```
bplist00—_WebMainResource’


_WebResourceFrameName_WebResourceData_WebResourceMIMEType_WebResourceTextEncodingName^
WebResourceURL]<!--frame1-->O CÄ9<!-- saved from url=(0094)https://
services.healthtech.dtu.dk/cgi-bin/webface2.cgi?jobid=60A3CDEE00005CFFAC8E6E0A&wait=20
--><html><head><meta http-equiv="Content-Type" content="text/html;
charset=windows-1252"></head><body link="#0000ff" bgcolor="#ffffff">

<script language="JavaScript" type="text/javascript">
  var loc = window.top.location.search.substring(1);
  if (loc != null && loc !== "" && loc.length > 1) {
      document.write('<center><h2>',loc,' Server Output - DTU Health Tech</h2></
center>');}
  </script><center><h2>NetMHCII-2.3 Server Output - DTU Health Tech</h2></center>
<hr>
<pre># Tmpdir made /scratch/netMHCIIsMiVJq
# Input is in FSA format

# Peptide length 15
          NetMHCII version 2.3.

Strong binder threshold   2.00. Weak binder threshold  10.00.

-----------------------------------------------------------------------------------------
----------
                Allele  pos              peptide       core Of 1-log50k(aff)
affinity(nM)    %Rank Relia     Identity Bind Level
-----------------------------------------------------------------------------------------
----------
             DRB1_0101    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.4028
640.0    65.00  0.47     Sequence
             DRB1_0101    2      SPIKEMFVFLVLLPL  FVFLVLLPL  6        0.4770
286.9    46.00  0.49     Sequence
             DRB1_0101    3      PIKEMFVFLVLLPLV  FVFLVLLPL  5        0.4967
231.6    42.00  0.61     Sequence
             DRB1_0101    4      IKEMFVFLVLLPLVS  FVFLVLLPL  4        0.5486
132.1    31.00  0.47     Sequence
             DRB1_0101    5      KEMFVFLVLLPLVSS  FVFLVLLPL  3        0.6057
71.2    22.00  0.32     Sequence
             DRB1_0101    6      EMFVFLVLLPLVSSQ  LVLLPLVSS  5        0.6135
65.5    20.00  0.36     Sequence
             DRB1_0101    7      MFVFLVLLPLVSSQC  LVLLPLVSS  4        0.6289
55.5    18.00  0.32     Sequence
             DRB1_0101    8      FVFLVLLPLVSSQCV  LLPLVSSQC  5        0.6522
43.1    15.00  0.31     Sequence
             DRB1_0101    9      VFLVLLPLVSSQCVN  LLPLVSSQC  4        0.6516
43.4    15.00  0.38     Sequence
             DRB1_0101   10      FLVLLPLVSSQCVNF  LLPLVSSQC  3        0.6552
41.7    14.00  0.42     Sequence
             DRB1_0101   11      LVLLPLVSSQCVNFT  LLPLVSSQC  2        0.6220
59.7    19.00  0.45     Sequence
             DRB1_0101   12      VLLPLVSSQCVNFTN  LLPLVSSQC  1        0.5614
115.0    29.00  0.44     Sequence
             DRB1_0101   13      LLPLVSSQCVNFTNR  LPLVSSQCV  1        0.5092
202.4    39.00  0.32     Sequence
             DRB1_0101   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.4123
577.7    60.00  0.38     Sequence
             DRB1_0101   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.3273
1448.1    80.00  0.45     Sequence
             DRB1_0101   16      LVSSQCVNFTNRTQL  VSSQCVNFT  1        0.2728
2611.4    90.00  0.29     Sequence
             DRB1_0101   17      VSSQCVNFTNRTQLP  CVNFTNRTQ  4        0.2023
5600.0    95.00  0.31     Sequence
             DRB1_0101   18      SSQCVNFTNRTQLPS  CVNFTNRTQ  3        0.2186
4694.5    95.00  0.32     Sequence
```

```
             DRB1_0101   19      SQCVNFTNRTQLPSA  FTNRTQLPS  5        0.2520
3270.5    90.00  0.31     Sequence
             DRB1_0101   20      QCVNFTNRTQLPSAY  FTNRTQLPS  4        0.3043
1857.6    85.00  0.38     Sequence
             DRB1_0101   21      CVNFTNRTQLPSAYT  RTQLPSAYT  6        0.4320
466.5    55.00  0.43     Sequence
             DRB1_0101   22      VNFTNRTQLPSAYTN  RTQLPSAYT  5        0.5079
205.2    39.00  0.58     Sequence
             DRB1_0101   23      NFTNRTQLPSAYTNS  RTQLPSAYT  4        0.5443
138.5    32.00  0.61     Sequence
             DRB1_0101   24      FTNRTQLPSAYTNSF  RTQLPSAYT  3        0.5588
118.4    30.00  0.69     Sequence
             DRB1_0101   25      TNRTQLPSAYTNSFT  RTQLPSAYT  2        0.5262
168.4    36.00  0.66     Sequence
             DRB1_0101   26      NRTQLPSAYTNSFTR  RTQLPSAYT  1        0.4787
281.6    45.00  0.66     Sequence
             DRB1_0101   27      RTQLPSAYTNSFTRG  RTQLPSAYT  0        0.3869
760.2    65.00  0.51     Sequence
             DRB1_0101   28      TQLPSAYTNSFTRGV  YTNSFTRGV  6        0.3616
1000.0    70.00  0.54     Sequence
             DRB1_0101   29      QLPSAYTNSFTRGVY  YTNSFTRGV  5        0.4566
357.5    50.00  0.68     Sequence
             DRB1_0101   30      LPSAYTNSFTRGVYY  YTNSFTRGV  4        0.5256
169.5    36.00  0.68     Sequence
             DRB1_0101   31      PSAYTNSFTRGVYYP  YTNSFTRGV  3        0.5113
197.8    39.00  0.69     Sequence
             DRB1_0101   32      SAYTNSFTRGVYYPD  YTNSFTRGV  2        0.4982
228.1    41.00  0.70     Sequence
             DRB1_0101   33      AYTNSFTRGVYYPDK  YTNSFTRGV  1        0.4657
324.2    48.00  0.53     Sequence
             DRB1_0101   34      YTNSFTRGVYYPDKV  NSFTRGVYY  2        0.3836
787.7    70.00  0.41     Sequence
             DRB1_0101   35      TNSFTRGVYYPDKVF  NSFTRGVYY  1        0.3335
1355.3    80.00  0.44     Sequence
             DRB1_0101   36      NSFTRGVYYPDKVFR  FTRGVYYPD  2        0.3072
1801.2    80.00  0.35     Sequence
             DRB1_0101   37      SFTRGVYYPDKVFRS  YYPDKVFRS  6        0.3248
1487.9    80.00  0.48     Sequence
             DRB1_0101   38      FTRGVYYPDKVFRSS  YYPDKVFRS  5        0.3712
900.8    70.00  0.68     Sequence
             DRB1_0101   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.4064
615.7    65.00  0.75     Sequence
             DRB1_0101   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.4930
241.1    42.00  0.56     Sequence
             DRB1_0101   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.5003
222.9    41.00  0.43     Sequence
             DRB1_0101   42      VYYPDKVFRSSVLHS  DKVFRSSVL  4        0.5074
206.3    40.00  0.41     Sequence
             DRB1_0101   43      YYPDKVFRSSVLHST  DKVFRSSVL  3        0.5361
151.4    34.00  0.40     Sequence
             DRB1_0101   44      YPDKVFRSSVLHSTQ  FRSSVLHST  5        0.5541
124.6    30.00  0.41     Sequence
             DRB1_0101   45      PDKVFRSSVLHSTQD  FRSSVLHST  4        0.5446
137.9    32.00  0.51     Sequence
             DRB1_0101   46      DKVFRSSVLHSTQDL  FRSSVLHST  3        0.5794
94.7    26.00  0.50     Sequence
             DRB1_0101   47      KVFRSSVLHSTQDLF  FRSSVLHST  2        0.5942
80.7    23.00  0.43     Sequence
             DRB1_0101   48      VFRSSVLHSTQDLFL  SVLHSTQDL  4        0.6085
69.1    21.00  0.49     Sequence
             DRB1_0101   49      FRSSVLHSTQDLFLP  SVLHSTQDL  3        0.5800
94.1    26.00  0.56     Sequence
             DRB1_0101   50      RSSVLHSTQDLFLPF  SVLHSTQDL  2        0.5649
110.7    28.00  0.56     Sequence
             DRB1_0101   51      SSVLHSTQDLFLPFF  LHSTQDLFL  3        0.5276
166.0    36.00  0.38     Sequence
```

```
             DRB1_0101   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2        0.4613
340.1    49.00  0.41     Sequence
             DRB1_0101   53      VLHSTQDLFLPFFSN  LHSTQDLFL  1        0.4337
458.4    55.00  0.34     Sequence
             DRB1_0101   54      LHSTQDLFLPFFSNV  DLFLPFFSN  5        0.4778
284.3    46.00  0.42     Sequence
             DRB1_0101   55      HSTQDLFLPFFSNVT  FLPFFSNVT  6        0.6619
38.8    14.00  0.58     Sequence
             DRB1_0101   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.7203
20.6     7.00  0.69     Sequence        WB
             DRB1_0101   57      TQDLFLPFFSNVTWF  FLPFFSNVT  4        0.7484
15.2     5.00  0.75     Sequence        WB
             DRB1_0101   58      QDLFLPFFSNVTWFH  FLPFFSNVT  3        0.7696
12.1     3.50  0.73     Sequence        WB
             DRB1_0101   59      DLFLPFFSNVTWFHA  FLPFFSNVT  2        0.7549
14.2     4.50  0.62     Sequence        WB
             DRB1_0101   60      LFLPFFSNVTWFHAI  FLPFFSNVT  1        0.7417
16.4     5.50  0.57     Sequence        WB
             DRB1_0101   61      FLPFFSNVTWFHAIH  FLPFFSNVT  0        0.6906
28.4    10.00  0.38     Sequence
             DRB1_0101   62      LPFFSNVTWFHAIHV  FFSNVTWFH  2        0.6409
48.7    16.00  0.34     Sequence
             DRB1_0101   63      PFFSNVTWFHAIHVS  FSNVTWFHA  2        0.6287
55.6    18.00  0.33     Sequence
             DRB1_0101   64      FFSNVTWFHAIHVSG  VTWFHAIHV  4        0.5857
88.4    25.00  0.30     Sequence
             DRB1_0101   65      FSNVTWFHAIHVSGT  VTWFHAIHV  3        0.5909
83.6    24.00  0.31     Sequence
             DRB1_0101   66      SNVTWFHAIHVSGTN  FHAIHVSGT  5        0.6357
51.5    17.00  0.52     Sequence
             DRB1_0101   67      NVTWFHAIHVSGTNG  FHAIHVSGT  4        0.6513
43.5    15.00  0.58     Sequence
             DRB1_0101   68      VTWFHAIHVSGTNGT  FHAIHVSGT  3        0.6457
46.2    16.00  0.62     Sequence
             DRB1_0101   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.6052
71.7    22.00  0.68     Sequence
             DRB1_0101   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1        0.5558
122.3    30.00  0.62     Sequence
             DRB1_0101   71      FHAIHVSGTNGTKRF  FHAIHVSGT  0        0.4819
271.8    45.00  0.43     Sequence
             DRB1_0101   72      HAIHVSGTNGTKRFD  IHVSGTNGT  2        0.3411
1247.2    75.00  0.47     Sequence
             DRB1_0101   73      AIHVSGTNGTKRFDN  IHVSGTNGT  1        0.2949
2057.9    85.00  0.45     Sequence
             DRB1_0101   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.2071
5321.6    95.00  0.39     Sequence
             DRB1_0101   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.1229
13222.7   100.00  0.50     Sequence
             DRB1_0101   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.2027
5578.9    95.00  0.61     Sequence
             DRB1_0101   77      SGTNGTKRFDNPVLP  TKRFDNPVL  5        0.2558
3140.2    90.00  0.61     Sequence
             DRB1_0101   78      GTNGTKRFDNPVLPF  TKRFDNPVL  4        0.3201
1565.4    80.00  0.59     Sequence
             DRB1_0101   79      TNGTKRFDNPVLPFN  TKRFDNPVL  3        0.3526
1102.0    75.00  0.52     Sequence
             DRB1_0101   80      NGTKRFDNPVLPFND  TKRFDNPVL  2        0.3371
1302.9    75.00  0.47     Sequence
             DRB1_0101   81      GTKRFDNPVLPFNDG  TKRFDNPVL  1        0.3125
1700.4    80.00  0.41     Sequence
             DRB1_0101   82      TKRFDNPVLPFNDGV  KRFDNPVLP  1        0.2616
2950.0    90.00  0.28     Sequence
             DRB1_0101   83      KRFDNPVLPFNDGVY  KRFDNPVLP  0        0.1958
6013.7    95.00  0.17     Sequence
             DRB1_0101   84      RFDNPVLPFNDGVYF  LPFNDGVYF  6        0.2088
5221.7    95.00  0.29     Sequence
```

```
             DRB1_0101   85      FDNPVLPFNDGVYFA  LPFNDGVYF  5        0.2416
3660.7    90.00  0.40     Sequence
             DRB1_0101   86      DNPVLPFNDGVYFAS  LPFNDGVYF  4        0.2612
2960.9    90.00  0.46     Sequence
             DRB1_0101   87      NPVLPFNDGVYFAST  LPFNDGVYF  3        0.2699
2696.0    90.00  0.45     Sequence
             DRB1_0101   88      PVLPFNDGVYFASTE  LPFNDGVYF  2        0.2508
3314.9    90.00  0.44     Sequence
             DRB1_0101   89      VLPFNDGVYFASTEK  LPFNDGVYF  1        0.2331
4013.8    95.00  0.34     Sequence
             DRB1_0101   90      LPFNDGVYFASTEKS  VYFASTEKS  6        0.2724
2622.9    90.00  0.41     Sequence
             DRB1_0101   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.3526
1101.9    75.00  0.68     Sequence
             DRB1_0101   92      FNDGVYFASTEKSNI  VYFASTEKS  4        0.4493
386.9    55.00  0.60     Sequence
             DRB1_0101   93      NDGVYFASTEKSNII  VYFASTEKS  3        0.5210
178.2    37.00  0.55     Sequence
             DRB1_0101   94      DGVYFASTEKSNIIR  VYFASTEKS  2        0.5368
150.2    34.00  0.44     Sequence
             DRB1_0101   95      GVYFASTEKSNIIRG  FASTEKSNI  3        0.5356
152.1    34.00  0.39     Sequence
             DRB1_0101   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.4760
289.8    46.00  0.53     Sequence
             DRB1_0101   97      YFASTEKSNIIRGWI  FASTEKSNI  1        0.3918
721.1    65.00  0.63     Sequence
             DRB1_0101   98      FASTEKSNIIRGWIF  SNIIRGWIF  6        0.4707
306.9    47.00  0.65     Sequence
             DRB1_0101   99      ASTEKSNIIRGWIFG  SNIIRGWIF  5        0.5233
173.7    36.00  0.82     Sequence
             DRB1_0101  100      STEKSNIIRGWIFGT  SNIIRGWIF  4        0.5765
97.7    26.00  0.75     Sequence
             DRB1_0101  101      TEKSNIIRGWIFGTT  SNIIRGWIF  3        0.6037
72.8    22.00  0.73     Sequence
             DRB1_0101  102      EKSNIIRGWIFGTTL  SNIIRGWIF  2        0.6048
71.9    22.00  0.65     Sequence
             DRB1_0101  103      KSNIIRGWIFGTTLD  SNIIRGWIF  1        0.5907
83.8    24.00  0.61     Sequence
             DRB1_0101  104      SNIIRGWIFGTTLDS  SNIIRGWIF  0        0.5544
124.1    30.00  0.43     Sequence
             DRB1_0101  105      NIIRGWIFGTTLDSK  WIFGTTLDS  5        0.5408
143.7    33.00  0.67     Sequence
             DRB1_0101  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.5424
141.3    33.00  0.73     Sequence
             DRB1_0101  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3        0.5493
131.1    31.00  0.75     Sequence
             DRB1_0101  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2        0.5316
158.8    35.00  0.72     Sequence
             DRB1_0101  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1        0.4887
252.7    43.00  0.61     Sequence
             DRB1_0101  110      WIFGTTLDSKTQSLL  WIFGTTLDS  0        0.4439
410.3    55.00  0.31     Sequence
             DRB1_0101  111      IFGTTLDSKTQSLLI  TLDSKTQSL  4        0.4244
506.8    60.00  0.28     Sequence
             DRB1_0101  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5        0.4592
347.7    50.00  0.26     Sequence
             DRB1_0101  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4        0.4561
359.4    50.00  0.37     Sequence
             DRB1_0101  114      TTLDSKTQSLLIVNN  DSKTQSLLI  3        0.4474
394.9    55.00  0.46     Sequence
             DRB1_0101  115      TLDSKTQSLLIVNNA  DSKTQSLLI  2        0.4437
411.0    55.00  0.37     Sequence
             DRB1_0101  116      LDSKTQSLLIVNNAT  QSLLIVNNA  5        0.4470
396.8    55.00  0.37     Sequence
             DRB1_0101  117      DSKTQSLLIVNNATN  QSLLIVNNA  4        0.4769
287.1    46.00  0.35     Sequence
```

```
             DRB1_0101  118      SKTQSLLIVNNATNV  LLIVNNATN  5        0.5381
148.0    33.00  0.31     Sequence
             DRB1_0101  119      KTQSLLIVNNATNVV  LLIVNNATN  4        0.5862
88.0    25.00  0.32     Sequence
             DRB1_0101  120      TQSLLIVNNATNVVI  LLIVNNATN  3        0.6044
72.3    22.00  0.37     Sequence
             DRB1_0101  121      QSLLIVNNATNVVIK  LIVNNATNV  3        0.6145
64.8    20.00  0.34     Sequence
             DRB1_0101  122      SLLIVNNATNVVIKV  LIVNNATNV  2        0.5953
79.7    23.00  0.31     Sequence
             DRB1_0101  123      LLIVNNATNVVIKVC  LIVNNATNV  1        0.5454
136.9    32.00  0.30     Sequence
             DRB1_0101  124      LIVNNATNVVIKVCE  VNNATNVVI  2        0.4460
401.0    55.00  0.29     Sequence
             DRB1_0101  125      IVNNATNVVIKVCEF  VNNATNVVI  1        0.3499
1134.3    75.00  0.34     Sequence
             DRB1_0101  126      VNNATNVVIKVCEFQ  NATNVVIKV  2        0.2729
2610.6    90.00  0.37     Sequence
             DRB1_0101  127      NNATNVVIKVCEFQF  NATNVVIKV  1        0.2665
2796.1    90.00  0.29     Sequence
             DRB1_0101  128      NATNVVIKVCEFQFC  VIKVCEFQF  5        0.2746
2563.5    90.00  0.31     Sequence
             DRB1_0101  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.2821
2362.5    85.00  0.44     Sequence
             DRB1_0101  130      TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.2970
2011.4    85.00  0.45     Sequence
             DRB1_0101  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.2765
2511.2    85.00  0.44     Sequence
             DRB1_0101  132      VVIKVCEFQFCNYPF  VIKVCEFQF  1        0.2617
2945.1    90.00  0.37     Sequence
             DRB1_0101  133      VIKVCEFQFCNYPFL  FQFCNYPFL  6        0.3331
1360.6    80.00  0.41     Sequence
             DRB1_0101  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.3501
1131.4    75.00  0.49     Sequence
             DRB1_0101  135      KVCEFQFCNYPFLGV  FQFCNYPFL  4        0.4142
565.5    60.00  0.45     Sequence
             DRB1_0101  136      VCEFQFCNYPFLGVY  FQFCNYPFL  3        0.4514
378.3    55.00  0.43     Sequence
             DRB1_0101  137      CEFQFCNYPFLGVYY  FQFCNYPFL  2        0.4719
302.9    47.00  0.35     Sequence
             DRB1_0101  138      EFQFCNYPFLGVYYH  FCNYPFLGV  3        0.4749
293.5    46.00  0.35     Sequence
             DRB1_0101  139      FQFCNYPFLGVYYHK  FCNYPFLGV  2        0.4566
357.5    50.00  0.35     Sequence
             DRB1_0101  140      QFCNYPFLGVYYHKN  FLGVYYHKN  6        0.4421
418.5    55.00  0.26     Sequence
             DRB1_0101  141      FCNYPFLGVYYHKNN  FLGVYYHKN  5        0.4399
428.3    55.00  0.42     Sequence
             DRB1_0101  142      CNYPFLGVYYHKNNK  FLGVYYHKN  4        0.4420
419.0    55.00  0.63     Sequence
             DRB1_0101  143      NYPFLGVYYHKNNKS  FLGVYYHKN  3        0.4760
290.0    46.00  0.54     Sequence
             DRB1_0101  144      YPFLGVYYHKNNKSW  FLGVYYHKN  2        0.5053
211.1    40.00  0.41     Sequence
             DRB1_0101  145      PFLGVYYHKNNKSWM  VYYHKNNKS  4        0.5427
140.9    33.00  0.43     Sequence
             DRB1_0101  146      FLGVYYHKNNKSWME  VYYHKNNKS  3        0.5401
144.9    33.00  0.41     Sequence
             DRB1_0101  147      LGVYYHKNNKSWMES  VYYHKNNKS  2        0.5241
172.2    36.00  0.40     Sequence
             DRB1_0101  148      GVYYHKNNKSWMESE  VYYHKNNKS  1        0.5002
223.2    41.00  0.32     Sequence
             DRB1_0101  149      VYYHKNNKSWMESEF  YHKNNKSWM  2        0.4495
386.2    55.00  0.31     Sequence
             DRB1_0101  150      YYHKNNKSWMESEFR  YHKNNKSWM  1        0.3539
1086.3    75.00  0.36     Sequence
```

```
             DRB1_0101  151      YHKNNKSWMESEFRV  SWMESEFRV  6        0.3226
1525.0    80.00  0.34     Sequence
             DRB1_0101  152      HKNNKSWMESEFRVY  SWMESEFRV  5        0.4082
603.9    60.00  0.54     Sequence
             DRB1_0101  153      KNNKSWMESEFRVYS  SWMESEFRV  4        0.4555
362.1    50.00  0.56     Sequence
             DRB1_0101  154      NNKSWMESEFRVYSS  SWMESEFRV  3        0.4765
288.4    46.00  0.56     Sequence
             DRB1_0101  155      NKSWMESEFRVYSSA  SWMESEFRV  2        0.4721
302.3    47.00  0.49     Sequence
             DRB1_0101  156      KSWMESEFRVYSSAN  SWMESEFRV  1        0.4412
422.6    55.00  0.43     Sequence
             DRB1_0101  157      SWMESEFRVYSSANN  FRVYSSANN  6        0.4299
477.4    60.00  0.42     Sequence
             DRB1_0101  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.4277
488.9    60.00  0.68     Sequence
             DRB1_0101  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.4540
367.8    55.00  0.75     Sequence
             DRB1_0101  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.5148
190.4    38.00  0.62     Sequence
             DRB1_0101  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.5295
162.6    35.00  0.54     Sequence
             DRB1_0101  162      EFRVYSSANNCTFEY  FRVYSSANN  1        0.5249
170.8    36.00  0.41     Sequence
             DRB1_0101  163      FRVYSSANNCTFEYV  YSSANNCTF  3        0.5007
222.0    41.00  0.41     Sequence
             DRB1_0101  164      RVYSSANNCTFEYVS  YSSANNCTF  2        0.4230
514.2    60.00  0.47     Sequence
             DRB1_0101  165      VYSSANNCTFEYVSQ  YSSANNCTF  1        0.3467
1174.2    75.00  0.50     Sequence
             DRB1_0101  166      YSSANNCTFEYVSQP  YSSANNCTF  0        0.2577
3076.2    90.00  0.34     Sequence
             DRB1_0101  167      SSANNCTFEYVSQPF  CTFEYVSQP  5        0.2271
4283.6    95.00  0.23     Sequence
             DRB1_0101  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.4946
237.1    42.00  0.79     Sequence
             DRB1_0101  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.6414
48.4    16.00  0.65     Sequence
             DRB1_0101  170      NNCTFEYVSQPFLMD  FEYVSQPFL  4        0.6777
32.7    12.00  0.54     Sequence
             DRB1_0101  171      NCTFEYVSQPFLMDL  FEYVSQPFL  3        0.7207
20.5     7.00  0.50     Sequence         WB
             DRB1_0101  172      CTFEYVSQPFLMDLE  FEYVSQPFL  2        0.7123
22.5     8.00  0.46     Sequence         WB
             DRB1_0101  173      TFEYVSQPFLMDLEG  FEYVSQPFL  1        0.6942
27.4     9.50  0.43     Sequence         WB
             DRB1_0101  174      FEYVSQPFLMDLEGK  EYVSQPFLM  1        0.6264
57.0    18.00  0.34     Sequence
             DRB1_0101  175      EYVSQPFLMDLEGKQ  YVSQPFLMD  1        0.4801
277.5    45.00  0.37     Sequence
             DRB1_0101  176      YVSQPFLMDLEGKQG  FLMDLEGKQ  5        0.4001
658.9    65.00  0.44     Sequence
             DRB1_0101  177      VSQPFLMDLEGKQGN  FLMDLEGKQ  4        0.4127
574.9    60.00  0.52     Sequence
             DRB1_0101  178      SQPFLMDLEGKQGNF  FLMDLEGKQ  3        0.4555
361.9    50.00  0.50     Sequence
             DRB1_0101  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2        0.4763
289.1    46.00  0.38     Sequence
             DRB1_0101  180      PFLMDLEGKQGNFKN  LMDLEGKQG  2        0.4561
359.7    50.00  0.36     Sequence
             DRB1_0101  181      FLMDLEGKQGNFKNL  LEGKQGNFK  4        0.4122
578.4    60.00  0.38     Sequence
             DRB1_0101  182      LMDLEGKQGNFKNLS  LEGKQGNFK  3        0.3618
997.4    70.00  0.57     Sequence
             DRB1_0101  183      MDLEGKQGNFKNLSE  LEGKQGNFK  2        0.3104
1738.7    80.00  0.67     Sequence
```

```
             DRB1_0101  184      DLEGKQGNFKNLSEF  LEGKQGNFK  1        0.2770
2495.9    85.00  0.60     Sequence
             DRB1_0101  185      LEGKQGNFKNLSEFV  NFKNLSEFV  6        0.3392
1273.1    75.00  0.44     Sequence
             DRB1_0101  186      EGKQGNFKNLSEFVF  FKNLSEFVF  6        0.4849
263.2    44.00  0.47     Sequence
             DRB1_0101  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5        0.5730
101.5    27.00  0.50     Sequence
             DRB1_0101  188      KQGNFKNLSEFVFKN  FKNLSEFVF  4        0.6047
72.0    22.00  0.55     Sequence
             DRB1_0101  189      QGNFKNLSEFVFKNI  FKNLSEFVF  3        0.5957
79.4    23.00  0.55     Sequence
             DRB1_0101  190      GNFKNLSEFVFKNID  FKNLSEFVF  2        0.5538
124.9    31.00  0.58     Sequence
             DRB1_0101  191      NFKNLSEFVFKNIDG  FKNLSEFVF  1        0.4816
272.7    45.00  0.62     Sequence
             DRB1_0101  192      FKNLSEFVFKNIDGY  FKNLSEFVF  0        0.3770
846.4    70.00  0.46     Sequence
             DRB1_0101  193      KNLSEFVFKNIDGYF  FVFKNIDGY  5        0.2827
2347.5    85.00  0.35     Sequence
             DRB1_0101  194      NLSEFVFKNIDGYFK  FKNIDGYFK  6        0.3826
796.4    70.00  0.42     Sequence
             DRB1_0101  195      LSEFVFKNIDGYFKI  FKNIDGYFK  5        0.4615
339.0    49.00  0.55     Sequence
             DRB1_0101  196      SEFVFKNIDGYFKIY  FKNIDGYFK  4        0.5038
214.6    40.00  0.57     Sequence
             DRB1_0101  197      EFVFKNIDGYFKIYS  FKNIDGYFK  3        0.5131
194.0    38.00  0.63     Sequence
             DRB1_0101  198      FVFKNIDGYFKIYSK  FKNIDGYFK  2        0.5001
223.4    41.00  0.64     Sequence
             DRB1_0101  199      VFKNIDGYFKIYSKH  FKNIDGYFK  1        0.4518
376.6    55.00  0.62     Sequence
             DRB1_0101  200      FKNIDGYFKIYSKHT  YFKIYSKHT  6        0.5511
128.6    31.00  0.56     Sequence
             DRB1_0101  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.5600
116.8    29.00  0.81     Sequence
             DRB1_0101  202      NIDGYFKIYSKHTPI  YFKIYSKHT  4        0.6181
62.3    20.00  0.83     Sequence
             DRB1_0101  203      IDGYFKIYSKHTPIN  YFKIYSKHT  3        0.6468
45.7    15.00  0.77     Sequence
             DRB1_0101  204      DGYFKIYSKHTPINL  YFKIYSKHT  2        0.6876
29.4    11.00  0.51     Sequence
             DRB1_0101  205      GYFKIYSKHTPINLV  YSKHTPINL  5        0.7383
17.0     5.50  0.38     Sequence        WB
             DRB1_0101  206      YFKIYSKHTPINLVR  YSKHTPINL  4        0.7425
16.2     5.50  0.56     Sequence        WB
             DRB1_0101  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.7195
20.8     7.00  0.67     Sequence        WB
             DRB1_0101  208      KIYSKHTPINLVRDL  YSKHTPINL  2        0.6993
25.9     9.00  0.58     Sequence        WB
             DRB1_0101  209      IYSKHTPINLVRDLP  YSKHTPINL  1        0.6178
62.5    20.00  0.59     Sequence
             DRB1_0101  210      YSKHTPINLVRDLPQ  SKHTPINLV  1        0.4924
242.8    43.00  0.47     Sequence
             DRB1_0101  211      SKHTPINLVRDLPQG  SKHTPINLV  0        0.3604
1012.4    70.00  0.48     Sequence
             DRB1_0101  212      KHTPINLVRDLPQGF  LVRDLPQGF  6        0.3600
1017.0    75.00  0.47     Sequence
             DRB1_0101  213      HTPINLVRDLPQGFS  LVRDLPQGF  5        0.4408
424.1    55.00  0.55     Sequence
             DRB1_0101  214      TPINLVRDLPQGFSA  LVRDLPQGF  4        0.4870
257.3    44.00  0.58     Sequence
             DRB1_0101  215      PINLVRDLPQGFSAL  LVRDLPQGF  3        0.5332
156.2    34.00  0.56     Sequence
             DRB1_0101  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.5255
169.8    36.00  0.53     Sequence
```

```
             DRB1_0101  217      NLVRDLPQGFSALEP  LVRDLPQGF  1        0.4802
277.1    45.00  0.49     Sequence
             DRB1_0101  218      LVRDLPQGFSALEPL  LVRDLPQGF  0        0.4242
507.7    60.00  0.25     Sequence
             DRB1_0101  219      VRDLPQGFSALEPLV  DLPQGFSAL  2        0.4010
652.3    65.00  0.22     Sequence
             DRB1_0101  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.4867
258.3    44.00  0.50     Sequence
             DRB1_0101  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.5646
111.2    29.00  0.63     Sequence
             DRB1_0101  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.5683
106.8    28.00  0.63     Sequence
             DRB1_0101  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.6225
59.4    19.00  0.56     Sequence
             DRB1_0101  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.6420
48.1    16.00  0.49     Sequence
             DRB1_0101  225      GFSALEPLVDLPIGI  LEPLVDLPI  4        0.6222
59.6    19.00  0.41     Sequence
             DRB1_0101  226      FSALEPLVDLPIGIN  LEPLVDLPI  3        0.5718
102.9    27.00  0.56     Sequence
             DRB1_0101  227      SALEPLVDLPIGINI  LEPLVDLPI  2        0.5162
187.6    38.00  0.63     Sequence
             DRB1_0101  228      ALEPLVDLPIGINIT  LEPLVDLPI  1        0.5057
210.2    40.00  0.50     Sequence
             DRB1_0101  229      LEPLVDLPIGINITR  VDLPIGINI  4        0.4686
314.1    48.00  0.28     Sequence
             DRB1_0101  230      EPLVDLPIGINITRF  VDLPIGINI  3        0.4414
421.6    55.00  0.43     Sequence
             DRB1_0101  231      PLVDLPIGINITRFQ  VDLPIGINI  2        0.4362
445.8    55.00  0.41     Sequence
             DRB1_0101  232      LVDLPIGINITRFQT  VDLPIGINI  1        0.4075
608.2    65.00  0.37     Sequence
             DRB1_0101  233      VDLPIGINITRFQTL  DLPIGINIT  1        0.3930
712.0    65.00  0.22     Sequence
             DRB1_0101  234      DLPIGINITRFQTLL  INITRFQTL  5        0.3857
770.3    65.00  0.38     Sequence
             DRB1_0101  235      LPIGINITRFQTLLA  ITRFQTLLA  6        0.4739
296.7    46.00  0.43     Sequence
             DRB1_0101  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.5460
136.0    32.00  0.49     Sequence
             DRB1_0101  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.5780
96.2    26.00  0.52     Sequence
             DRB1_0101  238      GINITRFQTLLALHR  FQTLLALHR  6        0.7331
17.9     6.00  0.60     Sequence         WB
             DRB1_0101  239      INITRFQTLLALHRS  FQTLLALHR  5        0.7643
12.8     4.00  0.65     Sequence         WB
             DRB1_0101  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.7777
11.1     3.50  0.71     Sequence         WB
             DRB1_0101  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.8016
8.6     2.00  0.62     Sequence         WB
             DRB1_0101  242      TRFQTLLALHRSYLT  FQTLLALHR  2        0.8132
7.5     1.60  0.49     Sequence         SB
             DRB1_0101  243      RFQTLLALHRSYLTP  FQTLLALHR  1        0.8015
8.6     2.00  0.40     Sequence         WB
             DRB1_0101  244      FQTLLALHRSYLTPG  LALHRSYLT  4        0.7702
12.0     3.50  0.40     Sequence         WB
             DRB1_0101  245      QTLLALHRSYLTPGD  LALHRSYLT  3        0.7162
21.6     7.50  0.51     Sequence         WB
             DRB1_0101  246      TLLALHRSYLTPGDS  LALHRSYLT  2        0.6632
38.3    13.00  0.58     Sequence
             DRB1_0101  247      LLALHRSYLTPGDSS  LALHRSYLT  1        0.5908
83.7    24.00  0.62     Sequence
             DRB1_0101  248      LALHRSYLTPGDSSS  LALHRSYLT  0        0.4404
426.1    55.00  0.65     Sequence
             DRB1_0101  249      ALHRSYLTPGDSSSG  SYLTPGDSS  4        0.2533
3224.9    90.00  0.32     Sequence
```

```
             DRB1_0101  250      LHRSYLTPGDSSSGW  SYLTPGDSS  3        0.2727
2615.6    90.00  0.34     Sequence
             DRB1_0101  251      HRSYLTPGDSSSGWT  LTPGDSSSG  4        0.2770
2495.8    85.00  0.40     Sequence
             DRB1_0101  252      RSYLTPGDSSSGWTA  LTPGDSSSG  3        0.3275
1445.9    80.00  0.35     Sequence
             DRB1_0101  253      SYLTPGDSSSGWTAG  GDSSSGWTA  5        0.3380
1290.4    75.00  0.48     Sequence
             DRB1_0101  254      YLTPGDSSSGWTAGA  GDSSSGWTA  4        0.3481
1157.0    75.00  0.60     Sequence
             DRB1_0101  255      LTPGDSSSGWTAGAA  GDSSSGWTA  3        0.3447
1200.3    75.00  0.70     Sequence
             DRB1_0101  256      TPGDSSSGWTAGAAA  GDSSSGWTA  2        0.3269
1454.3    80.00  0.70     Sequence
             DRB1_0101  257      PGDSSSGWTAGAAAY  GDSSSGWTA  1        0.3311
1389.7    80.00  0.56     Sequence
             DRB1_0101  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.4496
385.5    55.00  0.52     Sequence
             DRB1_0101  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.5569
120.8    30.00  0.57     Sequence
             DRB1_0101  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.6256
57.4    18.00  0.50     Sequence
             DRB1_0101  261      SSGWTAGAAAYYVGY  TAGAAAYYV  4        0.6659
37.1    13.00  0.50     Sequence
             DRB1_0101  262      SGWTAGAAAYYVGYL  TAGAAAYYV  3        0.6684
36.2    13.00  0.58     Sequence
             DRB1_0101  263      GWTAGAAAYYVGYLQ  TAGAAAYYV  2        0.6191
61.6    19.00  0.59     Sequence
             DRB1_0101  264      WTAGAAAYYVGYLQP  TAGAAAYYV  1        0.5431
140.3    33.00  0.65     Sequence
             DRB1_0101  265      TAGAAAYYVGYLQPR  TAGAAAYYV  0        0.4506
381.7    55.00  0.56     Sequence
             DRB1_0101  266      AGAAAYYVGYLQPRT  YVGYLQPRT  6        0.4295
479.6    60.00  0.46     Sequence
             DRB1_0101  267      GAAAYYVGYLQPRTF  YVGYLQPRT  5        0.5932
81.6    24.00  0.38     Sequence
             DRB1_0101  268      AAAYYVGYLQPRTFL  VGYLQPRTF  5        0.7076
23.7     8.50  0.36     Sequence         WB
             DRB1_0101  269      AAYYVGYLQPRTFLL  YLQPRTFLL  6        0.8264
6.5     1.20  0.41     Sequence         SB
             DRB1_0101  270      AYYVGYLQPRTFLLK  YLQPRTFLL  5        0.8627
4.4     0.40  0.54     Sequence         SB
             DRB1_0101  271      YYVGYLQPRTFLLKY  YLQPRTFLL  4        0.8736
3.9     0.30  0.63     Sequence         SB
             DRB1_0101  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.8685
4.1     0.40  0.69     Sequence         SB
             DRB1_0101  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.8399
5.7     0.80  0.77     Sequence         SB
             DRB1_0101  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.7936
9.3     2.50  0.81     Sequence         WB
             DRB1_0101  275      YLQPRTFLLKYNENG  YLQPRTFLL  0        0.6983
26.2     9.00  0.69     Sequence         WB
             DRB1_0101  276      LQPRTFLLKYNENGT  FLLKYNENG  5        0.5551
123.2    30.00  0.79     Sequence
             DRB1_0101  277      QPRTFLLKYNENGTI  FLLKYNENG  4        0.6353
51.7    17.00  0.79     Sequence
             DRB1_0101  278      PRTFLLKYNENGTIT  FLLKYNENG  3        0.6701
35.5    13.00  0.75     Sequence
             DRB1_0101  279      RTFLLKYNENGTITD  FLLKYNENG  2        0.6654
37.4    13.00  0.73     Sequence
             DRB1_0101  280      TFLLKYNENGTITDA  FLLKYNENG  1        0.6191
61.7    19.00  0.57     Sequence
             DRB1_0101  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.5340
154.7    34.00  0.38     Sequence
             DRB1_0101  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.4168
549.8    60.00  0.52     Sequence
```

```
             DRB1_0101  283      LKYNENGTITDAVDC  LKYNENGTI  0        0.3119
1712.1    80.00  0.44     Sequence
             DRB1_0101  284      KYNENGTITDAVDCA  YNENGTITD  1        0.2062
5371.1    95.00  0.39     Sequence
             DRB1_0101  285      YNENGTITDAVDCAL  GTITDAVDC  4        0.1900
6398.0   100.00  0.38     Sequence
             DRB1_0101  286      NENGTITDAVDCALD  GTITDAVDC  3        0.1900
6402.2   100.00  0.41     Sequence
             DRB1_0101  287      ENGTITDAVDCALDP  GTITDAVDC  2        0.1938
6145.2    95.00  0.37     Sequence
             DRB1_0101  288      NGTITDAVDCALDPL  GTITDAVDC  1        0.2152
4874.0    95.00  0.25     Sequence
             DRB1_0101  289      GTITDAVDCALDPLS  DAVDCALDP  4        0.2257
4350.5    95.00  0.23     Sequence
             DRB1_0101  290      TITDAVDCALDPLSE  DAVDCALDP  3        0.2260
4334.9    95.00  0.22     Sequence
             DRB1_0101  291      ITDAVDCALDPLSET  VDCALDPLS  4        0.2822
2361.1    85.00  0.25     Sequence
             DRB1_0101  292      TDAVDCALDPLSETK  CALDPLSET  5        0.3331
1361.2    80.00  0.34     Sequence
             DRB1_0101  293      DAVDCALDPLSETKC  CALDPLSET  4        0.3282
1434.7    80.00  0.38     Sequence
             DRB1_0101  294      AVDCALDPLSETKCT  CALDPLSET  3        0.3319
1378.1    80.00  0.40     Sequence
             DRB1_0101  295      VDCALDPLSETKCTL  CALDPLSET  2        0.3202
1565.0    80.00  0.35     Sequence
             DRB1_0101  296      DCALDPLSETKCTLK  LDPLSETKC  3        0.3061
1823.1    85.00  0.38     Sequence
             DRB1_0101  297      CALDPLSETKCTLKS  LDPLSETKC  2        0.2761
2520.4    85.00  0.38     Sequence
             DRB1_0101  298      ALDPLSETKCTLKSF  LDPLSETKC  1        0.2375
3828.7    95.00  0.41     Sequence
             DRB1_0101  299      LDPLSETKCTLKSFT  LSETKCTLK  3        0.2169
4781.4    95.00  0.26     Sequence
             DRB1_0101  300      DPLSETKCTLKSFTV  KCTLKSFTV  6        0.4219
520.5    60.00  0.71     Sequence
             DRB1_0101  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.5296
162.3    35.00  0.77     Sequence
             DRB1_0101  302      LSETKCTLKSFTVEK  KCTLKSFTV  4        0.5916
83.0    24.00  0.79     Sequence
             DRB1_0101  303      SETKCTLKSFTVEKG  KCTLKSFTV  3        0.6082
69.3    21.00  0.78     Sequence
             DRB1_0101  304      ETKCTLKSFTVEKGI  KCTLKSFTV  2        0.5999
75.9    23.00  0.70     Sequence
             DRB1_0101  305      TKCTLKSFTVEKGIY  KCTLKSFTV  1        0.5957
79.4    23.00  0.62     Sequence
             DRB1_0101  306      KCTLKSFTVEKGIYQ  FTVEKGIYQ  6        0.6345
52.2    17.00  0.52     Sequence
             DRB1_0101  307      CTLKSFTVEKGIYQT  FTVEKGIYQ  5        0.6357
51.5    17.00  0.81     Sequence
             DRB1_0101  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.6508
43.8    15.00  0.86     Sequence
             DRB1_0101  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.6586
40.2    14.00  0.89     Sequence
             DRB1_0101  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.6299
54.8    18.00  0.92     Sequence
             DRB1_0101  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.5699
105.0    28.00  0.82     Sequence
             DRB1_0101  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.5726
101.9    27.00  0.48     Sequence
             DRB1_0101  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.6389
49.8    17.00  0.76     Sequence
             DRB1_0101  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.6509
43.7    15.00  0.75     Sequence
             DRB1_0101  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.6683
36.2    13.00  0.78     Sequence
```

```
             DRB1_0101  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.6557
41.5    14.00  0.77     Sequence
             DRB1_0101  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.5960
79.1    23.00  0.71     Sequence
             DRB1_0101  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.5640
111.9    29.00  0.41     Sequence
             DRB1_0101  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.5855
88.7    25.00  0.81     Sequence
             DRB1_0101  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.6415
48.4    16.00  0.85     Sequence
             DRB1_0101  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.6665
36.9    13.00  0.85     Sequence
             DRB1_0101  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.6443
46.9    16.00  0.85     Sequence
             DRB1_0101  323      NFRVQPTESIVRFPN  FRVQPTESI  1        0.6018
74.3    22.00  0.80     Sequence
             DRB1_0101  324      FRVQPTESIVRFPNI  FRVQPTESI  0        0.4967
231.8    42.00  0.69     Sequence
             DRB1_0101  325      RVQPTESIVRFPNIT  VQPTESIVR  1        0.2501
3338.5    90.00  0.41     Sequence
             DRB1_0101  326      VQPTESIVRFPNITN  IVRFPNITN  6        0.2875
2229.1    85.00  0.46     Sequence
             DRB1_0101  327      QPTESIVRFPNITNL  IVRFPNITN  5        0.3595
1023.0    75.00  0.62     Sequence
             DRB1_0101  328      PTESIVRFPNITNLC  IVRFPNITN  4        0.3694
918.2    70.00  0.65     Sequence
             DRB1_0101  329      TESIVRFPNITNLCP  IVRFPNITN  3        0.3646
967.9    70.00  0.60     Sequence
             DRB1_0101  330      ESIVRFPNITNLCPF  IVRFPNITN  2        0.3528
1099.2    75.00  0.55     Sequence
             DRB1_0101  331      SIVRFPNITNLCPFG  IVRFPNITN  1        0.3338
1350.6    80.00  0.48     Sequence
             DRB1_0101  332      IVRFPNITNLCPFGE  FPNITNLCP  3        0.3126
1699.3    80.00  0.28     Sequence
             DRB1_0101  333      VRFPNITNLCPFGEV  ITNLCPFGE  5        0.3477
1161.5    75.00  0.50     Sequence
             DRB1_0101  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.3922
718.1    65.00  0.55     Sequence
             DRB1_0101  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.4096
594.6    60.00  0.59     Sequence
             DRB1_0101  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.4004
656.6    65.00  0.52     Sequence
             DRB1_0101  337      NITNLCPFGEVFNAT  ITNLCPFGE  1        0.3832
791.7    70.00  0.44     Sequence
             DRB1_0101  338      ITNLCPFGEVFNATR  NLCPFGEVF  2        0.3318
1379.5    80.00  0.28     Sequence
             DRB1_0101  339      TNLCPFGEVFNATRF  FGEVFNATR  5        0.3238
1504.0    80.00  0.23     Sequence
             DRB1_0101  340      NLCPFGEVFNATRFA  GEVFNATRF  5        0.3437
1212.7    75.00  0.31     Sequence
             DRB1_0101  341      LCPFGEVFNATRFAS  GEVFNATRF  4        0.3584
1035.1    75.00  0.37     Sequence
             DRB1_0101  342      CPFGEVFNATRFASV  FNATRFASV  6        0.4362
446.2    55.00  0.34     Sequence
             DRB1_0101  343      PFGEVFNATRFASVY  FNATRFASV  5        0.4811
274.3    45.00  0.51     Sequence
             DRB1_0101  344      FGEVFNATRFASVYA  FNATRFASV  4        0.5037
214.7    40.00  0.64     Sequence
             DRB1_0101  345      GEVFNATRFASVYAW  FNATRFASV  3        0.5188
182.5    37.00  0.65     Sequence
             DRB1_0101  346      EVFNATRFASVYAWN  FNATRFASV  2        0.5127
194.9    38.00  0.65     Sequence
             DRB1_0101  347      VFNATRFASVYAWNR  FASVYAWNR  6        0.5709
103.8    27.00  0.32     Sequence
             DRB1_0101  348      FNATRFASVYAWNRK  FASVYAWNR  5        0.6015
74.6    22.00  0.60     Sequence
```

```
             DRB1_0101  349      NATRFASVYAWNRKR  FASVYAWNR  4        0.6259
57.3    18.00  0.74     Sequence
             DRB1_0101  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.6404
49.0    16.00  0.74     Sequence
             DRB1_0101  351      TRFASVYAWNRKRIS  FASVYAWNR  2        0.6350
51.9    17.00  0.64     Sequence
             DRB1_0101  352      RFASVYAWNRKRISN  FASVYAWNR  1        0.6075
69.9    21.00  0.58     Sequence
             DRB1_0101  353      FASVYAWNRKRISNC  YAWNRKRIS  4        0.5181
183.9    37.00  0.34     Sequence
             DRB1_0101  354      ASVYAWNRKRISNCV  YAWNRKRIS  3        0.4594
347.0    50.00  0.44     Sequence
             DRB1_0101  355      SVYAWNRKRISNCVA  NRKRISNCV  5        0.4854
261.9    44.00  0.38     Sequence
             DRB1_0101  356      VYAWNRKRISNCVAD  NRKRISNCV  4        0.4709
306.5    47.00  0.44     Sequence
             DRB1_0101  357      YAWNRKRISNCVADY  NRKRISNCV  3        0.4588
349.1    50.00  0.55     Sequence
             DRB1_0101  358      AWNRKRISNCVADYS  NRKRISNCV  2        0.4273
490.8    60.00  0.51     Sequence
             DRB1_0101  359      WNRKRISNCVADYSV  NRKRISNCV  1        0.4286
484.3    60.00  0.35     Sequence
             DRB1_0101  360      NRKRISNCVADYSVL  ISNCVADYS  4        0.4237
510.4    60.00  0.46     Sequence
             DRB1_0101  361      RKRISNCVADYSVLY  ISNCVADYS  3        0.4684
314.8    48.00  0.45     Sequence
             DRB1_0101  362      KRISNCVADYSVLYN  CVADYSVLY  5        0.4728
300.2    47.00  0.40     Sequence
             DRB1_0101  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.4639
330.5    49.00  0.51     Sequence
             DRB1_0101  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.4439
410.3    55.00  0.59     Sequence
             DRB1_0101  365      SNCVADYSVLYNSAS  YSVLYNSAS  6        0.5314
159.2    35.00  0.50     Sequence
             DRB1_0101  366      NCVADYSVLYNSASF  YSVLYNSAS  5        0.5978
77.6    23.00  0.69     Sequence
             DRB1_0101  367      CVADYSVLYNSASFS  YSVLYNSAS  4        0.6283
55.8    18.00  0.81     Sequence
             DRB1_0101  368      VADYSVLYNSASFST  YSVLYNSAS  3        0.6582
40.4    14.00  0.78     Sequence
             DRB1_0101  369      ADYSVLYNSASFSTF  YSVLYNSAS  2        0.6621
38.7    14.00  0.68     Sequence
             DRB1_0101  370      DYSVLYNSASFSTFK  YSVLYNSAS  1        0.6519
43.2    15.00  0.54     Sequence
             DRB1_0101  371      YSVLYNSASFSTFKC  YSVLYNSAS  0        0.5949
80.1    23.00  0.44     Sequence
             DRB1_0101  372      SVLYNSASFSTFKCY  VLYNSASFS  1        0.4878
255.3    44.00  0.34     Sequence
             DRB1_0101  373      VLYNSASFSTFKCYG  YNSASFSTF  2        0.4221
519.6    60.00  0.29     Sequence
             DRB1_0101  374      LYNSASFSTFKCYGV  SASFSTFKC  3        0.4052
623.9    65.00  0.29     Sequence
             DRB1_0101  375      YNSASFSTFKCYGVS  FSTFKCYGV  5        0.4023
643.6    65.00  0.42     Sequence
             DRB1_0101  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.3753
861.7    70.00  0.54     Sequence
             DRB1_0101  377      SASFSTFKCYGVSPT  FKCYGVSPT  6        0.4880
254.5    43.00  0.44     Sequence
             DRB1_0101  378      ASFSTFKCYGVSPTK  FKCYGVSPT  5        0.5661
109.3    28.00  0.65     Sequence
             DRB1_0101  379      SFSTFKCYGVSPTKL  FKCYGVSPT  4        0.6617
38.9    14.00  0.56     Sequence
             DRB1_0101  380      FSTFKCYGVSPTKLN  FKCYGVSPT  3        0.7118
22.6     8.00  0.49     Sequence        WB
             DRB1_0101  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.7040
24.6     8.50  0.41     Sequence        WB
```

```
             DRB1_0101  382      TFKCYGVSPTKLNDL  CYGVSPTKL  3        0.6990
26.0     9.00  0.48     Sequence         WB
             DRB1_0101  383      FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.6368
50.9    17.00  0.57     Sequence
             DRB1_0101  384      KCYGVSPTKLNDLCF  CYGVSPTKL  1        0.5346
153.8    34.00  0.70     Sequence
             DRB1_0101  385      CYGVSPTKLNDLCFT  CYGVSPTKL  0        0.4233
513.0    60.00  0.56     Sequence
             DRB1_0101  386      YGVSPTKLNDLCFTN  PTKLNDLCF  4        0.2638
2880.1    90.00  0.29     Sequence
             DRB1_0101  387      GVSPTKLNDLCFTNV  PTKLNDLCF  3        0.2586
3047.5    90.00  0.31     Sequence
             DRB1_0101  388      VSPTKLNDLCFTNVY  PTKLNDLCF  2        0.2791
2441.6    85.00  0.27     Sequence
             DRB1_0101  389      SPTKLNDLCFTNVYA  DLCFTNVYA  6        0.3270
1453.5    80.00  0.22     Sequence
             DRB1_0101  390      PTKLNDLCFTNVYAD  DLCFTNVYA  5        0.3151
1653.4    80.00  0.27     Sequence
             DRB1_0101  391      TKLNDLCFTNVYADS  DLCFTNVYA  4        0.3074
1797.7    80.00  0.34     Sequence
             DRB1_0101  392      KLNDLCFTNVYADSF  DLCFTNVYA  3        0.3405
1256.4    75.00  0.28     Sequence
             DRB1_0101  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.3869
759.8    65.00  0.55     Sequence
             DRB1_0101  394      NDLCFTNVYADSFVI  FTNVYADSF  4        0.4698
310.0    47.00  0.43     Sequence
             DRB1_0101  395      DLCFTNVYADSFVIR  NVYADSFVI  5        0.5442
138.7    32.00  0.50     Sequence
             DRB1_0101  396      LCFTNVYADSFVIRG  NVYADSFVI  4        0.5691
105.9    28.00  0.54     Sequence
             DRB1_0101  397      CFTNVYADSFVIRGD  NVYADSFVI  3        0.5546
123.9    30.00  0.57     Sequence
             DRB1_0101  398      FTNVYADSFVIRGDE  NVYADSFVI  2        0.5282
164.8    35.00  0.65     Sequence
             DRB1_0101  399      TNVYADSFVIRGDEV  NVYADSFVI  1        0.4861
259.8    44.00  0.56     Sequence
             DRB1_0101  400      NVYADSFVIRGDEVR  NVYADSFVI  0        0.4683
315.1    48.00  0.32     Sequence
             DRB1_0101  401      VYADSFVIRGDEVRQ  SFVIRGDEV  4        0.4321
466.3    55.00  0.41     Sequence
             DRB1_0101  402      YADSFVIRGDEVRQI  FVIRGDEVR  4        0.4913
245.7    43.00  0.32     Sequence
             DRB1_0101  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.5308
160.3    35.00  0.30     Sequence
             DRB1_0101  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.5153
189.6    38.00  0.38     Sequence
             DRB1_0101  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.5007
221.9    41.00  0.46     Sequence
             DRB1_0101  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.4251
503.0    60.00  0.57     Sequence
             DRB1_0101  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.3904
731.8    65.00  0.42     Sequence
             DRB1_0101  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.4321
466.0    55.00  0.61     Sequence
             DRB1_0101  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.4483
391.2    55.00  0.77     Sequence
             DRB1_0101  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.4973
230.3    42.00  0.69     Sequence
             DRB1_0101  411      DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.5149
190.2    38.00  0.60     Sequence
             DRB1_0101  412      EVRQIAPGQTGTIAD  VRQIAPGQT  1        0.5038
214.6    40.00  0.55     Sequence
             DRB1_0101  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.4465
399.0    55.00  0.47     Sequence
             DRB1_0101  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.3422
1233.7    75.00  0.72     Sequence
```

```
             DRB1_0101  415      QIAPGQTGTIADYNY  IAPGQTGTI  1        0.2747
2558.4    90.00  0.71     Sequence
             DRB1_0101  416      IAPGQTGTIADYNYK  IAPGQTGTI  0        0.2216
4548.4    95.00  0.38     Sequence
             DRB1_0101  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.3022
1901.5    85.00  0.56     Sequence
             DRB1_0101  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.3838
786.3    70.00  0.70     Sequence
             DRB1_0101  419      GQTGTIADYNYKLPD  TIADYNYKL  4        0.4093
596.9    60.00  0.76     Sequence
             DRB1_0101  420      QTGTIADYNYKLPDD  TIADYNYKL  3        0.4068
612.8    65.00  0.77     Sequence
             DRB1_0101  421      TGTIADYNYKLPDDF  TIADYNYKL  2        0.3866
762.3    65.00  0.71     Sequence
             DRB1_0101  422      GTIADYNYKLPDDFT  TIADYNYKL  1        0.3594
1023.7    75.00  0.60     Sequence
             DRB1_0101  423      TIADYNYKLPDDFTG  YNYKLPDDF  4        0.3083
1778.8    80.00  0.41     Sequence
             DRB1_0101  424      IADYNYKLPDDFTGC  YNYKLPDDF  3        0.2671
2779.7    90.00  0.49     Sequence
             DRB1_0101  425      ADYNYKLPDDFTGCV  YNYKLPDDF  2        0.2861
2261.4    85.00  0.33     Sequence
             DRB1_0101  426      DYNYKLPDDFTGCVI  YKLPDDFTG  3        0.2996
1954.1    85.00  0.28     Sequence
             DRB1_0101  427      YNYKLPDDFTGCVIA  YKLPDDFTG  2        0.3170
1620.0    80.00  0.19     Sequence
             DRB1_0101  428      NYKLPDDFTGCVIAW  PDDFTGCVI  4        0.3107
1733.0    80.00  0.25     Sequence
             DRB1_0101  429      YKLPDDFTGCVIAWN  PDDFTGCVI  3        0.3150
1654.6    80.00  0.28     Sequence
             DRB1_0101  430      KLPDDFTGCVIAWNS  DDFTGCVIA  3        0.3359
1320.3    75.00  0.30     Sequence
             DRB1_0101  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.3401
1262.0    75.00  0.28     Sequence
             DRB1_0101  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.3414
1244.1    75.00  0.34     Sequence
             DRB1_0101  433      DDFTGCVIAWNSNNL  FTGCVIAWN  2        0.3587
1032.0    75.00  0.25     Sequence
             DRB1_0101  434      DFTGCVIAWNSNNLD  TGCVIAWNS  2        0.3665
948.4    70.00  0.20     Sequence
             DRB1_0101  435      FTGCVIAWNSNNLDS  IAWNSNNLD  5        0.3825
797.0    70.00  0.26     Sequence
             DRB1_0101  436      TGCVIAWNSNNLDSK  IAWNSNNLD  4        0.3861
767.2    65.00  0.40     Sequence
             DRB1_0101  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3        0.3761
854.7    70.00  0.45     Sequence
             DRB1_0101  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2        0.3422
1232.7    75.00  0.48     Sequence
             DRB1_0101  439      VIAWNSNNLDSKVGG  IAWNSNNLD  1        0.3092
1761.5    80.00  0.47     Sequence
             DRB1_0101  440      IAWNSNNLDSKVGGN  IAWNSNNLD  0        0.2439
3573.1    90.00  0.34     Sequence
             DRB1_0101  441      AWNSNNLDSKVGGNY  SNNLDSKVG  3        0.2065
5354.0    95.00  0.36     Sequence
             DRB1_0101  442      WNSNNLDSKVGGNYN  SNNLDSKVG  2        0.2036
5521.6    95.00  0.32     Sequence
             DRB1_0101  443      NSNNLDSKVGGNYNY  LDSKVGGNY  4        0.2201
4622.3    95.00  0.41     Sequence
             DRB1_0101  444      SNNLDSKVGGNYNYL  LDSKVGGNY  3        0.2848
2295.2    85.00  0.34     Sequence
             DRB1_0101  445      NNLDSKVGGNYNYLY  KVGGNYNYL  5        0.3450
1195.7    75.00  0.33     Sequence
             DRB1_0101  446      NLDSKVGGNYNYLYR  KVGGNYNYL  4        0.3934
708.8    65.00  0.35     Sequence
             DRB1_0101  447      LDSKVGGNYNYLYRL  KVGGNYNYL  3        0.4457
402.5    55.00  0.32     Sequence
```

```
             DRB1_0101  448      DSKVGGNYNYLYRLF  VGGNYNYLY  3        0.4697
310.4    47.00  0.28     Sequence
             DRB1_0101  449      SKVGGNYNYLYRLFR  GNYNYLYRL  4        0.4870
257.5    44.00  0.32     Sequence
             DRB1_0101  450      KVGGNYNYLYRLFRK  GNYNYLYRL  3        0.4902
248.6    43.00  0.35     Sequence
             DRB1_0101  451      VGGNYNYLYRLFRKS  YLYRLFRKS  6        0.5060
209.7    40.00  0.28     Sequence
             DRB1_0101  452      GGNYNYLYRLFRKSN  YLYRLFRKS  5        0.5328
156.8    34.00  0.41     Sequence
             DRB1_0101  453      GNYNYLYRLFRKSNL  YLYRLFRKS  4        0.6078
69.6    21.00  0.39     Sequence
             DRB1_0101  454      NYNYLYRLFRKSNLK  YRLFRKSNL  5        0.6486
44.8    15.00  0.42     Sequence
             DRB1_0101  455      YNYLYRLFRKSNLKP  YRLFRKSNL  4        0.6326
53.3    17.00  0.47     Sequence
             DRB1_0101  456      NYLYRLFRKSNLKPF  YRLFRKSNL  3        0.6277
56.1    18.00  0.51     Sequence
             DRB1_0101  457      YLYRLFRKSNLKPFE  YRLFRKSNL  2        0.5833
90.8    25.00  0.56     Sequence
             DRB1_0101  458      LYRLFRKSNLKPFER  YRLFRKSNL  1        0.5400
145.0    33.00  0.52     Sequence
             DRB1_0101  459      YRLFRKSNLKPFERD  YRLFRKSNL  0        0.4822
271.2    45.00  0.38     Sequence
             DRB1_0101  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.3617
998.6    70.00  0.47     Sequence
             DRB1_0101  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.3172
1615.9    80.00  0.41     Sequence
             DRB1_0101  462      FRKSNLKPFERDIST  KSNLKPFER  2        0.2504
3328.1    90.00  0.38     Sequence
             DRB1_0101  463      RKSNLKPFERDISTE  KSNLKPFER  1        0.2065
5354.5    95.00  0.43     Sequence
             DRB1_0101  464      KSNLKPFERDISTEI  FERDISTEI  6        0.2976
1998.0    85.00  0.62     Sequence
             DRB1_0101  465      SNLKPFERDISTEIY  FERDISTEI  5        0.4134
571.0    60.00  0.79     Sequence
             DRB1_0101  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.4567
357.4    50.00  0.82     Sequence
             DRB1_0101  467      LKPFERDISTEIYQA  FERDISTEI  3        0.4956
234.6    42.00  0.83     Sequence
             DRB1_0101  468      KPFERDISTEIYQAG  FERDISTEI  2        0.4771
286.4    46.00  0.75     Sequence
             DRB1_0101  469      PFERDISTEIYQAGS  FERDISTEI  1        0.4267
494.0    60.00  0.63     Sequence
             DRB1_0101  470      FERDISTEIYQAGST  FERDISTEI  0        0.3372
1301.1    75.00  0.42     Sequence
             DRB1_0101  471      ERDISTEIYQAGSTP  DISTEIYQA  2        0.2479
3419.7    90.00  0.42     Sequence
             DRB1_0101  472      RDISTEIYQAGSTPC  IYQAGSTPC  6        0.2950
2055.2    85.00  0.25     Sequence
             DRB1_0101  473      DISTEIYQAGSTPCN  IYQAGSTPC  5        0.3455
1189.3    75.00  0.41     Sequence
             DRB1_0101  474      ISTEIYQAGSTPCNG  IYQAGSTPC  4        0.3944
701.2    65.00  0.44     Sequence
             DRB1_0101  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.4314
469.8    60.00  0.46     Sequence
             DRB1_0101  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.4318
467.6    55.00  0.44     Sequence
             DRB1_0101  477      EIYQAGSTPCNGVKG  YQAGSTPCN  2        0.3865
763.9    65.00  0.43     Sequence
             DRB1_0101  478      IYQAGSTPCNGVKGF  YQAGSTPCN  1        0.3249
1487.4    80.00  0.44     Sequence
             DRB1_0101  479      YQAGSTPCNGVKGFN  YQAGSTPCN  0        0.2367
3859.5    95.00  0.32     Sequence
             DRB1_0101  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.2577
3075.7    90.00  0.43     Sequence
```

```
             DRB1_0101  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.3255
1477.5    80.00  0.67     Sequence
             DRB1_0101  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.3807
813.0    70.00  0.69     Sequence
             DRB1_0101  483      STPCNGVKGFNCYFP  CNGVKGFNC  3        0.3720
893.0    70.00  0.68     Sequence
             DRB1_0101  484      TPCNGVKGFNCYFPL  CNGVKGFNC  2        0.3899
736.1    65.00  0.53     Sequence
             DRB1_0101  485      PCNGVKGFNCYFPLQ  CNGVKGFNC  1        0.3931
711.1    65.00  0.44     Sequence
             DRB1_0101  486      CNGVKGFNCYFPLQS  CNGVKGFNC  0        0.3997
662.2    65.00  0.26     Sequence
             DRB1_0101  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.3795
823.6    70.00  0.39     Sequence
             DRB1_0101  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.3829
793.6    70.00  0.47     Sequence
             DRB1_0101  489      VKGFNCYFPLQSYGF  YFPLQSYGF  6        0.4887
252.7    43.00  0.48     Sequence
             DRB1_0101  490      KGFNCYFPLQSYGFQ  YFPLQSYGF  5        0.5452
137.2    32.00  0.57     Sequence
             DRB1_0101  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.5268
167.3    36.00  0.62     Sequence
             DRB1_0101  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.5267
167.5    36.00  0.68     Sequence
             DRB1_0101  493      NCYFPLQSYGFQPTY  YFPLQSYGF  2        0.5020
218.9    41.00  0.63     Sequence
             DRB1_0101  494      CYFPLQSYGFQPTYG  YFPLQSYGF  1        0.4786
282.0    45.00  0.56     Sequence
             DRB1_0101  495      YFPLQSYGFQPTYGV  YGFQPTYGV  6        0.4918
244.4    43.00  0.38     Sequence
             DRB1_0101  496      FPLQSYGFQPTYGVG  YGFQPTYGV  5        0.5032
215.9    40.00  0.65     Sequence
             DRB1_0101  497      PLQSYGFQPTYGVGY  YGFQPTYGV  4        0.5524
126.8    31.00  0.68     Sequence
             DRB1_0101  498      LQSYGFQPTYGVGYQ  YGFQPTYGV  3        0.5895
84.9    24.00  0.62     Sequence
             DRB1_0101  499      QSYGFQPTYGVGYQP  YGFQPTYGV  2        0.5722
102.4    27.00  0.60     Sequence
             DRB1_0101  500      SYGFQPTYGVGYQPY  YGFQPTYGV  1        0.5473
134.0    32.00  0.54     Sequence
             DRB1_0101  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.4665
321.2    48.00  0.41     Sequence
             DRB1_0101  502      GFQPTYGVGYQPYRV  GVGYQPYRV  6        0.4089
599.3    60.00  0.31     Sequence
             DRB1_0101  503      FQPTYGVGYQPYRVV  GVGYQPYRV  5        0.4921
243.7    43.00  0.46     Sequence
             DRB1_0101  504      QPTYGVGYQPYRVVV  GVGYQPYRV  4        0.5350
153.1    34.00  0.51     Sequence
             DRB1_0101  505      PTYGVGYQPYRVVVL  GVGYQPYRV  3        0.6217
59.9    19.00  0.41     Sequence
             DRB1_0101  506      TYGVGYQPYRVVVLS  GVGYQPYRV  2        0.6411
48.6    16.00  0.35     Sequence
             DRB1_0101  507      YGVGYQPYRVVVLSF  YQPYRVVVL  4        0.6394
49.5    17.00  0.40     Sequence
             DRB1_0101  508      GVGYQPYRVVVLSFE  YQPYRVVVL  3        0.5966
78.6    23.00  0.46     Sequence
             DRB1_0101  509      VGYQPYRVVVLSFEL  YQPYRVVVL  2        0.5323
157.6    35.00  0.49     Sequence
             DRB1_0101  510      GYQPYRVVVLSFELL  YQPYRVVVL  1        0.5178
184.4    37.00  0.36     Sequence
             DRB1_0101  511      YQPYRVVVLSFELLH  YRVVVLSFE  3        0.4708
306.6    47.00  0.22     Sequence
             DRB1_0101  512      QPYRVVVLSFELLHA  VVVLSFELL  4        0.4413
422.0    55.00  0.32     Sequence
             DRB1_0101  513      PYRVVVLSFELLHAP  VVVLSFELL  3        0.4281
487.0    60.00  0.31     Sequence
```

```
             DRB1_0101  514      YRVVVLSFELLHAPA  VVVLSFELL  2         0.4464
399.3    55.00  0.27     Sequence
             DRB1_0101  515      RVVVLSFELLHAPAT  FELLHAPAT  6         0.8315
6.2     1.00  0.86     Sequence          SB
             DRB1_0101  516      VVVLSFELLHAPATV  FELLHAPAT  5         0.8905
3.3     0.15  0.88     Sequence          SB
             DRB1_0101  517      VVLSFELLHAPATVC  FELLHAPAT  4         0.9010
2.9     0.08  0.87     Sequence          SB
             DRB1_0101  518      VLSFELLHAPATVCG  FELLHAPAT  3         0.9082
2.7     0.06  0.83     Sequence          SB
             DRB1_0101  519      LSFELLHAPATVCGP  FELLHAPAT  2         0.9033
2.8     0.07  0.82     Sequence          SB
             DRB1_0101  520      SFELLHAPATVCGPK  FELLHAPAT  1         0.8909
3.3     0.15  0.80     Sequence          SB
             DRB1_0101  521      FELLHAPATVCGPKK  FELLHAPAT  0         0.8406
5.6     0.80  0.75     Sequence          SB
             DRB1_0101  522      ELLHAPATVCGPKKS  LLHAPATVC  1         0.5324
157.5    35.00  0.69     Sequence
             DRB1_0101  523      LLHAPATVCGPKKST  LLHAPATVC  0         0.4180
542.7    60.00  0.53     Sequence
             DRB1_0101  524      LHAPATVCGPKKSTN  PATVCGPKK  3         0.2591
3029.0    90.00  0.40     Sequence
             DRB1_0101  525      HAPATVCGPKKSTNL  PATVCGPKK  2         0.2576
3080.5    90.00  0.38     Sequence
             DRB1_0101  526      APATVCGPKKSTNLV  CGPKKSTNL  5         0.2808
2396.0    85.00  0.33     Sequence
             DRB1_0101  527      PATVCGPKKSTNLVK  CGPKKSTNL  4         0.2956
2041.2    85.00  0.44     Sequence
             DRB1_0101  528      ATVCGPKKSTNLVKN  CGPKKSTNL  3         0.2951
2051.6    85.00  0.50     Sequence
             DRB1_0101  529      TVCGPKKSTNLVKNK  CGPKKSTNL  2         0.2913
2138.4    85.00  0.45     Sequence
             DRB1_0101  530      VCGPKKSTNLVKNKC  CGPKKSTNL  1         0.2646
2854.3    90.00  0.41     Sequence
             DRB1_0101  531      CGPKKSTNLVKNKCV  TNLVKNKCV  6         0.3777
840.2    70.00  0.62     Sequence
             DRB1_0101  532      GPKKSTNLVKNKCVN  TNLVKNKCV  5         0.4721
302.4    47.00  0.79     Sequence
             DRB1_0101  533      PKKSTNLVKNKCVNF  TNLVKNKCV  4         0.5546
123.9    30.00  0.75     Sequence
             DRB1_0101  534      KKSTNLVKNKCVNFN  TNLVKNKCV  3         0.6014
74.6    22.00  0.68     Sequence
             DRB1_0101  535      KSTNLVKNKCVNFNF  TNLVKNKCV  2         0.5969
78.4    23.00  0.58     Sequence
             DRB1_0101  536      STNLVKNKCVNFNFN  TNLVKNKCV  1         0.5782
95.9    26.00  0.49     Sequence
             DRB1_0101  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2         0.5171
185.9    38.00  0.34     Sequence
             DRB1_0101  538      NLVKNKCVNFNFNGL  LVKNKCVNF  1         0.4659
323.5    48.00  0.29     Sequence
             DRB1_0101  539      LVKNKCVNFNFNGLT  CVNFNFNGL  5         0.4538
368.8    55.00  0.42     Sequence
             DRB1_0101  540      VKNKCVNFNFNGLTG  CVNFNFNGL  4         0.4290
482.0    60.00  0.50     Sequence
             DRB1_0101  541      KNKCVNFNFNGLTGT  CVNFNFNGL  3         0.4635
331.8    49.00  0.47     Sequence
             DRB1_0101  542      NKCVNFNFNGLTGTG  CVNFNFNGL  2         0.4743
295.3    46.00  0.37     Sequence
             DRB1_0101  543      KCVNFNFNGLTGTGV  FNGLTGTGV  6         0.6789
32.3    12.00  0.68     Sequence
             DRB1_0101  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5         0.7761
11.3     3.50  0.83     Sequence          WB
             DRB1_0101  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4         0.8064
8.1     1.80  0.88     Sequence          SB
             DRB1_0101  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3         0.8104
7.8     1.70  0.89     Sequence          SB
```

```
             DRB1_0101  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.7938
9.3     2.50  0.88     Sequence         WB
             DRB1_0101  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.7490
15.1     5.00  0.86     Sequence         WB
             DRB1_0101  549      FNGLTGTGVLTESNK  FNGLTGTGV  0        0.6315
53.9    18.00  0.77     Sequence
             DRB1_0101  550      NGLTGTGVLTESNKK  GLTGTGVLT  1        0.3044
1855.3    85.00  0.56     Sequence
             DRB1_0101  551      GLTGTGVLTESNKKF  GVLTESNKK  5        0.2865
2253.9    85.00  0.29     Sequence
             DRB1_0101  552      LTGTGVLTESNKKFL  GVLTESNKK  4        0.3283
1433.0    80.00  0.38     Sequence
             DRB1_0101  553      TGTGVLTESNKKFLP  GVLTESNKK  3        0.3287
1426.7    80.00  0.38     Sequence
             DRB1_0101  554      GTGVLTESNKKFLPF  VLTESNKKF  3        0.3417
1239.2    75.00  0.37     Sequence
             DRB1_0101  555      TGVLTESNKKFLPFQ  VLTESNKKF  2        0.3312
1389.6    80.00  0.33     Sequence
             DRB1_0101  556      GVLTESNKKFLPFQQ  VLTESNKKF  1        0.2989
1970.4    85.00  0.29     Sequence
             DRB1_0101  557      VLTESNKKFLPFQQF  KKFLPFQQF  6        0.2945
2065.4    85.00  0.26     Sequence
             DRB1_0101  558      LTESNKKFLPFQQFG  KKFLPFQQF  5        0.2965
2022.1    85.00  0.38     Sequence
             DRB1_0101  559      TESNKKFLPFQQFGR  KKFLPFQQF  4        0.3655
957.9    70.00  0.34     Sequence
             DRB1_0101  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5        0.3691
921.7    70.00  0.35     Sequence
             DRB1_0101  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4        0.4161
554.3    60.00  0.36     Sequence
             DRB1_0101  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.4588
349.1    50.00  0.32     Sequence
             DRB1_0101  563      KKFLPFQQFGRDIAD  PFQQFGRDI  4        0.4436
411.8    55.00  0.38     Sequence
             DRB1_0101  564      KFLPFQQFGRDIADT  PFQQFGRDI  3        0.4168
550.0    60.00  0.47     Sequence
             DRB1_0101  565      FLPFQQFGRDIADTT  PFQQFGRDI  2        0.3895
739.3    65.00  0.35     Sequence
             DRB1_0101  566      LPFQQFGRDIADTTD  PFQQFGRDI  1        0.3573
1047.5    75.00  0.32     Sequence
             DRB1_0101  567      PFQQFGRDIADTTDA  FGRDIADTT  4        0.3337
1352.0    80.00  0.46     Sequence
             DRB1_0101  568      FQQFGRDIADTTDAV  FGRDIADTT  3        0.3089
1768.4    80.00  0.63     Sequence
             DRB1_0101  569      QQFGRDIADTTDAVR  FGRDIADTT  2        0.2737
2586.8    90.00  0.64     Sequence
             DRB1_0101  570      QFGRDIADTTDAVRD  FGRDIADTT  1        0.2496
3359.5    90.00  0.54     Sequence
             DRB1_0101  571      FGRDIADTTDAVRDP  FGRDIADTT  0        0.1942
6114.8    95.00  0.37     Sequence
             DRB1_0101  572      GRDIADTTDAVRDPQ  DIADTTDAV  2        0.1450
10417.6   100.00  0.35     Sequence
             DRB1_0101  573      RDIADTTDAVRDPQT  ADTTDAVRD  3        0.1380
11231.6   100.00  0.32     Sequence
             DRB1_0101  574      DIADTTDAVRDPQTL  ADTTDAVRD  2        0.1400
10993.5   100.00  0.25     Sequence
             DRB1_0101  575      IADTTDAVRDPQTLE  DAVRDPQTL  5        0.1445
10472.8   100.00  0.44     Sequence
             DRB1_0101  576      ADTTDAVRDPQTLEI  DAVRDPQTL  4        0.1773
7344.4   100.00  0.44     Sequence
             DRB1_0101  577      DTTDAVRDPQTLEIL  DAVRDPQTL  3        0.2254
4362.5    95.00  0.38     Sequence
             DRB1_0101  578      TTDAVRDPQTLEILD  DAVRDPQTL  2        0.2326
4034.7    95.00  0.34     Sequence
             DRB1_0101  579      TDAVRDPQTLEILDI  VRDPQTLEI  3        0.2678
2757.1    90.00  0.28     Sequence
```

```
             DRB1_0101  580      DAVRDPQTLEILDIT  PQTLEILDI  5        0.2832
2333.7    85.00  0.43     Sequence
             DRB1_0101  581      AVRDPQTLEILDITP  PQTLEILDI  4        0.2694
2711.3    90.00  0.47     Sequence
             DRB1_0101  582      VRDPQTLEILDITPC  LEILDITPC  6        0.3562
1060.1    75.00  0.51     Sequence
             DRB1_0101  583      RDPQTLEILDITPCS  LEILDITPC  5        0.4243
507.5    60.00  0.65     Sequence
             DRB1_0101  584      DPQTLEILDITPCSF  LEILDITPC  4        0.4709
306.5    47.00  0.66     Sequence
             DRB1_0101  585      PQTLEILDITPCSFG  LEILDITPC  3        0.4933
240.4    42.00  0.64     Sequence
             DRB1_0101  586      QTLEILDITPCSFGG  LEILDITPC  2        0.4876
255.7    44.00  0.62     Sequence
             DRB1_0101  587      TLEILDITPCSFGGV  LEILDITPC  1        0.4635
332.0    49.00  0.51     Sequence
             DRB1_0101  588      LEILDITPCSFGGVS  LEILDITPC  0        0.4067
613.8    65.00  0.36     Sequence
             DRB1_0101  589      EILDITPCSFGGVSV  PCSFGGVSV  6        0.3609
1006.8    70.00  0.28     Sequence
             DRB1_0101  590      ILDITPCSFGGVSVI  PCSFGGVSV  5        0.4427
415.5    55.00  0.34     Sequence
             DRB1_0101  591      LDITPCSFGGVSVIT  PCSFGGVSV  4        0.4754
291.8    46.00  0.38     Sequence
             DRB1_0101  592      DITPCSFGGVSVITP  PCSFGGVSV  3        0.5278
165.6    35.00  0.26     Sequence
             DRB1_0101  593      ITPCSFGGVSVITPG  FGGVSVITP  5        0.5786
95.5    26.00  0.38     Sequence
             DRB1_0101  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.6009
75.0    22.00  0.41     Sequence
             DRB1_0101  595      PCSFGGVSVITPGTN  FGGVSVITP  3        0.5956
79.5    23.00  0.41     Sequence
             DRB1_0101  596      CSFGGVSVITPGTNT  FGGVSVITP  2        0.5333
155.9    34.00  0.43     Sequence
             DRB1_0101  597      SFGGVSVITPGTNTS  FGGVSVITP  1        0.4935
239.8    42.00  0.35     Sequence
             DRB1_0101  598      FGGVSVITPGTNTSN  SVITPGTNT  4        0.4585
350.4    50.00  0.37     Sequence
             DRB1_0101  599      GGVSVITPGTNTSNQ  SVITPGTNT  3        0.4337
458.3    55.00  0.53     Sequence
             DRB1_0101  600      GVSVITPGTNTSNQV  SVITPGTNT  2        0.4142
565.9    60.00  0.54     Sequence
             DRB1_0101  601      VSVITPGTNTSNQVA  SVITPGTNT  1        0.3591
1027.4    75.00  0.58     Sequence
             DRB1_0101  602      SVITPGTNTSNQVAV  SVITPGTNT  0        0.2931
2097.1    85.00  0.41     Sequence
             DRB1_0101  603      VITPGTNTSNQVAVL  GTNTSNQVA  4        0.2775
2483.3    85.00  0.28     Sequence
             DRB1_0101  604      ITPGTNTSNQVAVLY  NTSNQVAVL  5        0.3240
1502.0    80.00  0.38     Sequence
             DRB1_0101  605      TPGTNTSNQVAVLYQ  NTSNQVAVL  4        0.3455
1189.3    75.00  0.39     Sequence
             DRB1_0101  606      PGTNTSNQVAVLYQG  NTSNQVAVL  3        0.3486
1150.4    75.00  0.40     Sequence
             DRB1_0101  607      GTNTSNQVAVLYQGV  NTSNQVAVL  2        0.3592
1026.3    75.00  0.32     Sequence
             DRB1_0101  608      TNTSNQVAVLYQGVN  QVAVLYQGV  5        0.3648
965.3    70.00  0.26     Sequence
             DRB1_0101  609      NTSNQVAVLYQGVNC  QVAVLYQGV  4        0.3345
1340.1    75.00  0.34     Sequence
             DRB1_0101  610      TSNQVAVLYQGVNCT  VLYQGVNCT  6        0.4502
383.1    55.00  0.46     Sequence
             DRB1_0101  611      SNQVAVLYQGVNCTE  VLYQGVNCT  5        0.5145
191.1    38.00  0.64     Sequence
             DRB1_0101  612      NQVAVLYQGVNCTEV  VLYQGVNCT  4        0.5591
118.0    30.00  0.69     Sequence
```

```
             DRB1_0101  613      QVAVLYQGVNCTEVP  VLYQGVNCT  3        0.5377
148.7    34.00  0.68     Sequence
             DRB1_0101  614      VAVLYQGVNCTEVPV  VLYQGVNCT  2        0.5050
211.7    40.00  0.68     Sequence
             DRB1_0101  615      AVLYQGVNCTEVPVA  VLYQGVNCT  1        0.4710
305.9    47.00  0.57     Sequence
             DRB1_0101  616      VLYQGVNCTEVPVAI  VLYQGVNCT  0        0.4009
653.4    65.00  0.33     Sequence
             DRB1_0101  617      LYQGVNCTEVPVAIH  NCTEVPVAI  5        0.3324
1371.1    80.00  0.31     Sequence
             DRB1_0101  618      YQGVNCTEVPVAIHA  NCTEVPVAI  4        0.3615
1000.2    70.00  0.38     Sequence
             DRB1_0101  619      QGVNCTEVPVAIHAD  NCTEVPVAI  3        0.3535
1091.0    75.00  0.38     Sequence
             DRB1_0101  620      GVNCTEVPVAIHADQ  NCTEVPVAI  2        0.3423
1232.1    75.00  0.36     Sequence
             DRB1_0101  621      VNCTEVPVAIHADQL  CTEVPVAIH  2        0.3490
1145.4    75.00  0.23     Sequence
             DRB1_0101  622      NCTEVPVAIHADQLT  PVAIHADQL  5        0.3638
976.2    70.00  0.40     Sequence
             DRB1_0101  623      CTEVPVAIHADQLTP  PVAIHADQL  4        0.3392
1274.4    75.00  0.47     Sequence
             DRB1_0101  624      TEVPVAIHADQLTPT  PVAIHADQL  3        0.3479
1159.3    75.00  0.50     Sequence
             DRB1_0101  625      EVPVAIHADQLTPTW  PVAIHADQL  2        0.3475
1164.5    75.00  0.44     Sequence
             DRB1_0101  626      VPVAIHADQLTPTWR  PVAIHADQL  1        0.3510
1121.1    75.00  0.41     Sequence
             DRB1_0101  627      PVAIHADQLTPTWRV  DQLTPTWRV  6        0.4734
298.2    47.00  0.56     Sequence
             DRB1_0101  628      VAIHADQLTPTWRVY  DQLTPTWRV  5        0.5382
148.0    33.00  0.74     Sequence
             DRB1_0101  629      AIHADQLTPTWRVYS  DQLTPTWRV  4        0.5622
114.0    29.00  0.78     Sequence
             DRB1_0101  630      IHADQLTPTWRVYST  DQLTPTWRV  3        0.5736
100.8    27.00  0.80     Sequence
             DRB1_0101  631      HADQLTPTWRVYSTG  DQLTPTWRV  2        0.5413
143.0    33.00  0.81     Sequence
             DRB1_0101  632      ADQLTPTWRVYSTGS  DQLTPTWRV  1        0.4982
227.9    41.00  0.80     Sequence
             DRB1_0101  633      DQLTPTWRVYSTGSN  DQLTPTWRV  0        0.3950
696.5    65.00  0.71     Sequence
             DRB1_0101  634      QLTPTWRVYSTGSNV  RVYSTGSNV  6        0.3028
1889.3    85.00  0.40     Sequence
             DRB1_0101  635      LTPTWRVYSTGSNVF  RVYSTGSNV  5        0.4008
653.7    65.00  0.51     Sequence
             DRB1_0101  636      TPTWRVYSTGSNVFQ  RVYSTGSNV  4        0.5187
182.6    37.00  0.41     Sequence
             DRB1_0101  637      PTWRVYSTGSNVFQT  YSTGSNVFQ  5        0.5817
92.3    26.00  0.38     Sequence
             DRB1_0101  638      TWRVYSTGSNVFQTR  YSTGSNVFQ  4        0.6119
66.6    21.00  0.44     Sequence
             DRB1_0101  639      WRVYSTGSNVFQTRA  YSTGSNVFQ  3        0.6114
67.0    21.00  0.54     Sequence
             DRB1_0101  640      RVYSTGSNVFQTRAG  YSTGSNVFQ  2        0.5819
92.2    25.00  0.60     Sequence
             DRB1_0101  641      VYSTGSNVFQTRAGC  YSTGSNVFQ  1        0.4577
353.2    50.00  0.68     Sequence
             DRB1_0101  642      YSTGSNVFQTRAGCL  VFQTRAGCL  6        0.4423
417.5    55.00  0.47     Sequence
             DRB1_0101  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.5433
139.9    32.00  0.56     Sequence
             DRB1_0101  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.5954
79.6    23.00  0.51     Sequence
             DRB1_0101  645      GSNVFQTRAGCLIGA  VFQTRAGCL  3        0.6302
54.7    18.00  0.50     Sequence
```

```
             DRB1_0101  646      SNVFQTRAGCLIGAE  VFQTRAGCL  2        0.6192
61.6    19.00  0.48     Sequence
             DRB1_0101  647      NVFQTRAGCLIGAEY  FQTRAGCLI  2        0.5768
97.4    26.00  0.45     Sequence
             DRB1_0101  648      VFQTRAGCLIGAEYV  GCLIGAEYV  6        0.6057
71.3    22.00  0.38     Sequence
             DRB1_0101  649      FQTRAGCLIGAEYVN  GCLIGAEYV  5        0.6044
72.2    22.00  0.57     Sequence
             DRB1_0101  650      QTRAGCLIGAEYVNN  GCLIGAEYV  4        0.6088
68.9    21.00  0.71     Sequence
             DRB1_0101  651      TRAGCLIGAEYVNNS  GCLIGAEYV  3        0.6282
55.9    18.00  0.74     Sequence
             DRB1_0101  652      RAGCLIGAEYVNNSY  GCLIGAEYV  2        0.6204
60.8    19.00  0.68     Sequence
             DRB1_0101  653      AGCLIGAEYVNNSYE  GCLIGAEYV  1        0.5778
96.3    26.00  0.65     Sequence
             DRB1_0101  654      GCLIGAEYVNNSYEC  GCLIGAEYV  0        0.5029
216.7    40.00  0.62     Sequence
             DRB1_0101  655      CLIGAEYVNNSYECD  IGAEYVNNS  2        0.2562
3125.4    90.00  0.38     Sequence
             DRB1_0101  656      LIGAEYVNNSYECDI  IGAEYVNNS  1        0.2270
4288.6    95.00  0.27     Sequence
             DRB1_0101  657      IGAEYVNNSYECDIP  YVNNSYECD  4        0.1918
6278.5   100.00  0.43     Sequence
             DRB1_0101  658      GAEYVNNSYECDIPI  YVNNSYECD  3        0.1930
6196.1   100.00  0.45     Sequence
             DRB1_0101  659      AEYVNNSYECDIPIG  YVNNSYECD  2        0.2119
5048.5    95.00  0.37     Sequence
             DRB1_0101  660      EYVNNSYECDIPIGA  YECDIPIGA  6        0.3168
1623.6    80.00  0.51     Sequence
             DRB1_0101  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.3738
875.7    70.00  0.69     Sequence
             DRB1_0101  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.4273
491.0    60.00  0.65     Sequence
             DRB1_0101  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.4410
423.4    55.00  0.61     Sequence
             DRB1_0101  664      NSYECDIPIGAGICA  YECDIPIGA  2        0.4407
424.9    55.00  0.50     Sequence
             DRB1_0101  665      SYECDIPIGAGICAS  YECDIPIGA  1        0.4210
525.9    60.00  0.40     Sequence
             DRB1_0101  666      YECDIPIGAGICASY  CDIPIGAGI  2        0.3920
719.7    65.00  0.25     Sequence
             DRB1_0101  667      ECDIPIGAGICASYQ  IPIGAGICA  3        0.3854
772.5    65.00  0.27     Sequence
             DRB1_0101  668      CDIPIGAGICASYQT  IPIGAGICA  2        0.3851
774.8    65.00  0.22     Sequence
             DRB1_0101  669      DIPIGAGICASYQTQ  GAGICASYQ  4        0.3640
973.7    70.00  0.31     Sequence
             DRB1_0101  670      IPIGAGICASYQTQT  GAGICASYQ  3        0.3553
1070.2    75.00  0.34     Sequence
             DRB1_0101  671      PIGAGICASYQTQTN  GAGICASYQ  2        0.3366
1310.5    75.00  0.33     Sequence
             DRB1_0101  672      IGAGICASYQTQTNS  GAGICASYQ  1        0.3210
1551.7    80.00  0.30     Sequence
             DRB1_0101  673      GAGICASYQTQTNSP  GICASYQTQ  2        0.2762
2518.3    85.00  0.29     Sequence
             DRB1_0101  674      AGICASYQTQTNSPR  YQTQTNSPR  6        0.2648
2848.0    90.00  0.31     Sequence
             DRB1_0101  675      GICASYQTQTNSPRR  YQTQTNSPR  5        0.3025
1894.1    85.00  0.61     Sequence
             DRB1_0101  676      ICASYQTQTNSPRRA  YQTQTNSPR  4        0.3439
1210.0    75.00  0.67     Sequence
             DRB1_0101  677      CASYQTQTNSPRRAR  YQTQTNSPR  3        0.3880
751.4    65.00  0.63     Sequence
             DRB1_0101  678      ASYQTQTNSPRRARS  YQTQTNSPR  2        0.3943
701.9    65.00  0.60     Sequence
```

```
             DRB1_0101  679      SYQTQTNSPRRARSV  YQTQTNSPR  1        0.3848
777.4    65.00  0.43     Sequence
             DRB1_0101  680      YQTQTNSPRRARSVA  TQTNSPRRA  2        0.3271
1452.2    80.00  0.41     Sequence
             DRB1_0101  681      QTQTNSPRRARSVAS  NSPRRARSV  4        0.3092
1763.0    80.00  0.33     Sequence
             DRB1_0101  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.3174
1612.5    80.00  0.40     Sequence
             DRB1_0101  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.3179
1603.3    80.00  0.51     Sequence
             DRB1_0101  684      TNSPRRARSVASQSI  PRRARSVAS  3        0.3525
1103.3    75.00  0.49     Sequence
             DRB1_0101  685      NSPRRARSVASQSII  ARSVASQSI  5        0.3997
662.1    65.00  0.41     Sequence
             DRB1_0101  686      SPRRARSVASQSIIA  SVASQSIIA  6        0.5243
171.9    36.00  0.43     Sequence
             DRB1_0101  687      PRRARSVASQSIIAY  SVASQSIIA  5        0.6160
63.7    20.00  0.59     Sequence
             DRB1_0101  688      RRARSVASQSIIAYT  SVASQSIIA  4        0.6502
44.0    15.00  0.63     Sequence
             DRB1_0101  689      RARSVASQSIIAYTM  SVASQSIIA  3        0.6695
35.7    13.00  0.65     Sequence
             DRB1_0101  690      ARSVASQSIIAYTMS  SVASQSIIA  2        0.6431
47.5    16.00  0.60     Sequence
             DRB1_0101  691      RSVASQSIIAYTMSL  SVASQSIIA  1        0.6220
59.7    19.00  0.44     Sequence
             DRB1_0101  692      SVASQSIIAYTMSLG  SQSIIAYTM  3        0.5656
109.9    28.00  0.29     Sequence
             DRB1_0101  693      VASQSIIAYTMSLGA  SIIAYTMSL  4        0.5812
92.8    26.00  0.34     Sequence
             DRB1_0101  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.6222
59.6    19.00  0.37     Sequence
             DRB1_0101  695      SQSIIAYTMSLGAEN  YTMSLGAEN  6        0.7324
18.1     6.00  0.49     Sequence        WB
             DRB1_0101  696      QSIIAYTMSLGAENS  YTMSLGAEN  5        0.7998
8.7     2.50  0.69     Sequence        WB
             DRB1_0101  697      SIIAYTMSLGAENSV  YTMSLGAEN  4        0.8331
6.1     1.00  0.76     Sequence        SB
             DRB1_0101  698      IIAYTMSLGAENSVA  YTMSLGAEN  3        0.8529
4.9     0.60  0.76     Sequence        SB
             DRB1_0101  699      IAYTMSLGAENSVAY  YTMSLGAEN  2        0.8429
5.5     0.80  0.74     Sequence        SB
             DRB1_0101  700      AYTMSLGAENSVAYS  YTMSLGAEN  1        0.8128
7.6     1.60  0.68     Sequence        SB
             DRB1_0101  701      YTMSLGAENSVAYSN  YTMSLGAEN  0        0.7236
19.9     7.00  0.53     Sequence        WB
             DRB1_0101  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.5288
163.8    35.00  0.37     Sequence
             DRB1_0101  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.4104
589.3    60.00  0.60     Sequence
             DRB1_0101  704      SLGAENSVAYSNNSI  LGAENSVAY  1        0.3381
1289.3    75.00  0.55     Sequence
             DRB1_0101  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.3686
926.8    70.00  0.46     Sequence
             DRB1_0101  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.4707
307.1    47.00  0.69     Sequence
             DRB1_0101  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.4816
272.9    45.00  0.66     Sequence
             DRB1_0101  708      ENSVAYSNNSIAIPT  VAYSNNSIA  3        0.5126
195.0    38.00  0.67     Sequence
             DRB1_0101  709      NSVAYSNNSIAIPTN  VAYSNNSIA  2        0.5162
187.6    38.00  0.63     Sequence
             DRB1_0101  710      SVAYSNNSIAIPTNF  VAYSNNSIA  1        0.4853
262.1    44.00  0.54     Sequence
             DRB1_0101  711      VAYSNNSIAIPTNFT  SIAIPTNFT  6        0.4788
281.3    45.00  0.29     Sequence
```

```
             DRB1_0101  712      AYSNNSIAIPTNFTI  SIAIPTNFT  5        0.5189
182.2    37.00  0.62     Sequence
             DRB1_0101  713      YSNNSIAIPTNFTIS  SIAIPTNFT  4        0.5562
121.7    30.00  0.70     Sequence
             DRB1_0101  714      SNNSIAIPTNFTISV  SIAIPTNFT  3        0.5797
94.4    26.00  0.70     Sequence
             DRB1_0101  715      NNSIAIPTNFTISVT  SIAIPTNFT  2        0.5541
124.5    30.00  0.64     Sequence
             DRB1_0101  716      NSIAIPTNFTISVTT  SIAIPTNFT  1        0.5116
197.2    39.00  0.63     Sequence
             DRB1_0101  717      SIAIPTNFTISVTTE  SIAIPTNFT  0        0.4204
528.9    60.00  0.47     Sequence
             DRB1_0101  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.4792
280.1    45.00  0.75     Sequence
             DRB1_0101  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.6098
68.1    21.00  0.84     Sequence
             DRB1_0101  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.6185
62.0    20.00  0.81     Sequence
             DRB1_0101  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.6462
46.0    16.00  0.81     Sequence
             DRB1_0101  722      TNFTISVTTEILPVS  FTISVTTEI  2        0.6355
51.6    17.00  0.75     Sequence
             DRB1_0101  723      NFTISVTTEILPVSM  FTISVTTEI  1        0.5825
91.6    25.00  0.73     Sequence
             DRB1_0101  724      FTISVTTEILPVSMT  FTISVTTEI  0        0.5102
200.2    39.00  0.34     Sequence
             DRB1_0101  725      TISVTTEILPVSMTK  TEILPVSMT  5        0.5014
220.3    41.00  0.59     Sequence
             DRB1_0101  726      ISVTTEILPVSMTKT  TEILPVSMT  4        0.5246
171.3    36.00  0.62     Sequence
             DRB1_0101  727      SVTTEILPVSMTKTS  TEILPVSMT  3        0.5485
132.3    32.00  0.59     Sequence
             DRB1_0101  728      VTTEILPVSMTKTSV  TEILPVSMT  2        0.5575
120.0    30.00  0.52     Sequence
             DRB1_0101  729      TTEILPVSMTKTSVD  TEILPVSMT  1        0.5513
128.3    31.00  0.47     Sequence
             DRB1_0101  730      TEILPVSMTKTSVDC  TEILPVSMT  0        0.4881
254.5    43.00  0.41     Sequence
             DRB1_0101  731      EILPVSMTKTSVDCT  ILPVSMTKT  1        0.3673
940.1    70.00  0.43     Sequence
             DRB1_0101  732      ILPVSMTKTSVDCTM  PVSMTKTSV  2        0.3235
1509.8    80.00  0.32     Sequence
             DRB1_0101  733      LPVSMTKTSVDCTMY  PVSMTKTSV  1        0.2882
2210.5    85.00  0.37     Sequence
             DRB1_0101  734      PVSMTKTSVDCTMYI  MTKTSVDCT  3        0.2672
2774.5    90.00  0.32     Sequence
             DRB1_0101  735      VSMTKTSVDCTMYIC  MTKTSVDCT  2        0.2146
4906.7    95.00  0.37     Sequence
             DRB1_0101  736      SMTKTSVDCTMYICG  MTKTSVDCT  1        0.1975
5901.7    95.00  0.34     Sequence
             DRB1_0101  737      MTKTSVDCTMYICGD  TSVDCTMYI  3        0.1623
8638.2   100.00  0.41     Sequence
             DRB1_0101  738      TKTSVDCTMYICGDS  TSVDCTMYI  2        0.1430
10645.5   100.00  0.44     Sequence
             DRB1_0101  739      KTSVDCTMYICGDST  TMYICGDST  6        0.1998
5753.1    95.00  0.44     Sequence
             DRB1_0101  740      TSVDCTMYICGDSTE  TMYICGDST  5        0.2360
3890.9    95.00  0.62     Sequence
             DRB1_0101  741      SVDCTMYICGDSTEC  TMYICGDST  4        0.2718
2642.0    90.00  0.57     Sequence
             DRB1_0101  742      VDCTMYICGDSTECS  TMYICGDST  3        0.3213
1545.2    80.00  0.49     Sequence
             DRB1_0101  743      DCTMYICGDSTECSN  TMYICGDST  2        0.3366
1309.9    75.00  0.41     Sequence
             DRB1_0101  744      CTMYICGDSTECSNL  YICGDSTEC  3        0.3550
1073.3    75.00  0.44     Sequence
```

```
             DRB1_0101  745      TMYICGDSTECSNLL  YICGDSTEC  2        0.3364
1312.9    75.00  0.40     Sequence
             DRB1_0101  746      MYICGDSTECSNLLL  YICGDSTEC  1        0.2978
1993.5    85.00  0.31     Sequence
             DRB1_0101  747      YICGDSTECSNLLLQ  DSTECSNLL  4        0.2864
2254.3    85.00  0.33     Sequence
             DRB1_0101  748      ICGDSTECSNLLLQY  DSTECSNLL  3        0.2774
2484.8    85.00  0.44     Sequence
             DRB1_0101  749      CGDSTECSNLLLQYG  DSTECSNLL  2        0.2889
2194.0    85.00  0.37     Sequence
             DRB1_0101  750      GDSTECSNLLLQYGS  CSNLLLQYG  5        0.3017
1912.0    85.00  0.28     Sequence
             DRB1_0101  751      DSTECSNLLLQYGSF  CSNLLLQYG  4        0.3303
1401.8    80.00  0.28     Sequence
             DRB1_0101  752      STECSNLLLQYGSFC  LLLQYGSFC  6        0.4308
472.9    60.00  0.55     Sequence
             DRB1_0101  753      TECSNLLLQYGSFCT  LLLQYGSFC  5        0.5267
167.6    36.00  0.51     Sequence
             DRB1_0101  754      ECSNLLLQYGSFCTQ  LLLQYGSFC  4        0.5840
90.1    25.00  0.49     Sequence
             DRB1_0101  755      CSNLLLQYGSFCTQL  LLLQYGSFC  3        0.6208
60.5    19.00  0.44     Sequence
             DRB1_0101  756      SNLLLQYGSFCTQLN  LLLQYGSFC  2        0.6319
53.7    18.00  0.41     Sequence
             DRB1_0101  757      NLLLQYGSFCTQLNR  LLQYGSFCT  2        0.6148
64.6    20.00  0.34     Sequence
             DRB1_0101  758      LLLQYGSFCTQLNRA  LLQYGSFCT  1        0.5734
101.1    27.00  0.30     Sequence
             DRB1_0101  759      LLQYGSFCTQLNRAL  FCTQLNRAL  6        0.6215
60.1    19.00  0.40     Sequence
             DRB1_0101  760      LQYGSFCTQLNRALT  FCTQLNRAL  5        0.6570
40.9    14.00  0.54     Sequence
             DRB1_0101  761      QYGSFCTQLNRALTG  FCTQLNRAL  4        0.6646
37.7    13.00  0.57     Sequence
             DRB1_0101  762      YGSFCTQLNRALTGI  FCTQLNRAL  3        0.6795
32.1    11.00  0.63     Sequence
             DRB1_0101  763      GSFCTQLNRALTGIA  FCTQLNRAL  2        0.6731
34.4    12.00  0.54     Sequence
             DRB1_0101  764      SFCTQLNRALTGIAV  NRALTGIAV  6        0.7564
14.0     4.50  0.49     Sequence         WB
             DRB1_0101  765      FCTQLNRALTGIAVE  NRALTGIAV  5        0.7850
10.2     3.00  0.65     Sequence         WB
             DRB1_0101  766      CTQLNRALTGIAVEQ  NRALTGIAV  4        0.7929
9.4     2.50  0.73     Sequence         WB
             DRB1_0101  767      TQLNRALTGIAVEQD  NRALTGIAV  3        0.7900
9.7     2.50  0.76     Sequence         WB
             DRB1_0101  768      QLNRALTGIAVEQDK  NRALTGIAV  2        0.7731
11.6     3.50  0.77     Sequence         WB
             DRB1_0101  769      LNRALTGIAVEQDKN  NRALTGIAV  1        0.7408
16.5     5.50  0.80     Sequence         WB
             DRB1_0101  770      NRALTGIAVEQDKNT  NRALTGIAV  0        0.6611
39.1    14.00  0.75     Sequence
             DRB1_0101  771      RALTGIAVEQDKNTQ  LTGIAVEQD  2        0.3090
1766.6    80.00  0.54     Sequence
             DRB1_0101  772      ALTGIAVEQDKNTQE  LTGIAVEQD  1        0.2283
4229.5    95.00  0.44     Sequence
             DRB1_0101  773      LTGIAVEQDKNTQEV  IAVEQDKNT  3        0.1995
5773.0    95.00  0.52     Sequence
             DRB1_0101  774      TGIAVEQDKNTQEVF  IAVEQDKNT  2        0.1638
8500.7   100.00  0.60     Sequence
             DRB1_0101  775      GIAVEQDKNTQEVFA  IAVEQDKNT  1        0.1763
7425.4   100.00  0.41     Sequence
             DRB1_0101  776      IAVEQDKNTQEVFAQ  DKNTQEVFA  5        0.1907
6352.9   100.00  0.30     Sequence
             DRB1_0101  777      AVEQDKNTQEVFAQV  NTQEVFAQV  6        0.2585
3051.3    90.00  0.28     Sequence
```

```
             DRB1_0101  778      VEQDKNTQEVFAQVK  NTQEVFAQV  5        0.3331
1360.3    80.00  0.38     Sequence
             DRB1_0101  779      EQDKNTQEVFAQVKQ  NTQEVFAQV  4        0.3521
1107.4    75.00  0.41     Sequence
             DRB1_0101  780      QDKNTQEVFAQVKQI  NTQEVFAQV  3        0.3940
703.8    65.00  0.35     Sequence
             DRB1_0101  781      DKNTQEVFAQVKQIY  EVFAQVKQI  5        0.4324
464.6    55.00  0.34     Sequence
             DRB1_0101  782      KNTQEVFAQVKQIYK  EVFAQVKQI  4        0.4701
309.1    47.00  0.36     Sequence
             DRB1_0101  783      NTQEVFAQVKQIYKT  EVFAQVKQI  3        0.4600
344.6    49.00  0.47     Sequence
             DRB1_0101  784      TQEVFAQVKQIYKTP  EVFAQVKQI  2        0.4361
446.5    55.00  0.47     Sequence
             DRB1_0101  785      QEVFAQVKQIYKTPP  EVFAQVKQI  1        0.4013
650.3    65.00  0.43     Sequence
             DRB1_0101  786      EVFAQVKQIYKTPPI  FAQVKQIYK  2        0.3516
1114.0    75.00  0.26     Sequence
             DRB1_0101  787      VFAQVKQIYKTPPIK  KQIYKTPPI  5        0.3374
1298.7    75.00  0.25     Sequence
             DRB1_0101  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6        0.4145
564.1    60.00  0.46     Sequence
             DRB1_0101  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.4979
228.7    41.00  0.62     Sequence
             DRB1_0101  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.5267
167.5    36.00  0.69     Sequence
             DRB1_0101  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.5348
153.5    34.00  0.74     Sequence
             DRB1_0101  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.5027
217.2    40.00  0.76     Sequence
             DRB1_0101  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.4134
570.9    60.00  0.74     Sequence
             DRB1_0101  794      IYKTPPIKDFGGFNF  IYKTPPIKD  0        0.3008
1930.0    85.00  0.44     Sequence
             DRB1_0101  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.2381
3802.9    95.00  0.53     Sequence
             DRB1_0101  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.2537
3212.8    90.00  0.60     Sequence
             DRB1_0101  797      TPPIKDFGGFNFSQI  FGGFNFSQI  6        0.3614
1002.0    70.00  0.41     Sequence
             DRB1_0101  798      PPIKDFGGFNFSQIL  FGGFNFSQI  5        0.4176
545.5    60.00  0.51     Sequence
             DRB1_0101  799      PIKDFGGFNFSQILP  FGGFNFSQI  4        0.4086
601.2    60.00  0.54     Sequence
             DRB1_0101  800      IKDFGGFNFSQILPD  FGGFNFSQI  3        0.4437
411.3    55.00  0.43     Sequence
             DRB1_0101  801      KDFGGFNFSQILPDP  FGGFNFSQI  2        0.4460
401.2    55.00  0.40     Sequence
             DRB1_0101  802      DFGGFNFSQILPDPS  FSQILPDPS  6        0.5597
117.2    29.00  0.49     Sequence
             DRB1_0101  803      FGGFNFSQILPDPSK  FSQILPDPS  5        0.6572
40.8    14.00  0.65     Sequence
             DRB1_0101  804      GGFNFSQILPDPSKP  FSQILPDPS  4        0.6501
44.1    15.00  0.71     Sequence
             DRB1_0101  805      GFNFSQILPDPSKPS  FSQILPDPS  3        0.6639
38.0    13.00  0.74     Sequence
             DRB1_0101  806      FNFSQILPDPSKPSK  FSQILPDPS  2        0.6456
46.3    16.00  0.78     Sequence
             DRB1_0101  807      NFSQILPDPSKPSKR  FSQILPDPS  1        0.5937
81.1    24.00  0.78     Sequence
             DRB1_0101  808      FSQILPDPSKPSKRS  FSQILPDPS  0        0.4890
251.8    43.00  0.64     Sequence
             DRB1_0101  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.2578
3073.5    90.00  0.50     Sequence
             DRB1_0101  810      QILPDPSKPSKRSFI  ILPDPSKPS  1        0.2550
3167.9    90.00  0.35     Sequence
```

```
             DRB1_0101  811      ILPDPSKPSKRSFIE  SKPSKRSFI  5        0.2551
3162.7    90.00  0.41     Sequence
             DRB1_0101  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.2315
4085.6    95.00  0.55     Sequence
             DRB1_0101  813      PDPSKPSKRSFIEDL  SKPSKRSFI  3        0.2661
2810.0    90.00  0.52     Sequence
             DRB1_0101  814      DPSKPSKRSFIEDLL  SKPSKRSFI  2        0.3042
1861.0    85.00  0.40     Sequence
             DRB1_0101  815      PSKPSKRSFIEDLLF  SKPSKRSFI  1        0.3245
1493.7    80.00  0.31     Sequence
             DRB1_0101  816      SKPSKRSFIEDLLFN  KRSFIEDLL  4        0.3150
1655.1    80.00  0.26     Sequence
             DRB1_0101  817      KPSKRSFIEDLLFNK  FIEDLLFNK  6        0.3493
1141.3    75.00  0.28     Sequence
             DRB1_0101  818      PSKRSFIEDLLFNKV  FIEDLLFNK  5        0.4240
508.6    60.00  0.31     Sequence
             DRB1_0101  819      SKRSFIEDLLFNKVT  IEDLLFNKV  5        0.4648
327.1    48.00  0.31     Sequence
             DRB1_0101  820      KRSFIEDLLFNKVTL  IEDLLFNKV  4        0.4946
237.0    42.00  0.32     Sequence
             DRB1_0101  821      RSFIEDLLFNKVTLA  LLFNKVTLA  6        0.5752
99.2    27.00  0.43     Sequence
             DRB1_0101  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5        0.5752
99.1    27.00  0.56     Sequence
             DRB1_0101  823      FIEDLLFNKVTLADA  LLFNKVTLA  4        0.6034
73.1    22.00  0.65     Sequence
             DRB1_0101  824      IEDLLFNKVTLADAG  LLFNKVTLA  3        0.6239
58.5    19.00  0.62     Sequence
             DRB1_0101  825      EDLLFNKVTLADAGF  LLFNKVTLA  2        0.6340
52.4    17.00  0.51     Sequence
             DRB1_0101  826      DLLFNKVTLADAGFI  FNKVTLADA  3        0.6461
46.0    16.00  0.40     Sequence
             DRB1_0101  827      LLFNKVTLADAGFIK  FNKVTLADA  2        0.6478
45.2    15.00  0.40     Sequence
             DRB1_0101  828      LFNKVTLADAGFIKQ  VTLADAGFI  4        0.6253
57.6    19.00  0.46     Sequence
             DRB1_0101  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.6130
65.9    20.00  0.62     Sequence
             DRB1_0101  830      NKVTLADAGFIKQYG  VTLADAGFI  2        0.5845
89.6    25.00  0.66     Sequence
             DRB1_0101  831      KVTLADAGFIKQYGD  VTLADAGFI  1        0.5319
158.3    35.00  0.66     Sequence
             DRB1_0101  832      VTLADAGFIKQYGDC  VTLADAGFI  0        0.3935
707.6    65.00  0.49     Sequence
             DRB1_0101  833      TLADAGFIKQYGDCL  FIKQYGDCL  6        0.5458
136.2    32.00  0.77     Sequence
             DRB1_0101  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.6433
47.4    16.00  0.87     Sequence
             DRB1_0101  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4        0.6580
40.5    14.00  0.86     Sequence
             DRB1_0101  836      DAGFIKQYGDCLGDI  FIKQYGDCL  3        0.6848
30.3    11.00  0.85     Sequence
             DRB1_0101  837      AGFIKQYGDCLGDIA  FIKQYGDCL  2        0.6853
30.1    11.00  0.81     Sequence
             DRB1_0101  838      GFIKQYGDCLGDIAA  FIKQYGDCL  1        0.6468
45.7    15.00  0.74     Sequence
             DRB1_0101  839      FIKQYGDCLGDIAAR  FIKQYGDCL  0        0.5528
126.3    31.00  0.58     Sequence
             DRB1_0101  840      IKQYGDCLGDIAARD  YGDCLGDIA  3        0.3686
926.2    70.00  0.57     Sequence
             DRB1_0101  841      KQYGDCLGDIAARDL  YGDCLGDIA  2        0.4052
623.7    65.00  0.41     Sequence
             DRB1_0101  842      QYGDCLGDIAARDLI  LGDIAARDL  5        0.4378
438.5    55.00  0.34     Sequence
             DRB1_0101  843      YGDCLGDIAARDLIC  LGDIAARDL  4        0.4226
516.8    60.00  0.37     Sequence
```

```
             DRB1_0101  844      GDCLGDIAARDLICA  LGDIAARDL  3        0.4269
493.1    60.00  0.44     Sequence
             DRB1_0101  845      DCLGDIAARDLICAQ  LGDIAARDL  2        0.4127
575.2    60.00  0.41     Sequence
             DRB1_0101  846      CLGDIAARDLICAQK  LGDIAARDL  1        0.3944
701.3    65.00  0.35     Sequence
             DRB1_0101  847      LGDIAARDLICAQKF  IAARDLICA  3        0.3786
832.0    70.00  0.31     Sequence
             DRB1_0101  848      GDIAARDLICAQKFN  RDLICAQKF  5        0.3539
1086.3    75.00  0.41     Sequence
             DRB1_0101  849      DIAARDLICAQKFNG  RDLICAQKF  4        0.3558
1064.7    75.00  0.46     Sequence
             DRB1_0101  850      IAARDLICAQKFNGL  RDLICAQKF  3        0.4214
523.6    60.00  0.40     Sequence
             DRB1_0101  851      AARDLICAQKFNGLT  ICAQKFNGL  5        0.4746
294.5    46.00  0.43     Sequence
             DRB1_0101  852      ARDLICAQKFNGLTV  ICAQKFNGL  4        0.5086
203.7    39.00  0.45     Sequence
             DRB1_0101  853      RDLICAQKFNGLTVL  ICAQKFNGL  3        0.5391
146.4    33.00  0.45     Sequence
             DRB1_0101  854      DLICAQKFNGLTVLP  ICAQKFNGL  2        0.5068
207.8    40.00  0.44     Sequence
             DRB1_0101  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.6331
53.0    17.00  0.60     Sequence
             DRB1_0101  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.7195
20.8     7.00  0.75     Sequence         WB
             DRB1_0101  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.7558
14.0     4.50  0.77     Sequence         WB
             DRB1_0101  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.8195
7.1     1.40  0.66     Sequence         SB
             DRB1_0101  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.8084
7.9     1.70  0.63     Sequence         SB
             DRB1_0101  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1        0.7721
11.8     3.50  0.55     Sequence         WB
             DRB1_0101  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.7017
25.2     9.00  0.54     Sequence         WB
             DRB1_0101  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.6162
63.6    20.00  0.83     Sequence
             DRB1_0101  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.5716
103.1    27.00  0.79     Sequence
             DRB1_0101  864      LTVLPPLLTDEMIAQ  LTVLPPLLT  0        0.5076
205.9    39.00  0.65     Sequence
             DRB1_0101  865      TVLPPLLTDEMIAQY  PLLTDEMIA  4        0.3619
996.1    70.00  0.37     Sequence
             DRB1_0101  866      VLPPLLTDEMIAQYT  PLLTDEMIA  3        0.4161
554.0    60.00  0.29     Sequence
             DRB1_0101  867      LPPLLTDEMIAQYTS  TDEMIAQYT  5        0.4679
316.5    48.00  0.44     Sequence
             DRB1_0101  868      PPLLTDEMIAQYTSA  TDEMIAQYT  4        0.5000
223.6    41.00  0.54     Sequence
             DRB1_0101  869      PLLTDEMIAQYTSAL  TDEMIAQYT  3        0.5784
95.8    26.00  0.41     Sequence
             DRB1_0101  870      LLTDEMIAQYTSALL  MIAQYTSAL  5        0.6655
37.3    13.00  0.55     Sequence
             DRB1_0101  871      LTDEMIAQYTSALLA  MIAQYTSAL  4        0.7206
20.5     7.00  0.59     Sequence         WB
             DRB1_0101  872      TDEMIAQYTSALLAG  MIAQYTSAL  3        0.7338
17.8     6.00  0.61     Sequence         WB
             DRB1_0101  873      DEMIAQYTSALLAGT  MIAQYTSAL  2        0.7293
18.7     6.50  0.51     Sequence         WB
             DRB1_0101  874      EMIAQYTSALLAGTI  MIAQYTSAL  1        0.7271
19.2     6.50  0.38     Sequence         WB
             DRB1_0101  875      MIAQYTSALLAGTIT  YTSALLAGT  4        0.7021
25.1     9.00  0.44     Sequence         WB
             DRB1_0101  876      IAQYTSALLAGTITS  YTSALLAGT  3        0.7037
24.7     8.50  0.50     Sequence         WB
```

```
             DRB1_0101  877      AQYTSALLAGTITSG  YTSALLAGT  2        0.6876
29.4    11.00  0.49     Sequence
             DRB1_0101  878      QYTSALLAGTITSGW  YTSALLAGT  1        0.6488
44.7    15.00  0.40     Sequence
             DRB1_0101  879      YTSALLAGTITSGWT  SALLAGTIT  2        0.5761
98.1    26.00  0.34     Sequence
             DRB1_0101  880      TSALLAGTITSGWTF  SALLAGTIT  1        0.5227
175.0    36.00  0.35     Sequence
             DRB1_0101  881      SALLAGTITSGWTFG  SALLAGTIT  0        0.4739
296.7    46.00  0.29     Sequence
             DRB1_0101  882      ALLAGTITSGWTFGA  GTITSGWTF  4        0.4332
460.5    55.00  0.39     Sequence
             DRB1_0101  883      LLAGTITSGWTFGAG  GTITSGWTF  3        0.4359
447.2    55.00  0.43     Sequence
             DRB1_0101  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.4604
343.1    49.00  0.52     Sequence
             DRB1_0101  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.4765
288.5    46.00  0.57     Sequence
             DRB1_0101  886      GTITSGWTFGAGAAL  WTFGAGAAL  6        0.5933
81.4    24.00  0.51     Sequence
             DRB1_0101  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.6425
47.8    16.00  0.68     Sequence
             DRB1_0101  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.7626
13.0     4.00  0.44     Sequence         WB
             DRB1_0101  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.8027
8.5     1.90  0.57     Sequence         SB
             DRB1_0101  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.8240
6.7     1.20  0.69     Sequence         SB
             DRB1_0101  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.8445
5.4     0.70  0.71     Sequence         SB
             DRB1_0101  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.8331
6.1     1.00  0.71     Sequence         SB
             DRB1_0101  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.8005
8.7     2.00  0.67     Sequence         WB
             DRB1_0101  894      FGAGAALQIPFAMQM  GAALQIPFA  3        0.7511
14.8     5.00  0.45     Sequence         WB
             DRB1_0101  895      GAGAALQIPFAMQMA  GAALQIPFA  2        0.6937
27.5     9.50  0.60     Sequence         WB
             DRB1_0101  896      AGAALQIPFAMQMAY  GAALQIPFA  1        0.6954
27.0     9.50  0.51     Sequence         WB
             DRB1_0101  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.6715
35.0    12.00  0.30     Sequence
             DRB1_0101  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.7286
18.8     6.50  0.61     Sequence         WB
             DRB1_0101  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.7845
10.3     3.00  0.83     Sequence         WB
             DRB1_0101  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.8069
8.1     1.80  0.86     Sequence         SB
             DRB1_0101  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.8164
7.3     1.50  0.87     Sequence         SB
             DRB1_0101  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.7893
9.8     2.50  0.88     Sequence         WB
             DRB1_0101  903      PFAMQMAYRFNGIGV  FAMQMAYRF  1        0.7451
15.8     5.00  0.85     Sequence         WB
             DRB1_0101  904      FAMQMAYRFNGIGVT  FAMQMAYRF  0        0.6583
40.3    14.00  0.61     Sequence
             DRB1_0101  905      AMQMAYRFNGIGVTQ  YRFNGIGVT  5        0.5135
193.2    38.00  0.34     Sequence
             DRB1_0101  906      MQMAYRFNGIGVTQN  YRFNGIGVT  4        0.5556
122.5    30.00  0.35     Sequence
             DRB1_0101  907      QMAYRFNGIGVTQNV  FNGIGVTQN  5        0.6074
70.0    21.00  0.38     Sequence
             DRB1_0101  908      MAYRFNGIGVTQNVL  FNGIGVTQN  4        0.6324
53.4    18.00  0.50     Sequence
             DRB1_0101  909      AYRFNGIGVTQNVLY  FNGIGVTQN  3        0.6507
43.8    15.00  0.56     Sequence
```

```
             DRB1_0101  910      YRFNGIGVTQNVLYE  FNGIGVTQN  2        0.6186
62.0    20.00  0.57     Sequence
             DRB1_0101  911      RFNGIGVTQNVLYEN  FNGIGVTQN  1        0.5758
98.4    26.00  0.50     Sequence
             DRB1_0101  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.5019
219.0    41.00  0.40     Sequence
             DRB1_0101  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.4309
472.4    60.00  0.49     Sequence
             DRB1_0101  914      GIGVTQNVLYENQKL  IGVTQNVLY  1        0.4294
480.1    60.00  0.37     Sequence
             DRB1_0101  915      IGVTQNVLYENQKLI  NVLYENQKL  5        0.4657
324.2    48.00  0.40     Sequence
             DRB1_0101  916      GVTQNVLYENQKLIA  NVLYENQKL  4        0.5145
191.2    38.00  0.46     Sequence
             DRB1_0101  917      VTQNVLYENQKLIAN  NVLYENQKL  3        0.5533
125.6    31.00  0.44     Sequence
             DRB1_0101  918      TQNVLYENQKLIANQ  VLYENQKLI  3        0.5680
107.2    28.00  0.40     Sequence
             DRB1_0101  919      QNVLYENQKLIANQF  VLYENQKLI  2        0.5545
124.0    30.00  0.34     Sequence
             DRB1_0101  920      NVLYENQKLIANQFN  NQKLIANQF  5        0.5292
163.0    35.00  0.25     Sequence
             DRB1_0101  921      VLYENQKLIANQFNS  NQKLIANQF  4        0.4870
257.3    44.00  0.44     Sequence
             DRB1_0101  922      LYENQKLIANQFNSA  NQKLIANQF  3        0.4984
227.5    41.00  0.51     Sequence
             DRB1_0101  923      YENQKLIANQFNSAI  NQKLIANQF  2        0.5582
119.1    30.00  0.34     Sequence
             DRB1_0101  924      ENQKLIANQFNSAIG  IANQFNSAI  5        0.6039
72.7    22.00  0.50     Sequence
             DRB1_0101  925      NQKLIANQFNSAIGK  IANQFNSAI  4        0.6393
49.5    17.00  0.60     Sequence
             DRB1_0101  926      QKLIANQFNSAIGKI  IANQFNSAI  3        0.6457
46.2    16.00  0.67     Sequence
             DRB1_0101  927      KLIANQFNSAIGKIQ  IANQFNSAI  2        0.6594
39.8    14.00  0.55     Sequence
             DRB1_0101  928      LIANQFNSAIGKIQD  FNSAIGKIQ  5        0.6375
50.5    17.00  0.46     Sequence
             DRB1_0101  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4        0.6098
68.1    21.00  0.71     Sequence
             DRB1_0101  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.6158
63.8    20.00  0.88     Sequence
             DRB1_0101  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.5926
82.1    24.00  0.85     Sequence
             DRB1_0101  932      QFNSAIGKIQDSLSS  FNSAIGKIQ  1        0.5530
126.0    31.00  0.71     Sequence
             DRB1_0101  933      FNSAIGKIQDSLSST  FNSAIGKIQ  0        0.4620
337.3    49.00  0.40     Sequence
             DRB1_0101  934      NSAIGKIQDSLSSTA  IGKIQDSLS  3        0.4378
438.1    55.00  0.47     Sequence
             DRB1_0101  935      SAIGKIQDSLSSTAS  IGKIQDSLS  2        0.4689
313.0    47.00  0.36     Sequence
             DRB1_0101  936      AIGKIQDSLSSTASA  IQDSLSSTA  4        0.4834
267.5    44.00  0.37     Sequence
             DRB1_0101  937      IGKIQDSLSSTASAL  IQDSLSSTA  3        0.5093
202.1    39.00  0.39     Sequence
             DRB1_0101  938      GKIQDSLSSTASALG  IQDSLSSTA  2        0.5084
204.1    39.00  0.33     Sequence
             DRB1_0101  939      KIQDSLSSTASALGK  LSSTASALG  5        0.5496
130.7    31.00  0.32     Sequence
             DRB1_0101  940      IQDSLSSTASALGKL  LSSTASALG  4        0.5684
106.7    28.00  0.44     Sequence
             DRB1_0101  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.5771
97.1    26.00  0.49     Sequence
             DRB1_0101  942      DSLSSTASALGKLQD  LSSTASALG  2        0.5512
128.6    31.00  0.47     Sequence
```

```
             DRB1_0101  943      SLSSTASALGKLQDV  LSSTASALG  1        0.5261
168.5    36.00  0.43     Sequence
             DRB1_0101  944      LSSTASALGKLQDVV  TASALGKLQ  3        0.4618
338.1    49.00  0.40     Sequence
             DRB1_0101  945      SSTASALGKLQDVVN  TASALGKLQ  2        0.4260
497.8    60.00  0.40     Sequence
             DRB1_0101  946      STASALGKLQDVVNQ  SALGKLQDV  3        0.4236
510.8    60.00  0.28     Sequence
             DRB1_0101  947      TASALGKLQDVVNQN  LGKLQDVVN  4        0.3988
668.1    65.00  0.32     Sequence
             DRB1_0101  948      ASALGKLQDVVNQNA  LGKLQDVVN  3        0.4034
635.6    65.00  0.38     Sequence
             DRB1_0101  949      SALGKLQDVVNQNAQ  LGKLQDVVN  2        0.3863
765.5    65.00  0.36     Sequence
             DRB1_0101  950      ALGKLQDVVNQNAQA  GKLQDVVNQ  2        0.3558
1064.1    75.00  0.31     Sequence
             DRB1_0101  951      LGKLQDVVNQNAQAL  VVNQNAQAL  6        0.4308
472.8    60.00  0.50     Sequence
             DRB1_0101  952      GKLQDVVNQNAQALN  VVNQNAQAL  5        0.5317
158.6    35.00  0.75     Sequence
             DRB1_0101  953      KLQDVVNQNAQALNT  VVNQNAQAL  4        0.5874
86.9    25.00  0.82     Sequence
             DRB1_0101  954      LQDVVNQNAQALNTL  VVNQNAQAL  3        0.6332
52.9    17.00  0.80     Sequence
             DRB1_0101  955      QDVVNQNAQALNTLV  VVNQNAQAL  2        0.6183
62.2    20.00  0.73     Sequence
             DRB1_0101  956      DVVNQNAQALNTLVK  VVNQNAQAL  1        0.5861
88.1    25.00  0.53     Sequence
             DRB1_0101  957      VVNQNAQALNTLVKQ  NAQALNTLV  4        0.5437
139.3    32.00  0.42     Sequence
             DRB1_0101  958      VNQNAQALNTLVKQL  NAQALNTLV  3        0.5215
177.3    37.00  0.60     Sequence
             DRB1_0101  959      NQNAQALNTLVKQLS  NAQALNTLV  2        0.5316
158.8    35.00  0.50     Sequence
             DRB1_0101  960      QNAQALNTLVKQLSS  NAQALNTLV  1        0.5181
183.9    37.00  0.34     Sequence
             DRB1_0101  961      NAQALNTLVKQLSSN  LNTLVKQLS  4        0.4958
234.1    42.00  0.51     Sequence
             DRB1_0101  962      AQALNTLVKQLSSNF  LVKQLSSNF  6        0.5725
102.0    27.00  0.43     Sequence
             DRB1_0101  963      QALNTLVKQLSSNFG  LVKQLSSNF  5        0.7243
19.8     7.00  0.41     Sequence         WB
             DRB1_0101  964      ALNTLVKQLSSNFGA  VKQLSSNFG  5        0.8094
7.9     1.70  0.52     Sequence         SB
             DRB1_0101  965      LNTLVKQLSSNFGAI  VKQLSSNFG  4        0.8337
6.0     1.00  0.52     Sequence         SB
             DRB1_0101  966      NTLVKQLSSNFGAIS  VKQLSSNFG  3        0.8330
6.1     1.00  0.56     Sequence         SB
             DRB1_0101  967      TLVKQLSSNFGAISS  VKQLSSNFG  2        0.8047
8.3     1.90  0.56     Sequence         SB
             DRB1_0101  968      LVKQLSSNFGAISSV  VKQLSSNFG  1        0.7362
17.4     6.00  0.59     Sequence         WB
             DRB1_0101  969      VKQLSSNFGAISSVL  LSSNFGAIS  3        0.6795
32.0    11.00  0.34     Sequence
             DRB1_0101  970      KQLSSNFGAISSVLN  FGAISSVLN  6        0.7452
15.7     5.00  0.69     Sequence         WB
             DRB1_0101  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.7916
9.5     2.50  0.81     Sequence         WB
             DRB1_0101  972      LSSNFGAISSVLNDI  FGAISSVLN  4        0.8149
7.4     1.50  0.86     Sequence         SB
             DRB1_0101  973      SSNFGAISSVLNDIL  FGAISSVLN  3        0.8297
6.3     1.10  0.87     Sequence         SB
             DRB1_0101  974      SNFGAISSVLNDILS  FGAISSVLN  2        0.8082
8.0     1.70  0.86     Sequence         SB
             DRB1_0101  975      NFGAISSVLNDILSR  FGAISSVLN  1        0.7532
14.5     4.50  0.82     Sequence         WB
```

```
             DRB1_0101  976      FGAISSVLNDILSRL  FGAISSVLN  0        0.6710
35.1    12.00  0.69     Sequence
             DRB1_0101  977      GAISSVLNDILSRLD  ISSVLNDIL  2        0.4265
495.4    60.00  0.46     Sequence
             DRB1_0101  978      AISSVLNDILSRLDK  ISSVLNDIL  1        0.4301
476.4    60.00  0.35     Sequence
             DRB1_0101  979      ISSVLNDILSRLDKV  SVLNDILSR  2        0.4171
548.2    60.00  0.20     Sequence
             DRB1_0101  980      SSVLNDILSRLDKVE  DILSRLDKV  5        0.3879
751.7    65.00  0.32     Sequence
             DRB1_0101  981      SVLNDILSRLDKVEA  DILSRLDKV  4        0.3846
779.0    65.00  0.47     Sequence
             DRB1_0101  982      VLNDILSRLDKVEAE  DILSRLDKV  3        0.3664
949.1    70.00  0.51     Sequence
             DRB1_0101  983      LNDILSRLDKVEAEV  DILSRLDKV  2        0.3561
1060.8    75.00  0.47     Sequence
             DRB1_0101  984      NDILSRLDKVEAEVQ  LSRLDKVEA  3        0.3571
1049.7    75.00  0.38     Sequence
             DRB1_0101  985      DILSRLDKVEAEVQI  LSRLDKVEA  2        0.3383
1286.1    75.00  0.40     Sequence
             DRB1_0101  986      ILSRLDKVEAEVQID  LSRLDKVEA  1        0.3162
1633.1    80.00  0.41     Sequence
             DRB1_0101  987      LSRLDKVEAEVQIDR  LDKVEAEVQ  3        0.3040
1863.6    85.00  0.39     Sequence
             DRB1_0101  988      SRLDKVEAEVQIDRL  LDKVEAEVQ  2        0.2998
1950.7    85.00  0.36     Sequence
             DRB1_0101  989      RLDKVEAEVQIDRLI  DKVEAEVQI  2        0.2986
1975.7    85.00  0.31     Sequence
             DRB1_0101  990      LDKVEAEVQIDRLIT  DKVEAEVQI  1        0.2713
2655.1    90.00  0.22     Sequence
             DRB1_0101  991      DKVEAEVQIDRLITG  AEVQIDRLI  4        0.2453
3517.5    90.00  0.22     Sequence
             DRB1_0101  992      KVEAEVQIDRLITGR  AEVQIDRLI  3        0.2495
3360.7    90.00  0.28     Sequence
             DRB1_0101  993      VEAEVQIDRLITGRL  IDRLITGRL  6        0.5494
131.0    31.00  0.77     Sequence
             DRB1_0101  994      EAEVQIDRLITGRLQ  IDRLITGRL  5        0.6552
41.7    14.00  0.75     Sequence
             DRB1_0101  995      AEVQIDRLITGRLQS  IDRLITGRL  4        0.6991
25.9     9.00  0.76     Sequence         WB
             DRB1_0101  996      EVQIDRLITGRLQSL  IDRLITGRL  3        0.7562
14.0     4.50  0.63     Sequence         WB
             DRB1_0101  997      VQIDRLITGRLQSLQ  IDRLITGRL  2        0.7760
11.3     3.50  0.53     Sequence         WB
             DRB1_0101  998      QIDRLITGRLQSLQT  IDRLITGRL  1        0.7844
10.3     3.00  0.41     Sequence         WB
             DRB1_0101  999      IDRLITGRLQSLQTY  LITGRLQSL  3        0.7946
9.2     2.50  0.30     Sequence         WB
             DRB1_0101 1000      DRLITGRLQSLQTYV  LITGRLQSL  2        0.7264
19.3     6.50  0.32     Sequence         WB
             DRB1_0101 1001      RLITGRLQSLQTYVT  LQSLQTYVT  6        0.7913
9.6     2.50  0.47     Sequence         WB
             DRB1_0101 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.8329
6.1     1.00  0.69     Sequence         SB
             DRB1_0101 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.8523
4.9     0.60  0.81     Sequence         SB
             DRB1_0101 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.8638
4.4     0.40  0.86     Sequence         SB
             DRB1_0101 1005      GRLQSLQTYVTQQLI  LQSLQTYVT  2        0.8386
5.7     0.90  0.88     Sequence         SB
             DRB1_0101 1006      RLQSLQTYVTQQLIR  LQSLQTYVT  1        0.8025
8.5     2.00  0.84     Sequence         WB
             DRB1_0101 1007      LQSLQTYVTQQLIRA  YVTQQLIRA  6        0.7881
9.9     3.00  0.49     Sequence         WB
             DRB1_0101 1008      QSLQTYVTQQLIRAA  YVTQQLIRA  5        0.8351
6.0     0.90  0.76     Sequence         SB
```

```
             DRB1_0101 1009      SLQTYVTQQLIRAAE  YVTQQLIRA  4        0.8532
4.9     0.60  0.77     Sequence         SB
             DRB1_0101 1010      LQTYVTQQLIRAAEI  YVTQQLIRA  3        0.8745
3.9     0.30  0.74     Sequence         SB
             DRB1_0101 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.8673
4.2     0.40  0.73     Sequence         SB
             DRB1_0101 1012      TYVTQQLIRAAEIRA  YVTQQLIRA  1        0.8219
6.9     1.30  0.67     Sequence         SB
             DRB1_0101 1013      YVTQQLIRAAEIRAS  YVTQQLIRA  0        0.7539
14.3     4.50  0.34     Sequence         WB
             DRB1_0101 1014      VTQQLIRAAEIRASA  QQLIRAAEI  2        0.7319
18.2     6.00  0.29     Sequence         WB
             DRB1_0101 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.7444
15.9     5.50  0.35     Sequence         WB
             DRB1_0101 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.7378
17.1     6.00  0.42     Sequence         WB
             DRB1_0101 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.6556
41.5    14.00  0.50     Sequence
             DRB1_0101 1018      LIRAAEIRASANLAA  EIRASANLA  5        0.6443
46.9    16.00  0.42     Sequence
             DRB1_0101 1019      IRAAEIRASANLAAI  EIRASANLA  4        0.6665
36.9    13.00  0.51     Sequence
             DRB1_0101 1020      RAAEIRASANLAAIK  EIRASANLA  3        0.7085
23.4     8.00  0.53     Sequence         WB
             DRB1_0101 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.7088
23.4     8.00  0.47     Sequence         WB
             DRB1_0101 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.6869
29.6    11.00  0.44     Sequence
             DRB1_0101 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.6216
60.0    19.00  0.45     Sequence
             DRB1_0101 1024      IRASANLAAIKMSEC  SANLAAIKM  3        0.5170
186.0    38.00  0.44     Sequence
             DRB1_0101 1025      RASANLAAIKMSECV  SANLAAIKM  2        0.4653
325.3    48.00  0.56     Sequence
             DRB1_0101 1026      ASANLAAIKMSECVL  SANLAAIKM  1        0.4536
369.5    55.00  0.39     Sequence
             DRB1_0101 1027      SANLAAIKMSECVLG  IKMSECVLG  6        0.4785
282.0    45.00  0.31     Sequence
             DRB1_0101 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.5020
218.8    41.00  0.50     Sequence
             DRB1_0101 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.5125
195.4    39.00  0.59     Sequence
             DRB1_0101 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.5187
182.6    37.00  0.70     Sequence
             DRB1_0101 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.4876
255.6    44.00  0.74     Sequence
             DRB1_0101 1032      AIKMSECVLGQSKRV  CVLGQSKRV  6        0.6138
65.3    20.00  0.59     Sequence
             DRB1_0101 1033      IKMSECVLGQSKRVD  CVLGQSKRV  5        0.6542
42.1    15.00  0.78     Sequence
             DRB1_0101 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.6872
29.5    11.00  0.88     Sequence
             DRB1_0101 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.6844
30.4    11.00  0.89     Sequence
             DRB1_0101 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.6634
38.2    13.00  0.88     Sequence
             DRB1_0101 1037      ECVLGQSKRVDFCGK  CVLGQSKRV  1        0.6176
62.7    20.00  0.88     Sequence
             DRB1_0101 1038      CVLGQSKRVDFCGKG  CVLGQSKRV  0        0.5114
197.7    39.00  0.79     Sequence
             DRB1_0101 1039      VLGQSKRVDFCGKGY  SKRVDFCGK  4        0.1587
8974.8   100.00  0.20     Sequence
             DRB1_0101 1040      LGQSKRVDFCGKGYH  SKRVDFCGK  3        0.1615
8714.4   100.00  0.24     Sequence
             DRB1_0101 1041      GQSKRVDFCGKGYHL  DFCGKGYHL  6        0.3557
1065.6    75.00  0.65     Sequence
```

```
             DRB1_0101 1042      QSKRVDFCGKGYHLM  DFCGKGYHL  5        0.5145
191.1    38.00  0.58     Sequence
             DRB1_0101 1043      SKRVDFCGKGYHLMS  DFCGKGYHL  4        0.5619
114.5    29.00  0.59     Sequence
             DRB1_0101 1044      KRVDFCGKGYHLMSF  DFCGKGYHL  3        0.5899
84.5    24.00  0.58     Sequence
             DRB1_0101 1045      RVDFCGKGYHLMSFP  DFCGKGYHL  2        0.5592
117.8    30.00  0.58     Sequence
             DRB1_0101 1046      VDFCGKGYHLMSFPQ  DFCGKGYHL  1        0.5221
176.1    37.00  0.49     Sequence
             DRB1_0101 1047      DFCGKGYHLMSFPQS  YHLMSFPQS  6        0.7112
22.7     8.00  0.62     Sequence         WB
             DRB1_0101 1048      FCGKGYHLMSFPQSA  YHLMSFPQS  5        0.8003
8.7     2.00  0.75     Sequence         WB
             DRB1_0101 1049      CGKGYHLMSFPQSAP  YHLMSFPQS  4        0.8087
7.9     1.70  0.75     Sequence         SB
             DRB1_0101 1050      GKGYHLMSFPQSAPH  YHLMSFPQS  3        0.8264
6.5     1.20  0.76     Sequence         SB
             DRB1_0101 1051      KGYHLMSFPQSAPHG  YHLMSFPQS  2        0.8223
6.8     1.30  0.76     Sequence         SB
             DRB1_0101 1052      GYHLMSFPQSAPHGV  YHLMSFPQS  1        0.7802
10.8     3.00  0.75     Sequence         WB
             DRB1_0101 1053      YHLMSFPQSAPHGVV  YHLMSFPQS  0        0.7088
23.4     8.00  0.64     Sequence         WB
             DRB1_0101 1054      HLMSFPQSAPHGVVF  FPQSAPHGV  4        0.5051
211.7    40.00  0.68     Sequence
             DRB1_0101 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.5210
178.1    37.00  0.79     Sequence
             DRB1_0101 1056      MSFPQSAPHGVVFLH  FPQSAPHGV  2        0.5013
220.6    41.00  0.75     Sequence
             DRB1_0101 1057      SFPQSAPHGVVFLHV  FPQSAPHGV  1        0.4825
270.1    45.00  0.56     Sequence
             DRB1_0101 1058      FPQSAPHGVVFLHVT  FPQSAPHGV  0        0.4306
473.9    60.00  0.28     Sequence
             DRB1_0101 1059      PQSAPHGVVFLHVTY  PHGVVFLHV  4        0.3869
760.3    65.00  0.38     Sequence
             DRB1_0101 1060      QSAPHGVVFLHVTYV  VVFLHVTYV  6        0.5137
192.8    38.00  0.49     Sequence
             DRB1_0101 1061      SAPHGVVFLHVTYVP  VVFLHVTYV  5        0.5251
170.4    36.00  0.56     Sequence
             DRB1_0101 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.6554
41.6    14.00  0.44     Sequence
             DRB1_0101 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.7083
23.5     8.00  0.52     Sequence         WB
             DRB1_0101 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.7029
24.9     8.50  0.55     Sequence         WB
             DRB1_0101 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.7067
23.9     8.50  0.60     Sequence         WB
             DRB1_0101 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.6828
30.9    11.00  0.59     Sequence
             DRB1_0101 1067      VFLHVTYVPAQEKNF  FLHVTYVPA  1        0.6481
45.0    15.00  0.56     Sequence
             DRB1_0101 1068      FLHVTYVPAQEKNFT  VTYVPAQEK  3        0.5947
80.3    23.00  0.40     Sequence
             DRB1_0101 1069      LHVTYVPAQEKNFTT  VTYVPAQEK  2        0.4784
282.3    45.00  0.56     Sequence
             DRB1_0101 1070      HVTYVPAQEKNFTTA  VTYVPAQEK  1        0.4646
328.1    48.00  0.45     Sequence
             DRB1_0101 1071      VTYVPAQEKNFTTAP  YVPAQEKNF  2        0.3987
668.9    65.00  0.34     Sequence
             DRB1_0101 1072      TYVPAQEKNFTTAPA  YVPAQEKNF  1        0.3258
1472.3    80.00  0.41     Sequence
             DRB1_0101 1073      YVPAQEKNFTTAPAI  PAQEKNFTT  2        0.3026
1892.3    85.00  0.31     Sequence
             DRB1_0101 1074      VPAQEKNFTTAPAIC  KNFTTAPAI  5        0.3337
1352.5    80.00  0.32     Sequence
```

```
             DRB1_0101 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.6314
53.9    18.00  0.81     Sequence
             DRB1_0101 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.7059
24.1      8.50  0.89     Sequence         WB
             DRB1_0101 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.7400
16.7      5.50  0.89     Sequence         WB
             DRB1_0101 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.7656
12.6      4.00  0.90     Sequence         WB
             DRB1_0101 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.7506
14.9      5.00  0.90     Sequence         WB
             DRB1_0101 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.6587
40.1    14.00  0.92     Sequence
             DRB1_0101 1081      FTTAPAICHDGKAHF  FTTAPAICH  0        0.5028
217.0    40.00  0.78     Sequence
             DRB1_0101 1082      TTAPAICHDGKAHFP  AICHDGKAH  4        0.2350
3932.3    95.00  0.24     Sequence
             DRB1_0101 1083      TAPAICHDGKAHFPR  CHDGKAHFP  5        0.2658
2819.2    90.00  0.26     Sequence
             DRB1_0101 1084      APAICHDGKAHFPRE  CHDGKAHFP  4        0.2566
3113.1    90.00  0.31     Sequence
             DRB1_0101 1085      PAICHDGKAHFPREG  CHDGKAHFP  3        0.2495
3362.0    90.00  0.36     Sequence
             DRB1_0101 1086      AICHDGKAHFPREGV  CHDGKAHFP  2        0.2402
3716.5    95.00  0.38     Sequence
             DRB1_0101 1087      ICHDGKAHFPREGVF  CHDGKAHFP  1        0.2197
4639.9    95.00  0.40     Sequence
             DRB1_0101 1088      CHDGKAHFPREGVFV  HFPREGVFV  6        0.2844
2303.4    85.00  0.49     Sequence
             DRB1_0101 1089      HDGKAHFPREGVFVS  HFPREGVFV  5        0.3625
989.7    70.00  0.54     Sequence
             DRB1_0101 1090      DGKAHFPREGVFVSN  HFPREGVFV  4        0.4001
659.2    65.00  0.55     Sequence
             DRB1_0101 1091      GKAHFPREGVFVSNG  HFPREGVFV  3        0.4154
558.6    60.00  0.56     Sequence
             DRB1_0101 1092      KAHFPREGVFVSNGT  HFPREGVFV  2        0.4032
637.3    65.00  0.56     Sequence
             DRB1_0101 1093      AHFPREGVFVSNGTH  HFPREGVFV  1        0.3473
1166.3    75.00  0.48     Sequence
             DRB1_0101 1094      HFPREGVFVSNGTHW  FPREGVFVS  1        0.2936
2087.2    85.00  0.28     Sequence
             DRB1_0101 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6        0.3194
1577.3    80.00  0.36     Sequence
             DRB1_0101 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.3944
700.7    65.00  0.43     Sequence
             DRB1_0101 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.4310
471.6    60.00  0.45     Sequence
             DRB1_0101 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.4348
452.7    55.00  0.51     Sequence
             DRB1_0101 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.4261
497.6    60.00  0.50     Sequence
             DRB1_0101 1100      VFVSNGTHWFVTQRN  FVSNGTHWF  1        0.3850
775.9    65.00  0.47     Sequence
             DRB1_0101 1101      FVSNGTHWFVTQRNF  FVSNGTHWF  0        0.3239
1503.4    80.00  0.32     Sequence
             DRB1_0101 1102      VSNGTHWFVTQRNFY  THWFVTQRN  4        0.2943
2070.2    85.00  0.34     Sequence
             DRB1_0101 1103      SNGTHWFVTQRNFYE  FVTQRNFYE  6        0.6124
66.3    20.00  0.85     Sequence
             DRB1_0101 1104      NGTHWFVTQRNFYEP  FVTQRNFYE  5        0.6670
36.7    13.00  0.90     Sequence
             DRB1_0101 1105      GTHWFVTQRNFYEPQ  FVTQRNFYE  4        0.6964
26.7      9.50  0.92     Sequence         WB
             DRB1_0101 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3        0.7118
22.6      8.00  0.94     Sequence         WB
             DRB1_0101 1107      HWFVTQRNFYEPQII  FVTQRNFYE  2        0.6824
31.1    11.00  0.93     Sequence
```

```
             DRB1_0101 1108      WFVTQRNFYEPQIIT  FVTQRNFYE  1        0.6274
56.4    18.00  0.88     Sequence
             DRB1_0101 1109      FVTQRNFYEPQIITT  FVTQRNFYE  0        0.5460
136.0    32.00  0.64     Sequence
             DRB1_0101 1110      VTQRNFYEPQIITTD  FYEPQIITT  5        0.3775
841.8    70.00  0.47     Sequence
             DRB1_0101 1111      TQRNFYEPQIITTDN  FYEPQIITT  4        0.4205
528.8    60.00  0.47     Sequence
             DRB1_0101 1112      QRNFYEPQIITTDNT  FYEPQIITT  3        0.4334
459.8    55.00  0.47     Sequence
             DRB1_0101 1113      RNFYEPQIITTDNTF  YEPQIITTD  3        0.4218
521.0    60.00  0.35     Sequence
             DRB1_0101 1114      NFYEPQIITTDNTFV  IITTDNTFV  6        0.4327
463.2    55.00  0.38     Sequence
             DRB1_0101 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.4587
349.4    50.00  0.66     Sequence
             DRB1_0101 1116      YEPQIITTDNTFVSG  IITTDNTFV  4        0.4687
313.6    48.00  0.84     Sequence
             DRB1_0101 1117      EPQIITTDNTFVSGN  IITTDNTFV  3        0.4823
270.7    45.00  0.85     Sequence
             DRB1_0101 1118      PQIITTDNTFVSGNC  IITTDNTFV  2        0.4630
333.8    49.00  0.86     Sequence
             DRB1_0101 1119      QIITTDNTFVSGNCD  IITTDNTFV  1        0.4130
572.9    60.00  0.81     Sequence
             DRB1_0101 1120      IITTDNTFVSGNCDV  IITTDNTFV  0        0.2736
2591.6    90.00  0.61     Sequence
             DRB1_0101 1121      ITTDNTFVSGNCDVV  FVSGNCDVV  6        0.2871
2237.6    85.00  0.59     Sequence
             DRB1_0101 1122      TTDNTFVSGNCDVVI  FVSGNCDVV  5        0.3805
814.3    70.00  0.65     Sequence
             DRB1_0101 1123      TDNTFVSGNCDVVIG  FVSGNCDVV  4        0.4152
559.5    60.00  0.71     Sequence
             DRB1_0101 1124      DNTFVSGNCDVVIGI  FVSGNCDVV  3        0.4396
429.8    55.00  0.70     Sequence
             DRB1_0101 1125      NTFVSGNCDVVIGIV  FVSGNCDVV  2        0.4382
436.6    55.00  0.67     Sequence
             DRB1_0101 1126      TFVSGNCDVVIGIVN  FVSGNCDVV  1        0.4184
540.9    60.00  0.57     Sequence
             DRB1_0101 1127      FVSGNCDVVIGIVNN  FVSGNCDVV  0        0.3624
991.0    70.00  0.37     Sequence
             DRB1_0101 1128      VSGNCDVVIGIVNNT  CDVVIGIVN  4        0.2848
2294.2    85.00  0.41     Sequence
             DRB1_0101 1129      SGNCDVVIGIVNNTV  VIGIVNNTV  6        0.3836
787.8    70.00  0.47     Sequence
             DRB1_0101 1130      GNCDVVIGIVNNTVY  VIGIVNNTV  5        0.5011
221.0    41.00  0.63     Sequence
             DRB1_0101 1131      NCDVVIGIVNNTVYD  VIGIVNNTV  4        0.5331
156.4    34.00  0.62     Sequence
             DRB1_0101 1132      CDVVIGIVNNTVYDP  VIGIVNNTV  3        0.5132
193.9    38.00  0.62     Sequence
             DRB1_0101 1133      DVVIGIVNNTVYDPL  VIGIVNNTV  2        0.5069
207.4    40.00  0.62     Sequence
             DRB1_0101 1134      VVIGIVNNTVYDPLQ  VIGIVNNTV  1        0.4775
285.3    46.00  0.57     Sequence
             DRB1_0101 1135      VIGIVNNTVYDPLQP  VIGIVNNTV  0        0.3700
912.9    70.00  0.43     Sequence
             DRB1_0101 1136      IGIVNNTVYDPLQPE  IGIVNNTVY  0        0.2510
3309.2    90.00  0.26     Sequence
             DRB1_0101 1137      GIVNNTVYDPLQPEL  TVYDPLQPE  5        0.2153
4867.8    95.00  0.24     Sequence
             DRB1_0101 1138      IVNNTVYDPLQPELD  YDPLQPELD  6        0.3314
1386.4    80.00  0.60     Sequence
             DRB1_0101 1139      VNNTVYDPLQPELDS  YDPLQPELD  5        0.4084
602.4    60.00  0.74     Sequence
             DRB1_0101 1140      NNTVYDPLQPELDSF  YDPLQPELD  4        0.4549
364.2    50.00  0.79     Sequence
```

```
             DRB1_0101 1141      NTVYDPLQPELDSFK  YDPLQPELD  3        0.4875
256.0    44.00  0.82     Sequence
             DRB1_0101 1142      TVYDPLQPELDSFKE  YDPLQPELD  2        0.4659
323.3    48.00  0.81     Sequence
             DRB1_0101 1143      VYDPLQPELDSFKEE  YDPLQPELD  1        0.4200
531.2    60.00  0.79     Sequence
             DRB1_0101 1144      YDPLQPELDSFKEEL  YDPLQPELD  0        0.3172
1616.2    80.00  0.57     Sequence
             DRB1_0101 1145      DPLQPELDSFKEELD  LQPELDSFK  2        0.1724
7738.6   100.00  0.49     Sequence
             DRB1_0101 1146      PLQPELDSFKEELDK  LQPELDSFK  1        0.1614
8718.3   100.00  0.44     Sequence
             DRB1_0101 1147      LQPELDSFKEELDKY  LDSFKEELD  4        0.1315
12055.8   100.00  0.31     Sequence
             DRB1_0101 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.1768
7379.9   100.00  0.51     Sequence
             DRB1_0101 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.2301
4145.6    95.00  0.69     Sequence
             DRB1_0101 1150      ELDSFKEELDKYFKN  FKEELDKYF  4        0.2602
2995.8    90.00  0.71     Sequence
             DRB1_0101 1151      LDSFKEELDKYFKNH  FKEELDKYF  3        0.2750
2551.2    90.00  0.72     Sequence
             DRB1_0101 1152      DSFKEELDKYFKNHT  FKEELDKYF  2        0.2568
3107.6    90.00  0.68     Sequence
             DRB1_0101 1153      SFKEELDKYFKNHTS  FKEELDKYF  1        0.2490
3378.6    90.00  0.51     Sequence
             DRB1_0101 1154      FKEELDKYFKNHTSP  DKYFKNHTS  5        0.2288
4206.6    95.00  0.30     Sequence
             DRB1_0101 1155      KEELDKYFKNHTSPD  DKYFKNHTS  4        0.2147
4900.5    95.00  0.44     Sequence
             DRB1_0101 1156      EELDKYFKNHTSPDV  FKNHTSPDV  6        0.4753
292.0    46.00  0.75     Sequence
             DRB1_0101 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.5914
83.1    24.00  0.82     Sequence
             DRB1_0101 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.6670
36.7    13.00  0.82     Sequence
             DRB1_0101 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.6791
32.2    11.00  0.85     Sequence
             DRB1_0101 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.6654
37.3    13.00  0.88     Sequence
             DRB1_0101 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.5548
123.6    30.00  0.89     Sequence
             DRB1_0101 1162      FKNHTSPDVDLGDIS  FKNHTSPDV  0        0.3682
930.6    70.00  0.80     Sequence
             DRB1_0101 1163      KNHTSPDVDLGDISG  NHTSPDVDL  1        0.1118
14917.0   100.00  0.41     Sequence
             DRB1_0101 1164      NHTSPDVDLGDISGI  VDLGDISGI  6        0.1628
8585.9   100.00  0.42     Sequence
             DRB1_0101 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.2031
5554.8    95.00  0.56     Sequence
             DRB1_0101 1166      TSPDVDLGDISGINA  LGDISGINA  6        0.3144
1666.6    80.00  0.44     Sequence
             DRB1_0101 1167      SPDVDLGDISGINAS  LGDISGINA  5        0.3908
728.9    65.00  0.55     Sequence
             DRB1_0101 1168      PDVDLGDISGINASF  LGDISGINA  4        0.4248
504.5    60.00  0.61     Sequence
             DRB1_0101 1169      DVDLGDISGINASFV  ISGINASFV  6        0.5426
141.0    33.00  0.40     Sequence
             DRB1_0101 1170      VDLGDISGINASFVN  ISGINASFV  5        0.5920
82.7    24.00  0.56     Sequence
             DRB1_0101 1171      DLGDISGINASFVNI  ISGINASFV  4        0.6054
71.5    22.00  0.65     Sequence
             DRB1_0101 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.6105
67.6    21.00  0.73     Sequence
             DRB1_0101 1173      GDISGINASFVNIQK  ISGINASFV  2        0.5857
88.5    25.00  0.73     Sequence
```

```
             DRB1_0101 1174      DISGINASFVNIQKE  ISGINASFV  1        0.5484
132.5    32.00  0.72     Sequence
             DRB1_0101 1175      ISGINASFVNIQKEI  ISGINASFV  0        0.4747
293.9    46.00  0.57     Sequence
             DRB1_0101 1176      SGINASFVNIQKEID  INASFVNIQ  2        0.3040
1864.2    85.00  0.38     Sequence
             DRB1_0101 1177      GINASFVNIQKEIDR  FVNIQKEID  5        0.2950
2055.4    85.00  0.32     Sequence
             DRB1_0101 1178      INASFVNIQKEIDRL  FVNIQKEID  4        0.3187
1590.6    80.00  0.43     Sequence
             DRB1_0101 1179      NASFVNIQKEIDRLN  FVNIQKEID  3        0.3387
1280.6    75.00  0.44     Sequence
             DRB1_0101 1180      ASFVNIQKEIDRLNE  FVNIQKEID  2        0.3322
1374.1    80.00  0.36     Sequence
             DRB1_0101 1181      SFVNIQKEIDRLNEV  FVNIQKEID  1        0.3195
1576.3    80.00  0.27     Sequence
             DRB1_0101 1182      FVNIQKEIDRLNEVA  NIQKEIDRL  2        0.2812
2384.8    85.00  0.28     Sequence
             DRB1_0101 1183      VNIQKEIDRLNEVAK  IQKEIDRLN  2        0.2541
3198.8    90.00  0.28     Sequence
             DRB1_0101 1184      NIQKEIDRLNEVAKN  IDRLNEVAK  5        0.2633
2894.8    90.00  0.34     Sequence
             DRB1_0101 1185      IQKEIDRLNEVAKNL  IDRLNEVAK  4        0.2927
2107.6    85.00  0.42     Sequence
             DRB1_0101 1186      QKEIDRLNEVAKNLN  IDRLNEVAK  3        0.3066
1813.2    85.00  0.44     Sequence
             DRB1_0101 1187      KEIDRLNEVAKNLNE  IDRLNEVAK  2        0.2873
2233.2    85.00  0.38     Sequence
             DRB1_0101 1188      EIDRLNEVAKNLNES  RLNEVAKNL  3        0.2545
3185.9    90.00  0.31     Sequence
             DRB1_0101 1189      IDRLNEVAKNLNESL  VAKNLNESL  6        0.2985
1979.5    85.00  0.43     Sequence
             DRB1_0101 1190      DRLNEVAKNLNESLI  VAKNLNESL  5        0.3782
835.3    70.00  0.68     Sequence
             DRB1_0101 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.4053
623.3    65.00  0.68     Sequence
             DRB1_0101 1192      LNEVAKNLNESLIDL  VAKNLNESL  3        0.4544
366.2    55.00  0.69     Sequence
             DRB1_0101 1193      NEVAKNLNESLIDLQ  VAKNLNESL  2        0.4434
412.3    55.00  0.60     Sequence
             DRB1_0101 1194      EVAKNLNESLIDLQE  VAKNLNESL  1        0.4060
618.5    65.00  0.49     Sequence
             DRB1_0101 1195      VAKNLNESLIDLQEL  VAKNLNESL  0        0.3526
1102.2    75.00  0.27     Sequence
             DRB1_0101 1196      AKNLNESLIDLQELG  LNESLIDLQ  3        0.2908
2150.6    85.00  0.32     Sequence
             DRB1_0101 1197      KNLNESLIDLQELGK  LNESLIDLQ  2        0.2682
2745.4    90.00  0.31     Sequence
             DRB1_0101 1198      NLNESLIDLQELGKY  ESLIDLQEL  3        0.2846
2299.3    85.00  0.25     Sequence
             DRB1_0101 1199      LNESLIDLQELGKYE  IDLQELGKY  5        0.2808
2394.9    85.00  0.30     Sequence
             DRB1_0101 1200      NESLIDLQELGKYEQ  IDLQELGKY  4        0.2900
2169.0    85.00  0.30     Sequence
             DRB1_0101 1201      ESLIDLQELGKYEQY  IDLQELGKY  3        0.2899
2171.4    85.00  0.35     Sequence
             DRB1_0101 1202      SLIDLQELGKYEQYI  IDLQELGKY  2        0.2931
2097.5    85.00  0.35     Sequence
             DRB1_0101 1203      LIDLQELGKYEQYIK  ELGKYEQYI  5        0.2717
2644.0    90.00  0.25     Sequence
             DRB1_0101 1204      IDLQELGKYEQYIKW  ELGKYEQYI  4        0.2868
2246.5    85.00  0.31     Sequence
             DRB1_0101 1205      DLQELGKYEQYIKWP  GKYEQYIKW  5        0.2704
2680.6    90.00  0.35     Sequence
             DRB1_0101 1206      LQELGKYEQYIKWPW  GKYEQYIKW  4        0.2812
2387.0    85.00  0.40     Sequence
```

```
             DRB1_0101 1207      QELGKYEQYIKWPWY  GKYEQYIKW  3        0.2894
2182.5    85.00  0.44     Sequence
             DRB1_0101 1208      ELGKYEQYIKWPWYI  GKYEQYIKW  2        0.3353
1328.5    75.00  0.31     Sequence
             DRB1_0101 1209      LGKYEQYIKWPWYIW  QYIKWPWYI  5        0.3782
835.1    70.00  0.37     Sequence
             DRB1_0101 1210      GKYEQYIKWPWYIWL  QYIKWPWYI  4        0.4143
565.4    60.00  0.38     Sequence
             DRB1_0101 1211      KYEQYIKWPWYIWLG  QYIKWPWYI  3        0.4125
576.2    60.00  0.41     Sequence
             DRB1_0101 1212      YEQYIKWPWYIWLGF  QYIKWPWYI  2        0.3954
693.6    65.00  0.37     Sequence
             DRB1_0101 1213      EQYIKWPWYIWLGFI  IKWPWYIWL  3        0.3913
725.0    65.00  0.32     Sequence
             DRB1_0101 1214      QYIKWPWYIWLGFIA  IKWPWYIWL  2        0.3813
807.7    70.00  0.26     Sequence
             DRB1_0101 1215      YIKWPWYIWLGFIAG  YIWLGFIAG  6        0.4227
516.3    60.00  0.42     Sequence
             DRB1_0101 1216      IKWPWYIWLGFIAGL  YIWLGFIAG  5        0.4666
321.1    48.00  0.45     Sequence
             DRB1_0101 1217      KWPWYIWLGFIAGLI  YIWLGFIAG  4        0.5189
182.2    37.00  0.34     Sequence
             DRB1_0101 1218      WPWYIWLGFIAGLIA  WLGFIAGLI  5        0.5881
86.2    24.00  0.28     Sequence
             DRB1_0101 1219      PWYIWLGFIAGLIAI  WLGFIAGLI  4        0.5969
78.4    23.00  0.26     Sequence
             DRB1_0101 1220      WYIWLGFIAGLIAIV  LGFIAGLIA  4        0.6142
65.0    20.00  0.26     Sequence
             DRB1_0101 1221      YIWLGFIAGLIAIVM  FIAGLIAIV  5        0.6112
67.2    21.00  0.22     Sequence
             DRB1_0101 1222      IWLGFIAGLIAIVMV  FIAGLIAIV  4        0.5634
112.6    29.00  0.29     Sequence
             DRB1_0101 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3        0.5130
194.3    38.00  0.35     Sequence
             DRB1_0101 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.4471
396.5    55.00  0.51     Sequence
             DRB1_0101 1225      GFIAGLIAIVMVTIM  FIAGLIAIV  1        0.4027
640.7    65.00  0.52     Sequence
             DRB1_0101 1226      FIAGLIAIVMVTIML  FIAGLIAIV  0        0.3375
1298.0    75.00  0.27     Sequence
             DRB1_0101 1227      IAGLIAIVMVTIMLC  IAGLIAIVM  0        0.2495
3362.6    90.00  0.22     Sequence
             DRB1_0101 1228      AGLIAIVMVTIMLCC  IAIVMVTIM  3        0.2171
4773.1    95.00  0.28     Sequence
             DRB1_0101 1229      GLIAIVMVTIMLCCM  MVTIMLCCM  6        0.2221
4524.1    95.00  0.25     Sequence
             DRB1_0101 1230      LIAIVMVTIMLCCMT  MVTIMLCCM  5        0.2290
4196.3    95.00  0.34     Sequence
             DRB1_0101 1231      IAIVMVTIMLCCMTS  MVTIMLCCM  4        0.2725
2619.8    90.00  0.34     Sequence
             DRB1_0101 1232      AIVMVTIMLCCMTSC  MVTIMLCCM  3        0.2924
2113.1    85.00  0.34     Sequence
             DRB1_0101 1233      IVMVTIMLCCMTSCC  MVTIMLCCM  2        0.2948
2059.6    85.00  0.29     Sequence
             DRB1_0101 1234      VMVTIMLCCMTSCCS  LCCMTSCCS  6        0.3582
1037.1    75.00  0.31     Sequence
             DRB1_0101 1235      MVTIMLCCMTSCCSC  LCCMTSCCS  5        0.3707
906.0    70.00  0.38     Sequence
             DRB1_0101 1236      VTIMLCCMTSCCSCL  LCCMTSCCS  4        0.4102
590.5    60.00  0.39     Sequence
             DRB1_0101 1237      TIMLCCMTSCCSCLK  LCCMTSCCS  3        0.4502
383.3    55.00  0.38     Sequence
             DRB1_0101 1238      IMLCCMTSCCSCLKG  LCCMTSCCS  2        0.4416
420.8    55.00  0.37     Sequence
             DRB1_0101 1239      MLCCMTSCCSCLKGC  LCCMTSCCS  1        0.4160
554.7    60.00  0.34     Sequence
```

```
             DRB1_0101 1240      LCCMTSCCSCLKGCC  CMTSCCSCL  2        0.3697
915.5    70.00  0.42     Sequence
             DRB1_0101 1241      CCMTSCCSCLKGCCS  CSCLKGCCS  6        0.4331
460.9    55.00  0.50     Sequence
             DRB1_0101 1242      CMTSCCSCLKGCCSC  CSCLKGCCS  5        0.4391
432.0    55.00  0.68     Sequence
             DRB1_0101 1243      MTSCCSCLKGCCSCG  CSCLKGCCS  4        0.4450
405.4    55.00  0.75     Sequence
             DRB1_0101 1244      TSCCSCLKGCCSCGS  CSCLKGCCS  3        0.4805
276.1    45.00  0.70     Sequence
             DRB1_0101 1245      SCCSCLKGCCSCGSC  CSCLKGCCS  2        0.4757
290.8    46.00  0.63     Sequence
             DRB1_0101 1246      CCSCLKGCCSCGSCC  CSCLKGCCS  1        0.4542
367.1    55.00  0.52     Sequence
             DRB1_0101 1247      CSCLKGCCSCGSCCK  CSCLKGCCS  0        0.4303
475.1    60.00  0.42     Sequence
             DRB1_0101 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2        0.3303
1402.7    80.00  0.36     Sequence
             DRB1_0101 1249      CLKGCCSCGSCCKFD  LKGCCSCGS  1        0.3067
1810.3    80.00  0.35     Sequence
             DRB1_0101 1250      LKGCCSCGSCCKFDE  CSCGSCCKF  4        0.2578
3072.5    90.00  0.24     Sequence
             DRB1_0101 1251      KGCCSCGSCCKFDED  CSCGSCCKF  3        0.2156
4853.6    95.00  0.34     Sequence
             DRB1_0101 1252      GCCSCGSCCKFDEDD  CSCGSCCKF  2        0.1741
7601.7   100.00  0.36     Sequence
             DRB1_0101 1253      CCSCGSCCKFDEDDS  CSCGSCCKF  1        0.1296
12298.2   100.00  0.46     Sequence
             DRB1_0101 1254      CSCGSCCKFDEDDSE  CSCGSCCKF  0        0.0985
17215.1   100.00  0.38     Sequence
             DRB1_0101 1255      SCGSCCKFDEDDSEP  CCKFDEDDS  4        0.0590
26418.3   100.00  0.20     Sequence
             DRB1_0101 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.1732
7672.2   100.00  0.76     Sequence
             DRB1_0101 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.2679
2754.6    90.00  0.82     Sequence
             DRB1_0101 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.3210
1551.2    80.00  0.82     Sequence
             DRB1_0101 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.3484
1152.8    75.00  0.76     Sequence
             DRB1_0101 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.3495
1138.9    75.00  0.68     Sequence
             DRB1_0101 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.3338
1349.7    80.00  0.60     Sequence
             DRB1_0101 1262      FDEDDSEPVLKGVKL  EPVLKGVKL  6        0.3879
751.7    65.00  0.48     Sequence
             DRB1_0101 1263      DEDDSEPVLKGVKLH  EPVLKGVKL  5        0.4725
301.0    47.00  0.67     Sequence
             DRB1_0101 1264      EDDSEPVLKGVKLHY  EPVLKGVKL  4        0.5507
129.2    31.00  0.65     Sequence
             DRB1_0101 1265      DDSEPVLKGVKLHYT  EPVLKGVKL  3        0.6285
55.7    18.00  0.60     Sequence
             DRB1_0301    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.1165
14172.0    95.00  0.54     Sequence
             DRB1_0301    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.1234
13158.2    90.00  0.44     Sequence
             DRB1_0301    3      PIKEMFVFLVLLPLV  FVFLVLLPL  5        0.1243
13032.0    90.00  0.28     Sequence
             DRB1_0301    4      IKEMFVFLVLLPLVS  FVFLVLLPL  4        0.1378
11263.0    90.00  0.33     Sequence
             DRB1_0301    5      KEMFVFLVLLPLVSS  FLVLLPLVS  5        0.1550
9344.8    85.00  0.26     Sequence
             DRB1_0301    6      EMFVFLVLLPLVSSQ  FLVLLPLVS  4        0.1731
7683.3    80.00  0.25     Sequence
             DRB1_0301    7      MFVFLVLLPLVSSQC  VLLPLVSSQ  5        0.1835
6863.9    75.00  0.31     Sequence
```

```
             DRB1_0301    8      FVFLVLLPLVSSQCV  VLLPLVSSQ  4        0.1907
6349.0    70.00  0.32     Sequence
             DRB1_0301    9      VFLVLLPLVSSQCVN  VLLPLVSSQ  3        0.2010
5680.4    70.00  0.34     Sequence
             DRB1_0301   10      FLVLLPLVSSQCVNF  LVSSQCVNF  6        0.2164
4811.3    65.00  0.32     Sequence
             DRB1_0301   11      LVLLPLVSSQCVNFT  LVSSQCVNF  5        0.2326
4035.9    60.00  0.47     Sequence
             DRB1_0301   12      VLLPLVSSQCVNFTN  LVSSQCVNF  4        0.2231
4472.5    60.00  0.57     Sequence
             DRB1_0301   13      LLPLVSSQCVNFTNR  LVSSQCVNF  3        0.2268
4299.2    60.00  0.67     Sequence
             DRB1_0301   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.2201
4618.8    65.00  0.61     Sequence
             DRB1_0301   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.1946
6090.2    70.00  0.49     Sequence
             DRB1_0301   16      LVSSQCVNFTNRTQL  VNFTNRTQL  6        0.2688
2729.1    47.00  0.59     Sequence
             DRB1_0301   17      VSSQCVNFTNRTQLP  VNFTNRTQL  5        0.3007
1932.8    38.00  0.63     Sequence
             DRB1_0301   18      SSQCVNFTNRTQLPS  VNFTNRTQL  4        0.3289
1424.5    32.00  0.66     Sequence
             DRB1_0301   19      SQCVNFTNRTQLPSA  VNFTNRTQL  3        0.3381
1288.8    30.00  0.62     Sequence
             DRB1_0301   20      QCVNFTNRTQLPSAY  VNFTNRTQL  2        0.3044
1855.7    37.00  0.55     Sequence
             DRB1_0301   21      CVNFTNRTQLPSAYT  VNFTNRTQL  1        0.2565
3117.4    50.00  0.43     Sequence
             DRB1_0301   22      VNFTNRTQLPSAYTN  VNFTNRTQL  0        0.1910
6332.4    70.00  0.31     Sequence
             DRB1_0301   23      NFTNRTQLPSAYTNS  NRTQLPSAY  3        0.0941
18066.2    95.00  0.35     Sequence
             DRB1_0301   24      FTNRTQLPSAYTNSF  NRTQLPSAY  2        0.0849
19961.0   100.00  0.36     Sequence
             DRB1_0301   25      TNRTQLPSAYTNSFT  LPSAYTNSF  5        0.0879
19326.4   100.00  0.43     Sequence
             DRB1_0301   26      NRTQLPSAYTNSFTR  LPSAYTNSF  4        0.1089
15392.0    95.00  0.47     Sequence
             DRB1_0301   27      RTQLPSAYTNSFTRG  LPSAYTNSF  3        0.1101
15199.2    95.00  0.43     Sequence
             DRB1_0301   28      TQLPSAYTNSFTRGV  LPSAYTNSF  2        0.1067
15756.1    95.00  0.32     Sequence
             DRB1_0301   29      QLPSAYTNSFTRGVY  AYTNSFTRG  4        0.1243
13034.7    90.00  0.25     Sequence
             DRB1_0301   30      LPSAYTNSFTRGVYY  AYTNSFTRG  3        0.1366
11400.1    90.00  0.20     Sequence
             DRB1_0301   31      PSAYTNSFTRGVYYP  NSFTRGVYY  5        0.1317
12024.9    90.00  0.28     Sequence
             DRB1_0301   32      SAYTNSFTRGVYYPD  NSFTRGVYY  4        0.1339
11742.1    90.00  0.30     Sequence
             DRB1_0301   33      AYTNSFTRGVYYPDK  NSFTRGVYY  3        0.1297
12294.8    90.00  0.34     Sequence
             DRB1_0301   34      YTNSFTRGVYYPDKV  FTRGVYYPD  4        0.1339
11739.5    90.00  0.26     Sequence
             DRB1_0301   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.1786
7237.1    75.00  0.26     Sequence
             DRB1_0301   36      NSFTRGVYYPDKVFR  VYYPDKVFR  6        0.4745
294.7    11.00  0.55     Sequence
             DRB1_0301   37      SFTRGVYYPDKVFRS  YYPDKVFRS  6        0.5924
82.3     4.00  0.54     Sequence         WB
             DRB1_0301   38      FTRGVYYPDKVFRSS  YYPDKVFRS  5        0.6371
50.7     2.50  0.60     Sequence         WB
             DRB1_0301   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.6616
38.9     1.70  0.62     Sequence         SB
             DRB1_0301   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.6540
42.2     1.80  0.67     Sequence         SB
```

```
             DRB1_0301   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.6064
70.7     3.50  0.62     Sequence         WB
             DRB1_0301   42      VYYPDKVFRSSVLHS  YYPDKVFRS  1        0.5197
180.7     7.50  0.50     Sequence         WB
             DRB1_0301   43      YYPDKVFRSSVLHST  VFRSSVLHS  5        0.3634
980.1    25.00  0.63     Sequence
             DRB1_0301   44      YPDKVFRSSVLHSTQ  VFRSSVLHS  4        0.3475
1164.9    28.00  0.79     Sequence
             DRB1_0301   45      PDKVFRSSVLHSTQD  VFRSSVLHS  3        0.3470
1170.4    28.00  0.79     Sequence
             DRB1_0301   46      DKVFRSSVLHSTQDL  VFRSSVLHS  2        0.3257
1474.4    33.00  0.74     Sequence
             DRB1_0301   47      KVFRSSVLHSTQDLF  VLHSTQDLF  6        0.4437
411.3    14.00  0.46     Sequence
             DRB1_0301   48      VFRSSVLHSTQDLFL  VLHSTQDLF  5        0.5272
166.6     7.00  0.61     Sequence         WB
             DRB1_0301   49      FRSSVLHSTQDLFLP  VLHSTQDLF  4        0.5233
173.7     7.00  0.62     Sequence         WB
             DRB1_0301   50      RSSVLHSTQDLFLPF  VLHSTQDLF  3        0.5562
121.7     5.50  0.59     Sequence         WB
             DRB1_0301   51      SSVLHSTQDLFLPFF  VLHSTQDLF  2        0.5334
155.8     6.50  0.52     Sequence         WB
             DRB1_0301   52      SVLHSTQDLFLPFFS  VLHSTQDLF  1        0.4857
261.2    10.00  0.45     Sequence
             DRB1_0301   53      VLHSTQDLFLPFFSN  LHSTQDLFL  1        0.3596
1021.7    26.00  0.29     Sequence
             DRB1_0301   54      LHSTQDLFLPFFSNV  STQDLFLPF  2        0.1656
8331.1    80.00  0.60     Sequence
             DRB1_0301   55      HSTQDLFLPFFSNVT  STQDLFLPF  1        0.1239
13086.4    90.00  0.50     Sequence
             DRB1_0301   56      STQDLFLPFFSNVTW  LFLPFFSNV  4        0.1043
16174.6    95.00  0.31     Sequence
             DRB1_0301   57      TQDLFLPFFSNVTWF  FFSNVTWFX  7        0.1307
12162.6    90.00  0.22     Sequence
             DRB1_0301   58      QDLFLPFFSNVTWFH  FFSNVTWFH  6        0.2337
3987.1    60.00  0.54     Sequence
             DRB1_0301   59      DLFLPFFSNVTWFHA  FFSNVTWFH  5        0.2792
2439.2    44.00  0.59     Sequence
             DRB1_0301   60      LFLPFFSNVTWFHAI  FFSNVTWFH  4        0.3002
1943.1    39.00  0.61     Sequence
             DRB1_0301   61      FLPFFSNVTWFHAIH  FFSNVTWFH  3        0.3015
1914.7    38.00  0.61     Sequence
             DRB1_0301   62      LPFFSNVTWFHAIHV  FFSNVTWFH  2        0.2900
2168.9    41.00  0.55     Sequence
             DRB1_0301   63      PFFSNVTWFHAIHVS  FFSNVTWFH  1        0.2505
3326.7    55.00  0.44     Sequence
             DRB1_0301   64      FFSNVTWFHAIHVSG  VTWFHAIHV  4        0.1959
6004.3    70.00  0.20     Sequence
             DRB1_0301   65      FSNVTWFHAIHVSGT  VTWFHAIHV  3        0.1650
8389.9    80.00  0.28     Sequence
             DRB1_0301   66      SNVTWFHAIHVSGTN  WFHAIHVSG  4        0.1735
7648.8    80.00  0.32     Sequence
             DRB1_0301   67      NVTWFHAIHVSGTNG  FHAIHVSGT  4        0.1643
8447.6    80.00  0.34     Sequence
             DRB1_0301   68      VTWFHAIHVSGTNGT  FHAIHVSGT  3        0.1802
7114.1    75.00  0.28     Sequence
             DRB1_0301   69      TWFHAIHVSGTNGTK  IHVSGTNGT  5        0.1964
5974.6    70.00  0.53     Sequence
             DRB1_0301   70      WFHAIHVSGTNGTKR  IHVSGTNGT  4        0.2824
2355.3    43.00  0.41     Sequence
             DRB1_0301   71      FHAIHVSGTNGTKRF  VSGTNGTKR  5        0.3456
1188.5    29.00  0.50     Sequence
             DRB1_0301   72      HAIHVSGTNGTKRFD  VSGTNGTKR  4        0.3604
1012.5    26.00  0.49     Sequence
             DRB1_0301   73      AIHVSGTNGTKRFDN  VSGTNGTKR  3        0.3561
1061.2    27.00  0.51     Sequence
```

```
             DRB1_0301   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.3068
1809.3    37.00  0.55     Sequence
             DRB1_0301   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.2477
3428.8    55.00  0.56     Sequence
             DRB1_0301   76      VSGTNGTKRFDNPVL  VSGTNGTKR  0        0.1968
5945.1    70.00  0.40     Sequence
             DRB1_0301   77      SGTNGTKRFDNPVLP  KRFDNPVLP  6        0.1994
5782.3    70.00  0.62     Sequence
             DRB1_0301   78      GTNGTKRFDNPVLPF  KRFDNPVLP  5        0.2998
1951.0    39.00  0.52     Sequence
             DRB1_0301   79      TNGTKRFDNPVLPFN  KRFDNPVLP  4        0.3449
1197.3    29.00  0.49     Sequence
             DRB1_0301   80      NGTKRFDNPVLPFND  KRFDNPVLP  3        0.3554
1068.8    27.00  0.47     Sequence
             DRB1_0301   81      GTKRFDNPVLPFNDG  RFDNPVLPF  3        0.3441
1207.7    29.00  0.45     Sequence
             DRB1_0301   82      TKRFDNPVLPFNDGV  RFDNPVLPF  2        0.3047
1849.7    37.00  0.49     Sequence
             DRB1_0301   83      KRFDNPVLPFNDGVY  RFDNPVLPF  1        0.2280
4243.5    60.00  0.47     Sequence
             DRB1_0301   84      RFDNPVLPFNDGVYF  LPFNDGVYF  6        0.2226
4499.2    60.00  0.34     Sequence
             DRB1_0301   85      FDNPVLPFNDGVYFA  PFNDGVYFA  6        0.2906
2155.1    41.00  0.36     Sequence
             DRB1_0301   86      DNPVLPFNDGVYFAS  PFNDGVYFA  5        0.3325
1370.2    31.00  0.43     Sequence
             DRB1_0301   87      NPVLPFNDGVYFAST  PFNDGVYFA  4        0.3506
1126.1    28.00  0.46     Sequence
             DRB1_0301   88      PVLPFNDGVYFASTE  PFNDGVYFA  3        0.3472
1168.6    28.00  0.50     Sequence
             DRB1_0301   89      VLPFNDGVYFASTEK  PFNDGVYFA  2        0.3203
1562.6    34.00  0.50     Sequence
             DRB1_0301   90      LPFNDGVYFASTEKS  PFNDGVYFA  1        0.2908
2150.8    41.00  0.43     Sequence
             DRB1_0301   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.2505
3327.0    55.00  0.44     Sequence
             DRB1_0301   92      FNDGVYFASTEKSNI  VYFASTEKS  4        0.2875
2229.5    42.00  0.47     Sequence
             DRB1_0301   93      NDGVYFASTEKSNII  VYFASTEKS  3        0.3261
1467.0    33.00  0.41     Sequence
             DRB1_0301   94      DGVYFASTEKSNIIR  FASTEKSNI  4        0.3586
1032.2    26.00  0.37     Sequence
             DRB1_0301   95      GVYFASTEKSNIIRG  FASTEKSNI  3        0.3396
1268.9    30.00  0.38     Sequence
             DRB1_0301   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.2786
2455.1    44.00  0.40     Sequence
             DRB1_0301   97      YFASTEKSNIIRGWI  TEKSNIIRG  4        0.2034
5538.7    70.00  0.38     Sequence
             DRB1_0301   98      FASTEKSNIIRGWIF  TEKSNIIRG  3        0.1834
6875.1    75.00  0.44     Sequence
             DRB1_0301   99      ASTEKSNIIRGWIFG  TEKSNIIRG  2        0.1717
7802.5    80.00  0.40     Sequence
             DRB1_0301  100      STEKSNIIRGWIFGT  IIRGWIFGT  6        0.1692
8012.8    80.00  0.41     Sequence
             DRB1_0301  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5        0.1580
9046.8    80.00  0.57     Sequence
             DRB1_0301  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.1592
8934.5    80.00  0.62     Sequence
             DRB1_0301  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3        0.1580
9047.6    80.00  0.62     Sequence
             DRB1_0301  104      SNIIRGWIFGTTLDS  IIRGWIFGT  2        0.1755
7488.7    75.00  0.43     Sequence
             DRB1_0301  105      NIIRGWIFGTTLDSK  IFGTTLDSK  6        0.2941
2073.8    40.00  0.51     Sequence
             DRB1_0301  106      IIRGWIFGTTLDSKT  IFGTTLDSK  5        0.3528
1099.6    27.00  0.61     Sequence
```

```
             DRB1_0301  107      IRGWIFGTTLDSKTQ   IFGTTLDSK  4        0.3818
803.5    22.00  0.62     Sequence
             DRB1_0301  108      RGWIFGTTLDSKTQS   IFGTTLDSK  3        0.4264
496.0    16.00  0.51     Sequence
             DRB1_0301  109      GWIFGTTLDSKTQSL   TTLDSKTQS  5        0.4244
506.4    16.00  0.44     Sequence
             DRB1_0301  110      WIFGTTLDSKTQSLL   TTLDSKTQS  4        0.4194
535.1    17.00  0.54     Sequence
             DRB1_0301  111      IFGTTLDSKTQSLLI   TTLDSKTQS  3        0.3900
735.5    21.00  0.60     Sequence
             DRB1_0301  112      FGTTLDSKTQSLLIV   TTLDSKTQS  2        0.3432
1220.4    29.00  0.64     Sequence
             DRB1_0301  113      GTTLDSKTQSLLIVN   TTLDSKTQS  1        0.3034
1875.6    38.00  0.52     Sequence
             DRB1_0301  114      TTLDSKTQSLLIVNN   TTLDSKTQS  0        0.2367
3862.3    60.00  0.31     Sequence
             DRB1_0301  115      TLDSKTQSLLIVNNA   DSKTQSLLI  2        0.1512
9738.5    85.00  0.36     Sequence
             DRB1_0301  116      LDSKTQSLLIVNNAT   DSKTQSLLI  1        0.0948
17924.5    95.00  0.38     Sequence
             DRB1_0301  117      DSKTQSLLIVNNATN   LIVNNATNX  7        0.0782
21460.4   100.00  0.19     Sequence
             DRB1_0301  118      SKTQSLLIVNNATNV   LIVNNATNV  6        0.2133
4976.1    65.00  0.64     Sequence
             DRB1_0301  119      KTQSLLIVNNATNVV   LIVNNATNV  5        0.3268
1455.9    32.00  0.55     Sequence
             DRB1_0301  120      TQSLLIVNNATNVVI   LIVNNATNV  4        0.3885
747.5    21.00  0.46     Sequence
             DRB1_0301  121      QSLLIVNNATNVVIK   IVNNATNVV  4        0.4355
449.4    15.00  0.46     Sequence
             DRB1_0301  122      SLLIVNNATNVVIKV   IVNNATNVV  3        0.4333
460.1    15.00  0.46     Sequence
             DRB1_0301  123      LLIVNNATNVVIKVC   IVNNATNVV  2        0.4030
638.9    19.00  0.44     Sequence
             DRB1_0301  124      LIVNNATNVVIKVCE   IVNNATNVV  1        0.3340
1347.7    31.00  0.38     Sequence
             DRB1_0301  125      IVNNATNVVIKVCEF   TNVVIKVCE  5        0.2027
5578.0    70.00  0.22     Sequence
             DRB1_0301  126      VNNATNVVIKVCEFQ   TNVVIKVCE  4        0.1733
7669.1    80.00  0.31     Sequence
             DRB1_0301  127      NNATNVVIKVCEFQF   TNVVIKVCE  3        0.1789
7216.9    75.00  0.34     Sequence
             DRB1_0301  128      NATNVVIKVCEFQFC   IKVCEFQFC  6        0.2132
4980.1    65.00  0.29     Sequence
             DRB1_0301  129      ATNVVIKVCEFQFCN   IKVCEFQFC  5        0.2407
3698.3    55.00  0.43     Sequence
             DRB1_0301  130      TNVVIKVCEFQFCNY   IKVCEFQFC  4        0.2604
2986.5    49.00  0.46     Sequence
             DRB1_0301  131      NVVIKVCEFQFCNYP   IKVCEFQFC  3        0.2451
3524.3    55.00  0.46     Sequence
             DRB1_0301  132      VVIKVCEFQFCNYPF   IKVCEFQFC  2        0.2488
3388.1    55.00  0.40     Sequence
             DRB1_0301  133      VIKVCEFQFCNYPFL   FQFCNYPFL  6        0.2434
3591.0    55.00  0.28     Sequence
             DRB1_0301  134      IKVCEFQFCNYPFLG   FQFCNYPFL  5        0.2262
4324.5    60.00  0.41     Sequence
             DRB1_0301  135      KVCEFQFCNYPFLGV   FQFCNYPFL  4        0.2293
4181.0    60.00  0.51     Sequence
             DRB1_0301  136      VCEFQFCNYPFLGVY   FQFCNYPFL  3        0.2378
3814.6    60.00  0.52     Sequence
             DRB1_0301  137      CEFQFCNYPFLGVYY   FQFCNYPFL  2        0.2390
3768.0    55.00  0.40     Sequence
             DRB1_0301  138      EFQFCNYPFLGVYYH   CNYPFLGVY  4        0.2324
4046.3    60.00  0.33     Sequence
             DRB1_0301  139      FQFCNYPFLGVYYHK   CNYPFLGVY  3        0.2081
5261.3    65.00  0.41     Sequence
```

```
            DRB1_0301  140      QFCNYPFLGVYYHKN  CNYPFLGVY  2        0.1695
7988.3    80.00  0.42     Sequence
            DRB1_0301  141      FCNYPFLGVYYHKNN  CNYPFLGVY  1        0.1329
11869.2    90.00  0.34     Sequence
            DRB1_0301  142      CNYPFLGVYYHKNNK  FLGVYYHKN  4        0.1223
13310.1    90.00  0.38     Sequence
            DRB1_0301  143      NYPFLGVYYHKNNKS  FLGVYYHKN  3        0.1249
12947.2    90.00  0.34     Sequence
            DRB1_0301  144      YPFLGVYYHKNNKSW  VYYHKNNKS  5        0.1454
10372.2    85.00  0.32     Sequence
            DRB1_0301  145      PFLGVYYHKNNKSWM  YHKNNKSWM  6        0.2369
3851.9    60.00  0.56     Sequence
            DRB1_0301  146      FLGVYYHKNNKSWME  YHKNNKSWM  5        0.2775
2481.9    44.00  0.65     Sequence
            DRB1_0301  147      LGVYYHKNNKSWMES  YHKNNKSWM  4        0.2965
2022.4    39.00  0.68     Sequence
            DRB1_0301  148      GVYYHKNNKSWMESE  YHKNNKSWM  3        0.2921
2120.2    41.00  0.71     Sequence
            DRB1_0301  149      VYYHKNNKSWMESEF  YHKNNKSWM  2        0.2697
2702.5    46.00  0.67     Sequence
            DRB1_0301  150      YYHKNNKSWMESEFR  YHKNNKSWM  1        0.2259
4340.1    60.00  0.52     Sequence
            DRB1_0301  151      YHKNNKSWMESEFRV  YHKNNKSWM  0        0.1817
7004.6    75.00  0.35     Sequence
            DRB1_0301  152      HKNNKSWMESEFRVY  MESEFRVYX  7        0.1535
9495.6    85.00  0.25     Sequence
            DRB1_0301  153      KNNKSWMESEFRVYS  MESEFRVYS  6        0.2309
4113.1    60.00  0.64     Sequence
            DRB1_0301  154      NNKSWMESEFRVYSS  MESEFRVYS  5        0.2692
2715.8    47.00  0.74     Sequence
            DRB1_0301  155      NKSWMESEFRVYSSA  MESEFRVYS  4        0.2815
2377.3    43.00  0.79     Sequence
            DRB1_0301  156      KSWMESEFRVYSSAN  MESEFRVYS  3        0.2771
2493.7    44.00  0.83     Sequence
            DRB1_0301  157      SWMESEFRVYSSANN  MESEFRVYS  2        0.2403
3711.7    55.00  0.82     Sequence
            DRB1_0301  158      WMESEFRVYSSANNC  MESEFRVYS  1        0.1811
7046.9    75.00  0.69     Sequence
            DRB1_0301  159      MESEFRVYSSANNCT  VYSSANNCT  6        0.1382
11207.0    90.00  0.35     Sequence
            DRB1_0301  160      ESEFRVYSSANNCTF  VYSSANNCT  5        0.1489
9980.2    85.00  0.58     Sequence
            DRB1_0301  161      SEFRVYSSANNCTFE  VYSSANNCT  4        0.1699
7954.5    80.00  0.61     Sequence
            DRB1_0301  162      EFRVYSSANNCTFEY  VYSSANNCT  3        0.1814
7022.4    75.00  0.61     Sequence
            DRB1_0301  163      FRVYSSANNCTFEYV  VYSSANNCT  2        0.1779
7291.1    75.00  0.52     Sequence
            DRB1_0301  164      RVYSSANNCTFEYVS  VYSSANNCT  1        0.1523
9619.9    85.00  0.43     Sequence
            DRB1_0301  165      VYSSANNCTFEYVSQ  CTFEYVSQX  7        0.1048
16080.8    95.00  0.21     Sequence
            DRB1_0301  166      YSSANNCTFEYVSQP  CTFEYVSQP  6        0.1072
15681.1    95.00  0.44     Sequence
            DRB1_0301  167      SSANNCTFEYVSQPF  CTFEYVSQP  5        0.1368
11379.2    90.00  0.63     Sequence
            DRB1_0301  168      SANNCTFEYVSQPFL  CTFEYVSQP  4        0.1831
6894.0    75.00  0.51     Sequence
            DRB1_0301  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.2447
3542.9    55.00  0.41     Sequence
            DRB1_0301  170      NNCTFEYVSQPFLMD  FEYVSQPFL  4        0.2605
2984.1    49.00  0.41     Sequence
            DRB1_0301  171      NCTFEYVSQPFLMDL  FEYVSQPFL  3        0.2630
2906.0    48.00  0.42     Sequence
            DRB1_0301  172      CTFEYVSQPFLMDLE  FEYVSQPFL  2        0.2481
3414.1    55.00  0.46     Sequence
```

```
              DRB1_0301  173      TFEYVSQPFLMDLEG  EYVSQPFLM  2        0.2278
4252.6    60.00  0.36    Sequence
              DRB1_0301  174      FEYVSQPFLMDLEGK  FLMDLEGKX  7        0.2628
2909.8    48.00  0.40    Sequence
              DRB1_0301  175      EYVSQPFLMDLEGKQ  FLMDLEGKQ  6        0.4476
394.1    14.00  0.86    Sequence
              DRB1_0301  176      YVSQPFLMDLEGKQG  FLMDLEGKQ  5        0.4711
305.5    11.00  0.90    Sequence
              DRB1_0301  177      VSQPFLMDLEGKQGN  FLMDLEGKQ  4        0.5039
214.4     8.50  0.83    Sequence         WB
              DRB1_0301  178      SQPFLMDLEGKQGNF  FLMDLEGKQ  3        0.5183
183.5     7.50  0.81    Sequence         WB
              DRB1_0301  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2        0.4976
229.5     9.00  0.71    Sequence         WB
              DRB1_0301  180      PFLMDLEGKQGNFKN  FLMDLEGKQ  1        0.4541
367.4    13.00  0.64    Sequence
              DRB1_0301  181      FLMDLEGKQGNFKNL  MDLEGKQGN  2        0.3434
1217.6    29.00  0.35    Sequence
              DRB1_0301  182      LMDLEGKQGNFKNLS  LEGKQGNFK  3        0.2012
5669.5    70.00  0.49    Sequence
              DRB1_0301  183      MDLEGKQGNFKNLSE  LEGKQGNFK  2        0.1464
10255.7    85.00  0.60    Sequence
              DRB1_0301  184      DLEGKQGNFKNLSEF  LEGKQGNFK  1        0.0978
17361.6    95.00  0.55    Sequence
              DRB1_0301  185      LEGKQGNFKNLSEFV  NFKNLSEFV  6        0.0805
20936.5   100.00  0.29    Sequence
              DRB1_0301  186      EGKQGNFKNLSEFVF  NFKNLSEFV  5        0.0973
17448.2    95.00  0.39    Sequence
              DRB1_0301  187      GKQGNFKNLSEFVFK  NFKNLSEFV  4        0.1287
12428.8    90.00  0.32    Sequence
              DRB1_0301  188      KQGNFKNLSEFVFKN  NFKNLSEFV  3        0.1470
10186.0    85.00  0.24    Sequence
              DRB1_0301  189      QGNFKNLSEFVFKNI  NLSEFVFKN  5        0.1543
9414.8    85.00  0.28    Sequence
              DRB1_0301  190      GNFKNLSEFVFKNID  NLSEFVFKN  4        0.1488
9995.3    85.00  0.29    Sequence
              DRB1_0301  191      NFKNLSEFVFKNIDG  NLSEFVFKN  3        0.1308
12144.2    90.00  0.34    Sequence
              DRB1_0301  192      FKNLSEFVFKNIDGY  FVFKNIDGY  6        0.1632
8554.0    80.00  0.26    Sequence
              DRB1_0301  193      KNLSEFVFKNIDGYF  VFKNIDGYF  6        0.2363
3879.6    60.00  0.44    Sequence
              DRB1_0301  194      NLSEFVFKNIDGYFK  VFKNIDGYF  5        0.2884
2206.0    41.00  0.51    Sequence
              DRB1_0301  195      LSEFVFKNIDGYFKI  VFKNIDGYF  4        0.3222
1530.8    33.00  0.56    Sequence
              DRB1_0301  196      SEFVFKNIDGYFKIY  VFKNIDGYF  3        0.3343
1343.4    31.00  0.53    Sequence
              DRB1_0301  197      EFVFKNIDGYFKIYS  VFKNIDGYF  2        0.3230
1517.4    33.00  0.49    Sequence
              DRB1_0301  198      FVFKNIDGYFKIYSK  VFKNIDGYF  1        0.2909
2148.4    41.00  0.38    Sequence
              DRB1_0301  199      VFKNIDGYFKIYSKH  KNIDGYFKI  2        0.2217
4541.3    65.00  0.34    Sequence
              DRB1_0301  200      FKNIDGYFKIYSKHT  IDGYFKIYS  3        0.1646
8423.2    80.00  0.45    Sequence
              DRB1_0301  201      KNIDGYFKIYSKHTP  IDGYFKIYS  2        0.1320
11984.8    90.00  0.47    Sequence
              DRB1_0301  202      NIDGYFKIYSKHTPI  IDGYFKIYS  1        0.1274
12596.1    90.00  0.27    Sequence
              DRB1_0301  203      IDGYFKIYSKHTPIN  IYSKHTPIN  6        0.1380
11228.2    90.00  0.28    Sequence
              DRB1_0301  204      DGYFKIYSKHTPINL  IYSKHTPIN  5        0.1712
7843.4    80.00  0.37    Sequence
              DRB1_0301  205      GYFKIYSKHTPINLV  IYSKHTPIN  4        0.2047
5455.9    70.00  0.38    Sequence
```

```
             DRB1_0301  206      YFKIYSKHTPINLVR  IYSKHTPIN  3        0.2267
4304.4    60.00  0.35     Sequence
             DRB1_0301  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.2203
4609.0    65.00  0.29     Sequence
             DRB1_0301  208      KIYSKHTPINLVRDL  YSKHTPINL  2        0.1997
5764.2    70.00  0.28     Sequence
             DRB1_0301  209      IYSKHTPINLVRDLP  YSKHTPINL  1        0.1639
8489.3    80.00  0.25     Sequence
             DRB1_0301  210      YSKHTPINLVRDLPQ  INLVRDLPQ  6        0.1900
6403.1    75.00  0.33     Sequence
             DRB1_0301  211      SKHTPINLVRDLPQG  LVRDLPQGX  7        0.2865
2252.0    42.00  0.36     Sequence
             DRB1_0301  212      KHTPINLVRDLPQGF  LVRDLPQGF  6        0.6263
57.0     2.50  0.90     Sequence         WB
             DRB1_0301  213      HTPINLVRDLPQGFS  LVRDLPQGF  5        0.7021
25.1     1.00  0.93     Sequence         SB
             DRB1_0301  214      TPINLVRDLPQGFSA  LVRDLPQGF  4        0.7240
19.8     0.70  0.93     Sequence         SB
             DRB1_0301  215      PINLVRDLPQGFSAL  LVRDLPQGF  3        0.7227
20.1     0.70  0.94     Sequence         SB
             DRB1_0301  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.6887
29.0     1.20  0.93     Sequence         SB
             DRB1_0301  217      NLVRDLPQGFSALEP  LVRDLPQGF  1        0.5917
82.9     4.00  0.86     Sequence         WB
             DRB1_0301  218      LVRDLPQGFSALEPL  LVRDLPQGF  0        0.3255
1477.7    33.00  0.54     Sequence
             DRB1_0301  219      VRDLPQGFSALEPLV  GFSALEPLV  6        0.0690
23696.0   100.00  0.21     Sequence
             DRB1_0301  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.1088
15407.3    95.00  0.44     Sequence
             DRB1_0301  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.1566
9186.9    85.00  0.50     Sequence
             DRB1_0301  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.1577
9072.2    80.00  0.44     Sequence
             DRB1_0301  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.1751
7519.7    75.00  0.38     Sequence
             DRB1_0301  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.1748
7541.9    75.00  0.37     Sequence
             DRB1_0301  225      GFSALEPLVDLPIGI  PLVDLPIGI  6        0.2299
4154.2    60.00  0.50     Sequence
             DRB1_0301  226      FSALEPLVDLPIGIN  PLVDLPIGI  5        0.2600
3001.3    49.00  0.59     Sequence
             DRB1_0301  227      SALEPLVDLPIGINI  PLVDLPIGI  4        0.2824
2356.0    43.00  0.63     Sequence
             DRB1_0301  228      ALEPLVDLPIGINIT  PLVDLPIGI  3        0.2933
2093.4    40.00  0.62     Sequence
             DRB1_0301  229      LEPLVDLPIGINITR  PLVDLPIGI  2        0.3106
1735.7    36.00  0.50     Sequence
             DRB1_0301  230      EPLVDLPIGINITRF  PLVDLPIGI  1        0.3112
1725.4    36.00  0.34     Sequence
             DRB1_0301  231      PLVDLPIGINITRFQ  LPIGINITR  4        0.3084
1777.7    37.00  0.37     Sequence
             DRB1_0301  232      LVDLPIGINITRFQT  LPIGINITR  3        0.3105
1736.7    36.00  0.38     Sequence
             DRB1_0301  233      VDLPIGINITRFQTL  IGINITRFQ  4        0.3090
1765.0    36.00  0.40     Sequence
             DRB1_0301  234      DLPIGINITRFQTLL  IGINITRFQ  3        0.2977
1994.9    39.00  0.41     Sequence
             DRB1_0301  235      LPIGINITRFQTLLA  IGINITRFQ  2        0.3141
1671.4    35.00  0.31     Sequence
             DRB1_0301  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.3200
1567.3    34.00  0.43     Sequence
             DRB1_0301  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.3096
1753.9    36.00  0.56     Sequence
             DRB1_0301  238      GINITRFQTLLALHR  ITRFQTLLA  3        0.3369
1305.1    30.00  0.47     Sequence
```

```
             DRB1_0301  239      INITRFQTLLALHRS  ITRFQTLLA  2        0.3430
1221.8    29.00  0.41     Sequence
             DRB1_0301  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.3478
1160.3    28.00  0.37     Sequence
             DRB1_0301  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.3543
1082.0    27.00  0.37     Sequence
             DRB1_0301  242      TRFQTLLALHRSYLT  TLLALHRSY  4        0.3562
1059.7    27.00  0.28     Sequence
             DRB1_0301  243      RFQTLLALHRSYLTP  TLLALHRSY  3        0.3548
1075.5    27.00  0.24     Sequence
             DRB1_0301  244      FQTLLALHRSYLTPG  LHRSYLTPG  6        0.3426
1227.7    29.00  0.28     Sequence
             DRB1_0301  245      QTLLALHRSYLTPGD  LHRSYLTPG  5        0.3462
1180.8    29.00  0.45     Sequence
             DRB1_0301  246      TLLALHRSYLTPGDS  LHRSYLTPG  4        0.3077
1792.0    37.00  0.63     Sequence
             DRB1_0301  247      LLALHRSYLTPGDSS  LHRSYLTPG  3        0.2876
2225.8    42.00  0.76     Sequence
             DRB1_0301  248      LALHRSYLTPGDSSS  LHRSYLTPG  2        0.2462
3485.4    55.00  0.83     Sequence
             DRB1_0301  249      ALHRSYLTPGDSSSG  LHRSYLTPG  1        0.1896
6430.5    75.00  0.71     Sequence
             DRB1_0301  250      LHRSYLTPGDSSSGW  LHRSYLTPG  0        0.1128
14762.1    95.00  0.40     Sequence
             DRB1_0301  251      HRSYLTPGDSSSGWT  LTPGDSSSG  4        0.0597
26196.0   100.00  0.40     Sequence
             DRB1_0301  252      RSYLTPGDSSSGWTA  LTPGDSSSG  3        0.0634
25174.3   100.00  0.34     Sequence
             DRB1_0301  253      SYLTPGDSSSGWTAG  LTPGDSSSG  2        0.0570
26975.2   100.00  0.32     Sequence
             DRB1_0301  254      YLTPGDSSSGWTAGA  LTPGDSSSG  1        0.0483
29647.1   100.00  0.28     Sequence
             DRB1_0301  255      LTPGDSSSGWTAGAA  DSSSGWTAG  4        0.0423
31622.6   100.00  0.24     Sequence
             DRB1_0301  256      TPGDSSSGWTAGAAA  DSSSGWTAG  3        0.0337
34705.5   100.00  0.31     Sequence
             DRB1_0301  257      PGDSSSGWTAGAAAY  DSSSGWTAG  2        0.0342
34519.8   100.00  0.22     Sequence
             DRB1_0301  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.0782
21461.3   100.00  0.44     Sequence
             DRB1_0301  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.1220
13349.8    90.00  0.52     Sequence
             DRB1_0301  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.1236
13130.6    90.00  0.51     Sequence
             DRB1_0301  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.1392
11083.6    90.00  0.48     Sequence
             DRB1_0301  262      SGWTAGAAAYYVGYL  WTAGAAAYY  2        0.1368
11376.3    90.00  0.38     Sequence
             DRB1_0301  263      GWTAGAAAYYVGYLQ  WTAGAAAYY  1        0.1244
13016.5    90.00  0.32     Sequence
             DRB1_0301  264      WTAGAAAYYVGYLQP  GAAAYYVGY  3        0.0910
18670.3   100.00  0.34     Sequence
             DRB1_0301  265      TAGAAAYYVGYLQPR  GAAAYYVGY  2        0.0795
21154.2   100.00  0.31     Sequence
             DRB1_0301  266      AGAAAYYVGYLQPRT  YYVGYLQPR  5        0.0912
18643.7   100.00  0.34     Sequence
             DRB1_0301  267      GAAAYYVGYLQPRTF  YYVGYLQPR  4        0.1273
12616.0    90.00  0.25     Sequence
             DRB1_0301  268      AAAYYVGYLQPRTFL  GYLQPRTFL  6        0.1774
7335.9    75.00  0.32     Sequence
             DRB1_0301  269      AAYYVGYLQPRTFLL  GYLQPRTFL  5        0.2272
4280.6    60.00  0.34     Sequence
             DRB1_0301  270      AYYVGYLQPRTFLLK  GYLQPRTFL  4        0.2785
2457.6    44.00  0.33     Sequence
             DRB1_0301  271      YYVGYLQPRTFLLKY  GYLQPRTFL  3        0.3016
1912.2    38.00  0.31     Sequence
```

```
             DRB1_0301  272      YVGYLQPRTFLLKYN  GYLQPRTFL  2        0.2963
2027.1    39.00  0.26     Sequence
             DRB1_0301  273      VGYLQPRTFLLKYNE  LQPRTFLLK  3        0.2603
2991.7    49.00  0.38     Sequence
             DRB1_0301  274      GYLQPRTFLLKYNEN  LQPRTFLLK  2        0.1955
6027.3    70.00  0.41     Sequence
             DRB1_0301  275      YLQPRTFLLKYNENG  LQPRTFLLK  1        0.1397
11030.4    85.00  0.39     Sequence
             DRB1_0301  276      LQPRTFLLKYNENGT  FLLKYNENG  5        0.1353
11564.3    90.00  0.32     Sequence
             DRB1_0301  277      QPRTFLLKYNENGTI  LKYNENGTI  6        0.1908
6347.4    70.00  0.47     Sequence
             DRB1_0301  278      PRTFLLKYNENGTIT  LKYNENGTI  5        0.2362
3883.5    60.00  0.58     Sequence
             DRB1_0301  279      RTFLLKYNENGTITD  LKYNENGTI  4        0.2557
3143.1    50.00  0.56     Sequence
             DRB1_0301  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.2533
3225.2    55.00  0.58     Sequence
             DRB1_0301  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.2372
3842.1    60.00  0.55     Sequence
             DRB1_0301  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.1826
6932.3    75.00  0.47     Sequence
             DRB1_0301  283      LKYNENGTITDAVDC  YNENGTITD  2        0.1178
13975.4    95.00  0.43     Sequence
             DRB1_0301  284      KYNENGTITDAVDCA  TITDAVDCA  6        0.1404
10946.8    85.00  0.48     Sequence
             DRB1_0301  285      YNENGTITDAVDCAL  TITDAVDCA  5        0.1876
6571.6    75.00  0.58     Sequence
             DRB1_0301  286      NENGTITDAVDCALD  TITDAVDCA  4        0.2252
4372.9    60.00  0.47     Sequence
             DRB1_0301  287      ENGTITDAVDCALDP  TITDAVDCA  3        0.2292
4187.2    60.00  0.43     Sequence
             DRB1_0301  288      NGTITDAVDCALDPL  TITDAVDCA  2        0.2419
3651.7    55.00  0.36     Sequence
             DRB1_0301  289      GTITDAVDCALDPLS  DAVDCALDP  4        0.2629
2908.2    48.00  0.29     Sequence
             DRB1_0301  290      TITDAVDCALDPLSE  DAVDCALDP  3        0.2712
2657.8    46.00  0.25     Sequence
             DRB1_0301  291      ITDAVDCALDPLSET  CALDPLSET  6        0.3155
1646.1    35.00  0.61     Sequence
             DRB1_0301  292      TDAVDCALDPLSETK  CALDPLSET  5        0.3771
845.1    23.00  0.74     Sequence
             DRB1_0301  293      DAVDCALDPLSETKC  CALDPLSET  4        0.3857
770.3    22.00  0.81     Sequence
             DRB1_0301  294      AVDCALDPLSETKCT  CALDPLSET  3        0.3885
746.9    21.00  0.83     Sequence
             DRB1_0301  295      VDCALDPLSETKCTL  CALDPLSET  2        0.3652
961.8    25.00  0.81     Sequence
             DRB1_0301  296      DCALDPLSETKCTLK  CALDPLSET  1        0.3011
1923.9    38.00  0.58     Sequence
             DRB1_0301  297      CALDPLSETKCTLKS  PLSETKCTL  4        0.2362
3881.7    60.00  0.38     Sequence
             DRB1_0301  298      ALDPLSETKCTLKSF  PLSETKCTL  3        0.2163
4812.9    65.00  0.44     Sequence
             DRB1_0301  299      LDPLSETKCTLKSFT  LSETKCTLK  3        0.2090
5209.1    65.00  0.37     Sequence
             DRB1_0301  300      DPLSETKCTLKSFTV  LSETKCTLK  2        0.2051
5437.5    70.00  0.31     Sequence
             DRB1_0301  301      PLSETKCTLKSFTVE  TKCTLKSFT  4        0.1897
6417.6    75.00  0.28     Sequence
             DRB1_0301  302      LSETKCTLKSFTVEK  TLKSFTVEK  6        0.2074
5301.3    65.00  0.33     Sequence
             DRB1_0301  303      SETKCTLKSFTVEKG  TLKSFTVEK  5        0.2159
4836.8    65.00  0.41     Sequence
             DRB1_0301  304      ETKCTLKSFTVEKGI  TLKSFTVEK  4        0.2267
4300.2    60.00  0.44     Sequence
```

```
             DRB1_0301  305      TKCTLKSFTVEKGIY  TLKSFTVEK  3        0.2485
3399.9    55.00  0.43     Sequence
             DRB1_0301  306      KCTLKSFTVEKGIYQ  FTVEKGIYQ  6        0.2908
2150.1    41.00  0.41     Sequence
             DRB1_0301  307      CTLKSFTVEKGIYQT  FTVEKGIYQ  5        0.3008
1929.6    38.00  0.55     Sequence
             DRB1_0301  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.3030
1884.7    38.00  0.62     Sequence
             DRB1_0301  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.2876
2227.1    42.00  0.70     Sequence
             DRB1_0301  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.2591
3029.4    49.00  0.68     Sequence
             DRB1_0301  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.2175
4752.7    65.00  0.49     Sequence
             DRB1_0301  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.1932
6182.4    70.00  0.41     Sequence
             DRB1_0301  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.1959
6001.8    70.00  0.63     Sequence
             DRB1_0301  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.1840
6828.0    75.00  0.63     Sequence
             DRB1_0301  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.1862
6669.5    75.00  0.62     Sequence
             DRB1_0301  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.1759
7456.1    75.00  0.55     Sequence
             DRB1_0301  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.1506
9802.4    85.00  0.43     Sequence
             DRB1_0301  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.1466
10237.9    85.00  0.52     Sequence
             DRB1_0301  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.1947
6085.2    70.00  0.63     Sequence
             DRB1_0301  320      QTSNFRVQPTESIVR  VQPTESIVR  6        0.3047
1849.2    37.00  0.46     Sequence
             DRB1_0301  321      TSNFRVQPTESIVRF  VQPTESIVR  5        0.3703
910.2    24.00  0.62     Sequence
             DRB1_0301  322      SNFRVQPTESIVRFP  VQPTESIVR  4        0.3535
1090.9    27.00  0.62     Sequence
             DRB1_0301  323      NFRVQPTESIVRFPN  VQPTESIVR  3        0.3426
1228.1    29.00  0.65     Sequence
             DRB1_0301  324      FRVQPTESIVRFPNI  VQPTESIVR  2        0.3064
1816.9    37.00  0.70     Sequence
             DRB1_0301  325      RVQPTESIVRFPNIT  VQPTESIVR  1        0.2370
3848.3    60.00  0.64     Sequence
             DRB1_0301  326      VQPTESIVRFPNITN  VQPTESIVR  0        0.1424
10707.7    85.00  0.35     Sequence
             DRB1_0301  327      QPTESIVRFPNITNL  VRFPNITNL  6        0.1113
14989.0    95.00  0.29     Sequence
             DRB1_0301  328      PTESIVRFPNITNLC  VRFPNITNL  5        0.1376
11279.2    90.00  0.38     Sequence
             DRB1_0301  329      TESIVRFPNITNLCP  VRFPNITNL  4        0.1351
11585.6    90.00  0.38     Sequence
             DRB1_0301  330      ESIVRFPNITNLCPF  RFPNITNLC  4        0.1514
9718.0    85.00  0.38     Sequence
             DRB1_0301  331      SIVRFPNITNLCPFG  RFPNITNLC  3        0.1541
9433.0    85.00  0.38     Sequence
             DRB1_0301  332      IVRFPNITNLCPFGE  RFPNITNLC  2        0.1385
11177.9    90.00  0.34     Sequence
             DRB1_0301  333      VRFPNITNLCPFGEV  RFPNITNLC  1        0.1212
13471.5    90.00  0.24     Sequence
             DRB1_0301  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.1054
15977.6    95.00  0.25     Sequence
             DRB1_0301  335      FPNITNLCPFGEVFN  TNLCPFGEV  4        0.1011
16745.0    95.00  0.22     Sequence
             DRB1_0301  336      PNITNLCPFGEVFNA  TNLCPFGEV  3        0.1087
15431.0    95.00  0.21     Sequence
             DRB1_0301  337      NITNLCPFGEVFNAT  CPFGEVFNA  5        0.1056
15951.1    95.00  0.32     Sequence
```

```
             DRB1_0301  338      ITNLCPFGEVFNATR  CPFGEVFNA  4        0.1080
15537.9    95.00  0.37     Sequence
             DRB1_0301  339      TNLCPFGEVFNATRF  CPFGEVFNA  3        0.1330
11854.8    90.00  0.35     Sequence
             DRB1_0301  340      NLCPFGEVFNATRFA  VFNATRFAX  7        0.1914
6300.3    70.00  0.34     Sequence
             DRB1_0301  341      LCPFGEVFNATRFAS  VFNATRFAS  6        0.3048
1847.9    37.00  0.74     Sequence
             DRB1_0301  342      CPFGEVFNATRFASV  VFNATRFAS  5        0.3662
950.9    25.00  0.81     Sequence
             DRB1_0301  343      PFGEVFNATRFASVY  VFNATRFAS  4        0.3999
660.7    19.00  0.81     Sequence
             DRB1_0301  344      FGEVFNATRFASVYA  VFNATRFAS  3        0.3969
681.9    20.00  0.80     Sequence
             DRB1_0301  345      GEVFNATRFASVYAW  VFNATRFAS  2        0.3750
865.1    23.00  0.76     Sequence
             DRB1_0301  346      EVFNATRFASVYAWN  VFNATRFAS  1        0.3175
1611.3    34.00  0.65     Sequence
             DRB1_0301  347      VFNATRFASVYAWNR  FASVYAWNR  6        0.2210
4575.1    65.00  0.34     Sequence
             DRB1_0301  348      FNATRFASVYAWNRK  FASVYAWNR  5        0.2259
4338.5    60.00  0.55     Sequence
             DRB1_0301  349      NATRFASVYAWNRKR  FASVYAWNR  4        0.2959
2034.7    40.00  0.47     Sequence
             DRB1_0301  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.3633
981.6    25.00  0.34     Sequence
             DRB1_0301  351      TRFASVYAWNRKRIS  VYAWNRKRI  5        0.3986
670.0    20.00  0.30     Sequence
             DRB1_0301  352      RFASVYAWNRKRISN  VYAWNRKRI  4        0.4037
634.0    19.00  0.33     Sequence
             DRB1_0301  353      FASVYAWNRKRISNC  YAWNRKRIS  4        0.3689
923.5    24.00  0.34     Sequence
             DRB1_0301  354      ASVYAWNRKRISNCV  YAWNRKRIS  3        0.3459
1184.1    29.00  0.41     Sequence
             DRB1_0301  355      SVYAWNRKRISNCVA  YAWNRKRIS  2        0.3026
1893.2    38.00  0.42     Sequence
             DRB1_0301  356      VYAWNRKRISNCVAD  YAWNRKRIS  1        0.2080
5266.7    65.00  0.43     Sequence
             DRB1_0301  357      YAWNRKRISNCVADY  KRISNCVAD  5        0.1614
8717.9    80.00  0.21     Sequence
             DRB1_0301  358      AWNRKRISNCVADYS  ISNCVADYS  6        0.2018
5630.8    70.00  0.47     Sequence
             DRB1_0301  359      WNRKRISNCVADYSV  ISNCVADYS  5        0.2725
2619.8    46.00  0.51     Sequence
             DRB1_0301  360      NRKRISNCVADYSVL  ISNCVADYS  4        0.3708
904.7    24.00  0.47     Sequence
             DRB1_0301  361      RKRISNCVADYSVLY  CVADYSVLY  6        0.5523
126.9     5.50  0.68     Sequence         WB
             DRB1_0301  362      KRISNCVADYSVLYN  CVADYSVLY  5        0.6024
73.8     3.50  0.82     Sequence         WB
             DRB1_0301  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.6226
59.3     3.00  0.88     Sequence         WB
             DRB1_0301  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.6194
61.4     3.00  0.91     Sequence         WB
             DRB1_0301  365      SNCVADYSVLYNSAS  CVADYSVLY  2        0.5916
83.0     4.00  0.89     Sequence         WB
             DRB1_0301  366      NCVADYSVLYNSASF  CVADYSVLY  1        0.5294
162.8     7.00  0.80     Sequence         WB
             DRB1_0301  367      CVADYSVLYNSASFS  CVADYSVLY  0        0.3963
686.5    20.00  0.44     Sequence
             DRB1_0301  368      VADYSVLYNSASFST  VLYNSASFS  5        0.3106
1735.9    36.00  0.68     Sequence
             DRB1_0301  369      ADYSVLYNSASFSTF  VLYNSASFS  4        0.3647
966.2    25.00  0.66     Sequence
             DRB1_0301  370      DYSVLYNSASFSTFK  VLYNSASFS  3        0.3892
741.5    21.00  0.61     Sequence
```

```
             DRB1_0301  371      YSVLYNSASFSTFKC  VLYNSASFS  2        0.3807
813.1    22.00  0.61     Sequence
             DRB1_0301  372      SVLYNSASFSTFKCY  VLYNSASFS  1        0.3398
1265.7    30.00  0.54     Sequence
             DRB1_0301  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.2185
4699.8    65.00  0.41     Sequence
             DRB1_0301  374      LYNSASFSTFKCYGV  ASFSTFKCY  4        0.1000
16948.6    95.00  0.28     Sequence
             DRB1_0301  375      YNSASFSTFKCYGVS  ASFSTFKCY  3        0.0950
17887.5    95.00  0.35     Sequence
             DRB1_0301  376      NSASFSTFKCYGVSP  ASFSTFKCY  2        0.0894
18999.0   100.00  0.32     Sequence
             DRB1_0301  377      SASFSTFKCYGVSPT  SFSTFKCYG  2        0.0863
19656.5   100.00  0.30     Sequence
             DRB1_0301  378      ASFSTFKCYGVSPTK  FKCYGVSPT  5        0.0791
21252.4   100.00  0.31     Sequence
             DRB1_0301  379      SFSTFKCYGVSPTKL  CYGVSPTKL  6        0.1001
16920.9    95.00  0.29     Sequence
             DRB1_0301  380      FSTFKCYGVSPTKLN  CYGVSPTKL  5        0.1311
12105.7    90.00  0.37     Sequence
             DRB1_0301  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.1432
10617.9    85.00  0.34     Sequence
             DRB1_0301  382      TFKCYGVSPTKLNDL  CYGVSPTKL  3        0.1518
9678.9    85.00  0.34     Sequence
             DRB1_0301  383      FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.1442
10504.9    85.00  0.32     Sequence
             DRB1_0301  384      KCYGVSPTKLNDLCF  GVSPTKLND  3        0.1515
9707.5    85.00  0.25     Sequence
             DRB1_0301  385      CYGVSPTKLNDLCFT  TKLNDLCFT  6        0.1826
6932.4    75.00  0.25     Sequence
             DRB1_0301  386      YGVSPTKLNDLCFTN  TKLNDLCFT  5        0.2113
5085.3    65.00  0.38     Sequence
             DRB1_0301  387      GVSPTKLNDLCFTNV  TKLNDLCFT  4        0.2415
3665.7    55.00  0.39     Sequence
             DRB1_0301  388      VSPTKLNDLCFTNVY  KLNDLCFTN  4        0.2621
2931.9    49.00  0.38     Sequence
             DRB1_0301  389      SPTKLNDLCFTNVYA  KLNDLCFTN  3        0.2608
2976.0    49.00  0.35     Sequence
             DRB1_0301  390      PTKLNDLCFTNVYAD  KLNDLCFTN  2        0.2511
3305.1    55.00  0.31     Sequence
             DRB1_0301  391      TKLNDLCFTNVYADS  CFTNVYADS  6        0.2357
3902.0    60.00  0.22     Sequence
             DRB1_0301  392      KLNDLCFTNVYADSF  CFTNVYADS  5        0.2207
4591.7    65.00  0.37     Sequence
             DRB1_0301  393      LNDLCFTNVYADSFV  CFTNVYADS  4        0.2455
3511.3    55.00  0.40     Sequence
             DRB1_0301  394      NDLCFTNVYADSFVI  CFTNVYADS  3        0.2883
2209.3    42.00  0.29     Sequence
             DRB1_0301  395      DLCFTNVYADSFVIR  VYADSFVIR  6        0.4899
249.4     9.50  0.70     Sequence         WB
             DRB1_0301  396      LCFTNVYADSFVIRG  VYADSFVIR  5        0.5112
198.0     8.00  0.77     Sequence         WB
             DRB1_0301  397      CFTNVYADSFVIRGD  VYADSFVIR  4        0.5188
182.4     7.50  0.84     Sequence         WB
             DRB1_0301  398      FTNVYADSFVIRGDE  VYADSFVIR  3        0.5258
169.1     7.00  0.84     Sequence         WB
             DRB1_0301  399      TNVYADSFVIRGDEV  VYADSFVIR  2        0.5143
191.5     8.00  0.84     Sequence         WB
             DRB1_0301  400      NVYADSFVIRGDEVR  VYADSFVIR  1        0.4864
259.2    10.00  0.70     Sequence
             DRB1_0301  401      VYADSFVIRGDEVRQ  IRGDEVRQX  7        0.4854
261.8    10.00  0.35     Sequence
             DRB1_0301  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.5663
109.1     5.00  0.69     Sequence         WB
             DRB1_0301  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.6432
47.5     2.50  0.79     Sequence         WB
```

```
             DRB1_0301  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.6333
52.9     2.50  0.79     Sequence         WB
             DRB1_0301  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.6220
59.7     3.00  0.81     Sequence         WB
             DRB1_0301  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.5713
103.3     4.50  0.81     Sequence         WB
             DRB1_0301  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.4373
440.8    15.00  0.75     Sequence
             DRB1_0301  408      IRGDEVRQIAPGQTG  IRGDEVRQI  0        0.2075
5296.3    65.00  0.42     Sequence
             DRB1_0301  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.1048
16093.6    95.00  0.44     Sequence
             DRB1_0301  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.1228
13241.9    90.00  0.39     Sequence
             DRB1_0301  411      DEVRQIAPGQTGTIA  IAPGQTGTI  5        0.1308
12138.9    90.00  0.38     Sequence
             DRB1_0301  412      EVRQIAPGQTGTIAD  IAPGQTGTI  4        0.1253
12888.2    90.00  0.45     Sequence
             DRB1_0301  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.1120
14879.9    95.00  0.54     Sequence
             DRB1_0301  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.0919
18507.6   100.00  0.54     Sequence
             DRB1_0301  415      QIAPGQTGTIADYNY  IAPGQTGTI  1        0.0683
23891.1   100.00  0.34     Sequence
             DRB1_0301  416      IAPGQTGTIADYNYK  TIADYNYKX  7        0.0901
18861.2   100.00  0.28     Sequence
             DRB1_0301  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.2653
2832.2    48.00  0.75     Sequence
             DRB1_0301  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.3214
1544.9    34.00  0.68     Sequence
             DRB1_0301  419      GQTGTIADYNYKLPD  TIADYNYKL  4        0.3514
1116.1    27.00  0.60     Sequence
             DRB1_0301  420      QTGTIADYNYKLPDD  TIADYNYKL  3        0.3593
1025.0    26.00  0.56     Sequence
             DRB1_0301  421      TGTIADYNYKLPDDF  TIADYNYKL  2        0.3540
1085.7    27.00  0.52     Sequence
             DRB1_0301  422      GTIADYNYKLPDDFT  TIADYNYKL  1        0.3207
1556.1    34.00  0.45     Sequence
             DRB1_0301  423      TIADYNYKLPDDFTG  ADYNYKLPD  2        0.2412
3676.0    55.00  0.50     Sequence
             DRB1_0301  424      IADYNYKLPDDFTGC  ADYNYKLPD  1        0.1261
12780.6    90.00  0.43     Sequence
             DRB1_0301  425      ADYNYKLPDDFTGCV  LPDDFTGCV  6        0.0884
19219.9   100.00  0.31     Sequence
             DRB1_0301  426      DYNYKLPDDFTGCVI  LPDDFTGCV  5        0.1042
16196.3    95.00  0.43     Sequence
             DRB1_0301  427      YNYKLPDDFTGCVIA  LPDDFTGCV  4        0.1100
15216.3    95.00  0.46     Sequence
             DRB1_0301  428      NYKLPDDFTGCVIAW  LPDDFTGCV  3        0.1101
15197.2    95.00  0.49     Sequence
             DRB1_0301  429      YKLPDDFTGCVIAWN  LPDDFTGCV  2        0.1001
16927.5    95.00  0.47     Sequence
             DRB1_0301  430      KLPDDFTGCVIAWNS  LPDDFTGCV  1        0.0898
18922.9   100.00  0.39     Sequence
             DRB1_0301  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.0786
21357.3   100.00  0.28     Sequence
             DRB1_0301  432      PDDFTGCVIAWNSNN  CVIAWNSNN  6        0.0945
17979.1    95.00  0.41     Sequence
             DRB1_0301  433      DDFTGCVIAWNSNNL  CVIAWNSNN  5        0.1411
10863.8    85.00  0.39     Sequence
             DRB1_0301  434      DFTGCVIAWNSNNLD  IAWNSNNLD  6        0.1946
6088.0    70.00  0.53     Sequence
             DRB1_0301  435      FTGCVIAWNSNNLDS  IAWNSNNLD  5        0.2335
3995.9    60.00  0.61     Sequence
             DRB1_0301  436      TGCVIAWNSNNLDSK  IAWNSNNLD  4        0.2700
2694.3    46.00  0.61     Sequence
```

```
             DRB1_0301  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3        0.2870
2240.7    42.00  0.62     Sequence
             DRB1_0301  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2        0.2768
2503.2    45.00  0.54     Sequence
             DRB1_0301  439      VIAWNSNNLDSKVGG  NNLDSKVGG  6        0.2743
2569.4    45.00  0.37     Sequence
             DRB1_0301  440      IAWNSNNLDSKVGGN  NNLDSKVGG  5        0.2431
3603.3    55.00  0.65     Sequence
             DRB1_0301  441      AWNSNNLDSKVGGNY  NNLDSKVGG  4        0.2529
3238.8    55.00  0.81     Sequence
             DRB1_0301  442      WNSNNLDSKVGGNYN  NNLDSKVGG  3        0.2577
3076.0    50.00  0.83     Sequence
             DRB1_0301  443      NSNNLDSKVGGNYNY  NNLDSKVGG  2        0.2390
3768.1    55.00  0.79     Sequence
             DRB1_0301  444      SNNLDSKVGGNYNYL  NNLDSKVGG  1        0.2005
5710.8    70.00  0.64     Sequence
             DRB1_0301  445      NNLDSKVGGNYNYLY  VGGNYNYLY  6        0.1434
10592.9    85.00  0.34     Sequence
             DRB1_0301  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.1679
8128.6    80.00  0.58     Sequence
             DRB1_0301  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4        0.1917
6280.4    70.00  0.64     Sequence
             DRB1_0301  448      DSKVGGNYNYLYRLF  VGGNYNYLY  3        0.2082
5258.1    65.00  0.60     Sequence
             DRB1_0301  449      SKVGGNYNYLYRLFR  YNYLYRLFR  6        0.2722
2630.1    46.00  0.38     Sequence
             DRB1_0301  450      KVGGNYNYLYRLFRK  YNYLYRLFR  5        0.2984
1980.8    39.00  0.53     Sequence
             DRB1_0301  451      VGGNYNYLYRLFRKS  YNYLYRLFR  4        0.2887
2198.7    41.00  0.67     Sequence
             DRB1_0301  452      GGNYNYLYRLFRKSN  YNYLYRLFR  3        0.2852
2285.0    42.00  0.67     Sequence
             DRB1_0301  453      GNYNYLYRLFRKSNL  YNYLYRLFR  2        0.2750
2551.3    45.00  0.56     Sequence
             DRB1_0301  454      NYNYLYRLFRKSNLK  YNYLYRLFR  1        0.2663
2803.4    47.00  0.38     Sequence
             DRB1_0301  455      YNYLYRLFRKSNLKP  YRLFRKSNL  4        0.2332
4012.4    60.00  0.25     Sequence
             DRB1_0301  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6        0.2681
2748.7    47.00  0.31     Sequence
             DRB1_0301  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.2876
2226.8    42.00  0.46     Sequence
             DRB1_0301  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.3135
1682.6    35.00  0.49     Sequence
             DRB1_0301  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.2966
2020.4    39.00  0.52     Sequence
             DRB1_0301  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.2657
2820.2    48.00  0.54     Sequence
             DRB1_0301  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.2157
4848.8    65.00  0.44     Sequence
             DRB1_0301  462      FRKSNLKPFERDIST  LKPFERDIS  5        0.1764
7417.6    75.00  0.34     Sequence
             DRB1_0301  463      RKSNLKPFERDISTE  LKPFERDIS  4        0.1977
5891.1    70.00  0.47     Sequence
             DRB1_0301  464      KSNLKPFERDISTEI  FERDISTEI  6        0.4265
495.2    16.00  0.89     Sequence
             DRB1_0301  465      SNLKPFERDISTEIY  FERDISTEI  5        0.5260
168.8     7.00  0.91     Sequence          WB
             DRB1_0301  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.5485
132.3     6.00  0.93     Sequence          WB
             DRB1_0301  467      LKPFERDISTEIYQA  FERDISTEI  3        0.5571
120.5     5.50  0.91     Sequence          WB
             DRB1_0301  468      KPFERDISTEIYQAG  FERDISTEI  2        0.5216
177.1     7.50  0.85     Sequence          WB
             DRB1_0301  469      PFERDISTEIYQAGS  FERDISTEI  1        0.4461
400.4    14.00  0.74     Sequence
```

```
             DRB1_0301  470      FERDISTEIYQAGST  FERDISTEI  0        0.3005
1935.7    38.00  0.44     Sequence
             DRB1_0301  471      ERDISTEIYQAGSTP  ISTEIYQAG  3        0.1674
8170.6    80.00  0.69     Sequence
             DRB1_0301  472      RDISTEIYQAGSTPC  ISTEIYQAG  2        0.1755
7488.7    75.00  0.49     Sequence
             DRB1_0301  473      DISTEIYQAGSTPCN  IYQAGSTPC  5        0.1662
8277.3    80.00  0.54     Sequence
             DRB1_0301  474      ISTEIYQAGSTPCNG  IYQAGSTPC  4        0.1440
10527.1    85.00  0.66     Sequence
             DRB1_0301  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.1453
10379.1    85.00  0.74     Sequence
             DRB1_0301  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.1337
11769.4    90.00  0.70     Sequence
             DRB1_0301  477      EIYQAGSTPCNGVKG  IYQAGSTPC  1        0.1060
15881.9    95.00  0.60     Sequence
             DRB1_0301  478      IYQAGSTPCNGVKGF  IYQAGSTPC  0        0.0519
28513.8   100.00  0.25     Sequence
             DRB1_0301  479      YQAGSTPCNGVKGFN  TPCNGVKGF  5        0.0358
33945.3   100.00  0.33     Sequence
             DRB1_0301  480      QAGSTPCNGVKGFNC  TPCNGVKGF  4        0.0414
31946.2   100.00  0.34     Sequence
             DRB1_0301  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.0501
29087.5   100.00  0.29     Sequence
             DRB1_0301  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.0582
26645.9   100.00  0.31     Sequence
             DRB1_0301  483      STPCNGVKGFNCYFP  CNGVKGFNC  3        0.0595
26268.6   100.00  0.29     Sequence
             DRB1_0301  484      TPCNGVKGFNCYFPL  GVKGFNCYF  4        0.0625
25427.7   100.00  0.26     Sequence
             DRB1_0301  485      PCNGVKGFNCYFPLQ  GVKGFNCYF  3        0.0642
24962.7   100.00  0.26     Sequence
             DRB1_0301  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.0869
19535.8   100.00  0.32     Sequence
             DRB1_0301  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.1144
14507.8    95.00  0.41     Sequence
             DRB1_0301  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.1152
14368.9    95.00  0.39     Sequence
             DRB1_0301  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3        0.1249
12943.9    90.00  0.38     Sequence
             DRB1_0301  490      KGFNCYFPLQSYGFQ  FNCYFPLQS  2        0.1174
14045.2    95.00  0.36     Sequence
             DRB1_0301  491      GFNCYFPLQSYGFQP  FNCYFPLQS  1        0.0976
17394.5    95.00  0.31     Sequence
             DRB1_0301  492      FNCYFPLQSYGFQPT  CYFPLQSYG  2        0.0840
20157.4   100.00  0.29     Sequence
             DRB1_0301  493      NCYFPLQSYGFQPTY  LQSYGFQPT  5        0.0845
20034.8   100.00  0.23     Sequence
             DRB1_0301  494      CYFPLQSYGFQPTYG  LQSYGFQPT  4        0.0757
22052.1   100.00  0.23     Sequence
             DRB1_0301  495      YFPLQSYGFQPTYGV  LQSYGFQPT  3        0.0760
21969.5   100.00  0.27     Sequence
             DRB1_0301  496      FPLQSYGFQPTYGVG  QSYGFQPTY  3        0.0696
23537.3   100.00  0.29     Sequence
             DRB1_0301  497      PLQSYGFQPTYGVGY  FQPTYGVGY  6        0.1015
16671.1    95.00  0.47     Sequence
             DRB1_0301  498      LQSYGFQPTYGVGYQ  FQPTYGVGY  5        0.1192
13769.7    90.00  0.66     Sequence
             DRB1_0301  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4        0.1052
16022.4    95.00  0.72     Sequence
             DRB1_0301  500      SYGFQPTYGVGYQPY  FQPTYGVGY  3        0.1147
14453.4    95.00  0.69     Sequence
             DRB1_0301  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.1332
11837.1    90.00  0.46     Sequence
             DRB1_0301  502      GFQPTYGVGYQPYRV  YGVGYQPYR  5        0.1483
10047.2    85.00  0.40     Sequence
```

```
             DRB1_0301  503      FQPTYGVGYQPYRVV  YGVGYQPYR  4        0.1665
8254.9    80.00  0.43     Sequence
             DRB1_0301  504      QPTYGVGYQPYRVVV  YGVGYQPYR  3        0.1833
6881.9    75.00  0.42     Sequence
             DRB1_0301  505      PTYGVGYQPYRVVVL  YGVGYQPYR  2        0.1877
6563.2    75.00  0.34     Sequence
             DRB1_0301  506      TYGVGYQPYRVVVLS  GYQPYRVVV  4        0.1776
7317.1    75.00  0.27     Sequence
             DRB1_0301  507      YGVGYQPYRVVVLSF  GYQPYRVVV  3        0.1625
8619.5    80.00  0.28     Sequence
             DRB1_0301  508      GVGYQPYRVVVLSFE  GYQPYRVVV  2        0.1451
10404.2    85.00  0.29     Sequence
             DRB1_0301  509      VGYQPYRVVVLSFEL  PYRVVVLSF  4        0.1338
11757.2    90.00  0.28     Sequence
             DRB1_0301  510      GYQPYRVVVLSFELL  VVLSFELLX  7        0.1786
7237.3    75.00  0.34     Sequence
             DRB1_0301  511      YQPYRVVVLSFELLH  VVLSFELLH  6        0.3517
1112.3    27.00  0.85     Sequence
             DRB1_0301  512      QPYRVVVLSFELLHA  VVLSFELLH  5        0.4310
471.5    15.00  0.87     Sequence
             DRB1_0301  513      PYRVVVLSFELLHAP  VVLSFELLH  4        0.4222
518.9    17.00  0.83     Sequence
             DRB1_0301  514      YRVVVLSFELLHAPA  VVLSFELLH  3        0.4294
479.9    16.00  0.82     Sequence
             DRB1_0301  515      RVVVLSFELLHAPAT  VVLSFELLH  2        0.4051
624.2    19.00  0.76     Sequence
             DRB1_0301  516      VVVLSFELLHAPATV  VVLSFELLH  1        0.3331
1361.0    31.00  0.64     Sequence
             DRB1_0301  517      VVLSFELLHAPATVC  VVLSFELLH  0        0.2341
3970.9    60.00  0.34     Sequence
             DRB1_0301  518      VLSFELLHAPATVCG  LLHAPATVC  5        0.1420
10757.5    85.00  0.26     Sequence
             DRB1_0301  519      LSFELLHAPATVCGP  LLHAPATVC  4        0.1144
14495.8    95.00  0.32     Sequence
             DRB1_0301  520      SFELLHAPATVCGPK  LHAPATVCG  4        0.1133
14671.5    95.00  0.38     Sequence
             DRB1_0301  521      FELLHAPATVCGPKK  LHAPATVCG  3        0.1053
15995.7    95.00  0.46     Sequence
             DRB1_0301  522      ELLHAPATVCGPKKS  LHAPATVCG  2        0.1051
16030.4    95.00  0.39     Sequence
             DRB1_0301  523      LLHAPATVCGPKKST  ATVCGPKKS  5        0.0947
17953.4    95.00  0.32     Sequence
             DRB1_0301  524      LHAPATVCGPKKSTN  ATVCGPKKS  4        0.0822
20548.7   100.00  0.40     Sequence
             DRB1_0301  525      HAPATVCGPKKSTNL  ATVCGPKKS  3        0.0859
19741.1   100.00  0.44     Sequence
             DRB1_0301  526      APATVCGPKKSTNLV  ATVCGPKKS  2        0.0852
19885.6   100.00  0.37     Sequence
             DRB1_0301  527      PATVCGPKKSTNLVK  ATVCGPKKS  1        0.0795
21146.4   100.00  0.28     Sequence
             DRB1_0301  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5        0.0692
23654.0   100.00  0.28     Sequence
             DRB1_0301  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.0689
23719.4   100.00  0.43     Sequence
             DRB1_0301  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3        0.0670
24229.0   100.00  0.48     Sequence
             DRB1_0301  531      CGPKKSTNLVKNKCV  PKKSTNLVK  2        0.0737
22525.5   100.00  0.32     Sequence
             DRB1_0301  532      GPKKSTNLVKNKCVN  NLVKNKCVN  6        0.0991
17108.0    95.00  0.22     Sequence
             DRB1_0301  533      PKKSTNLVKNKCVNF  LVKNKCVNF  6        0.1604
8812.9    80.00  0.52     Sequence
             DRB1_0301  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.1982
5856.1    70.00  0.64     Sequence
             DRB1_0301  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.2218
4538.3    65.00  0.67     Sequence
```

```
             DRB1_0301  536      STNLVKNKCVNFNFN  LVKNKCVNF  3        0.2178
4735.8    65.00  0.65     Sequence
             DRB1_0301  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2        0.1954
6039.9    70.00  0.65     Sequence
             DRB1_0301  538      NLVKNKCVNFNFNGL  LVKNKCVNF  1        0.1728
7709.7    80.00  0.55     Sequence
             DRB1_0301  539      LVKNKCVNFNFNGLT  VNFNFNGLT  6        0.1742
7590.6    80.00  0.47     Sequence
             DRB1_0301  540      VKNKCVNFNFNGLTG  VNFNFNGLT  5        0.1822
6962.6    75.00  0.62     Sequence
             DRB1_0301  541      KNKCVNFNFNGLTGT  VNFNFNGLT  4        0.2166
4797.0    65.00  0.56     Sequence
             DRB1_0301  542      NKCVNFNFNGLTGTG  VNFNFNGLT  3        0.2156
4849.3    65.00  0.54     Sequence
             DRB1_0301  543      KCVNFNFNGLTGTGV  VNFNFNGLT  2        0.2131
4982.7    65.00  0.47     Sequence
             DRB1_0301  544      CVNFNFNGLTGTGVL  FNFNGLTGT  3        0.1816
7009.0    75.00  0.51     Sequence
             DRB1_0301  545      VNFNFNGLTGTGVLT  FNFNGLTGT  2        0.1567
9176.6    85.00  0.57     Sequence
             DRB1_0301  546      NFNFNGLTGTGVLTE  LTGTGVLTE  6        0.1450
10410.1    85.00  0.44     Sequence
             DRB1_0301  547      FNFNGLTGTGVLTES  LTGTGVLTE  5        0.1501
9855.1    85.00  0.71     Sequence
             DRB1_0301  548      NFNGLTGTGVLTESN  LTGTGVLTE  4        0.1546
9385.6    85.00  0.83     Sequence
             DRB1_0301  549      FNGLTGTGVLTESNK  LTGTGVLTE  3        0.1649
8397.0    80.00  0.85     Sequence
             DRB1_0301  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.1599
8862.0    80.00  0.74     Sequence
             DRB1_0301  551      GLTGTGVLTESNKKF  VLTESNKKF  6        0.2589
3038.0    50.00  0.49     Sequence
             DRB1_0301  552      LTGTGVLTESNKKFL  LTESNKKFL  6        0.4577
353.5    13.00  0.50     Sequence
             DRB1_0301  553      TGTGVLTESNKKFLP  LTESNKKFL  5        0.5047
212.6     8.50  0.55     Sequence         WB
             DRB1_0301  554      GTGVLTESNKKFLPF  LTESNKKFL  4        0.5586
118.6     5.50  0.55     Sequence         WB
             DRB1_0301  555      TGVLTESNKKFLPFQ  LTESNKKFL  3        0.5618
114.5     5.00  0.56     Sequence         WB
             DRB1_0301  556      GVLTESNKKFLPFQQ  LTESNKKFL  2        0.5160
188.1     7.50  0.56     Sequence         WB
             DRB1_0301  557      VLTESNKKFLPFQQF  LTESNKKFL  1        0.4305
474.1    16.00  0.57     Sequence
             DRB1_0301  558      LTESNKKFLPFQQFG  LTESNKKFL  0        0.2509
3312.6    55.00  0.48     Sequence
             DRB1_0301  559      TESNKKFLPFQQFGR  FLPFQQFGR  6        0.1162
14229.2    95.00  0.45     Sequence
             DRB1_0301  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5        0.1405
10937.7    85.00  0.51     Sequence
             DRB1_0301  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4        0.1574
9107.3    85.00  0.50     Sequence
             DRB1_0301  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.1824
6950.5    75.00  0.40     Sequence
             DRB1_0301  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.1971
5924.2    70.00  0.29     Sequence
             DRB1_0301  564      KFLPFQQFGRDIADT  FQQFGRDIA  4        0.2200
4627.0    65.00  0.34     Sequence
             DRB1_0301  565      FLPFQQFGRDIADTT  FGRDIADTT  6        0.2842
2308.5    43.00  0.60     Sequence
             DRB1_0301  566      LPFQQFGRDIADTTD  FGRDIADTT  5        0.3185
1592.7    34.00  0.76     Sequence
             DRB1_0301  567      PFQQFGRDIADTTDA  FGRDIADTT  4        0.3396
1268.6    30.00  0.81     Sequence
             DRB1_0301  568      FQQFGRDIADTTDAV  FGRDIADTT  3        0.3583
1035.9    26.00  0.74     Sequence
```

```
             DRB1_0301  569      QQFGRDIADTTDAVR  FGRDIADTT  2        0.3832
791.7    22.00  0.59     Sequence
             DRB1_0301  570      QFGRDIADTTDAVRD  FGRDIADTT  1        0.3575
1044.8    26.00  0.41     Sequence
             DRB1_0301  571      FGRDIADTTDAVRDP  DIADTTDAV  3        0.2922
2118.0    41.00  0.48     Sequence
             DRB1_0301  572      GRDIADTTDAVRDPQ  DIADTTDAV  2        0.2612
2963.4    49.00  0.47     Sequence
             DRB1_0301  573      RDIADTTDAVRDPQT  DIADTTDAV  1        0.2353
3920.5    60.00  0.39     Sequence
             DRB1_0301  574      DIADTTDAVRDPQTL  IADTTDAVR  1        0.1799
7142.3    75.00  0.28     Sequence
             DRB1_0301  575      IADTTDAVRDPQTLE  AVRDPQTLE  6        0.1830
6905.9    75.00  0.50     Sequence
             DRB1_0301  576      ADTTDAVRDPQTLEI  AVRDPQTLE  5        0.2204
4605.6    65.00  0.70     Sequence
             DRB1_0301  577      DTTDAVRDPQTLEIL  AVRDPQTLE  4        0.2521
3268.6    55.00  0.68     Sequence
             DRB1_0301  578      TTDAVRDPQTLEILD  AVRDPQTLE  3        0.2604
2987.2    49.00  0.68     Sequence
             DRB1_0301  579      TDAVRDPQTLEILDI  AVRDPQTLE  2        0.2531
3233.0    55.00  0.67     Sequence
             DRB1_0301  580      DAVRDPQTLEILDIT  AVRDPQTLE  1        0.2217
4542.5    65.00  0.56     Sequence
             DRB1_0301  581      AVRDPQTLEILDITP  AVRDPQTLE  0        0.1430
10646.8    85.00  0.33     Sequence
             DRB1_0301  582      VRDPQTLEILDITPC  EILDITPCX  7        0.1279
12535.5    90.00  0.25     Sequence
             DRB1_0301  583      RDPQTLEILDITPCS  EILDITPCS  6        0.2665
2797.5    47.00  0.65     Sequence
             DRB1_0301  584      DPQTLEILDITPCSF  EILDITPCS  5        0.3732
881.6    24.00  0.62     Sequence
             DRB1_0301  585      PQTLEILDITPCSFG  EILDITPCS  4        0.3941
703.5    20.00  0.58     Sequence
             DRB1_0301  586      QTLEILDITPCSFGG  EILDITPCS  3        0.3891
742.1    21.00  0.58     Sequence
             DRB1_0301  587      TLEILDITPCSFGGV  EILDITPCS  2        0.3757
858.3    23.00  0.50     Sequence
             DRB1_0301  588      LEILDITPCSFGGVS  EILDITPCS  1        0.3369
1306.3    30.00  0.46     Sequence
             DRB1_0301  589      EILDITPCSFGGVSV  EILDITPCS  0        0.2636
2887.7    48.00  0.25     Sequence
             DRB1_0301  590      ILDITPCSFGGVSVI  ITPCSFGGV  3        0.1689
8043.7    80.00  0.33     Sequence
             DRB1_0301  591      LDITPCSFGGVSVIT  CSFGGVSVI  5        0.1384
11187.7    90.00  0.50     Sequence
             DRB1_0301  592      DITPCSFGGVSVITP  CSFGGVSVI  4        0.1298
12280.1    90.00  0.49     Sequence
             DRB1_0301  593      ITPCSFGGVSVITPG  CSFGGVSVI  3        0.1213
13454.4    90.00  0.52     Sequence
             DRB1_0301  594      TPCSFGGVSVITPGT  CSFGGVSVI  2        0.1087
15416.8    95.00  0.51     Sequence
             DRB1_0301  595      PCSFGGVSVITPGTN  CSFGGVSVI  1        0.1008
16798.2    95.00  0.35     Sequence
             DRB1_0301  596      CSFGGVSVITPGTNT  FGGVSVITP  2        0.0824
20506.5   100.00  0.25     Sequence
             DRB1_0301  597      SFGGVSVITPGTNTS  VITPGTNTS  6        0.0987
17184.6    95.00  0.25     Sequence
             DRB1_0301  598      FGGVSVITPGTNTSN  VITPGTNTS  5        0.1132
14686.2    95.00  0.37     Sequence
             DRB1_0301  599      GGVSVITPGTNTSNQ  VITPGTNTS  4        0.1280
12516.4    90.00  0.38     Sequence
             DRB1_0301  600      GVSVITPGTNTSNQV  ITPGTNTSN  4        0.1410
10877.0    85.00  0.45     Sequence
             DRB1_0301  601      VSVITPGTNTSNQVA  ITPGTNTSN  3        0.1352
11583.3    90.00  0.48     Sequence
```

```
             DRB1_0301  602      SVITPGTNTSNQVAV  ITPGTNTSN  2        0.1266
12713.2    90.00  0.35     Sequence
             DRB1_0301  603      VITPGTNTSNQVAVL  TNTSNQVAV  5        0.1333
11824.6    90.00  0.61     Sequence
             DRB1_0301  604      ITPGTNTSNQVAVLY  TNTSNQVAV  4        0.1651
8376.7    80.00  0.62     Sequence
             DRB1_0301  605      TPGTNTSNQVAVLYQ  TNTSNQVAV  3        0.1789
7212.8    75.00  0.56     Sequence
             DRB1_0301  606      PGTNTSNQVAVLYQG  TNTSNQVAV  2        0.1629
8582.6    80.00  0.50     Sequence
             DRB1_0301  607      GTNTSNQVAVLYQGV  TNTSNQVAV  1        0.1403
10959.2    85.00  0.35     Sequence
             DRB1_0301  608      TNTSNQVAVLYQGVN  SNQVAVLYQ  3        0.1037
16284.4    95.00  0.20     Sequence
             DRB1_0301  609      NTSNQVAVLYQGVNC  VLYQGVNCX  7        0.1009
16783.8    95.00  0.17     Sequence
             DRB1_0301  610      TSNQVAVLYQGVNCT  VLYQGVNCT  6        0.1287
12424.2    90.00  0.50     Sequence
             DRB1_0301  611      SNQVAVLYQGVNCTE  VLYQGVNCT  5        0.1633
8539.6    80.00  0.50     Sequence
             DRB1_0301  612      NQVAVLYQGVNCTEV  VLYQGVNCT  4        0.1954
6037.8    70.00  0.47     Sequence
             DRB1_0301  613      QVAVLYQGVNCTEVP  VLYQGVNCT  3        0.1883
6517.9    75.00  0.47     Sequence
             DRB1_0301  614      VAVLYQGVNCTEVPV  VLYQGVNCT  2        0.1874
6583.7    75.00  0.40     Sequence
             DRB1_0301  615      AVLYQGVNCTEVPVA  LYQGVNCTE  2        0.1751
7516.0    75.00  0.29     Sequence
             DRB1_0301  616      VLYQGVNCTEVPVAI  VNCTEVPVA  5        0.1734
7658.5    80.00  0.38     Sequence
             DRB1_0301  617      LYQGVNCTEVPVAIH  VNCTEVPVA  4        0.1876
6569.0    75.00  0.44     Sequence
             DRB1_0301  618      YQGVNCTEVPVAIHA  VNCTEVPVA  3        0.1966
5959.7    70.00  0.39     Sequence
             DRB1_0301  619      QGVNCTEVPVAIHAD  VNCTEVPVA  2        0.1925
6230.8    70.00  0.34     Sequence
             DRB1_0301  620      GVNCTEVPVAIHADQ  NCTEVPVAI  2        0.1684
8087.4    80.00  0.25     Sequence
             DRB1_0301  621      VNCTEVPVAIHADQL  CTEVPVAIH  2        0.1516
9694.8    85.00  0.23     Sequence
             DRB1_0301  622      NCTEVPVAIHADQLT  VPVAIHADQ  4        0.1512
9734.0    85.00  0.31     Sequence
             DRB1_0301  623      CTEVPVAIHADQLTP  IHADQLTPX  7        0.2835
2327.5    43.00  0.41     Sequence
             DRB1_0301  624      TEVPVAIHADQLTPT  IHADQLTPT  6        0.6031
73.3     3.50  0.94     Sequence         WB
             DRB1_0301  625      EVPVAIHADQLTPTW  IHADQLTPT  5        0.7091
23.3     0.90  0.96     Sequence         SB
             DRB1_0301  626      VPVAIHADQLTPTWR  IHADQLTPT  4        0.7602
13.4     0.40  0.96     Sequence         SB
             DRB1_0301  627      PVAIHADQLTPTWRV  IHADQLTPT  3        0.7728
11.7     0.25  0.96     Sequence         SB
             DRB1_0301  628      VAIHADQLTPTWRVY  IHADQLTPT  2        0.7512
14.8     0.40  0.93     Sequence         SB
             DRB1_0301  629      AIHADQLTPTWRVYS  IHADQLTPT  1        0.6749
33.7     1.40  0.82     Sequence         SB
             DRB1_0301  630      IHADQLTPTWRVYST  IHADQLTPT  0        0.4739
296.6    11.00  0.42     Sequence
             DRB1_0301  631      HADQLTPTWRVYSTG  LTPTWRVYS  4        0.2793
2435.9    44.00  0.73     Sequence
             DRB1_0301  632      ADQLTPTWRVYSTGS  LTPTWRVYS  3        0.2689
2724.1    47.00  0.79     Sequence
             DRB1_0301  633      DQLTPTWRVYSTGSN  LTPTWRVYS  2        0.2376
3823.9    60.00  0.81     Sequence
             DRB1_0301  634      QLTPTWRVYSTGSNV  LTPTWRVYS  1        0.1941
6124.0    70.00  0.62     Sequence
```

```
             DRB1_0301  635      LTPTWRVYSTGSNVF  VYSTGSNVF  6        0.1568
9162.7    85.00  0.40     Sequence
             DRB1_0301  636      TPTWRVYSTGSNVFQ  VYSTGSNVF  5        0.1640
8475.4    80.00  0.58     Sequence
             DRB1_0301  637      PTWRVYSTGSNVFQT  VYSTGSNVF  4        0.1877
6563.3    75.00  0.61     Sequence
             DRB1_0301  638      TWRVYSTGSNVFQTR  VYSTGSNVF  3        0.2091
5202.6    65.00  0.60     Sequence
             DRB1_0301  639      WRVYSTGSNVFQTRA  VYSTGSNVF  2        0.1931
6189.4    70.00  0.56     Sequence
             DRB1_0301  640      RVYSTGSNVFQTRAG  VYSTGSNVF  1        0.1632
8552.2    80.00  0.50     Sequence
             DRB1_0301  641      VYSTGSNVFQTRAGC  STGSNVFQT  2        0.0989
17146.2    95.00  0.22     Sequence
             DRB1_0301  642      YSTGSNVFQTRAGCL  VFQTRAGCL  6        0.1101
15197.4    95.00  0.31     Sequence
             DRB1_0301  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.1517
9685.6    85.00  0.44     Sequence
             DRB1_0301  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.1623
8639.5    80.00  0.38     Sequence
             DRB1_0301  645      GSNVFQTRAGCLIGA  VFQTRAGCL  3        0.1750
7530.0    75.00  0.37     Sequence
             DRB1_0301  646      SNVFQTRAGCLIGAE  VFQTRAGCL  2        0.1701
7939.9    80.00  0.34     Sequence
             DRB1_0301  647      NVFQTRAGCLIGAEY  FQTRAGCLI  2        0.1526
9591.3    85.00  0.24     Sequence
             DRB1_0301  648      VFQTRAGCLIGAEYV  TRAGCLIGA  3        0.1405
10930.1    85.00  0.29     Sequence
             DRB1_0301  649      FQTRAGCLIGAEYVN  TRAGCLIGA  2        0.1348
11627.9    90.00  0.22     Sequence
             DRB1_0301  650      QTRAGCLIGAEYVNN  LIGAEYVNN  6        0.1479
10093.3    85.00  0.25     Sequence
             DRB1_0301  651      TRAGCLIGAEYVNNS  IGAEYVNNS  6        0.1797
7154.9    75.00  0.31     Sequence
             DRB1_0301  652      RAGCLIGAEYVNNSY  IGAEYVNNS  5        0.2130
4988.8    65.00  0.44     Sequence
             DRB1_0301  653      AGCLIGAEYVNNSYE  IGAEYVNNS  4        0.2119
5050.8    65.00  0.46     Sequence
             DRB1_0301  654      GCLIGAEYVNNSYEC  IGAEYVNNS  3        0.2016
5644.1    70.00  0.52     Sequence
             DRB1_0301  655      CLIGAEYVNNSYECD  IGAEYVNNS  2        0.1719
7784.7    80.00  0.50     Sequence
             DRB1_0301  656      LIGAEYVNNSYECDI  IGAEYVNNS  1        0.1613
8733.4    80.00  0.38     Sequence
             DRB1_0301  657      IGAEYVNNSYECDIP  VNNSYECDI  5        0.1249
12943.0    90.00  0.43     Sequence
             DRB1_0301  658      GAEYVNNSYECDIPI  VNNSYECDI  4        0.1212
13471.3    90.00  0.54     Sequence
             DRB1_0301  659      AEYVNNSYECDIPIG  YECDIPIGX  7        0.1681
8112.1    80.00  0.27     Sequence
             DRB1_0301  660      EYVNNSYECDIPIGA  YECDIPIGA  6        0.3480
1158.2    28.00  0.79     Sequence
             DRB1_0301  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.3768
848.3    23.00  0.83     Sequence
             DRB1_0301  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.4009
653.4    19.00  0.87     Sequence
             DRB1_0301  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.3920
719.4    21.00  0.86     Sequence
             DRB1_0301  664      NSYECDIPIGAGICA  YECDIPIGA  2        0.3724
889.1    24.00  0.79     Sequence
             DRB1_0301  665      SYECDIPIGAGICAS  YECDIPIGA  1        0.3212
1547.0    34.00  0.69     Sequence
             DRB1_0301  666      YECDIPIGAGICASY  YECDIPIGA  0        0.2007
5699.5    70.00  0.34     Sequence
             DRB1_0301  667      ECDIPIGAGICASYQ  IGAGICASY  5        0.1458
10328.3    85.00  0.38     Sequence
```

```
             DRB1_0301  668      CDIPIGAGICASYQT  IGAGICASY  4        0.1473
10161.3    85.00  0.49     Sequence
             DRB1_0301  669      DIPIGAGICASYQTQ  IGAGICASY  3        0.1576
9084.7    80.00  0.50     Sequence
             DRB1_0301  670      IPIGAGICASYQTQT  ICASYQTQT  6        0.2222
4519.0    60.00  0.52     Sequence
             DRB1_0301  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.2601
2996.6    49.00  0.68     Sequence
             DRB1_0301  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.2707
2672.1    46.00  0.80     Sequence
             DRB1_0301  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.2407
3699.4    55.00  0.82     Sequence
             DRB1_0301  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.2264
4317.8    60.00  0.78     Sequence
             DRB1_0301  675      GICASYQTQTNSPRR  ICASYQTQT  1        0.2038
5510.8    70.00  0.56     Sequence
             DRB1_0301  676      ICASYQTQTNSPRRA  ICASYQTQT  0        0.1494
9934.7    85.00  0.28     Sequence
             DRB1_0301  677      CASYQTQTNSPRRAR  TQTNSPRRA  5        0.1550
9344.2    85.00  0.31     Sequence
             DRB1_0301  678      ASYQTQTNSPRRARS  TQTNSPRRA  4        0.1824
6951.8    75.00  0.27     Sequence
             DRB1_0301  679      SYQTQTNSPRRARSV  TQTNSPRRA  3        0.1937
6151.0    70.00  0.25     Sequence
             DRB1_0301  680      YQTQTNSPRRARSVA  QTNSPRRAR  3        0.1851
6745.1    75.00  0.34     Sequence
             DRB1_0301  681      QTQTNSPRRARSVAS  QTNSPRRAR  2        0.1612
8735.8    80.00  0.33     Sequence
             DRB1_0301  682      TQTNSPRRARSVASQ  TNSPRRARS  2        0.1271
12637.3    90.00  0.28     Sequence
             DRB1_0301  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.1073
15654.7    95.00  0.31     Sequence
             DRB1_0301  684      TNSPRRARSVASQSI  PRRARSVAS  3        0.1046
16130.1    95.00  0.34     Sequence
             DRB1_0301  685      NSPRRARSVASQSII  RARSVASQS  4        0.1256
12851.5    90.00  0.28     Sequence
             DRB1_0301  686      SPRRARSVASQSIIA  SVASQSIIA  6        0.1596
8888.5    80.00  0.23     Sequence
             DRB1_0301  687      PRRARSVASQSIIAY  VASQSIIAY  6        0.2367
3861.3    60.00  0.40     Sequence
             DRB1_0301  688      RRARSVASQSIIAYT  VASQSIIAY  5        0.2867
2249.0    42.00  0.51     Sequence
             DRB1_0301  689      RARSVASQSIIAYTM  VASQSIIAY  4        0.3028
1888.7    38.00  0.56     Sequence
             DRB1_0301  690      ARSVASQSIIAYTMS  VASQSIIAY  3        0.2887
2198.6    41.00  0.62     Sequence
             DRB1_0301  691      RSVASQSIIAYTMSL  VASQSIIAY  2        0.2738
2584.7    45.00  0.55     Sequence
             DRB1_0301  692      SVASQSIIAYTMSLG  VASQSIIAY  1        0.2501
3341.5    55.00  0.38     Sequence
             DRB1_0301  693      VASQSIIAYTMSLGA  IAYTMSLGA  6        0.2570
3100.7    50.00  0.49     Sequence
             DRB1_0301  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.2756
2535.3    45.00  0.56     Sequence
             DRB1_0301  695      SQSIIAYTMSLGAEN  IAYTMSLGA  4        0.2846
2299.5    42.00  0.56     Sequence
             DRB1_0301  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.2821
2361.6    43.00  0.59     Sequence
             DRB1_0301  697      SIIAYTMSLGAENSV  IAYTMSLGA  2        0.2496
3357.3    55.00  0.54     Sequence
             DRB1_0301  698      IIAYTMSLGAENSVA  YTMSLGAEN  3        0.1990
5802.8    70.00  0.34     Sequence
             DRB1_0301  699      IAYTMSLGAENSVAY  LGAENSVAY  6        0.2691
2718.6    47.00  0.58     Sequence
             DRB1_0301  700      AYTMSLGAENSVAYS  LGAENSVAY  5        0.3426
1228.2    29.00  0.70     Sequence
```

```
             DRB1_0301  701      YTMSLGAENSVAYSN  LGAENSVAY  4        0.3659
953.7    25.00  0.78     Sequence
             DRB1_0301  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.3682
930.7    24.00  0.80     Sequence
             DRB1_0301  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.3299
1408.9    32.00  0.79     Sequence
             DRB1_0301  704      SLGAENSVAYSNNSI  LGAENSVAY  1        0.2642
2867.9    48.00  0.70     Sequence
             DRB1_0301  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.1919
6266.5    70.00  0.31     Sequence
             DRB1_0301  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.2068
5336.6    65.00  0.50     Sequence
             DRB1_0301  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.2098
5163.8    65.00  0.44     Sequence
             DRB1_0301  708      ENSVAYSNNSIAIPT  AYSNNSIAI  4        0.2273
4275.0    60.00  0.50     Sequence
             DRB1_0301  709      NSVAYSNNSIAIPTN  AYSNNSIAI  3        0.2210
4573.7    65.00  0.54     Sequence
             DRB1_0301  710      SVAYSNNSIAIPTNF  AYSNNSIAI  2        0.1934
6169.2    70.00  0.50     Sequence
             DRB1_0301  711      VAYSNNSIAIPTNFT  AYSNNSIAI  1        0.1303
12211.2    90.00  0.40     Sequence
             DRB1_0301  712      AYSNNSIAIPTNFTI  IAIPTNFTI  6        0.0902
18836.1   100.00  0.29     Sequence
             DRB1_0301  713      YSNNSIAIPTNFTIS  IAIPTNFTI  5        0.1069
15722.0    95.00  0.41     Sequence
             DRB1_0301  714      SNNSIAIPTNFTISV  IPTNFTISV  6        0.1354
11552.4    90.00  0.43     Sequence
             DRB1_0301  715      NNSIAIPTNFTISVT  IPTNFTISV  5        0.1533
9521.6    85.00  0.53     Sequence
             DRB1_0301  716      NSIAIPTNFTISVTT  IPTNFTISV  4        0.1582
9031.7    80.00  0.58     Sequence
             DRB1_0301  717      SIAIPTNFTISVTTE  IPTNFTISV  3        0.1714
7824.0    80.00  0.56     Sequence
             DRB1_0301  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.2040
5497.4    70.00  0.55     Sequence
             DRB1_0301  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.2391
3762.4    55.00  0.72     Sequence
             DRB1_0301  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.2556
3146.6    50.00  0.56     Sequence
             DRB1_0301  721      PTNFTISVTTEILPV  ISVTTEILP  5        0.2858
2271.0    42.00  0.47     Sequence
             DRB1_0301  722      TNFTISVTTEILPVS  ISVTTEILP  4        0.2947
2061.4    40.00  0.51     Sequence
             DRB1_0301  723      NFTISVTTEILPVSM  ISVTTEILP  3        0.2956
2040.5    40.00  0.52     Sequence
             DRB1_0301  724      FTISVTTEILPVSMT  ISVTTEILP  2        0.2920
2122.0    41.00  0.43     Sequence
             DRB1_0301  725      TISVTTEILPVSMTK  ISVTTEILP  1        0.2931
2098.0    40.00  0.28     Sequence
             DRB1_0301  726      ISVTTEILPVSMTKT  VTTEILPVS  2        0.2662
2805.0    47.00  0.28     Sequence
             DRB1_0301  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.2459
3494.8    55.00  0.25     Sequence
             DRB1_0301  728      VTTEILPVSMTKTSV  LPVSMTKTS  5        0.2569
3101.6    50.00  0.28     Sequence
             DRB1_0301  729      TTEILPVSMTKTSVD  LPVSMTKTS  4        0.2548
3173.3    55.00  0.33     Sequence
             DRB1_0301  730      TEILPVSMTKTSVDC  LPVSMTKTS  3        0.2494
3366.7    55.00  0.34     Sequence
             DRB1_0301  731      EILPVSMTKTSVDCT  VSMTKTSVD  4        0.2474
3438.4    55.00  0.33     Sequence
             DRB1_0301  732      ILPVSMTKTSVDCTM  MTKTSVDCT  5        0.2609
2971.1    49.00  0.34     Sequence
             DRB1_0301  733      LPVSMTKTSVDCTMY  MTKTSVDCT  4        0.3013
1919.0    38.00  0.37     Sequence
```

```
             DRB1_0301  734      PVSMTKTSVDCTMYI  TSVDCTMYI  6        0.3961
687.9    20.00  0.49     Sequence
             DRB1_0301  735      VSMTKTSVDCTMYIC  TSVDCTMYI  5        0.4283
485.5    16.00  0.56     Sequence
             DRB1_0301  736      SMTKTSVDCTMYICG  TSVDCTMYI  4        0.4042
630.7    19.00  0.60     Sequence
             DRB1_0301  737      MTKTSVDCTMYICGD  TSVDCTMYI  3        0.3666
947.4    25.00  0.68     Sequence
             DRB1_0301  738      TKTSVDCTMYICGDS  TSVDCTMYI  2        0.3200
1568.7    34.00  0.68     Sequence
             DRB1_0301  739      KTSVDCTMYICGDST  TSVDCTMYI  1        0.2599
3004.6    49.00  0.60     Sequence
             DRB1_0301  740      TSVDCTMYICGDSTE  VDCTMYICG  2        0.1590
8954.7    80.00  0.38     Sequence
             DRB1_0301  741      SVDCTMYICGDSTEC  ICGDSTECX  7        0.1367
11387.9    90.00  0.22     Sequence
             DRB1_0301  742      VDCTMYICGDSTECS  ICGDSTECS  6        0.2330
4020.0    60.00  0.65     Sequence
             DRB1_0301  743      DCTMYICGDSTECSN  ICGDSTECS  5        0.2896
2177.6    41.00  0.75     Sequence
             DRB1_0301  744      CTMYICGDSTECSNL  ICGDSTECS  4        0.3221
1533.4    33.00  0.79     Sequence
             DRB1_0301  745      TMYICGDSTECSNLL  ICGDSTECS  3        0.3386
1282.6    30.00  0.79     Sequence
             DRB1_0301  746      MYICGDSTECSNLLL  ICGDSTECS  2        0.3078
1788.4    37.00  0.70     Sequence
             DRB1_0301  747      YICGDSTECSNLLLQ  ICGDSTECS  1        0.2736
2590.6    45.00  0.55     Sequence
             DRB1_0301  748      ICGDSTECSNLLLQY  TECSNLLLQ  5        0.2191
4672.4    65.00  0.33     Sequence
             DRB1_0301  749      CGDSTECSNLLLQYG  TECSNLLLQ  4        0.1666
8240.3    80.00  0.43     Sequence
             DRB1_0301  750      GDSTECSNLLLQYGS  TECSNLLLQ  3        0.1726
7727.0    80.00  0.44     Sequence
             DRB1_0301  751      DSTECSNLLLQYGSF  TECSNLLLQ  2        0.1587
8982.5    80.00  0.42     Sequence
             DRB1_0301  752      STECSNLLLQYGSFC  TECSNLLLQ  1        0.1275
12589.7    90.00  0.31     Sequence
             DRB1_0301  753      TECSNLLLQYGSFCT  LLLQYGSFC  5        0.1113
14995.0    95.00  0.43     Sequence
             DRB1_0301  754      ECSNLLLQYGSFCTQ  LLLQYGSFC  4        0.1194
13733.5    90.00  0.46     Sequence
             DRB1_0301  755      CSNLLLQYGSFCTQL  LLLQYGSFC  3        0.1404
10943.5    85.00  0.44     Sequence
             DRB1_0301  756      SNLLLQYGSFCTQLN  LLLQYGSFC  2        0.1481
10066.1    85.00  0.41     Sequence
             DRB1_0301  757      NLLLQYGSFCTQLNR  GSFCTQLNR  6        0.1718
7789.1    80.00  0.31     Sequence
             DRB1_0301  758      LLLQYGSFCTQLNRA  GSFCTQLNR  5        0.1871
6602.6    75.00  0.43     Sequence
             DRB1_0301  759      LLQYGSFCTQLNRAL  GSFCTQLNR  4        0.1945
6096.2    70.00  0.48     Sequence
             DRB1_0301  760      LQYGSFCTQLNRALT  GSFCTQLNR  3        0.2152
4872.6    65.00  0.45     Sequence
             DRB1_0301  761      QYGSFCTQLNRALTG  GSFCTQLNR  2        0.2150
4883.8    65.00  0.34     Sequence
             DRB1_0301  762      YGSFCTQLNRALTGI  CTQLNRALT  4        0.2152
4874.0    65.00  0.28     Sequence
             DRB1_0301  763      GSFCTQLNRALTGIA  TQLNRALTG  4        0.2280
4240.1    60.00  0.28     Sequence
             DRB1_0301  764      SFCTQLNRALTGIAV  LNRALTGIA  5        0.2513
3298.4    55.00  0.44     Sequence
             DRB1_0301  765      FCTQLNRALTGIAVE  LNRALTGIA  4        0.2518
3278.7    55.00  0.54     Sequence
             DRB1_0301  766      CTQLNRALTGIAVEQ  LNRALTGIA  3        0.2415
3664.5    55.00  0.63     Sequence
```

```
             DRB1_0301  767      TQLNRALTGIAVEQD  LNRALTGIA  2        0.2367
3862.9    60.00  0.60     Sequence
             DRB1_0301  768      QLNRALTGIAVEQDK  LNRALTGIA  1        0.2120
5045.5    65.00  0.40     Sequence
             DRB1_0301  769      LNRALTGIAVEQDKN  LTGIAVEQD  4        0.1766
7400.3    75.00  0.31     Sequence
             DRB1_0301  770      NRALTGIAVEQDKNT  IAVEQDKNT  6        0.2057
5402.0    70.00  0.38     Sequence
             DRB1_0301  771      RALTGIAVEQDKNTQ  IAVEQDKNT  5        0.2466
3469.2    55.00  0.51     Sequence
             DRB1_0301  772      ALTGIAVEQDKNTQE  IAVEQDKNT  4        0.2761
2521.6    45.00  0.52     Sequence
             DRB1_0301  773      LTGIAVEQDKNTQEV  IAVEQDKNT  3        0.3184
1594.8    34.00  0.48     Sequence
             DRB1_0301  774      TGIAVEQDKNTQEVF  VEQDKNTQE  4        0.3233
1513.1    33.00  0.52     Sequence
             DRB1_0301  775      GIAVEQDKNTQEVFA  VEQDKNTQE  3        0.3077
1790.1    37.00  0.56     Sequence
             DRB1_0301  776      IAVEQDKNTQEVFAQ  VEQDKNTQE  2        0.2618
2941.7    49.00  0.60     Sequence
             DRB1_0301  777      AVEQDKNTQEVFAQV  VEQDKNTQE  1        0.1864
6656.7    75.00  0.54     Sequence
             DRB1_0301  778      VEQDKNTQEVFAQVK  VEQDKNTQE  0        0.1432
10618.5    85.00  0.25     Sequence
             DRB1_0301  779      EQDKNTQEVFAQVKQ  KNTQEVFAQ  3        0.1286
12439.8    90.00  0.24     Sequence
             DRB1_0301  780      QDKNTQEVFAQVKQI  VFAQVKQIX  7        0.1543
9420.0    85.00  0.26     Sequence
             DRB1_0301  781      DKNTQEVFAQVKQIY  VFAQVKQIY  6        0.3198
1570.9    34.00  0.81     Sequence
             DRB1_0301  782      KNTQEVFAQVKQIYK  VFAQVKQIY  5        0.4256
499.9    16.00  0.83     Sequence
             DRB1_0301  783      NTQEVFAQVKQIYKT  VFAQVKQIY  4        0.4574
354.7    13.00  0.82     Sequence
             DRB1_0301  784      TQEVFAQVKQIYKTP  VFAQVKQIY  3        0.4351
451.2    15.00  0.82     Sequence
             DRB1_0301  785      QEVFAQVKQIYKTPP  VFAQVKQIY  2        0.3944
701.0    20.00  0.76     Sequence
             DRB1_0301  786      EVFAQVKQIYKTPPI  VFAQVKQIY  1        0.3185
1592.6    34.00  0.66     Sequence
             DRB1_0301  787      VFAQVKQIYKTPPIK  VFAQVKQIY  0        0.2481
3411.7    55.00  0.36     Sequence
             DRB1_0301  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6        0.2614
2956.3    49.00  0.66     Sequence
             DRB1_0301  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.3285
1430.2    32.00  0.75     Sequence
             DRB1_0301  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.3216
1541.3    34.00  0.81     Sequence
             DRB1_0301  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.3009
1928.5    38.00  0.85     Sequence
             DRB1_0301  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.2629
2908.3    48.00  0.86     Sequence
             DRB1_0301  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.1908
6342.4    70.00  0.73     Sequence
             DRB1_0301  794      IYKTPPIKDFGGFNF  IYKTPPIKD  0        0.1006
16843.1    95.00  0.25     Sequence
             DRB1_0301  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.0974
17430.1    95.00  0.41     Sequence
             DRB1_0301  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.1116
14950.8    95.00  0.38     Sequence
             DRB1_0301  797      TPPIKDFGGFNFSQI  IKDFGGFNF  3        0.1233
13168.0    90.00  0.34     Sequence
             DRB1_0301  798      PPIKDFGGFNFSQIL  IKDFGGFNF  2        0.1269
12668.6    90.00  0.31     Sequence
             DRB1_0301  799      PIKDFGGFNFSQILP  FNFSQILPX  7        0.1291
12367.7    90.00  0.22     Sequence
```

```
             DRB1_0301  800      IKDFGGFNFSQILPD  FNFSQILPD  6        0.2363
3877.8    60.00  0.73     Sequence
             DRB1_0301  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.2575
3082.1    50.00  0.83     Sequence
             DRB1_0301  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.2820
2365.1    43.00  0.85     Sequence
             DRB1_0301  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.3009
1928.7    38.00  0.81     Sequence
             DRB1_0301  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.2970
2010.2    39.00  0.71     Sequence
             DRB1_0301  805      GFNFSQILPDPSKPS  ILPDPSKPS  6        0.3271
1452.2    32.00  0.52     Sequence
             DRB1_0301  806      FNFSQILPDPSKPSK  ILPDPSKPS  5        0.3490
1146.2    28.00  0.79     Sequence
             DRB1_0301  807      NFSQILPDPSKPSKR  ILPDPSKPS  4        0.3793
825.5    23.00  0.87     Sequence
             DRB1_0301  808      FSQILPDPSKPSKRS  ILPDPSKPS  3        0.3913
724.9    21.00  0.91     Sequence
             DRB1_0301  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.3728
886.0    24.00  0.88     Sequence
             DRB1_0301  810      QILPDPSKPSKRSFI  ILPDPSKPS  1        0.3094
1759.0    36.00  0.78     Sequence
             DRB1_0301  811      ILPDPSKPSKRSFIE  ILPDPSKPS  0        0.1744
7579.6    80.00  0.45     Sequence
             DRB1_0301  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.0753
22133.4   100.00  0.47     Sequence
             DRB1_0301  813      PDPSKPSKRSFIEDL  SKPSKRSFI  3        0.0809
20836.4   100.00  0.41     Sequence
             DRB1_0301  814      DPSKPSKRSFIEDLL  SKRSFIEDL  5        0.1078
15573.7    95.00  0.41     Sequence
             DRB1_0301  815      PSKPSKRSFIEDLLF  SKRSFIEDL  4        0.1654
8353.1    80.00  0.29     Sequence
             DRB1_0301  816      SKPSKRSFIEDLLFN  FIEDLLFNX  7        0.2685
2735.9    47.00  0.37     Sequence
             DRB1_0301  817      KPSKRSFIEDLLFNK  FIEDLLFNK  6        0.3958
690.1    20.00  0.73     Sequence
             DRB1_0301  818      PSKRSFIEDLLFNKV  FIEDLLFNK  5        0.4443
408.6    14.00  0.81     Sequence
             DRB1_0301  819      SKRSFIEDLLFNKVT  FIEDLLFNK  4        0.4556
361.4    13.00  0.83     Sequence
             DRB1_0301  820      KRSFIEDLLFNKVTL  FIEDLLFNK  3        0.4659
323.3    12.00  0.78     Sequence
             DRB1_0301  821      RSFIEDLLFNKVTLA  FIEDLLFNK  2        0.4786
281.7    11.00  0.55     Sequence
             DRB1_0301  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5        0.4693
311.7    12.00  0.41     Sequence
             DRB1_0301  823      FIEDLLFNKVTLADA  LLFNKVTLA  4        0.4333
460.0    15.00  0.55     Sequence
             DRB1_0301  824      IEDLLFNKVTLADAG  LLFNKVTLA  3        0.3966
684.5    20.00  0.62     Sequence
             DRB1_0301  825      EDLLFNKVTLADAGF  LLFNKVTLA  2        0.3668
944.8    25.00  0.56     Sequence
             DRB1_0301  826      DLLFNKVTLADAGFI  LLFNKVTLA  1        0.3739
874.7    24.00  0.36     Sequence
             DRB1_0301  827      LLFNKVTLADAGFIK  TLADAGFIK  6        0.3963
686.6    20.00  0.35     Sequence
             DRB1_0301  828      LFNKVTLADAGFIKQ  TLADAGFIK  5        0.4160
555.1    17.00  0.54     Sequence
             DRB1_0301  829      FNKVTLADAGFIKQY  TLADAGFIK  4        0.4521
375.4    13.00  0.56     Sequence
             DRB1_0301  830      NKVTLADAGFIKQYG  TLADAGFIK  3        0.4460
401.0    14.00  0.60     Sequence
             DRB1_0301  831      KVTLADAGFIKQYGD  TLADAGFIK  2        0.4193
535.4    17.00  0.58     Sequence
             DRB1_0301  832      VTLADAGFIKQYGDC  TLADAGFIK  1        0.3339
1349.3    31.00  0.56     Sequence
```

```
             DRB1_0301  833      TLADAGFIKQYGDCL  TLADAGFIK  0        0.1194
13743.2    90.00  0.31     Sequence
             DRB1_0301  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.0876
19378.8   100.00  0.40     Sequence
             DRB1_0301  835      ADAGFIKQYGDCLGD  IKQYGDCLG  5        0.0992
17100.0    95.00  0.33     Sequence
             DRB1_0301  836      DAGFIKQYGDCLGDI  IKQYGDCLG  4        0.1199
13657.5    90.00  0.34     Sequence
             DRB1_0301  837      AGFIKQYGDCLGDIA  IKQYGDCLG  3        0.1347
11637.1    90.00  0.34     Sequence
             DRB1_0301  838      GFIKQYGDCLGDIAA  QYGDCLGDI  4        0.1394
11066.0    90.00  0.30     Sequence
             DRB1_0301  839      FIKQYGDCLGDIAAR  CLGDIAARX  7        0.2542
3194.2    55.00  0.36     Sequence
             DRB1_0301  840      IKQYGDCLGDIAARD  CLGDIAARD  6        0.4433
413.1    14.00  0.85     Sequence
             DRB1_0301  841      KQYGDCLGDIAARDL  CLGDIAARD  5        0.5333
156.0     6.50  0.92     Sequence         WB
             DRB1_0301  842      QYGDCLGDIAARDLI  CLGDIAARD  4        0.5725
102.0     4.50  0.90     Sequence         WB
             DRB1_0301  843      YGDCLGDIAARDLIC  CLGDIAARD  3        0.5758
98.4     4.50  0.88     Sequence         WB
             DRB1_0301  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.5607
116.0     5.00  0.82     Sequence         WB
             DRB1_0301  845      DCLGDIAARDLICAQ  CLGDIAARD  1        0.5289
163.6     7.00  0.70     Sequence         WB
             DRB1_0301  846      CLGDIAARDLICAQK  AARDLICAQ  5        0.3987
668.8    20.00  0.44     Sequence
             DRB1_0301  847      LGDIAARDLICAQKF  AARDLICAQ  4        0.3372
1301.1    30.00  0.62     Sequence
             DRB1_0301  848      GDIAARDLICAQKFN  AARDLICAQ  3        0.3544
1080.0    27.00  0.61     Sequence
             DRB1_0301  849      DIAARDLICAQKFNG  AARDLICAQ  2        0.3635
979.6    25.00  0.47     Sequence
             DRB1_0301  850      IAARDLICAQKFNGL  LICAQKFNG  5        0.3688
924.6    24.00  0.53     Sequence
             DRB1_0301  851      AARDLICAQKFNGLT  LICAQKFNG  4        0.3376
1296.4    30.00  0.73     Sequence
             DRB1_0301  852      ARDLICAQKFNGLTV  LICAQKFNG  3        0.3340
1347.9    31.00  0.76     Sequence
             DRB1_0301  853      RDLICAQKFNGLTVL  LICAQKFNG  2        0.3340
1348.0    31.00  0.65     Sequence
             DRB1_0301  854      DLICAQKFNGLTVLP  LICAQKFNG  1        0.2669
2786.3    47.00  0.47     Sequence
             DRB1_0301  855      LICAQKFNGLTVLPP  QKFNGLTVL  4        0.2029
5567.5    70.00  0.23     Sequence
             DRB1_0301  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.1834
6876.9    75.00  0.41     Sequence
             DRB1_0301  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.1831
6898.2    75.00  0.48     Sequence
             DRB1_0301  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.2067
5344.2    65.00  0.43     Sequence
             DRB1_0301  859      QKFNGLTVLPPLLTD  LTVLPPLLT  5        0.2019
5624.3    70.00  0.30     Sequence
             DRB1_0301  860      KFNGLTVLPPLLTDE  LTVLPPLLT  4        0.1837
6851.8    75.00  0.37     Sequence
             DRB1_0301  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.1812
7040.5    75.00  0.44     Sequence
             DRB1_0301  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.1862
6666.7    75.00  0.38     Sequence
             DRB1_0301  863      GLTVLPPLLTDEMIA  LLTDEMIAX  7        0.2521
3269.0    55.00  0.28     Sequence
             DRB1_0301  864      LTVLPPLLTDEMIAQ  LLTDEMIAQ  6        0.3296
1412.5    32.00  0.64     Sequence
             DRB1_0301  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.3976
677.0    20.00  0.63     Sequence
```

```
             DRB1_0301  866      VLPPLLTDEMIAQYT  LLTDEMIAQ  4        0.4458
401.8    14.00  0.56     Sequence
             DRB1_0301  867      LPPLLTDEMIAQYTS  LLTDEMIAQ  3        0.4589
348.9    13.00  0.56     Sequence
             DRB1_0301  868      PPLLTDEMIAQYTSA  LLTDEMIAQ  2        0.4438
410.7    14.00  0.51     Sequence
             DRB1_0301  869      PLLTDEMIAQYTSAL  LTDEMIAQY  2        0.3880
751.2    21.00  0.39     Sequence
             DRB1_0301  870      LLTDEMIAQYTSALL  MIAQYTSAL  5        0.3213
1545.9    34.00  0.44     Sequence
             DRB1_0301  871      LTDEMIAQYTSALLA  MIAQYTSAL  4        0.2936
2085.8    40.00  0.63     Sequence
             DRB1_0301  872      TDEMIAQYTSALLAG  MIAQYTSAL  3        0.2696
2704.3    46.00  0.64     Sequence
             DRB1_0301  873      DEMIAQYTSALLAGT  MIAQYTSAL  2        0.2611
2965.1    49.00  0.58     Sequence
             DRB1_0301  874      EMIAQYTSALLAGTI  MIAQYTSAL  1        0.2261
4330.5    60.00  0.44     Sequence
             DRB1_0301  875      MIAQYTSALLAGTIT  AQYTSALLA  2        0.1522
9628.7    85.00  0.52     Sequence
             DRB1_0301  876      IAQYTSALLAGTITS  AQYTSALLA  1        0.0996
17018.1    95.00  0.50     Sequence
             DRB1_0301  877      AQYTSALLAGTITSG  LLAGTITSG  6        0.0891
19061.8   100.00  0.42     Sequence
             DRB1_0301  878      QYTSALLAGTITSGW  LLAGTITSG  5        0.1278
12538.7    90.00  0.47     Sequence
             DRB1_0301  879      YTSALLAGTITSGWT  LLAGTITSG  4        0.1586
8991.0    80.00  0.43     Sequence
             DRB1_0301  880      TSALLAGTITSGWTF  LAGTITSGW  4        0.1882
6529.0    75.00  0.43     Sequence
             DRB1_0301  881      SALLAGTITSGWTFG  LAGTITSGW  3        0.1870
6608.1    75.00  0.41     Sequence
             DRB1_0301  882      ALLAGTITSGWTFGA  LAGTITSGW  2        0.1811
7046.1    75.00  0.32     Sequence
             DRB1_0301  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.1504
9823.5    85.00  0.43     Sequence
             DRB1_0301  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.1309
12130.5    90.00  0.59     Sequence
             DRB1_0301  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.1234
13155.2    90.00  0.66     Sequence
             DRB1_0301  886      GTITSGWTFGAGAAL  ITSGWTFGA  2        0.1081
15516.9    95.00  0.57     Sequence
             DRB1_0301  887      TITSGWTFGAGAALQ  ITSGWTFGA  1        0.0981
17291.8    95.00  0.37     Sequence
             DRB1_0301  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.1013
16709.9    95.00  0.40     Sequence
             DRB1_0301  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.0957
17761.5    95.00  0.55     Sequence
             DRB1_0301  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.1150
14404.8    95.00  0.54     Sequence
             DRB1_0301  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.1203
13604.7    90.00  0.53     Sequence
             DRB1_0301  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.1258
12819.5    90.00  0.41     Sequence
             DRB1_0301  893      TFGAGAALQIPFAMQ  AALQIPFAM  5        0.1372
11335.9    90.00  0.29     Sequence
             DRB1_0301  894      FGAGAALQIPFAMQM  LQIPFAMQM  6        0.1952
6051.0    70.00  0.54     Sequence
             DRB1_0301  895      GAGAALQIPFAMQMA  LQIPFAMQM  5        0.2428
3613.4    55.00  0.60     Sequence
             DRB1_0301  896      AGAALQIPFAMQMAY  LQIPFAMQM  4        0.3356
1324.6    31.00  0.44     Sequence
             DRB1_0301  897      GAALQIPFAMQMAYR  IPFAMQMAY  5        0.4325
464.3    15.00  0.52     Sequence
             DRB1_0301  898      AALQIPFAMQMAYRF  IPFAMQMAY  4        0.4919
244.2     9.50  0.52     Sequence         WB
```

```
             DRB1_0301  899      ALQIPFAMQMAYRFN  IPFAMQMAY  3        0.5106
199.4     8.00  0.50     Sequence         WB
             DRB1_0301  900      LQIPFAMQMAYRFNG  IPFAMQMAY  2        0.5084
204.2     8.00  0.39     Sequence         WB
             DRB1_0301  901      QIPFAMQMAYRFNGI  MQMAYRFNG  5        0.5030
216.5     8.50  0.40     Sequence         WB
             DRB1_0301  902      IPFAMQMAYRFNGIG  MQMAYRFNG  4        0.4339
457.4    15.00  0.53     Sequence
             DRB1_0301  903      PFAMQMAYRFNGIGV  MQMAYRFNG  3        0.3883
748.7    21.00  0.57     Sequence
             DRB1_0301  904      FAMQMAYRFNGIGVT  MQMAYRFNG  2        0.3199
1568.9    34.00  0.66     Sequence
             DRB1_0301  905      AMQMAYRFNGIGVTQ  MQMAYRFNG  1        0.2634
2892.5    48.00  0.50     Sequence
             DRB1_0301  906      MQMAYRFNGIGVTQN  YRFNGIGVT  4        0.2167
4796.6    65.00  0.44     Sequence
             DRB1_0301  907      QMAYRFNGIGVTQNV  YRFNGIGVT  3        0.1916
6287.2    70.00  0.54     Sequence
             DRB1_0301  908      MAYRFNGIGVTQNVL  YRFNGIGVT  2        0.1890
6469.2    75.00  0.49     Sequence
             DRB1_0301  909      AYRFNGIGVTQNVLY  IGVTQNVLY  6        0.2210
4574.5    65.00  0.38     Sequence
             DRB1_0301  910      YRFNGIGVTQNVLYE  IGVTQNVLY  5        0.2503
3332.8    55.00  0.62     Sequence
             DRB1_0301  911      RFNGIGVTQNVLYEN  IGVTQNVLY  4        0.2688
2729.5    47.00  0.65     Sequence
             DRB1_0301  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.2691
2720.7    47.00  0.66     Sequence
             DRB1_0301  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.2709
2666.9    46.00  0.63     Sequence
             DRB1_0301  914      GIGVTQNVLYENQKL  IGVTQNVLY  1        0.2673
2774.1    47.00  0.51     Sequence
             DRB1_0301  915      IGVTQNVLYENQKLI  VLYENQKLI  6        0.4197
533.0    17.00  0.46     Sequence
             DRB1_0301  916      GVTQNVLYENQKLIA  LYENQKLIA  6        0.5706
104.1     4.50  0.64     Sequence         WB
             DRB1_0301  917      VTQNVLYENQKLIAN  LYENQKLIA  5        0.6316
53.8     2.50  0.69     Sequence         WB
             DRB1_0301  918      TQNVLYENQKLIANQ  LYENQKLIA  4        0.6508
43.8     1.90  0.71     Sequence         SB
             DRB1_0301  919      QNVLYENQKLIANQF  LYENQKLIA  3        0.6504
43.9     1.90  0.76     Sequence         SB
             DRB1_0301  920      NVLYENQKLIANQFN  LYENQKLIA  2        0.6004
75.4     3.50  0.76     Sequence         WB
             DRB1_0301  921      VLYENQKLIANQFNS  LYENQKLIA  1        0.5008
221.6     8.50  0.74     Sequence         WB
             DRB1_0301  922      LYENQKLIANQFNSA  LYENQKLIA  0        0.2762
2518.0    45.00  0.40     Sequence
             DRB1_0301  923      YENQKLIANQFNSAI  LIANQFNSA  5        0.2323
4049.5    60.00  0.62     Sequence
             DRB1_0301  924      ENQKLIANQFNSAIG  LIANQFNSA  4        0.2365
3870.2    60.00  0.60     Sequence
             DRB1_0301  925      NQKLIANQFNSAIGK  LIANQFNSA  3        0.2546
3182.2    55.00  0.57     Sequence
             DRB1_0301  926      QKLIANQFNSAIGKI  LIANQFNSA  2        0.2397
3739.5    55.00  0.50     Sequence
             DRB1_0301  927      KLIANQFNSAIGKIQ  LIANQFNSA  1        0.2006
5705.0    70.00  0.46     Sequence
             DRB1_0301  928      LIANQFNSAIGKIQD  NQFNSAIGK  3        0.1417
10797.9    85.00  0.28     Sequence
             DRB1_0301  929      IANQFNSAIGKIQDS  NQFNSAIGK  2        0.1013
16701.8    95.00  0.37     Sequence
             DRB1_0301  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.0879
19321.8   100.00  0.34     Sequence
             DRB1_0301  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.0882
19248.6   100.00  0.29     Sequence
```

```
             DRB1_0301  932      QFNSAIGKIQDSLSS  IGKIQDSLS  5        0.0958
17737.0    95.00  0.35     Sequence
             DRB1_0301  933      FNSAIGKIQDSLSST  IGKIQDSLS  4        0.1029
16427.6    95.00  0.41     Sequence
             DRB1_0301  934      NSAIGKIQDSLSSTA  IQDSLSSTA  6        0.1325
11919.0    90.00  0.40     Sequence
             DRB1_0301  935      SAIGKIQDSLSSTAS  IQDSLSSTA  5        0.1576
9088.9    80.00  0.49     Sequence
             DRB1_0301  936      AIGKIQDSLSSTASA  IQDSLSSTA  4        0.1676
8156.2    80.00  0.57     Sequence
             DRB1_0301  937      IGKIQDSLSSTASAL  IQDSLSSTA  3        0.1692
8018.1    80.00  0.60     Sequence
             DRB1_0301  938      GKIQDSLSSTASALG  IQDSLSSTA  2        0.1433
10610.7    85.00  0.55     Sequence
             DRB1_0301  939      KIQDSLSSTASALGK  IQDSLSSTA  1        0.1276
12565.5    90.00  0.34     Sequence
             DRB1_0301  940      IQDSLSSTASALGKL  LSSTASALG  4        0.1083
15488.7    95.00  0.41     Sequence
             DRB1_0301  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.0948
17934.2    95.00  0.49     Sequence
             DRB1_0301  942      DSLSSTASALGKLQD  LSSTASALG  2        0.0855
19825.8   100.00  0.43     Sequence
             DRB1_0301  943      SLSSTASALGKLQDV  ASALGKLQD  5        0.0804
20951.3   100.00  0.24     Sequence
             DRB1_0301  944      LSSTASALGKLQDVV  ASALGKLQD  4        0.0692
23657.6   100.00  0.43     Sequence
             DRB1_0301  945      SSTASALGKLQDVVN  ASALGKLQD  3        0.0696
23553.6   100.00  0.43     Sequence
             DRB1_0301  946      STASALGKLQDVVNQ  ASALGKLQD  2        0.0770
21735.2   100.00  0.29     Sequence
             DRB1_0301  947      TASALGKLQDVVNQN  KLQDVVNQN  6        0.0948
17919.4    95.00  0.25     Sequence
             DRB1_0301  948      ASALGKLQDVVNQNA  KLQDVVNQN  5        0.1160
14256.6    95.00  0.34     Sequence
             DRB1_0301  949      SALGKLQDVVNQNAQ  KLQDVVNQN  4        0.1302
12225.4    90.00  0.36     Sequence
             DRB1_0301  950      ALGKLQDVVNQNAQA  KLQDVVNQN  3        0.1386
11161.2    90.00  0.33     Sequence
             DRB1_0301  951      LGKLQDVVNQNAQAL  KLQDVVNQN  2        0.1570
9146.7    85.00  0.23     Sequence
             DRB1_0301  952      GKLQDVVNQNAQALN  VNQNAQALN  6        0.1764
7411.4    75.00  0.22     Sequence
             DRB1_0301  953      KLQDVVNQNAQALNT  VNQNAQALN  5        0.1921
6253.7    70.00  0.40     Sequence
             DRB1_0301  954      LQDVVNQNAQALNTL  VNQNAQALN  4        0.2040
5500.9    70.00  0.52     Sequence
             DRB1_0301  955      QDVVNQNAQALNTLV  VNQNAQALN  3        0.1963
5976.3    70.00  0.59     Sequence
             DRB1_0301  956      DVVNQNAQALNTLVK  VNQNAQALN  2        0.1786
7239.8    75.00  0.50     Sequence
             DRB1_0301  957      VVNQNAQALNTLVKQ  VNQNAQALN  1        0.1654
8350.0    80.00  0.36     Sequence
             DRB1_0301  958      VNQNAQALNTLVKQL  AQALNTLVK  4        0.1601
8848.3    80.00  0.38     Sequence
             DRB1_0301  959      NQNAQALNTLVKQLS  LNTLVKQLS  6        0.2145
4910.3    65.00  0.56     Sequence
             DRB1_0301  960      QNAQALNTLVKQLSS  LNTLVKQLS  5        0.2750
2551.1    45.00  0.70     Sequence
             DRB1_0301  961      NAQALNTLVKQLSSN  LNTLVKQLS  4        0.2925
2110.6    40.00  0.80     Sequence
             DRB1_0301  962      AQALNTLVKQLSSNF  LNTLVKQLS  3        0.2974
2001.4    39.00  0.79     Sequence
             DRB1_0301  963      QALNTLVKQLSSNFG  LNTLVKQLS  2        0.2632
2899.9    48.00  0.73     Sequence
             DRB1_0301  964      ALNTLVKQLSSNFGA  LNTLVKQLS  1        0.2066
5349.6    65.00  0.52     Sequence
```

```
             DRB1_0301  965      LNTLVKQLSSNFGAI  LVKQLSSNF  3        0.1506
9799.7    85.00  0.51     Sequence
             DRB1_0301  966      NTLVKQLSSNFGAIS  LVKQLSSNF  2        0.1352
11577.9    90.00  0.50     Sequence
             DRB1_0301  967      TLVKQLSSNFGAISS  LSSNFGAIS  5        0.1366
11402.7    90.00  0.38     Sequence
             DRB1_0301  968      LVKQLSSNFGAISSV  LSSNFGAIS  4        0.1313
12081.5    90.00  0.60     Sequence
             DRB1_0301  969      VKQLSSNFGAISSVL  LSSNFGAIS  3        0.1263
12754.0    90.00  0.69     Sequence
             DRB1_0301  970      KQLSSNFGAISSVLN  LSSNFGAIS  2        0.1159
14271.1    95.00  0.55     Sequence
             DRB1_0301  971      QLSSNFGAISSVLND  LSSNFGAIS  1        0.0954
17804.4    95.00  0.31     Sequence
             DRB1_0301  972      LSSNFGAISSVLNDI  GAISSVLND  5        0.0929
18291.0    95.00  0.25     Sequence
             DRB1_0301  973      SSNFGAISSVLNDIL  GAISSVLND  4        0.1169
14113.6    95.00  0.27     Sequence
             DRB1_0301  974      SNFGAISSVLNDILS  ISSVLNDIL  5        0.1464
10260.5    85.00  0.41     Sequence
             DRB1_0301  975      NFGAISSVLNDILSR  VLNDILSRX  7        0.3597
1020.7    26.00  0.35     Sequence
             DRB1_0301  976      FGAISSVLNDILSRL  VLNDILSRL  6        0.4837
266.7    10.00  0.59     Sequence
             DRB1_0301  977      GAISSVLNDILSRLD  VLNDILSRL  5        0.5216
177.0     7.50  0.70     Sequence         WB
             DRB1_0301  978      AISSVLNDILSRLDK  VLNDILSRL  4        0.5546
123.9     5.50  0.74     Sequence         WB
             DRB1_0301  979      ISSVLNDILSRLDKV  VLNDILSRL  3        0.5566
121.2     5.50  0.73     Sequence         WB
             DRB1_0301  980      SSVLNDILSRLDKVE  VLNDILSRL  2        0.5255
169.7     7.00  0.72     Sequence         WB
             DRB1_0301  981      SVLNDILSRLDKVEA  VLNDILSRL  1        0.4805
276.2    11.00  0.59     Sequence
             DRB1_0301  982      VLNDILSRLDKVEAE  SRLDKVEAE  6        0.4157
556.9    17.00  0.45     Sequence
             DRB1_0301  983      LNDILSRLDKVEAEV  SRLDKVEAE  5        0.4478
393.5    14.00  0.62     Sequence
             DRB1_0301  984      NDILSRLDKVEAEVQ  SRLDKVEAE  4        0.4697
310.4    12.00  0.62     Sequence
             DRB1_0301  985      DILSRLDKVEAEVQI  SRLDKVEAE  3        0.4770
286.7    11.00  0.63     Sequence
             DRB1_0301  986      ILSRLDKVEAEVQID  SRLDKVEAE  2        0.4626
335.1    12.00  0.62     Sequence
             DRB1_0301  987      LSRLDKVEAEVQIDR  VEAEVQIDR  6        0.4714
304.5    11.00  0.41     Sequence
             DRB1_0301  988      SRLDKVEAEVQIDRL  VEAEVQIDR  5        0.4700
309.5    11.00  0.73     Sequence
             DRB1_0301  989      RLDKVEAEVQIDRLI  VEAEVQIDR  4        0.4969
231.1     9.00  0.80     Sequence         WB
             DRB1_0301  990      LDKVEAEVQIDRLIT  VEAEVQIDR  3        0.5604
116.3     5.00  0.64     Sequence         WB
             DRB1_0301  991      DKVEAEVQIDRLITG  VQIDRLITG  6        0.6208
60.5     3.00  0.60     Sequence         WB
             DRB1_0301  992      KVEAEVQIDRLITGR  VQIDRLITG  5        0.6761
33.3     1.40  0.76     Sequence         SB
             DRB1_0301  993      VEAEVQIDRLITGRL  VQIDRLITG  4        0.6789
32.3     1.30  0.86     Sequence         SB
             DRB1_0301  994      EAEVQIDRLITGRLQ  VQIDRLITG  3        0.6708
35.2     1.50  0.89     Sequence         SB
             DRB1_0301  995      AEVQIDRLITGRLQS  VQIDRLITG  2        0.6490
44.6     1.90  0.85     Sequence         SB
             DRB1_0301  996      EVQIDRLITGRLQSL  VQIDRLITG  1        0.5625
113.7     5.00  0.74     Sequence         WB
             DRB1_0301  997      VQIDRLITGRLQSLQ  VQIDRLITG  0        0.4073
609.8    18.00  0.35     Sequence
```

```
             DRB1_0301  998      QIDRLITGRLQSLQT  IDRLITGRL  1        0.2972
2007.6    39.00  0.28     Sequence
             DRB1_0301  999      IDRLITGRLQSLQTY  ITGRLQSLQ  4        0.2697
2702.1    46.00  0.27     Sequence
             DRB1_0301 1000      DRLITGRLQSLQTYV  ITGRLQSLQ  3        0.2169
4784.2    65.00  0.31     Sequence
             DRB1_0301 1001      RLITGRLQSLQTYVT  ITGRLQSLQ  2        0.2043
5484.3    70.00  0.27     Sequence
             DRB1_0301 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.1903
6376.6    75.00  0.43     Sequence
             DRB1_0301 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.1888
6485.9    75.00  0.54     Sequence
             DRB1_0301 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.1861
6677.5    75.00  0.46     Sequence
             DRB1_0301 1005      GRLQSLQTYVTQQLI  LQSLQTYVT  2        0.1935
6161.0    70.00  0.34     Sequence
             DRB1_0301 1006      RLQSLQTYVTQQLIR  LQTYVTQQL  4        0.2335
3995.2    60.00  0.38     Sequence
             DRB1_0301 1007      LQSLQTYVTQQLIRA  TYVTQQLIR  5        0.2465
3473.4    55.00  0.34     Sequence
             DRB1_0301 1008      QSLQTYVTQQLIRAA  TYVTQQLIR  4        0.2522
3263.9    55.00  0.42     Sequence
             DRB1_0301 1009      SLQTYVTQQLIRAAE  TYVTQQLIR  3        0.2408
3693.5    55.00  0.42     Sequence
             DRB1_0301 1010      LQTYVTQQLIRAAEI  TYVTQQLIR  2        0.2271
4283.2    60.00  0.37     Sequence
             DRB1_0301 1011      QTYVTQQLIRAAEIR  TYVTQQLIR  1        0.2412
3676.9    55.00  0.28     Sequence
             DRB1_0301 1012      TYVTQQLIRAAEIRA  LIRAAEIRA  6        0.2831
2338.1    43.00  0.43     Sequence
             DRB1_0301 1013      YVTQQLIRAAEIRAS  LIRAAEIRA  5        0.3902
733.7    21.00  0.41     Sequence
             DRB1_0301 1014      VTQQLIRAAEIRASA  IRAAEIRAS  5        0.4750
293.2    11.00  0.54     Sequence
             DRB1_0301 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.4973
230.3     9.00  0.56     Sequence         WB
             DRB1_0301 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.5001
223.3     9.00  0.56     Sequence         WB
             DRB1_0301 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.4879
254.9     9.50  0.52     Sequence         WB
             DRB1_0301 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.4756
291.1    11.00  0.46     Sequence
             DRB1_0301 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.4611
340.7    12.00  0.84     Sequence
             DRB1_0301 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.4875
256.0     9.50  0.94     Sequence         WB
             DRB1_0301 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.4868
258.0    10.00  0.94     Sequence
             DRB1_0301 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.4580
352.3    13.00  0.86     Sequence
             DRB1_0301 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.4474
395.2    14.00  0.49     Sequence
             DRB1_0301 1024      IRASANLAAIKMSEC  NLAAIKMSE  5        0.3829
793.9    22.00  0.79     Sequence
             DRB1_0301 1025      RASANLAAIKMSECV  NLAAIKMSE  4        0.4095
595.6    18.00  0.82     Sequence
             DRB1_0301 1026      ASANLAAIKMSECVL  NLAAIKMSE  3        0.4160
554.9    17.00  0.77     Sequence
             DRB1_0301 1027      SANLAAIKMSECVLG  NLAAIKMSE  2        0.4298
477.9    16.00  0.56     Sequence
             DRB1_0301 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.4203
529.4    17.00  0.61     Sequence
             DRB1_0301 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.4027
640.6    19.00  0.76     Sequence
             DRB1_0301 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.4151
560.2    17.00  0.81     Sequence
```

```
             DRB1_0301 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.4008
653.7    19.00  0.75     Sequence
             DRB1_0301 1032      AIKMSECVLGQSKRV  IKMSECVLG  1        0.3690
923.1    24.00  0.56     Sequence
             DRB1_0301 1033      IKMSECVLGQSKRVD  CVLGQSKRV  5        0.2897
2177.2    41.00  0.33     Sequence
             DRB1_0301 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.3164
1629.5    35.00  0.40     Sequence
             DRB1_0301 1035      MSECVLGQSKRVDFC  LGQSKRVDF  5        0.3491
1143.8    28.00  0.44     Sequence
             DRB1_0301 1036      SECVLGQSKRVDFCG  LGQSKRVDF  4        0.3383
1285.7    30.00  0.49     Sequence
             DRB1_0301 1037      ECVLGQSKRVDFCGK  LGQSKRVDF  3        0.3293
1417.3    32.00  0.52     Sequence
             DRB1_0301 1038      CVLGQSKRVDFCGKG  LGQSKRVDF  2        0.2654
2830.9    48.00  0.61     Sequence
             DRB1_0301 1039      VLGQSKRVDFCGKGY  LGQSKRVDF  1        0.2514
3294.9    55.00  0.55     Sequence
             DRB1_0301 1040      LGQSKRVDFCGKGYH  VDFCGKGYH  6        0.2159
4836.9    65.00  0.41     Sequence
             DRB1_0301 1041      GQSKRVDFCGKGYHL  VDFCGKGYH  5        0.2278
4253.7    60.00  0.59     Sequence
             DRB1_0301 1042      QSKRVDFCGKGYHLM  VDFCGKGYH  4        0.2582
3059.3    50.00  0.56     Sequence
             DRB1_0301 1043      SKRVDFCGKGYHLMS  VDFCGKGYH  3        0.2850
2290.4    42.00  0.47     Sequence
             DRB1_0301 1044      KRVDFCGKGYHLMSF  VDFCGKGYH  2        0.3039
1865.8    38.00  0.38     Sequence
             DRB1_0301 1045      RVDFCGKGYHLMSFP  CGKGYHLMS  4        0.2689
2724.8    47.00  0.43     Sequence
             DRB1_0301 1046      VDFCGKGYHLMSFPQ  CGKGYHLMS  3        0.2211
4572.0    65.00  0.56     Sequence
             DRB1_0301 1047      DFCGKGYHLMSFPQS  CGKGYHLMS  2        0.1720
7774.3    80.00  0.63     Sequence
             DRB1_0301 1048      FCGKGYHLMSFPQSA  CGKGYHLMS  1        0.1700
7948.8    80.00  0.43     Sequence
             DRB1_0301 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.1384
11181.3    90.00  0.60     Sequence
             DRB1_0301 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.1603
8826.1    80.00  0.55     Sequence
             DRB1_0301 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.1617
8690.1    80.00  0.51     Sequence
             DRB1_0301 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.1598
8874.4    80.00  0.41     Sequence
             DRB1_0301 1053      YHLMSFPQSAPHGVV  HLMSFPQSA  1        0.1597
8884.0    80.00  0.29     Sequence
             DRB1_0301 1054      HLMSFPQSAPHGVVF  FPQSAPHGV  4        0.1408
10901.9    85.00  0.35     Sequence
             DRB1_0301 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.1270
12657.2    90.00  0.40     Sequence
             DRB1_0301 1056      MSFPQSAPHGVVFLH  FPQSAPHGV  2        0.1180
13941.0    95.00  0.33     Sequence
             DRB1_0301 1057      SFPQSAPHGVVFLHV  FPQSAPHGV  1        0.1107
15088.6    95.00  0.21     Sequence
             DRB1_0301 1058      FPQSAPHGVVFLHVT  APHGVVFLH  4        0.1012
16734.1    95.00  0.29     Sequence
             DRB1_0301 1059      PQSAPHGVVFLHVTY  PHGVVFLHV  4        0.1062
15853.8    95.00  0.23     Sequence
             DRB1_0301 1060      QSAPHGVVFLHVTYV  PHGVVFLHV  3        0.0988
17169.0    95.00  0.21     Sequence
             DRB1_0301 1061      SAPHGVVFLHVTYVP  PHGVVFLHV  2        0.1064
15818.5    95.00  0.19     Sequence
             DRB1_0301 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.1333
11822.6    90.00  0.20     Sequence
             DRB1_0301 1063      PHGVVFLHVTYVPAQ  LHVTYVPAQ  6        0.1668
8225.8    80.00  0.37     Sequence
```

```
             DRB1_0301 1064      HGVVFLHVTYVPAQE  LHVTYVPAQ  5        0.1924
6233.4    70.00  0.49     Sequence
             DRB1_0301 1065      GVVFLHVTYVPAQEK  LHVTYVPAQ  4        0.2549
3171.7    55.00  0.41     Sequence
             DRB1_0301 1066      VVFLHVTYVPAQEKN  VTYVPAQEK  5        0.2837
2322.7    43.00  0.42     Sequence
             DRB1_0301 1067      VFLHVTYVPAQEKNF  VTYVPAQEK  4        0.3002
1942.7    39.00  0.50     Sequence
             DRB1_0301 1068      FLHVTYVPAQEKNFT  VTYVPAQEK  3        0.2889
2194.1    41.00  0.53     Sequence
             DRB1_0301 1069      LHVTYVPAQEKNFTT  VTYVPAQEK  2        0.2623
2927.0    49.00  0.54     Sequence
             DRB1_0301 1070      HVTYVPAQEKNFTTA  VTYVPAQEK  1        0.2218
4538.4    65.00  0.44     Sequence
             DRB1_0301 1071      VTYVPAQEKNFTTAP  VPAQEKNFT  3        0.1624
8625.8    80.00  0.31     Sequence
             DRB1_0301 1072      TYVPAQEKNFTTAPA  VPAQEKNFT  2        0.0892
19045.8   100.00  0.39     Sequence
             DRB1_0301 1073      YVPAQEKNFTTAPAI  VPAQEKNFT  1        0.0597
26219.5   100.00  0.33     Sequence
             DRB1_0301 1074      VPAQEKNFTTAPAIC  KNFTTAPAI  5        0.0499
29129.4   100.00  0.28     Sequence
             DRB1_0301 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.1147
14446.8    95.00  0.65     Sequence
             DRB1_0301 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.1437
10557.9    85.00  0.70     Sequence
             DRB1_0301 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.1406
10916.9    85.00  0.70     Sequence
             DRB1_0301 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.1468
10216.9    85.00  0.75     Sequence
             DRB1_0301 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.1410
10879.0    85.00  0.72     Sequence
             DRB1_0301 1080      NFTTAPAICHDGKAH  ICHDGKAHX  7        0.1665
8252.7    80.00  0.35     Sequence
             DRB1_0301 1081      FTTAPAICHDGKAHF  ICHDGKAHF  6        0.4798
278.2    11.00  0.87     Sequence
             DRB1_0301 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.5297
162.1     7.00  0.86     Sequence         WB
             DRB1_0301 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.5861
88.1     4.00  0.83     Sequence         WB
             DRB1_0301 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.5976
77.7     3.50  0.82     Sequence         WB
             DRB1_0301 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.5797
94.4     4.50  0.79     Sequence         WB
             DRB1_0301 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.5255
169.7     7.00  0.71     Sequence         WB
             DRB1_0301 1087      ICHDGKAHFPREGVF  ICHDGKAHF  0        0.3673
939.9    25.00  0.50     Sequence
             DRB1_0301 1088      CHDGKAHFPREGVFV  KAHFPREGV  4        0.0957
17746.0    95.00  0.32     Sequence
             DRB1_0301 1089      HDGKAHFPREGVFVS  FPREGVFVS  6        0.1314
12069.6    90.00  0.44     Sequence
             DRB1_0301 1090      DGKAHFPREGVFVSN  FPREGVFVS  5        0.1531
9538.9    85.00  0.52     Sequence
             DRB1_0301 1091      GKAHFPREGVFVSNG  FPREGVFVS  4        0.1497
9902.5    85.00  0.56     Sequence
             DRB1_0301 1092      KAHFPREGVFVSNGT  FPREGVFVS  3        0.1411
10859.0    85.00  0.63     Sequence
             DRB1_0301 1093      AHFPREGVFVSNGTH  FPREGVFVS  2        0.1206
13555.6    90.00  0.60     Sequence
             DRB1_0301 1094      HFPREGVFVSNGTHW  VFVSNGTHW  6        0.2152
4871.2    65.00  0.44     Sequence
             DRB1_0301 1095      FPREGVFVSNGTHWF  VFVSNGTHW  5        0.3168
1623.5    35.00  0.43     Sequence
             DRB1_0301 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.4020
645.5    19.00  0.38     Sequence
```

```
             DRB1_0301 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.4415
421.2    14.00  0.34     Sequence
             DRB1_0301 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.4344
454.7    15.00  0.31     Sequence
             DRB1_0301 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.4258
499.2    16.00  0.28     Sequence
             DRB1_0301 1100      VFVSNGTHWFVTQRN  VSNGTHWFV  2        0.3505
1126.6    28.00  0.40     Sequence
             DRB1_0301 1101      FVSNGTHWFVTQRNF  VSNGTHWFV  1        0.2427
3616.8    55.00  0.32     Sequence
             DRB1_0301 1102      VSNGTHWFVTQRNFY  WFVTQRNFY  6        0.2854
2280.1    42.00  0.48     Sequence
             DRB1_0301 1103      SNGTHWFVTQRNFYE  WFVTQRNFY  5        0.3082
1781.7    37.00  0.57     Sequence
             DRB1_0301 1104      NGTHWFVTQRNFYEP  WFVTQRNFY  4        0.2998
1950.7    39.00  0.58     Sequence
             DRB1_0301 1105      GTHWFVTQRNFYEPQ  WFVTQRNFY  3        0.3036
1871.5    38.00  0.58     Sequence
             DRB1_0301 1106      THWFVTQRNFYEPQI  WFVTQRNFY  2        0.2925
2111.6    40.00  0.54     Sequence
             DRB1_0301 1107      HWFVTQRNFYEPQII  WFVTQRNFY  1        0.2740
2578.7    45.00  0.46     Sequence
             DRB1_0301 1108      WFVTQRNFYEPQIIT  WFVTQRNFY  0        0.2519
3275.9    55.00  0.26     Sequence
             DRB1_0301 1109      FVTQRNFYEPQIITT  NFYEPQIIT  5        0.2003
5723.2    70.00  0.54     Sequence
             DRB1_0301 1110      VTQRNFYEPQIITTD  NFYEPQIIT  4        0.1976
5891.6    70.00  0.58     Sequence
             DRB1_0301 1111      TQRNFYEPQIITTDN  NFYEPQIIT  3        0.1903
6381.1    75.00  0.62     Sequence
             DRB1_0301 1112      QRNFYEPQIITTDNT  NFYEPQIIT  2        0.1730
7689.9    80.00  0.58     Sequence
             DRB1_0301 1113      RNFYEPQIITTDNTF  NFYEPQIIT  1        0.1644
8440.4    80.00  0.46     Sequence
             DRB1_0301 1114      NFYEPQIITTDNTFV  ITTDNTFVX  7        0.3168
1623.5    35.00  0.40     Sequence
             DRB1_0301 1115      FYEPQIITTDNTFVS  ITTDNTFVS  6        0.6773
32.9     1.40  0.90     Sequence         SB
             DRB1_0301 1116      YEPQIITTDNTFVSG  ITTDNTFVS  5        0.7249
19.6     0.70  0.93     Sequence         SB
             DRB1_0301 1117      EPQIITTDNTFVSGN  ITTDNTFVS  4        0.7454
15.7     0.50  0.94     Sequence         SB
             DRB1_0301 1118      PQIITTDNTFVSGNC  ITTDNTFVS  3        0.7487
15.2     0.50  0.94     Sequence         SB
             DRB1_0301 1119      QIITTDNTFVSGNCD  ITTDNTFVS  2        0.7144
22.0     0.80  0.93     Sequence         SB
             DRB1_0301 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.6201
61.0     3.00  0.85     Sequence         WB
             DRB1_0301 1121      ITTDNTFVSGNCDVV  ITTDNTFVS  0        0.3524
1104.7    27.00  0.54     Sequence
             DRB1_0301 1122      TTDNTFVSGNCDVVI  TFVSGNCDV  4        0.1013
16704.7    95.00  0.41     Sequence
             DRB1_0301 1123      TDNTFVSGNCDVVIG  GNCDVVIGX  7        0.1344
11678.7    90.00  0.23     Sequence
             DRB1_0301 1124      DNTFVSGNCDVVIGI  GNCDVVIGI  6        0.1985
5834.8    70.00  0.50     Sequence
             DRB1_0301 1125      NTFVSGNCDVVIGIV  GNCDVVIGI  5        0.2466
3469.0    55.00  0.61     Sequence
             DRB1_0301 1126      TFVSGNCDVVIGIVN  GNCDVVIGI  4        0.2628
2910.7    48.00  0.63     Sequence
             DRB1_0301 1127      FVSGNCDVVIGIVNN  GNCDVVIGI  3        0.2629
2908.0    48.00  0.64     Sequence
             DRB1_0301 1128      VSGNCDVVIGIVNNT  GNCDVVIGI  2        0.2497
3353.9    55.00  0.60     Sequence
             DRB1_0301 1129      SGNCDVVIGIVNNTV  GNCDVVIGI  1        0.2177
4742.8    65.00  0.45     Sequence
```

```
             DRB1_0301 1130      GNCDVVIGIVNNTVY  CDVVIGIVN  2        0.1935
6160.4    70.00  0.23     Sequence
             DRB1_0301 1131      NCDVVIGIVNNTVYD  IGIVNNTVY  5        0.2278
4251.3    60.00  0.25     Sequence
             DRB1_0301 1132      CDVVIGIVNNTVYDP  IVNNTVYDP  6        0.2371
3846.2    60.00  0.28     Sequence
             DRB1_0301 1133      DVVIGIVNNTVYDPL  IVNNTVYDP  5        0.2707
2673.9    46.00  0.39     Sequence
             DRB1_0301 1134      VVIGIVNNTVYDPLQ  IVNNTVYDP  4        0.2796
2427.8    44.00  0.41     Sequence
             DRB1_0301 1135      VIGIVNNTVYDPLQP  IVNNTVYDP  3        0.2564
3118.6    50.00  0.44     Sequence
             DRB1_0301 1136      IGIVNNTVYDPLQPE  IVNNTVYDP  2        0.2585
3050.5    50.00  0.41     Sequence
             DRB1_0301 1137      GIVNNTVYDPLQPEL  TVYDPLQPE  5        0.2546
3182.6    55.00  0.47     Sequence
             DRB1_0301 1138      IVNNTVYDPLQPELD  TVYDPLQPE  4        0.2152
4872.8    65.00  0.69     Sequence
             DRB1_0301 1139      VNNTVYDPLQPELDS  TVYDPLQPE  3        0.2070
5324.3    65.00  0.76     Sequence
             DRB1_0301 1140      NNTVYDPLQPELDSF  TVYDPLQPE  2        0.1845
6791.2    75.00  0.69     Sequence
             DRB1_0301 1141      NTVYDPLQPELDSFK  TVYDPLQPE  1        0.1716
7807.9    80.00  0.51     Sequence
             DRB1_0301 1142      TVYDPLQPELDSFKE  LQPELDSFK  5        0.1303
12203.1    90.00  0.35     Sequence
             DRB1_0301 1143      VYDPLQPELDSFKEE  LQPELDSFK  4        0.1154
14341.7    95.00  0.54     Sequence
             DRB1_0301 1144      YDPLQPELDSFKEEL  LQPELDSFK  3        0.1359
11494.1    90.00  0.45     Sequence
             DRB1_0301 1145      DPLQPELDSFKEELD  LQPELDSFK  2        0.1463
10270.3    85.00  0.35     Sequence
             DRB1_0301 1146      PLQPELDSFKEELDK  ELDSFKEEL  4        0.1536
9491.5    85.00  0.25     Sequence
             DRB1_0301 1147      LQPELDSFKEELDKY  ELDSFKEEL  3        0.1524
9615.9    85.00  0.28     Sequence
             DRB1_0301 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.1941
6123.9    70.00  0.35     Sequence
             DRB1_0301 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.2541
3199.8    55.00  0.49     Sequence
             DRB1_0301 1150      ELDSFKEELDKYFKN  FKEELDKYF  4        0.2765
2509.3    45.00  0.55     Sequence
             DRB1_0301 1151      LDSFKEELDKYFKNH  FKEELDKYF  3        0.2830
2339.7    43.00  0.56     Sequence
             DRB1_0301 1152      DSFKEELDKYFKNHT  FKEELDKYF  2        0.2660
2810.8    47.00  0.46     Sequence
             DRB1_0301 1153      SFKEELDKYFKNHTS  FKEELDKYF  1        0.2467
3464.0    55.00  0.38     Sequence
             DRB1_0301 1154      FKEELDKYFKNHTSP  LDKYFKNHT  4        0.1818
6995.7    75.00  0.30     Sequence
             DRB1_0301 1155      KEELDKYFKNHTSPD  LDKYFKNHT  3        0.1284
12458.0    90.00  0.47     Sequence
             DRB1_0301 1156      EELDKYFKNHTSPDV  LDKYFKNHT  2        0.1180
13945.4    95.00  0.37     Sequence
             DRB1_0301 1157      ELDKYFKNHTSPDVD  YFKNHTSPD  4        0.1144
14504.6    95.00  0.47     Sequence
             DRB1_0301 1158      LDKYFKNHTSPDVDL  YFKNHTSPD  3        0.1076
15610.7    95.00  0.51     Sequence
             DRB1_0301 1159      DKYFKNHTSPDVDLG  YFKNHTSPD  2        0.1055
15964.8    95.00  0.47     Sequence
             DRB1_0301 1160      KYFKNHTSPDVDLGD  TSPDVDLGD  6        0.1132
14695.1    95.00  0.31     Sequence
             DRB1_0301 1161      YFKNHTSPDVDLGDI  TSPDVDLGD  5        0.1172
14063.1    95.00  0.44     Sequence
             DRB1_0301 1162      FKNHTSPDVDLGDIS  TSPDVDLGD  4        0.1352
11580.1    90.00  0.43     Sequence
```

```
             DRB1_0301 1163      KNHTSPDVDLGDISG  TSPDVDLGD  3        0.1466
10239.7    85.00  0.37     Sequence
             DRB1_0301 1164      NHTSPDVDLGDISGI  VDLGDISGI  6        0.1778
7299.9    75.00  0.37     Sequence
             DRB1_0301 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.2001
5735.0    70.00  0.47     Sequence
             DRB1_0301 1166      TSPDVDLGDISGINA  VDLGDISGI  4        0.2018
5631.7    70.00  0.54     Sequence
             DRB1_0301 1167      SPDVDLGDISGINAS  VDLGDISGI  3        0.2011
5677.8    70.00  0.53     Sequence
             DRB1_0301 1168      PDVDLGDISGINASF  VDLGDISGI  2        0.1810
7057.6    75.00  0.48     Sequence
             DRB1_0301 1169      DVDLGDISGINASFV  VDLGDISGI  1        0.1586
8985.6    80.00  0.38     Sequence
             DRB1_0301 1170      VDLGDISGINASFVN  ISGINASFV  5        0.1363
11439.7    90.00  0.26     Sequence
             DRB1_0301 1171      DLGDISGINASFVNI  ISGINASFV  4        0.1143
14521.9    95.00  0.43     Sequence
             DRB1_0301 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.1355
11547.2    90.00  0.35     Sequence
             DRB1_0301 1173      GDISGINASFVNIQK  INASFVNIQ  5        0.1593
8919.6    80.00  0.49     Sequence
             DRB1_0301 1174      DISGINASFVNIQKE  INASFVNIQ  4        0.1544
9406.1    85.00  0.60     Sequence
             DRB1_0301 1175      ISGINASFVNIQKEI  INASFVNIQ  3        0.1556
9282.9    85.00  0.63     Sequence
             DRB1_0301 1176      SGINASFVNIQKEID  INASFVNIQ  2        0.1547
9380.5    85.00  0.48     Sequence
             DRB1_0301 1177      GINASFVNIQKEIDR  FVNIQKEID  5        0.1912
6318.6    70.00  0.29     Sequence
             DRB1_0301 1178      INASFVNIQKEIDRL  VNIQKEIDR  5        0.2319
4066.4    60.00  0.37     Sequence
             DRB1_0301 1179      NASFVNIQKEIDRLN  VNIQKEIDR  4        0.2658
2816.9    48.00  0.37     Sequence
             DRB1_0301 1180      ASFVNIQKEIDRLNE  IQKEIDRLN  5        0.2925
2112.0    40.00  0.34     Sequence
             DRB1_0301 1181      SFVNIQKEIDRLNEV  IQKEIDRLN  4        0.3042
1861.0    38.00  0.44     Sequence
             DRB1_0301 1182      FVNIQKEIDRLNEVA  IQKEIDRLN  3        0.2947
2060.7    40.00  0.51     Sequence
             DRB1_0301 1183      VNIQKEIDRLNEVAK  IQKEIDRLN  2        0.2856
2273.8    42.00  0.46     Sequence
             DRB1_0301 1184      NIQKEIDRLNEVAKN  IDRLNEVAK  5        0.2630
2904.0    48.00  0.31     Sequence
             DRB1_0301 1185      IQKEIDRLNEVAKNL  IDRLNEVAK  4        0.2367
3859.3    60.00  0.46     Sequence
             DRB1_0301 1186      QKEIDRLNEVAKNLN  IDRLNEVAK  3        0.2343
3960.7    60.00  0.44     Sequence
             DRB1_0301 1187      KEIDRLNEVAKNLNE  IDRLNEVAK  2        0.2456
3508.4    55.00  0.34     Sequence
             DRB1_0301 1188      EIDRLNEVAKNLNES  LNEVAKNLN  4        0.2397
3737.6    55.00  0.51     Sequence
             DRB1_0301 1189      IDRLNEVAKNLNESL  LNEVAKNLN  3        0.2314
4087.5    60.00  0.53     Sequence
             DRB1_0301 1190      DRLNEVAKNLNESLI  LNEVAKNLN  2        0.2191
4671.9    65.00  0.47     Sequence
             DRB1_0301 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.2099
5161.7    65.00  0.51     Sequence
             DRB1_0301 1192      LNEVAKNLNESLIDL  VAKNLNESL  3        0.1885
6502.0    75.00  0.61     Sequence
             DRB1_0301 1193      NEVAKNLNESLIDLQ  VAKNLNESL  2        0.1926
6219.0    70.00  0.43     Sequence
             DRB1_0301 1194      EVAKNLNESLIDLQE  LNESLIDLQ  5        0.2083
5249.4    65.00  0.39     Sequence
             DRB1_0301 1195      VAKNLNESLIDLQEL  LNESLIDLQ  4        0.2143
4919.1    65.00  0.50     Sequence
```

```
              DRB1_0301 1196      AKNLNESLIDLQELG  LNESLIDLQ  3        0.2290
4194.7    60.00  0.44     Sequence
              DRB1_0301 1197      KNLNESLIDLQELGK  SLIDLQELG  5        0.2518
3277.8    55.00  0.38     Sequence
              DRB1_0301 1198      NLNESLIDLQELGKY  SLIDLQELG  4        0.2800
2416.4    44.00  0.43     Sequence
              DRB1_0301 1199      LNESLIDLQELGKYE  SLIDLQELG  3        0.3009
1928.2    38.00  0.37     Sequence
              DRB1_0301 1200      NESLIDLQELGKYEQ  IDLQELGKY  4        0.3072
1801.7    37.00  0.40     Sequence
              DRB1_0301 1201      ESLIDLQELGKYEQY  IDLQELGKY  3        0.3075
1795.3    37.00  0.43     Sequence
              DRB1_0301 1202      SLIDLQELGKYEQYI  IDLQELGKY  2        0.2848
2294.5    42.00  0.45     Sequence
              DRB1_0301 1203      LIDLQELGKYEQYIK  LQELGKYEQ  3        0.2362
3881.9    60.00  0.39     Sequence
              DRB1_0301 1204      IDLQELGKYEQYIKW  LQELGKYEQ  2        0.1939
6138.5    70.00  0.34     Sequence
              DRB1_0301 1205      DLQELGKYEQYIKWP  LQELGKYEQ  1        0.1301
12230.8    90.00  0.29     Sequence
              DRB1_0301 1206      LQELGKYEQYIKWPW  LGKYEQYIK  3        0.1176
14000.7    95.00  0.21     Sequence
              DRB1_0301 1207      QELGKYEQYIKWPWY  YEQYIKWPW  5        0.1321
11979.1    90.00  0.31     Sequence
              DRB1_0301 1208      ELGKYEQYIKWPWYI  YEQYIKWPW  4        0.1438
10546.5    85.00  0.41     Sequence
              DRB1_0301 1209      LGKYEQYIKWPWYIW  YEQYIKWPW  3        0.1473
10157.9    85.00  0.40     Sequence
              DRB1_0301 1210      GKYEQYIKWPWYIWL  YEQYIKWPW  2        0.1514
9713.9    85.00  0.35     Sequence
              DRB1_0301 1211      KYEQYIKWPWYIWLG  IKWPWYIWL  5        0.1447
10444.5    85.00  0.31     Sequence
              DRB1_0301 1212      YEQYIKWPWYIWLGF  IKWPWYIWL  4        0.1364
11426.4    90.00  0.37     Sequence
              DRB1_0301 1213      EQYIKWPWYIWLGFI  IKWPWYIWL  3        0.1276
12577.3    90.00  0.41     Sequence
              DRB1_0301 1214      QYIKWPWYIWLGFIA  IKWPWYIWL  2        0.1112
15011.9    95.00  0.37     Sequence
              DRB1_0301 1215      YIKWPWYIWLGFIAG  WPWYIWLGF  3        0.0914
18603.4   100.00  0.32     Sequence
              DRB1_0301 1216      IKWPWYIWLGFIAGL  IWLGFIAGL  6        0.1041
16205.6    95.00  0.35     Sequence
              DRB1_0301 1217      KWPWYIWLGFIAGLI  IWLGFIAGL  5        0.1170
14105.5    95.00  0.40     Sequence
              DRB1_0301 1218      WPWYIWLGFIAGLIA  IWLGFIAGL  4        0.1273
12609.9    90.00  0.43     Sequence
              DRB1_0301 1219      PWYIWLGFIAGLIAI  IWLGFIAGL  3        0.1344
11683.2    90.00  0.43     Sequence
              DRB1_0301 1220      WYIWLGFIAGLIAIV  IWLGFIAGL  2        0.1352
11578.7    90.00  0.35     Sequence
              DRB1_0301 1221      YIWLGFIAGLIAIVM  LGFIAGLIA  3        0.1399
11004.0    85.00  0.28     Sequence
              DRB1_0301 1222      IWLGFIAGLIAIVMV  IAGLIAIVM  5        0.1430
10639.8    85.00  0.33     Sequence
              DRB1_0301 1223      WLGFIAGLIAIVMVT  IAGLIAIVM  4        0.1405
10932.7    85.00  0.44     Sequence
              DRB1_0301 1224      LGFIAGLIAIVMVTI  IAGLIAIVM  3        0.1457
10337.4    85.00  0.43     Sequence
              DRB1_0301 1225      GFIAGLIAIVMVTIM  IAIVMVTIM  6        0.1574
9106.2    85.00  0.36     Sequence
              DRB1_0301 1226      FIAGLIAIVMVTIML  IAIVMVTIM  5        0.1833
6883.1    75.00  0.47     Sequence
              DRB1_0301 1227      IAGLIAIVMVTIMLC  IVMVTIMLC  6        0.2372
3840.8    60.00  0.35     Sequence
              DRB1_0301 1228      AGLIAIVMVTIMLCC  IVMVTIMLC  5        0.2571
3095.3    50.00  0.41     Sequence
```

```
             DRB1_0301 1229      GLIAIVMVTIMLCCM  IVMVTIMLC  4        0.2704
2681.7    46.00  0.47     Sequence
             DRB1_0301 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3        0.2665
2797.7    47.00  0.50     Sequence
             DRB1_0301 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2        0.2540
3201.6    55.00  0.49     Sequence
             DRB1_0301 1232      AIVMVTIMLCCMTSC  IVMVTIMLC  1        0.2280
4243.6    60.00  0.41     Sequence
             DRB1_0301 1233      IVMVTIMLCCMTSCC  MVTIMLCCM  2        0.1752
7508.9    75.00  0.24     Sequence
             DRB1_0301 1234      VMVTIMLCCMTSCCS  MLCCMTSCC  5        0.1558
9265.5    85.00  0.36     Sequence
             DRB1_0301 1235      MVTIMLCCMTSCCSC  MLCCMTSCC  4        0.1586
8989.4    80.00  0.41     Sequence
             DRB1_0301 1236      VTIMLCCMTSCCSCL  MLCCMTSCC  3        0.1667
8231.7    80.00  0.41     Sequence
             DRB1_0301 1237      TIMLCCMTSCCSCLK  MLCCMTSCC  2        0.1803
7104.8    75.00  0.29     Sequence
             DRB1_0301 1238      IMLCCMTSCCSCLKG  MLCCMTSCC  1        0.1753
7502.4    75.00  0.23     Sequence
             DRB1_0301 1239      MLCCMTSCCSCLKGC  MTSCCSCLK  4        0.1534
9510.4    85.00  0.28     Sequence
             DRB1_0301 1240      LCCMTSCCSCLKGCC  MTSCCSCLK  3        0.1371
11338.0    90.00  0.31     Sequence
             DRB1_0301 1241      CCMTSCCSCLKGCCS  MTSCCSCLK  2        0.1045
16137.4    95.00  0.28     Sequence
             DRB1_0301 1242      CMTSCCSCLKGCCSC  CCSCLKGCC  4        0.0937
18144.0    95.00  0.30     Sequence
             DRB1_0301 1243      MTSCCSCLKGCCSCG  CCSCLKGCC  3        0.0784
21402.9   100.00  0.35     Sequence
             DRB1_0301 1244      TSCCSCLKGCCSCGS  CCSCLKGCC  2        0.0696
23538.1   100.00  0.34     Sequence
             DRB1_0301 1245      SCCSCLKGCCSCGSC  CLKGCCSCG  4        0.0620
25571.8   100.00  0.30     Sequence
             DRB1_0301 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.0575
26849.4   100.00  0.31     Sequence
             DRB1_0301 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.0620
25570.4   100.00  0.29     Sequence
             DRB1_0301 1248      SCLKGCCSCGSCCKF  CSCGSCCKF  6        0.0839
20165.7   100.00  0.31     Sequence
             DRB1_0301 1249      CLKGCCSCGSCCKFD  CSCGSCCKF  5        0.1007
16811.6    95.00  0.41     Sequence
             DRB1_0301 1250      LKGCCSCGSCCKFDE  CSCGSCCKF  4        0.1161
14241.8    95.00  0.45     Sequence
             DRB1_0301 1251      KGCCSCGSCCKFDED  CSCGSCCKF  3        0.1202
13624.6    90.00  0.44     Sequence
             DRB1_0301 1252      GCCSCGSCCKFDEDD  CSCGSCCKF  2        0.1092
15336.0    95.00  0.40     Sequence
             DRB1_0301 1253      CCSCGSCCKFDEDDS  CGSCCKFDE  3        0.1014
16687.9    95.00  0.40     Sequence
             DRB1_0301 1254      CSCGSCCKFDEDDSE  CKFDEDDSE  6        0.1234
13162.1    90.00  0.50     Sequence
             DRB1_0301 1255      SCGSCCKFDEDDSEP  CKFDEDDSE  5        0.1221
13346.6    90.00  0.57     Sequence
             DRB1_0301 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.1821
6971.9    75.00  0.40     Sequence
             DRB1_0301 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.2285
4218.7    60.00  0.46     Sequence
             DRB1_0301 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.2575
3082.0    50.00  0.47     Sequence
             DRB1_0301 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.2450
3530.9    55.00  0.49     Sequence
             DRB1_0301 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.2385
3786.5    55.00  0.52     Sequence
             DRB1_0301 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.2180
4726.8    65.00  0.54     Sequence
```

```
             DRB1_0301 1262      FDEDDSEPVLKGVKL  EDDSEPVLK  2        0.1372
11325.1    90.00  0.20     Sequence
             DRB1_0301 1263      DEDDSEPVLKGVKLH  VLKGVKLHX  7        0.1199
13668.4    90.00  0.26     Sequence
             DRB1_0301 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.3358
1321.9    31.00  0.79     Sequence
             DRB1_0301 1265      DDSEPVLKGVKLHYT  VLKGVKLHY  5        0.4176
545.2    17.00  0.78     Sequence
             DRB1_0401    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.3301
1405.7    46.00  0.79     Sequence
             DRB1_0401    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.3887
745.6    31.00  0.52     Sequence
             DRB1_0401    3      PIKEMFVFLVLLPLV  FVFLVLLPL  5        0.3892
741.1    31.00  0.43     Sequence
             DRB1_0401    4      IKEMFVFLVLLPLVS  FVFLVLLPL  4        0.3997
661.6    29.00  0.43     Sequence
             DRB1_0401    5      KEMFVFLVLLPLVSS  FVFLVLLPL  3        0.4083
602.9    27.00  0.38     Sequence
             DRB1_0401    6      EMFVFLVLLPLVSSQ  FLVLLPLVS  4        0.4366
443.8    22.00  0.34     Sequence
             DRB1_0401    7      MFVFLVLLPLVSSQC  LLPLVSSQC  6        0.4879
254.9    14.00  0.35     Sequence
             DRB1_0401    8      FVFLVLLPLVSSQCV  LLPLVSSQC  5        0.5029
216.6    12.00  0.44     Sequence
             DRB1_0401    9      VFLVLLPLVSSQCVN  LLPLVSSQC  4        0.4988
226.5    13.00  0.56     Sequence
             DRB1_0401   10      FLVLLPLVSSQCVNF  LLPLVSSQC  3        0.5159
188.2    11.00  0.56     Sequence
             DRB1_0401   11      LVLLPLVSSQCVNFT  LLPLVSSQC  2        0.5450
137.4     7.50  0.47     Sequence         WB
             DRB1_0401   12      VLLPLVSSQCVNFTN  VSSQCVNFT  5        0.5710
103.8     5.50  0.54     Sequence         WB
             DRB1_0401   13      LLPLVSSQCVNFTNR  VSSQCVNFT  4        0.5641
111.7     6.00  0.76     Sequence         WB
             DRB1_0401   14      LPLVSSQCVNFTNRT  VSSQCVNFT  3        0.5540
124.6     7.00  0.87     Sequence         WB
             DRB1_0401   15      PLVSSQCVNFTNRTQ  VSSQCVNFT  2        0.5574
120.2     6.50  0.80     Sequence         WB
             DRB1_0401   16      LVSSQCVNFTNRTQL  VSSQCVNFT  1        0.5351
152.9     8.50  0.69     Sequence         WB
             DRB1_0401   17      VSSQCVNFTNRTQLP  CVNFTNRTQ  4        0.3656
956.9    37.00  0.36     Sequence
             DRB1_0401   18      SSQCVNFTNRTQLPS  CVNFTNRTQ  3        0.2846
2300.6    60.00  0.51     Sequence
             DRB1_0401   19      SQCVNFTNRTQLPSA  CVNFTNRTQ  2        0.2801
2413.0    60.00  0.46     Sequence
             DRB1_0401   20      QCVNFTNRTQLPSAY  CVNFTNRTQ  1        0.2666
2793.6    65.00  0.38     Sequence
             DRB1_0401   21      CVNFTNRTQLPSAYT  FTNRTQLPS  3        0.2443
3556.4    75.00  0.26     Sequence
             DRB1_0401   22      VNFTNRTQLPSAYTN  RTQLPSAYT  5        0.2224
4505.1    80.00  0.34     Sequence
             DRB1_0401   23      NFTNRTQLPSAYTNS  RTQLPSAYT  4        0.2247
4397.3    80.00  0.41     Sequence
             DRB1_0401   24      FTNRTQLPSAYTNSF  RTQLPSAYT  3        0.2643
2865.3    65.00  0.38     Sequence
             DRB1_0401   25      TNRTQLPSAYTNSFT  LPSAYTNSF  5        0.2707
2674.1    65.00  0.40     Sequence
             DRB1_0401   26      NRTQLPSAYTNSFTR  LPSAYTNSF  4        0.2877
2223.3    60.00  0.47     Sequence
             DRB1_0401   27      RTQLPSAYTNSFTRG  LPSAYTNSF  3        0.2819
2367.2    60.00  0.46     Sequence
             DRB1_0401   28      TQLPSAYTNSFTRGV  YTNSFTRGV  6        0.3501
1132.0    40.00  0.50     Sequence
             DRB1_0401   29      QLPSAYTNSFTRGVY  YTNSFTRGV  5        0.3841
784.0    32.00  0.69     Sequence
```

```
             DRB1_0401   30      LPSAYTNSFTRGVYY  YTNSFTRGV  4        0.3980
673.9    29.00  0.75     Sequence
             DRB1_0401   31      PSAYTNSFTRGVYYP  YTNSFTRGV  3        0.3886
746.2    31.00  0.82     Sequence
             DRB1_0401   32      SAYTNSFTRGVYYPD  YTNSFTRGV  2        0.3872
757.6    31.00  0.75     Sequence
             DRB1_0401   33      AYTNSFTRGVYYPDK  YTNSFTRGV  1        0.3628
986.7    37.00  0.57     Sequence
             DRB1_0401   34      YTNSFTRGVYYPDKV  FTRGVYYPD  4        0.2976
1998.5    55.00  0.56     Sequence
             DRB1_0401   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.2552
3161.7    70.00  0.77     Sequence
             DRB1_0401   36      NSFTRGVYYPDKVFR  FTRGVYYPD  2        0.2917
2128.8    60.00  0.55     Sequence
             DRB1_0401   37      SFTRGVYYPDKVFRS  YYPDKVFRS  6        0.5673
107.9     6.00  0.86     Sequence         WB
             DRB1_0401   38      FTRGVYYPDKVFRSS  YYPDKVFRS  5        0.6383
50.1     2.50  0.94     Sequence         WB
             DRB1_0401   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.6612
39.1     1.50  0.95     Sequence         SB
             DRB1_0401   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.6665
36.9     1.40  0.95     Sequence         SB
             DRB1_0401   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.6420
48.1     2.00  0.90     Sequence         WB
             DRB1_0401   42      VYYPDKVFRSSVLHS  YYPDKVFRS  1        0.6152
64.3     3.50  0.72     Sequence         WB
             DRB1_0401   43      YYPDKVFRSSVLHST  FRSSVLHST  6        0.6203
60.8     3.00  0.51     Sequence         WB
             DRB1_0401   44      YPDKVFRSSVLHSTQ  FRSSVLHST  5        0.6183
62.1     3.00  0.72     Sequence         WB
             DRB1_0401   45      PDKVFRSSVLHSTQD  FRSSVLHST  4        0.6201
61.0     3.00  0.70     Sequence         WB
             DRB1_0401   46      DKVFRSSVLHSTQDL  FRSSVLHST  3        0.6184
62.1     3.00  0.74     Sequence         WB
             DRB1_0401   47      KVFRSSVLHSTQDLF  FRSSVLHST  2        0.6037
72.8     4.00  0.75     Sequence         WB
             DRB1_0401   48      VFRSSVLHSTQDLFL  FRSSVLHST  1        0.5331
156.2     9.00  0.81     Sequence         WB
             DRB1_0401   49      FRSSVLHSTQDLFLP  FRSSVLHST  0        0.3562
1060.3    39.00  0.51     Sequence
             DRB1_0401   50      RSSVLHSTQDLFLPF  LHSTQDLFL  4        0.2347
3946.1    75.00  0.52     Sequence
             DRB1_0401   51      SSVLHSTQDLFLPFF  LHSTQDLFL  3        0.2510
3307.3    70.00  0.51     Sequence
             DRB1_0401   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2        0.2496
3357.4    70.00  0.48     Sequence
             DRB1_0401   53      VLHSTQDLFLPFFSN  LHSTQDLFL  1        0.2439
3571.6    75.00  0.39     Sequence
             DRB1_0401   54      LHSTQDLFLPFFSNV  FLPFFSNVX  7        0.2961
2029.5    55.00  0.23     Sequence
             DRB1_0401   55      HSTQDLFLPFFSNVT  FLPFFSNVT  6        0.5428
140.8     8.00  0.77     Sequence         WB
             DRB1_0401   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.5907
83.8     4.50  0.80     Sequence         WB
             DRB1_0401   57      TQDLFLPFFSNVTWF  FLPFFSNVT  4        0.6131
65.8     3.50  0.81     Sequence         WB
             DRB1_0401   58      QDLFLPFFSNVTWFH  FLPFFSNVT  3        0.6526
42.9     1.70  0.70     Sequence         SB
             DRB1_0401   59      DLFLPFFSNVTWFHA  FLPFFSNVT  2        0.6790
32.2     1.10  0.54     Sequence         SB
             DRB1_0401   60      LFLPFFSNVTWFHAI  FLPFFSNVT  1        0.6780
32.6     1.10  0.46     Sequence         SB
             DRB1_0401   61      FLPFFSNVTWFHAIH  FSNVTWFHA  4        0.6085
69.1     3.50  0.40     Sequence         WB
             DRB1_0401   62      LPFFSNVTWFHAIHV  FSNVTWFHA  3        0.5508
129.1     7.00  0.55     Sequence         WB
```

```
             DRB1_0401   63      PFFSNVTWFHAIHVS  FSNVTWFHA  2        0.5389
146.8     8.50  0.52     Sequence         WB
             DRB1_0401   64      FFSNVTWFHAIHVSG  FSNVTWFHA  1        0.5090
202.9    11.00  0.47     Sequence
             DRB1_0401   65      FSNVTWFHAIHVSGT  FHAIHVSGT  6        0.4971
230.9    13.00  0.44     Sequence
             DRB1_0401   66      SNVTWFHAIHVSGTN  FHAIHVSGT  5        0.5117
197.0    11.00  0.62     Sequence
             DRB1_0401   67      NVTWFHAIHVSGTNG  FHAIHVSGT  4        0.5238
172.8     9.50  0.63     Sequence         WB
             DRB1_0401   68      VTWFHAIHVSGTNGT  FHAIHVSGT  3        0.5337
155.3     8.50  0.52     Sequence         WB
             DRB1_0401   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.5372
149.5     8.50  0.46     Sequence         WB
             DRB1_0401   70      WFHAIHVSGTNGTKR  IHVSGTNGT  4        0.5251
170.5     9.50  0.48     Sequence         WB
             DRB1_0401   71      FHAIHVSGTNGTKRF  IHVSGTNGT  3        0.4826
270.0    15.00  0.62     Sequence
             DRB1_0401   72      HAIHVSGTNGTKRFD  IHVSGTNGT  2        0.4339
457.0    22.00  0.71     Sequence
             DRB1_0401   73      AIHVSGTNGTKRFDN  IHVSGTNGT  1        0.3930
711.8    30.00  0.71     Sequence
             DRB1_0401   74      IHVSGTNGTKRFDNP  IHVSGTNGT  0        0.2814
2381.6    60.00  0.47     Sequence
             DRB1_0401   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.1285
12454.6   100.00  0.50     Sequence
             DRB1_0401   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.1038
16262.2   100.00  0.34     Sequence
             DRB1_0401   77      SGTNGTKRFDNPVLP  KRFDNPVLP  6        0.1404
10948.9    95.00  0.39     Sequence
             DRB1_0401   78      GTNGTKRFDNPVLPF  KRFDNPVLP  5        0.2302
4144.0    75.00  0.32     Sequence
             DRB1_0401   79      TNGTKRFDNPVLPFN  RFDNPVLPF  5        0.3188
1587.7    49.00  0.30     Sequence
             DRB1_0401   80      NGTKRFDNPVLPFND  FDNPVLPFN  5        0.3461
1181.6    41.00  0.33     Sequence
             DRB1_0401   81      GTKRFDNPVLPFNDG  FDNPVLPFN  4        0.3510
1121.4    40.00  0.37     Sequence
             DRB1_0401   82      TKRFDNPVLPFNDGV  FDNPVLPFN  3        0.3277
1443.2    46.00  0.40     Sequence
             DRB1_0401   83      KRFDNPVLPFNDGVY  FDNPVLPFN  2        0.2875
2228.3    60.00  0.40     Sequence
             DRB1_0401   84      RFDNPVLPFNDGVYF  FDNPVLPFN  1        0.2198
4637.3    80.00  0.40     Sequence
             DRB1_0401   85      FDNPVLPFNDGVYFA  PFNDGVYFA  6        0.1803
7104.5    90.00  0.35     Sequence
             DRB1_0401   86      DNPVLPFNDGVYFAS  FNDGVYFAS  6        0.2607
2977.4    70.00  0.47     Sequence
             DRB1_0401   87      NPVLPFNDGVYFAST  FNDGVYFAS  5        0.3048
1847.7    55.00  0.53     Sequence
             DRB1_0401   88      PVLPFNDGVYFASTE  FNDGVYFAS  4        0.3167
1624.3    49.00  0.55     Sequence
             DRB1_0401   89      VLPFNDGVYFASTEK  FNDGVYFAS  3        0.3369
1306.2    44.00  0.54     Sequence
             DRB1_0401   90      LPFNDGVYFASTEKS  VYFASTEKS  6        0.4844
264.7    14.00  0.62     Sequence
             DRB1_0401   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.5377
148.7     8.50  0.77     Sequence         WB
             DRB1_0401   92      FNDGVYFASTEKSNI  VYFASTEKS  4        0.5532
125.8     7.00  0.81     Sequence         WB
             DRB1_0401   93      NDGVYFASTEKSNII  VYFASTEKS  3        0.5652
110.4     6.00  0.76     Sequence         WB
             DRB1_0401   94      DGVYFASTEKSNIIR  VYFASTEKS  2        0.5596
117.3     6.50  0.66     Sequence         WB
             DRB1_0401   95      GVYFASTEKSNIIRG  VYFASTEKS  1        0.5331
156.3     9.00  0.60     Sequence         WB
```

```
             DRB1_0401   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.4293
480.3    23.00  0.29     Sequence
             DRB1_0401   97      YFASTEKSNIIRGWI  FASTEKSNI  1        0.3116
1716.2    55.00  0.38     Sequence
             DRB1_0401   98      FASTEKSNIIRGWIF  ASTEKSNII  1        0.2462
3485.4    70.00  0.33     Sequence
             DRB1_0401   99      ASTEKSNIIRGWIFG  ASTEKSNII  0        0.1757
7473.2    90.00  0.20     Sequence
             DRB1_0401  100      STEKSNIIRGWIFGT  IIRGWIFGT  6        0.2309
4111.5    75.00  0.57     Sequence
             DRB1_0401  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5        0.2705
2679.7    65.00  0.64     Sequence
             DRB1_0401  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.2788
2449.7    60.00  0.64     Sequence
             DRB1_0401  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3        0.2855
2276.1    60.00  0.63     Sequence
             DRB1_0401  104      SNIIRGWIFGTTLDS  WIFGTTLDS  6        0.3582
1036.9    38.00  0.43     Sequence
             DRB1_0401  105      NIIRGWIFGTTLDSK  WIFGTTLDS  5        0.3799
820.1    33.00  0.52     Sequence
             DRB1_0401  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.3955
692.9    30.00  0.56     Sequence
             DRB1_0401  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3        0.4187
538.9    25.00  0.51     Sequence
             DRB1_0401  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2        0.4302
475.8    23.00  0.49     Sequence
             DRB1_0401  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1        0.4150
561.0    26.00  0.37     Sequence
             DRB1_0401  110      WIFGTTLDSKTQSLL  FGTTLDSKT  2        0.3750
865.1    34.00  0.37     Sequence
             DRB1_0401  111      IFGTTLDSKTQSLLI  FGTTLDSKT  1        0.3197
1573.4    49.00  0.39     Sequence
             DRB1_0401  112      FGTTLDSKTQSLLIV  TLDSKTQSL  3        0.2748
2556.7    65.00  0.37     Sequence
             DRB1_0401  113      GTTLDSKTQSLLIVN  TLDSKTQSL  2        0.2466
3469.8    70.00  0.40     Sequence
             DRB1_0401  114      TTLDSKTQSLLIVNN  TLDSKTQSL  1        0.2316
4078.3    75.00  0.31     Sequence
             DRB1_0401  115      TLDSKTQSLLIVNNA  DSKTQSLLI  2        0.2305
4127.6    75.00  0.19     Sequence
             DRB1_0401  116      LDSKTQSLLIVNNAT  SLLIVNNAT  6        0.3223
1528.6    48.00  0.31     Sequence
             DRB1_0401  117      DSKTQSLLIVNNATN  LLIVNNATN  6        0.5190
182.0    10.00  0.69     Sequence
             DRB1_0401  118      SKTQSLLIVNNATNV  LLIVNNATN  5        0.5802
93.9     5.00  0.71     Sequence        WB
             DRB1_0401  119      KTQSLLIVNNATNVV  LLIVNNATN  4        0.6072
70.1     3.50  0.64     Sequence        WB
             DRB1_0401  120      TQSLLIVNNATNVVI  LLIVNNATN  3        0.6140
65.2     3.50  0.61     Sequence        WB
             DRB1_0401  121      QSLLIVNNATNVVIK  LLIVNNATN  2        0.6078
69.7     3.50  0.56     Sequence        WB
             DRB1_0401  122      SLLIVNNATNVVIKV  LLIVNNATN  1        0.5755
98.8     5.50  0.50     Sequence        WB
             DRB1_0401  123      LLIVNNATNVVIKVC  IVNNATNVV  2        0.4833
268.0    15.00  0.28     Sequence
             DRB1_0401  124      LIVNNATNVVIKVCE  IVNNATNVV  1        0.3496
1138.1    41.00  0.47     Sequence
             DRB1_0401  125      IVNNATNVVIKVCEF  VNNATNVVI  1        0.2494
3364.2    70.00  0.43     Sequence
             DRB1_0401  126      VNNATNVVIKVCEFQ  NATNVVIKV  2        0.1605
8802.5    95.00  0.31     Sequence
             DRB1_0401  127      NNATNVVIKVCEFQF  VVIKVCEFQ  5        0.1703
7923.4    90.00  0.28     Sequence
             DRB1_0401  128      NATNVVIKVCEFQFC  VIKVCEFQF  5        0.1870
6611.0    90.00  0.34     Sequence
```

```
            DRB1_0401  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.2091
5207.7    80.00  0.35     Sequence
            DRB1_0401  130      TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.2238
4437.3    80.00  0.34     Sequence
            DRB1_0401  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.2439
3570.2    75.00  0.31     Sequence
            DRB1_0401  132      VVIKVCEFQFCNYPF  CEFQFCNYP  5        0.2699
2696.1    65.00  0.32     Sequence
            DRB1_0401  133      VIKVCEFQFCNYPFL  FQFCNYPFL  6        0.3251
1483.6    47.00  0.40     Sequence
            DRB1_0401  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.3564
1057.8    39.00  0.43     Sequence
            DRB1_0401  135      KVCEFQFCNYPFLGV  FCNYPFLGV  6        0.4304
474.7    23.00  0.38     Sequence
            DRB1_0401  136      VCEFQFCNYPFLGVY  FCNYPFLGV  5        0.4562
359.1    18.00  0.47     Sequence
            DRB1_0401  137      CEFQFCNYPFLGVYY  FCNYPFLGV  4        0.4556
361.7    19.00  0.52     Sequence
            DRB1_0401  138      EFQFCNYPFLGVYYH  FCNYPFLGV  3        0.4531
371.3    19.00  0.55     Sequence
            DRB1_0401  139      FQFCNYPFLGVYYHK  FCNYPFLGV  2        0.4199
531.8    25.00  0.62     Sequence
            DRB1_0401  140      QFCNYPFLGVYYHKN  FCNYPFLGV  1        0.3975
677.7    29.00  0.51     Sequence
            DRB1_0401  141      FCNYPFLGVYYHKNN  FLGVYYHKN  5        0.3374
1299.4    44.00  0.44     Sequence
            DRB1_0401  142      CNYPFLGVYYHKNNK  FLGVYYHKN  4        0.3365
1311.4    44.00  0.57     Sequence
            DRB1_0401  143      NYPFLGVYYHKNNKS  VYYHKNNKS  6        0.5183
183.5    11.00  0.62     Sequence
            DRB1_0401  144      YPFLGVYYHKNNKSW  VYYHKNNKS  5        0.5754
98.9     5.50  0.63     Sequence         WB
            DRB1_0401  145      PFLGVYYHKNNKSWM  VYYHKNNKS  4        0.5957
79.4     4.00  0.63     Sequence         WB
            DRB1_0401  146      FLGVYYHKNNKSWME  VYYHKNNKS  3        0.6012
74.8     4.00  0.64     Sequence         WB
            DRB1_0401  147      LGVYYHKNNKSWMES  VYYHKNNKS  2        0.5960
79.2     4.00  0.61     Sequence         WB
            DRB1_0401  148      GVYYHKNNKSWMESE  VYYHKNNKS  1        0.5656
110.0     6.00  0.56     Sequence         WB
            DRB1_0401  149      VYYHKNNKSWMESEF  VYYHKNNKS  0        0.4497
385.2    20.00  0.34     Sequence
            DRB1_0401  150      YYHKNNKSWMESEFR  YHKNNKSWM  1        0.3184
1594.7    49.00  0.33     Sequence
            DRB1_0401  151      YHKNNKSWMESEFRV  KSWMESEFR  5        0.2477
3426.5    70.00  0.36     Sequence
            DRB1_0401  152      HKNNKSWMESEFRVY  KSWMESEFR  4        0.2028
5572.5    85.00  0.55     Sequence
            DRB1_0401  153      KNNKSWMESEFRVYS  KSWMESEFR  3        0.2324
4043.1    75.00  0.41     Sequence
            DRB1_0401  154      NNKSWMESEFRVYSS  MESEFRVYS  5        0.2534
3223.0    70.00  0.42     Sequence
            DRB1_0401  155      NKSWMESEFRVYSSA  MESEFRVYS  4        0.2622
2931.3    65.00  0.46     Sequence
            DRB1_0401  156      KSWMESEFRVYSSAN  MESEFRVYS  3        0.2803
2409.7    60.00  0.44     Sequence
            DRB1_0401  157      SWMESEFRVYSSANN  FRVYSSANN  6        0.3355
1325.6    44.00  0.56     Sequence
            DRB1_0401  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.3504
1128.3    40.00  0.60     Sequence
            DRB1_0401  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.3990
667.2    29.00  0.44     Sequence
            DRB1_0401  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.4673
318.6    17.00  0.38     Sequence
            DRB1_0401  161      SEFRVYSSANNCTFE  VYSSANNCT  4        0.4893
251.1    14.00  0.37     Sequence
```

```
             DRB1_0401  162      EFRVYSSANNCTFEY  VYSSANNCT  3        0.4841
265.6    14.00  0.38     Sequence
             DRB1_0401  163      FRVYSSANNCTFEYV  VYSSANNCT  2        0.4503
382.9    19.00  0.39     Sequence
             DRB1_0401  164      RVYSSANNCTFEYVS  YSSANNCTF  2        0.4159
555.7    26.00  0.44     Sequence
             DRB1_0401  165      VYSSANNCTFEYVSQ  YSSANNCTF  1        0.3263
1465.3    47.00  0.44     Sequence
             DRB1_0401  166      YSSANNCTFEYVSQP  YSSANNCTF  0        0.2290
4194.6    75.00  0.26     Sequence
             DRB1_0401  167      SSANNCTFEYVSQPF  CTFEYVSQP  5        0.2405
3705.3    75.00  0.28     Sequence
             DRB1_0401  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.3133
1685.5    50.00  0.49     Sequence
             DRB1_0401  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.3839
785.4    32.00  0.44     Sequence
             DRB1_0401  170      NNCTFEYVSQPFLMD  YVSQPFLMD  6        0.4629
334.1    17.00  0.42     Sequence
             DRB1_0401  171      NCTFEYVSQPFLMDL  YVSQPFLMD  5        0.4958
234.0    13.00  0.57     Sequence
             DRB1_0401  172      CTFEYVSQPFLMDLE  YVSQPFLMD  4        0.4941
238.3    13.00  0.64     Sequence
             DRB1_0401  173      TFEYVSQPFLMDLEG  YVSQPFLMD  3        0.4865
258.8    14.00  0.69     Sequence
             DRB1_0401  174      FEYVSQPFLMDLEGK  YVSQPFLMD  2        0.4341
456.0    22.00  0.77     Sequence
             DRB1_0401  175      EYVSQPFLMDLEGKQ  YVSQPFLMD  1        0.4209
526.0    25.00  0.59     Sequence
             DRB1_0401  176      YVSQPFLMDLEGKQG  FLMDLEGKQ  5        0.3402
1259.5    43.00  0.57     Sequence
             DRB1_0401  177      VSQPFLMDLEGKQGN  FLMDLEGKQ  4        0.3354
1327.5    44.00  0.69     Sequence
             DRB1_0401  178      SQPFLMDLEGKQGNF  FLMDLEGKQ  3        0.3563
1059.0    39.00  0.69     Sequence
             DRB1_0401  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2        0.3505
1127.5    40.00  0.58     Sequence
             DRB1_0401  180      PFLMDLEGKQGNFKN  FLMDLEGKQ  1        0.3224
1527.2    48.00  0.50     Sequence
             DRB1_0401  181      FLMDLEGKQGNFKNL  LMDLEGKQG  1        0.2607
2978.5    70.00  0.30     Sequence
             DRB1_0401  182      LMDLEGKQGNFKNLS  LEGKQGNFK  3        0.1970
5930.1    85.00  0.35     Sequence
             DRB1_0401  183      MDLEGKQGNFKNLSE  LEGKQGNFK  2        0.1878
6553.7    90.00  0.37     Sequence
             DRB1_0401  184      DLEGKQGNFKNLSEF  LEGKQGNFK  1        0.1871
6602.1    90.00  0.31     Sequence
             DRB1_0401  185      LEGKQGNFKNLSEFV  KQGNFKNLS  3        0.2014
5654.3    85.00  0.25     Sequence
             DRB1_0401  186      EGKQGNFKNLSEFVF  FKNLSEFVF  6        0.2325
4039.7    75.00  0.49     Sequence
             DRB1_0401  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5        0.2708
2670.6    65.00  0.58     Sequence
             DRB1_0401  188      KQGNFKNLSEFVFKN  FKNLSEFVF  4        0.3352
1329.5    44.00  0.50     Sequence
             DRB1_0401  189      QGNFKNLSEFVFKNI  FKNLSEFVF  3        0.3557
1065.7    39.00  0.45     Sequence
             DRB1_0401  190      GNFKNLSEFVFKNID  NLSEFVFKN  4        0.3547
1076.9    39.00  0.41     Sequence
             DRB1_0401  191      NFKNLSEFVFKNIDG  NLSEFVFKN  3        0.3363
1314.8    44.00  0.44     Sequence
             DRB1_0401  192      FKNLSEFVFKNIDGY  NLSEFVFKN  2        0.3196
1574.1    49.00  0.42     Sequence
             DRB1_0401  193      KNLSEFVFKNIDGYF  NLSEFVFKN  1        0.3675
937.4    36.00  0.29     Sequence
             DRB1_0401  194      NLSEFVFKNIDGYFK  FKNIDGYFK  6        0.4020
645.5    28.00  0.34     Sequence
```

```
             DRB1_0401  195      LSEFVFKNIDGYFKI  FKNIDGYFK  5        0.4115
582.6    26.00  0.49     Sequence
             DRB1_0401  196      SEFVFKNIDGYFKIY  FKNIDGYFK  4        0.4188
538.5    25.00  0.56     Sequence
             DRB1_0401  197      EFVFKNIDGYFKIYS  FKNIDGYFK  3        0.4087
600.4    27.00  0.61     Sequence
             DRB1_0401  198      FVFKNIDGYFKIYSK  FKNIDGYFK  2        0.4008
654.0    29.00  0.63     Sequence
             DRB1_0401  199      VFKNIDGYFKIYSKH  FKNIDGYFK  1        0.3807
813.3    33.00  0.59     Sequence
             DRB1_0401  200      FKNIDGYFKIYSKHT  YFKIYSKHT  6        0.3499
1134.4    40.00  0.39     Sequence
             DRB1_0401  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.4002
658.2    29.00  0.43     Sequence
             DRB1_0401  202      NIDGYFKIYSKHTPI  YFKIYSKHT  4        0.4408
424.5    21.00  0.41     Sequence
             DRB1_0401  203      IDGYFKIYSKHTPIN  YFKIYSKHT  3        0.4871
257.2    14.00  0.32     Sequence
             DRB1_0401  204      DGYFKIYSKHTPINL  YFKIYSKHT  2        0.5177
184.6    11.00  0.27     Sequence
             DRB1_0401  205      GYFKIYSKHTPINLV  YSKHTPINL  5        0.5278
165.6     9.50  0.28     Sequence         WB
             DRB1_0401  206      YFKIYSKHTPINLVR  YSKHTPINL  4        0.5171
185.8    11.00  0.38     Sequence
             DRB1_0401  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.4757
290.8    16.00  0.47     Sequence
             DRB1_0401  208      KIYSKHTPINLVRDL  YSKHTPINL  2        0.4135
570.0    26.00  0.56     Sequence
             DRB1_0401  209      IYSKHTPINLVRDLP  YSKHTPINL  1        0.3215
1542.8    48.00  0.54     Sequence
             DRB1_0401  210      YSKHTPINLVRDLPQ  INLVRDLPQ  6        0.3310
1392.4    45.00  0.62     Sequence
             DRB1_0401  211      SKHTPINLVRDLPQG  INLVRDLPQ  5        0.3647
966.9    37.00  0.83     Sequence
             DRB1_0401  212      KHTPINLVRDLPQGF  INLVRDLPQ  4        0.4173
546.9    25.00  0.77     Sequence
             DRB1_0401  213      HTPINLVRDLPQGFS  INLVRDLPQ  3        0.4447
406.6    20.00  0.68     Sequence
             DRB1_0401  214      TPINLVRDLPQGFSA  INLVRDLPQ  2        0.4545
365.8    19.00  0.62     Sequence
             DRB1_0401  215      PINLVRDLPQGFSAL  INLVRDLPQ  1        0.4308
473.0    23.00  0.54     Sequence
             DRB1_0401  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.3639
974.6    37.00  0.32     Sequence
             DRB1_0401  217      NLVRDLPQGFSALEP  LVRDLPQGF  1        0.2703
2683.2    65.00  0.41     Sequence
             DRB1_0401  218      LVRDLPQGFSALEPL  LPQGFSALE  4        0.2294
4180.8    75.00  0.31     Sequence
             DRB1_0401  219      VRDLPQGFSALEPLV  LPQGFSALE  3        0.2479
3419.2    70.00  0.36     Sequence
             DRB1_0401  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.3535
1091.0    40.00  0.67     Sequence
             DRB1_0401  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.4086
601.2    27.00  0.80     Sequence
             DRB1_0401  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.4259
498.7    24.00  0.82     Sequence
             DRB1_0401  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.4320
466.7    23.00  0.81     Sequence
             DRB1_0401  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.4232
513.0    24.00  0.74     Sequence
             DRB1_0401  225      GFSALEPLVDLPIGI  FSALEPLVD  1        0.3844
781.4    32.00  0.67     Sequence
             DRB1_0401  226      FSALEPLVDLPIGIN  LEPLVDLPI  3        0.2617
2947.3    65.00  0.42     Sequence
             DRB1_0401  227      SALEPLVDLPIGINI  LEPLVDLPI  2        0.2179
4732.9    80.00  0.52     Sequence
```

```
             DRB1_0401  228      ALEPLVDLPIGINIT  LEPLVDLPI  1        0.2303
4139.3    75.00  0.37     Sequence
             DRB1_0401  229      LEPLVDLPIGINITR  LPIGINITR  6        0.2599
3005.5    70.00  0.32     Sequence
             DRB1_0401  230      EPLVDLPIGINITRF  LPIGINITR  5        0.2874
2231.9    60.00  0.41     Sequence
             DRB1_0401  231      PLVDLPIGINITRFQ  LPIGINITR  4        0.3160
1637.5    50.00  0.39     Sequence
             DRB1_0401  232      LVDLPIGINITRFQT  LPIGINITR  3        0.3187
1589.3    49.00  0.38     Sequence
             DRB1_0401  233      VDLPIGINITRFQTL  LPIGINITR  2        0.3160
1637.7    50.00  0.34     Sequence
             DRB1_0401  234      DLPIGINITRFQTLL  IGINITRFQ  3        0.3178
1606.1    49.00  0.30     Sequence
             DRB1_0401  235      LPIGINITRFQTLLA  ITRFQTLLA  6        0.4085
601.8    27.00  0.54    Sequence
             DRB1_0401  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.4415
421.0    21.00  0.69    Sequence
             DRB1_0401  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.5000
223.6    13.00  0.63    Sequence
             DRB1_0401  238      GINITRFQTLLALHR  ITRFQTLLA  3        0.5978
77.6     4.00  0.50    Sequence        WB
             DRB1_0401  239      INITRFQTLLALHRS  FQTLLALHR  5        0.6096
68.3     3.50  0.54    Sequence        WB
             DRB1_0401  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.6098
68.2     3.50  0.61    Sequence        WB
             DRB1_0401  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.5880
86.3     4.50  0.62    Sequence        WB
             DRB1_0401  242      TRFQTLLALHRSYLT  LALHRSYLT  6        0.6563
41.2     1.60  0.50    Sequence        SB
             DRB1_0401  243      RFQTLLALHRSYLTP  LALHRSYLT  5        0.6712
35.1     1.30  0.62    Sequence        SB
             DRB1_0401  244      FQTLLALHRSYLTPG  LALHRSYLT  4        0.6473
45.4     1.90  0.77    Sequence        SB
             DRB1_0401  245      QTLLALHRSYLTPGD  LALHRSYLT  3        0.6251
57.8     3.00  0.87    Sequence        WB
             DRB1_0401  246      TLLALHRSYLTPGDS  LALHRSYLT  2        0.6133
65.6     3.50  0.85    Sequence        WB
             DRB1_0401  247      LLALHRSYLTPGDSS  LALHRSYLT  1        0.5740
100.4     5.50  0.79    Sequence        WB
             DRB1_0401  248      LALHRSYLTPGDSSS  LALHRSYLT  0        0.4366
443.9    22.00  0.44    Sequence
             DRB1_0401  249      ALHRSYLTPGDSSSG  YLTPGDSSS  5        0.2966
2019.0    55.00  0.32     Sequence
             DRB1_0401  250      LHRSYLTPGDSSSGW  YLTPGDSSS  4        0.2943
2071.5    60.00  0.38     Sequence
             DRB1_0401  251      HRSYLTPGDSSSGWT  YLTPGDSSS  3        0.2792
2436.7    60.00  0.44     Sequence
             DRB1_0401  252      RSYLTPGDSSSGWTA  YLTPGDSSS  2        0.2790
2443.3    60.00  0.40     Sequence
             DRB1_0401  253      SYLTPGDSSSGWTAG  LTPGDSSSG  2        0.2447
3542.9    70.00  0.31     Sequence
             DRB1_0401  254      YLTPGDSSSGWTAGA  LTPGDSSSG  1        0.2086
5234.5    80.00  0.28     Sequence
             DRB1_0401  255      LTPGDSSSGWTAGAA  SSSGWTAGA  5        0.1619
8675.7    95.00  0.22     Sequence
             DRB1_0401  256      TPGDSSSGWTAGAAA  SSSGWTAGA  4        0.1498
9888.4    95.00  0.26     Sequence
             DRB1_0401  257      PGDSSSGWTAGAAAY  SSSGWTAGA  3        0.1636
8519.3    95.00  0.24     Sequence
             DRB1_0401  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.2264
4317.5    80.00  0.41     Sequence
             DRB1_0401  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.2672
2775.8    65.00  0.50     Sequence
             DRB1_0401  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.2806
2401.5    60.00  0.52     Sequence
```

```
             DRB1_0401  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.2868
2245.4    60.00  0.56     Sequence
             DRB1_0401  262      SGWTAGAAAYYVGYL  WTAGAAAYY  2        0.2714
2653.6    65.00  0.52     Sequence
             DRB1_0401  263      GWTAGAAAYYVGYLQ  WTAGAAAYY  1        0.2492
3371.2    70.00  0.47     Sequence
             DRB1_0401  264      WTAGAAAYYVGYLQP  TAGAAAYYV  1        0.2170
4780.6    80.00  0.28     Sequence
             DRB1_0401  265      TAGAAAYYVGYLQPR  YYVGYLQPR  6        0.2867
2248.3    60.00  0.38     Sequence
             DRB1_0401  266      AGAAAYYVGYLQPRT  YVGYLQPRT  6        0.4383
435.7    21.00  0.54     Sequence
             DRB1_0401  267      GAAAYYVGYLQPRTF  YVGYLQPRT  5        0.5043
213.5    12.00  0.62     Sequence
             DRB1_0401  268      AAAYYVGYLQPRTFL  YVGYLQPRT  4        0.5288
163.7     9.00  0.60     Sequence         WB
             DRB1_0401  269      AAYYVGYLQPRTFLL  YVGYLQPRT  3        0.5517
127.7     7.00  0.51     Sequence         WB
             DRB1_0401  270      AYYVGYLQPRTFLLK  YVGYLQPRT  2        0.5598
117.1     6.50  0.41     Sequence         WB
             DRB1_0401  271      YYVGYLQPRTFLLKY  YLQPRTFLL  4        0.5466
135.0     7.50  0.50     Sequence         WB
             DRB1_0401  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.4959
233.8    13.00  0.63     Sequence
             DRB1_0401  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.4527
373.0    19.00  0.75     Sequence
             DRB1_0401  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.4406
425.2    21.00  0.65     Sequence
             DRB1_0401  275      YLQPRTFLLKYNENG  FLLKYNENG  6        0.4029
639.6    28.00  0.55     Sequence
             DRB1_0401  276      LQPRTFLLKYNENGT  FLLKYNENG  5        0.4027
640.7    28.00  0.74     Sequence
             DRB1_0401  277      QPRTFLLKYNENGTI  FLLKYNENG  4        0.4650
326.5    17.00  0.62     Sequence
             DRB1_0401  278      PRTFLLKYNENGTIT  FLLKYNENG  3        0.4969
231.3    13.00  0.53     Sequence
             DRB1_0401  279      RTFLLKYNENGTITD  FLLKYNENG  2        0.5013
220.5    12.00  0.47     Sequence
             DRB1_0401  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.4885
253.3    14.00  0.40     Sequence
             DRB1_0401  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.4425
416.5    21.00  0.43     Sequence
             DRB1_0401  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.3828
794.7    32.00  0.47     Sequence
             DRB1_0401  283      LKYNENGTITDAVDC  YNENGTITD  2        0.3144
1666.1    50.00  0.56     Sequence
             DRB1_0401  284      KYNENGTITDAVDCA  YNENGTITD  1        0.2340
3977.7    75.00  0.60     Sequence
             DRB1_0401  285      YNENGTITDAVDCAL  TITDAVDCA  5        0.2079
5275.2    85.00  0.39     Sequence
             DRB1_0401  286      NENGTITDAVDCALD  TITDAVDCA  4        0.2133
4974.1    80.00  0.47     Sequence
             DRB1_0401  287      ENGTITDAVDCALDP  TITDAVDCA  3        0.2373
3835.7    75.00  0.40     Sequence
             DRB1_0401  288      NGTITDAVDCALDPL  TITDAVDCA  2        0.2470
3454.5    70.00  0.37     Sequence
             DRB1_0401  289      GTITDAVDCALDPLS  VDCALDPLS  6        0.3060
1823.5    55.00  0.24     Sequence
             DRB1_0401  290      TITDAVDCALDPLSE  VDCALDPLS  5        0.3164
1630.4    49.00  0.38     Sequence
             DRB1_0401  291      ITDAVDCALDPLSET  VDCALDPLS  4        0.3138
1676.9    50.00  0.46     Sequence
             DRB1_0401  292      TDAVDCALDPLSETK  VDCALDPLS  3        0.3236
1507.3    47.00  0.47     Sequence
             DRB1_0401  293      DAVDCALDPLSETKC  VDCALDPLS  2        0.2903
2162.5    60.00  0.49     Sequence
```

```
             DRB1_0401  294      AVDCALDPLSETKCT  VDCALDPLS  1        0.2555
3150.4    70.00  0.47     Sequence
             DRB1_0401  295      VDCALDPLSETKCTL  VDCALDPLS  0        0.1974
5909.3    85.00  0.28     Sequence
             DRB1_0401  296      DCALDPLSETKCTLK  CALDPLSET  1        0.1336
11782.0   100.00  0.29     Sequence
             DRB1_0401  297      CALDPLSETKCTLKS  SETKCTLKS  6        0.1279
12526.1   100.00  0.27     Sequence
             DRB1_0401  298      ALDPLSETKCTLKSF  SETKCTLKS  5        0.1382
11204.5    95.00  0.45     Sequence
             DRB1_0401  299      LDPLSETKCTLKSFT  SETKCTLKS  4        0.1437
10556.0    95.00  0.49     Sequence
             DRB1_0401  300      DPLSETKCTLKSFTV  SETKCTLKS  3        0.1698
7966.3    90.00  0.41     Sequence
             DRB1_0401  301      PLSETKCTLKSFTVE  SETKCTLKS  2        0.1852
6739.7    90.00  0.34     Sequence
             DRB1_0401  302      LSETKCTLKSFTVEK  TLKSFTVEK  6        0.2609
2972.8    70.00  0.26     Sequence
             DRB1_0401  303      SETKCTLKSFTVEKG  LKSFTVEKG  6        0.4040
632.1    28.00  0.63     Sequence
             DRB1_0401  304      ETKCTLKSFTVEKGI  LKSFTVEKG  5        0.4684
314.7    17.00  0.71     Sequence
             DRB1_0401  305      TKCTLKSFTVEKGIY  LKSFTVEKG  4        0.5115
197.4    11.00  0.69     Sequence
             DRB1_0401  306      KCTLKSFTVEKGIYQ  LKSFTVEKG  3        0.5548
123.6     7.00  0.58     Sequence         WB
             DRB1_0401  307      CTLKSFTVEKGIYQT  LKSFTVEKG  2        0.5408
143.8     8.00  0.47     Sequence         WB
             DRB1_0401  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.5336
155.5     8.50  0.51     Sequence         WB
             DRB1_0401  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.4641
329.8    17.00  0.80     Sequence
             DRB1_0401  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.4400
428.0    21.00  0.85     Sequence
             DRB1_0401  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.4495
386.1    20.00  0.62     Sequence
             DRB1_0401  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.4371
441.8    22.00  0.38     Sequence
             DRB1_0401  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.4651
326.3    17.00  0.58     Sequence
             DRB1_0401  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.4882
254.2    14.00  0.59     Sequence
             DRB1_0401  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.4960
233.5    13.00  0.58     Sequence
             DRB1_0401  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.4828
269.4    15.00  0.61     Sequence
             DRB1_0401  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.4278
488.4    23.00  0.62     Sequence
             DRB1_0401  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.5126
195.2    11.00  0.79     Sequence
             DRB1_0401  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.5556
122.5     7.00  0.89     Sequence         WB
             DRB1_0401  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.5994
76.3     4.00  0.86     Sequence         WB
             DRB1_0401  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.6193
61.5     3.00  0.81     Sequence         WB
             DRB1_0401  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.6068
70.4     3.50  0.77     Sequence         WB
             DRB1_0401  323      NFRVQPTESIVRFPN  FRVQPTESI  1        0.5683
106.8     6.00  0.69     Sequence         WB
             DRB1_0401  324      FRVQPTESIVRFPNI  FRVQPTESI  0        0.4637
331.2    17.00  0.47     Sequence
             DRB1_0401  325      RVQPTESIVRFPNIT  VQPTESIVR  1        0.2947
2061.5    60.00  0.66     Sequence
             DRB1_0401  326      VQPTESIVRFPNITN  IVRFPNITN  6        0.3316
1382.7    45.00  0.70     Sequence
```

```
             DRB1_0401  327      QPTESIVRFPNITNL  IVRFPNITN  5         0.3630
985.0    37.00  0.87     Sequence
             DRB1_0401  328      PTESIVRFPNITNLC  IVRFPNITN  4         0.4113
583.7    26.00  0.74     Sequence
             DRB1_0401  329      TESIVRFPNITNLCP  IVRFPNITN  3         0.4908
247.0    14.00  0.49     Sequence
             DRB1_0401  330      ESIVRFPNITNLCPF  FPNITNLCP  5         0.5250
170.6     9.50  0.56     Sequence         WB
             DRB1_0401  331      SIVRFPNITNLCPFG  FPNITNLCP  4         0.5340
154.7     8.50  0.62     Sequence         WB
             DRB1_0401  332      IVRFPNITNLCPFGE  FPNITNLCP  3         0.5126
195.1    11.00  0.72     Sequence
             DRB1_0401  333      VRFPNITNLCPFGEV  FPNITNLCP  2         0.4854
261.9    14.00  0.74     Sequence
             DRB1_0401  334      RFPNITNLCPFGEVF  FPNITNLCP  1         0.4471
396.4    20.00  0.70     Sequence
             DRB1_0401  335      FPNITNLCPFGEVFN  FPNITNLCP  0         0.2920
2121.8    60.00  0.39     Sequence
             DRB1_0401  336      PNITNLCPFGEVFNA  ITNLCPFGE  2         0.2006
5705.2    85.00  0.52     Sequence
             DRB1_0401  337      NITNLCPFGEVFNAT  ITNLCPFGE  1         0.2080
5265.1    80.00  0.38     Sequence
             DRB1_0401  338      ITNLCPFGEVFNATR  FGEVFNATR  6         0.2960
2033.0    55.00  0.61     Sequence
             DRB1_0401  339      TNLCPFGEVFNATRF  FGEVFNATR  5         0.3471
1169.3    41.00  0.67     Sequence
             DRB1_0401  340      NLCPFGEVFNATRFA  FGEVFNATR  4         0.3808
811.9    33.00  0.67     Sequence
             DRB1_0401  341      LCPFGEVFNATRFAS  FGEVFNATR  3         0.4039
632.3    28.00  0.60     Sequence
             DRB1_0401  342      CPFGEVFNATRFASV  FGEVFNATR  2         0.4386
434.4    21.00  0.44     Sequence
             DRB1_0401  343      PFGEVFNATRFASVY  FNATRFASV  5         0.4556
361.3    19.00  0.38     Sequence
             DRB1_0401  344      FGEVFNATRFASVYA  FNATRFASV  4         0.4331
461.1    22.00  0.56     Sequence
             DRB1_0401  345      GEVFNATRFASVYAW  FNATRFASV  3         0.4177
544.9    25.00  0.61     Sequence
             DRB1_0401  346      EVFNATRFASVYAWN  FNATRFASV  2         0.4072
610.5    27.00  0.55     Sequence
             DRB1_0401  347      VFNATRFASVYAWNR  FNATRFASV  1         0.4250
503.6    24.00  0.34     Sequence
             DRB1_0401  348      FNATRFASVYAWNRK  FASVYAWNR  5         0.4152
559.9    26.00  0.44     Sequence
             DRB1_0401  349      NATRFASVYAWNRKR  FASVYAWNR  4         0.4286
484.2    23.00  0.56     Sequence
             DRB1_0401  350      ATRFASVYAWNRKRI  FASVYAWNR  3         0.4153
559.1    26.00  0.63     Sequence
             DRB1_0401  351      TRFASVYAWNRKRIS  FASVYAWNR  2         0.3951
695.4    30.00  0.67     Sequence
             DRB1_0401  352      RFASVYAWNRKRISN  FASVYAWNR  1         0.3339
1349.2    45.00  0.65     Sequence
             DRB1_0401  353      FASVYAWNRKRISNC  FASVYAWNR  0         0.2424
3631.4    75.00  0.29     Sequence
             DRB1_0401  354      ASVYAWNRKRISNCV  YAWNRKRIS  3         0.2047
5459.8    85.00  0.37     Sequence
             DRB1_0401  355      SVYAWNRKRISNCVA  YAWNRKRIS  2         0.2181
4721.8    80.00  0.32     Sequence
             DRB1_0401  356      VYAWNRKRISNCVAD  WNRKRISNC  3         0.2123
5027.9    80.00  0.26     Sequence
             DRB1_0401  357      YAWNRKRISNCVADY  WNRKRISNC  2         0.2334
4003.2    75.00  0.20     Sequence
             DRB1_0401  358      AWNRKRISNCVADYS  ISNCVADYS  6         0.2809
2392.3    60.00  0.38     Sequence
             DRB1_0401  359      WNRKRISNCVADYSV  ISNCVADYS  5         0.3138
1677.0    50.00  0.51     Sequence
```

```
             DRB1_0401  360      NRKRISNCVADYSVL  ISNCVADYS  4        0.3356
1323.7    44.00  0.57     Sequence
             DRB1_0401  361      RKRISNCVADYSVLY  CVADYSVLY  6        0.4560
359.8    18.00  0.50     Sequence
             DRB1_0401  362      KRISNCVADYSVLYN  CVADYSVLY  5        0.4943
237.9    13.00  0.61     Sequence
             DRB1_0401  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.5018
219.2    12.00  0.69     Sequence
             DRB1_0401  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.5096
201.5    11.00  0.70     Sequence
             DRB1_0401  365      SNCVADYSVLYNSAS  CVADYSVLY  2        0.5812
92.9     5.00  0.47     Sequence         WB
             DRB1_0401  366      NCVADYSVLYNSASF  YSVLYNSAS  5        0.5918
82.8     4.50  0.46     Sequence         WB
             DRB1_0401  367      CVADYSVLYNSASFS  YSVLYNSAS  4        0.5653
110.3     6.00  0.54     Sequence         WB
             DRB1_0401  368      VADYSVLYNSASFST  YSVLYNSAS  3        0.5487
132.1     7.50  0.62     Sequence         WB
             DRB1_0401  369      ADYSVLYNSASFSTF  YSVLYNSAS  2        0.5589
118.2     6.50  0.55     Sequence         WB
             DRB1_0401  370      DYSVLYNSASFSTFK  YSVLYNSAS  1        0.5527
126.5     7.00  0.44     Sequence         WB
             DRB1_0401  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.4965
232.3    13.00  0.26     Sequence
             DRB1_0401  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.4246
505.5    24.00  0.35     Sequence
             DRB1_0401  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.3623
992.2    37.00  0.40     Sequence
             DRB1_0401  374      LYNSASFSTFKCYGV  YNSASFSTF  1        0.2998
1951.2    55.00  0.28     Sequence
             DRB1_0401  375      YNSASFSTFKCYGVS  FSTFKCYGV  5        0.2386
3783.9    75.00  0.52     Sequence
             DRB1_0401  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.2403
3711.7    75.00  0.63     Sequence
             DRB1_0401  377      SASFSTFKCYGVSPT  FKCYGVSPT  6        0.3347
1337.0    44.00  0.49     Sequence
             DRB1_0401  378      ASFSTFKCYGVSPTK  FKCYGVSPT  5        0.3829
793.8    32.00  0.56     Sequence
             DRB1_0401  379      SFSTFKCYGVSPTKL  FKCYGVSPT  4        0.4081
604.3    27.00  0.56     Sequence
             DRB1_0401  380      FSTFKCYGVSPTKLN  FKCYGVSPT  3        0.4212
524.6    24.00  0.53     Sequence
             DRB1_0401  381      STFKCYGVSPTKLND  FKCYGVSPT  2        0.4110
585.4    26.00  0.49     Sequence
             DRB1_0401  382      TFKCYGVSPTKLNDL  FKCYGVSPT  1        0.3884
748.4    31.00  0.39     Sequence
             DRB1_0401  383      FKCYGVSPTKLNDLC  YGVSPTKLN  3        0.3143
1668.0    50.00  0.37     Sequence
             DRB1_0401  384      KCYGVSPTKLNDLCF  YGVSPTKLN  2        0.2434
3589.4    75.00  0.57     Sequence
             DRB1_0401  385      CYGVSPTKLNDLCFT  YGVSPTKLN  1        0.1793
7181.5    90.00  0.58     Sequence
             DRB1_0401  386      YGVSPTKLNDLCFTN  YGVSPTKLN  0        0.1547
9375.1    95.00  0.31     Sequence
             DRB1_0401  387      GVSPTKLNDLCFTNV  LNDLCFTNV  6        0.1758
7462.0    90.00  0.38     Sequence
             DRB1_0401  388      VSPTKLNDLCFTNVY  LNDLCFTNV  5        0.2111
5095.9    80.00  0.46     Sequence
             DRB1_0401  389      SPTKLNDLCFTNVYA  LNDLCFTNV  4        0.2610
2968.2    70.00  0.46     Sequence
             DRB1_0401  390      PTKLNDLCFTNVYAD  LCFTNVYAD  6        0.3158
1640.9    50.00  0.31     Sequence
             DRB1_0401  391      TKLNDLCFTNVYADS  LCFTNVYAD  5        0.3509
1122.2    40.00  0.38     Sequence
             DRB1_0401  392      KLNDLCFTNVYADSF  LCFTNVYAD  4        0.3842
782.8    32.00  0.38     Sequence
```

```
             DRB1_0401  393      LNDLCFTNVYADSFV  LCFTNVYAD  3        0.3821
800.5    33.00  0.43     Sequence
             DRB1_0401  394      NDLCFTNVYADSFVI  FTNVYADSF  4        0.3851
774.9    32.00  0.40     Sequence
             DRB1_0401  395      DLCFTNVYADSFVIR  FTNVYADSF  3        0.4080
605.2    27.00  0.39     Sequence
             DRB1_0401  396      LCFTNVYADSFVIRG  YADSFVIRG  6        0.4599
345.0    18.00  0.41     Sequence
             DRB1_0401  397      CFTNVYADSFVIRGD  YADSFVIRG  5        0.4536
369.6    19.00  0.54     Sequence
             DRB1_0401  398      FTNVYADSFVIRGDE  YADSFVIRG  4        0.4427
415.6    21.00  0.64     Sequence
             DRB1_0401  399      TNVYADSFVIRGDEV  YADSFVIRG  3        0.4250
503.3    24.00  0.69     Sequence
             DRB1_0401  400      NVYADSFVIRGDEVR  YADSFVIRG  2        0.4061
617.8    27.00  0.64     Sequence
             DRB1_0401  401      VYADSFVIRGDEVRQ  YADSFVIRG  1        0.3721
892.1    35.00  0.52     Sequence
             DRB1_0401  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.4570
356.2    18.00  0.66     Sequence
             DRB1_0401  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.5347
153.7     8.50  0.82     Sequence         WB
             DRB1_0401  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.5583
119.0     6.50  0.85     Sequence         WB
             DRB1_0401  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.5612
115.3     6.50  0.85     Sequence         WB
             DRB1_0401  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.5346
153.7     8.50  0.82     Sequence         WB
             DRB1_0401  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.4894
250.8    14.00  0.80     Sequence
             DRB1_0401  408      IRGDEVRQIAPGQTG  IRGDEVRQI  0        0.3250
1485.1    47.00  0.47     Sequence
             DRB1_0401  409      RGDEVRQIAPGQTGT  EVRQIAPGQ  3        0.1983
5850.7    85.00  0.47     Sequence
             DRB1_0401  410      GDEVRQIAPGQTGTI  EVRQIAPGQ  2        0.1794
7176.1    90.00  0.38     Sequence
             DRB1_0401  411      DEVRQIAPGQTGTIA  EVRQIAPGQ  1        0.1651
8375.6    95.00  0.29     Sequence
             DRB1_0401  412      EVRQIAPGQTGTIAD  IAPGQTGTI  4        0.1440
10521.8    95.00  0.33     Sequence
             DRB1_0401  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.1357
11522.0    95.00  0.43     Sequence
             DRB1_0401  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.1279
12529.0   100.00  0.41     Sequence
             DRB1_0401  415      QIAPGQTGTIADYNY  IAPGQTGTI  1        0.1172
14063.9   100.00  0.31     Sequence
             DRB1_0401  416      IAPGQTGTIADYNYK  PGQTGTIAD  2        0.1217
13395.8   100.00  0.17     Sequence
             DRB1_0401  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.1954
6034.9    85.00  0.55     Sequence
             DRB1_0401  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.2402
3718.7    75.00  0.66     Sequence
             DRB1_0401  419      GQTGTIADYNYKLPD  TIADYNYKL  4        0.2502
3336.2    70.00  0.64     Sequence
             DRB1_0401  420      QTGTIADYNYKLPDD  TIADYNYKL  3        0.2403
3715.4    75.00  0.67     Sequence
             DRB1_0401  421      TGTIADYNYKLPDDF  TIADYNYKL  2        0.2356
3908.6    75.00  0.67     Sequence
             DRB1_0401  422      GTIADYNYKLPDDFT  TIADYNYKL  1        0.2344
3957.9    75.00  0.54     Sequence
             DRB1_0401  423      TIADYNYKLPDDFTG  YKLPDDFTG  6        0.2141
4933.1    80.00  0.32     Sequence
             DRB1_0401  424      IADYNYKLPDDFTGC  YKLPDDFTG  5        0.1880
6538.3    85.00  0.47     Sequence
             DRB1_0401  425      ADYNYKLPDDFTGCV  YKLPDDFTG  4        0.2022
5606.3    85.00  0.47     Sequence
```

```
             DRB1_0401  426      DYNYKLPDDFTGCVI  YKLPDDFTG  3        0.2101
5149.1    80.00  0.43     Sequence
             DRB1_0401  427      YNYKLPDDFTGCVIA  YKLPDDFTG  2        0.2115
5069.5    80.00  0.40     Sequence
             DRB1_0401  428      NYKLPDDFTGCVIAW  YKLPDDFTG  1        0.2124
5019.9    80.00  0.35     Sequence
             DRB1_0401  429      YKLPDDFTGCVIAWN  FTGCVIAWN  6        0.3244
1495.1    47.00  0.68     Sequence
             DRB1_0401  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.3797
822.0    33.00  0.77     Sequence
             DRB1_0401  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.4090
598.9    27.00  0.76     Sequence
             DRB1_0401  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.4567
357.4    18.00  0.65     Sequence
             DRB1_0401  433      DDFTGCVIAWNSNNL  FTGCVIAWN  2        0.5019
219.0    12.00  0.52     Sequence
             DRB1_0401  434      DFTGCVIAWNSNNLD  IAWNSNNLD  6        0.5689
106.1     6.00  0.39     Sequence         WB
             DRB1_0401  435      FTGCVIAWNSNNLDS  IAWNSNNLD  5        0.5780
96.2     5.50  0.56     Sequence         WB
             DRB1_0401  436      TGCVIAWNSNNLDSK  IAWNSNNLD  4        0.5817
92.4     5.00  0.71     Sequence         WB
             DRB1_0401  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3        0.5841
90.0     5.00  0.73     Sequence         WB
             DRB1_0401  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2        0.5426
141.1     8.00  0.74     Sequence         WB
             DRB1_0401  439      VIAWNSNNLDSKVGG  IAWNSNNLD  1        0.4981
228.3    13.00  0.79     Sequence
             DRB1_0401  440      IAWNSNNLDSKVGGN  IAWNSNNLD  0        0.3467
1174.8    41.00  0.56     Sequence
             DRB1_0401  441      AWNSNNLDSKVGGNY  WNSNNLDSK  1        0.1352
11575.3   100.00  0.42     Sequence
             DRB1_0401  442      WNSNNLDSKVGGNYN  DSKVGGNYN  6        0.1033
16347.1   100.00  0.19     Sequence
             DRB1_0401  443      NSNNLDSKVGGNYNY  DSKVGGNYN  5        0.1131
14703.2   100.00  0.26     Sequence
             DRB1_0401  444      SNNLDSKVGGNYNYL  DSKVGGNYN  4        0.1332
11837.1   100.00  0.22     Sequence
             DRB1_0401  445      NNLDSKVGGNYNYLY  VGGNYNYLY  6        0.2437
3581.1    75.00  0.61     Sequence
             DRB1_0401  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.3140
1672.2    50.00  0.71     Sequence
             DRB1_0401  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4        0.3345
1340.1    44.00  0.74     Sequence
             DRB1_0401  448      DSKVGGNYNYLYRLF  VGGNYNYLY  3        0.3488
1147.5    41.00  0.72     Sequence
             DRB1_0401  449      SKVGGNYNYLYRLFR  VGGNYNYLY  2        0.3765
851.0    34.00  0.56     Sequence
             DRB1_0401  450      KVGGNYNYLYRLFRK  VGGNYNYLY  1        0.3905
731.0    31.00  0.40     Sequence
             DRB1_0401  451      VGGNYNYLYRLFRKS  YNYLYRLFR  4        0.3782
835.7    34.00  0.49     Sequence
             DRB1_0401  452      GGNYNYLYRLFRKSN  YNYLYRLFR  3        0.3826
796.7    33.00  0.51     Sequence
             DRB1_0401  453      GNYNYLYRLFRKSNL  YNYLYRLFR  2        0.3884
747.7    31.00  0.38     Sequence
             DRB1_0401  454      NYNYLYRLFRKSNLK  LYRLFRKSN  4        0.3874
756.4    31.00  0.29     Sequence
             DRB1_0401  455      YNYLYRLFRKSNLKP  LYRLFRKSN  3        0.3857
770.1    32.00  0.29     Sequence
             DRB1_0401  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6        0.4294
480.0    23.00  0.31     Sequence
             DRB1_0401  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.4430
414.4    21.00  0.40     Sequence
             DRB1_0401  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.4604
343.2    18.00  0.51     Sequence
```

```
             DRB1_0401  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.4376
439.2    22.00  0.56     Sequence
             DRB1_0401  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.4149
561.3    26.00  0.57     Sequence
             DRB1_0401  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.3485
1151.7    41.00  0.55     Sequence
             DRB1_0401  462      FRKSNLKPFERDIST  LKPFERDIS  5        0.2211
4573.5    80.00  0.27     Sequence
             DRB1_0401  463      RKSNLKPFERDISTE  LKPFERDIS  4        0.1801
7127.1    90.00  0.44     Sequence
             DRB1_0401  464      KSNLKPFERDISTEI  FERDISTEI  6        0.3548
1076.2    39.00  0.77     Sequence
             DRB1_0401  465      SNLKPFERDISTEIY  FERDISTEI  5        0.4160
554.6    25.00  0.85     Sequence
             DRB1_0401  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.4408
424.3    21.00  0.88     Sequence
             DRB1_0401  467      LKPFERDISTEIYQA  FERDISTEI  3        0.4651
326.1    17.00  0.77     Sequence
             DRB1_0401  468      KPFERDISTEIYQAG  FERDISTEI  2        0.4747
294.0    16.00  0.65     Sequence
             DRB1_0401  469      PFERDISTEIYQAGS  FERDISTEI  1        0.4438
410.5    20.00  0.54     Sequence
             DRB1_0401  470      FERDISTEIYQAGST  DISTEIYQA  3        0.3765
850.8    34.00  0.34     Sequence
             DRB1_0401  471      ERDISTEIYQAGSTP  DISTEIYQA  2        0.3126
1698.7    55.00  0.38     Sequence
             DRB1_0401  472      RDISTEIYQAGSTPC  IYQAGSTPC  6        0.4327
463.0    22.00  0.58     Sequence
             DRB1_0401  473      DISTEIYQAGSTPCN  IYQAGSTPC  5        0.4950
235.9    13.00  0.65     Sequence
             DRB1_0401  474      ISTEIYQAGSTPCNG  IYQAGSTPC  4        0.5163
187.5    11.00  0.69     Sequence
             DRB1_0401  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.5249
170.8     9.50  0.68     Sequence         WB
             DRB1_0401  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.5087
203.5    12.00  0.61     Sequence
             DRB1_0401  477      EIYQAGSTPCNGVKG  IYQAGSTPC  1        0.4619
337.8    18.00  0.56     Sequence
             DRB1_0401  478      IYQAGSTPCNGVKGF  YQAGSTPCN  1        0.3454
1190.8    42.00  0.62     Sequence
             DRB1_0401  479      YQAGSTPCNGVKGFN  YQAGSTPCN  0        0.1581
9033.4    95.00  0.41     Sequence
             DRB1_0401  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.1013
16717.9   100.00  0.28     Sequence
             DRB1_0401  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.1107
15095.4   100.00  0.40     Sequence
             DRB1_0401  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.1461
10288.5    95.00  0.38     Sequence
             DRB1_0401  483      STPCNGVKGFNCYFP  CNGVKGFNC  3        0.1713
7831.8    90.00  0.34     Sequence
             DRB1_0401  484      TPCNGVKGFNCYFPL  VKGFNCYFP  5        0.1919
6272.4    85.00  0.29     Sequence
             DRB1_0401  485      PCNGVKGFNCYFPLQ  VKGFNCYFP  4        0.2149
4886.6    80.00  0.25     Sequence
             DRB1_0401  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.3564
1057.7    39.00  0.50     Sequence
             DRB1_0401  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.3971
680.5    29.00  0.56     Sequence
             DRB1_0401  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.4128
574.3    26.00  0.60     Sequence
             DRB1_0401  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3        0.4598
345.5    18.00  0.52     Sequence
             DRB1_0401  490      KGFNCYFPLQSYGFQ  FNCYFPLQS  2        0.4848
263.7    14.00  0.44     Sequence
             DRB1_0401  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.4770
286.8    15.00  0.46     Sequence
```

```
             DRB1_0401  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.4415
421.2    21.00  0.50     Sequence
             DRB1_0401  493      NCYFPLQSYGFQPTY  YFPLQSYGF  2        0.3788
830.2    33.00  0.60     Sequence
             DRB1_0401  494      CYFPLQSYGFQPTYG  YFPLQSYGF  1        0.3624
990.5    37.00  0.53     Sequence
             DRB1_0401  495      YFPLQSYGFQPTYGV  YGFQPTYGV  6        0.4264
495.7    24.00  0.57     Sequence
             DRB1_0401  496      FPLQSYGFQPTYGVG  YGFQPTYGV  5        0.4324
464.6    22.00  0.74     Sequence
             DRB1_0401  497      PLQSYGFQPTYGVGY  YGFQPTYGV  4        0.4869
257.6    14.00  0.66     Sequence
             DRB1_0401  498      LQSYGFQPTYGVGYQ  YGFQPTYGV  3        0.4986
226.9    13.00  0.64     Sequence
             DRB1_0401  499      QSYGFQPTYGVGYQP  YGFQPTYGV  2        0.4857
261.0    14.00  0.61     Sequence
             DRB1_0401  500      SYGFQPTYGVGYQPY  YGFQPTYGV  1        0.4606
342.5    18.00  0.54     Sequence
             DRB1_0401  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.4036
634.7    28.00  0.46     Sequence
             DRB1_0401  502      GFQPTYGVGYQPYRV  FQPTYGVGY  1        0.3193
1579.1    49.00  0.51     Sequence
             DRB1_0401  503      FQPTYGVGYQPYRVV  YGVGYQPYR  4        0.2701
2689.9    65.00  0.43     Sequence
             DRB1_0401  504      QPTYGVGYQPYRVVV  YGVGYQPYR  3        0.2574
3087.8    70.00  0.45     Sequence
             DRB1_0401  505      PTYGVGYQPYRVVVL  YQPYRVVVL  6        0.3272
1449.6    46.00  0.53     Sequence
             DRB1_0401  506      TYGVGYQPYRVVVLS  YQPYRVVVL  5        0.3593
1024.7    38.00  0.67     Sequence
             DRB1_0401  507      YGVGYQPYRVVVLSF  YQPYRVVVL  4        0.3796
822.6    33.00  0.68     Sequence
             DRB1_0401  508      GVGYQPYRVVVLSFE  YQPYRVVVL  3        0.4173
547.1    25.00  0.56     Sequence
             DRB1_0401  509      VGYQPYRVVVLSFEL  YQPYRVVVL  2        0.4183
541.5    25.00  0.44     Sequence
             DRB1_0401  510      GYQPYRVVVLSFELL  YQPYRVVVL  1        0.4045
628.7    28.00  0.40     Sequence
             DRB1_0401  511      YQPYRVVVLSFELLH  YRVVVLSFE  3        0.3827
795.4    32.00  0.33     Sequence
             DRB1_0401  512      QPYRVVVLSFELLHA  VVLSFELLH  5        0.4375
439.9    22.00  0.28     Sequence
             DRB1_0401  513      PYRVVVLSFELLHAP  VVLSFELLH  4        0.4613
340.0    18.00  0.30     Sequence
             DRB1_0401  514      YRVVVLSFELLHAPA  VLSFELLHA  4        0.5045
213.0    12.00  0.31     Sequence
             DRB1_0401  515      RVVVLSFELLHAPAT  FELLHAPAT  6        0.5661
109.3     6.00  0.38     Sequence         WB
             DRB1_0401  516      VVVLSFELLHAPATV  FELLHAPAT  5        0.5750
99.3     5.50  0.51     Sequence         WB
             DRB1_0401  517      VVLSFELLHAPATVC  FELLHAPAT  4        0.5647
111.0     6.00  0.51     Sequence         WB
             DRB1_0401  518      VLSFELLHAPATVCG  FELLHAPAT  3        0.5308
160.3     9.00  0.65     Sequence         WB
             DRB1_0401  519      LSFELLHAPATVCGP  FELLHAPAT  2        0.5099
201.0    11.00  0.69     Sequence
             DRB1_0401  520      SFELLHAPATVCGPK  FELLHAPAT  1        0.4814
273.4    15.00  0.61     Sequence
             DRB1_0401  521      FELLHAPATVCGPKK  LLHAPATVC  2        0.3958
690.8    30.00  0.32     Sequence
             DRB1_0401  522      ELLHAPATVCGPKKS  LLHAPATVC  1        0.2875
2229.3    60.00  0.42     Sequence
             DRB1_0401  523      LLHAPATVCGPKKST  LHAPATVCG  1        0.2221
4522.6    80.00  0.43     Sequence
             DRB1_0401  524      LHAPATVCGPKKSTN  PATVCGPKK  3        0.1445
10465.1    95.00  0.33     Sequence
```

```
             DRB1_0401  525      HAPATVCGPKKSTNL  PATVCGPKK  2        0.1101
15198.4   100.00  0.41     Sequence
             DRB1_0401  526      APATVCGPKKSTNLV  PATVCGPKK  1        0.1131
14699.1   100.00  0.32     Sequence
             DRB1_0401  527      PATVCGPKKSTNLVK  PKKSTNLVK  6        0.1332
11828.7   100.00  0.43     Sequence
             DRB1_0401  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5        0.1659
8304.2    90.00  0.50     Sequence
             DRB1_0401  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.1924
6235.4    85.00  0.55     Sequence
             DRB1_0401  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3        0.1873
6587.8    90.00  0.57     Sequence
             DRB1_0401  531      CGPKKSTNLVKNKCV  PKKSTNLVK  2        0.1892
6452.4    85.00  0.54     Sequence
             DRB1_0401  532      GPKKSTNLVKNKCVN  PKKSTNLVK  1        0.1892
6458.3    85.00  0.46     Sequence
             DRB1_0401  533      PKKSTNLVKNKCVNF  TNLVKNKCV  4        0.2130
4991.4    80.00  0.23     Sequence
             DRB1_0401  534      KKSTNLVKNKCVNFN  VKNKCVNFN  6        0.2908
2150.3    60.00  0.55     Sequence
             DRB1_0401  535      KSTNLVKNKCVNFNF  VKNKCVNFN  5        0.3559
1063.7    39.00  0.67     Sequence
             DRB1_0401  536      STNLVKNKCVNFNFN  VKNKCVNFN  4        0.3829
793.7    32.00  0.72     Sequence
             DRB1_0401  537      TNLVKNKCVNFNFNG  VKNKCVNFN  3        0.3846
779.2    32.00  0.69     Sequence
             DRB1_0401  538      NLVKNKCVNFNFNGL  VKNKCVNFN  2        0.3808
812.3    33.00  0.60     Sequence
             DRB1_0401  539      LVKNKCVNFNFNGLT  VKNKCVNFN  1        0.4371
441.6    22.00  0.37     Sequence
             DRB1_0401  540      VKNKCVNFNFNGLTG  VNFNFNGLT  5        0.4008
653.9    29.00  0.56     Sequence
             DRB1_0401  541      KNKCVNFNFNGLTGT  VNFNFNGLT  4        0.4059
618.8    27.00  0.56     Sequence
             DRB1_0401  542      NKCVNFNFNGLTGTG  VNFNFNGLT  3        0.4257
499.6    24.00  0.55     Sequence
             DRB1_0401  543      KCVNFNFNGLTGTGV  VNFNFNGLT  2        0.4542
367.1    19.00  0.42     Sequence
             DRB1_0401  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5        0.4533
370.8    19.00  0.45     Sequence
             DRB1_0401  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.4336
458.7    22.00  0.51     Sequence
             DRB1_0401  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3        0.3948
698.1    30.00  0.61     Sequence
             DRB1_0401  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.3738
876.0    35.00  0.60     Sequence
             DRB1_0401  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.3512
1118.3    40.00  0.54     Sequence
             DRB1_0401  549      FNGLTGTGVLTESNK  LTGTGVLTE  3        0.2968
2015.5    55.00  0.52     Sequence
             DRB1_0401  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.2993
1962.3    55.00  0.46     Sequence
             DRB1_0401  551      GLTGTGVLTESNKKF  VLTESNKKF  6        0.3689
923.5    36.00  0.43     Sequence
             DRB1_0401  552      LTGTGVLTESNKKFL  VLTESNKKF  5        0.3860
767.8    32.00  0.60     Sequence
             DRB1_0401  553      TGTGVLTESNKKFLP  VLTESNKKF  4        0.3894
739.7    31.00  0.67     Sequence
             DRB1_0401  554      GTGVLTESNKKFLPF  VLTESNKKF  3        0.3914
724.1    31.00  0.70     Sequence
             DRB1_0401  555      TGVLTESNKKFLPFQ  VLTESNKKF  2        0.3491
1143.8    41.00  0.73     Sequence
             DRB1_0401  556      GVLTESNKKFLPFQQ  VLTESNKKF  1        0.2941
2074.8    60.00  0.70     Sequence
             DRB1_0401  557      VLTESNKKFLPFQQF  VLTESNKKF  0        0.1906
6361.1    85.00  0.39     Sequence
```

```
             DRB1_0401  558      LTESNKKFLPFQQFG  KKFLPFQQF  5        0.1410
10880.2    95.00  0.23     Sequence
             DRB1_0401  559      TESNKKFLPFQQFGR  FLPFQQFGR  6        0.1806
7088.5    90.00  0.32     Sequence
             DRB1_0401  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5        0.1860
6684.4    90.00  0.41     Sequence
             DRB1_0401  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4        0.1862
6671.1    90.00  0.44     Sequence
             DRB1_0401  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.1981
5863.2    85.00  0.43     Sequence
             DRB1_0401  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.1841
6821.1    90.00  0.39     Sequence
             DRB1_0401  564      KFLPFQQFGRDIADT  FQQFGRDIA  4        0.1759
7452.5    90.00  0.40     Sequence
             DRB1_0401  565      FLPFQQFGRDIADTT  FGRDIADTT  6        0.2493
3367.8    70.00  0.54     Sequence
             DRB1_0401  566      LPFQQFGRDIADTTD  FGRDIADTT  5        0.2652
2836.6    65.00  0.67     Sequence
             DRB1_0401  567      PFQQFGRDIADTTDA  FGRDIADTT  4        0.2924
2112.8    60.00  0.70     Sequence
             DRB1_0401  568      FQQFGRDIADTTDAV  FGRDIADTT  3        0.3508
1123.4    40.00  0.52     Sequence
             DRB1_0401  569      QQFGRDIADTTDAVR  FGRDIADTT  2        0.4075
608.1    27.00  0.37     Sequence
             DRB1_0401  570      QFGRDIADTTDAVRD  DIADTTDAV  4        0.4010
652.8    28.00  0.34     Sequence
             DRB1_0401  571      FGRDIADTTDAVRDP  DIADTTDAV  3        0.3759
856.1    34.00  0.43     Sequence
             DRB1_0401  572      GRDIADTTDAVRDPQ  DIADTTDAV  2        0.3449
1197.4    42.00  0.49     Sequence
             DRB1_0401  573      RDIADTTDAVRDPQT  DIADTTDAV  1        0.3017
1910.1    55.00  0.44     Sequence
             DRB1_0401  574      DIADTTDAVRDPQTL  IADTTDAVR  1        0.2204
4607.6    80.00  0.44     Sequence
             DRB1_0401  575      IADTTDAVRDPQTLE  IADTTDAVR  0        0.1233
13166.3   100.00  0.23     Sequence
             DRB1_0401  576      ADTTDAVRDPQTLEI  VRDPQTLEI  6        0.1127
14775.6   100.00  0.26     Sequence
             DRB1_0401  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5        0.1296
12306.2   100.00  0.34     Sequence
             DRB1_0401  578      TTDAVRDPQTLEILD  VRDPQTLEI  4        0.1311
12102.6   100.00  0.41     Sequence
             DRB1_0401  579      TDAVRDPQTLEILDI  VRDPQTLEI  3        0.1287
12422.1   100.00  0.44     Sequence
             DRB1_0401  580      DAVRDPQTLEILDIT  VRDPQTLEI  2        0.1250
12923.2   100.00  0.40     Sequence
             DRB1_0401  581      AVRDPQTLEILDITP  VRDPQTLEI  1        0.1400
10995.1    95.00  0.26     Sequence
             DRB1_0401  582      VRDPQTLEILDITPC  LEILDITPC  6        0.2133
4974.5    80.00  0.45     Sequence
             DRB1_0401  583      RDPQTLEILDITPCS  EILDITPCS  6        0.3404
1257.2    43.00  0.47     Sequence
             DRB1_0401  584      DPQTLEILDITPCSF  EILDITPCS  5        0.4180
542.9    25.00  0.47     Sequence
             DRB1_0401  585      PQTLEILDITPCSFG  EILDITPCS  4        0.4413
422.0    21.00  0.47     Sequence
             DRB1_0401  586      QTLEILDITPCSFGG  EILDITPCS  3        0.4420
419.0    21.00  0.47     Sequence
             DRB1_0401  587      TLEILDITPCSFGGV  EILDITPCS  2        0.4206
528.2    25.00  0.44     Sequence
             DRB1_0401  588      LEILDITPCSFGGVS  EILDITPCS  1        0.3671
941.8    36.00  0.44     Sequence
             DRB1_0401  589      EILDITPCSFGGVSV  EILDITPCS  0        0.2598
3008.9    70.00  0.31     Sequence
             DRB1_0401  590      ILDITPCSFGGVSVI  DITPCSFGG  2        0.1710
7863.1    90.00  0.28     Sequence
```

```
             DRB1_0401  591      LDITPCSFGGVSVIT  DITPCSFGG  1        0.1453
10382.8    95.00  0.31     Sequence
             DRB1_0401  592      DITPCSFGGVSVITP  FGGVSVITP  6        0.2110
5100.3    80.00  0.57     Sequence
             DRB1_0401  593      ITPCSFGGVSVITPG  FGGVSVITP  5        0.2670
2783.1    65.00  0.65     Sequence
             DRB1_0401  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.3580
1039.8    38.00  0.47     Sequence
             DRB1_0401  595      PCSFGGVSVITPGTN  GVSVITPGT  5        0.4034
635.8    28.00  0.50     Sequence
             DRB1_0401  596      CSFGGVSVITPGTNT  GVSVITPGT  4        0.4171
548.3    25.00  0.54     Sequence
             DRB1_0401  597      SFGGVSVITPGTNTS  GVSVITPGT  3        0.4607
342.1    18.00  0.49     Sequence
             DRB1_0401  598      FGGVSVITPGTNTSN  GVSVITPGT  2        0.4667
320.5    17.00  0.38     Sequence
             DRB1_0401  599      GGVSVITPGTNTSNQ  VITPGTNTS  4        0.4695
311.1    16.00  0.37     Sequence
             DRB1_0401  600      GVSVITPGTNTSNQV  VITPGTNTS  3        0.4380
437.3    21.00  0.40     Sequence
             DRB1_0401  601      VSVITPGTNTSNQVA  ITPGTNTSN  3        0.4007
654.5    29.00  0.49     Sequence
             DRB1_0401  602      SVITPGTNTSNQVAV  ITPGTNTSN  2        0.3788
829.8    33.00  0.51     Sequence
             DRB1_0401  603      VITPGTNTSNQVAVL  ITPGTNTSN  1        0.3072
1800.0    55.00  0.52     Sequence
             DRB1_0401  604      ITPGTNTSNQVAVLY  ITPGTNTSN  0        0.1987
5822.9    85.00  0.27     Sequence
             DRB1_0401  605      TPGTNTSNQVAVLYQ  TSNQVAVLY  5        0.1839
6835.3    90.00  0.27     Sequence
             DRB1_0401  606      PGTNTSNQVAVLYQG  TSNQVAVLY  4        0.1891
6461.0    85.00  0.31     Sequence
             DRB1_0401  607      GTNTSNQVAVLYQGV  TSNQVAVLY  3        0.1843
6804.3    90.00  0.32     Sequence
             DRB1_0401  608      TNTSNQVAVLYQGVN  SNQVAVLYQ  3        0.1769
7376.7    90.00  0.31     Sequence
             DRB1_0401  609      NTSNQVAVLYQGVNC  VLYQGVNCX  7        0.2064
5358.1    85.00  0.20     Sequence
             DRB1_0401  610      TSNQVAVLYQGVNCT  VLYQGVNCT  6        0.3784
833.9    33.00  0.75     Sequence
             DRB1_0401  611      SNQVAVLYQGVNCTE  VLYQGVNCT  5        0.4312
470.8    23.00  0.80     Sequence
             DRB1_0401  612      NQVAVLYQGVNCTEV  VLYQGVNCT  4        0.4618
338.2    18.00  0.77     Sequence
             DRB1_0401  613      QVAVLYQGVNCTEVP  VLYQGVNCT  3        0.4712
305.5    16.00  0.76     Sequence
             DRB1_0401  614      VAVLYQGVNCTEVPV  VLYQGVNCT  2        0.4618
337.9    18.00  0.73     Sequence
             DRB1_0401  615      AVLYQGVNCTEVPVA  VLYQGVNCT  1        0.4381
436.9    21.00  0.64     Sequence
             DRB1_0401  616      VLYQGVNCTEVPVAI  YQGVNCTEV  2        0.3269
1455.6    47.00  0.31     Sequence
             DRB1_0401  617      LYQGVNCTEVPVAIH  YQGVNCTEV  1        0.2612
2962.6    70.00  0.26     Sequence
             DRB1_0401  618      YQGVNCTEVPVAIHA  CTEVPVAIH  5        0.2584
3052.2    70.00  0.34     Sequence
             DRB1_0401  619      QGVNCTEVPVAIHAD  CTEVPVAIH  4        0.2397
3738.0    75.00  0.40     Sequence
             DRB1_0401  620      GVNCTEVPVAIHADQ  CTEVPVAIH  3        0.2272
4279.8    75.00  0.40     Sequence
             DRB1_0401  621      VNCTEVPVAIHADQL  CTEVPVAIH  2        0.1841
6822.8    90.00  0.41     Sequence
             DRB1_0401  622      NCTEVPVAIHADQLT  VAIHADQLT  6        0.1748
7547.6    90.00  0.35     Sequence
             DRB1_0401  623      CTEVPVAIHADQLTP  VAIHADQLT  5        0.1782
7273.2    90.00  0.49     Sequence
```

```
             DRB1_0401  624      TEVPVAIHADQLTPT  VAIHADQLT  4        0.2330
4019.4    75.00  0.40     Sequence
             DRB1_0401  625      EVPVAIHADQLTPTW  IHADQLTPT  5        0.3051
1842.1    55.00  0.37     Sequence
             DRB1_0401  626      VPVAIHADQLTPTWR  IHADQLTPT  4        0.3610
1006.5    38.00  0.43     Sequence
             DRB1_0401  627      PVAIHADQLTPTWRV  HADQLTPTW  4        0.3799
820.2    33.00  0.33     Sequence
             DRB1_0401  628      VAIHADQLTPTWRVY  HADQLTPTW  3        0.3745
869.1    34.00  0.36     Sequence
             DRB1_0401  629      AIHADQLTPTWRVYS  HADQLTPTW  2        0.3508
1123.5    40.00  0.34     Sequence
             DRB1_0401  630      IHADQLTPTWRVYST  HADQLTPTW  1        0.3053
1838.2    55.00  0.32     Sequence
             DRB1_0401  631      HADQLTPTWRVYSTG  LTPTWRVYS  4        0.2543
3191.0    70.00  0.46     Sequence
             DRB1_0401  632      ADQLTPTWRVYSTGS  LTPTWRVYS  3        0.2506
3321.9    70.00  0.50     Sequence
             DRB1_0401  633      DQLTPTWRVYSTGSN  WRVYSTGSN  6        0.2734
2594.5    65.00  0.37     Sequence
             DRB1_0401  634      QLTPTWRVYSTGSNV  WRVYSTGSN  5        0.3080
1785.2    55.00  0.41     Sequence
             DRB1_0401  635      LTPTWRVYSTGSNVF  VYSTGSNVF  6        0.4563
358.6    18.00  0.53     Sequence
             DRB1_0401  636      TPTWRVYSTGSNVFQ  VYSTGSNVF  5        0.5795
94.6     5.00  0.50     Sequence         WB
             DRB1_0401  637      PTWRVYSTGSNVFQT  YSTGSNVFQ  5        0.6307
54.4     2.50  0.45     Sequence         WB
             DRB1_0401  638      TWRVYSTGSNVFQTR  YSTGSNVFQ  4        0.6692
35.8     1.30  0.52     Sequence         SB
             DRB1_0401  639      WRVYSTGSNVFQTRA  YSTGSNVFQ  3        0.6670
36.7     1.40  0.60     Sequence         SB
             DRB1_0401  640      RVYSTGSNVFQTRAG  YSTGSNVFQ  2        0.6667
36.8     1.40  0.62     Sequence         SB
             DRB1_0401  641      VYSTGSNVFQTRAGC  YSTGSNVFQ  1        0.5781
96.0     5.50  0.76     Sequence         WB
             DRB1_0401  642      YSTGSNVFQTRAGCL  YSTGSNVFQ  0        0.3549
1074.5    39.00  0.54     Sequence
             DRB1_0401  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.1395
11053.2    95.00  0.31     Sequence
             DRB1_0401  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.1491
9957.5    95.00  0.34     Sequence
             DRB1_0401  645      GSNVFQTRAGCLIGA  TRAGCLIGA  6        0.1878
6550.6    90.00  0.27     Sequence
             DRB1_0401  646      SNVFQTRAGCLIGAE  TRAGCLIGA  5        0.2060
5383.8    85.00  0.38     Sequence
             DRB1_0401  647      NVFQTRAGCLIGAEY  TRAGCLIGA  4        0.2130
4989.9    80.00  0.44     Sequence
             DRB1_0401  648      VFQTRAGCLIGAEYV  TRAGCLIGA  3        0.2053
5422.0    85.00  0.45     Sequence
             DRB1_0401  649      FQTRAGCLIGAEYVN  TRAGCLIGA  2        0.2073
5309.0    85.00  0.46     Sequence
             DRB1_0401  650      QTRAGCLIGAEYVNN  TRAGCLIGA  1        0.2345
3953.1    75.00  0.35     Sequence
             DRB1_0401  651      TRAGCLIGAEYVNNS  IGAEYVNNS  6        0.2918
2127.4    60.00  0.38     Sequence
             DRB1_0401  652      RAGCLIGAEYVNNSY  IGAEYVNNS  5        0.3477
1162.0    41.00  0.46     Sequence
             DRB1_0401  653      AGCLIGAEYVNNSYE  IGAEYVNNS  4        0.3618
997.8    37.00  0.49     Sequence
             DRB1_0401  654      GCLIGAEYVNNSYEC  IGAEYVNNS  3        0.3558
1064.8    39.00  0.53     Sequence
             DRB1_0401  655      CLIGAEYVNNSYECD  IGAEYVNNS  2        0.3249
1486.8    47.00  0.49     Sequence
             DRB1_0401  656      LIGAEYVNNSYECDI  IGAEYVNNS  1        0.2960
2032.7    55.00  0.49     Sequence
```

```
             DRB1_0401  657      IGAEYVNNSYECDIP  YVNNSYECD  4        0.2008
5696.3    85.00  0.25     Sequence
             DRB1_0401  658      GAEYVNNSYECDIPI  YVNNSYECD  3        0.1614
8721.1    95.00  0.37     Sequence
             DRB1_0401  659      AEYVNNSYECDIPIG  YVNNSYECD  2        0.1730
7689.7    90.00  0.30     Sequence
             DRB1_0401  660      EYVNNSYECDIPIGA  YECDIPIGA  6        0.3697
916.1    36.00  0.71     Sequence
             DRB1_0401  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.4193
535.3    25.00  0.81     Sequence
             DRB1_0401  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.4359
447.5    22.00  0.86     Sequence
             DRB1_0401  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.4278
488.3    23.00  0.88     Sequence
             DRB1_0401  664      NSYECDIPIGAGICA  YECDIPIGA  2        0.4053
623.0    28.00  0.87     Sequence
             DRB1_0401  665      SYECDIPIGAGICAS  YECDIPIGA  1        0.3612
1004.3    38.00  0.79     Sequence
             DRB1_0401  666      YECDIPIGAGICASY  YECDIPIGA  0        0.2682
2745.5    65.00  0.51     Sequence
             DRB1_0401  667      ECDIPIGAGICASYQ  IGAGICASY  5        0.1760
7448.2    90.00  0.25     Sequence
             DRB1_0401  668      CDIPIGAGICASYQT  GAGICASYQ  5        0.2017
5638.9    85.00  0.29     Sequence
             DRB1_0401  669      DIPIGAGICASYQTQ  GAGICASYQ  4        0.2229
4483.8    80.00  0.28     Sequence
             DRB1_0401  670      IPIGAGICASYQTQT  GAGICASYQ  3        0.2345
3953.6    75.00  0.25     Sequence
             DRB1_0401  671      PIGAGICASYQTQTN  CASYQTQTN  6        0.2970
2011.2    55.00  0.37     Sequence
             DRB1_0401  672      IGAGICASYQTQTNS  CASYQTQTN  5        0.3269
1454.8    47.00  0.47     Sequence
             DRB1_0401  673      GAGICASYQTQTNSP  CASYQTQTN  4        0.3661
952.5    36.00  0.47     Sequence
             DRB1_0401  674      AGICASYQTQTNSPR  YQTQTNSPR  6        0.5020
218.9    12.00  0.57     Sequence
             DRB1_0401  675      GICASYQTQTNSPRR  YQTQTNSPR  5        0.5585
118.7     6.50  0.73     Sequence         WB
             DRB1_0401  676      ICASYQTQTNSPRRA  YQTQTNSPR  4        0.5829
91.2     5.00  0.80     Sequence         WB
             DRB1_0401  677      CASYQTQTNSPRRAR  YQTQTNSPR  3        0.5951
79.9     4.50  0.86     Sequence         WB
             DRB1_0401  678      ASYQTQTNSPRRARS  YQTQTNSPR  2        0.5945
80.4     4.50  0.88     Sequence         WB
             DRB1_0401  679      SYQTQTNSPRRARSV  YQTQTNSPR  1        0.5370
149.9     8.50  0.86     Sequence         WB
             DRB1_0401  680      YQTQTNSPRRARSVA  YQTQTNSPR  0        0.3466
1175.5    41.00  0.56     Sequence
             DRB1_0401  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.2003
5722.1    85.00  0.69     Sequence
             DRB1_0401  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.2653
2835.0    65.00  0.81     Sequence
             DRB1_0401  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.3154
1647.9    50.00  0.72     Sequence
             DRB1_0401  684      TNSPRRARSVASQSI  PRRARSVAS  3        0.3491
1144.3    41.00  0.62     Sequence
             DRB1_0401  685      NSPRRARSVASQSII  PRRARSVAS  2        0.3521
1108.0    40.00  0.53     Sequence
             DRB1_0401  686      SPRRARSVASQSIIA  PRRARSVAS  1        0.3560
1062.1    39.00  0.38     Sequence
             DRB1_0401  687      PRRARSVASQSIIAY  VASQSIIAY  6        0.3702
910.7    35.00  0.26     Sequence
             DRB1_0401  688      RRARSVASQSIIAYT  VASQSIIAY  5        0.3856
770.8    32.00  0.38     Sequence
             DRB1_0401  689      RARSVASQSIIAYTM  VASQSIIAY  4        0.3870
759.1    32.00  0.44     Sequence
```

```
             DRB1_0401  690      ARSVASQSIIAYTMS  VASQSIIAY  3        0.3618
997.8    37.00  0.47     Sequence
             DRB1_0401  691      RSVASQSIIAYTMSL  VASQSIIAY  2        0.3587
1031.6    38.00  0.45     Sequence
             DRB1_0401  692      SVASQSIIAYTMSLG  VASQSIIAY  1        0.3253
1480.2    47.00  0.35     Sequence
             DRB1_0401  693      VASQSIIAYTMSLGA  IAYTMSLGA  6        0.3574
1046.4    39.00  0.38     Sequence
             DRB1_0401  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.3752
862.5    34.00  0.41     Sequence
             DRB1_0401  695      SQSIIAYTMSLGAEN  IAYTMSLGA  4        0.4365
444.7    22.00  0.31     Sequence
             DRB1_0401  696      QSIIAYTMSLGAENS  YTMSLGAEN  5        0.4696
310.6    16.00  0.45     Sequence
             DRB1_0401  697      SIIAYTMSLGAENSV  YTMSLGAEN  4        0.4760
290.0    16.00  0.49     Sequence
             DRB1_0401  698      IIAYTMSLGAENSVA  YTMSLGAEN  3        0.4738
297.0    16.00  0.50     Sequence
             DRB1_0401  699      IAYTMSLGAENSVAY  YTMSLGAEN  2        0.4906
247.6    14.00  0.41     Sequence
             DRB1_0401  700      AYTMSLGAENSVAYS  LGAENSVAY  5        0.5065
208.4    12.00  0.46     Sequence
             DRB1_0401  701      YTMSLGAENSVAYSN  LGAENSVAY  4        0.4864
259.2    14.00  0.60     Sequence
             DRB1_0401  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.4467
398.0    20.00  0.73     Sequence
             DRB1_0401  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.4263
496.5    24.00  0.69     Sequence
             DRB1_0401  704      SLGAENSVAYSNNSI  LGAENSVAY  1        0.3982
672.8    29.00  0.63     Sequence
             DRB1_0401  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.3953
693.9    30.00  0.47     Sequence
             DRB1_0401  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.4441
409.4    20.00  0.68     Sequence
             DRB1_0401  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.4857
261.0    14.00  0.62     Sequence
             DRB1_0401  708      ENSVAYSNNSIAIPT  VAYSNNSIA  3        0.5124
195.4    11.00  0.58     Sequence
             DRB1_0401  709      NSVAYSNNSIAIPTN  VAYSNNSIA  2        0.5129
194.4    11.00  0.52     Sequence
             DRB1_0401  710      SVAYSNNSIAIPTNF  VAYSNNSIA  1        0.4783
282.8    15.00  0.46     Sequence
             DRB1_0401  711      VAYSNNSIAIPTNFT  YSNNSIAIP  2        0.4303
475.1    23.00  0.34     Sequence
             DRB1_0401  712      AYSNNSIAIPTNFTI  SIAIPTNFT  5        0.4120
579.4    26.00  0.41     Sequence
             DRB1_0401  713      YSNNSIAIPTNFTIS  SIAIPTNFT  4        0.3917
721.4    30.00  0.47     Sequence
             DRB1_0401  714      SNNSIAIPTNFTISV  SIAIPTNFT  3        0.4120
579.3    26.00  0.47     Sequence
             DRB1_0401  715      NNSIAIPTNFTISVT  SIAIPTNFT  2        0.4097
593.9    27.00  0.41     Sequence
             DRB1_0401  716      NSIAIPTNFTISVTT  SIAIPTNFT  1        0.3865
763.4    32.00  0.34     Sequence
             DRB1_0401  717      SIAIPTNFTISVTTE  IPTNFTISV  3        0.3369
1306.3    44.00  0.31     Sequence
             DRB1_0401  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.4472
395.8    20.00  0.72     Sequence
             DRB1_0401  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.4868
257.9    14.00  0.80     Sequence
             DRB1_0401  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.5015
220.0    12.00  0.81     Sequence
             DRB1_0401  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.5126
195.2    11.00  0.78     Sequence
             DRB1_0401  722      TNFTISVTTEILPVS  FTISVTTEI  2        0.5226
175.1    10.00  0.68     Sequence
```

```
             DRB1_0401  723       NFTISVTTEILPVSM  FTISVTTEI  1         0.5057
210.1    12.00  0.57     Sequence
             DRB1_0401  724       FTISVTTEILPVSMT  FTISVTTEI  0         0.4454
403.8    20.00  0.38     Sequence
             DRB1_0401  725       TISVTTEILPVSMTK  VTTEILPVS  3         0.3551
1072.6    39.00  0.45     Sequence
             DRB1_0401  726       ISVTTEILPVSMTKT  VTTEILPVS  2         0.3492
1142.9    41.00  0.41     Sequence
             DRB1_0401  727       SVTTEILPVSMTKTS  ILPVSMTKT  5         0.3411
1247.8    43.00  0.41     Sequence
             DRB1_0401  728       VTTEILPVSMTKTSV  ILPVSMTKT  4         0.3063
1819.2    55.00  0.51     Sequence
             DRB1_0401  729       TTEILPVSMTKTSVD  ILPVSMTKT  3         0.2913
2139.4    60.00  0.56     Sequence
             DRB1_0401  730       TEILPVSMTKTSVDC  ILPVSMTKT  2         0.2728
2611.6    65.00  0.54     Sequence
             DRB1_0401  731       EILPVSMTKTSVDCT  ILPVSMTKT  1         0.2433
3596.1    75.00  0.45     Sequence
             DRB1_0401  732       ILPVSMTKTSVDCTM  VSMTKTSVD  3         0.1777
7307.2    90.00  0.40     Sequence
             DRB1_0401  733       LPVSMTKTSVDCTMY  VSMTKTSVD  2         0.1749
7538.7    90.00  0.37     Sequence
             DRB1_0401  734       PVSMTKTSVDCTMYI  TSVDCTMYI  6         0.2440
3567.9    75.00  0.47     Sequence
             DRB1_0401  735       VSMTKTSVDCTMYIC  TSVDCTMYI  5         0.2623
2926.2    65.00  0.67     Sequence
             DRB1_0401  736       SMTKTSVDCTMYICG  TSVDCTMYI  4         0.2839
2316.1    60.00  0.73     Sequence
             DRB1_0401  737       MTKTSVDCTMYICGD  TSVDCTMYI  3         0.2838
2320.5    60.00  0.81     Sequence
             DRB1_0401  738       TKTSVDCTMYICGDS  TSVDCTMYI  2         0.2714
2652.5    65.00  0.79     Sequence
             DRB1_0401  739       KTSVDCTMYICGDST  TSVDCTMYI  1         0.2491
3376.9    70.00  0.70     Sequence
             DRB1_0401  740       TSVDCTMYICGDSTE  TSVDCTMYI  0         0.1733
7664.2    90.00  0.30     Sequence
             DRB1_0401  741       SVDCTMYICGDSTEC  TMYICGDST  4         0.1619
8675.4    95.00  0.31     Sequence
             DRB1_0401  742       VDCTMYICGDSTECS  ICGDSTECS  6         0.2625
2920.0    65.00  0.55     Sequence
             DRB1_0401  743       DCTMYICGDSTECSN  ICGDSTECS  5         0.3221
1532.6    48.00  0.63     Sequence
             DRB1_0401  744       CTMYICGDSTECSNL  ICGDSTECS  4         0.3459
1184.1    41.00  0.69     Sequence
             DRB1_0401  745       TMYICGDSTECSNLL  ICGDSTECS  3         0.3723
890.8    35.00  0.69     Sequence
             DRB1_0401  746       MYICGDSTECSNLLL  ICGDSTECS  2         0.3575
1045.5    39.00  0.67     Sequence
             DRB1_0401  747       YICGDSTECSNLLLQ  ICGDSTECS  1         0.3214
1543.7    48.00  0.61     Sequence
             DRB1_0401  748       ICGDSTECSNLLLQY  DSTECSNLL  3         0.2428
3613.0    75.00  0.34     Sequence
             DRB1_0401  749       CGDSTECSNLLLQYG  DSTECSNLL  2         0.1915
6299.5    85.00  0.47     Sequence
             DRB1_0401  750       GDSTECSNLLLQYGS  DSTECSNLL  1         0.2022
5608.7    85.00  0.38     Sequence
             DRB1_0401  751       DSTECSNLLLQYGSF  CSNLLLQYG  4         0.1889
6473.1    85.00  0.32     Sequence
             DRB1_0401  752       STECSNLLLQYGSFC  LLLQYGSFC  6         0.2210
4576.2    80.00  0.41     Sequence
             DRB1_0401  753       TECSNLLLQYGSFCT  LLLQYGSFC  5         0.2654
2829.6    65.00  0.40     Sequence
             DRB1_0401  754       ECSNLLLQYGSFCTQ  LLLQYGSFC  4         0.2832
2335.2    60.00  0.41     Sequence
             DRB1_0401  755       CSNLLLQYGSFCTQL  LLQYGSFCT  4         0.3306
1398.4    46.00  0.36     Sequence
```

```
             DRB1_0401  756      SNLLLQYGSFCTQLN  YGSFCTQLN  6        0.4878
255.3    14.00  0.60     Sequence
             DRB1_0401  757      NLLLQYGSFCTQLNR  YGSFCTQLN  5        0.5574
120.2     6.50  0.69     Sequence         WB
             DRB1_0401  758      LLLQYGSFCTQLNRA  YGSFCTQLN  4        0.5963
78.9     4.00  0.75     Sequence         WB
             DRB1_0401  759      LLQYGSFCTQLNRAL  YGSFCTQLN  3        0.6398
49.3     2.50  0.64     Sequence         WB
             DRB1_0401  760      LQYGSFCTQLNRALT  YGSFCTQLN  2        0.6512
43.6     1.80  0.56     Sequence         SB
             DRB1_0401  761      QYGSFCTQLNRALTG  YGSFCTQLN  1        0.6356
51.6     2.50  0.49     Sequence         WB
             DRB1_0401  762      YGSFCTQLNRALTGI  FCTQLNRAL  3        0.5718
102.8     5.50  0.58     Sequence         WB
             DRB1_0401  763      GSFCTQLNRALTGIA  FCTQLNRAL  2        0.5329
156.7     9.00  0.55     Sequence         WB
             DRB1_0401  764      SFCTQLNRALTGIAV  FCTQLNRAL  1        0.5249
170.8     9.50  0.41     Sequence         WB
             DRB1_0401  765      FCTQLNRALTGIAVE  LNRALTGIA  4        0.4683
315.0    17.00  0.56     Sequence
             DRB1_0401  766      CTQLNRALTGIAVEQ  LNRALTGIA  3        0.4289
482.6    23.00  0.72     Sequence
             DRB1_0401  767      TQLNRALTGIAVEQD  LNRALTGIA  2        0.4256
500.3    24.00  0.69     Sequence
             DRB1_0401  768      QLNRALTGIAVEQDK  LNRALTGIA  1        0.3851
775.2    32.00  0.57     Sequence
             DRB1_0401  769      LNRALTGIAVEQDKN  LTGIAVEQD  4        0.3128
1694.3    55.00  0.46     Sequence
             DRB1_0401  770      NRALTGIAVEQDKNT  LTGIAVEQD  3        0.2480
3415.8    70.00  0.66     Sequence
             DRB1_0401  771      RALTGIAVEQDKNTQ  LTGIAVEQD  2        0.2767
2505.1    65.00  0.52     Sequence
             DRB1_0401  772      ALTGIAVEQDKNTQE  VEQDKNTQE  6        0.3133
1686.6    50.00  0.44     Sequence
             DRB1_0401  773      LTGIAVEQDKNTQEV  VEQDKNTQE  5        0.3314
1386.0    45.00  0.64     Sequence
             DRB1_0401  774      TGIAVEQDKNTQEVF  VEQDKNTQE  4        0.3493
1141.4    41.00  0.73     Sequence
             DRB1_0401  775      GIAVEQDKNTQEVFA  VEQDKNTQE  3        0.3495
1139.6    41.00  0.75     Sequence
             DRB1_0401  776      IAVEQDKNTQEVFAQ  VEQDKNTQE  2        0.3223
1529.2    48.00  0.69     Sequence
             DRB1_0401  777      AVEQDKNTQEVFAQV  VEQDKNTQE  1        0.2987
1974.3    55.00  0.59     Sequence
             DRB1_0401  778      VEQDKNTQEVFAQVK  KNTQEVFAQ  4        0.2091
5202.9    80.00  0.43     Sequence
             DRB1_0401  779      EQDKNTQEVFAQVKQ  KNTQEVFAQ  3        0.1915
6299.3    85.00  0.52     Sequence
             DRB1_0401  780      QDKNTQEVFAQVKQI  KNTQEVFAQ  2        0.1879
6548.1    90.00  0.47     Sequence
             DRB1_0401  781      DKNTQEVFAQVKQIY  KNTQEVFAQ  1        0.2351
3928.9    75.00  0.26     Sequence
             DRB1_0401  782      KNTQEVFAQVKQIYK  FAQVKQIYK  6        0.2786
2454.9    60.00  0.38     Sequence
             DRB1_0401  783      NTQEVFAQVKQIYKT  FAQVKQIYK  5        0.3013
1919.3    55.00  0.58     Sequence
             DRB1_0401  784      TQEVFAQVKQIYKTP  FAQVKQIYK  4        0.3139
1675.5    50.00  0.64     Sequence
             DRB1_0401  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.3304
1400.2    46.00  0.56     Sequence
             DRB1_0401  786      EVFAQVKQIYKTPPI  FAQVKQIYK  2        0.3509
1122.5    40.00  0.47     Sequence
             DRB1_0401  787      VFAQVKQIYKTPPIK  FAQVKQIYK  1        0.3613
1002.4    38.00  0.39     Sequence
             DRB1_0401  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6        0.3362
1316.1    44.00  0.36     Sequence
```

```
            DRB1_0401  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.3746
868.5    34.00  0.49     Sequence
            DRB1_0401  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.3765
850.8    34.00  0.56     Sequence
            DRB1_0401  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.3519
1109.9    40.00  0.62     Sequence
            DRB1_0401  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.3088
1770.0    55.00  0.67     Sequence
            DRB1_0401  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.2310
4107.4    75.00  0.71     Sequence
            DRB1_0401  794      IYKTPPIKDFGGFNF  IYKTPPIKD  0        0.1531
9543.2    95.00  0.31     Sequence
            DRB1_0401  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.1294
12329.8   100.00  0.33     Sequence
            DRB1_0401  796      KTPPIKDFGGFNFSQ  DFGGFNFSQ  6        0.1702
7931.5    90.00  0.31     Sequence
            DRB1_0401  797      TPPIKDFGGFNFSQI  FGGFNFSQI  6        0.2254
4365.6    80.00  0.29     Sequence
            DRB1_0401  798      PPIKDFGGFNFSQIL  FGGFNFSQI  5        0.2525
3254.5    70.00  0.32     Sequence
            DRB1_0401  799      PIKDFGGFNFSQILP  FGGFNFSQI  4        0.2779
2472.3    65.00  0.35     Sequence
            DRB1_0401  800      IKDFGGFNFSQILPD  FNFSQILPD  6        0.3116
1716.7    55.00  0.37     Sequence
            DRB1_0401  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.3198
1571.6    49.00  0.41     Sequence
            DRB1_0401  802      DFGGFNFSQILPDPS  FSQILPDPS  6        0.3961
688.1    30.00  0.41     Sequence
            DRB1_0401  803      FGGFNFSQILPDPSK  FSQILPDPS  5        0.4294
479.8    23.00  0.53     Sequence
            DRB1_0401  804      GGFNFSQILPDPSKP  FSQILPDPS  4        0.4338
457.5    22.00  0.58     Sequence
            DRB1_0401  805      GFNFSQILPDPSKPS  FSQILPDPS  3        0.4675
317.9    17.00  0.45     Sequence
            DRB1_0401  806      FNFSQILPDPSKPSK  ILPDPSKPS  5        0.4584
350.7    18.00  0.47     Sequence
            DRB1_0401  807      NFSQILPDPSKPSKR  ILPDPSKPS  4        0.4564
358.4    18.00  0.62     Sequence
            DRB1_0401  808      FSQILPDPSKPSKRS  ILPDPSKPS  3        0.4131
572.6    26.00  0.80     Sequence
            DRB1_0401  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.3636
978.7    37.00  0.93     Sequence
            DRB1_0401  810      QILPDPSKPSKRSFI  ILPDPSKPS  1        0.3129
1692.8    50.00  0.85     Sequence
            DRB1_0401  811      ILPDPSKPSKRSFIE  ILPDPSKPS  0        0.1898
6412.3    85.00  0.54     Sequence
            DRB1_0401  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.0695
23564.6   100.00  0.44     Sequence
            DRB1_0401  813      PDPSKPSKRSFIEDL  SKPSKRSFI  3        0.0874
19418.2   100.00  0.38     Sequence
            DRB1_0401  814      DPSKPSKRSFIEDLL  SKRSFIEDL  5        0.1023
16522.7   100.00  0.28     Sequence
            DRB1_0401  815      PSKPSKRSFIEDLLF  RSFIEDLLF  6        0.1338
11754.4   100.00  0.37     Sequence
            DRB1_0401  816      SKPSKRSFIEDLLFN  RSFIEDLLF  5        0.1910
6329.3    85.00  0.41     Sequence
            DRB1_0401  817      KPSKRSFIEDLLFNK  FIEDLLFNK  6        0.3007
1931.7    55.00  0.51     Sequence
            DRB1_0401  818      PSKRSFIEDLLFNKV  FIEDLLFNK  5        0.3539
1086.6    39.00  0.55     Sequence
            DRB1_0401  819      SKRSFIEDLLFNKVT  FIEDLLFNK  4        0.3748
866.8    34.00  0.55     Sequence
            DRB1_0401  820      KRSFIEDLLFNKVTL  FIEDLLFNK  3        0.3728
885.8    35.00  0.54     Sequence
            DRB1_0401  821      RSFIEDLLFNKVTLA  LLFNKVTLA  6        0.4991
225.7    13.00  0.45     Sequence
```

```
             DRB1_0401  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5        0.5163
187.5    11.00  0.54     Sequence
             DRB1_0401  823      FIEDLLFNKVTLADA  LLFNKVTLA  4        0.5493
131.2     7.50  0.51     Sequence         WB
             DRB1_0401  824      IEDLLFNKVTLADAG  LLFNKVTLA  3        0.5578
119.7     6.50  0.52     Sequence         WB
             DRB1_0401  825      EDLLFNKVTLADAGF  LLFNKVTLA  2        0.5677
107.5     6.00  0.46     Sequence         WB
             DRB1_0401  826      DLLFNKVTLADAGFI  LLFNKVTLA  1        0.5659
109.6     6.00  0.41     Sequence         WB
             DRB1_0401  827      LLFNKVTLADAGFIK  FNKVTLADA  2        0.5244
171.7     9.50  0.37     Sequence         WB
             DRB1_0401  828      LFNKVTLADAGFIKQ  FNKVTLADA  1        0.3885
746.8    31.00  0.41     Sequence
             DRB1_0401  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.3343
1343.3    45.00  0.33     Sequence
             DRB1_0401  830      NKVTLADAGFIKQYG  LADAGFIKQ  4        0.3010
1925.6    55.00  0.43     Sequence
             DRB1_0401  831      KVTLADAGFIKQYGD  LADAGFIKQ  3        0.2678
2759.1    65.00  0.47     Sequence
             DRB1_0401  832      VTLADAGFIKQYGDC  LADAGFIKQ  2        0.1990
5803.8    85.00  0.61     Sequence
             DRB1_0401  833      TLADAGFIKQYGDCL  FIKQYGDCL  6        0.2567
3108.6    70.00  0.51     Sequence
             DRB1_0401  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.2571
3097.3    70.00  0.68     Sequence
             DRB1_0401  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4        0.2552
3160.3    70.00  0.74     Sequence
             DRB1_0401  836      DAGFIKQYGDCLGDI  FIKQYGDCL  3        0.2691
2718.8    65.00  0.70     Sequence
             DRB1_0401  837      AGFIKQYGDCLGDIA  FIKQYGDCL  2        0.3048
1847.1    55.00  0.51     Sequence
             DRB1_0401  838      GFIKQYGDCLGDIAA  FIKQYGDCL  1        0.3128
1695.4    55.00  0.41     Sequence
             DRB1_0401  839      FIKQYGDCLGDIAAR  YGDCLGDIA  4        0.3039
1865.7    55.00  0.48     Sequence
             DRB1_0401  840      IKQYGDCLGDIAARD  YGDCLGDIA  3        0.3125
1699.8    55.00  0.50     Sequence
             DRB1_0401  841      KQYGDCLGDIAARDL  CLGDIAARD  5        0.3267
1458.5    47.00  0.43     Sequence
             DRB1_0401  842      QYGDCLGDIAARDLI  CLGDIAARD  4        0.3135
1682.9    50.00  0.49     Sequence
             DRB1_0401  843      YGDCLGDIAARDLIC  CLGDIAARD  3        0.2840
2313.8    60.00  0.57     Sequence
             DRB1_0401  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.2764
2511.6    65.00  0.58     Sequence
             DRB1_0401  845      DCLGDIAARDLICAQ  CLGDIAARD  1        0.2762
2517.3    65.00  0.40     Sequence
             DRB1_0401  846      CLGDIAARDLICAQK  IAARDLICA  4        0.2638
2878.8    65.00  0.36     Sequence
             DRB1_0401  847      LGDIAARDLICAQKF  IAARDLICA  3        0.2581
3061.9    70.00  0.44     Sequence
             DRB1_0401  848      GDIAARDLICAQKFN  IAARDLICA  2        0.2551
3163.5    70.00  0.41     Sequence
             DRB1_0401  849      DIAARDLICAQKFNG  IAARDLICA  1        0.2366
3864.8    75.00  0.34     Sequence
             DRB1_0401  850      IAARDLICAQKFNGL  ICAQKFNGL  6        0.2569
3103.9    70.00  0.38     Sequence
             DRB1_0401  851      AARDLICAQKFNGLT  ICAQKFNGL  5        0.2696
2703.5    65.00  0.52     Sequence
             DRB1_0401  852      ARDLICAQKFNGLTV  ICAQKFNGL  4        0.2801
2415.0    60.00  0.56     Sequence
             DRB1_0401  853      RDLICAQKFNGLTVL  ICAQKFNGL  3        0.2762
2519.5    65.00  0.56     Sequence
             DRB1_0401  854      DLICAQKFNGLTVLP  ICAQKFNGL  2        0.3005
1936.0    55.00  0.45     Sequence
```

```
             DRB1_0401  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.4530
371.8    19.00  0.70     Sequence
             DRB1_0401  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.4992
225.6    13.00  0.82     Sequence
             DRB1_0401  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.5153
189.4    11.00  0.89     Sequence
             DRB1_0401  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.5500
130.2     7.50  0.82     Sequence         WB
             DRB1_0401  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.5445
138.1     8.00  0.75     Sequence         WB
             DRB1_0401  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1        0.5068
207.7    12.00  0.68     Sequence
             DRB1_0401  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.3681
931.9    36.00  0.51     Sequence
             DRB1_0401  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.2797
2425.1    60.00  0.77     Sequence
             DRB1_0401  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.2505
3326.5    70.00  0.73     Sequence
             DRB1_0401  864      LTVLPPLLTDEMIAQ  LLTDEMIAQ  6        0.2574
3087.1    70.00  0.43     Sequence
             DRB1_0401  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.3205
1559.9    48.00  0.60     Sequence
             DRB1_0401  866      VLPPLLTDEMIAQYT  LLTDEMIAQ  4        0.3656
957.0    37.00  0.58     Sequence
             DRB1_0401  867      LPPLLTDEMIAQYTS  LLTDEMIAQ  3        0.3951
696.0    30.00  0.58     Sequence
             DRB1_0401  868      PPLLTDEMIAQYTSA  LLTDEMIAQ  2        0.3925
715.6    30.00  0.55     Sequence
             DRB1_0401  869      PLLTDEMIAQYTSAL  LLTDEMIAQ  1        0.4113
583.8    26.00  0.38     Sequence
             DRB1_0401  870      LLTDEMIAQYTSALL  IAQYTSALL  6        0.4085
602.0    27.00  0.32     Sequence
             DRB1_0401  871      LTDEMIAQYTSALLA  IAQYTSALL  5        0.4007
654.6    29.00  0.50     Sequence
             DRB1_0401  872      TDEMIAQYTSALLAG  IAQYTSALL  4        0.4197
533.3    25.00  0.49     Sequence
             DRB1_0401  873      DEMIAQYTSALLAGT  YTSALLAGT  6        0.4993
225.4    13.00  0.40     Sequence
             DRB1_0401  874      EMIAQYTSALLAGTI  YTSALLAGT  5        0.5376
148.8     8.50  0.56     Sequence         WB
             DRB1_0401  875      MIAQYTSALLAGTIT  YTSALLAGT  4        0.5386
147.3     8.50  0.66     Sequence         WB
             DRB1_0401  876      IAQYTSALLAGTITS  YTSALLAGT  3        0.5024
217.8    12.00  0.76     Sequence
             DRB1_0401  877      AQYTSALLAGTITSG  YTSALLAGT  2        0.4814
273.6    15.00  0.75     Sequence
             DRB1_0401  878      QYTSALLAGTITSGW  YTSALLAGT  1        0.4605
342.8    18.00  0.54     Sequence
             DRB1_0401  879      YTSALLAGTITSGWT  LAGTITSGW  5        0.4081
604.4    27.00  0.48     Sequence
             DRB1_0401  880      TSALLAGTITSGWTF  LAGTITSGW  4        0.3981
673.3    29.00  0.60     Sequence
             DRB1_0401  881      SALLAGTITSGWTFG  LAGTITSGW  3        0.4038
633.5    28.00  0.56     Sequence
             DRB1_0401  882      ALLAGTITSGWTFGA  LAGTITSGW  2        0.4381
437.0    21.00  0.38     Sequence
             DRB1_0401  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.4498
384.7    19.00  0.56     Sequence
             DRB1_0401  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.4401
427.4    21.00  0.77     Sequence
             DRB1_0401  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.4354
450.0    22.00  0.92     Sequence
             DRB1_0401  886      GTITSGWTFGAGAAL  ITSGWTFGA  2        0.4475
394.7    20.00  0.79     Sequence
             DRB1_0401  887      TITSGWTFGAGAALQ  ITSGWTFGA  1        0.4418
419.9    21.00  0.54     Sequence
```

```
             DRB1_0401  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.5112
198.1    11.00  0.73     Sequence
             DRB1_0401  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.5735
100.9     5.50  0.82     Sequence         WB
             DRB1_0401  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.6086
69.0     3.50  0.86     Sequence         WB
             DRB1_0401  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.6184
62.1     3.00  0.85     Sequence         WB
             DRB1_0401  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.5951
79.9     4.50  0.79     Sequence         WB
             DRB1_0401  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.5862
88.0     5.00  0.75     Sequence         WB
             DRB1_0401  894      FGAGAALQIPFAMQM  FGAGAALQI  0        0.4654
325.0    17.00  0.41     Sequence
             DRB1_0401  895      GAGAALQIPFAMQMA  LQIPFAMQM  5        0.3706
906.6    35.00  0.32     Sequence
             DRB1_0401  896      AGAALQIPFAMQMAY  LQIPFAMQM  4        0.3624
990.5    37.00  0.46     Sequence
             DRB1_0401  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.3733
880.9    35.00  0.49     Sequence
             DRB1_0401  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.4220
519.9    24.00  0.50     Sequence
             DRB1_0401  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.4318
467.8    23.00  0.62     Sequence
             DRB1_0401  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.4236
511.2    24.00  0.71     Sequence
             DRB1_0401  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.4028
640.0    28.00  0.80     Sequence
             DRB1_0401  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.3893
740.4    31.00  0.77     Sequence
             DRB1_0401  903      PFAMQMAYRFNGIGV  FAMQMAYRF  1        0.3731
882.5    35.00  0.62     Sequence
             DRB1_0401  904      FAMQMAYRFNGIGVT  YRFNGIGVT  6        0.3464
1177.9    41.00  0.46     Sequence
             DRB1_0401  905      AMQMAYRFNGIGVTQ  YRFNGIGVT  5        0.3817
803.9    33.00  0.54     Sequence
             DRB1_0401  906      MQMAYRFNGIGVTQN  FNGIGVTQN  6        0.5273
166.4     9.50  0.58     Sequence         WB
             DRB1_0401  907      QMAYRFNGIGVTQNV  FNGIGVTQN  5        0.5851
89.0     5.00  0.66     Sequence         WB
             DRB1_0401  908      MAYRFNGIGVTQNVL  FNGIGVTQN  4        0.5954
79.6     4.50  0.70     Sequence         WB
             DRB1_0401  909      AYRFNGIGVTQNVLY  FNGIGVTQN  3        0.5974
77.9     4.00  0.70     Sequence         WB
             DRB1_0401  910      YRFNGIGVTQNVLYE  FNGIGVTQN  2        0.5628
113.3     6.50  0.70     Sequence         WB
             DRB1_0401  911      RFNGIGVTQNVLYEN  FNGIGVTQN  1        0.5065
208.4    12.00  0.63     Sequence
             DRB1_0401  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.3712
901.2    35.00  0.41     Sequence
             DRB1_0401  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.3151
1652.9    50.00  0.52     Sequence
             DRB1_0401  914      GIGVTQNVLYENQKL  IGVTQNVLY  1        0.3027
1890.8    55.00  0.41     Sequence
             DRB1_0401  915      IGVTQNVLYENQKLI  NVLYENQKL  5        0.2606
2982.0    70.00  0.28     Sequence
             DRB1_0401  916      GVTQNVLYENQKLIA  NVLYENQKL  4        0.2509
3310.2    70.00  0.29     Sequence
             DRB1_0401  917      VTQNVLYENQKLIAN  YENQKLIAN  6        0.3285
1429.5    46.00  0.62     Sequence
             DRB1_0401  918      TQNVLYENQKLIANQ  YENQKLIAN  5        0.3806
813.5    33.00  0.71     Sequence
             DRB1_0401  919      QNVLYENQKLIANQF  YENQKLIAN  4        0.4050
624.8    28.00  0.74     Sequence
             DRB1_0401  920      NVLYENQKLIANQFN  YENQKLIAN  3        0.4054
622.4    28.00  0.75     Sequence
```

```
             DRB1_0401  921      VLYENQKLIANQFNS  YENQKLIAN  2        0.3839
785.5    32.00  0.69     Sequence
             DRB1_0401  922      LYENQKLIANQFNSA  YENQKLIAN  1        0.4281
486.7    23.00  0.40     Sequence
             DRB1_0401  923      YENQKLIANQFNSAI  IANQFNSAI  6        0.4615
339.3    18.00  0.44     Sequence
             DRB1_0401  924      ENQKLIANQFNSAIG  IANQFNSAI  5        0.4829
268.9    15.00  0.52     Sequence
             DRB1_0401  925      NQKLIANQFNSAIGK  IANQFNSAI  4        0.5053
211.1    12.00  0.55     Sequence
             DRB1_0401  926      QKLIANQFNSAIGKI  IANQFNSAI  3        0.4986
227.1    13.00  0.57     Sequence
             DRB1_0401  927      KLIANQFNSAIGKIQ  IANQFNSAI  2        0.5354
152.5     8.50  0.46     Sequence         WB
             DRB1_0401  928      LIANQFNSAIGKIQD  FNSAIGKIQ  5        0.5164
187.2    11.00  0.46     Sequence
             DRB1_0401  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4        0.4337
458.2    22.00  0.78     Sequence
             DRB1_0401  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.4255
500.8    24.00  0.86     Sequence
             DRB1_0401  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.4345
454.3    22.00  0.71     Sequence
             DRB1_0401  932      QFNSAIGKIQDSLSS  FNSAIGKIQ  1        0.4530
371.8    19.00  0.45     Sequence
             DRB1_0401  933      FNSAIGKIQDSLSST  GKIQDSLSS  5        0.4316
468.5    23.00  0.41     Sequence
             DRB1_0401  934      NSAIGKIQDSLSSTA  IQDSLSSTA  6        0.4964
232.5    13.00  0.38     Sequence
             DRB1_0401  935      SAIGKIQDSLSSTAS  IQDSLSSTA  5        0.5299
161.7     9.00  0.47     Sequence         WB
             DRB1_0401  936      AIGKIQDSLSSTASA  IQDSLSSTA  4        0.5429
140.5     8.00  0.56     Sequence         WB
             DRB1_0401  937      IGKIQDSLSSTASAL  IQDSLSSTA  3        0.5402
144.7     8.00  0.58     Sequence         WB
             DRB1_0401  938      GKIQDSLSSTASALG  IQDSLSSTA  2        0.5312
159.6     9.00  0.47     Sequence         WB
             DRB1_0401  939      KIQDSLSSTASALGK  LSSTASALG  5        0.5412
143.2     8.00  0.57     Sequence         WB
             DRB1_0401  940      IQDSLSSTASALGKL  LSSTASALG  4        0.5236
173.2     9.50  0.77     Sequence         WB
             DRB1_0401  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.5148
190.5    11.00  0.88     Sequence
             DRB1_0401  942      DSLSSTASALGKLQD  LSSTASALG  2        0.4857
261.0    14.00  0.92     Sequence
             DRB1_0401  943      SLSSTASALGKLQDV  LSSTASALG  1        0.4368
442.8    22.00  0.91     Sequence
             DRB1_0401  944      LSSTASALGKLQDVV  LSSTASALG  0        0.2427
3620.4    75.00  0.51     Sequence
             DRB1_0401  945      SSTASALGKLQDVVN  LGKLQDVVN  6        0.1151
14385.5   100.00  0.26     Sequence
             DRB1_0401  946      STASALGKLQDVVNQ  GKLQDVVNQ  6        0.1494
9930.1    95.00  0.31     Sequence
             DRB1_0401  947      TASALGKLQDVVNQN  GKLQDVVNQ  5        0.2248
4391.8    80.00  0.25     Sequence
             DRB1_0401  948      ASALGKLQDVVNQNA  LQDVVNQNA  6        0.3792
826.0    33.00  0.57     Sequence
             DRB1_0401  949      SALGKLQDVVNQNAQ  LQDVVNQNA  5        0.4403
426.5    21.00  0.68     Sequence
             DRB1_0401  950      ALGKLQDVVNQNAQA  LQDVVNQNA  4        0.4725
301.1    16.00  0.69     Sequence
             DRB1_0401  951      LGKLQDVVNQNAQAL  LQDVVNQNA  3        0.4776
284.9    15.00  0.71     Sequence
             DRB1_0401  952      GKLQDVVNQNAQALN  LQDVVNQNA  2        0.4584
350.9    18.00  0.69     Sequence
             DRB1_0401  953      KLQDVVNQNAQALNT  LQDVVNQNA  1        0.3973
679.5    29.00  0.62     Sequence
```

```
             DRB1_0401  954      LQDVVNQNAQALNTL  VVNQNAQAL  3        0.2715
2648.5    65.00 0.31      Sequence
             DRB1_0401  955      QDVVNQNAQALNTLV  VVNQNAQAL  2        0.2039
5503.7    85.00 0.42      Sequence
             DRB1_0401  956      DVVNQNAQALNTLVK  AQALNTLVK  6        0.2116
5063.6    80.00 0.24      Sequence
             DRB1_0401  957      VVNQNAQALNTLVKQ  AQALNTLVK  5        0.2308
4116.7    75.00 0.34      Sequence
             DRB1_0401  958      VNQNAQALNTLVKQL  AQALNTLVK  4        0.2430
3608.6    75.00 0.40      Sequence
             DRB1_0401  959      NQNAQALNTLVKQLS  AQALNTLVK  3        0.2946
2063.6    60.00 0.28      Sequence
             DRB1_0401  960      QNAQALNTLVKQLSS  LNTLVKQLS  5        0.3241
1499.9    47.00 0.41      Sequence
             DRB1_0401  961      NAQALNTLVKQLSSN  LNTLVKQLS  4        0.3500
1133.3    40.00 0.44      Sequence
             DRB1_0401  962      AQALNTLVKQLSSNF  LVKQLSSNF  6        0.4837
266.7    14.00 0.36      Sequence
             DRB1_0401  963      QALNTLVKQLSSNFG  VKQLSSNFG  6        0.6193
61.5     3.00  0.64     Sequence         WB
             DRB1_0401  964      ALNTLVKQLSSNFGA  VKQLSSNFG  5        0.7168
21.4     0.60  0.74     Sequence         SB
             DRB1_0401  965      LNTLVKQLSSNFGAI  VKQLSSNFG  4        0.7424
16.2     0.30  0.75     Sequence         SB
             DRB1_0401  966      NTLVKQLSSNFGAIS  VKQLSSNFG  3        0.7440
16.0     0.30  0.77     Sequence         SB
             DRB1_0401  967      TLVKQLSSNFGAISS  VKQLSSNFG  2        0.7142
22.0     0.60  0.76     Sequence         SB
             DRB1_0401  968      LVKQLSSNFGAISSV  VKQLSSNFG  1        0.6534
42.5     1.70  0.77     Sequence         SB
             DRB1_0401  969      VKQLSSNFGAISSVL  LSSNFGAIS  3        0.5034
215.4    12.00 0.28      Sequence
             DRB1_0401  970      KQLSSNFGAISSVLN  FGAISSVLN  6        0.5300
161.7     9.00  0.69     Sequence         WB
             DRB1_0401  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.5572
120.5     6.50  0.81     Sequence         WB
             DRB1_0401  972      LSSNFGAISSVLNDI  FGAISSVLN  4        0.5666
108.7     6.00  0.85     Sequence         WB
             DRB1_0401  973      SSNFGAISSVLNDIL  FGAISSVLN  3        0.5745
99.9     5.50  0.86     Sequence         WB
             DRB1_0401  974      SNFGAISSVLNDILS  FGAISSVLN  2        0.5620
114.3     6.50  0.83     Sequence         WB
             DRB1_0401  975      NFGAISSVLNDILSR  FGAISSVLN  1        0.5316
158.8     9.00  0.72     Sequence         WB
             DRB1_0401  976      FGAISSVLNDILSRL  ISSVLNDIL  3        0.4606
342.4    18.00 0.41      Sequence
             DRB1_0401  977      GAISSVLNDILSRLD  ISSVLNDIL  2        0.3400
1263.1    43.00 0.66      Sequence
             DRB1_0401  978      AISSVLNDILSRLDK  ISSVLNDIL  1        0.3214
1544.1    48.00 0.47      Sequence
             DRB1_0401  979      ISSVLNDILSRLDKV  LNDILSRLD  4        0.2639
2876.3    65.00 0.47      Sequence
             DRB1_0401  980      SSVLNDILSRLDKVE  LNDILSRLD  3        0.2505
3326.4    70.00 0.49      Sequence
             DRB1_0401  981      SVLNDILSRLDKVEA  LNDILSRLD  2        0.2459
3495.8    70.00 0.44      Sequence
             DRB1_0401  982      VLNDILSRLDKVEAE  LNDILSRLD  1        0.2400
3724.7    75.00 0.36      Sequence
             DRB1_0401  983      LNDILSRLDKVEAEV  LSRLDKVEA  4        0.2239
4436.8    80.00 0.35      Sequence
             DRB1_0401  984      NDILSRLDKVEAEVQ  LSRLDKVEA  3        0.2352
3926.1    75.00 0.35      Sequence
             DRB1_0401  985      DILSRLDKVEAEVQI  SRLDKVEAE  3        0.2356
3909.1    75.00 0.26      Sequence
             DRB1_0401  986      ILSRLDKVEAEVQID  SRLDKVEAE  2        0.2299
4156.2    75.00 0.23      Sequence
```

```
             DRB1_0401  987      LSRLDKVEAEVQIDR  DKVEAEVQI  4        0.2204
4605.5    80.00  0.29     Sequence
             DRB1_0401  988      SRLDKVEAEVQIDRL  DKVEAEVQI  3        0.1870
6609.6    90.00  0.36     Sequence
             DRB1_0401  989      RLDKVEAEVQIDRLI  DKVEAEVQI  2        0.1780
7289.8    90.00  0.34     Sequence
             DRB1_0401  990      LDKVEAEVQIDRLIT  VEAEVQIDR  3        0.1808
7069.5    90.00  0.30     Sequence
             DRB1_0401  991      DKVEAEVQIDRLITG  VQIDRLITG  6        0.2454
3513.7    70.00  0.64     Sequence
             DRB1_0401  992      KVEAEVQIDRLITGR  VQIDRLITG  5        0.3165
1627.8    49.00  0.73     Sequence
             DRB1_0401  993      VEAEVQIDRLITGRL  VQIDRLITG  4        0.3404
1257.3    43.00  0.69     Sequence
             DRB1_0401  994      EAEVQIDRLITGRLQ  VQIDRLITG  3        0.3582
1036.6    38.00  0.67     Sequence
             DRB1_0401  995      AEVQIDRLITGRLQS  VQIDRLITG  2        0.3651
962.5    37.00  0.56     Sequence
             DRB1_0401  996      EVQIDRLITGRLQSL  VQIDRLITG  1        0.3748
866.8    34.00  0.29     Sequence
             DRB1_0401  997      VQIDRLITGRLQSLQ  LITGRLQSL  5        0.3750
864.2    34.00  0.46     Sequence
             DRB1_0401  998      QIDRLITGRLQSLQT  LITGRLQSL  4        0.3931
711.3    30.00  0.46     Sequence
             DRB1_0401  999      IDRLITGRLQSLQTY  LITGRLQSL  3        0.4157
556.5    26.00  0.47     Sequence
             DRB1_0401 1000      DRLITGRLQSLQTYV  LITGRLQSL  2        0.3966
684.3    29.00  0.46     Sequence
             DRB1_0401 1001      RLITGRLQSLQTYVT  LQSLQTYVT  6        0.4157
556.5    26.00  0.36     Sequence
             DRB1_0401 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.4442
409.0    20.00  0.71     Sequence
             DRB1_0401 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.4840
265.9    14.00  0.79     Sequence
             DRB1_0401 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.5068
207.8    12.00  0.75     Sequence
             DRB1_0401 1005      GRLQSLQTYVTQQLI  LQSLQTYVT  2        0.4877
255.6    14.00  0.71     Sequence
             DRB1_0401 1006      RLQSLQTYVTQQLIR  LQSLQTYVT  1        0.4393
431.1    21.00  0.56     Sequence
             DRB1_0401 1007      LQSLQTYVTQQLIRA  YVTQQLIRA  6        0.4555
361.8    19.00  0.58     Sequence
             DRB1_0401 1008      QSLQTYVTQQLIRAA  YVTQQLIRA  5        0.5287
163.9     9.00  0.75     Sequence         WB
             DRB1_0401 1009      SLQTYVTQQLIRAAE  YVTQQLIRA  4        0.5496
130.7     7.50  0.76     Sequence         WB
             DRB1_0401 1010      LQTYVTQQLIRAAEI  YVTQQLIRA  3        0.5408
143.7     8.00  0.83     Sequence         WB
             DRB1_0401 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.5126
195.1    11.00  0.84     Sequence
             DRB1_0401 1012      TYVTQQLIRAAEIRA  YVTQQLIRA  1        0.4588
349.2    18.00  0.74     Sequence
             DRB1_0401 1013      YVTQQLIRAAEIRAS  IRAAEIRAS  6        0.4350
451.8    22.00  0.47     Sequence
             DRB1_0401 1014      VTQQLIRAAEIRASA  IRAAEIRAS  5        0.5024
217.8    12.00  0.71     Sequence
             DRB1_0401 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.5412
143.2     8.00  0.74     Sequence         WB
             DRB1_0401 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.5498
130.5     7.50  0.74     Sequence         WB
             DRB1_0401 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.5644
111.4     6.00  0.63     Sequence         WB
             DRB1_0401 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.5867
87.5     4.50  0.43     Sequence         WB
             DRB1_0401 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.5733
101.2     5.50  0.73     Sequence         WB
```

```
             DRB1_0401 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.5861
88.1     5.00  0.89     Sequence        WB
             DRB1_0401 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.5889
85.5     4.50  0.93     Sequence        WB
             DRB1_0401 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.5814
92.7     5.00  0.92     Sequence        WB
             DRB1_0401 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.5489
131.7     7.50  0.90     Sequence        WB
             DRB1_0401 1024      IRASANLAAIKMSEC  IRASANLAA  0        0.3586
1033.0    38.00  0.56     Sequence
             DRB1_0401 1025      RASANLAAIKMSECV  LAAIKMSEC  5        0.1719
7785.4    90.00  0.33     Sequence
             DRB1_0401 1026      ASANLAAIKMSECVL  LAAIKMSEC  4        0.1690
8033.5    90.00  0.41     Sequence
             DRB1_0401 1027      SANLAAIKMSECVLG  IKMSECVLG  6        0.2525
3253.5    70.00  0.48     Sequence
             DRB1_0401 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.3385
1283.5    43.00  0.49     Sequence
             DRB1_0401 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.3868
760.8    32.00  0.48     Sequence
             DRB1_0401 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.4160
555.0    26.00  0.47     Sequence
             DRB1_0401 1031      AAIKMSECVLGQSKR  KMSECVLGQ  3        0.4244
506.5    24.00  0.50     Sequence
             DRB1_0401 1032      AIKMSECVLGQSKRV  KMSECVLGQ  2        0.4009
653.5    29.00  0.50     Sequence
             DRB1_0401 1033      IKMSECVLGQSKRVD  KMSECVLGQ  1        0.3358
1321.2    44.00  0.51     Sequence
             DRB1_0401 1034      KMSECVLGQSKRVDF  KMSECVLGQ  0        0.2316
4078.8    75.00  0.28     Sequence
             DRB1_0401 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.1692
8018.5    90.00  0.50     Sequence
             DRB1_0401 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.1629
8584.9    95.00  0.49     Sequence
             DRB1_0401 1037      ECVLGQSKRVDFCGK  CVLGQSKRV  1        0.1548
9367.3    95.00  0.38     Sequence
             DRB1_0401 1038      CVLGQSKRVDFCGKG  VLGQSKRVD  1        0.1370
11350.6    95.00  0.23     Sequence
             DRB1_0401 1039      VLGQSKRVDFCGKGY  KRVDFCGKG  5        0.1347
11642.4   100.00  0.28     Sequence
             DRB1_0401 1040      LGQSKRVDFCGKGYH  KRVDFCGKG  4        0.1381
11218.6    95.00  0.28     Sequence
             DRB1_0401 1041      GQSKRVDFCGKGYHL  KRVDFCGKG  3        0.1353
11561.7   100.00  0.30     Sequence
             DRB1_0401 1042      QSKRVDFCGKGYHLM  FCGKGYHLM  6        0.1661
8285.3    90.00  0.25     Sequence
             DRB1_0401 1043      SKRVDFCGKGYHLMS  FCGKGYHLM  5        0.2011
5677.1    85.00  0.27     Sequence
             DRB1_0401 1044      KRVDFCGKGYHLMSF  CGKGYHLMS  5        0.2252
4370.8    80.00  0.34     Sequence
             DRB1_0401 1045      RVDFCGKGYHLMSFP  CGKGYHLMS  4        0.2239
4434.8    80.00  0.37     Sequence
             DRB1_0401 1046      VDFCGKGYHLMSFPQ  CGKGYHLMS  3        0.2709
2666.4    65.00  0.31     Sequence
             DRB1_0401 1047      DFCGKGYHLMSFPQS  YHLMSFPQS  6        0.4454
403.6    20.00  0.60     Sequence
             DRB1_0401 1048      FCGKGYHLMSFPQSA  YHLMSFPQS  5        0.5432
140.1     8.00  0.61     Sequence        WB
             DRB1_0401 1049      CGKGYHLMSFPQSAP  YHLMSFPQS  4        0.5725
102.1     5.50  0.57     Sequence        WB
             DRB1_0401 1050      GKGYHLMSFPQSAPH  YHLMSFPQS  3        0.5819
92.2     5.00  0.60     Sequence        WB
             DRB1_0401 1051      KGYHLMSFPQSAPHG  YHLMSFPQS  2        0.5590
118.1     6.50  0.56     Sequence        WB
             DRB1_0401 1052      GYHLMSFPQSAPHGV  YHLMSFPQS  1        0.5133
193.7    11.00  0.52     Sequence
```

```
             DRB1_0401 1053      YHLMSFPQSAPHGVV  YHLMSFPQS  0        0.3926
714.7    30.00  0.37     Sequence
             DRB1_0401 1054      HLMSFPQSAPHGVVF  LMSFPQSAP  1        0.2687
2731.5    65.00  0.34     Sequence
             DRB1_0401 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.1898
6414.3    85.00  0.41     Sequence
             DRB1_0401 1056      MSFPQSAPHGVVFLH  FPQSAPHGV  2        0.1787
7230.4    90.00  0.44     Sequence
             DRB1_0401 1057      SFPQSAPHGVVFLHV  FPQSAPHGV  1        0.1566
9190.3    95.00  0.38     Sequence
             DRB1_0401 1058      FPQSAPHGVVFLHVT  SAPHGVVFL  3        0.1416
10807.7    95.00  0.32     Sequence
             DRB1_0401 1059      PQSAPHGVVFLHVTY  SAPHGVVFL  2        0.1459
10318.6    95.00  0.29     Sequence
             DRB1_0401 1060      QSAPHGVVFLHVTYV  VVFLHVTYV  6        0.2154
4861.8    80.00  0.49     Sequence
             DRB1_0401 1061      SAPHGVVFLHVTYVP  VVFLHVTYV  5        0.2755
2537.2    65.00  0.46     Sequence
             DRB1_0401 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.3953
694.3    30.00  0.43     Sequence
             DRB1_0401 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.4501
383.5    19.00  0.43     Sequence
             DRB1_0401 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.4733
298.4    16.00  0.40     Sequence
             DRB1_0401 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.4960
233.4    13.00  0.40     Sequence
             DRB1_0401 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.4716
303.9    16.00  0.41     Sequence
             DRB1_0401 1067      VFLHVTYVPAQEKNF  FLHVTYVPA  1        0.4424
417.1    21.00  0.39     Sequence
             DRB1_0401 1068      FLHVTYVPAQEKNFT  LHVTYVPAQ  1        0.3763
852.4    34.00  0.32     Sequence
             DRB1_0401 1069      LHVTYVPAQEKNFTT  VTYVPAQEK  2        0.2838
2320.0    60.00  0.23     Sequence
             DRB1_0401 1070      HVTYVPAQEKNFTTA  PAQEKNFTT  5        0.2658
2818.5    65.00  0.31     Sequence
             DRB1_0401 1071      VTYVPAQEKNFTTAP  PAQEKNFTT  4        0.2588
3039.2    70.00  0.39     Sequence
             DRB1_0401 1072      TYVPAQEKNFTTAPA  PAQEKNFTT  3        0.2736
2588.8    65.00  0.40     Sequence
             DRB1_0401 1073      YVPAQEKNFTTAPAI  PAQEKNFTT  2        0.2617
2944.6    65.00  0.33     Sequence
             DRB1_0401 1074      VPAQEKNFTTAPAIC  FTTAPAICX  7        0.3032
1879.6    55.00  0.25     Sequence
             DRB1_0401 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.5320
158.2     9.00  0.82     Sequence         WB
             DRB1_0401 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.5812
92.9     5.00  0.90     Sequence         WB
             DRB1_0401 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.6019
74.3     4.00  0.94     Sequence         WB
             DRB1_0401 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.6166
63.3     3.00  0.96     Sequence         WB
             DRB1_0401 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.6031
73.3     4.00  0.96     Sequence         WB
             DRB1_0401 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.5342
154.5     8.50  0.92     Sequence         WB
             DRB1_0401 1081      FTTAPAICHDGKAHF  FTTAPAICH  0        0.3532
1094.7    40.00  0.59     Sequence
             DRB1_0401 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.1511
9750.7    95.00  0.50     Sequence
             DRB1_0401 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.1702
7926.4    90.00  0.54     Sequence
             DRB1_0401 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.1712
7843.5    90.00  0.52     Sequence
             DRB1_0401 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.1666
8244.2    90.00  0.48     Sequence
```

```
             DRB1_0401 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.1626
8610.3    95.00  0.38     Sequence
             DRB1_0401 1087      ICHDGKAHFPREGVF  CHDGKAHFP  1        0.1349
11615.2   100.00  0.28     Sequence
             DRB1_0401 1088      CHDGKAHFPREGVFV  FPREGVFVX  7        0.1419
10764.3    95.00  0.27     Sequence
             DRB1_0401 1089      HDGKAHFPREGVFVS  FPREGVFVS  6        0.2908
2150.4    60.00  0.80     Sequence
             DRB1_0401 1090      DGKAHFPREGVFVSN  FPREGVFVS  5        0.3475
1164.6    41.00  0.83     Sequence
             DRB1_0401 1091      GKAHFPREGVFVSNG  FPREGVFVS  4        0.3676
936.4    36.00  0.83     Sequence
             DRB1_0401 1092      KAHFPREGVFVSNGT  FPREGVFVS  3        0.3709
903.8    35.00  0.79     Sequence
             DRB1_0401 1093      AHFPREGVFVSNGTH  FPREGVFVS  2        0.3558
1064.3    39.00  0.69     Sequence
             DRB1_0401 1094      HFPREGVFVSNGTHW  FPREGVFVS  1        0.3749
865.4    34.00  0.49     Sequence
             DRB1_0401 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6        0.4724
301.3    16.00  0.69     Sequence
             DRB1_0401 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.5203
179.5    10.00  0.80     Sequence
             DRB1_0401 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.5422
141.7     8.00  0.82     Sequence         WB
             DRB1_0401 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.5404
144.4     8.00  0.83     Sequence         WB
             DRB1_0401 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.5298
162.0     9.00  0.86     Sequence         WB
             DRB1_0401 1100      VFVSNGTHWFVTQRN  FVSNGTHWF  1        0.4996
224.5    13.00  0.78     Sequence
             DRB1_0401 1101      FVSNGTHWFVTQRNF  FVSNGTHWF  0        0.3397
1267.2    43.00  0.39     Sequence
             DRB1_0401 1102      VSNGTHWFVTQRNFY  THWFVTQRN  4        0.3830
793.4    32.00  0.40     Sequence
             DRB1_0401 1103      SNGTHWFVTQRNFYE  FVTQRNFYE  6        0.5188
182.5    10.00  0.69     Sequence
             DRB1_0401 1104      NGTHWFVTQRNFYEP  FVTQRNFYE  5        0.5634
112.6     6.00  0.78     Sequence         WB
             DRB1_0401 1105      GTHWFVTQRNFYEPQ  FVTQRNFYE  4        0.5863
87.9     5.00  0.80     Sequence         WB
             DRB1_0401 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3        0.5739
100.5     5.50  0.88     Sequence         WB
             DRB1_0401 1107      HWFVTQRNFYEPQII  FVTQRNFYE  2        0.5518
127.7     7.00  0.90     Sequence         WB
             DRB1_0401 1108      WFVTQRNFYEPQIIT  FVTQRNFYE  1        0.5195
181.2    10.00  0.88     Sequence
             DRB1_0401 1109      FVTQRNFYEPQIITT  FVTQRNFYE  0        0.4416
420.5    21.00  0.46     Sequence
             DRB1_0401 1110      VTQRNFYEPQIITTD  YEPQIITTD  6        0.4099
592.9    27.00  0.64     Sequence
             DRB1_0401 1111      TQRNFYEPQIITTDN  YEPQIITTD  5        0.4603
343.7    18.00  0.70     Sequence
             DRB1_0401 1112      QRNFYEPQIITTDNT  YEPQIITTD  4        0.4762
289.3    16.00  0.72     Sequence
             DRB1_0401 1113      RNFYEPQIITTDNTF  YEPQIITTD  3        0.4893
251.0    14.00  0.64     Sequence
             DRB1_0401 1114      NFYEPQIITTDNTFV  YEPQIITTD  2        0.5050
211.8    12.00  0.46     Sequence
             DRB1_0401 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.5532
125.7     7.00  0.35     Sequence         WB
             DRB1_0401 1116      YEPQIITTDNTFVSG  ITTDNTFVS  5        0.5650
110.7     6.00  0.52     Sequence         WB
             DRB1_0401 1117      EPQIITTDNTFVSGN  ITTDNTFVS  4        0.5808
93.2     5.00  0.62     Sequence         WB
             DRB1_0401 1118      PQIITTDNTFVSGNC  ITTDNTFVS  3        0.5789
95.2     5.00  0.62     Sequence         WB
```

```
             DRB1_0401 1119      QIITTDNTFVSGNCD  ITTDNTFVS  2        0.5552
123.1     7.00  0.68     Sequence         WB
             DRB1_0401 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.4518
376.6    19.00  0.83     Sequence
             DRB1_0401 1121      ITTDNTFVSGNCDVV  ITTDNTFVS  0        0.2896
2179.1    60.00  0.54     Sequence
             DRB1_0401 1122      TTDNTFVSGNCDVVI  FVSGNCDVV  5        0.1733
7667.5    90.00  0.49     Sequence
             DRB1_0401 1123      TDNTFVSGNCDVVIG  FVSGNCDVV  4        0.1956
6025.2    85.00  0.47     Sequence
             DRB1_0401 1124      DNTFVSGNCDVVIGI  FVSGNCDVV  3        0.2103
5138.1    80.00  0.44     Sequence
             DRB1_0401 1125      NTFVSGNCDVVIGIV  FVSGNCDVV  2        0.2168
4788.1    80.00  0.41     Sequence
             DRB1_0401 1126      TFVSGNCDVVIGIVN  FVSGNCDVV  1        0.2045
5469.6    85.00  0.34     Sequence
             DRB1_0401 1127      FVSGNCDVVIGIVNN  VSGNCDVVI  1        0.1717
7797.6    90.00  0.29     Sequence
             DRB1_0401 1128      VSGNCDVVIGIVNNT  VVIGIVNNT  6        0.1787
7231.9    90.00  0.28     Sequence
             DRB1_0401 1129      SGNCDVVIGIVNNTV  VIGIVNNTV  6        0.2401
3721.2    75.00  0.44     Sequence
             DRB1_0401 1130      GNCDVVIGIVNNTVY  VIGIVNNTV  5        0.3063
1818.9    55.00  0.42     Sequence
             DRB1_0401 1131      NCDVVIGIVNNTVYD  VIGIVNNTV  4        0.3164
1629.6    49.00  0.40     Sequence
             DRB1_0401 1132      CDVVIGIVNNTVYDP  VIGIVNNTV  3        0.3314
1386.5    45.00  0.37     Sequence
             DRB1_0401 1133      DVVIGIVNNTVYDPL  VIGIVNNTV  2        0.3556
1066.2    39.00  0.35     Sequence
             DRB1_0401 1134      VVIGIVNNTVYDPLQ  VIGIVNNTV  1        0.3430
1222.5    42.00  0.34     Sequence
             DRB1_0401 1135      VIGIVNNTVYDPLQP  IVNNTVYDP  3        0.2914
2136.0    60.00  0.35     Sequence
             DRB1_0401 1136      IGIVNNTVYDPLQPE  IVNNTVYDP  2        0.2406
3702.0    75.00  0.46     Sequence
             DRB1_0401 1137      GIVNNTVYDPLQPEL  IVNNTVYDP  1        0.2120
5044.5    80.00  0.41     Sequence
             DRB1_0401 1138      IVNNTVYDPLQPELD  IVNNTVYDP  0        0.1656
8333.6    90.00  0.17     Sequence
             DRB1_0401 1139      VNNTVYDPLQPELDS  YDPLQPELD  5        0.1408
10892.5    95.00  0.32     Sequence
             DRB1_0401 1140      NNTVYDPLQPELDSF  YDPLQPELD  4        0.1664
8261.3    90.00  0.34     Sequence
             DRB1_0401 1141      NTVYDPLQPELDSFK  LQPELDSFK  6        0.2924
2114.1    60.00  0.66     Sequence
             DRB1_0401 1142      TVYDPLQPELDSFKE  LQPELDSFK  5        0.3465
1177.0    41.00  0.80     Sequence
             DRB1_0401 1143      VYDPLQPELDSFKEE  LQPELDSFK  4        0.3627
987.5    37.00  0.83     Sequence
             DRB1_0401 1144      YDPLQPELDSFKEEL  LQPELDSFK  3        0.3609
1007.5    38.00  0.88     Sequence
             DRB1_0401 1145      DPLQPELDSFKEELD  LQPELDSFK  2        0.3446
1202.1    42.00  0.89     Sequence
             DRB1_0401 1146      PLQPELDSFKEELDK  LQPELDSFK  1        0.3067
1810.8    55.00  0.85     Sequence
             DRB1_0401 1147      LQPELDSFKEELDKY  LQPELDSFK  0        0.1902
6387.5    85.00  0.52     Sequence
             DRB1_0401 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.1413
10836.0    95.00  0.63     Sequence
             DRB1_0401 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.1809
7064.8    90.00  0.70     Sequence
             DRB1_0401 1150      ELDSFKEELDKYFKN  FKEELDKYF  4        0.2012
5671.7    85.00  0.73     Sequence
             DRB1_0401 1151      LDSFKEELDKYFKNH  FKEELDKYF  3        0.2094
5186.7    80.00  0.70     Sequence
```

```
             DRB1_0401 1152      DSFKEELDKYFKNHT  FKEELDKYF  2        0.2187
4693.7    80.00  0.59     Sequence
             DRB1_0401 1153      SFKEELDKYFKNHTS  FKEELDKYF  1        0.2457
3503.7    70.00  0.42     Sequence
             DRB1_0401 1154      FKEELDKYFKNHTSP  DKYFKNHTS  5        0.2388
3774.8    75.00  0.39     Sequence
             DRB1_0401 1155      KEELDKYFKNHTSPD  DKYFKNHTS  4        0.3123
1704.6    55.00  0.32     Sequence
             DRB1_0401 1156      EELDKYFKNHTSPDV  FKNHTSPDV  6        0.4459
401.6    20.00  0.65     Sequence
             DRB1_0401 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.4930
241.2    13.00  0.74     Sequence
             DRB1_0401 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.5158
188.5    11.00  0.76     Sequence
             DRB1_0401 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.5029
216.8    12.00  0.82     Sequence
             DRB1_0401 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.4792
280.1    15.00  0.88     Sequence
             DRB1_0401 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.3989
667.8    29.00  0.85     Sequence
             DRB1_0401 1162      FKNHTSPDVDLGDIS  FKNHTSPDV  0        0.2365
3867.8    75.00  0.55     Sequence
             DRB1_0401 1163      KNHTSPDVDLGDISG  TSPDVDLGD  3        0.1015
16678.8   100.00  0.54     Sequence
             DRB1_0401 1164      NHTSPDVDLGDISGI  TSPDVDLGD  2        0.1094
15309.4   100.00  0.43     Sequence
             DRB1_0401 1165      HTSPDVDLGDISGIN  DLGDISGIN  6        0.1268
12682.1   100.00  0.31     Sequence
             DRB1_0401 1166      TSPDVDLGDISGINA  DLGDISGIN  5        0.1594
8915.6    95.00  0.35     Sequence
             DRB1_0401 1167      SPDVDLGDISGINAS  DLGDISGIN  4        0.1954
6037.4    85.00  0.32     Sequence
             DRB1_0401 1168      PDVDLGDISGINASF  DISGINASF  6        0.2625
2922.2    65.00  0.26     Sequence
             DRB1_0401 1169      DVDLGDISGINASFV  DISGINASF  5        0.3023
1899.5    55.00  0.31     Sequence
             DRB1_0401 1170      VDLGDISGINASFVN  DISGINASF  4        0.3198
1571.8    49.00  0.32     Sequence
             DRB1_0401 1171      DLGDISGINASFVNI  DISGINASF  3        0.3255
1476.7    47.00  0.34     Sequence
             DRB1_0401 1172      LGDISGINASFVNIQ  INASFVNIQ  6        0.3990
667.3    29.00  0.46     Sequence
             DRB1_0401 1173      GDISGINASFVNIQK  INASFVNIQ  5        0.4585
350.3    18.00  0.58     Sequence
             DRB1_0401 1174      DISGINASFVNIQKE  INASFVNIQ  4        0.4552
363.0    19.00  0.69     Sequence
             DRB1_0401 1175      ISGINASFVNIQKEI  INASFVNIQ  3        0.4399
428.5    21.00  0.78     Sequence
             DRB1_0401 1176      SGINASFVNIQKEID  INASFVNIQ  2        0.4315
469.3    23.00  0.75     Sequence
             DRB1_0401 1177      GINASFVNIQKEIDR  INASFVNIQ  1        0.3921
718.9    30.00  0.70     Sequence
             DRB1_0401 1178      INASFVNIQKEIDRL  INASFVNIQ  0        0.2845
2303.2    60.00  0.38     Sequence
             DRB1_0401 1179      NASFVNIQKEIDRLN  IQKEIDRLN  6        0.2796
2427.3    60.00  0.50     Sequence
             DRB1_0401 1180      ASFVNIQKEIDRLNE  IQKEIDRLN  5        0.3137
1677.6    50.00  0.61     Sequence
             DRB1_0401 1181      SFVNIQKEIDRLNEV  IQKEIDRLN  4        0.3281
1436.9    46.00  0.67     Sequence
             DRB1_0401 1182      FVNIQKEIDRLNEVA  IQKEIDRLN  3        0.3324
1371.4    45.00  0.69     Sequence
             DRB1_0401 1183      VNIQKEIDRLNEVAK  IQKEIDRLN  2        0.3344
1341.9    44.00  0.63     Sequence
             DRB1_0401 1184      NIQKEIDRLNEVAKN  IQKEIDRLN  1        0.3180
1602.9    49.00  0.54     Sequence
```

```
             DRB1_0401 1185      IQKEIDRLNEVAKNL  IDRLNEVAK  4        0.2580
3065.1    70.00  0.29     Sequence
             DRB1_0401 1186      QKEIDRLNEVAKNLN  IDRLNEVAK  3        0.2164
4809.6    80.00  0.32     Sequence
             DRB1_0401 1187      KEIDRLNEVAKNLNE  IDRLNEVAK  2        0.2190
4675.5    80.00  0.28     Sequence
             DRB1_0401 1188      EIDRLNEVAKNLNES  LNEVAKNLN  4        0.2057
5400.8    85.00  0.28     Sequence
             DRB1_0401 1189      IDRLNEVAKNLNESL  VAKNLNESL  6        0.2280
4244.3    75.00  0.34     Sequence
             DRB1_0401 1190      DRLNEVAKNLNESLI  VAKNLNESL  5        0.2360
3890.4    75.00  0.50     Sequence
             DRB1_0401 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.2266
4308.4    75.00  0.56     Sequence
             DRB1_0401 1192      LNEVAKNLNESLIDL  VAKNLNESL  3        0.2117
5058.1    80.00  0.62     Sequence
             DRB1_0401 1193      NEVAKNLNESLIDLQ  VAKNLNESL  2        0.2057
5402.4    85.00  0.57     Sequence
             DRB1_0401 1194      EVAKNLNESLIDLQE  VAKNLNESL  1        0.2089
5216.2    80.00  0.41     Sequence
             DRB1_0401 1195      VAKNLNESLIDLQEL  LNESLIDLQ  4        0.1902
6383.7    85.00  0.41     Sequence
             DRB1_0401 1196      AKNLNESLIDLQELG  LNESLIDLQ  3        0.1649
8397.9    95.00  0.48     Sequence
             DRB1_0401 1197      KNLNESLIDLQELGK  LNESLIDLQ  2        0.1600
8853.1    95.00  0.45     Sequence
             DRB1_0401 1198      NLNESLIDLQELGKY  LNESLIDLQ  1        0.1578
9069.9    95.00  0.31     Sequence
             DRB1_0401 1199      LNESLIDLQELGKYE  LIDLQELGK  4        0.1463
10270.1    95.00  0.28     Sequence
             DRB1_0401 1200      NESLIDLQELGKYEQ  LIDLQELGK  3        0.1350
11600.0   100.00  0.34     Sequence
             DRB1_0401 1201      ESLIDLQELGKYEQY  IDLQELGKY  3        0.1391
11095.5    95.00  0.25     Sequence
             DRB1_0401 1202      SLIDLQELGKYEQYI  IDLQELGKY  2        0.1359
11494.4    95.00  0.25     Sequence
             DRB1_0401 1203      LIDLQELGKYEQYIK  IDLQELGKY  1        0.1250
12933.9   100.00  0.22     Sequence
             DRB1_0401 1204      IDLQELGKYEQYIKW  GKYEQYIKW  6        0.1308
12148.0   100.00  0.28     Sequence
             DRB1_0401 1205      DLQELGKYEQYIKWP  GKYEQYIKW  5        0.1317
12031.8   100.00  0.37     Sequence
             DRB1_0401 1206      LQELGKYEQYIKWPW  GKYEQYIKW  4        0.1694
7996.1    90.00  0.31     Sequence
             DRB1_0401 1207      QELGKYEQYIKWPWY  YEQYIKWPW  5        0.1958
6008.8    85.00  0.31     Sequence
             DRB1_0401 1208      ELGKYEQYIKWPWYI  YEQYIKWPW  4        0.2255
4357.6    80.00  0.32     Sequence
             DRB1_0401 1209      LGKYEQYIKWPWYIW  YIKWPWYIW  6        0.2666
2794.7    65.00  0.19     Sequence
             DRB1_0401 1210      GKYEQYIKWPWYIWL  YIKWPWYIW  5        0.2810
2390.5    60.00  0.24     Sequence
             DRB1_0401 1211      KYEQYIKWPWYIWLG  YIKWPWYIW  4        0.2654
2829.2    65.00  0.31     Sequence
             DRB1_0401 1212      YEQYIKWPWYIWLGF  YIKWPWYIW  3        0.2542
3193.7    70.00  0.35     Sequence
             DRB1_0401 1213      EQYIKWPWYIWLGFI  YIKWPWYIW  2        0.2319
4066.9    75.00  0.38     Sequence
             DRB1_0401 1214      QYIKWPWYIWLGFIA  YIKWPWYIW  1        0.2233
4462.2    80.00  0.34     Sequence
             DRB1_0401 1215      YIKWPWYIWLGFIAG  IKWPWYIWL  1        0.2147
4899.1    80.00  0.23     Sequence
             DRB1_0401 1216      IKWPWYIWLGFIAGL  YIWLGFIAG  5        0.2055
5413.6    85.00  0.29     Sequence
             DRB1_0401 1217      KWPWYIWLGFIAGLI  YIWLGFIAG  4        0.2146
4904.0    80.00  0.25     Sequence
```

```
             DRB1_0401 1218      WPWYIWLGFIAGLIA  IWLGFIAGL  4        0.2455
3510.1    70.00  0.25     Sequence
             DRB1_0401 1219      PWYIWLGFIAGLIAI  LGFIAGLIA  5        0.2750
2551.9    65.00  0.22     Sequence
             DRB1_0401 1220      WYIWLGFIAGLIAIV  FIAGLIAIV  6        0.3660
953.1    36.00  0.48     Sequence
             DRB1_0401 1221      YIWLGFIAGLIAIVM  FIAGLIAIV  5        0.3966
684.4    29.00  0.56     Sequence
             DRB1_0401 1222      IWLGFIAGLIAIVMV  FIAGLIAIV  4        0.3951
695.3    30.00  0.61     Sequence
             DRB1_0401 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3        0.3918
721.3    30.00  0.68     Sequence
             DRB1_0401 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.3910
727.4    31.00  0.69     Sequence
             DRB1_0401 1225      GFIAGLIAIVMVTIM  FIAGLIAIV  1        0.3549
1074.8    39.00  0.68     Sequence
             DRB1_0401 1226      FIAGLIAIVMVTIML  FIAGLIAIV  0        0.2550
3169.3    70.00  0.38     Sequence
             DRB1_0401 1227      IAGLIAIVMVTIMLC  IVMVTIMLC  6        0.1987
5823.6    85.00  0.36     Sequence
             DRB1_0401 1228      AGLIAIVMVTIMLCC  IVMVTIMLC  5        0.2033
5539.6    85.00  0.44     Sequence
             DRB1_0401 1229      GLIAIVMVTIMLCCM  IVMVTIMLC  4        0.2057
5399.3    85.00  0.49     Sequence
             DRB1_0401 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3        0.1937
6145.7    85.00  0.53     Sequence
             DRB1_0401 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2        0.2416
3661.1    75.00  0.48     Sequence
             DRB1_0401 1232      AIVMVTIMLCCMTSC  IVMVTIMLC  1        0.2647
2850.7    65.00  0.37     Sequence
             DRB1_0401 1233      IVMVTIMLCCMTSCC  IMLCCMTSC  5        0.2635
2890.3    65.00  0.34     Sequence
             DRB1_0401 1234      VMVTIMLCCMTSCCS  IMLCCMTSC  4        0.2910
2145.7    60.00  0.36     Sequence
             DRB1_0401 1235      MVTIMLCCMTSCCSC  LCCMTSCCS  5        0.3065
1815.1    55.00  0.31     Sequence
             DRB1_0401 1236      VTIMLCCMTSCCSCL  LCCMTSCCS  4        0.3268
1456.4    47.00  0.32     Sequence
             DRB1_0401 1237      TIMLCCMTSCCSCLK  LCCMTSCCS  3        0.3319
1379.0    45.00  0.34     Sequence
             DRB1_0401 1238      IMLCCMTSCCSCLKG  LCCMTSCCS  2        0.2645
2857.7    65.00  0.40     Sequence
             DRB1_0401 1239      MLCCMTSCCSCLKGC  LCCMTSCCS  1        0.2451
3527.6    70.00  0.40     Sequence
             DRB1_0401 1240      LCCMTSCCSCLKGCC  CMTSCCSCL  2        0.2028
5572.8    85.00  0.44     Sequence
             DRB1_0401 1241      CCMTSCCSCLKGCCS  CMTSCCSCL  1        0.1454
10368.5    95.00  0.44     Sequence
             DRB1_0401 1242      CMTSCCSCLKGCCSC  MTSCCSCLK  1        0.1022
16546.2   100.00  0.39     Sequence
             DRB1_0401 1243      MTSCCSCLKGCCSCG  CLKGCCSCG  6        0.0917
18533.3   100.00  0.28     Sequence
             DRB1_0401 1244      TSCCSCLKGCCSCGS  LKGCCSCGS  6        0.1607
8786.2    95.00  0.62     Sequence
             DRB1_0401 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5        0.1874
6582.2    90.00  0.68     Sequence
             DRB1_0401 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.1932
6179.5    85.00  0.70     Sequence
             DRB1_0401 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.2136
4957.8    80.00  0.69     Sequence
             DRB1_0401 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2        0.2248
4393.6    80.00  0.64     Sequence
             DRB1_0401 1249      CLKGCCSCGSCCKFD  LKGCCSCGS  1        0.2001
5739.5    85.00  0.59     Sequence
             DRB1_0401 1250      LKGCCSCGSCCKFDE  LKGCCSCGS  0        0.1562
9224.1    95.00  0.41     Sequence
```

```
             DRB1_0401 1251      KGCCSCGSCCKFDED  CCSCGSCCK  2        0.0965
17603.3   100.00  0.46     Sequence
             DRB1_0401 1252      GCCSCGSCCKFDEDD  CCSCGSCCK  1        0.0796
21136.6   100.00  0.39     Sequence
             DRB1_0401 1253      CCSCGSCCKFDEDDS  CGSCCKFDE  3        0.0661
24465.9   100.00  0.31     Sequence
             DRB1_0401 1254      CSCGSCCKFDEDDSE  CKFDEDDSE  6        0.0917
18541.7   100.00  0.43     Sequence
             DRB1_0401 1255      SCGSCCKFDEDDSEP  CKFDEDDSE  5        0.1148
14440.9   100.00  0.41     Sequence
             DRB1_0401 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.1997
5762.6    85.00  0.51     Sequence
             DRB1_0401 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.2390
3766.1    75.00  0.63     Sequence
             DRB1_0401 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.2644
2862.0    65.00  0.65     Sequence
             DRB1_0401 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.2759
2526.3    65.00  0.61     Sequence
             DRB1_0401 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.2801
2413.1    60.00  0.61     Sequence
             DRB1_0401 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.2721
2632.8    65.00  0.55     Sequence
             DRB1_0401 1262      FDEDDSEPVLKGVKL  DDSEPVLKG  3        0.2101
5149.3    80.00  0.46     Sequence
             DRB1_0401 1263      DEDDSEPVLKGVKLH  DDSEPVLKG  2        0.1300
12246.8   100.00  0.67     Sequence
             DRB1_0401 1264      EDDSEPVLKGVKLHY  DDSEPVLKG  1        0.1692
8011.2    90.00  0.38     Sequence
             DRB1_0401 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.2672
2776.8    65.00  0.65     Sequence
             DRB1_0405    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.3098
1749.8    55.00  0.69     Sequence
             DRB1_0405    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.2866
2250.4    60.00  0.65     Sequence
             DRB1_0405    3      PIKEMFVFLVLLPLV  IKEMFVFLV  1        0.2500
3343.3    70.00  0.44     Sequence
             DRB1_0405    4      IKEMFVFLVLLPLVS  FLVLLPLVS  6        0.2838
2318.5    65.00  0.43     Sequence
             DRB1_0405    5      KEMFVFLVLLPLVSS  LVLLPLVSS  6        0.3312
1388.7    48.00  0.47     Sequence
             DRB1_0405    6      EMFVFLVLLPLVSSQ  LVLLPLVSS  5        0.3997
662.0    32.00  0.44     Sequence
             DRB1_0405    7      MFVFLVLLPLVSSQC  LLPLVSSQC  6        0.5130
194.2    13.00  0.54     Sequence
             DRB1_0405    8      FVFLVLLPLVSSQCV  LLPLVSSQC  5        0.5519
127.6     8.00  0.60    Sequence         WB
             DRB1_0405    9      VFLVLLPLVSSQCVN  LLPLVSSQC  4        0.5681
107.0     6.50  0.62    Sequence         WB
             DRB1_0405   10      FLVLLPLVSSQCVNF  LLPLVSSQC  3        0.5687
106.3     6.50  0.58    Sequence         WB
             DRB1_0405   11      LVLLPLVSSQCVNFT  LLPLVSSQC  2        0.5600
116.8     7.50  0.56    Sequence         WB
             DRB1_0405   12      VLLPLVSSQCVNFTN  LLPLVSSQC  1        0.5285
164.3    11.00  0.42    Sequence
             DRB1_0405   13      LLPLVSSQCVNFTNR  VSSQCVNFT  4        0.4584
350.6    21.00  0.33    Sequence
             DRB1_0405   14      LPLVSSQCVNFTNRT  VSSQCVNFT  3        0.3804
815.5    36.00  0.41    Sequence
             DRB1_0405   15      PLVSSQCVNFTNRTQ  VSSQCVNFT  2        0.3610
1006.1    41.00  0.39     Sequence
             DRB1_0405   16      LVSSQCVNFTNRTQL  VSSQCVNFT  1        0.3133
1685.2    55.00  0.29     Sequence
             DRB1_0405   17      VSSQCVNFTNRTQLP  CVNFTNRTQ  4        0.2733
2597.9    65.00  0.38     Sequence
             DRB1_0405   18      SSQCVNFTNRTQLPS  CVNFTNRTQ  3        0.2534
3221.3    70.00  0.38     Sequence
```

```
             DRB1_0405   19      SQCVNFTNRTQLPSA  CVNFTNRTQ  2        0.2392
3760.0    75.00  0.34     Sequence
             DRB1_0405   20      QCVNFTNRTQLPSAY  FTNRTQLPS  4        0.2164
4808.6    80.00  0.22     Sequence
             DRB1_0405   21      CVNFTNRTQLPSAYT  RTQLPSAYT  6        0.2291
4191.0    75.00  0.41     Sequence
             DRB1_0405   22      VNFTNRTQLPSAYTN  RTQLPSAYT  5        0.2498
3352.2    70.00  0.55     Sequence
             DRB1_0405   23      NFTNRTQLPSAYTNS  RTQLPSAYT  4        0.2627
2913.0    70.00  0.57     Sequence
             DRB1_0405   24      FTNRTQLPSAYTNSF  RTQLPSAYT  3        0.2953
2048.9    60.00  0.45     Sequence
             DRB1_0405   25      TNRTQLPSAYTNSFT  LPSAYTNSF  5        0.3239
1503.4    50.00  0.38     Sequence
             DRB1_0405   26      NRTQLPSAYTNSFTR  LPSAYTNSF  4        0.3310
1392.4    48.00  0.34     Sequence
             DRB1_0405   27      RTQLPSAYTNSFTRG  LPSAYTNSF  3        0.3280
1438.5    49.00  0.32     Sequence
             DRB1_0405   28      TQLPSAYTNSFTRGV  YTNSFTRGV  6        0.4016
648.5    32.00  0.50     Sequence
             DRB1_0405   29      QLPSAYTNSFTRGVY  YTNSFTRGV  5        0.4206
527.7    28.00  0.62     Sequence
             DRB1_0405   30      LPSAYTNSFTRGVYY  YTNSFTRGV  4        0.4123
577.4    29.00  0.69     Sequence
             DRB1_0405   31      PSAYTNSFTRGVYYP  YTNSFTRGV  3        0.3993
664.9    32.00  0.74     Sequence
             DRB1_0405   32      SAYTNSFTRGVYYPD  YTNSFTRGV  2        0.4580
352.3    21.00  0.46     Sequence
             DRB1_0405   33      AYTNSFTRGVYYPDK  FTRGVYYPD  5        0.4557
361.1    21.00  0.56     Sequence
             DRB1_0405   34      YTNSFTRGVYYPDKV  FTRGVYYPD  4        0.4358
447.8    25.00  0.66     Sequence
             DRB1_0405   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.4269
493.3    26.00  0.69     Sequence
             DRB1_0405   36      NSFTRGVYYPDKVFR  FTRGVYYPD  2        0.4293
480.3    26.00  0.54     Sequence
             DRB1_0405   37      SFTRGVYYPDKVFRS  YYPDKVFRS  6        0.4993
225.2    14.00  0.60     Sequence
             DRB1_0405   38      FTRGVYYPDKVFRSS  YYPDKVFRS  5        0.5093
202.2    13.00  0.80     Sequence
             DRB1_0405   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.5140
192.2    12.00  0.84     Sequence
             DRB1_0405   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.5193
181.5    12.00  0.79     Sequence
             DRB1_0405   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.5130
194.3    13.00  0.67     Sequence
             DRB1_0405   42      VYYPDKVFRSSVLHS  YYPDKVFRS  1        0.5126
195.2    13.00  0.41     Sequence
             DRB1_0405   43      YYPDKVFRSSVLHST  FRSSVLHST  6        0.5476
133.6     8.50  0.31     Sequence         WB
             DRB1_0405   44      YPDKVFRSSVLHSTQ  FRSSVLHST  5        0.5759
98.3     6.00  0.44     Sequence         WB
             DRB1_0405   45      PDKVFRSSVLHSTQD  FRSSVLHST  4        0.5970
78.3     4.50  0.49     Sequence         WB
             DRB1_0405   46      DKVFRSSVLHSTQDL  FRSSVLHST  3        0.5774
96.8     6.00  0.48     Sequence         WB
             DRB1_0405   47      KVFRSSVLHSTQDLF  FRSSVLHST  2        0.5694
105.6     6.50  0.41     Sequence         WB
             DRB1_0405   48      VFRSSVLHSTQDLFL  LHSTQDLFL  6        0.5466
135.1     8.50  0.35     Sequence         WB
             DRB1_0405   49      FRSSVLHSTQDLFLP  LHSTQDLFL  5        0.5151
189.8    12.00  0.57     Sequence
             DRB1_0405   50      RSSVLHSTQDLFLPF  LHSTQDLFL  4        0.5005
222.4    14.00  0.70     Sequence
             DRB1_0405   51      SSVLHSTQDLFLPFF  LHSTQDLFL  3        0.4916
245.0    15.00  0.75     Sequence
```

```
             DRB1_0405   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2        0.4681
315.9    19.00  0.72     Sequence
             DRB1_0405   53      VLHSTQDLFLPFFSN  LHSTQDLFL  1        0.4041
631.2    31.00  0.51     Sequence
             DRB1_0405   54      LHSTQDLFLPFFSNV  FLPFFSNVX  7        0.4275
489.8    26.00  0.33     Sequence
             DRB1_0405   55      HSTQDLFLPFFSNVT  FLPFFSNVT  6        0.5712
103.5     6.50  0.66     Sequence         WB
             DRB1_0405   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.5932
81.5     5.00  0.67     Sequence         WB
             DRB1_0405   57      TQDLFLPFFSNVTWF  FLPFFSNVT  4        0.5950
80.0     5.00  0.67     Sequence         WB
             DRB1_0405   58      QDLFLPFFSNVTWFH  FLPFFSNVT  3        0.6302
54.7     3.00  0.49     Sequence         WB
             DRB1_0405   59      DLFLPFFSNVTWFHA  FLPFFSNVT  2        0.6454
46.4     2.00  0.37     Sequence         WB
             DRB1_0405   60      LFLPFFSNVTWFHAI  FFSNVTWFH  4        0.6185
62.0     3.50  0.36     Sequence         WB
             DRB1_0405   61      FLPFFSNVTWFHAIH  FFSNVTWFH  3        0.5871
87.2     5.50  0.45     Sequence         WB
             DRB1_0405   62      LPFFSNVTWFHAIHV  FFSNVTWFH  2        0.5656
110.0     7.00  0.46     Sequence         WB
             DRB1_0405   63      PFFSNVTWFHAIHVS  FFSNVTWFH  1        0.5381
148.0     9.50  0.35     Sequence         WB
             DRB1_0405   64      FFSNVTWFHAIHVSG  VTWFHAIHV  4        0.5015
220.0    14.00  0.25     Sequence
             DRB1_0405   65      FSNVTWFHAIHVSGT  FHAIHVSGT  6        0.4830
268.7    17.00  0.41     Sequence
             DRB1_0405   66      SNVTWFHAIHVSGTN  FHAIHVSGT  5        0.4931
240.8    15.00  0.49     Sequence
             DRB1_0405   67      NVTWFHAIHVSGTNG  FHAIHVSGT  4        0.4570
356.1    21.00  0.54     Sequence
             DRB1_0405   68      VTWFHAIHVSGTNGT  FHAIHVSGT  3        0.4443
408.7    23.00  0.55     Sequence
             DRB1_0405   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.4276
489.5    26.00  0.46     Sequence
             DRB1_0405   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1        0.3673
940.2    39.00  0.34     Sequence
             DRB1_0405   71      FHAIHVSGTNGTKRF  IHVSGTNGT  3        0.2807
2397.6    65.00  0.47     Sequence
             DRB1_0405   72      HAIHVSGTNGTKRFD  IHVSGTNGT  2        0.2607
2979.5    70.00  0.56     Sequence
             DRB1_0405   73      AIHVSGTNGTKRFDN  VSGTNGTKR  3        0.2231
4474.7    80.00  0.37     Sequence
             DRB1_0405   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.1673
8181.5    90.00  0.48     Sequence
             DRB1_0405   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.1196
13706.5   100.00  0.29     Sequence
             DRB1_0405   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.1926
6219.4    85.00  0.52     Sequence
             DRB1_0405   77      SGTNGTKRFDNPVLP  TKRFDNPVL  5        0.2399
3730.6    75.00  0.56     Sequence
             DRB1_0405   78      GTNGTKRFDNPVLPF  TKRFDNPVL  4        0.2602
2994.5    70.00  0.50     Sequence
             DRB1_0405   79      TNGTKRFDNPVLPFN  TKRFDNPVL  3        0.3149
1657.1    55.00  0.40     Sequence
             DRB1_0405   80      NGTKRFDNPVLPFND  DNPVLPFND  6        0.3437
1213.7    45.00  0.35     Sequence
             DRB1_0405   81      GTKRFDNPVLPFNDG  DNPVLPFND  5        0.3239
1503.7    50.00  0.42     Sequence
             DRB1_0405   82      TKRFDNPVLPFNDGV  DNPVLPFND  4        0.2983
1982.6    60.00  0.50     Sequence
             DRB1_0405   83      KRFDNPVLPFNDGVY  DNPVLPFND  3        0.2711
2662.4    65.00  0.57     Sequence
             DRB1_0405   84      RFDNPVLPFNDGVYF  DNPVLPFND  2        0.2474
3437.5    70.00  0.50     Sequence
```

```
             DRB1_0405   85      FDNPVLPFNDGVYFA  VLPFNDGVY  4        0.1995
5776.1    85.00  0.38     Sequence
             DRB1_0405   86      DNPVLPFNDGVYFAS  VLPFNDGVY  3        0.2015
5648.8    85.00  0.35     Sequence
             DRB1_0405   87      NPVLPFNDGVYFAST  FNDGVYFAS  5        0.2142
4926.6    80.00  0.41     Sequence
             DRB1_0405   88      PVLPFNDGVYFASTE  FNDGVYFAS  4        0.2487
3392.6    70.00  0.35     Sequence
             DRB1_0405   89      VLPFNDGVYFASTEK  FNDGVYFAS  3        0.2761
2521.5    65.00  0.29     Sequence
             DRB1_0405   90      LPFNDGVYFASTEKS  VYFASTEKS  6        0.3371
1303.6    47.00  0.50     Sequence
             DRB1_0405   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.3705
908.2    39.00  0.57     Sequence
             DRB1_0405   92      FNDGVYFASTEKSNI  VYFASTEKS  4        0.3751
863.5    38.00  0.54     Sequence
             DRB1_0405   93      NDGVYFASTEKSNII  VYFASTEKS  3        0.3861
767.0    35.00  0.47     Sequence
             DRB1_0405   94      DGVYFASTEKSNIIR  VYFASTEKS  2        0.3744
870.0    38.00  0.46     Sequence
             DRB1_0405   95      GVYFASTEKSNIIRG  FASTEKSNI  3        0.3394
1271.4    46.00  0.32     Sequence
             DRB1_0405   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.2934
2091.3    60.00  0.34     Sequence
             DRB1_0405   97      YFASTEKSNIIRGWI  ASTEKSNII  2        0.2415
3664.6    75.00  0.24     Sequence
             DRB1_0405   98      FASTEKSNIIRGWIF  SNIIRGWIF  6        0.1988
5821.6    85.00  0.37     Sequence
             DRB1_0405   99      ASTEKSNIIRGWIFG  SNIIRGWIF  5        0.1879
6549.5    85.00  0.46     Sequence
             DRB1_0405  100      STEKSNIIRGWIFGT  SNIIRGWIF  4        0.2219
4529.5    80.00  0.36     Sequence
             DRB1_0405  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5        0.2370
3847.5    75.00  0.37     Sequence
             DRB1_0405  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.2541
3197.1    70.00  0.37     Sequence
             DRB1_0405  103      KSNIIRGWIFGTTLD  GWIFGTTLD  6        0.3167
1625.1    55.00  0.29     Sequence
             DRB1_0405  104      SNIIRGWIFGTTLDS  WIFGTTLDS  6        0.3699
913.6    39.00  0.37     Sequence
             DRB1_0405  105      NIIRGWIFGTTLDSK  WIFGTTLDS  5        0.4176
545.5    28.00  0.39     Sequence
             DRB1_0405  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.4465
398.9    23.00  0.37     Sequence
             DRB1_0405  107      IRGWIFGTTLDSKTQ  FGTTLDSKT  5        0.4696
310.7    19.00  0.32     Sequence
             DRB1_0405  108      RGWIFGTTLDSKTQS  FGTTLDSKT  4        0.4635
331.8    20.00  0.37     Sequence
             DRB1_0405  109      GWIFGTTLDSKTQSL  FGTTLDSKT  3        0.4089
599.2    30.00  0.45     Sequence
             DRB1_0405  110      WIFGTTLDSKTQSLL  FGTTLDSKT  2        0.3423
1231.5    46.00  0.59     Sequence
             DRB1_0405  111      IFGTTLDSKTQSLLI  FGTTLDSKT  1        0.2942
2072.5    60.00  0.45     Sequence
             DRB1_0405  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5        0.2254
4361.7    80.00  0.41     Sequence
             DRB1_0405  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4        0.2177
4741.1    80.00  0.44     Sequence
             DRB1_0405  114      TTLDSKTQSLLIVNN  DSKTQSLLI  3        0.2421
3641.8    75.00  0.42     Sequence
             DRB1_0405  115      TLDSKTQSLLIVNNA  TQSLLIVNN  5        0.3095
1757.3    55.00  0.26     Sequence
             DRB1_0405  116      LDSKTQSLLIVNNAT  LLIVNNATX  7        0.4459
401.5    23.00  0.35     Sequence
             DRB1_0405  117      DSKTQSLLIVNNATN  LLIVNNATN  6        0.5924
82.3     5.00  0.75     Sequence         WB
```

```
             DRB1_0405  118      SKTQSLLIVNNATNV  LLIVNNATN  5        0.6362
51.2     2.50  0.81     Sequence        WB
             DRB1_0405  119      KTQSLLIVNNATNVV  LLIVNNATN  4        0.6496
44.3     1.90  0.80     Sequence        SB
             DRB1_0405  120      TQSLLIVNNATNVVI  LLIVNNATN  3        0.6500
44.1     1.90  0.75     Sequence        SB
             DRB1_0405  121      QSLLIVNNATNVVIK  LLIVNNATN  2        0.6389
49.7     2.50  0.69     Sequence        WB
             DRB1_0405  122      SLLIVNNATNVVIKV  LLIVNNATN  1        0.5660
109.5     7.00  0.54     Sequence        WB
             DRB1_0405  123      LLIVNNATNVVIKVC  VNNATNVVI  3        0.4540
367.8    21.00  0.60     Sequence
             DRB1_0405  124      LIVNNATNVVIKVCE  VNNATNVVI  2        0.3916
722.3    34.00  0.73     Sequence
             DRB1_0405  125      IVNNATNVVIKVCEF  VNNATNVVI  1        0.2862
2259.4    60.00  0.50     Sequence
             DRB1_0405  126      VNNATNVVIKVCEFQ  NVVIKVCEF  5        0.2455
3510.3    75.00  0.23     Sequence
             DRB1_0405  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.2562
3126.0    70.00  0.39     Sequence
             DRB1_0405  128      NATNVVIKVCEFQFC  VIKVCEFQF  5        0.2725
2620.5    65.00  0.41     Sequence
             DRB1_0405  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.2783
2462.4    65.00  0.41     Sequence
             DRB1_0405  130      TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.2706
2676.8    65.00  0.46     Sequence
             DRB1_0405  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.2617
2944.7    70.00  0.44     Sequence
             DRB1_0405  132      VVIKVCEFQFCNYPF  EFQFCNYPF  6        0.2851
2288.1    60.00  0.25     Sequence
             DRB1_0405  133      VIKVCEFQFCNYPFL  FQFCNYPFL  6        0.3409
1250.9    46.00  0.44     Sequence
             DRB1_0405  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.3634
980.8    40.00  0.40     Sequence
             DRB1_0405  135      KVCEFQFCNYPFLGV  FCNYPFLGV  6        0.4153
559.2    29.00  0.37     Sequence
             DRB1_0405  136      VCEFQFCNYPFLGVY  FCNYPFLGV  5        0.4342
455.8    25.00  0.44     Sequence
             DRB1_0405  137      CEFQFCNYPFLGVYY  FCNYPFLGV  4        0.4467
397.9    23.00  0.44     Sequence
             DRB1_0405  138      EFQFCNYPFLGVYYH  FCNYPFLGV  3        0.4449
405.8    23.00  0.44     Sequence
             DRB1_0405  139      FQFCNYPFLGVYYHK  FCNYPFLGV  2        0.4625
335.6    20.00  0.33     Sequence
             DRB1_0405  140      QFCNYPFLGVYYHKN  FLGVYYHKN  6        0.5157
188.7    12.00  0.46     Sequence
             DRB1_0405  141      FCNYPFLGVYYHKNN  FLGVYYHKN  5        0.5275
166.0    11.00  0.61     Sequence
             DRB1_0405  142      CNYPFLGVYYHKNNK  FLGVYYHKN  4        0.5246
171.4    11.00  0.68     Sequence
             DRB1_0405  143      NYPFLGVYYHKNNKS  FLGVYYHKN  3        0.5088
203.2    13.00  0.71     Sequence
             DRB1_0405  144      YPFLGVYYHKNNKSW  FLGVYYHKN  2        0.4758
290.6    18.00  0.64     Sequence
             DRB1_0405  145      PFLGVYYHKNNKSWM  FLGVYYHKN  1        0.4091
597.8    30.00  0.44     Sequence
             DRB1_0405  146      FLGVYYHKNNKSWME  VYYHKNNKS  3        0.3376
1295.7    47.00  0.38     Sequence
             DRB1_0405  147      LGVYYHKNNKSWMES  VYYHKNNKS  2        0.3168
1622.7    55.00  0.40     Sequence
             DRB1_0405  148      GVYYHKNNKSWMESE  HKNNKSWME  4        0.3004
1938.1    60.00  0.38     Sequence
             DRB1_0405  149      VYYHKNNKSWMESEF  HKNNKSWME  3        0.2823
2357.3    65.00  0.43     Sequence
             DRB1_0405  150      YYHKNNKSWMESEFR  HKNNKSWME  2        0.2758
2530.1    65.00  0.41     Sequence
```

```
             DRB1_0405  151      YHKNNKSWMESEFRV  KSWMESEFR  5        0.2500
3342.0    70.00  0.40     Sequence
             DRB1_0405  152      HKNNKSWMESEFRVY  KSWMESEFR  4        0.2350
3933.1    75.00  0.42     Sequence
             DRB1_0405  153      KNNKSWMESEFRVYS  KSWMESEFR  3        0.2387
3780.4    75.00  0.40     Sequence
             DRB1_0405  154      NNKSWMESEFRVYSS  KSWMESEFR  2        0.2308
4117.2    75.00  0.32     Sequence
             DRB1_0405  155      NKSWMESEFRVYSSA  MESEFRVYS  4        0.2431
3603.9    75.00  0.23     Sequence
             DRB1_0405  156      KSWMESEFRVYSSAN  FRVYSSANX  7        0.3687
925.6    39.00  0.43     Sequence
             DRB1_0405  157      SWMESEFRVYSSANN  FRVYSSANN  6        0.5300
161.6    11.00  0.80     Sequence
             DRB1_0405  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.5732
101.3     6.50  0.77     Sequence         WB
             DRB1_0405  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.5937
81.2     5.00  0.71     Sequence         WB
             DRB1_0405  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.6075
69.9     4.00  0.62     Sequence         WB
             DRB1_0405  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.6060
71.0     4.00  0.57     Sequence         WB
             DRB1_0405  162      EFRVYSSANNCTFEY  YSSANNCTF  4        0.5497
130.7     8.50  0.28     Sequence         WB
             DRB1_0405  163      FRVYSSANNCTFEYV  YSSANNCTF  3        0.4567
357.1    21.00  0.51     Sequence
             DRB1_0405  164      RVYSSANNCTFEYVS  YSSANNCTF  2        0.3853
773.1    35.00  0.69     Sequence
             DRB1_0405  165      VYSSANNCTFEYVSQ  YSSANNCTF  1        0.2794
2431.7    65.00  0.49     Sequence
             DRB1_0405  166      YSSANNCTFEYVSQP  NCTFEYVSQ  5        0.2337
3986.8    75.00  0.22     Sequence
             DRB1_0405  167      SSANNCTFEYVSQPF  FEYVSQPFX  7        0.2654
2829.9    70.00  0.26     Sequence
             DRB1_0405  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.3861
767.0    35.00  0.60     Sequence
             DRB1_0405  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.4592
347.6    21.00  0.55     Sequence
             DRB1_0405  170      NNCTFEYVSQPFLMD  YVSQPFLMD  6        0.5765
97.7     6.00  0.52     Sequence         WB
             DRB1_0405  171      NCTFEYVSQPFLMDL  YVSQPFLMD  5        0.6008
75.1     4.50  0.59     Sequence         WB
             DRB1_0405  172      CTFEYVSQPFLMDLE  YVSQPFLMD  4        0.6135
65.5     3.50  0.65     Sequence         WB
             DRB1_0405  173      TFEYVSQPFLMDLEG  YVSQPFLMD  3        0.5895
84.9     5.00  0.70     Sequence         WB
             DRB1_0405  174      FEYVSQPFLMDLEGK  YVSQPFLMD  2        0.5388
147.0     9.50  0.80     Sequence         WB
             DRB1_0405  175      EYVSQPFLMDLEGKQ  YVSQPFLMD  1        0.4523
374.6    22.00  0.62     Sequence
             DRB1_0405  176      YVSQPFLMDLEGKQG  FLMDLEGKQ  5        0.3303
1403.2    49.00  0.25     Sequence
             DRB1_0405  177      VSQPFLMDLEGKQGN  FLMDLEGKQ  4        0.2717
2643.8    65.00  0.44     Sequence
             DRB1_0405  178      SQPFLMDLEGKQGNF  FLMDLEGKQ  3        0.2652
2837.5    70.00  0.49     Sequence
             DRB1_0405  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2        0.2426
3624.4    75.00  0.49     Sequence
             DRB1_0405  180      PFLMDLEGKQGNFKN  LMDLEGKQG  2        0.2110
5100.1    80.00  0.40     Sequence
             DRB1_0405  181      FLMDLEGKQGNFKNL  LMDLEGKQG  1        0.1520
9655.9    95.00  0.30     Sequence
             DRB1_0405  182      LMDLEGKQGNFKNLS  QGNFKNLSX  7        0.1288
12412.4   100.00  0.28     Sequence
             DRB1_0405  183      MDLEGKQGNFKNLSE  QGNFKNLSE  6        0.2502
3336.9    70.00  0.74     Sequence
```

```
            DRB1_0405  184      DLEGKQGNFKNLSEF  QGNFKNLSE  5        0.2935
2087.5    60.00  0.74     Sequence
            DRB1_0405  185      LEGKQGNFKNLSEFV  QGNFKNLSE  4        0.3357
1323.5    47.00  0.59     Sequence
            DRB1_0405  186      EGKQGNFKNLSEFVF  QGNFKNLSE  3        0.3535
1090.7    43.00  0.50     Sequence
            DRB1_0405  187      GKQGNFKNLSEFVFK  QGNFKNLSE  2        0.3529
1097.7    43.00  0.44     Sequence
            DRB1_0405  188      KQGNFKNLSEFVFKN  FKNLSEFVF  4        0.3437
1213.6    45.00  0.32     Sequence
            DRB1_0405  189      QGNFKNLSEFVFKNI  FKNLSEFVF  3        0.3126
1698.2    55.00  0.38     Sequence
            DRB1_0405  190      GNFKNLSEFVFKNID  NLSEFVFKN  4        0.3502
1131.2    44.00  0.28     Sequence
            DRB1_0405  191      NFKNLSEFVFKNIDG  EFVFKNIDG  6        0.3635
979.4    40.00  0.44     Sequence
            DRB1_0405  192      FKNLSEFVFKNIDGY  EFVFKNIDG  5        0.3869
760.2    35.00  0.50     Sequence
            DRB1_0405  193      KNLSEFVFKNIDGYF  EFVFKNIDG  4        0.4449
405.7    23.00  0.41     Sequence
            DRB1_0405  194      NLSEFVFKNIDGYFK  FKNIDGYFK  6        0.4820
271.8    17.00  0.47     Sequence
            DRB1_0405  195      LSEFVFKNIDGYFKI  FKNIDGYFK  5        0.4927
242.0    15.00  0.56     Sequence
            DRB1_0405  196      SEFVFKNIDGYFKIY  FKNIDGYFK  4        0.4816
272.7    17.00  0.63     Sequence
            DRB1_0405  197      EFVFKNIDGYFKIYS  FKNIDGYFK  3        0.4549
364.3    21.00  0.69     Sequence
            DRB1_0405  198      FVFKNIDGYFKIYSK  FKNIDGYFK  2        0.4367
443.3    25.00  0.69     Sequence
            DRB1_0405  199      VFKNIDGYFKIYSKH  FKNIDGYFK  1        0.3646
967.4    40.00  0.48     Sequence
            DRB1_0405  200      FKNIDGYFKIYSKHT  YFKIYSKHT  6        0.4049
625.5    31.00  0.61     Sequence
            DRB1_0405  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.4470
396.9    23.00  0.69     Sequence
            DRB1_0405  202      NIDGYFKIYSKHTPI  YFKIYSKHT  4        0.4539
368.1    21.00  0.69     Sequence
            DRB1_0405  203      IDGYFKIYSKHTPIN  YFKIYSKHT  3        0.4625
335.3    20.00  0.65     Sequence
            DRB1_0405  204      DGYFKIYSKHTPINL  YFKIYSKHT  2        0.4721
302.2    18.00  0.54     Sequence
            DRB1_0405  205      GYFKIYSKHTPINLV  YFKIYSKHT  1        0.4620
337.5    20.00  0.34     Sequence
            DRB1_0405  206      YFKIYSKHTPINLVR  SKHTPINLV  5        0.4279
487.8    26.00  0.31     Sequence
            DRB1_0405  207      FKIYSKHTPINLVRD  SKHTPINLV  4        0.4211
524.8    28.00  0.33     Sequence
            DRB1_0405  208      KIYSKHTPINLVRDL  SKHTPINLV  3        0.4223
518.5    27.00  0.30     Sequence
            DRB1_0405  209      IYSKHTPINLVRDLP  HTPINLVRD  4        0.4263
496.2    27.00  0.28     Sequence
            DRB1_0405  210      YSKHTPINLVRDLPQ  INLVRDLPQ  6        0.4914
245.5    15.00  0.64     Sequence
            DRB1_0405  211      SKHTPINLVRDLPQG  INLVRDLPQ  5        0.4979
228.7    15.00  0.70     Sequence
            DRB1_0405  212      KHTPINLVRDLPQGF  INLVRDLPQ  4        0.4988
226.4    14.00  0.68     Sequence
            DRB1_0405  213      HTPINLVRDLPQGFS  INLVRDLPQ  3        0.4885
253.2    16.00  0.68     Sequence
            DRB1_0405  214      TPINLVRDLPQGFSA  INLVRDLPQ  2        0.4672
318.9    19.00  0.65     Sequence
            DRB1_0405  215      PINLVRDLPQGFSAL  INLVRDLPQ  1        0.3980
674.0    33.00  0.51     Sequence
            DRB1_0405  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.3480
1158.5    44.00  0.24     Sequence
```

```
             DRB1_0405  217      NLVRDLPQGFSALEP  PQGFSALEP  6        0.3234
1511.1    50.00  0.33     Sequence
             DRB1_0405  218      LVRDLPQGFSALEPL  PQGFSALEP  5        0.3420
1235.5    46.00  0.37     Sequence
             DRB1_0405  219      VRDLPQGFSALEPLV  PQGFSALEP  4        0.4025
642.0    32.00  0.28     Sequence
             DRB1_0405  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.5525
126.7     8.00  0.72     Sequence         WB
             DRB1_0405  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.5896
84.8     5.00  0.77     Sequence         WB
             DRB1_0405  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.6009
75.1     4.50  0.75     Sequence         WB
             DRB1_0405  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.6117
66.8     3.50  0.70     Sequence         WB
             DRB1_0405  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.5836
90.5     5.50  0.67     Sequence         WB
             DRB1_0405  225      GFSALEPLVDLPIGI  FSALEPLVD  1        0.5080
205.0    13.00  0.47     Sequence
             DRB1_0405  226      FSALEPLVDLPIGIN  LEPLVDLPI  3        0.4379
437.6    24.00  0.52     Sequence
             DRB1_0405  227      SALEPLVDLPIGINI  LEPLVDLPI  2        0.3505
1126.6    44.00  0.67     Sequence
             DRB1_0405  228      ALEPLVDLPIGINIT  LEPLVDLPI  1        0.2848
2293.5    60.00  0.45     Sequence
             DRB1_0405  229      LEPLVDLPIGINITR  LVDLPIGIN  3        0.2377
3819.0    75.00  0.31     Sequence
             DRB1_0405  230      EPLVDLPIGINITRF  PIGINITRF  6        0.2403
3713.2    75.00  0.28     Sequence
             DRB1_0405  231      PLVDLPIGINITRFQ  PIGINITRF  5        0.2612
2962.9    70.00  0.35     Sequence
             DRB1_0405  232      LVDLPIGINITRFQT  PIGINITRF  4        0.2663
2803.3    65.00  0.35     Sequence
             DRB1_0405  233      VDLPIGINITRFQTL  PIGINITRF  3        0.2972
2006.4    60.00  0.29     Sequence
             DRB1_0405  234      DLPIGINITRFQTLL  ITRFQTLLX  7        0.3824
798.3    36.00  0.41     Sequence
             DRB1_0405  235      LPIGINITRFQTLLA  ITRFQTLLA  6        0.5110
198.4    13.00  0.82     Sequence
             DRB1_0405  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.5504
129.5     8.50  0.81     Sequence         WB
             DRB1_0405  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.6405
48.9     2.50  0.56     Sequence         WB
             DRB1_0405  238      GINITRFQTLLALHR  FQTLLALHR  6        0.7068
23.9     0.60  0.56     Sequence         SB
             DRB1_0405  239      INITRFQTLLALHRS  FQTLLALHR  5        0.7179
21.2     0.50  0.62     Sequence         SB
             DRB1_0405  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.7120
22.5     0.50  0.68     Sequence         SB
             DRB1_0405  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.6966
26.6     0.80  0.73     Sequence         SB
             DRB1_0405  242      TRFQTLLALHRSYLT  FQTLLALHR  2        0.6715
34.9     1.30  0.72     Sequence         SB
             DRB1_0405  243      RFQTLLALHRSYLTP  FQTLLALHR  1        0.5721
102.5     6.50  0.51     Sequence         WB
             DRB1_0405  244      FQTLLALHRSYLTPG  LALHRSYLT  4        0.4034
635.9    31.00  0.34     Sequence
             DRB1_0405  245      QTLLALHRSYLTPGD  LALHRSYLT  3        0.4112
584.5    30.00  0.32     Sequence
             DRB1_0405  246      TLLALHRSYLTPGDS  HRSYLTPGD  5        0.4103
590.3    30.00  0.47     Sequence
             DRB1_0405  247      LLALHRSYLTPGDSS  HRSYLTPGD  4        0.3845
780.0    36.00  0.61     Sequence
             DRB1_0405  248      LALHRSYLTPGDSSS  HRSYLTPGD  3        0.3690
922.4    39.00  0.63     Sequence
             DRB1_0405  249      ALHRSYLTPGDSSSG  HRSYLTPGD  2        0.3451
1195.4    45.00  0.62     Sequence
```

```
             DRB1_0405  250      LHRSYLTPGDSSSGW  HRSYLTPGD  1        0.3022
1901.7    60.00  0.46     Sequence
             DRB1_0405  251      HRSYLTPGDSSSGWT  YLTPGDSSS  3        0.2352
3922.7    75.00  0.30     Sequence
             DRB1_0405  252      RSYLTPGDSSSGWTA  YLTPGDSSS  2        0.1708
7874.5    90.00  0.40     Sequence
             DRB1_0405  253      SYLTPGDSSSGWTAG  LTPGDSSSG  2        0.1265
12721.3   100.00  0.47     Sequence
             DRB1_0405  254      YLTPGDSSSGWTAGA  LTPGDSSSG  1        0.0776
21592.4   100.00  0.34     Sequence
             DRB1_0405  255      LTPGDSSSGWTAGAA  SSSGWTAGA  5        0.0534
28055.4   100.00  0.26     Sequence
             DRB1_0405  256      TPGDSSSGWTAGAAA  SSSGWTAGA  4        0.0567
27063.2   100.00  0.30     Sequence
             DRB1_0405  257      PGDSSSGWTAGAAAY  WTAGAAAYX  7        0.0852
19889.0   100.00  0.28     Sequence
             DRB1_0405  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.1638
8495.5    90.00  0.63     Sequence
             DRB1_0405  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.1971
5925.3    85.00  0.65     Sequence
             DRB1_0405  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.1944
6099.5    85.00  0.64     Sequence
             DRB1_0405  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.1974
5906.0    85.00  0.62     Sequence
             DRB1_0405  262      SGWTAGAAAYYVGYL  WTAGAAAYY  2        0.1964
5974.6    85.00  0.47     Sequence
             DRB1_0405  263      GWTAGAAAYYVGYLQ  AAYYVGYLQ  6        0.1911
6325.4    85.00  0.24     Sequence
             DRB1_0405  264      WTAGAAAYYVGYLQP  AAYYVGYLQ  5        0.1972
5920.3    85.00  0.26     Sequence
             DRB1_0405  265      TAGAAAYYVGYLQPR  YVGYLQPRX  7        0.3454
1191.3    45.00  0.34     Sequence
             DRB1_0405  266      AGAAAYYVGYLQPRT  YVGYLQPRT  6        0.5231
174.2    11.00  0.64     Sequence
             DRB1_0405  267      GAAAYYVGYLQPRTF  YVGYLQPRT  5        0.5785
95.6     6.00  0.67     Sequence         WB
             DRB1_0405  268      AAAYYVGYLQPRTFL  YVGYLQPRT  4        0.5971
78.2     4.50  0.67     Sequence         WB
             DRB1_0405  269      AAYYVGYLQPRTFLL  YVGYLQPRT  3        0.6274
56.3     3.00  0.51     Sequence         WB
             DRB1_0405  270      AYYVGYLQPRTFLLK  YVGYLQPRT  2        0.6227
59.3     3.00  0.47     Sequence         WB
             DRB1_0405  271      YYVGYLQPRTFLLKY  YLQPRTFLL  4        0.5851
89.0     5.50  0.46     Sequence         WB
             DRB1_0405  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.4908
246.9    16.00  0.69     Sequence
             DRB1_0405  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.4362
446.2    25.00  0.79     Sequence
             DRB1_0405  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.4115
582.9    30.00  0.47     Sequence
             DRB1_0405  275      YLQPRTFLLKYNENG  FLLKYNENG  6        0.3852
774.4    35.00  0.35     Sequence
             DRB1_0405  276      LQPRTFLLKYNENGT  FLLKYNENG  5        0.3651
962.7    40.00  0.46     Sequence
             DRB1_0405  277      QPRTFLLKYNENGTI  FLLKYNENG  4        0.3923
717.4    34.00  0.40     Sequence
             DRB1_0405  278      PRTFLLKYNENGTIT  FLLKYNENG  3        0.3873
756.5    35.00  0.38     Sequence
             DRB1_0405  279      RTFLLKYNENGTITD  FLLKYNENG  2        0.3903
732.9    34.00  0.29     Sequence
             DRB1_0405  280      TFLLKYNENGTITDA  YNENGTITD  5        0.3751
863.8    38.00  0.45     Sequence
             DRB1_0405  281      FLLKYNENGTITDAV  YNENGTITD  4        0.3558
1064.2    42.00  0.56     Sequence
             DRB1_0405  282      LLKYNENGTITDAVD  YNENGTITD  3        0.3295
1415.2    49.00  0.66     Sequence
```

```
             DRB1_0405  283      LKYNENGTITDAVDC  YNENGTITD  2        0.3074
1796.8    55.00  0.65     Sequence
             DRB1_0405  284      KYNENGTITDAVDCA  YNENGTITD  1        0.2607
2978.2    70.00  0.48     Sequence
             DRB1_0405  285      YNENGTITDAVDCAL  NGTITDAVD  3        0.1963
5975.5    85.00  0.31     Sequence
             DRB1_0405  286      NENGTITDAVDCALD  NGTITDAVD  2        0.1914
6303.8    85.00  0.25     Sequence
             DRB1_0405  287      ENGTITDAVDCALDP  ITDAVDCAL  4        0.1951
6059.2    85.00  0.29     Sequence
             DRB1_0405  288      NGTITDAVDCALDPL  TDAVDCALD  4        0.2147
4899.9    80.00  0.34     Sequence
             DRB1_0405  289      GTITDAVDCALDPLS  VDCALDPLS  6        0.2757
2531.8    65.00  0.44     Sequence
             DRB1_0405  290      TITDAVDCALDPLSE  VDCALDPLS  5        0.3273
1448.1    49.00  0.49     Sequence
             DRB1_0405  291      ITDAVDCALDPLSET  VDCALDPLS  4        0.3389
1278.4    46.00  0.52     Sequence
             DRB1_0405  292      TDAVDCALDPLSETK  VDCALDPLS  3        0.3365
1310.9    47.00  0.51     Sequence
             DRB1_0405  293      DAVDCALDPLSETKC  VDCALDPLS  2        0.3214
1544.3    55.00  0.47     Sequence
             DRB1_0405  294      AVDCALDPLSETKCT  VDCALDPLS  1        0.2798
2420.9    65.00  0.38     Sequence
             DRB1_0405  295      VDCALDPLSETKCTL  DCALDPLSE  1        0.1974
5910.2    85.00  0.30     Sequence
             DRB1_0405  296      DCALDPLSETKCTLK  LDPLSETKC  3        0.1434
10594.9    95.00  0.31     Sequence
             DRB1_0405  297      CALDPLSETKCTLKS  LSETKCTLK  5        0.1186
13856.5   100.00  0.39     Sequence
             DRB1_0405  298      ALDPLSETKCTLKSF  LSETKCTLK  4        0.1214
13448.8   100.00  0.39     Sequence
             DRB1_0405  299      LDPLSETKCTLKSFT  LSETKCTLK  3        0.1411
10865.2    95.00  0.33     Sequence
             DRB1_0405  300      DPLSETKCTLKSFTV  KCTLKSFTV  6        0.2006
5704.0    85.00  0.56     Sequence
             DRB1_0405  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.2616
2950.1    70.00  0.63     Sequence
             DRB1_0405  302      LSETKCTLKSFTVEK  KCTLKSFTV  4        0.3128
1695.0    55.00  0.49     Sequence
             DRB1_0405  303      SETKCTLKSFTVEKG  LKSFTVEKG  6        0.3548
1076.0    42.00  0.48     Sequence
             DRB1_0405  304      ETKCTLKSFTVEKGI  LKSFTVEKG  5        0.3706
906.5    39.00  0.55     Sequence
             DRB1_0405  305      TKCTLKSFTVEKGIY  LKSFTVEKG  4        0.4023
643.9    32.00  0.46     Sequence
             DRB1_0405  306      KCTLKSFTVEKGIYQ  FTVEKGIYQ  6        0.4846
264.2    16.00  0.57     Sequence
             DRB1_0405  307      CTLKSFTVEKGIYQT  FTVEKGIYQ  5        0.5026
217.5    14.00  0.73     Sequence
             DRB1_0405  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.4968
231.5    15.00  0.85     Sequence
             DRB1_0405  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.4896
250.3    16.00  0.88     Sequence
             DRB1_0405  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.4720
302.7    18.00  0.86     Sequence
             DRB1_0405  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.3934
708.3    34.00  0.52     Sequence
             DRB1_0405  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.4273
490.8    26.00  0.67     Sequence
             DRB1_0405  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.4956
234.5    15.00  0.76     Sequence
             DRB1_0405  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.5214
177.4    12.00  0.75     Sequence
             DRB1_0405  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.5225
175.2    11.00  0.74     Sequence
```

```
             DRB1_0405  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.5281
165.1    11.00  0.69     Sequence
             DRB1_0405  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.5090
202.8    13.00  0.50     Sequence
             DRB1_0405  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.5834
90.7     5.50  0.77     Sequence         WB
             DRB1_0405  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.6190
61.7     3.50  0.81     Sequence         WB
             DRB1_0405  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.6359
51.4     2.50  0.79     Sequence         WB
             DRB1_0405  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.6354
51.7     2.50  0.80     Sequence         WB
             DRB1_0405  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.6086
69.0     4.00  0.77     Sequence         WB
             DRB1_0405  323      NFRVQPTESIVRFPN  FRVQPTESI  1        0.4960
233.5    15.00  0.56     Sequence
             DRB1_0405  324      FRVQPTESIVRFPNI  VQPTESIVR  2        0.3895
739.0    34.00  0.50     Sequence
             DRB1_0405  325      RVQPTESIVRFPNIT  IVRFPNITX  7        0.4281
486.7    26.00  0.49     Sequence
             DRB1_0405  326      VQPTESIVRFPNITN  IVRFPNITN  6        0.6229
59.1     3.00  0.93     Sequence         WB
             DRB1_0405  327      QPTESIVRFPNITNL  IVRFPNITN  5        0.6713
35.0     1.30  0.90     Sequence         SB
             DRB1_0405  328      PTESIVRFPNITNLC  IVRFPNITN  4        0.7078
23.6     0.60  0.81     Sequence         SB
             DRB1_0405  329      TESIVRFPNITNLCP  IVRFPNITN  3        0.7191
20.9     0.50  0.75     Sequence         SB
             DRB1_0405  330      ESIVRFPNITNLCPF  IVRFPNITN  2        0.7105
22.9     0.60  0.71     Sequence         SB
             DRB1_0405  331      SIVRFPNITNLCPFG  IVRFPNITN  1        0.6661
37.1     1.40  0.56     Sequence         SB
             DRB1_0405  332      IVRFPNITNLCPFGE  FPNITNLCP  3        0.5922
82.5     5.00  0.47     Sequence         WB
             DRB1_0405  333      VRFPNITNLCPFGEV  FPNITNLCP  2        0.5301
161.5    11.00  0.54     Sequence
             DRB1_0405  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.4521
375.6    22.00  0.51     Sequence
             DRB1_0405  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.3682
930.5    39.00  0.66     Sequence
             DRB1_0405  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.3496
1138.0    44.00  0.73     Sequence
             DRB1_0405  337      NITNLCPFGEVFNAT  ITNLCPFGE  1        0.3000
1946.3    60.00  0.43     Sequence
             DRB1_0405  338      ITNLCPFGEVFNATR  FGEVFNATR  6        0.3718
895.3    38.00  0.57     Sequence
             DRB1_0405  339      TNLCPFGEVFNATRF  FGEVFNATR  5        0.4141
566.4    29.00  0.58     Sequence
             DRB1_0405  340      NLCPFGEVFNATRFA  FGEVFNATR  4        0.4269
493.0    26.00  0.56     Sequence
             DRB1_0405  341      LCPFGEVFNATRFAS  FGEVFNATR  3        0.4306
473.8    26.00  0.55     Sequence
             DRB1_0405  342      CPFGEVFNATRFASV  FGEVFNATR  2        0.4296
479.1    26.00  0.41     Sequence
             DRB1_0405  343      PFGEVFNATRFASVY  FNATRFASV  5        0.4127
574.9    29.00  0.31     Sequence
             DRB1_0405  344      FGEVFNATRFASVYA  FNATRFASV  4        0.3815
806.3    36.00  0.35     Sequence
             DRB1_0405  345      GEVFNATRFASVYAW  FNATRFASV  3        0.3795
823.2    37.00  0.35     Sequence
             DRB1_0405  346      EVFNATRFASVYAWN  ATRFASVYA  4        0.4545
365.7    21.00  0.24     Sequence
             DRB1_0405  347      VFNATRFASVYAWNR  FASVYAWNR  6        0.5448
137.7     9.00  0.62     Sequence         WB
             DRB1_0405  348      FNATRFASVYAWNRK  FASVYAWNR  5        0.5852
88.9     5.50  0.73     Sequence         WB
```

```
             DRB1_0405  349      NATRFASVYAWNRKR  FASVYAWNR  4        0.5997
76.0     4.50  0.75     Sequence         WB
             DRB1_0405  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.5843
89.9     5.50  0.79     Sequence         WB
             DRB1_0405  351      TRFASVYAWNRKRIS  FASVYAWNR  2        0.5451
137.3     9.00  0.83     Sequence         WB
             DRB1_0405  352      RFASVYAWNRKRISN  FASVYAWNR  1        0.4036
634.4    31.00  0.60     Sequence
             DRB1_0405  353      FASVYAWNRKRISNC  WNRKRISNC  6        0.2451
3527.2    75.00  0.26     Sequence
             DRB1_0405  354      ASVYAWNRKRISNCV  WNRKRISNC  5        0.2172
4767.5    80.00  0.33     Sequence
             DRB1_0405  355      SVYAWNRKRISNCVA  RKRISNCVA  6        0.2521
3268.2    70.00  0.34     Sequence
             DRB1_0405  356      VYAWNRKRISNCVAD  RKRISNCVA  5        0.3045
1854.7    55.00  0.38     Sequence
             DRB1_0405  357      YAWNRKRISNCVADY  RKRISNCVA  4        0.3408
1251.8    46.00  0.31     Sequence
             DRB1_0405  358      AWNRKRISNCVADYS  ISNCVADYS  6        0.3875
755.5    35.00  0.29     Sequence
             DRB1_0405  359      WNRKRISNCVADYSV  ISNCVADYS  5        0.4004
657.1    32.00  0.38     Sequence
             DRB1_0405  360      NRKRISNCVADYSVL  ISNCVADYS  4        0.4014
650.0    32.00  0.40     Sequence
             DRB1_0405  361      RKRISNCVADYSVLY  ISNCVADYS  3        0.3973
679.2    33.00  0.38     Sequence
             DRB1_0405  362      KRISNCVADYSVLYN  ISNCVADYS  2        0.3745
869.6    38.00  0.35     Sequence
             DRB1_0405  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.3390
1277.0    46.00  0.40     Sequence
             DRB1_0405  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.3710
902.7    39.00  0.32     Sequence
             DRB1_0405  365      SNCVADYSVLYNSAS  YSVLYNSAS  6        0.5834
90.7     5.50  0.77     Sequence         WB
             DRB1_0405  366      NCVADYSVLYNSASF  YSVLYNSAS  5        0.6141
65.0     3.50  0.80     Sequence         WB
             DRB1_0405  367      CVADYSVLYNSASFS  YSVLYNSAS  4        0.6344
52.2     2.50  0.75     Sequence         WB
             DRB1_0405  368      VADYSVLYNSASFST  YSVLYNSAS  3        0.6376
50.4     2.50  0.71     Sequence         WB
             DRB1_0405  369      ADYSVLYNSASFSTF  YSVLYNSAS  2        0.6272
56.5     3.00  0.63     Sequence         WB
             DRB1_0405  370      DYSVLYNSASFSTFK  YSVLYNSAS  1        0.5884
85.9     5.00  0.43     Sequence         WB
             DRB1_0405  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.5179
184.3    12.00  0.25     Sequence
             DRB1_0405  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.4331
461.1    25.00  0.35     Sequence
             DRB1_0405  373      VLYNSASFSTFKCYG  YNSASFSTF  2        0.3861
767.0    35.00  0.26     Sequence
             DRB1_0405  374      LYNSASFSTFKCYGV  FSTFKCYGV  6        0.3899
735.8    34.00  0.47     Sequence
             DRB1_0405  375      YNSASFSTFKCYGVS  FSTFKCYGV  5        0.3842
782.4    36.00  0.66     Sequence
             DRB1_0405  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.4027
640.5    32.00  0.59     Sequence
             DRB1_0405  377      SASFSTFKCYGVSPT  FSTFKCYGV  3        0.4761
289.5    18.00  0.44     Sequence
             DRB1_0405  378      ASFSTFKCYGVSPTK  FKCYGVSPT  5        0.4934
240.2    15.00  0.48     Sequence
             DRB1_0405  379      SFSTFKCYGVSPTKL  FKCYGVSPT  4        0.4770
286.7    18.00  0.54     Sequence
             DRB1_0405  380      FSTFKCYGVSPTKLN  FKCYGVSPT  3        0.5121
196.1    13.00  0.38     Sequence
             DRB1_0405  381      STFKCYGVSPTKLND  YGVSPTKLN  5        0.5323
157.6    10.00  0.47     Sequence
```

```
             DRB1_0405  382      TFKCYGVSPTKLNDL  YGVSPTKLN  4        0.5085
204.0    13.00  0.55     Sequence
             DRB1_0405  383      FKCYGVSPTKLNDLC  YGVSPTKLN  3        0.4641
329.6    20.00  0.67     Sequence
             DRB1_0405  384      KCYGVSPTKLNDLCF  YGVSPTKLN  2        0.4213
524.0    28.00  0.71     Sequence
             DRB1_0405  385      CYGVSPTKLNDLCFT  YGVSPTKLN  1        0.3202
1564.2    55.00  0.61     Sequence
             DRB1_0405  386      YGVSPTKLNDLCFTN  YGVSPTKLN  0        0.2405
3707.3    75.00  0.28     Sequence
             DRB1_0405  387      GVSPTKLNDLCFTNV  LNDLCFTNV  6        0.2102
5145.1    80.00  0.28     Sequence
             DRB1_0405  388      VSPTKLNDLCFTNVY  LNDLCFTNV  5        0.2407
3695.9    75.00  0.28     Sequence
             DRB1_0405  389      SPTKLNDLCFTNVYA  DLCFTNVYA  6        0.2774
2487.2    65.00  0.37     Sequence
             DRB1_0405  390      PTKLNDLCFTNVYAD  DLCFTNVYA  5        0.3476
1163.2    44.00  0.35     Sequence
             DRB1_0405  391      TKLNDLCFTNVYADS  DLCFTNVYA  4        0.3787
831.0    37.00  0.28     Sequence
             DRB1_0405  392      KLNDLCFTNVYADSF  FTNVYADSF  6        0.4274
490.6    26.00  0.35     Sequence
             DRB1_0405  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.4392
431.6    24.00  0.44     Sequence
             DRB1_0405  394      NDLCFTNVYADSFVI  FTNVYADSF  4        0.4376
439.2    24.00  0.47     Sequence
             DRB1_0405  395      DLCFTNVYADSFVIR  FTNVYADSF  3        0.4338
457.5    25.00  0.47     Sequence
             DRB1_0405  396      LCFTNVYADSFVIRG  FTNVYADSF  2        0.4179
543.8    28.00  0.41     Sequence
             DRB1_0405  397      CFTNVYADSFVIRGD  YADSFVIRG  5        0.3949
697.2    33.00  0.37     Sequence
             DRB1_0405  398      FTNVYADSFVIRGDE  YADSFVIRG  4        0.3676
936.3    39.00  0.57     Sequence
             DRB1_0405  399      TNVYADSFVIRGDEV  YADSFVIRG  3        0.3259
1471.0    50.00  0.62     Sequence
             DRB1_0405  400      NVYADSFVIRGDEVR  YADSFVIRG  2        0.2939
2078.9    60.00  0.59     Sequence
             DRB1_0405  401      VYADSFVIRGDEVRQ  YADSFVIRG  1        0.2646
2854.5    70.00  0.40     Sequence
             DRB1_0405  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.2548
3175.2    70.00  0.43     Sequence
             DRB1_0405  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.2658
2819.0    70.00  0.56     Sequence
             DRB1_0405  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.2702
2688.6    65.00  0.60     Sequence
             DRB1_0405  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.2578
3073.0    70.00  0.60     Sequence
             DRB1_0405  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.2425
3625.3    75.00  0.51     Sequence
             DRB1_0405  407      VIRGDEVRQIAPGQT  VRQIAPGQT  6        0.2432
3598.6    75.00  0.47     Sequence
             DRB1_0405  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.2361
3884.6    75.00  0.59     Sequence
             DRB1_0405  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.2359
3893.9    75.00  0.65     Sequence
             DRB1_0405  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.2232
4470.1    80.00  0.65     Sequence
             DRB1_0405  411      DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.1985
5840.4    85.00  0.62     Sequence
             DRB1_0405  412      EVRQIAPGQTGTIAD  VRQIAPGQT  1        0.1486
10012.9    95.00  0.43     Sequence
             DRB1_0405  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.1158
14277.6   100.00  0.29     Sequence
             DRB1_0405  414      RQIAPGQTGTIADYN  PGQTGTIAD  4        0.1224
13298.6   100.00  0.31     Sequence
```

```
             DRB1_0405  415      QIAPGQTGTIADYNY  PGQTGTIAD  3        0.1291
12368.0   100.00  0.31     Sequence
             DRB1_0405  416      IAPGQTGTIADYNYK  TGTIADYNY  5        0.1402
10963.5    95.00  0.25     Sequence
             DRB1_0405  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.1654
8351.2    90.00  0.31     Sequence
             DRB1_0405  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.1744
7579.4    90.00  0.43     Sequence
             DRB1_0405  419      GQTGTIADYNYKLPD  TIADYNYKL  4        0.1789
7213.4    90.00  0.47     Sequence
             DRB1_0405  420      QTGTIADYNYKLPDD  TIADYNYKL  3        0.1885
6502.3    85.00  0.47     Sequence
             DRB1_0405  421      TGTIADYNYKLPDDF  TIADYNYKL  2        0.2290
4197.1    75.00  0.29     Sequence
             DRB1_0405  422      GTIADYNYKLPDDFT  YNYKLPDDF  5        0.2482
3408.7    70.00  0.28     Sequence
             DRB1_0405  423      TIADYNYKLPDDFTG  YNYKLPDDF  4        0.2412
3676.6    75.00  0.29     Sequence
             DRB1_0405  424      IADYNYKLPDDFTGC  YKLPDDFTG  5        0.2419
3650.1    75.00  0.24     Sequence
             DRB1_0405  425      ADYNYKLPDDFTGCV  YKLPDDFTG  4        0.2335
3998.0    75.00  0.29     Sequence
             DRB1_0405  426      DYNYKLPDDFTGCVI  YKLPDDFTG  3        0.2054
5416.4    85.00  0.37     Sequence
             DRB1_0405  427      YNYKLPDDFTGCVIA  YKLPDDFTG  2        0.1714
7826.1    90.00  0.42     Sequence
             DRB1_0405  428      NYKLPDDFTGCVIAW  FTGCVIAWX  7        0.1699
7955.6    90.00  0.33     Sequence
             DRB1_0405  429      YKLPDDFTGCVIAWN  FTGCVIAWN  6        0.2836
2325.1    65.00  0.73     Sequence
             DRB1_0405  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.3226
1523.7    55.00  0.73     Sequence
             DRB1_0405  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.3470
1171.2    44.00  0.69     Sequence
             DRB1_0405  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.3703
909.7    39.00  0.56     Sequence
             DRB1_0405  433      DDFTGCVIAWNSNNL  FTGCVIAWN  2        0.3756
858.8    37.00  0.41     Sequence
             DRB1_0405  434      DFTGCVIAWNSNNLD  IAWNSNNLD  6        0.4305
474.5    26.00  0.31     Sequence
             DRB1_0405  435      FTGCVIAWNSNNLDS  IAWNSNNLD  5        0.4378
438.5    24.00  0.44     Sequence
             DRB1_0405  436      TGCVIAWNSNNLDSK  IAWNSNNLD  4        0.4370
442.3    25.00  0.47     Sequence
             DRB1_0405  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3        0.4241
508.6    27.00  0.51     Sequence
             DRB1_0405  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2        0.3748
866.6    38.00  0.56     Sequence
             DRB1_0405  439      VIAWNSNNLDSKVGG  IAWNSNNLD  1        0.2969
2012.7    60.00  0.49     Sequence
             DRB1_0405  440      IAWNSNNLDSKVGGN  IAWNSNNLD  0        0.1976
5894.3    85.00  0.28     Sequence
             DRB1_0405  441      AWNSNNLDSKVGGNY  NSNNLDSKV  2        0.1161
14241.0   100.00  0.18     Sequence
             DRB1_0405  442      WNSNNLDSKVGGNYN  NLDSKVGGN  4        0.0933
18228.8   100.00  0.23     Sequence
             DRB1_0405  443      NSNNLDSKVGGNYNY  NLDSKVGGN  3        0.0860
19712.5   100.00  0.22     Sequence
             DRB1_0405  444      SNNLDSKVGGNYNYL  VGGNYNYLX  7        0.1081
15517.9   100.00  0.27     Sequence
             DRB1_0405  445      NNLDSKVGGNYNYLY  VGGNYNYLY  6        0.1573
9118.1    95.00  0.57     Sequence
             DRB1_0405  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.1849
6762.1    90.00  0.66     Sequence
             DRB1_0405  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4        0.2138
4948.6    80.00  0.58     Sequence
```

```
             DRB1_0405  448      DSKVGGNYNYLYRLF  VGGNYNYLY  3        0.2634
2892.1    70.00  0.40     Sequence
             DRB1_0405  449      SKVGGNYNYLYRLFR  YNYLYRLFR  6        0.3574
1046.1    42.00  0.48     Sequence
             DRB1_0405  450      KVGGNYNYLYRLFRK  YNYLYRLFR  5        0.3823
799.1    36.00  0.54     Sequence
             DRB1_0405  451      VGGNYNYLYRLFRKS  YNYLYRLFR  4        0.4054
622.2    31.00  0.50     Sequence
             DRB1_0405  452      GGNYNYLYRLFRKSN  YNYLYRLFR  3        0.4523
374.6    22.00  0.34     Sequence
             DRB1_0405  453      GNYNYLYRLFRKSNL  YRLFRKSNL  6        0.5037
214.9    14.00  0.43     Sequence
             DRB1_0405  454      NYNYLYRLFRKSNLK  YRLFRKSNL  5        0.5226
175.0    11.00  0.52     Sequence
             DRB1_0405  455      YNYLYRLFRKSNLKP  YRLFRKSNL  4        0.5183
183.4    12.00  0.57     Sequence
             DRB1_0405  456      NYLYRLFRKSNLKPF  YRLFRKSNL  3        0.5169
186.3    12.00  0.52     Sequence
             DRB1_0405  457      YLYRLFRKSNLKPFE  YRLFRKSNL  2        0.5134
193.4    13.00  0.44     Sequence
             DRB1_0405  458      LYRLFRKSNLKPFER  YRLFRKSNL  1        0.4759
290.3    18.00  0.33     Sequence
             DRB1_0405  459      YRLFRKSNLKPFERD  LFRKSNLKP  2        0.4240
508.7    27.00  0.32     Sequence
             DRB1_0405  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.3522
1106.5    43.00  0.25     Sequence
             DRB1_0405  461      LFRKSNLKPFERDIS  KSNLKPFER  3        0.2843
2308.0    65.00  0.25     Sequence
             DRB1_0405  462      FRKSNLKPFERDIST  LKPFERDIS  5        0.2486
3393.3    70.00  0.34     Sequence
             DRB1_0405  463      RKSNLKPFERDISTE  LKPFERDIS  4        0.2272
4280.1    80.00  0.43     Sequence
             DRB1_0405  464      KSNLKPFERDISTEI  FERDISTEI  6        0.3452
1193.3    45.00  0.62     Sequence
             DRB1_0405  465      SNLKPFERDISTEIY  FERDISTEI  5        0.3905
731.3    34.00  0.68     Sequence
             DRB1_0405  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.4100
591.8    30.00  0.69     Sequence
             DRB1_0405  467      LKPFERDISTEIYQA  FERDISTEI  3        0.4231
513.9    27.00  0.62     Sequence
             DRB1_0405  468      KPFERDISTEIYQAG  FERDISTEI  2        0.4108
587.2    30.00  0.58     Sequence
             DRB1_0405  469      PFERDISTEIYQAGS  FERDISTEI  1        0.3472
1168.3    44.00  0.40     Sequence
             DRB1_0405  470      FERDISTEIYQAGST  DISTEIYQA  3        0.2653
2833.7    70.00  0.40     Sequence
             DRB1_0405  471      ERDISTEIYQAGSTP  DISTEIYQA  2        0.2574
3085.5    70.00  0.41     Sequence
             DRB1_0405  472      RDISTEIYQAGSTPC  IYQAGSTPC  6        0.3715
897.8    38.00  0.63     Sequence
             DRB1_0405  473      DISTEIYQAGSTPCN  IYQAGSTPC  5        0.4410
423.3    24.00  0.65     Sequence
             DRB1_0405  474      ISTEIYQAGSTPCNG  IYQAGSTPC  4        0.4450
405.6    23.00  0.64     Sequence
             DRB1_0405  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.4431
413.6    23.00  0.62     Sequence
             DRB1_0405  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.4125
576.3    29.00  0.57     Sequence
             DRB1_0405  477      EIYQAGSTPCNGVKG  YQAGSTPCN  2        0.3383
1286.8    47.00  0.50     Sequence
             DRB1_0405  478      IYQAGSTPCNGVKGF  YQAGSTPCN  1        0.2339
3981.4    75.00  0.51     Sequence
             DRB1_0405  479      YQAGSTPCNGVKGFN  CNGVKGFNX  7        0.1463
10272.0    95.00  0.29     Sequence
             DRB1_0405  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.1427
10678.0    95.00  0.61     Sequence
```

```
             DRB1_0405  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.1672
8194.5    90.00  0.67     Sequence
             DRB1_0405  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.2380
3805.5    75.00  0.41     Sequence
             DRB1_0405  483      STPCNGVKGFNCYFP  VKGFNCYFP  6        0.2739
2580.8    65.00  0.40     Sequence
             DRB1_0405  484      TPCNGVKGFNCYFPL  VKGFNCYFP  5        0.2907
2153.6    60.00  0.41     Sequence
             DRB1_0405  485      PCNGVKGFNCYFPLQ  FNCYFPLQX  7        0.3661
951.9    40.00  0.30     Sequence
             DRB1_0405  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.4817
272.7    17.00  0.63     Sequence
             DRB1_0405  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.5299
161.8    11.00  0.66     Sequence
             DRB1_0405  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.5388
146.9     9.50  0.65     Sequence         WB
             DRB1_0405  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3        0.6059
71.1     4.00  0.48     Sequence         WB
             DRB1_0405  490      KGFNCYFPLQSYGFQ  YFPLQSYGF  5        0.6346
52.1     2.50  0.48     Sequence         WB
             DRB1_0405  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.6059
71.1     4.00  0.58     Sequence         WB
             DRB1_0405  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.5586
118.6     7.50  0.68     Sequence         WB
             DRB1_0405  493      NCYFPLQSYGFQPTY  YFPLQSYGF  2        0.5306
160.5    11.00  0.71     Sequence
             DRB1_0405  494      CYFPLQSYGFQPTYG  YFPLQSYGF  1        0.4697
310.3    19.00  0.49     Sequence
             DRB1_0405  495      YFPLQSYGFQPTYGV  YGFQPTYGV  6        0.4384
435.6    24.00  0.41     Sequence
             DRB1_0405  496      FPLQSYGFQPTYGVG  YGFQPTYGV  5        0.4105
589.1    30.00  0.57     Sequence
             DRB1_0405  497      PLQSYGFQPTYGVGY  YGFQPTYGV  4        0.4342
455.6    25.00  0.52     Sequence
             DRB1_0405  498      LQSYGFQPTYGVGYQ  YGFQPTYGV  3        0.4408
424.3    24.00  0.47     Sequence
             DRB1_0405  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4        0.4360
446.8    25.00  0.46     Sequence
             DRB1_0405  500      SYGFQPTYGVGYQPY  FQPTYGVGY  3        0.3948
698.3    33.00  0.50     Sequence
             DRB1_0405  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.3834
789.3    36.00  0.51     Sequence
             DRB1_0405  502      GFQPTYGVGYQPYRV  GVGYQPYRV  6        0.3608
1008.1    41.00  0.34     Sequence
             DRB1_0405  503      FQPTYGVGYQPYRVV  GVGYQPYRV  5        0.3447
1200.3    45.00  0.49     Sequence
             DRB1_0405  504      QPTYGVGYQPYRVVV  GVGYQPYRV  4        0.3625
990.0    41.00  0.49     Sequence
             DRB1_0405  505      PTYGVGYQPYRVVVL  YQPYRVVVL  6        0.4214
523.6    28.00  0.47     Sequence
             DRB1_0405  506      TYGVGYQPYRVVVLS  YQPYRVVVL  5        0.4169
549.6    29.00  0.56     Sequence
             DRB1_0405  507      YGVGYQPYRVVVLSF  YQPYRVVVL  4        0.4266
495.0    27.00  0.53     Sequence
             DRB1_0405  508      GVGYQPYRVVVLSFE  YRVVVLSFE  6        0.5274
166.2    11.00  0.50     Sequence
             DRB1_0405  509      VGYQPYRVVVLSFEL  YRVVVLSFE  5        0.5466
135.1     8.50  0.54     Sequence         WB
             DRB1_0405  510      GYQPYRVVVLSFELL  YRVVVLSFE  4        0.5303
161.1    11.00  0.54     Sequence
             DRB1_0405  511      YQPYRVVVLSFELLH  YRVVVLSFE  3        0.5467
134.8     8.50  0.51     Sequence         WB
             DRB1_0405  512      QPYRVVVLSFELLHA  YRVVVLSFE  2        0.5568
120.9     7.50  0.44     Sequence         WB
             DRB1_0405  513      PYRVVVLSFELLHAP  VLSFELLHA  5        0.5501
130.0     8.50  0.30     Sequence         WB
```

```
             DRB1_0405  514      YRVVVLSFELLHAPA  VLSFELLHA  4        0.5397
145.5     9.50  0.32     Sequence         WB
             DRB1_0405  515      RVVVLSFELLHAPAT  FELLHAPAT  6        0.6096
68.3     4.00  0.63     Sequence         WB
             DRB1_0405  516      VVVLSFELLHAPATV  FELLHAPAT  5        0.6466
45.8     2.00  0.65     Sequence         WB
             DRB1_0405  517      VVLSFELLHAPATVC  FELLHAPAT  4        0.6646
37.7     1.40  0.57     Sequence         SB
             DRB1_0405  518      VLSFELLHAPATVCG  FELLHAPAT  3        0.6538
42.4     1.80  0.56     Sequence         SB
             DRB1_0405  519      LSFELLHAPATVCGP  FELLHAPAT  2        0.6327
53.2     2.50  0.54     Sequence         WB
             DRB1_0405  520      SFELLHAPATVCGPK  LLHAPATVC  3        0.5638
112.1     7.00  0.52     Sequence         WB
             DRB1_0405  521      FELLHAPATVCGPKK  LLHAPATVC  2        0.4577
353.4    21.00  0.75     Sequence
             DRB1_0405  522      ELLHAPATVCGPKKS  LLHAPATVC  1        0.2951
2051.6    60.00  0.69     Sequence
             DRB1_0405  523      LLHAPATVCGPKKST  LLHAPATVC  0        0.1443
10493.8    95.00  0.37     Sequence
             DRB1_0405  524      LHAPATVCGPKKSTN  PATVCGPKK  3        0.0619
25580.3   100.00  0.31     Sequence
             DRB1_0405  525      HAPATVCGPKKSTNL  PATVCGPKK  2        0.0631
25256.7   100.00  0.31     Sequence
             DRB1_0405  526      APATVCGPKKSTNLV  PKKSTNLVX  7        0.0747
22280.9   100.00  0.26     Sequence
             DRB1_0405  527      PATVCGPKKSTNLVK  PKKSTNLVK  6        0.1213
13461.8   100.00  0.50     Sequence
             DRB1_0405  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5        0.1661
8288.3    90.00  0.45     Sequence
             DRB1_0405  529      TVCGPKKSTNLVKNK  KKSTNLVKN  5        0.1978
5880.1    85.00  0.32     Sequence
             DRB1_0405  530      VCGPKKSTNLVKNKC  KKSTNLVKN  4        0.2318
4070.1    75.00  0.29     Sequence
             DRB1_0405  531      CGPKKSTNLVKNKCV  TNLVKNKCV  6        0.2598
3007.6    70.00  0.44     Sequence
             DRB1_0405  532      GPKKSTNLVKNKCVN  TNLVKNKCV  5        0.2668
2788.7    65.00  0.50     Sequence
             DRB1_0405  533      PKKSTNLVKNKCVNF  TNLVKNKCV  4        0.2620
2935.9    70.00  0.54     Sequence
             DRB1_0405  534      KKSTNLVKNKCVNFN  TNLVKNKCV  3        0.2644
2860.0    70.00  0.46     Sequence
             DRB1_0405  535      KSTNLVKNKCVNFNF  TNLVKNKCV  2        0.2720
2636.0    65.00  0.28     Sequence
             DRB1_0405  536      STNLVKNKCVNFNFN  KNKCVNFNF  5        0.2600
2999.5    70.00  0.29     Sequence
             DRB1_0405  537      TNLVKNKCVNFNFNG  KNKCVNFNF  4        0.2425
3625.4    75.00  0.31     Sequence
             DRB1_0405  538      NLVKNKCVNFNFNGL  KNKCVNFNF  3        0.2451
3525.2    75.00  0.29     Sequence
             DRB1_0405  539      LVKNKCVNFNFNGLT  VNFNFNGLT  6        0.2543
3190.3    70.00  0.25     Sequence
             DRB1_0405  540      VKNKCVNFNFNGLTG  VNFNFNGLT  5        0.2418
3653.4    75.00  0.32     Sequence
             DRB1_0405  541      KNKCVNFNFNGLTGT  VNFNFNGLT  4        0.2680
2752.6    65.00  0.34     Sequence
             DRB1_0405  542      NKCVNFNFNGLTGTG  FNGLTGTGX  7        0.3218
1538.2    55.00  0.35     Sequence
             DRB1_0405  543      KCVNFNFNGLTGTGV  FNGLTGTGV  6        0.4401
427.5    24.00  0.75     Sequence
             DRB1_0405  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5        0.4818
272.3    17.00  0.82     Sequence
             DRB1_0405  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.4867
258.2    16.00  0.84     Sequence
             DRB1_0405  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3        0.5038
214.7    14.00  0.77     Sequence
```

```
             DRB1_0405  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.4926
242.3    15.00  0.71     Sequence
             DRB1_0405  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.4193
535.5    28.00  0.49     Sequence
             DRB1_0405  549      FNGLTGTGVLTESNK  LTGTGVLTE  3        0.3321
1375.3    48.00  0.62     Sequence
             DRB1_0405  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.3234
1510.7    50.00  0.60     Sequence
             DRB1_0405  551      GLTGTGVLTESNKKF  GVLTESNKK  5        0.2946
2063.8    60.00  0.32     Sequence
             DRB1_0405  552      LTGTGVLTESNKKFL  GVLTESNKK  4        0.2591
3028.8    70.00  0.47     Sequence
             DRB1_0405  553      TGTGVLTESNKKFLP  GVLTESNKK  3        0.2436
3584.6    75.00  0.49     Sequence
             DRB1_0405  554      GTGVLTESNKKFLPF  GVLTESNKK  2        0.2305
4129.8    75.00  0.44     Sequence
             DRB1_0405  555      TGVLTESNKKFLPFQ  VLTESNKKF  2        0.2095
5180.0    80.00  0.37     Sequence
             DRB1_0405  556      GVLTESNKKFLPFQQ  NKKFLPFQQ  6        0.2115
5074.0    80.00  0.41     Sequence
             DRB1_0405  557      VLTESNKKFLPFQQF  NKKFLPFQQ  5        0.2490
3378.5    70.00  0.46     Sequence
             DRB1_0405  558      LTESNKKFLPFQQFG  NKKFLPFQQ  4        0.3093
1760.1    55.00  0.34     Sequence
             DRB1_0405  559      TESNKKFLPFQQFGR  FLPFQQFGR  6        0.4394
430.8    24.00  0.65     Sequence
             DRB1_0405  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5        0.4908
246.9    16.00  0.71     Sequence
             DRB1_0405  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4        0.4949
236.3    15.00  0.75     Sequence
             DRB1_0405  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.4850
262.9    16.00  0.73     Sequence
             DRB1_0405  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.4703
308.5    19.00  0.69     Sequence
             DRB1_0405  564      KFLPFQQFGRDIADT  FLPFQQFGR  1        0.3991
666.1    32.00  0.54     Sequence
             DRB1_0405  565      FLPFQQFGRDIADTT  FGRDIADTT  6        0.3317
1380.7    48.00  0.28     Sequence
             DRB1_0405  566      LPFQQFGRDIADTTD  FGRDIADTT  5        0.3194
1577.5    55.00  0.47     Sequence
             DRB1_0405  567      PFQQFGRDIADTTDA  FGRDIADTT  4        0.3181
1600.1    55.00  0.53     Sequence
             DRB1_0405  568      FQQFGRDIADTTDAV  FGRDIADTT  3        0.2938
2082.3    60.00  0.55     Sequence
             DRB1_0405  569      QQFGRDIADTTDAVR  FGRDIADTT  2        0.2770
2495.6    65.00  0.50     Sequence
             DRB1_0405  570      QFGRDIADTTDAVRD  FGRDIADTT  1        0.2671
2779.6    65.00  0.30     Sequence
             DRB1_0405  571      FGRDIADTTDAVRDP  ADTTDAVRD  5        0.2347
3945.5    75.00  0.34     Sequence
             DRB1_0405  572      GRDIADTTDAVRDPQ  ADTTDAVRD  4        0.2189
4679.2    80.00  0.45     Sequence
             DRB1_0405  573      RDIADTTDAVRDPQT  ADTTDAVRD  3        0.2178
4739.3    80.00  0.43     Sequence
             DRB1_0405  574      DIADTTDAVRDPQTL  ADTTDAVRD  2        0.1890
6470.9    85.00  0.40     Sequence
             DRB1_0405  575      IADTTDAVRDPQTLE  TDAVRDPQT  4        0.1844
6800.9    90.00  0.40     Sequence
             DRB1_0405  576      ADTTDAVRDPQTLEI  TDAVRDPQT  3        0.1686
8069.3    90.00  0.44     Sequence
             DRB1_0405  577      DTTDAVRDPQTLEIL  TDAVRDPQT  2        0.1576
9082.6    95.00  0.34     Sequence
             DRB1_0405  578      TTDAVRDPQTLEILD  AVRDPQTLE  3        0.1612
8742.9    90.00  0.29     Sequence
             DRB1_0405  579      TDAVRDPQTLEILDI  AVRDPQTLE  2        0.1600
8851.8    95.00  0.25     Sequence
```

```
             DRB1_0405  580      DAVRDPQTLEILDIT  PQTLEILDI  5        0.1936
6152.6    85.00  0.27     Sequence
             DRB1_0405  581      AVRDPQTLEILDITP  LEILDITPX  7        0.2670
2782.1    65.00  0.37     Sequence
             DRB1_0405  582      VRDPQTLEILDITPC  LEILDITPC  6        0.3834
789.8    36.00  0.70     Sequence
             DRB1_0405  583      RDPQTLEILDITPCS  LEILDITPC  5        0.4253
501.8    27.00  0.70     Sequence
             DRB1_0405  584      DPQTLEILDITPCSF  LEILDITPC  4        0.4409
424.0    24.00  0.65     Sequence
             DRB1_0405  585      PQTLEILDITPCSFG  LEILDITPC  3        0.4301
476.1    26.00  0.63     Sequence
             DRB1_0405  586      QTLEILDITPCSFGG  LEILDITPC  2        0.3895
739.5    34.00  0.61     Sequence
             DRB1_0405  587      TLEILDITPCSFGGV  LEILDITPC  1        0.3206
1557.1    55.00  0.46     Sequence
             DRB1_0405  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.2296
4167.7    75.00  0.50     Sequence
             DRB1_0405  589      EILDITPCSFGGVSV  LDITPCSFG  2        0.1637
8506.7    90.00  0.35     Sequence
             DRB1_0405  590      ILDITPCSFGGVSVI  PCSFGGVSV  5        0.1623
8640.1    90.00  0.26     Sequence
             DRB1_0405  591      LDITPCSFGGVSVIT  FGGVSVITX  7        0.2246
4401.5    80.00  0.47     Sequence
             DRB1_0405  592      DITPCSFGGVSVITP  FGGVSVITP  6        0.2978
1994.0    60.00  0.73     Sequence
             DRB1_0405  593      ITPCSFGGVSVITPG  FGGVSVITP  5        0.3110
1727.6    55.00  0.75     Sequence
             DRB1_0405  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.3355
1325.7    47.00  0.63     Sequence
             DRB1_0405  595      PCSFGGVSVITPGTN  FGGVSVITP  3        0.3525
1103.4    43.00  0.55     Sequence
             DRB1_0405  596      CSFGGVSVITPGTNT  FGGVSVITP  2        0.3362
1316.3    47.00  0.49     Sequence
             DRB1_0405  597      SFGGVSVITPGTNTS  GVSVITPGT  3        0.2812
2384.7    65.00  0.28     Sequence
             DRB1_0405  598      FGGVSVITPGTNTSN  VSVITPGTN  3        0.2461
3487.6    75.00  0.30     Sequence
             DRB1_0405  599      GGVSVITPGTNTSNQ  ITPGTNTSN  5        0.2428
3615.1    75.00  0.34     Sequence
             DRB1_0405  600      GVSVITPGTNTSNQV  ITPGTNTSN  4        0.2173
4761.2    80.00  0.40     Sequence
             DRB1_0405  601      VSVITPGTNTSNQVA  ITPGTNTSN  3        0.2013
5661.2    85.00  0.49     Sequence
             DRB1_0405  602      SVITPGTNTSNQVAV  ITPGTNTSN  2        0.1887
6488.0    85.00  0.48     Sequence
             DRB1_0405  603      VITPGTNTSNQVAVL  GTNTSNQVA  4        0.1684
8086.1    90.00  0.29     Sequence
             DRB1_0405  604      ITPGTNTSNQVAVLY  TSNQVAVLY  6        0.1769
7377.9    90.00  0.32     Sequence
             DRB1_0405  605      TPGTNTSNQVAVLYQ  TSNQVAVLY  5        0.1959
6001.5    85.00  0.37     Sequence
             DRB1_0405  606      PGTNTSNQVAVLYQG  TSNQVAVLY  4        0.1870
6612.1    85.00  0.32     Sequence
             DRB1_0405  607      GTNTSNQVAVLYQGV  TSNQVAVLY  3        0.1814
7021.7    90.00  0.28     Sequence
             DRB1_0405  608      TNTSNQVAVLYQGVN  VAVLYQGVN  6        0.2146
4905.0    80.00  0.22     Sequence
             DRB1_0405  609      NTSNQVAVLYQGVNC  AVLYQGVNC  6        0.2415
3665.0    75.00  0.31     Sequence
             DRB1_0405  610      TSNQVAVLYQGVNCT  AVLYQGVNC  5        0.2608
2976.4    70.00  0.35     Sequence
             DRB1_0405  611      SNQVAVLYQGVNCTE  AVLYQGVNC  4        0.3250
1485.6    50.00  0.26     Sequence
             DRB1_0405  612      NQVAVLYQGVNCTEV  AVLYQGVNC  3        0.3570
1050.8    42.00  0.24     Sequence
```

```
             DRB1_0405  613      QVAVLYQGVNCTEVP  YQGVNCTEV  5        0.3647
966.4    40.00  0.34     Sequence
             DRB1_0405  614      VAVLYQGVNCTEVPV  YQGVNCTEV  4        0.3519
1110.2    43.00  0.37     Sequence
             DRB1_0405  615      AVLYQGVNCTEVPVA  YQGVNCTEV  3        0.3336
1353.3    48.00  0.39     Sequence
             DRB1_0405  616      VLYQGVNCTEVPVAI  YQGVNCTEV  2        0.3093
1760.8    55.00  0.38     Sequence
             DRB1_0405  617      LYQGVNCTEVPVAIH  VNCTEVPVA  4        0.2700
2694.2    65.00  0.35     Sequence
             DRB1_0405  618      YQGVNCTEVPVAIHA  VNCTEVPVA  3        0.2229
4482.3    80.00  0.42     Sequence
             DRB1_0405  619      QGVNCTEVPVAIHAD  VNCTEVPVA  2        0.2183
4711.7    80.00  0.38     Sequence
             DRB1_0405  620      GVNCTEVPVAIHADQ  EVPVAIHAD  5        0.2054
5415.6    85.00  0.28     Sequence
             DRB1_0405  621      VNCTEVPVAIHADQL  EVPVAIHAD  4        0.1988
5819.2    85.00  0.29     Sequence
             DRB1_0405  622      NCTEVPVAIHADQLT  EVPVAIHAD  3        0.1910
6327.6    85.00  0.28     Sequence
             DRB1_0405  623      CTEVPVAIHADQLTP  EVPVAIHAD  2        0.1921
6258.3    85.00  0.23     Sequence
             DRB1_0405  624      TEVPVAIHADQLTPT  VAIHADQLT  4        0.1895
6437.2    85.00  0.22     Sequence
             DRB1_0405  625      EVPVAIHADQLTPTW  IHADQLTPT  5        0.1806
7087.2    90.00  0.29     Sequence
             DRB1_0405  626      VPVAIHADQLTPTWR  IHADQLTPT  4        0.1834
6870.9    90.00  0.28     Sequence
             DRB1_0405  627      PVAIHADQLTPTWRV  DQLTPTWRV  6        0.2100
5153.5    80.00  0.34     Sequence
             DRB1_0405  628      VAIHADQLTPTWRVY  DQLTPTWRV  5        0.2158
4840.9    80.00  0.41     Sequence
             DRB1_0405  629      AIHADQLTPTWRVYS  DQLTPTWRV  4        0.2238
4439.1    80.00  0.42     Sequence
             DRB1_0405  630      IHADQLTPTWRVYST  DQLTPTWRV  3        0.2243
4414.7    80.00  0.39     Sequence
             DRB1_0405  631      HADQLTPTWRVYSTG  DQLTPTWRV  2        0.2225
4504.2    80.00  0.37     Sequence
             DRB1_0405  632      ADQLTPTWRVYSTGS  WRVYSTGSX  7        0.2870
2240.7    60.00  0.34     Sequence
             DRB1_0405  633      DQLTPTWRVYSTGSN  WRVYSTGSN  6        0.4675
317.7    19.00  0.80     Sequence
             DRB1_0405  634      QLTPTWRVYSTGSNV  WRVYSTGSN  5        0.5103
200.0    13.00  0.80     Sequence
             DRB1_0405  635      LTPTWRVYSTGSNVF  WRVYSTGSN  4        0.5474
133.9     8.50  0.69     Sequence         WB
             DRB1_0405  636      TPTWRVYSTGSNVFQ  WRVYSTGSN  3        0.6036
72.9     4.00  0.51     Sequence         WB
             DRB1_0405  637      PTWRVYSTGSNVFQT  YSTGSNVFQ  5        0.6126
66.1     3.50  0.44     Sequence         WB
             DRB1_0405  638      TWRVYSTGSNVFQTR  YSTGSNVFQ  4        0.5907
83.8     5.00  0.58     Sequence         WB
             DRB1_0405  639      WRVYSTGSNVFQTRA  YSTGSNVFQ  3        0.5615
114.9     7.50  0.66     Sequence         WB
             DRB1_0405  640      RVYSTGSNVFQTRAG  YSTGSNVFQ  2        0.5223
175.6    12.00  0.75     Sequence
             DRB1_0405  641      VYSTGSNVFQTRAGC  YSTGSNVFQ  1        0.4236
511.3    27.00  0.62     Sequence
             DRB1_0405  642      YSTGSNVFQTRAGCL  YSTGSNVFQ  0        0.2773
2487.9    65.00  0.29     Sequence
             DRB1_0405  643      STGSNVFQTRAGCLI  SNVFQTRAG  3        0.2063
5367.1    85.00  0.32     Sequence
             DRB1_0405  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.1951
6058.6    85.00  0.29     Sequence
             DRB1_0405  645      GSNVFQTRAGCLIGA  VFQTRAGCL  3        0.1747
7549.6    90.00  0.34     Sequence
```

```
             DRB1_0405  646      SNVFQTRAGCLIGAE  VFQTRAGCL  2        0.1828
6917.8    90.00  0.25     Sequence
             DRB1_0405  647      NVFQTRAGCLIGAEY  QTRAGCLIG  3        0.1800
7133.7    90.00  0.24     Sequence
             DRB1_0405  648      VFQTRAGCLIGAEYV  QTRAGCLIG  2        0.1861
6674.8    85.00  0.22     Sequence
             DRB1_0405  649      FQTRAGCLIGAEYVN  LIGAEYVNX  7        0.1970
5935.6    85.00  0.23     Sequence
             DRB1_0405  650      QTRAGCLIGAEYVNN  LIGAEYVNN  6        0.2350
3934.6    75.00  0.51     Sequence
             DRB1_0405  651      TRAGCLIGAEYVNNS  LIGAEYVNN  5        0.2681
2750.3    65.00  0.60     Sequence
             DRB1_0405  652      RAGCLIGAEYVNNSY  LIGAEYVNN  4        0.2905
2158.3    60.00  0.58     Sequence
             DRB1_0405  653      AGCLIGAEYVNNSYE  LIGAEYVNN  3        0.3435
1215.4    45.00  0.45     Sequence
             DRB1_0405  654      GCLIGAEYVNNSYEC  AEYVNNSYE  5        0.3607
1009.3    41.00  0.35     Sequence
             DRB1_0405  655      CLIGAEYVNNSYECD  AEYVNNSYE  4        0.3754
860.7    38.00  0.37     Sequence
             DRB1_0405  656      LIGAEYVNNSYECDI  AEYVNNSYE  3        0.3661
952.0    40.00  0.43     Sequence
             DRB1_0405  657      IGAEYVNNSYECDIP  AEYVNNSYE  2        0.3523
1105.1    43.00  0.38     Sequence
             DRB1_0405  658      GAEYVNNSYECDIPI  YVNNSYECD  3        0.3291
1420.1    49.00  0.41     Sequence
             DRB1_0405  659      AEYVNNSYECDIPIG  YVNNSYECD  2        0.3288
1425.8    49.00  0.34     Sequence
             DRB1_0405  660      EYVNNSYECDIPIGA  YECDIPIGA  6        0.3983
672.2    32.00  0.69     Sequence
             DRB1_0405  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.4060
618.0    31.00  0.80     Sequence
             DRB1_0405  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.4125
576.5    29.00  0.83     Sequence
             DRB1_0405  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.4069
612.1    31.00  0.82     Sequence
             DRB1_0405  664      NSYECDIPIGAGICA  YECDIPIGA  2        0.3833
790.6    36.00  0.83     Sequence
             DRB1_0405  665      SYECDIPIGAGICAS  YECDIPIGA  1        0.2995
1958.1    60.00  0.71     Sequence
             DRB1_0405  666      YECDIPIGAGICASY  YECDIPIGA  0        0.1660
8294.9    90.00  0.36     Sequence
             DRB1_0405  667      ECDIPIGAGICASYQ  GAGICASYQ  6        0.1487
10002.8    95.00  0.46     Sequence
             DRB1_0405  668      CDIPIGAGICASYQT  GAGICASYQ  5        0.1789
7217.2    90.00  0.44     Sequence
             DRB1_0405  669      DIPIGAGICASYQTQ  GAGICASYQ  4        0.2054
5417.2    85.00  0.42     Sequence
             DRB1_0405  670      IPIGAGICASYQTQT  GAGICASYQ  3        0.2490
3381.8    70.00  0.30     Sequence
             DRB1_0405  671      PIGAGICASYQTQTN  CASYQTQTN  6        0.2945
2065.2    60.00  0.35     Sequence
             DRB1_0405  672      IGAGICASYQTQTNS  CASYQTQTN  5        0.3089
1768.6    55.00  0.40     Sequence
             DRB1_0405  673      GAGICASYQTQTNSP  CASYQTQTN  4        0.3666
947.3    40.00  0.27     Sequence
             DRB1_0405  674      AGICASYQTQTNSPR  YQTQTNSPR  6        0.5189
182.2    12.00  0.73     Sequence
             DRB1_0405  675      GICASYQTQTNSPRR  YQTQTNSPR  5        0.5738
100.6     6.50  0.77     Sequence         WB
             DRB1_0405  676      ICASYQTQTNSPRRA  YQTQTNSPR  4        0.5809
93.2     5.50  0.80     Sequence         WB
             DRB1_0405  677      CASYQTQTNSPRRAR  YQTQTNSPR  3        0.5732
101.3     6.50  0.83     Sequence         WB
             DRB1_0405  678      ASYQTQTNSPRRARS  YQTQTNSPR  2        0.5418
142.3     9.00  0.81     Sequence         WB
```

```
             DRB1_0405  679      SYQTQTNSPRRARSV  YQTQTNSPR  1        0.4229
515.1    27.00  0.63     Sequence
             DRB1_0405  680      YQTQTNSPRRARSVA  YQTQTNSPR  0        0.2253
4369.7    80.00  0.38     Sequence
             DRB1_0405  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.1730
7696.0    90.00  0.70     Sequence
             DRB1_0405  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.2341
3972.4    75.00  0.71     Sequence
             DRB1_0405  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.3491
1143.8    44.00  0.32     Sequence
             DRB1_0405  684      TNSPRRARSVASQSI  ARSVASQSI  6        0.4210
525.5    28.00  0.47     Sequence
             DRB1_0405  685      NSPRRARSVASQSII  ARSVASQSI  5        0.4461
400.6    23.00  0.47     Sequence
             DRB1_0405  686      SPRRARSVASQSIIA  ARSVASQSI  4        0.4602
343.8    20.00  0.47     Sequence
             DRB1_0405  687      PRRARSVASQSIIAY  ARSVASQSI  3        0.4518
376.8    22.00  0.42     Sequence
             DRB1_0405  688      RRARSVASQSIIAYT  ARSVASQSI  2        0.4218
521.3    28.00  0.34     Sequence
             DRB1_0405  689      RARSVASQSIIAYTM  SVASQSIIA  3        0.3666
947.1    40.00  0.39     Sequence
             DRB1_0405  690      ARSVASQSIIAYTMS  SVASQSIIA  2        0.3260
1469.4    50.00  0.34     Sequence
             DRB1_0405  691      RSVASQSIIAYTMSL  VASQSIIAY  2        0.3473
1167.3    44.00  0.18     Sequence
             DRB1_0405  692      SVASQSIIAYTMSLG  IIAYTMSLG  6        0.3629
985.5    41.00  0.54     Sequence
             DRB1_0405  693      VASQSIIAYTMSLGA  IIAYTMSLG  5        0.3833
790.8    36.00  0.56     Sequence
             DRB1_0405  694      ASQSIIAYTMSLGAE  IIAYTMSLG  4        0.4260
498.1    27.00  0.49     Sequence
             DRB1_0405  695      SQSIIAYTMSLGAEN  YTMSLGAEN  6        0.5151
189.9    12.00  0.43     Sequence
             DRB1_0405  696      QSIIAYTMSLGAENS  YTMSLGAEN  5        0.5534
125.5     8.00  0.55     Sequence         WB
             DRB1_0405  697      SIIAYTMSLGAENSV  YTMSLGAEN  4        0.5436
139.5     9.00  0.62     Sequence         WB
             DRB1_0405  698      IIAYTMSLGAENSVA  YTMSLGAEN  3        0.5109
198.6    13.00  0.70     Sequence
             DRB1_0405  699      IAYTMSLGAENSVAY  YTMSLGAEN  2        0.4916
244.8    15.00  0.68     Sequence
             DRB1_0405  700      AYTMSLGAENSVAYS  YTMSLGAEN  1        0.4330
461.5    25.00  0.57     Sequence
             DRB1_0405  701      YTMSLGAENSVAYSN  LGAENSVAY  4        0.3055
1834.9    55.00  0.41     Sequence
             DRB1_0405  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.2526
3251.4    70.00  0.51     Sequence
             DRB1_0405  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.2394
3751.6    75.00  0.43     Sequence
             DRB1_0405  704      SLGAENSVAYSNNSI  LGAENSVAY  1        0.2334
4001.6    75.00  0.23     Sequence
             DRB1_0405  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.2687
2731.0    65.00  0.45     Sequence
             DRB1_0405  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.3049
1846.3    55.00  0.47     Sequence
             DRB1_0405  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.3467
1174.2    45.00  0.44     Sequence
             DRB1_0405  708      ENSVAYSNNSIAIPT  VAYSNNSIA  3        0.3607
1009.9    41.00  0.40     Sequence
             DRB1_0405  709      NSVAYSNNSIAIPTN  YSNNSIAIP  4        0.3620
995.3    41.00  0.35     Sequence
             DRB1_0405  710      SVAYSNNSIAIPTNF  YSNNSIAIP  3        0.3475
1163.8    44.00  0.37     Sequence
             DRB1_0405  711      VAYSNNSIAIPTNFT  YSNNSIAIP  2        0.3326
1367.4    48.00  0.34     Sequence
```

```
             DRB1_0405  712      AYSNNSIAIPTNFTI  SIAIPTNFT  5        0.3171
1617.7    55.00  0.43      Sequence
             DRB1_0405  713      YSNNSIAIPTNFTIS  SIAIPTNFT  4        0.2860
2266.0    60.00  0.56      Sequence
             DRB1_0405  714      SNNSIAIPTNFTISV  SIAIPTNFT  3        0.2730
2608.2    65.00  0.56      Sequence
             DRB1_0405  715      NNSIAIPTNFTISVT  SIAIPTNFT  2        0.2506
3321.2    70.00  0.56      Sequence
             DRB1_0405  716      NSIAIPTNFTISVTT  SIAIPTNFT  1        0.2229
4481.3    80.00  0.33      Sequence
             DRB1_0405  717      SIAIPTNFTISVTTE  FTISVTTEX  7        0.2634
2893.4    70.00  0.31      Sequence
             DRB1_0405  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.3784
833.5    37.00  0.65      Sequence
             DRB1_0405  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.4228
515.6    27.00  0.64      Sequence
             DRB1_0405  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.4371
441.7    25.00  0.65      Sequence
             DRB1_0405  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.4343
455.2    25.00  0.65      Sequence
             DRB1_0405  722      TNFTISVTTEILPVS  FTISVTTEI  2        0.3926
715.0    34.00  0.63      Sequence
             DRB1_0405  723      NFTISVTTEILPVSM  FTISVTTEI  1        0.3339
1348.7    48.00  0.46      Sequence
             DRB1_0405  724      FTISVTTEILPVSMT  TEILPVSMT  6        0.2754
2539.4    65.00  0.31      Sequence
             DRB1_0405  725      TISVTTEILPVSMTK  TEILPVSMT  5        0.2925
2112.1    60.00  0.38      Sequence
             DRB1_0405  726      ISVTTEILPVSMTKT  ILPVSMTKT  6        0.3237
1507.0    50.00  0.43      Sequence
             DRB1_0405  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.3475
1164.7    44.00  0.53      Sequence
             DRB1_0405  728      VTTEILPVSMTKTSV  ILPVSMTKT  4        0.3577
1042.9    42.00  0.47      Sequence
             DRB1_0405  729      TTEILPVSMTKTSVD  VSMTKTSVD  6        0.4513
378.6    22.00  0.50      Sequence
             DRB1_0405  730      TEILPVSMTKTSVDC  VSMTKTSVD  5        0.4672
318.7    19.00  0.63      Sequence
             DRB1_0405  731      EILPVSMTKTSVDCT  VSMTKTSVD  4        0.4467
398.2    23.00  0.75      Sequence
             DRB1_0405  732      ILPVSMTKTSVDCTM  VSMTKTSVD  3        0.4208
526.9    28.00  0.82      Sequence
             DRB1_0405  733      LPVSMTKTSVDCTMY  VSMTKTSVD  2        0.3989
667.6    32.00  0.80      Sequence
             DRB1_0405  734      PVSMTKTSVDCTMYI  VSMTKTSVD  1        0.3155
1646.3    55.00  0.57      Sequence
             DRB1_0405  735      VSMTKTSVDCTMYIC  VSMTKTSVD  0        0.2206
4595.5    80.00  0.28      Sequence
             DRB1_0405  736      SMTKTSVDCTMYICG  TSVDCTMYI  4        0.1513
9732.2    95.00  0.29      Sequence
             DRB1_0405  737      MTKTSVDCTMYICGD  VDCTMYICG  5        0.1902
6385.3    85.00  0.25      Sequence
             DRB1_0405  738      TKTSVDCTMYICGDS  VDCTMYICG  4        0.2090
5211.7    80.00  0.25      Sequence
             DRB1_0405  739      KTSVDCTMYICGDST  VDCTMYICG  3        0.2126
5014.1    80.00  0.23      Sequence
             DRB1_0405  740      TSVDCTMYICGDSTE  MYICGDSTE  6        0.2692
2716.1    65.00  0.25      Sequence
             DRB1_0405  741      SVDCTMYICGDSTEC  MYICGDSTE  5        0.3175
1611.5    55.00  0.29      Sequence
             DRB1_0405  742      VDCTMYICGDSTECS  ICGDSTECS  6        0.3513
1117.1    43.00  0.31      Sequence
             DRB1_0405  743      DCTMYICGDSTECSN  ICGDSTECS  5        0.3625
990.0    41.00  0.34      Sequence
             DRB1_0405  744      CTMYICGDSTECSNL  ICGDSTECS  4        0.3501
1132.5    44.00  0.39      Sequence
```

```
             DRB1_0405  745      TMYICGDSTECSNLL  ICGDSTECS  3        0.3254
1478.8    50.00  0.44     Sequence
             DRB1_0405  746      MYICGDSTECSNLLL  ICGDSTECS  2        0.2875
2229.2    60.00  0.46     Sequence
             DRB1_0405  747      YICGDSTECSNLLLQ  ICGDSTECS  1        0.1926
6219.6    85.00  0.28     Sequence
             DRB1_0405  748      ICGDSTECSNLLLQY  STECSNLLL  4        0.1564
9206.1    95.00  0.35     Sequence
             DRB1_0405  749      CGDSTECSNLLLQYG  STECSNLLL  3        0.1489
9987.1    95.00  0.35     Sequence
             DRB1_0405  750      GDSTECSNLLLQYGS  STECSNLLL  2        0.1716
7809.6    90.00  0.26     Sequence
             DRB1_0405  751      DSTECSNLLLQYGSF  SNLLLQYGS  5        0.2139
4942.1    80.00  0.21     Sequence
             DRB1_0405  752      STECSNLLLQYGSFC  LLLQYGSFC  6        0.3643
971.2    40.00  0.44     Sequence
             DRB1_0405  753      TECSNLLLQYGSFCT  LLQYGSFCT  6        0.4467
398.2    23.00  0.52     Sequence
             DRB1_0405  754      ECSNLLLQYGSFCTQ  LLQYGSFCT  5        0.5026
217.4    14.00  0.57     Sequence
             DRB1_0405  755      CSNLLLQYGSFCTQL  LLQYGSFCT  4        0.5704
104.4     6.50  0.43     Sequence         WB
             DRB1_0405  756      SNLLLQYGSFCTQLN  YGSFCTQLN  6        0.6434
47.4     2.50  0.53     Sequence         WB
             DRB1_0405  757      NLLLQYGSFCTQLNR  YGSFCTQLN  5        0.6582
40.4     1.60  0.63     Sequence         SB
             DRB1_0405  758      LLLQYGSFCTQLNRA  YGSFCTQLN  4        0.6379
50.3     2.50  0.71     Sequence         WB
             DRB1_0405  759      LLQYGSFCTQLNRAL  YGSFCTQLN  3        0.6243
58.3     3.00  0.71     Sequence         WB
             DRB1_0405  760      LQYGSFCTQLNRALT  YGSFCTQLN  2        0.6130
65.9     3.50  0.65     Sequence         WB
             DRB1_0405  761      QYGSFCTQLNRALTG  YGSFCTQLN  1        0.5330
156.5    10.00  0.54     Sequence
             DRB1_0405  762      YGSFCTQLNRALTGI  FCTQLNRAL  3        0.3986
669.6    32.00  0.47     Sequence
             DRB1_0405  763      GSFCTQLNRALTGIA  LNRALTGIA  6        0.4482
391.6    22.00  0.51     Sequence
             DRB1_0405  764      SFCTQLNRALTGIAV  LNRALTGIA  5        0.4587
349.7    21.00  0.61     Sequence
             DRB1_0405  765      FCTQLNRALTGIAVE  LNRALTGIA  4        0.4844
264.7    17.00  0.67     Sequence
             DRB1_0405  766      CTQLNRALTGIAVEQ  LNRALTGIA  3        0.4917
244.6    15.00  0.64     Sequence
             DRB1_0405  767      TQLNRALTGIAVEQD  LNRALTGIA  2        0.5086
203.7    13.00  0.48     Sequence
             DRB1_0405  768      QLNRALTGIAVEQDK  LTGIAVEQD  5        0.4864
259.0    16.00  0.50     Sequence
             DRB1_0405  769      LNRALTGIAVEQDKN  LTGIAVEQD  4        0.4496
385.7    22.00  0.70     Sequence
             DRB1_0405  770      NRALTGIAVEQDKNT  LTGIAVEQD  3        0.4168
549.9    29.00  0.82     Sequence
             DRB1_0405  771      RALTGIAVEQDKNTQ  LTGIAVEQD  2        0.3892
741.3    34.00  0.81     Sequence
             DRB1_0405  772      ALTGIAVEQDKNTQE  LTGIAVEQD  1        0.3192
1580.8    55.00  0.43     Sequence
             DRB1_0405  773      LTGIAVEQDKNTQEV  VEQDKNTQE  5        0.2763
2514.9    65.00  0.68     Sequence
             DRB1_0405  774      TGIAVEQDKNTQEVF  VEQDKNTQE  4        0.2681
2748.8    65.00  0.77     Sequence
             DRB1_0405  775      GIAVEQDKNTQEVFA  VEQDKNTQE  3        0.2623
2926.4    70.00  0.79     Sequence
             DRB1_0405  776      IAVEQDKNTQEVFAQ  VEQDKNTQE  2        0.2577
3075.4    70.00  0.71     Sequence
             DRB1_0405  777      AVEQDKNTQEVFAQV  VEQDKNTQE  1        0.2272
4279.7    80.00  0.47     Sequence
```

```
            DRB1_0405  778      VEQDKNTQEVFAQVK  KNTQEVFAQ  4        0.1944
6103.4    85.00  0.32     Sequence
            DRB1_0405  779      EQDKNTQEVFAQVKQ  KNTQEVFAQ  3        0.1937
6149.4    85.00  0.32     Sequence
            DRB1_0405  780      QDKNTQEVFAQVKQI  QEVFAQVKQ  5        0.2089
5216.1    80.00  0.32     Sequence
            DRB1_0405  781      DKNTQEVFAQVKQIY  QEVFAQVKQ  4        0.2264
4314.2    80.00  0.28     Sequence
            DRB1_0405  782      KNTQEVFAQVKQIYK  FAQVKQIYK  6        0.2575
3081.9    70.00  0.44     Sequence
            DRB1_0405  783      NTQEVFAQVKQIYKT  FAQVKQIYK  5        0.2665
2796.2    65.00  0.50     Sequence
            DRB1_0405  784      TQEVFAQVKQIYKTP  FAQVKQIYK  4        0.2757
2532.8    65.00  0.56     Sequence
            DRB1_0405  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.3165
1627.9    55.00  0.40     Sequence
            DRB1_0405  786      EVFAQVKQIYKTPPI  VKQIYKTPP  5        0.3493
1142.1    44.00  0.32     Sequence
            DRB1_0405  787      VFAQVKQIYKTPPIK  KQIYKTPPI  5        0.3838
786.0    36.00  0.40     Sequence
            DRB1_0405  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6        0.5019
219.0    14.00  0.55     Sequence
            DRB1_0405  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.5373
149.3     9.50  0.65     Sequence         WB
            DRB1_0405  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.5202
179.7    12.00  0.69     Sequence
            DRB1_0405  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.4843
265.0    17.00  0.75     Sequence
            DRB1_0405  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.4476
394.3    23.00  0.81     Sequence
            DRB1_0405  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.3502
1131.4    44.00  0.67     Sequence
            DRB1_0405  794      IYKTPPIKDFGGFNF  IKDFGGFNF  6        0.2462
3482.6    75.00  0.43     Sequence
            DRB1_0405  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.2033
5541.5    85.00  0.67     Sequence
            DRB1_0405  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.2438
3577.6    75.00  0.56     Sequence
            DRB1_0405  797      TPPIKDFGGFNFSQI  FGGFNFSQI  6        0.2940
2076.4    60.00  0.38     Sequence
            DRB1_0405  798      PPIKDFGGFNFSQIL  FGGFNFSQI  5        0.3178
1606.4    55.00  0.47     Sequence
            DRB1_0405  799      PIKDFGGFNFSQILP  FGGFNFSQI  4        0.3534
1092.3    43.00  0.41     Sequence
            DRB1_0405  800      IKDFGGFNFSQILPD  FNFSQILPD  6        0.5230
174.3    11.00  0.69     Sequence
            DRB1_0405  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.5794
94.7     6.00  0.69     Sequence         WB
            DRB1_0405  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.6407
48.8     2.50  0.52     Sequence         WB
            DRB1_0405  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.6643
37.8     1.40  0.45     Sequence         SB
            DRB1_0405  804      GGFNFSQILPDPSKP  FSQILPDPS  4        0.6607
39.3     1.60  0.43     Sequence         SB
            DRB1_0405  805      GFNFSQILPDPSKPS  FSQILPDPS  3        0.6289
55.4     3.00  0.46     Sequence         WB
            DRB1_0405  806      FNFSQILPDPSKPSK  FSQILPDPS  2        0.5604
116.3     7.50  0.60     Sequence         WB
            DRB1_0405  807      NFSQILPDPSKPSKR  FSQILPDPS  1        0.4405
425.7    24.00  0.53     Sequence
            DRB1_0405  808      FSQILPDPSKPSKRS  ILPDPSKPS  3        0.3062
1820.5    55.00  0.40     Sequence
            DRB1_0405  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.1828
6918.9    90.00  0.69     Sequence
            DRB1_0405  810      QILPDPSKPSKRSFI  ILPDPSKPS  1        0.1402
10964.9    95.00  0.46     Sequence
```

```
             DRB1_0405  811      ILPDPSKPSKRSFIE  SKPSKRSFI  5        0.1179
13968.6   100.00  0.40     Sequence
             DRB1_0405  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.1293
12345.0    95.00  0.41     Sequence
             DRB1_0405  813      PDPSKPSKRSFIEDL  SKPSKRSFI  3        0.1603
8822.5    95.00  0.29     Sequence
             DRB1_0405  814      DPSKPSKRSFIEDLL  KRSFIEDLL  6        0.2448
3537.4    75.00  0.32     Sequence
             DRB1_0405  815      PSKPSKRSFIEDLLF  RSFIEDLLF  6        0.3079
1786.8    55.00  0.50     Sequence
             DRB1_0405  816      SKPSKRSFIEDLLFN  RSFIEDLLF  5        0.3601
1016.2    41.00  0.44     Sequence
             DRB1_0405  817      KPSKRSFIEDLLFNK  FIEDLLFNK  6        0.4419
419.4    24.00  0.43     Sequence
             DRB1_0405  818      PSKRSFIEDLLFNKV  FIEDLLFNK  5        0.4676
317.6    19.00  0.50     Sequence
             DRB1_0405  819      SKRSFIEDLLFNKVT  FIEDLLFNK  4        0.4630
333.8    20.00  0.54     Sequence
             DRB1_0405  820      KRSFIEDLLFNKVTL  FIEDLLFNK  3        0.4520
375.7    22.00  0.54     Sequence
             DRB1_0405  821      RSFIEDLLFNKVTLA  FIEDLLFNK  2        0.4205
528.7    28.00  0.45     Sequence
             DRB1_0405  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5        0.4230
514.5    27.00  0.30     Sequence
             DRB1_0405  823      FIEDLLFNKVTLADA  FNKVTLADA  6        0.4498
384.8    22.00  0.29     Sequence
             DRB1_0405  824      IEDLLFNKVTLADAG  FNKVTLADA  5        0.4489
388.7    22.00  0.37     Sequence
             DRB1_0405  825      EDLLFNKVTLADAGF  FNKVTLADA  4        0.4480
392.4    23.00  0.37     Sequence
             DRB1_0405  826      DLLFNKVTLADAGFI  FNKVTLADA  3        0.4342
455.5    25.00  0.37     Sequence
             DRB1_0405  827      LLFNKVTLADAGFIK  FNKVTLADA  2        0.4030
639.0    31.00  0.40     Sequence
             DRB1_0405  828      LFNKVTLADAGFIKQ  VTLADAGFI  4        0.3496
1138.2    44.00  0.31     Sequence
             DRB1_0405  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.2806
2400.8    65.00  0.51     Sequence
             DRB1_0405  830      NKVTLADAGFIKQYG  VTLADAGFI  2        0.2420
3645.3    75.00  0.61     Sequence
             DRB1_0405  831      KVTLADAGFIKQYGD  VTLADAGFI  1        0.1959
6001.4    85.00  0.48     Sequence
             DRB1_0405  832      VTLADAGFIKQYGDC  LADAGFIKQ  2        0.1567
9176.7    95.00  0.19     Sequence
             DRB1_0405  833      TLADAGFIKQYGDCL  FIKQYGDCL  6        0.2399
3730.7    75.00  0.47     Sequence
             DRB1_0405  834      LADAGFIKQYGDCLG  IKQYGDCLG  6        0.2618
2941.5    70.00  0.44     Sequence
             DRB1_0405  835      ADAGFIKQYGDCLGD  IKQYGDCLG  5        0.2868
2246.1    60.00  0.50     Sequence
             DRB1_0405  836      DAGFIKQYGDCLGDI  IKQYGDCLG  4        0.2913
2137.6    60.00  0.47     Sequence
             DRB1_0405  837      AGFIKQYGDCLGDIA  IKQYGDCLG  3        0.3083
1778.6    55.00  0.41     Sequence
             DRB1_0405  838      GFIKQYGDCLGDIAA  IKQYGDCLG  2        0.2871
2239.2    60.00  0.36     Sequence
             DRB1_0405  839      FIKQYGDCLGDIAAR  YGDCLGDIA  4        0.2484
3403.7    70.00  0.32     Sequence
             DRB1_0405  840      IKQYGDCLGDIAARD  CLGDIAARD  6        0.2659
2815.2    70.00  0.34     Sequence
             DRB1_0405  841      KQYGDCLGDIAARDL  CLGDIAARD  5        0.2907
2153.8    60.00  0.40     Sequence
             DRB1_0405  842      QYGDCLGDIAARDLI  CLGDIAARD  4        0.2858
2269.3    60.00  0.45     Sequence
             DRB1_0405  843      YGDCLGDIAARDLIC  CLGDIAARD  3        0.2684
2740.4    65.00  0.49     Sequence
```

```
              DRB1_0405  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.2453
3520.0    75.00  0.47     Sequence
              DRB1_0405  845      DCLGDIAARDLICAQ  CLGDIAARD  1        0.2336
3992.5    75.00  0.34     Sequence
              DRB1_0405  846      CLGDIAARDLICAQK  DIAARDLIC  3        0.2173
4764.1    80.00  0.28     Sequence
              DRB1_0405  847      LGDIAARDLICAQKF  RDLICAQKF  6        0.2021
5611.8    85.00  0.35     Sequence
              DRB1_0405  848      GDIAARDLICAQKFN  RDLICAQKF  5        0.2096
5175.7    80.00  0.47     Sequence
              DRB1_0405  849      DIAARDLICAQKFNG  RDLICAQKF  4        0.2016
5643.4    85.00  0.46     Sequence
              DRB1_0405  850      IAARDLICAQKFNGL  RDLICAQKF  3        0.2042
5490.1    85.00  0.38     Sequence
              DRB1_0405  851      AARDLICAQKFNGLT  RDLICAQKF  2        0.2139
4943.3    80.00  0.32     Sequence
              DRB1_0405  852      ARDLICAQKFNGLTV  LICAQKFNG  3        0.2131
4986.0    80.00  0.29     Sequence
              DRB1_0405  853      RDLICAQKFNGLTVL  AQKFNGLTV  5        0.2376
3825.1    75.00  0.29     Sequence
              DRB1_0405  854      DLICAQKFNGLTVLP  FNGLTVLPX  7        0.3934
708.7    34.00  0.49     Sequence
              DRB1_0405  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.5493
131.1     8.50  0.81     Sequence         WB
              DRB1_0405  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.5877
86.5     5.00  0.83     Sequence         WB
              DRB1_0405  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.6058
71.2     4.00  0.76     Sequence         WB
              DRB1_0405  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.6240
58.5     3.00  0.68     Sequence         WB
              DRB1_0405  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.6246
58.1     3.00  0.58     Sequence         WB
              DRB1_0405  860      KFNGLTVLPPLLTDE  LTVLPPLLT  4        0.5554
122.8     8.00  0.47     Sequence         WB
              DRB1_0405  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.4487
389.6    22.00  0.73     Sequence
              DRB1_0405  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.4249
503.9    27.00  0.78     Sequence
              DRB1_0405  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.3531
1095.3    43.00  0.64     Sequence
              DRB1_0405  864      LTVLPPLLTDEMIAQ  LLTDEMIAQ  6        0.2818
2370.7    65.00  0.44     Sequence
              DRB1_0405  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.2813
2382.3    65.00  0.68     Sequence
              DRB1_0405  866      VLPPLLTDEMIAQYT  LLTDEMIAQ  4        0.2870
2239.6    60.00  0.70     Sequence
              DRB1_0405  867      LPPLLTDEMIAQYTS  LLTDEMIAQ  3        0.2992
1963.0    60.00  0.64     Sequence
              DRB1_0405  868      PPLLTDEMIAQYTSA  LLTDEMIAQ  2        0.3076
1792.1    55.00  0.58     Sequence
              DRB1_0405  869      PLLTDEMIAQYTSAL  MIAQYTSAL  6        0.3408
1252.3    46.00  0.44     Sequence
              DRB1_0405  870      LLTDEMIAQYTSALL  MIAQYTSAL  5        0.4178
544.0    28.00  0.42     Sequence
              DRB1_0405  871      LTDEMIAQYTSALLA  IAQYTSALL  5        0.4410
423.4    24.00  0.48     Sequence
              DRB1_0405  872      TDEMIAQYTSALLAG  IAQYTSALL  4        0.4320
466.7    25.00  0.47     Sequence
              DRB1_0405  873      DEMIAQYTSALLAGT  YTSALLAGT  6        0.4574
354.6    21.00  0.34     Sequence
              DRB1_0405  874      EMIAQYTSALLAGTI  YTSALLAGT  5        0.4560
360.0    21.00  0.54     Sequence
              DRB1_0405  875      MIAQYTSALLAGTIT  YTSALLAGT  4        0.4390
432.7    24.00  0.66     Sequence
              DRB1_0405  876      IAQYTSALLAGTITS  YTSALLAGT  3        0.4248
504.7    27.00  0.70     Sequence
```

```
             DRB1_0405  877      AQYTSALLAGTITSG  YTSALLAGT  2         0.3937
706.4    33.00  0.65     Sequence
             DRB1_0405  878      QYTSALLAGTITSGW  YTSALLAGT  1         0.3622
993.3    41.00  0.35     Sequence
             DRB1_0405  879      YTSALLAGTITSGWT  LAGTITSGW  5         0.3211
1550.0    55.00  0.49     Sequence
             DRB1_0405  880      TSALLAGTITSGWTF  LAGTITSGW  4         0.3074
1796.1    55.00  0.56     Sequence
             DRB1_0405  881      SALLAGTITSGWTFG  LAGTITSGW  3         0.2851
2286.7    60.00  0.57     Sequence
             DRB1_0405  882      ALLAGTITSGWTFGA  LAGTITSGW  2         0.2630
2904.3    70.00  0.55     Sequence
             DRB1_0405  883      LLAGTITSGWTFGAG  ITSGWTFGA  5         0.2082
5254.0    80.00  0.39     Sequence
             DRB1_0405  884      LAGTITSGWTFGAGA  ITSGWTFGA  4         0.1630
8572.1    90.00  0.62     Sequence
             DRB1_0405  885      AGTITSGWTFGAGAA  ITSGWTFGA  3         0.1488
9993.0    95.00  0.68     Sequence
             DRB1_0405  886      GTITSGWTFGAGAAL  ITSGWTFGA  2         0.1534
9512.5    95.00  0.55     Sequence
             DRB1_0405  887      TITSGWTFGAGAALQ  WTFGAGAAL  5         0.1680
8117.9    90.00  0.22     Sequence
             DRB1_0405  888      ITSGWTFGAGAALQI  FGAGAALQI  6         0.2389
3770.3    75.00  0.55     Sequence
             DRB1_0405  889      TSGWTFGAGAALQIP  FGAGAALQI  5         0.2785
2457.1    65.00  0.59     Sequence
             DRB1_0405  890      SGWTFGAGAALQIPF  FGAGAALQI  4         0.2890
2193.0    60.00  0.58     Sequence
             DRB1_0405  891      GWTFGAGAALQIPFA  FGAGAALQI  3         0.2959
2035.9    60.00  0.55     Sequence
             DRB1_0405  892      WTFGAGAALQIPFAM  FGAGAALQI  2         0.2929
2101.0    60.00  0.48     Sequence
             DRB1_0405  893      TFGAGAALQIPFAMQ  FGAGAALQI  1         0.2850
2288.6    60.00  0.28     Sequence
             DRB1_0405  894      FGAGAALQIPFAMQM  ALQIPFAMQ  5         0.2655
2827.8    70.00  0.31     Sequence
             DRB1_0405  895      GAGAALQIPFAMQMA  ALQIPFAMQ  4         0.2673
2773.8    65.00  0.31     Sequence
             DRB1_0405  896      AGAALQIPFAMQMAY  ALQIPFAMQ  3         0.2710
2664.2    65.00  0.31     Sequence
             DRB1_0405  897      GAALQIPFAMQMAYR  FAMQMAYRX  7         0.3295
1414.9    49.00  0.31     Sequence
             DRB1_0405  898      AALQIPFAMQMAYRF  FAMQMAYRF  6         0.4402
426.8    24.00  0.65     Sequence
             DRB1_0405  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5         0.4822
271.0    17.00  0.70     Sequence
             DRB1_0405  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4         0.4711
305.5    19.00  0.71     Sequence
             DRB1_0405  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3         0.4632
333.0    20.00  0.69     Sequence
             DRB1_0405  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2         0.4332
460.4    25.00  0.70     Sequence
             DRB1_0405  903      PFAMQMAYRFNGIGV  FAMQMAYRF  1         0.3696
917.1    39.00  0.50     Sequence
             DRB1_0405  904      FAMQMAYRFNGIGVT  AYRFNGIGV  5         0.3157
1642.6    55.00  0.32     Sequence
             DRB1_0405  905      AMQMAYRFNGIGVTQ  FNGIGVTQX  7         0.4451
404.8    23.00  0.42     Sequence
             DRB1_0405  906      MQMAYRFNGIGVTQN  FNGIGVTQN  6         0.5943
80.6     5.00  0.71     Sequence         WB
             DRB1_0405  907      QMAYRFNGIGVTQNV  FNGIGVTQN  5         0.6308
54.3     3.00  0.77     Sequence         WB
             DRB1_0405  908      MAYRFNGIGVTQNVL  FNGIGVTQN  4         0.6408
48.7     2.50  0.77     Sequence         WB
             DRB1_0405  909      AYRFNGIGVTQNVLY  FNGIGVTQN  3         0.6470
45.6     2.00  0.75     Sequence         WB
```

```
             DRB1_0405  910      YRFNGIGVTQNVLYE  FNGIGVTQN  2        0.6290
55.3      3.00  0.69      Sequence         WB
             DRB1_0405  911      RFNGIGVTQNVLYEN  FNGIGVTQN  1        0.5540
124.7     8.00  0.50      Sequence         WB
             DRB1_0405  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.4361
446.3    25.00  0.64      Sequence
             DRB1_0405  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.4124
576.7    29.00  0.63      Sequence
             DRB1_0405  914      GIGVTQNVLYENQKL  IGVTQNVLY  1        0.3829
793.6    36.00  0.41      Sequence
             DRB1_0405  915      IGVTQNVLYENQKLI  NVLYENQKL  5        0.3290
1422.8    49.00  0.52      Sequence
             DRB1_0405  916      GVTQNVLYENQKLIA  NVLYENQKL  4        0.3145
1664.4    55.00  0.68      Sequence
             DRB1_0405  917      VTQNVLYENQKLIAN  NVLYENQKL  3        0.3376
1296.0    47.00  0.55      Sequence
             DRB1_0405  918      TQNVLYENQKLIANQ  NVLYENQKL  2        0.3497
1137.5    44.00  0.42      Sequence
             DRB1_0405  919      QNVLYENQKLIANQF  YENQKLIAN  4        0.3521
1107.3    43.00  0.44      Sequence
             DRB1_0405  920      NVLYENQKLIANQFN  QKLIANQFN  6        0.3715
898.0    38.00  0.35      Sequence
             DRB1_0405  921      VLYENQKLIANQFNS  QKLIANQFN  5        0.3790
828.4    37.00  0.44      Sequence
             DRB1_0405  922      LYENQKLIANQFNSA  QKLIANQFN  4        0.3737
876.5    38.00  0.50      Sequence
             DRB1_0405  923      YENQKLIANQFNSAI  QKLIANQFN  3        0.3981
673.8    33.00  0.42      Sequence
             DRB1_0405  924      ENQKLIANQFNSAIG  QKLIANQFN  2        0.3968
682.8    33.00  0.36      Sequence
             DRB1_0405  925      NQKLIANQFNSAIGK  IANQFNSAI  4        0.3810
810.1    36.00  0.39      Sequence
             DRB1_0405  926      QKLIANQFNSAIGKI  IANQFNSAI  3        0.3452
1194.3    45.00  0.47      Sequence
             DRB1_0405  927      KLIANQFNSAIGKIQ  FNSAIGKIQ  6        0.3788
829.6    37.00  0.41      Sequence
             DRB1_0405  928      LIANQFNSAIGKIQD  FNSAIGKIQ  5        0.3922
717.6    34.00  0.61      Sequence
             DRB1_0405  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4        0.3930
711.5    34.00  0.70      Sequence
             DRB1_0405  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.3995
663.0    32.00  0.67      Sequence
             DRB1_0405  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.4214
523.2    28.00  0.50      Sequence
             DRB1_0405  932      QFNSAIGKIQDSLSS  IGKIQDSLS  5        0.3988
668.2    32.00  0.55      Sequence
             DRB1_0405  933      FNSAIGKIQDSLSST  IGKIQDSLS  4        0.3735
878.8    38.00  0.69      Sequence
             DRB1_0405  934      NSAIGKIQDSLSSTA  IGKIQDSLS  3        0.3685
927.5    39.00  0.65      Sequence
             DRB1_0405  935      SAIGKIQDSLSSTAS  IGKIQDSLS  2        0.3691
921.5    39.00  0.55      Sequence
             DRB1_0405  936      AIGKIQDSLSSTASA  IQDSLSSTA  4        0.3354
1327.1    47.00  0.29      Sequence
             DRB1_0405  937      IGKIQDSLSSTASAL  IQDSLSSTA  3        0.3347
1337.6    48.00  0.29      Sequence
             DRB1_0405  938      GKIQDSLSSTASALG  LSSTASALG  6        0.3682
931.2    39.00  0.50      Sequence
             DRB1_0405  939      KIQDSLSSTASALGK  LSSTASALG  5        0.3889
744.0    35.00  0.67      Sequence
             DRB1_0405  940      IQDSLSSTASALGKL  LSSTASALG  4        0.3809
811.3    36.00  0.77      Sequence
             DRB1_0405  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.3701
911.8    39.00  0.82      Sequence
             DRB1_0405  942      DSLSSTASALGKLQD  LSSTASALG  2        0.3433
1218.5    45.00  0.78      Sequence
```

```
             DRB1_0405  943      SLSSTASALGKLQDV  LSSTASALG  1        0.2697
2701.4    65.00  0.54     Sequence
             DRB1_0405  944      LSSTASALGKLQDVV  ASALGKLQD  4        0.2080
5266.5    80.00  0.41     Sequence
             DRB1_0405  945      SSTASALGKLQDVVN  LGKLQDVVN  6        0.2641
2871.1    70.00  0.61     Sequence
             DRB1_0405  946      STASALGKLQDVVNQ  LGKLQDVVN  5        0.3093
1760.3    55.00  0.63     Sequence
             DRB1_0405  947      TASALGKLQDVVNQN  LGKLQDVVN  4        0.3663
950.0    40.00  0.51     Sequence
             DRB1_0405  948      ASALGKLQDVVNQNA  LGKLQDVVN  3        0.3987
668.9    32.00  0.44     Sequence
             DRB1_0405  949      SALGKLQDVVNQNAQ  LQDVVNQNA  5        0.4107
587.9    30.00  0.45     Sequence
             DRB1_0405  950      ALGKLQDVVNQNAQA  LQDVVNQNA  4        0.3958
690.4    33.00  0.54     Sequence
             DRB1_0405  951      LGKLQDVVNQNAQAL  LQDVVNQNA  3        0.3760
855.1    37.00  0.55     Sequence
             DRB1_0405  952      GKLQDVVNQNAQALN  LQDVVNQNA  2        0.3509
1122.0    43.00  0.50     Sequence
             DRB1_0405  953      KLQDVVNQNAQALNT  LQDVVNQNA  1        0.2829
2341.6    65.00  0.33     Sequence
             DRB1_0405  954      LQDVVNQNAQALNTL  DVVNQNAQA  2        0.2313
4091.8    75.00  0.30     Sequence
             DRB1_0405  955      QDVVNQNAQALNTLV  NAQALNTLV  6        0.3513
1118.0    43.00  0.50     Sequence
             DRB1_0405  956      DVVNQNAQALNTLVK  NAQALNTLV  5        0.3885
747.6    35.00  0.55     Sequence
             DRB1_0405  957      VVNQNAQALNTLVKQ  NAQALNTLV  4        0.4076
607.9    30.00  0.56     Sequence
             DRB1_0405  958      VNQNAQALNTLVKQL  NAQALNTLV  3        0.4079
605.5    30.00  0.55     Sequence
             DRB1_0405  959      NQNAQALNTLVKQLS  NAQALNTLV  2        0.4111
585.3    30.00  0.45     Sequence
             DRB1_0405  960      QNAQALNTLVKQLSS  LNTLVKQLS  5        0.3859
768.3    35.00  0.27     Sequence
             DRB1_0405  961      NAQALNTLVKQLSSN  LNTLVKQLS  4        0.3375
1297.3    47.00  0.44     Sequence
             DRB1_0405  962      AQALNTLVKQLSSNF  LVKQLSSNF  6        0.3859
768.5    35.00  0.34     Sequence
             DRB1_0405  963      QALNTLVKQLSSNFG  VKQLSSNFG  6        0.4569
356.3    21.00  0.55     Sequence
             DRB1_0405  964      ALNTLVKQLSSNFGA  VKQLSSNFG  5        0.4794
279.5    17.00  0.60     Sequence
             DRB1_0405  965      LNTLVKQLSSNFGAI  VKQLSSNFG  4        0.4814
273.5    17.00  0.61     Sequence
             DRB1_0405  966      NTLVKQLSSNFGAIS  VKQLSSNFG  3        0.4778
284.4    18.00  0.57     Sequence
             DRB1_0405  967      TLVKQLSSNFGAISS  VKQLSSNFG  2        0.4483
391.3    22.00  0.58     Sequence
             DRB1_0405  968      LVKQLSSNFGAISSV  VKQLSSNFG  1        0.3821
801.1    36.00  0.44     Sequence
             DRB1_0405  969      VKQLSSNFGAISSVL  LSSNFGAIS  3        0.3710
903.2    39.00  0.22     Sequence
             DRB1_0405  970      KQLSSNFGAISSVLN  FGAISSVLN  6        0.4754
292.0    18.00  0.69     Sequence
             DRB1_0405  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.5208
178.5    12.00  0.81     Sequence
             DRB1_0405  972      LSSNFGAISSVLNDI  FGAISSVLN  4        0.5316
158.8    10.00  0.81     Sequence
             DRB1_0405  973      SSNFGAISSVLNDIL  FGAISSVLN  3        0.5602
116.6     7.50  0.65     Sequence         WB
             DRB1_0405  974      SNFGAISSVLNDILS  FGAISSVLN  2        0.5577
119.7     7.50  0.56     Sequence         WB
             DRB1_0405  975      NFGAISSVLNDILSR  ISSVLNDIL  4        0.5228
174.7    11.00  0.38     Sequence
```

```
             DRB1_0405  976      FGAISSVLNDILSRL  ISSVLNDIL  3        0.4736
297.4    18.00  0.48     Sequence
             DRB1_0405  977      GAISSVLNDILSRLD  ISSVLNDIL  2        0.4763
288.8    18.00  0.38     Sequence
             DRB1_0405  978      AISSVLNDILSRLDK  LNDILSRLD  5        0.4639
330.6    20.00  0.46     Sequence
             DRB1_0405  979      ISSVLNDILSRLDKV  LNDILSRLD  4        0.4365
444.6    25.00  0.61     Sequence
             DRB1_0405  980      SSVLNDILSRLDKVE  LNDILSRLD  3        0.4332
460.7    25.00  0.62     Sequence
             DRB1_0405  981      SVLNDILSRLDKVEA  LNDILSRLD  2        0.4115
582.8    30.00  0.56     Sequence
             DRB1_0405  982      VLNDILSRLDKVEAE  LSRLDKVEA  5        0.3872
757.4    35.00  0.41     Sequence
             DRB1_0405  983      LNDILSRLDKVEAEV  LSRLDKVEA  4        0.3463
1179.1    45.00  0.57     Sequence
             DRB1_0405  984      NDILSRLDKVEAEVQ  LSRLDKVEA  3        0.3222
1530.4    55.00  0.57     Sequence
             DRB1_0405  985      DILSRLDKVEAEVQI  LSRLDKVEA  2        0.3065
1814.8    55.00  0.54     Sequence
             DRB1_0405  986      ILSRLDKVEAEVQID  LDKVEAEVQ  4        0.2759
2525.7    65.00  0.35     Sequence
             DRB1_0405  987      LSRLDKVEAEVQIDR  LDKVEAEVQ  3        0.2516
3285.4    70.00  0.44     Sequence
             DRB1_0405  988      SRLDKVEAEVQIDRL  LDKVEAEVQ  2        0.2449
3531.9    75.00  0.35     Sequence
             DRB1_0405  989      RLDKVEAEVQIDRLI  KVEAEVQID  3        0.2134
4967.3    80.00  0.40     Sequence
             DRB1_0405  990      LDKVEAEVQIDRLIT  KVEAEVQID  2        0.2031
5555.5    85.00  0.34     Sequence
             DRB1_0405  991      DKVEAEVQIDRLITG  KVEAEVQID  1        0.1896
6424.3    85.00  0.22     Sequence
             DRB1_0405  992      KVEAEVQIDRLITGR  IDRLITGRX  7        0.2070
5325.8    85.00  0.28     Sequence
             DRB1_0405  993      VEAEVQIDRLITGRL  IDRLITGRL  6        0.3083
1779.8    55.00  0.73     Sequence
             DRB1_0405  994      EAEVQIDRLITGRLQ  IDRLITGRL  5        0.3546
1078.5    43.00  0.76     Sequence
             DRB1_0405  995      AEVQIDRLITGRLQS  IDRLITGRL  4        0.3681
931.4    39.00  0.75     Sequence
             DRB1_0405  996      EVQIDRLITGRLQSL  IDRLITGRL  3        0.3658
955.2    40.00  0.71     Sequence
             DRB1_0405  997      VQIDRLITGRLQSLQ  IDRLITGRL  2        0.3633
981.0    40.00  0.61     Sequence
             DRB1_0405  998      QIDRLITGRLQSLQT  IDRLITGRL  1        0.3487
1149.6    44.00  0.37     Sequence
             DRB1_0405  999      IDRLITGRLQSLQTY  TGRLQSLQT  5        0.3353
1329.0    47.00  0.47     Sequence
             DRB1_0405 1000      DRLITGRLQSLQTYV  TGRLQSLQT  4        0.4147
563.0    29.00  0.35     Sequence
             DRB1_0405 1001      RLITGRLQSLQTYVT  LQSLQTYVT  6        0.4705
307.7    19.00  0.53     Sequence
             DRB1_0405 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.5012
220.7    14.00  0.64     Sequence
             DRB1_0405 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.5393
146.2     9.50  0.57     Sequence         WB
             DRB1_0405 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.5614
115.1     7.50  0.47     Sequence         WB
             DRB1_0405 1005      GRLQSLQTYVTQQLI  LQSLQTYVT  2        0.5525
126.7     8.00  0.44     Sequence         WB
             DRB1_0405 1006      RLQSLQTYVTQQLIR  LQTYVTQQL  4        0.5125
195.3    13.00  0.44     Sequence
             DRB1_0405 1007      LQSLQTYVTQQLIRA  YVTQQLIRA  6        0.5414
142.9     9.00  0.50     Sequence         WB
             DRB1_0405 1008      QSLQTYVTQQLIRAA  YVTQQLIRA  5        0.5620
114.3     7.00  0.59     Sequence         WB
```

```
             DRB1_0405 1009      SLQTYVTQQLIRAAE  YVTQQLIRA  4        0.5603
116.5     7.50  0.71     Sequence         WB
             DRB1_0405 1010      LQTYVTQQLIRAAEI  YVTQQLIRA  3        0.5459
136.1     9.00  0.74     Sequence         WB
             DRB1_0405 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.5332
156.1    10.00  0.66     Sequence
             DRB1_0405 1012      TYVTQQLIRAAEIRA  YVTQQLIRA  1        0.4857
261.0    16.00  0.46     Sequence
             DRB1_0405 1013      YVTQQLIRAAEIRAS  LIRAAEIRA  5        0.4185
540.2    28.00  0.42     Sequence
             DRB1_0405 1014      VTQQLIRAAEIRASA  LIRAAEIRA  4        0.4076
607.6    30.00  0.51     Sequence
             DRB1_0405 1015      TQQLIRAAEIRASAN  LIRAAEIRA  3        0.4100
592.4    30.00  0.47     Sequence
             DRB1_0405 1016      QQLIRAAEIRASANL  LIRAAEIRA  2        0.4065
614.8    31.00  0.43     Sequence
             DRB1_0405 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.4097
593.8    30.00  0.29     Sequence
             DRB1_0405 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.4455
403.4    23.00  0.62     Sequence
             DRB1_0405 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.4646
327.9    20.00  0.81     Sequence
             DRB1_0405 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.4800
277.5    17.00  0.83     Sequence
             DRB1_0405 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.4714
304.6    19.00  0.85     Sequence
             DRB1_0405 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.4548
364.7    21.00  0.81     Sequence
             DRB1_0405 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.3986
670.1    32.00  0.51     Sequence
             DRB1_0405 1024      IRASANLAAIKMSEC  LAAIKMSEC  6        0.3343
1342.8    48.00  0.50     Sequence
             DRB1_0405 1025      RASANLAAIKMSECV  LAAIKMSEC  5        0.3508
1123.4    43.00  0.62     Sequence
             DRB1_0405 1026      ASANLAAIKMSECVL  LAAIKMSEC  4        0.3544
1081.0    43.00  0.66     Sequence
             DRB1_0405 1027      SANLAAIKMSECVLG  LAAIKMSEC  3        0.3483
1154.3    44.00  0.65     Sequence
             DRB1_0405 1028      ANLAAIKMSECVLGQ  LAAIKMSEC  2        0.3276
1444.3    49.00  0.57     Sequence
             DRB1_0405 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.2674
2770.8    65.00  0.42     Sequence
             DRB1_0405 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.2235
4455.9    80.00  0.52     Sequence
             DRB1_0405 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.2133
4974.0    80.00  0.51     Sequence
             DRB1_0405 1032      AIKMSECVLGQSKRV  IKMSECVLG  1        0.1888
6486.2    85.00  0.34     Sequence
             DRB1_0405 1033      IKMSECVLGQSKRVD  CVLGQSKRV  5        0.1631
8558.8    90.00  0.37     Sequence
             DRB1_0405 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.1589
8957.1    95.00  0.34     Sequence
             DRB1_0405 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.1520
9656.6    95.00  0.36     Sequence
             DRB1_0405 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.1386
11156.5    95.00  0.32     Sequence
             DRB1_0405 1037      ECVLGQSKRVDFCGK  LGQSKRVDF  3        0.1235
13144.8   100.00  0.25     Sequence
             DRB1_0405 1038      CVLGQSKRVDFCGKG  LGQSKRVDF  2        0.1032
16376.3   100.00  0.31     Sequence
             DRB1_0405 1039      VLGQSKRVDFCGKGY  LGQSKRVDF  1        0.0873
19449.1   100.00  0.21     Sequence
             DRB1_0405 1040      LGQSKRVDFCGKGYH  VDFCGKGYH  6        0.0787
21334.7   100.00  0.20     Sequence
             DRB1_0405 1041      GQSKRVDFCGKGYHL  VDFCGKGYH  5        0.0888
19134.2   100.00  0.23     Sequence
```

```
             DRB1_0405 1042      QSKRVDFCGKGYHLM  FCGKGYHLM  6        0.1315
12057.1    95.00  0.49     Sequence
             DRB1_0405 1043      SKRVDFCGKGYHLMS  FCGKGYHLM  5        0.1600
8853.4    95.00  0.50     Sequence
             DRB1_0405 1044      KRVDFCGKGYHLMSF  FCGKGYHLM  4        0.1772
7352.7    90.00  0.46     Sequence
             DRB1_0405 1045      RVDFCGKGYHLMSFP  FCGKGYHLM  3        0.2110
5097.4    80.00  0.37     Sequence
             DRB1_0405 1046      VDFCGKGYHLMSFPQ  GYHLMSFPQ  6        0.3686
927.2    39.00  0.47     Sequence
             DRB1_0405 1047      DFCGKGYHLMSFPQS  YHLMSFPQS  6        0.5194
181.3    12.00  0.56     Sequence
             DRB1_0405 1048      FCGKGYHLMSFPQSA  YHLMSFPQS  5        0.5756
98.7     6.00  0.54     Sequence        WB
             DRB1_0405 1049      CGKGYHLMSFPQSAP  YHLMSFPQS  4        0.5987
76.9     4.50  0.47     Sequence        WB
             DRB1_0405 1050      GKGYHLMSFPQSAPH  YHLMSFPQS  3        0.6092
68.6     4.00  0.44     Sequence        WB
             DRB1_0405 1051      KGYHLMSFPQSAPHG  YHLMSFPQS  2        0.5845
89.6     5.50  0.41     Sequence        WB
             DRB1_0405 1052      GYHLMSFPQSAPHGV  LMSFPQSAP  3        0.5115
197.4    13.00  0.42     Sequence
             DRB1_0405 1053      YHLMSFPQSAPHGVV  LMSFPQSAP  2        0.4080
605.0    30.00  0.56     Sequence
             DRB1_0405 1054      HLMSFPQSAPHGVVF  LMSFPQSAP  1        0.2606
2980.9    70.00  0.51     Sequence
             DRB1_0405 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.1624
8627.6    90.00  0.31     Sequence
             DRB1_0405 1056      MSFPQSAPHGVVFLH  FPQSAPHGV  2        0.1287
12416.4   100.00  0.29     Sequence
             DRB1_0405 1057      SFPQSAPHGVVFLHV  APHGVVFLH  5        0.1276
12567.5   100.00  0.31     Sequence
             DRB1_0405 1058      FPQSAPHGVVFLHVT  APHGVVFLH  4        0.1345
11667.9    95.00  0.32     Sequence
             DRB1_0405 1059      PQSAPHGVVFLHVTY  VVFLHVTYX  7        0.1906
6358.6    85.00  0.31     Sequence
             DRB1_0405 1060      QSAPHGVVFLHVTYV  VVFLHVTYV  6        0.2459
3496.2    75.00  0.52     Sequence
             DRB1_0405 1061      SAPHGVVFLHVTYVP  VVFLHVTYV  5        0.2972
2005.6    60.00  0.46     Sequence
             DRB1_0405 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.5296
162.3    11.00  0.57     Sequence
             DRB1_0405 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.5982
77.2     4.50  0.56     Sequence        WB
             DRB1_0405 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.6629
38.4     1.50  0.49     Sequence        SB
             DRB1_0405 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.6920
28.0     0.80  0.46     Sequence        SB
             DRB1_0405 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.6921
28.0     0.80  0.42     Sequence        SB
             DRB1_0405 1067      VFLHVTYVPAQEKNF  VTYVPAQEK  4        0.6738
34.1     1.20  0.35     Sequence        SB
             DRB1_0405 1068      FLHVTYVPAQEKNFT  VTYVPAQEK  3        0.6140
65.2     3.50  0.47     Sequence        WB
             DRB1_0405 1069      LHVTYVPAQEKNFTT  VTYVPAQEK  2        0.4745
294.6    18.00  0.65     Sequence
             DRB1_0405 1070      HVTYVPAQEKNFTTA  VTYVPAQEK  1        0.3080
1784.5    55.00  0.50     Sequence
             DRB1_0405 1071      VTYVPAQEKNFTTAP  YVPAQEKNF  2        0.1659
8306.8    90.00  0.30     Sequence
             DRB1_0405 1072      TYVPAQEKNFTTAPA  EKNFTTAPA  6        0.2194
4658.2    80.00  0.65     Sequence
             DRB1_0405 1073      YVPAQEKNFTTAPAI  EKNFTTAPA  5        0.2718
2642.0    65.00  0.66     Sequence
             DRB1_0405 1074      VPAQEKNFTTAPAIC  EKNFTTAPA  4        0.3787
830.9    37.00  0.46     Sequence
```

```
            DRB1_0405 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.5802
93.9     6.00  0.80     Sequence        WB
            DRB1_0405 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.6485
44.8     1.90  0.87     Sequence        SB
            DRB1_0405 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.6469
45.6     2.00  0.89     Sequence        WB
            DRB1_0405 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.6479
45.1     2.00  0.90     Sequence        WB
            DRB1_0405 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.6308
54.3     3.00  0.93     Sequence        WB
            DRB1_0405 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.4550
363.9    21.00  0.77     Sequence
            DRB1_0405 1081      FTTAPAICHDGKAHF  FTTAPAICH  0        0.2170
4777.6    80.00  0.40     Sequence
            DRB1_0405 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.1030
16396.3   100.00  0.55     Sequence
            DRB1_0405 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.1128
14750.2   100.00  0.59     Sequence
            DRB1_0405 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.1304
12197.4    95.00  0.53     Sequence
            DRB1_0405 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.1250
12927.3   100.00  0.49     Sequence
            DRB1_0405 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.1131
14706.4   100.00  0.32     Sequence
            DRB1_0405 1087      ICHDGKAHFPREGVF  KAHFPREGV  5        0.1142
14531.5   100.00  0.26     Sequence
            DRB1_0405 1088      CHDGKAHFPREGVFV  FPREGVFVX  7        0.1700
7943.5    90.00  0.32     Sequence
            DRB1_0405 1089      HDGKAHFPREGVFVS  FPREGVFVS  6        0.2400
3726.5    75.00  0.59     Sequence
            DRB1_0405 1090      DGKAHFPREGVFVSN  FPREGVFVS  5        0.2871
2237.5    60.00  0.58     Sequence
            DRB1_0405 1091      GKAHFPREGVFVSNG  FPREGVFVS  4        0.2866
2249.6    60.00  0.57     Sequence
            DRB1_0405 1092      KAHFPREGVFVSNGT  FPREGVFVS  3        0.3075
1794.6    55.00  0.49     Sequence
            DRB1_0405 1093      AHFPREGVFVSNGTH  FPREGVFVS  2        0.3114
1721.0    55.00  0.39     Sequence
            DRB1_0405 1094      HFPREGVFVSNGTHW  GVFVSNGTH  5        0.3104
1739.4    55.00  0.16     Sequence
            DRB1_0405 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6        0.3704
909.0    39.00  0.44     Sequence
            DRB1_0405 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.3969
681.9    33.00  0.50     Sequence
            DRB1_0405 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.3865
763.4    35.00  0.55     Sequence
            DRB1_0405 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.3736
878.2    38.00  0.58     Sequence
            DRB1_0405 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.3717
896.5    38.00  0.51     Sequence
            DRB1_0405 1100      VFVSNGTHWFVTQRN  THWFVTQRN  6        0.3619
996.6    41.00  0.31     Sequence
            DRB1_0405 1101      FVSNGTHWFVTQRNF  THWFVTQRN  5        0.3185
1594.1    55.00  0.47     Sequence
            DRB1_0405 1102      VSNGTHWFVTQRNFY  THWFVTQRN  4        0.4074
609.1    31.00  0.34     Sequence
            DRB1_0405 1103      SNGTHWFVTQRNFYE  FVTQRNFYE  6        0.5728
101.7     6.50  0.69     Sequence        WB
            DRB1_0405 1104      NGTHWFVTQRNFYEP  FVTQRNFYE  5        0.6227
59.3     3.00  0.80     Sequence        WB
            DRB1_0405 1105      GTHWFVTQRNFYEPQ  FVTQRNFYE  4        0.6398
49.3     2.50  0.84     Sequence        WB
            DRB1_0405 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3        0.6342
52.4     2.50  0.86     Sequence        WB
            DRB1_0405 1107      HWFVTQRNFYEPQII  FVTQRNFYE  2        0.6167
63.3     3.50  0.88     Sequence        WB
```

```
             DRB1_0405 1108      WFVTQRNFYEPQIIT  FVTQRNFYE  1        0.5329
156.6    10.00  0.71     Sequence
             DRB1_0405 1109      FVTQRNFYEPQIITT  FVTQRNFYE  0        0.4381
436.6    24.00  0.41     Sequence
             DRB1_0405 1110      VTQRNFYEPQIITTD  YEPQIITTD  6        0.4250
503.6    27.00  0.64     Sequence
             DRB1_0405 1111      TQRNFYEPQIITTDN  YEPQIITTD  5        0.4740
296.3    18.00  0.69     Sequence
             DRB1_0405 1112      QRNFYEPQIITTDNT  YEPQIITTD  4        0.4791
280.3    17.00  0.69     Sequence
             DRB1_0405 1113      RNFYEPQIITTDNTF  YEPQIITTD  3        0.5034
215.6    14.00  0.62     Sequence
             DRB1_0405 1114      NFYEPQIITTDNTFV  IITTDNTFV  6        0.5501
130.0     8.50  0.49     Sequence         WB
             DRB1_0405 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.5648
110.9     7.00  0.60     Sequence         WB
             DRB1_0405 1116      YEPQIITTDNTFVSG  IITTDNTFV  4        0.5402
144.8     9.50  0.70     Sequence         WB
             DRB1_0405 1117      EPQIITTDNTFVSGN  IITTDNTFV  3        0.5360
151.5     9.50  0.74     Sequence         WB
             DRB1_0405 1118      PQIITTDNTFVSGNC  IITTDNTFV  2        0.5215
177.1    12.00  0.70     Sequence
             DRB1_0405 1119      QIITTDNTFVSGNCD  IITTDNTFV  1        0.4347
453.3    25.00  0.56     Sequence
             DRB1_0405 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.2701
2690.4    65.00  0.34     Sequence
             DRB1_0405 1121      ITTDNTFVSGNCDVV  FVSGNCDVV  6        0.2080
5268.6    80.00  0.22     Sequence
             DRB1_0405 1122      TTDNTFVSGNCDVVI  VSGNCDVVI  6        0.2324
4043.9    75.00  0.35     Sequence
             DRB1_0405 1123      TDNTFVSGNCDVVIG  VSGNCDVVI  5        0.2292
4189.8    75.00  0.41     Sequence
             DRB1_0405 1124      DNTFVSGNCDVVIGI  VSGNCDVVI  4        0.2288
4206.4    75.00  0.45     Sequence
             DRB1_0405 1125      NTFVSGNCDVVIGIV  VSGNCDVVI  3        0.2222
4516.9    80.00  0.44     Sequence
             DRB1_0405 1126      TFVSGNCDVVIGIVN  VSGNCDVVI  2        0.2077
5285.5    80.00  0.41     Sequence
             DRB1_0405 1127      FVSGNCDVVIGIVNN  CDVVIGIVN  5        0.1810
7058.0    90.00  0.28     Sequence
             DRB1_0405 1128      VSGNCDVVIGIVNNT  VIGIVNNTX  7        0.2239
4436.7    80.00  0.32     Sequence
             DRB1_0405 1129      SGNCDVVIGIVNNTV  VIGIVNNTV  6        0.3691
921.8    39.00  0.67     Sequence
             DRB1_0405 1130      GNCDVVIGIVNNTVY  VIGIVNNTV  5        0.4228
515.5    27.00  0.68     Sequence
             DRB1_0405 1131      NCDVVIGIVNNTVYD  VIGIVNNTV  4        0.4690
312.7    19.00  0.64     Sequence
             DRB1_0405 1132      CDVVIGIVNNTVYDP  VIGIVNNTV  3        0.4843
265.1    17.00  0.58     Sequence
             DRB1_0405 1133      DVVIGIVNNTVYDPL  VIGIVNNTV  2        0.4780
283.8    17.00  0.51     Sequence
             DRB1_0405 1134      VVIGIVNNTVYDPLQ  VIGIVNNTV  1        0.4423
417.5    24.00  0.38     Sequence
             DRB1_0405 1135      VIGIVNNTVYDPLQP  IVNNTVYDP  3        0.3719
894.3    38.00  0.26     Sequence
             DRB1_0405 1136      IGIVNNTVYDPLQPE  IVNNTVYDP  2        0.3183
1597.0    55.00  0.29     Sequence
             DRB1_0405 1137      GIVNNTVYDPLQPEL  NNTVYDPLQ  3        0.3024
1896.2    60.00  0.20     Sequence
             DRB1_0405 1138      IVNNTVYDPLQPELD  YDPLQPELD  6        0.3973
679.7    33.00  0.73     Sequence
             DRB1_0405 1139      VNNTVYDPLQPELDS  YDPLQPELD  5        0.4295
479.6    26.00  0.79     Sequence
             DRB1_0405 1140      NNTVYDPLQPELDSF  YDPLQPELD  4        0.4270
492.5    26.00  0.84     Sequence
```

```
             DRB1_0405 1141      NTVYDPLQPELDSFK  YDPLQPELD  3         0.4299
477.3    26.00  0.79     Sequence
             DRB1_0405 1142      TVYDPLQPELDSFKE  YDPLQPELD  2         0.4160
555.1    29.00  0.66     Sequence
             DRB1_0405 1143      VYDPLQPELDSFKEE  YDPLQPELD  1         0.3599
1017.7    41.00  0.45     Sequence
             DRB1_0405 1144      YDPLQPELDSFKEEL  LQPELDSFK  3         0.2998
1951.3    60.00  0.54     Sequence
             DRB1_0405 1145      DPLQPELDSFKEELD  LQPELDSFK  2         0.2756
2535.7    65.00  0.51     Sequence
             DRB1_0405 1146      PLQPELDSFKEELDK  LDSFKEELD  5         0.2619
2939.5    70.00  0.52     Sequence
             DRB1_0405 1147      LQPELDSFKEELDKY  LDSFKEELD  4         0.2370
3848.1    75.00  0.66     Sequence
             DRB1_0405 1148      QPELDSFKEELDKYF  FKEELDKYF  6         0.3068
1808.5    55.00  0.41     Sequence
             DRB1_0405 1149      PELDSFKEELDKYFK  FKEELDKYF  5         0.3242
1498.6    50.00  0.48     Sequence
             DRB1_0405 1150      ELDSFKEELDKYFKN  FKEELDKYF  4         0.3182
1598.6    55.00  0.55     Sequence
             DRB1_0405 1151      LDSFKEELDKYFKNH  FKEELDKYF  3         0.3112
1725.0    55.00  0.58     Sequence
             DRB1_0405 1152      DSFKEELDKYFKNHT  FKEELDKYF  2         0.3103
1742.1    55.00  0.51     Sequence
             DRB1_0405 1153      SFKEELDKYFKNHTS  FKEELDKYF  1         0.2958
2037.3    60.00  0.36     Sequence
             DRB1_0405 1154      FKEELDKYFKNHTSP  DKYFKNHTS  5         0.2504
3329.5    70.00  0.28     Sequence
             DRB1_0405 1155      KEELDKYFKNHTSPD  YFKNHTSPD  6         0.3375
1297.1    47.00  0.38     Sequence
             DRB1_0405 1156      EELDKYFKNHTSPDV  FKNHTSPDV  6         0.4099
592.9    30.00  0.44     Sequence
             DRB1_0405 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5         0.4607
341.9    20.00  0.49     Sequence
             DRB1_0405 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4         0.4710
306.1    19.00  0.51     Sequence
             DRB1_0405 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3         0.4532
371.0    22.00  0.54     Sequence
             DRB1_0405 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2         0.4304
475.0    26.00  0.56     Sequence
             DRB1_0405 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1         0.3376
1295.8    47.00  0.47     Sequence
             DRB1_0405 1162      FKNHTSPDVDLGDIS  NHTSPDVDL  2         0.1801
7124.9    90.00  0.30     Sequence
             DRB1_0405 1163      KNHTSPDVDLGDISG  TSPDVDLGD  3         0.1288
12405.0    100.00  0.44     Sequence
             DRB1_0405 1164      NHTSPDVDLGDISGI  TSPDVDLGD  2         0.1107
15099.7    100.00  0.44     Sequence
             DRB1_0405 1165      HTSPDVDLGDISGIN  DVDLGDISG  4         0.1187
13841.1    100.00  0.23     Sequence
             DRB1_0405 1166      TSPDVDLGDISGINA  LGDISGINA  6         0.1402
10965.6    95.00  0.41     Sequence
             DRB1_0405 1167      SPDVDLGDISGINAS  LGDISGINA  5         0.1744
7578.2    90.00  0.43     Sequence
             DRB1_0405 1168      PDVDLGDISGINASF  ISGINASFX  7         0.2373
3836.6    75.00  0.34     Sequence
             DRB1_0405 1169      DVDLGDISGINASFV  ISGINASFV  6         0.3269
1454.4    49.00  0.71     Sequence
             DRB1_0405 1170      VDLGDISGINASFVN  ISGINASFV  5         0.3728
885.1    38.00  0.79     Sequence
             DRB1_0405 1171      DLGDISGINASFVNI  ISGINASFV  4         0.3959
689.7    33.00  0.72     Sequence
             DRB1_0405 1172      LGDISGINASFVNIQ  ISGINASFV  3         0.4794
279.5    17.00  0.44     Sequence
             DRB1_0405 1173      GDISGINASFVNIQK  INASFVNIQ  5         0.5076
206.0    13.00  0.40     Sequence
```

```
             DRB1_0405 1174      DISGINASFVNIQKE  INASFVNIQ  4        0.5242
172.0    11.00  0.47     Sequence
             DRB1_0405 1175      ISGINASFVNIQKEI  INASFVNIQ  3        0.5315
159.0    10.00  0.47     Sequence
             DRB1_0405 1176      SGINASFVNIQKEID  FVNIQKEID  6        0.5565
121.3     7.50  0.35     Sequence         WB
             DRB1_0405 1177      GINASFVNIQKEIDR  FVNIQKEID  5        0.5575
120.0     7.50  0.49     Sequence         WB
             DRB1_0405 1178      INASFVNIQKEIDRL  FVNIQKEID  4        0.5313
159.4    10.00  0.62     Sequence
             DRB1_0405 1179      NASFVNIQKEIDRLN  FVNIQKEID  3        0.5071
207.0    13.00  0.68     Sequence
             DRB1_0405 1180      ASFVNIQKEIDRLNE  FVNIQKEID  2        0.4724
301.5    18.00  0.66     Sequence
             DRB1_0405 1181      SFVNIQKEIDRLNEV  FVNIQKEID  1        0.3838
785.9    36.00  0.50     Sequence
             DRB1_0405 1182      FVNIQKEIDRLNEVA  IQKEIDRLN  3        0.2756
2534.0    65.00  0.37     Sequence
             DRB1_0405 1183      VNIQKEIDRLNEVAK  IQKEIDRLN  2        0.1934
6167.3    85.00  0.52     Sequence
             DRB1_0405 1184      NIQKEIDRLNEVAKN  DRLNEVAKN  6        0.2157
4844.1    80.00  0.28     Sequence
             DRB1_0405 1185      IQKEIDRLNEVAKNL  DRLNEVAKN  5        0.2277
4254.9    75.00  0.34     Sequence
             DRB1_0405 1186      QKEIDRLNEVAKNLN  DRLNEVAKN  4        0.2480
3416.1    70.00  0.34     Sequence
             DRB1_0405 1187      KEIDRLNEVAKNLNE  DRLNEVAKN  3        0.2929
2102.6    60.00  0.25     Sequence
             DRB1_0405 1188      EIDRLNEVAKNLNES  NEVAKNLNE  5        0.2947
2062.2    60.00  0.40     Sequence
             DRB1_0405 1189      IDRLNEVAKNLNESL  NEVAKNLNE  4        0.3003
1939.4    60.00  0.40     Sequence
             DRB1_0405 1190      DRLNEVAKNLNESLI  NEVAKNLNE  3        0.2866
2251.4    60.00  0.39     Sequence
             DRB1_0405 1191      RLNEVAKNLNESLID  KNLNESLID  6        0.3262
1466.9    50.00  0.35     Sequence
             DRB1_0405 1192      LNEVAKNLNESLIDL  KNLNESLID  5        0.3318
1379.4    48.00  0.45     Sequence
             DRB1_0405 1193      NEVAKNLNESLIDLQ  KNLNESLID  4        0.3676
936.5    39.00  0.41     Sequence
             DRB1_0405 1194      EVAKNLNESLIDLQE  KNLNESLID  3        0.4005
656.0    32.00  0.34     Sequence
             DRB1_0405 1195      VAKNLNESLIDLQEL  NESLIDLQE  5        0.4049
625.4    31.00  0.43     Sequence
             DRB1_0405 1196      AKNLNESLIDLQELG  NESLIDLQE  4        0.3793
825.4    37.00  0.44     Sequence
             DRB1_0405 1197      KNLNESLIDLQELGK  NESLIDLQE  3        0.3508
1123.0    43.00  0.50     Sequence
             DRB1_0405 1198      NLNESLIDLQELGKY  NESLIDLQE  2        0.3029
1886.4    60.00  0.49     Sequence
             DRB1_0405 1199      LNESLIDLQELGKYE  LIDLQELGK  4        0.2613
2960.4    70.00  0.52     Sequence
             DRB1_0405 1200      NESLIDLQELGKYEQ  LIDLQELGK  3        0.2215
4551.1    80.00  0.62     Sequence
             DRB1_0405 1201      ESLIDLQELGKYEQY  LIDLQELGK  2        0.1913
6310.3    85.00  0.61     Sequence
             DRB1_0405 1202      SLIDLQELGKYEQYI  LIDLQELGK  1        0.1530
9555.4    95.00  0.38     Sequence
             DRB1_0405 1203      LIDLQELGKYEQYIK  LGKYEQYIK  6        0.1133
14682.1   100.00  0.25     Sequence
             DRB1_0405 1204      IDLQELGKYEQYIKW  LGKYEQYIK  5        0.1178
13984.2   100.00  0.34     Sequence
             DRB1_0405 1205      DLQELGKYEQYIKWP  YEQYIKWPX  7        0.1586
8988.9    95.00  0.31     Sequence
             DRB1_0405 1206      LQELGKYEQYIKWPW  YEQYIKWPW  6        0.2668
2786.9    65.00  0.66     Sequence
```

```
             DRB1_0405 1207      QELGKYEQYIKWPWY  YEQYIKWPW  5        0.2988
1971.2    60.00  0.69     Sequence
             DRB1_0405 1208      ELGKYEQYIKWPWYI  YEQYIKWPW  4        0.3294
1415.6    49.00  0.55     Sequence
             DRB1_0405 1209      LGKYEQYIKWPWYIW  YIKWPWYIW  6        0.3987
669.4    32.00  0.43     Sequence
             DRB1_0405 1210      GKYEQYIKWPWYIWL  YIKWPWYIW  5        0.4077
606.7    30.00  0.50     Sequence
             DRB1_0405 1211      KYEQYIKWPWYIWLG  YIKWPWYIW  4        0.3800
819.4    36.00  0.56     Sequence
             DRB1_0405 1212      YEQYIKWPWYIWLGF  YIKWPWYIW  3        0.3531
1096.5    43.00  0.61     Sequence
             DRB1_0405 1213      EQYIKWPWYIWLGFI  YIKWPWYIW  2        0.3513
1117.6    43.00  0.55     Sequence
             DRB1_0405 1214      QYIKWPWYIWLGFIA  YIKWPWYIW  1        0.3593
1024.8    41.00  0.38     Sequence
             DRB1_0405 1215      YIKWPWYIWLGFIAG  WYIWLGFIA  5        0.3006
1933.6    60.00  0.23     Sequence
             DRB1_0405 1216      IKWPWYIWLGFIAGL  YIWLGFIAG  5        0.3190
1585.2    55.00  0.24     Sequence
             DRB1_0405 1217      KWPWYIWLGFIAGLI  WLGFIAGLI  6        0.3917
721.6    34.00  0.44     Sequence
             DRB1_0405 1218      WPWYIWLGFIAGLIA  WLGFIAGLI  5        0.3914
724.5    34.00  0.49     Sequence
             DRB1_0405 1219      PWYIWLGFIAGLIAI  WLGFIAGLI  4        0.3995
663.5    32.00  0.46     Sequence
             DRB1_0405 1220      WYIWLGFIAGLIAIV  WLGFIAGLI  3        0.4221
519.7    27.00  0.35     Sequence
             DRB1_0405 1221      YIWLGFIAGLIAIVM  FIAGLIAIV  5        0.4355
449.2    25.00  0.28     Sequence
             DRB1_0405 1222      IWLGFIAGLIAIVMV  FIAGLIAIV  4        0.4243
507.5    27.00  0.36     Sequence
             DRB1_0405 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3        0.3997
661.8    32.00  0.41     Sequence
             DRB1_0405 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.3723
889.9    38.00  0.47     Sequence
             DRB1_0405 1225      GFIAGLIAIVMVTIM  IAGLIAIVM  2        0.3405
1256.2    46.00  0.44     Sequence
             DRB1_0405 1226      FIAGLIAIVMVTIML  IAGLIAIVM  1        0.2469
3458.9    75.00  0.27     Sequence
             DRB1_0405 1227      IAGLIAIVMVTIMLC  LIAIVMVTI  3        0.1761
7438.8    90.00  0.37     Sequence
             DRB1_0405 1228      AGLIAIVMVTIMLCC  LIAIVMVTI  2        0.1660
8298.2    90.00  0.38     Sequence
             DRB1_0405 1229      GLIAIVMVTIMLCCM  IAIVMVTIM  2        0.1458
10328.4    95.00  0.24     Sequence
             DRB1_0405 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3        0.1351
11590.4    95.00  0.27     Sequence
             DRB1_0405 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2        0.1566
9182.3    95.00  0.19     Sequence
             DRB1_0405 1232      AIVMVTIMLCCMTSC  IMLCCMTSC  6        0.1857
6703.5    85.00  0.34     Sequence
             DRB1_0405 1233      IVMVTIMLCCMTSCC  IMLCCMTSC  5        0.2169
4783.5    80.00  0.29     Sequence
             DRB1_0405 1234      VMVTIMLCCMTSCCS  LCCMTSCCS  6        0.2791
2439.9    65.00  0.32     Sequence
             DRB1_0405 1235      MVTIMLCCMTSCCSC  LCCMTSCCS  5        0.2952
2051.2    60.00  0.34     Sequence
             DRB1_0405 1236      VTIMLCCMTSCCSCL  LCCMTSCCS  4        0.3076
1792.8    55.00  0.39     Sequence
             DRB1_0405 1237      TIMLCCMTSCCSCLK  LCCMTSCCS  3        0.3047
1849.8    55.00  0.41     Sequence
             DRB1_0405 1238      IMLCCMTSCCSCLKG  LCCMTSCCS  2        0.2822
2359.4    65.00  0.40     Sequence
             DRB1_0405 1239      MLCCMTSCCSCLKGC  MTSCCSCLK  4        0.2566
3112.9    70.00  0.43     Sequence
```

```
             DRB1_0405 1240      LCCMTSCCSCLKGCC  MTSCCSCLK  3        0.2340
3973.6    75.00  0.51     Sequence
             DRB1_0405 1241      CCMTSCCSCLKGCCS  MTSCCSCLK  2        0.2020
5618.3    85.00  0.56     Sequence
             DRB1_0405 1242      CMTSCCSCLKGCCSC  MTSCCSCLK  1        0.1738
7624.3    90.00  0.42     Sequence
             DRB1_0405 1243      MTSCCSCLKGCCSCG  CSCLKGCCS  4        0.1559
9252.5    95.00  0.34     Sequence
             DRB1_0405 1244      TSCCSCLKGCCSCGS  LKGCCSCGS  6        0.1920
6263.1    85.00  0.61     Sequence
             DRB1_0405 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5        0.2075
5294.6    85.00  0.65     Sequence
             DRB1_0405 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.2038
5509.4    85.00  0.68     Sequence
             DRB1_0405 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.1998
5756.0    85.00  0.70     Sequence
             DRB1_0405 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2        0.1892
6457.7    85.00  0.69     Sequence
             DRB1_0405 1249      CLKGCCSCGSCCKFD  LKGCCSCGS  1        0.1498
9891.2    95.00  0.48     Sequence
             DRB1_0405 1250      LKGCCSCGSCCKFDE  CGSCCKFDE  6        0.1228
13240.0   100.00  0.26     Sequence
             DRB1_0405 1251      KGCCSCGSCCKFDED  CGSCCKFDE  5        0.1259
12802.2   100.00  0.38     Sequence
             DRB1_0405 1252      GCCSCGSCCKFDEDD  CGSCCKFDE  4        0.1299
12264.3    95.00  0.41     Sequence
             DRB1_0405 1253      CCSCGSCCKFDEDDS  CGSCCKFDE  3        0.1366
11409.1    95.00  0.35     Sequence
             DRB1_0405 1254      CSCGSCCKFDEDDSE  CGSCCKFDE  2        0.1547
9372.6    95.00  0.29     Sequence
             DRB1_0405 1255      SCGSCCKFDEDDSEP  CKFDEDDSE  5        0.1585
8997.5    95.00  0.23     Sequence
             DRB1_0405 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.1824
6951.1    90.00  0.46     Sequence
             DRB1_0405 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.1957
6014.9    85.00  0.52     Sequence
             DRB1_0405 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.2051
5435.6    85.00  0.50     Sequence
             DRB1_0405 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.1947
6082.0    85.00  0.54     Sequence
             DRB1_0405 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.1831
6897.4    90.00  0.52     Sequence
             DRB1_0405 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.1531
9545.0    95.00  0.42     Sequence
             DRB1_0405 1262      FDEDDSEPVLKGVKL  DDSEPVLKG  3        0.1078
15568.5   100.00  0.35     Sequence
             DRB1_0405 1263      DEDDSEPVLKGVKLH  DDSEPVLKG  2        0.0992
17091.7   100.00  0.34     Sequence
             DRB1_0405 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.1724
7741.8    90.00  0.40     Sequence
             DRB1_0405 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.2338
3983.3    75.00  0.56     Sequence
             DRB1_0701    1      PSPIKEMFVFLVLLP  PSPIKEMFV  0        0.2919
2124.4    65.00  0.35     Sequence
             DRB1_0701    2      SPIKEMFVFLVLLPL  FVFLVLLPL  6        0.3079
1787.6    65.00  0.52     Sequence
             DRB1_0701    3      PIKEMFVFLVLLPLV  FVFLVLLPL  5        0.2870
2240.5    70.00  0.41     Sequence
             DRB1_0701    4      IKEMFVFLVLLPLVS  FVFLVLLPL  4        0.2845
2303.1    70.00  0.38     Sequence
             DRB1_0701    5      KEMFVFLVLLPLVSS  FVFLVLLPL  3        0.2619
2940.6    75.00  0.38     Sequence
             DRB1_0701    6      EMFVFLVLLPLVSSQ  FVFLVLLPL  2        0.2443
3555.8    75.00  0.40     Sequence
             DRB1_0701    7      MFVFLVLLPLVSSQC  LLPLVSSQC  6        0.3679
933.5    48.00  0.57     Sequence
```

```
             DRB1_0701    8       FVFLVLLPLVSSQCV  LLPLVSSQC  5        0.4645
328.2    29.00  0.44     Sequence
             DRB1_0701    9       VFLVLLPLVSSQCVN  LLPLVSSQC  4        0.4656
324.5    29.00  0.45     Sequence
             DRB1_0701   10       FLVLLPLVSSQCVNF  LLPLVSSQC  3        0.4997
224.4    23.00  0.37     Sequence
             DRB1_0701   11       LVLLPLVSSQCVNFT  LLPLVSSQC  2        0.4780
283.8    27.00  0.38     Sequence
             DRB1_0701   12       VLLPLVSSQCVNFTN  LLPLVSSQC  1        0.4634
332.3    29.00  0.38     Sequence
             DRB1_0701   13       LLPLVSSQCVNFTNR  LPLVSSQCV  1        0.4331
461.3    35.00  0.28     Sequence
             DRB1_0701   14       LPLVSSQCVNFTNRT  LPLVSSQCV  0        0.3400
1263.0    55.00  0.31     Sequence
             DRB1_0701   15       PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.2575
3082.8    75.00  0.40     Sequence
             DRB1_0701   16       LVSSQCVNFTNRTQL  VNFTNRTQL  6        0.4330
461.7    35.00  0.76     Sequence
             DRB1_0701   17       VSSQCVNFTNRTQLP  VNFTNRTQL  5        0.3928
713.1    43.00  0.81     Sequence
             DRB1_0701   18       SSQCVNFTNRTQLPS  VNFTNRTQL  4        0.3792
826.4    45.00  0.80     Sequence
             DRB1_0701   19       SQCVNFTNRTQLPSA  VNFTNRTQL  3        0.3645
968.6    49.00  0.75     Sequence
             DRB1_0701   20       QCVNFTNRTQLPSAY  VNFTNRTQL  2        0.3478
1160.8    55.00  0.75     Sequence
             DRB1_0701   21       CVNFTNRTQLPSAYT  VNFTNRTQL  1        0.3331
1361.3    60.00  0.68     Sequence
             DRB1_0701   22       VNFTNRTQLPSAYTN  VNFTNRTQL  0        0.2937
2083.7    65.00  0.60     Sequence
             DRB1_0701   23       NFTNRTQLPSAYTNS  RTQLPSAYT  4        0.1688
8046.1    90.00  0.40     Sequence
             DRB1_0701   24       FTNRTQLPSAYTNSF  RTQLPSAYT  3        0.1790
7211.6    90.00  0.36     Sequence
             DRB1_0701   25       TNRTQLPSAYTNSFT  RTQLPSAYT  2        0.1746
7561.1    90.00  0.33     Sequence
             DRB1_0701   26       NRTQLPSAYTNSFTR  SAYTNSFTR  6        0.2393
3752.4    80.00  0.48     Sequence
             DRB1_0701   27       RTQLPSAYTNSFTRG  SAYTNSFTR  5        0.2403
3715.1    80.00  0.55     Sequence
             DRB1_0701   28       TQLPSAYTNSFTRGV  YTNSFTRGV  6        0.4689
312.9    28.00  0.75     Sequence
             DRB1_0701   29       QLPSAYTNSFTRGVY  YTNSFTRGV  5        0.4793
279.8    26.00  0.73     Sequence
             DRB1_0701   30       LPSAYTNSFTRGVYY  YTNSFTRGV  4        0.5436
139.5    17.00  0.50     Sequence
             DRB1_0701   31       PSAYTNSFTRGVYYP  YTNSFTRGV  3        0.5136
193.1    21.00  0.47     Sequence
             DRB1_0701   32       SAYTNSFTRGVYYPD  YTNSFTRGV  2        0.5211
178.0    20.00  0.48     Sequence
             DRB1_0701   33       AYTNSFTRGVYYPDK  YTNSFTRGV  1        0.4898
249.7    25.00  0.43     Sequence
             DRB1_0701   34       YTNSFTRGVYYPDKV  NSFTRGVYY  2        0.4541
367.5    31.00  0.37     Sequence
             DRB1_0701   35       TNSFTRGVYYPDKVF  NSFTRGVYY  1        0.4083
602.9    39.00  0.43     Sequence
             DRB1_0701   36       NSFTRGVYYPDKVFR  FTRGVYYPD  2        0.3751
863.6    46.00  0.44     Sequence
             DRB1_0701   37       SFTRGVYYPDKVFRS  FTRGVYYPD  1        0.3468
1173.6    55.00  0.46     Sequence
             DRB1_0701   38       FTRGVYYPDKVFRSS  FTRGVYYPD  0        0.3187
1589.5    60.00  0.39     Sequence
             DRB1_0701   39       TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.2615
2952.6    75.00  0.47     Sequence
             DRB1_0701   40       RGVYYPDKVFRSSVL  DKVFRSSVL  6        0.5995
76.2    11.00  0.82     Sequence
```

```
             DRB1_0701   41      GVYYPDKVFRSSVLH  DKVFRSSVL  5         0.5776
96.6    13.00  0.81     Sequence
             DRB1_0701   42      VYYPDKVFRSSVLHS  DKVFRSSVL  4         0.5845
89.6    12.00  0.71     Sequence
             DRB1_0701   43      YYPDKVFRSSVLHST  DKVFRSSVL  3         0.6308
54.3     8.00  0.45     Sequence         WB
             DRB1_0701   44      YPDKVFRSSVLHSTQ  FRSSVLHST  5         0.6135
65.5     9.50  0.45     Sequence         WB
             DRB1_0701   45      PDKVFRSSVLHSTQD  FRSSVLHST  4         0.5852
88.9    12.00  0.49     Sequence
             DRB1_0701   46      DKVFRSSVLHSTQDL  FRSSVLHST  3         0.5868
87.4    12.00  0.52     Sequence
             DRB1_0701   47      KVFRSSVLHSTQDLF  FRSSVLHST  2         0.6282
55.9     8.00  0.35     Sequence         WB
             DRB1_0701   48      VFRSSVLHSTQDLFL  LHSTQDLFL  6         0.6936
27.5     4.00  0.40     Sequence         WB
             DRB1_0701   49      FRSSVLHSTQDLFLP  LHSTQDLFL  5         0.6506
43.8     6.50  0.44     Sequence         WB
             DRB1_0701   50      RSSVLHSTQDLFLPF  LHSTQDLFL  4         0.6325
53.3     8.00  0.51     Sequence         WB
             DRB1_0701   51      SSVLHSTQDLFLPFF  LHSTQDLFL  3         0.6117
66.7     9.50  0.52     Sequence         WB
             DRB1_0701   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2         0.5812
92.9    13.00  0.52     Sequence
             DRB1_0701   53      VLHSTQDLFLPFFSN  LHSTQDLFL  1         0.5184
183.3    20.00  0.61     Sequence
             DRB1_0701   54      LHSTQDLFLPFFSNV  LHSTQDLFL  0         0.3979
675.1    42.00  0.75     Sequence
             DRB1_0701   55      HSTQDLFLPFFSNVT  FLPFFSNVT  6         0.6544
42.1     6.50  0.94     Sequence         WB
             DRB1_0701   56      STQDLFLPFFSNVTW  FLPFFSNVT  5         0.6600
39.6     6.00  0.94     Sequence         WB
             DRB1_0701   57      TQDLFLPFFSNVTWF  FLPFFSNVT  4         0.6790
32.3     5.00  0.90     Sequence         WB
             DRB1_0701   58      QDLFLPFFSNVTWFH  FLPFFSNVT  3         0.6999
25.7     4.00  0.73     Sequence         WB
             DRB1_0701   59      DLFLPFFSNVTWFHA  FLPFFSNVT  2         0.7399
16.7     2.50  0.51     Sequence         WB
             DRB1_0701   60      LFLPFFSNVTWFHAI  FLPFFSNVT  1         0.7609
13.3     1.50  0.38     Sequence         SB
             DRB1_0701   61      FLPFFSNVTWFHAIH  FSNVTWFHA  4         0.7405
16.6     2.50  0.38     Sequence         WB
             DRB1_0701   62      LPFFSNVTWFHAIHV  VTWFHAIHV  6         0.7652
12.7     1.40  0.43     Sequence         SB
             DRB1_0701   63      PFFSNVTWFHAIHVS  VTWFHAIHV  5         0.7508
14.8     1.80  0.40     Sequence         SB
             DRB1_0701   64      FFSNVTWFHAIHVSG  VTWFHAIHV  4         0.7323
18.1     2.50  0.35     Sequence         WB
             DRB1_0701   65      FSNVTWFHAIHVSGT  VTWFHAIHV  3         0.7138
22.1     3.00  0.38     Sequence         WB
             DRB1_0701   66      SNVTWFHAIHVSGTN  VTWFHAIHV  2         0.6418
48.2     7.00  0.50     Sequence         WB
             DRB1_0701   67      NVTWFHAIHVSGTNG  VTWFHAIHV  1         0.6284
55.7     8.00  0.49     Sequence         WB
             DRB1_0701   68      VTWFHAIHVSGTNGT  VTWFHAIHV  0         0.6628
38.4     6.00  0.34     Sequence         WB
             DRB1_0701   69      TWFHAIHVSGTNGTK  IHVSGTNGT  5         0.5804
93.6    13.00  0.49     Sequence
             DRB1_0701   70      WFHAIHVSGTNGTKR  IHVSGTNGT  4         0.5962
79.0    11.00  0.41     Sequence
             DRB1_0701   71      FHAIHVSGTNGTKRF  IHVSGTNGT  3         0.5954
79.7    11.00  0.41     Sequence
             DRB1_0701   72      HAIHVSGTNGTKRFD  VSGTNGTKR  4         0.5629
113.2    15.00  0.42     Sequence
             DRB1_0701   73      AIHVSGTNGTKRFDN  VSGTNGTKR  3         0.5348
153.5    18.00  0.44     Sequence
```

```
             DRB1_0701   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.4600
344.8    30.00  0.52     Sequence
             DRB1_0701   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.3648
965.2    49.00  0.79     Sequence
             DRB1_0701   76      VSGTNGTKRFDNPVL  VSGTNGTKR  0        0.3227
1523.5    60.00  0.46     Sequence
             DRB1_0701   77      SGTNGTKRFDNPVLP  TKRFDNPVL  5        0.2139
4939.6    85.00  0.59     Sequence
             DRB1_0701   78      GTNGTKRFDNPVLPF  TKRFDNPVL  4        0.2726
2618.9    70.00  0.42     Sequence
             DRB1_0701   79      TNGTKRFDNPVLPFN  RFDNPVLPF  5        0.2672
2775.3    70.00  0.39     Sequence
             DRB1_0701   80      NGTKRFDNPVLPFND  RFDNPVLPF  4        0.2581
3062.5    75.00  0.41     Sequence
             DRB1_0701   81      GTKRFDNPVLPFNDG  RFDNPVLPF  3        0.2321
4060.4    80.00  0.41     Sequence
             DRB1_0701   82      TKRFDNPVLPFNDGV  RFDNPVLPF  2        0.2096
5176.0    85.00  0.46     Sequence
             DRB1_0701   83      KRFDNPVLPFNDGVY  RFDNPVLPF  1        0.1950
6065.1    85.00  0.44     Sequence
             DRB1_0701   84      RFDNPVLPFNDGVYF  VLPFNDGVY  5        0.1891
6459.9    90.00  0.40     Sequence
             DRB1_0701   85      FDNPVLPFNDGVYFA  VLPFNDGVY  4        0.1602
8832.1    95.00  0.52     Sequence
             DRB1_0701   86      DNPVLPFNDGVYFAS  VLPFNDGVY  3        0.1730
7689.2    90.00  0.38     Sequence
             DRB1_0701   87      NPVLPFNDGVYFAST  VLPFNDGVY  2        0.1739
7620.0    90.00  0.40     Sequence
             DRB1_0701   88      PVLPFNDGVYFASTE  VLPFNDGVY  1        0.1662
8280.3    90.00  0.37     Sequence
             DRB1_0701   89      VLPFNDGVYFASTEK  GVYFASTEK  6        0.2046
5464.2    85.00  0.39     Sequence
             DRB1_0701   90      LPFNDGVYFASTEKS  VYFASTEKS  6        0.3471
1169.5    55.00  0.66     Sequence
             DRB1_0701   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.3875
755.3    44.00  0.55     Sequence
             DRB1_0701   92      FNDGVYFASTEKSNI  FASTEKSNI  6        0.5831
91.0    12.00  0.65     Sequence
             DRB1_0701   93      NDGVYFASTEKSNII  FASTEKSNI  5        0.6250
57.8     8.50  0.65     Sequence         WB
             DRB1_0701   94      DGVYFASTEKSNIIR  FASTEKSNI  4        0.6112
67.2     9.50  0.69     Sequence         WB
             DRB1_0701   95      GVYFASTEKSNIIRG  FASTEKSNI  3        0.5829
91.2    13.00  0.62     Sequence
             DRB1_0701   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.5552
123.0    16.00  0.69     Sequence
             DRB1_0701   97      YFASTEKSNIIRGWI  FASTEKSNI  1        0.5074
206.3    22.00  0.77     Sequence
             DRB1_0701   98      FASTEKSNIIRGWIF  SNIIRGWIF  6        0.5291
163.3    19.00  0.56     Sequence
             DRB1_0701   99      ASTEKSNIIRGWIFG  SNIIRGWIF  5        0.4563
358.8    30.00  0.78     Sequence
             DRB1_0701  100      STEKSNIIRGWIFGT  SNIIRGWIF  4        0.4569
356.4    30.00  0.74     Sequence
             DRB1_0701  101      TEKSNIIRGWIFGTT  SNIIRGWIF  3        0.4476
394.1    32.00  0.73     Sequence
             DRB1_0701  102      EKSNIIRGWIFGTTL  SNIIRGWIF  2        0.4539
368.3    31.00  0.64     Sequence
             DRB1_0701  103      KSNIIRGWIFGTTLD  SNIIRGWIF  1        0.4376
439.5    34.00  0.62     Sequence
             DRB1_0701  104      SNIIRGWIFGTTLDS  SNIIRGWIF  0        0.3815
805.7    45.00  0.47     Sequence
             DRB1_0701  105      NIIRGWIFGTTLDSK  RGWIFGTTL  3        0.2824
2354.7    70.00  0.27     Sequence
             DRB1_0701  106      IIRGWIFGTTLDSKT  FGTTLDSKT  6        0.3162
1634.4    60.00  0.38     Sequence
```

```
             DRB1_0701  107      IRGWIFGTTLDSKTQ  FGTTLDSKT  5        0.2975
2000.3    65.00  0.43     Sequence
             DRB1_0701  108      RGWIFGTTLDSKTQS  FGTTLDSKT  4        0.2787
2450.9    70.00  0.48     Sequence
             DRB1_0701  109      GWIFGTTLDSKTQSL  FGTTLDSKT  3        0.3262
1465.6    60.00  0.44     Sequence
             DRB1_0701  110      WIFGTTLDSKTQSLL  TLDSKTQSL  5        0.3339
1348.3    55.00  0.41     Sequence
             DRB1_0701  111      IFGTTLDSKTQSLLI  DSKTQSLLI  6        0.6849
30.3     4.50  0.89     Sequence         WB
             DRB1_0701  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5        0.7013
25.3     4.00  0.92     Sequence         WB
             DRB1_0701  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4        0.6853
30.1     4.50  0.94     Sequence         WB
             DRB1_0701  114      TTLDSKTQSLLIVNN  DSKTQSLLI  3        0.6707
35.3     5.50  0.94     Sequence         WB
             DRB1_0701  115      TLDSKTQSLLIVNNA  DSKTQSLLI  2        0.6504
44.0     6.50  0.94     Sequence         WB
             DRB1_0701  116      LDSKTQSLLIVNNAT  DSKTQSLLI  1        0.6158
63.9     9.00  0.93     Sequence         WB
             DRB1_0701  117      DSKTQSLLIVNNATN  DSKTQSLLI  0        0.5329
156.6    18.00  0.71     Sequence
             DRB1_0701  118      SKTQSLLIVNNATNV  LIVNNATNV  6        0.4538
368.7    31.00  0.56     Sequence
             DRB1_0701  119      KTQSLLIVNNATNVV  LIVNNATNV  5        0.4798
278.3    26.00  0.49     Sequence
             DRB1_0701  120      TQSLLIVNNATNVVI  LIVNNATNV  4        0.5294
162.6    19.00  0.41     Sequence
             DRB1_0701  121      QSLLIVNNATNVVIK  LIVNNATNV  3        0.5125
195.4    21.00  0.41     Sequence
             DRB1_0701  122      SLLIVNNATNVVIKV  LIVNNATNV  2        0.5137
192.8    21.00  0.34     Sequence
             DRB1_0701  123      LLIVNNATNVVIKVC  LIVNNATNV  1        0.4883
253.8    25.00  0.34     Sequence
             DRB1_0701  124      LIVNNATNVVIKVCE  VNNATNVVI  2        0.4239
509.6    36.00  0.28     Sequence
             DRB1_0701  125      IVNNATNVVIKVCEF  NVVIKVCEF  6        0.4241
508.5    36.00  0.37     Sequence
             DRB1_0701  126      VNNATNVVIKVCEFQ  NVVIKVCEF  5        0.3672
940.6    48.00  0.41     Sequence
             DRB1_0701  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.4745
294.8    27.00  0.60     Sequence
             DRB1_0701  128      NATNVVIKVCEFQFC  VIKVCEFQF  5        0.4543
366.6    31.00  0.61     Sequence
             DRB1_0701  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.4363
445.3    34.00  0.61     Sequence
             DRB1_0701  130      TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.4252
502.1    36.00  0.60     Sequence
             DRB1_0701  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.3984
671.2    41.00  0.63     Sequence
             DRB1_0701  132      VVIKVCEFQFCNYPF  EFQFCNYPF  6        0.5133
193.5    21.00  0.54     Sequence
             DRB1_0701  133      VIKVCEFQFCNYPFL  EFQFCNYPF  5        0.5579
119.5    15.00  0.56     Sequence
             DRB1_0701  134      IKVCEFQFCNYPFLG  EFQFCNYPF  4        0.5085
203.9    22.00  0.64     Sequence
             DRB1_0701  135      KVCEFQFCNYPFLGV  EFQFCNYPF  3        0.5582
119.1    15.00  0.50     Sequence
             DRB1_0701  136      VCEFQFCNYPFLGVY  EFQFCNYPF  2        0.5413
143.1    17.00  0.45     Sequence
             DRB1_0701  137      CEFQFCNYPFLGVYY  EFQFCNYPF  1        0.5444
138.4    17.00  0.41     Sequence
             DRB1_0701  138      EFQFCNYPFLGVYYH  FCNYPFLGV  3        0.5142
191.8    21.00  0.31     Sequence
             DRB1_0701  139      FQFCNYPFLGVYYHK  FCNYPFLGV  2        0.4157
556.9    38.00  0.52     Sequence
```

```
             DRB1_0701  140      QFCNYPFLGVYYHKN  FLGVYYHKN  6        0.4800
277.7    26.00  0.50     Sequence
             DRB1_0701  141      FCNYPFLGVYYHKNN  FLGVYYHKN  5        0.4666
320.9    29.00  0.56     Sequence
             DRB1_0701  142      CNYPFLGVYYHKNNK  FLGVYYHKN  4        0.4179
543.8    38.00  0.73     Sequence
             DRB1_0701  143      NYPFLGVYYHKNNKS  VYYHKNNKS  6        0.5380
148.2    18.00  0.54     Sequence
             DRB1_0701  144      YPFLGVYYHKNNKSW  VYYHKNNKS  5        0.5699
105.0    14.00  0.51     Sequence
             DRB1_0701  145      PFLGVYYHKNNKSWM  VYYHKNNKS  4        0.6095
68.4    10.00  0.43     Sequence
             DRB1_0701  146      FLGVYYHKNNKSWME  VYYHKNNKS  3        0.5928
82.0    12.00  0.44     Sequence
             DRB1_0701  147      LGVYYHKNNKSWMES  VYYHKNNKS  2        0.5532
125.8    16.00  0.50     Sequence
             DRB1_0701  148      GVYYHKNNKSWMESE  VYYHKNNKS  1        0.5260
168.7    19.00  0.47     Sequence
             DRB1_0701  149      VYYHKNNKSWMESEF  VYYHKNNKS  0        0.4751
292.7    27.00  0.36     Sequence
             DRB1_0701  150      YYHKNNKSWMESEFR  YHKNNKSWM  1        0.3579
1040.0    50.00  0.42     Sequence
             DRB1_0701  151      YHKNNKSWMESEFRV  YHKNNKSWM  0        0.3123
1704.0    60.00  0.38     Sequence
             DRB1_0701  152      HKNNKSWMESEFRVY  WMESEFRVY  6        0.5380
148.3    18.00  0.79     Sequence
             DRB1_0701  153      KNNKSWMESEFRVYS  WMESEFRVY  5        0.5479
133.2    17.00  0.82     Sequence
             DRB1_0701  154      NNKSWMESEFRVYSS  WMESEFRVY  4        0.5391
146.5    18.00  0.81     Sequence
             DRB1_0701  155      NKSWMESEFRVYSSA  WMESEFRVY  3        0.5251
170.5    20.00  0.82     Sequence
             DRB1_0701  156      KSWMESEFRVYSSAN  WMESEFRVY  2        0.5396
145.7    18.00  0.73     Sequence
             DRB1_0701  157      SWMESEFRVYSSANN  WMESEFRVY  1        0.5733
101.2    14.00  0.44     Sequence
             DRB1_0701  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.5483
132.6    16.00  0.44     Sequence
             DRB1_0701  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.5106
199.4    22.00  0.57     Sequence
             DRB1_0701  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.5642
111.6    15.00  0.44     Sequence
             DRB1_0701  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.5540
124.7    16.00  0.44     Sequence
             DRB1_0701  162      EFRVYSSANNCTFEY  FRVYSSANN  1        0.5328
156.9    19.00  0.44     Sequence
             DRB1_0701  163      FRVYSSANNCTFEYV  FRVYSSANN  0        0.4891
251.5    25.00  0.37     Sequence
             DRB1_0701  164      RVYSSANNCTFEYVS  YSSANNCTF  2        0.3683
929.5    48.00  0.51     Sequence
             DRB1_0701  165      VYSSANNCTFEYVSQ  YSSANNCTF  1        0.2969
2013.1    65.00  0.61     Sequence
             DRB1_0701  166      YSSANNCTFEYVSQP  YSSANNCTF  0        0.2048
5454.1    85.00  0.65     Sequence
             DRB1_0701  167      SSANNCTFEYVSQPF  TFEYVSQPF  6        0.4085
602.0    39.00  0.84     Sequence
             DRB1_0701  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.5790
95.1    13.00  0.52     Sequence
             DRB1_0701  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.6276
56.2     8.00  0.38     Sequence         WB
             DRB1_0701  170      NNCTFEYVSQPFLMD  FEYVSQPFL  4        0.6148
64.6     9.50  0.39     Sequence         WB
             DRB1_0701  171      NCTFEYVSQPFLMDL  FEYVSQPFL  3        0.6176
62.7     9.00  0.39     Sequence         WB
             DRB1_0701  172      CTFEYVSQPFLMDLE  FEYVSQPFL  2        0.5963
78.9    11.00  0.39     Sequence
```

```
             DRB1_0701  173      TFEYVSQPFLMDLEG  FEYVSQPFL  1        0.5703
104.5    14.00  0.43     Sequence
             DRB1_0701  174      FEYVSQPFLMDLEGK  FEYVSQPFL  0        0.4631
333.3    29.00  0.49     Sequence
             DRB1_0701  175      EYVSQPFLMDLEGKQ  EYVSQPFLM  0        0.2671
2779.0    70.00  0.62     Sequence
             DRB1_0701  176      YVSQPFLMDLEGKQG  FLMDLEGKQ  5        0.1301
12240.5    95.00  0.27     Sequence
             DRB1_0701  177      VSQPFLMDLEGKQGN  LMDLEGKQG  5        0.1154
14342.3   100.00  0.40     Sequence
             DRB1_0701  178      SQPFLMDLEGKQGNF  LMDLEGKQG  4        0.1397
11033.8    95.00  0.31     Sequence
             DRB1_0701  179      QPFLMDLEGKQGNFK  LMDLEGKQG  3        0.1540
9449.0    95.00  0.25     Sequence
             DRB1_0701  180      PFLMDLEGKQGNFKN  LMDLEGKQG  2        0.1509
9771.0    95.00  0.25     Sequence
             DRB1_0701  181      FLMDLEGKQGNFKNL  DLEGKQGNF  3        0.1564
9201.2    95.00  0.23     Sequence
             DRB1_0701  182      LMDLEGKQGNFKNLS  LEGKQGNFK  3        0.1300
12250.3    95.00  0.30     Sequence
             DRB1_0701  183      MDLEGKQGNFKNLSE  LEGKQGNFK  2        0.1048
16086.2   100.00  0.34     Sequence
             DRB1_0701  184      DLEGKQGNFKNLSEF  LEGKQGNFK  1        0.0974
17422.6   100.00  0.30     Sequence
             DRB1_0701  185      LEGKQGNFKNLSEFV  NFKNLSEFV  6        0.2318
4070.5    80.00  0.75     Sequence
             DRB1_0701  186      EGKQGNFKNLSEFVF  FKNLSEFVF  6        0.3477
1161.7    55.00  0.52     Sequence
             DRB1_0701  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5        0.3523
1105.6    55.00  0.53     Sequence
             DRB1_0701  188      KQGNFKNLSEFVFKN  FKNLSEFVF  4        0.3508
1123.3    55.00  0.50     Sequence
             DRB1_0701  189      QGNFKNLSEFVFKNI  LSEFVFKNI  6        0.4571
355.6    30.00  0.50     Sequence
             DRB1_0701  190      GNFKNLSEFVFKNID  LSEFVFKNI  5        0.4435
412.2    33.00  0.51     Sequence
             DRB1_0701  191      NFKNLSEFVFKNIDG  LSEFVFKNI  4        0.4239
509.4    36.00  0.47     Sequence
             DRB1_0701  192      FKNLSEFVFKNIDGY  LSEFVFKNI  3        0.4096
594.7    39.00  0.48     Sequence
             DRB1_0701  193      KNLSEFVFKNIDGYF  LSEFVFKNI  2        0.4240
508.9    36.00  0.42     Sequence
             DRB1_0701  194      NLSEFVFKNIDGYFK  LSEFVFKNI  1        0.4373
440.9    34.00  0.34     Sequence
             DRB1_0701  195      LSEFVFKNIDGYFKI  VFKNIDGYF  4        0.4797
278.6    26.00  0.25     Sequence
             DRB1_0701  196      SEFVFKNIDGYFKIY  VFKNIDGYF  3        0.4491
387.6    32.00  0.30     Sequence
             DRB1_0701  197      EFVFKNIDGYFKIYS  VFKNIDGYF  2        0.4342
455.7    34.00  0.31     Sequence
             DRB1_0701  198      FVFKNIDGYFKIYSK  VFKNIDGYF  1        0.4029
639.6    41.00  0.32     Sequence
             DRB1_0701  199      VFKNIDGYFKIYSKH  FKNIDGYFK  1        0.3484
1152.7    55.00  0.28     Sequence
             DRB1_0701  200      FKNIDGYFKIYSKHT  YFKIYSKHT  6        0.4906
247.5    25.00  0.77     Sequence
             DRB1_0701  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.4931
240.9    24.00  0.79     Sequence
             DRB1_0701  202      NIDGYFKIYSKHTPI  KIYSKHTPI  6        0.6969
26.6     4.00  0.64     Sequence         WB
             DRB1_0701  203      IDGYFKIYSKHTPIN  KIYSKHTPI  5        0.6994
25.9     4.00  0.63     Sequence         WB
             DRB1_0701  204      DGYFKIYSKHTPINL  KIYSKHTPI  4        0.7493
15.1     1.80  0.47     Sequence         SB
             DRB1_0701  205      GYFKIYSKHTPINLV  KIYSKHTPI  3        0.7740
11.5     1.20  0.40     Sequence         SB
```

```
             DRB1_0701  206      YFKIYSKHTPINLVR  KIYSKHTPI  2        0.7615
13.2     1.50  0.41     Sequence         SB
             DRB1_0701  207      FKIYSKHTPINLVRD  KIYSKHTPI  1        0.7194
20.8     3.00  0.41     Sequence         WB
             DRB1_0701  208      KIYSKHTPINLVRDL  YSKHTPINL  2        0.6670
36.7     5.50  0.42     Sequence         WB
             DRB1_0701  209      IYSKHTPINLVRDLP  YSKHTPINL  1        0.5600
116.8    15.00  0.58     Sequence
             DRB1_0701  210      YSKHTPINLVRDLPQ  YSKHTPINL  0        0.5095
201.8    22.00  0.41     Sequence
             DRB1_0701  211      SKHTPINLVRDLPQG  INLVRDLPQ  5        0.3484
1152.8    55.00  0.47     Sequence
             DRB1_0701  212      KHTPINLVRDLPQGF  INLVRDLPQ  4        0.3145
1664.1    60.00  0.56     Sequence
             DRB1_0701  213      HTPINLVRDLPQGFS  INLVRDLPQ  3        0.3085
1776.4    65.00  0.55     Sequence
             DRB1_0701  214      TPINLVRDLPQGFSA  INLVRDLPQ  2        0.3020
1905.5    65.00  0.55     Sequence
             DRB1_0701  215      PINLVRDLPQGFSAL  INLVRDLPQ  1        0.3018
1908.7    65.00  0.47     Sequence
             DRB1_0701  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.2865
2252.1    70.00  0.47     Sequence
             DRB1_0701  217      NLVRDLPQGFSALEP  LVRDLPQGF  1        0.2344
3956.6    80.00  0.52     Sequence
             DRB1_0701  218      LVRDLPQGFSALEPL  QGFSALEPL  6        0.2640
2873.4    75.00  0.31     Sequence
             DRB1_0701  219      VRDLPQGFSALEPLV  QGFSALEPL  5        0.2449
3534.2    75.00  0.38     Sequence
             DRB1_0701  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.3314
1386.4    60.00  0.55     Sequence
             DRB1_0701  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.3732
881.6    47.00  0.65     Sequence
             DRB1_0701  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.3622
992.9    49.00  0.66     Sequence
             DRB1_0701  223      PQGFSALEPLVDLPI  LEPLVDLPI  6        0.4974
230.1    24.00  0.50     Sequence
             DRB1_0701  224      QGFSALEPLVDLPIG  LEPLVDLPI  5        0.4779
284.0    27.00  0.51     Sequence
             DRB1_0701  225      GFSALEPLVDLPIGI  LEPLVDLPI  4        0.4921
243.7    24.00  0.54     Sequence
             DRB1_0701  226      FSALEPLVDLPIGIN  LEPLVDLPI  3        0.4524
374.3    31.00  0.59     Sequence
             DRB1_0701  227      SALEPLVDLPIGINI  LEPLVDLPI  2        0.4271
492.2    36.00  0.56     Sequence
             DRB1_0701  228      ALEPLVDLPIGINIT  LEPLVDLPI  1        0.4056
620.7    40.00  0.54     Sequence
             DRB1_0701  229      LEPLVDLPIGINITR  LEPLVDLPI  0        0.3642
971.8    49.00  0.44     Sequence
             DRB1_0701  230      EPLVDLPIGINITRF  PIGINITRF  6        0.3235
1510.1    60.00  0.28     Sequence
             DRB1_0701  231      PLVDLPIGINITRFQ  PIGINITRF  5        0.3110
1727.6    60.00  0.28     Sequence
             DRB1_0701  232      LVDLPIGINITRFQT  PIGINITRF  4        0.2886
2201.1    65.00  0.32     Sequence
             DRB1_0701  233      VDLPIGINITRFQTL  INITRFQTL  6        0.4911
246.2    25.00  0.76     Sequence
             DRB1_0701  234      DLPIGINITRFQTLL  INITRFQTL  5        0.4739
296.6    27.00  0.75     Sequence
             DRB1_0701  235      LPIGINITRFQTLLA  INITRFQTL  4        0.5139
192.4    21.00  0.55     Sequence
             DRB1_0701  236      PIGINITRFQTLLAL  INITRFQTL  3        0.5190
182.2    20.00  0.54     Sequence
             DRB1_0701  237      IGINITRFQTLLALH  INITRFQTL  2        0.5161
187.8    21.00  0.55     Sequence
             DRB1_0701  238      GINITRFQTLLALHR  INITRFQTL  1        0.5477
133.4    17.00  0.41     Sequence
```

```
             DRB1_0701  239      INITRFQTLLALHRS  FQTLLALHR  5        0.5236
173.1    20.00  0.42     Sequence
             DRB1_0701  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.5021
218.6    23.00  0.47     Sequence
             DRB1_0701  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.5579
119.5    15.00  0.37     Sequence
             DRB1_0701  242      TRFQTLLALHRSYLT  LALHRSYLT  6        0.7620
13.1     1.50  0.81     Sequence        SB
             DRB1_0701  243      RFQTLLALHRSYLTP  LALHRSYLT  5        0.7467
15.5     1.90  0.83     Sequence        SB
             DRB1_0701  244      FQTLLALHRSYLTPG  LALHRSYLT  4        0.7126
22.4     3.50  0.82     Sequence        WB
             DRB1_0701  245      QTLLALHRSYLTPGD  LALHRSYLT  3        0.6849
30.3     4.50  0.88     Sequence        WB
             DRB1_0701  246      TLLALHRSYLTPGDS  LALHRSYLT  2        0.6672
36.6     5.50  0.87     Sequence        WB
             DRB1_0701  247      LLALHRSYLTPGDSS  LALHRSYLT  1        0.6378
50.3     7.50  0.86     Sequence        WB
             DRB1_0701  248      LALHRSYLTPGDSSS  LALHRSYLT  0        0.5419
142.1    17.00  0.77     Sequence
             DRB1_0701  249      ALHRSYLTPGDSSSG  LHRSYLTPG  1        0.2074
5298.7    85.00  0.37     Sequence
             DRB1_0701  250      LHRSYLTPGDSSSGW  LTPGDSSSG  5        0.1915
6294.6    90.00  0.28     Sequence
             DRB1_0701  251      HRSYLTPGDSSSGWT  PGDSSSGWT  6        0.1868
6621.7    90.00  0.28     Sequence
             DRB1_0701  252      RSYLTPGDSSSGWTA  PGDSSSGWT  5        0.1924
6233.7    90.00  0.27     Sequence
             DRB1_0701  253      SYLTPGDSSSGWTAG  PGDSSSGWT  4        0.1739
7614.6    90.00  0.27     Sequence
             DRB1_0701  254      YLTPGDSSSGWTAGA  PGDSSSGWT  3        0.1519
9670.0    95.00  0.31     Sequence
             DRB1_0701  255      LTPGDSSSGWTAGAA  PGDSSSGWT  2        0.1346
11649.4    95.00  0.29     Sequence
             DRB1_0701  256      TPGDSSSGWTAGAAA  SGWTAGAAA  6        0.2350
3932.4    80.00  0.58     Sequence
             DRB1_0701  257      PGDSSSGWTAGAAAY  SGWTAGAAA  5        0.2683
2743.0    70.00  0.62     Sequence
             DRB1_0701  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.3917
722.0    43.00  0.59     Sequence
             DRB1_0701  259      DSSSGWTAGAAAYYV  TAGAAAYYV  6        0.5693
105.7    14.00  0.64     Sequence
             DRB1_0701  260      SSSGWTAGAAAYYVG  TAGAAAYYV  5        0.5547
123.7    16.00  0.66     Sequence
             DRB1_0701  261      SSGWTAGAAAYYVGY  TAGAAAYYV  4        0.5479
133.2    17.00  0.65     Sequence
             DRB1_0701  262      SGWTAGAAAYYVGYL  TAGAAAYYV  3        0.5474
133.9    17.00  0.71     Sequence
             DRB1_0701  263      GWTAGAAAYYVGYLQ  TAGAAAYYV  2        0.5181
183.9    21.00  0.77     Sequence
             DRB1_0701  264      WTAGAAAYYVGYLQP  TAGAAAYYV  1        0.4772
286.2    27.00  0.77     Sequence
             DRB1_0701  265      TAGAAAYYVGYLQPR  TAGAAAYYV  0        0.3732
881.6    47.00  0.75     Sequence
             DRB1_0701  266      AGAAAYYVGYLQPRT  YVGYLQPRT  6        0.1901
6391.2    90.00  0.37     Sequence
             DRB1_0701  267      GAAAYYVGYLQPRTF  VGYLQPRTF  6        0.3400
1262.7    55.00  0.66     Sequence
             DRB1_0701  268      AAAYYVGYLQPRTFL  VGYLQPRTF  5        0.3794
824.6    45.00  0.68     Sequence
             DRB1_0701  269      AAYYVGYLQPRTFLL  YLQPRTFLL  6        0.5949
80.1    11.00  0.65     Sequence
             DRB1_0701  270      AYYVGYLQPRTFLLK  YLQPRTFLL  5        0.5779
96.2    13.00  0.68     Sequence
             DRB1_0701  271      YYVGYLQPRTFLLKY  YLQPRTFLL  4        0.5606
116.1    15.00  0.68     Sequence
```

```
             DRB1_0701  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.5315
159.0    19.00  0.69     Sequence
             DRB1_0701  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.4815
273.1    26.00  0.77     Sequence
             DRB1_0701  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.4384
435.5    34.00  0.83     Sequence
             DRB1_0701  275      YLQPRTFLLKYNENG  YLQPRTFLL  0        0.3649
964.6    49.00  0.77     Sequence
             DRB1_0701  276      LQPRTFLLKYNENGT  LLKYNENGT  6        0.2090
5211.2    85.00  0.58     Sequence
             DRB1_0701  277      QPRTFLLKYNENGTI  LKYNENGTI  6        0.4027
640.4    41.00  0.62     Sequence
             DRB1_0701  278      PRTFLLKYNENGTIT  LKYNENGTI  5        0.4005
656.3    41.00  0.61     Sequence
             DRB1_0701  279      RTFLLKYNENGTITD  LKYNENGTI  4        0.3945
700.5    42.00  0.58     Sequence
             DRB1_0701  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.3773
843.1    46.00  0.60     Sequence
             DRB1_0701  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.3652
960.9    48.00  0.60     Sequence
             DRB1_0701  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.3296
1412.7    60.00  0.62     Sequence
             DRB1_0701  283      LKYNENGTITDAVDC  LKYNENGTI  0        0.3057
1829.6    65.00  0.46     Sequence
             DRB1_0701  284      KYNENGTITDAVDCA  GTITDAVDC  5        0.2270
4289.0    80.00  0.57     Sequence
             DRB1_0701  285      YNENGTITDAVDCAL  GTITDAVDC  4        0.2926
2108.3    65.00  0.45     Sequence
             DRB1_0701  286      NENGTITDAVDCALD  GTITDAVDC  3        0.2741
2576.2    70.00  0.47     Sequence
             DRB1_0701  287      ENGTITDAVDCALDP  GTITDAVDC  2        0.2589
3035.3    75.00  0.49     Sequence
             DRB1_0701  288      NGTITDAVDCALDPL  GTITDAVDC  1        0.2559
3136.5    75.00  0.47     Sequence
             DRB1_0701  289      GTITDAVDCALDPLS  ITDAVDCAL  2        0.2126
5012.1    85.00  0.43     Sequence
             DRB1_0701  290      TITDAVDCALDPLSE  ITDAVDCAL  1        0.1469
10197.5    95.00  0.63     Sequence
             DRB1_0701  291      ITDAVDCALDPLSET  ITDAVDCAL  0        0.1250
12925.3   100.00  0.47     Sequence
             DRB1_0701  292      TDAVDCALDPLSETK  CALDPLSET  5        0.0659
24496.1   100.00  0.19     Sequence
             DRB1_0701  293      DAVDCALDPLSETKC  LDPLSETKC  6        0.1112
15019.4   100.00  0.50     Sequence
             DRB1_0701  294      AVDCALDPLSETKCT  LDPLSETKC  5        0.1166
14164.7   100.00  0.52     Sequence
             DRB1_0701  295      VDCALDPLSETKCTL  LDPLSETKC  4        0.1862
6671.9    90.00  0.35     Sequence
             DRB1_0701  296      DCALDPLSETKCTLK  LSETKCTLK  6        0.2109
5103.6    85.00  0.32     Sequence
             DRB1_0701  297      CALDPLSETKCTLKS  LSETKCTLK  5        0.2090
5212.8    85.00  0.32     Sequence
             DRB1_0701  298      ALDPLSETKCTLKSF  LSETKCTLK  4        0.2186
4696.0    85.00  0.32     Sequence
             DRB1_0701  299      LDPLSETKCTLKSFT  LSETKCTLK  3        0.2219
4530.6    80.00  0.24     Sequence
             DRB1_0701  300      DPLSETKCTLKSFTV  KCTLKSFTV  6        0.5231
174.2    20.00  0.80     Sequence
             DRB1_0701  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.5087
203.6    22.00  0.81     Sequence
             DRB1_0701  302      LSETKCTLKSFTVEK  KCTLKSFTV  4        0.4997
224.5    23.00  0.77     Sequence
             DRB1_0701  303      SETKCTLKSFTVEKG  KCTLKSFTV  3        0.4879
254.9    25.00  0.65     Sequence
             DRB1_0701  304      ETKCTLKSFTVEKGI  KCTLKSFTV  2        0.5298
162.0    19.00  0.43     Sequence
```

```
             DRB1_0701  305      TKCTLKSFTVEKGIY  KCTLKSFTV  1        0.5218
176.7    20.00  0.39     Sequence
             DRB1_0701  306      KCTLKSFTVEKGIYQ  KCTLKSFTV  0        0.4934
240.2    24.00  0.27     Sequence
             DRB1_0701  307      CTLKSFTVEKGIYQT  LKSFTVEKG  2        0.4141
566.4    38.00  0.29     Sequence
             DRB1_0701  308      TLKSFTVEKGIYQTS  LKSFTVEKG  1        0.3936
706.8    42.00  0.28     Sequence
             DRB1_0701  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.3330
1362.2    60.00  0.31     Sequence
             DRB1_0701  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.2914
2137.0    65.00  0.37     Sequence
             DRB1_0701  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.2382
3797.8    80.00  0.40     Sequence
             DRB1_0701  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.5690
105.9    14.00  0.89     Sequence
             DRB1_0701  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.5768
97.4    13.00  0.89     Sequence
             DRB1_0701  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.5598
117.1    15.00  0.88     Sequence
             DRB1_0701  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.5453
137.0    17.00  0.87     Sequence
             DRB1_0701  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.5359
151.6    18.00  0.88     Sequence
             DRB1_0701  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.5160
188.0    21.00  0.76     Sequence
             DRB1_0701  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.6222
59.6     8.50  0.56     Sequence         WB
             DRB1_0701  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.6128
66.0     9.50  0.70     Sequence         WB
             DRB1_0701  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.6217
59.9     8.50  0.60     Sequence         WB
             DRB1_0701  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.6325
53.3     8.00  0.58     Sequence         WB
             DRB1_0701  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.6132
65.7     9.50  0.56     Sequence         WB
             DRB1_0701  323      NFRVQPTESIVRFPN  FRVQPTESI  1        0.5810
93.1    13.00  0.56     Sequence
             DRB1_0701  324      FRVQPTESIVRFPNI  FRVQPTESI  0        0.5172
185.7    21.00  0.47     Sequence
             DRB1_0701  325      RVQPTESIVRFPNIT  VQPTESIVR  1        0.3684
928.8    48.00  0.58     Sequence
             DRB1_0701  326      VQPTESIVRFPNITN  VQPTESIVR  0        0.2899
2170.6    65.00  0.35     Sequence
             DRB1_0701  327      QPTESIVRFPNITNL  VRFPNITNL  6        0.3087
1771.9    65.00  0.31     Sequence
             DRB1_0701  328      PTESIVRFPNITNLC  VRFPNITNL  5        0.2911
2142.8    65.00  0.29     Sequence
             DRB1_0701  329      TESIVRFPNITNLCP  VRFPNITNL  4        0.2919
2125.9    65.00  0.25     Sequence
             DRB1_0701  330      ESIVRFPNITNLCPF  PNITNLCPF  6        0.3418
1239.0    55.00  0.29     Sequence
             DRB1_0701  331      SIVRFPNITNLCPFG  PNITNLCPF  5        0.3242
1497.8    60.00  0.31     Sequence
             DRB1_0701  332      IVRFPNITNLCPFGE  PNITNLCPF  4        0.3146
1662.7    60.00  0.32     Sequence
             DRB1_0701  333      VRFPNITNLCPFGEV  PNITNLCPF  3        0.3003
1939.4    65.00  0.35     Sequence
             DRB1_0701  334      RFPNITNLCPFGEVF  PNITNLCPF  2        0.2860
2265.3    70.00  0.35     Sequence
             DRB1_0701  335      FPNITNLCPFGEVFN  PNITNLCPF  1        0.2637
2882.6    75.00  0.33     Sequence
             DRB1_0701  336      PNITNLCPFGEVFNA  PNITNLCPF  0        0.2135
4962.1    85.00  0.26     Sequence
             DRB1_0701  337      NITNLCPFGEVFNAT  ITNLCPFGE  1        0.1750
7531.2    90.00  0.25     Sequence
```

```
             DRB1_0701  338      ITNLCPFGEVFNATR  FGEVFNATR  6        0.1943
6111.1    85.00  0.34     Sequence
             DRB1_0701  339      TNLCPFGEVFNATRF  GEVFNATRF  6        0.3843
781.6    44.00  0.75     Sequence
             DRB1_0701  340      NLCPFGEVFNATRFA  GEVFNATRF  5        0.4015
649.0    41.00  0.74     Sequence
             DRB1_0701  341      LCPFGEVFNATRFAS  GEVFNATRF  4        0.4067
613.8    40.00  0.69     Sequence
             DRB1_0701  342      CPFGEVFNATRFASV  FNATRFASV  6        0.6644
37.8     5.50  0.75     Sequence         WB
             DRB1_0701  343      PFGEVFNATRFASVY  FNATRFASV  5        0.6579
40.5     6.00  0.75     Sequence         WB
             DRB1_0701  344      FGEVFNATRFASVYA  FNATRFASV  4        0.6554
41.6     6.50  0.67     Sequence         WB
             DRB1_0701  345      GEVFNATRFASVYAW  FNATRFASV  3        0.6373
50.6     7.50  0.65     Sequence         WB
             DRB1_0701  346      EVFNATRFASVYAWN  FNATRFASV  2        0.6251
57.8     8.50  0.69     Sequence         WB
             DRB1_0701  347      VFNATRFASVYAWNR  FNATRFASV  1        0.6485
44.8     6.50  0.52     Sequence         WB
             DRB1_0701  348      FNATRFASVYAWNRK  FNATRFASV  0        0.6090
68.8    10.00  0.38     Sequence
             DRB1_0701  349      NATRFASVYAWNRKR  FASVYAWNR  4        0.5155
189.1    21.00  0.44     Sequence
             DRB1_0701  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.5372
149.6    18.00  0.44     Sequence
             DRB1_0701  351      TRFASVYAWNRKRIS  FASVYAWNR  2        0.5357
151.9    18.00  0.44     Sequence
             DRB1_0701  352      RFASVYAWNRKRISN  FASVYAWNR  1        0.5052
211.3    22.00  0.46     Sequence
             DRB1_0701  353      FASVYAWNRKRISNC  FASVYAWNR  0        0.4304
474.7    35.00  0.35     Sequence
             DRB1_0701  354      ASVYAWNRKRISNCV  NRKRISNCV  6        0.4181
542.5    37.00  0.36     Sequence
             DRB1_0701  355      SVYAWNRKRISNCVA  NRKRISNCV  5        0.4291
481.3    35.00  0.32     Sequence
             DRB1_0701  356      VYAWNRKRISNCVAD  NRKRISNCV  4        0.3982
672.7    42.00  0.38     Sequence
             DRB1_0701  357      YAWNRKRISNCVADY  NRKRISNCV  3        0.3499
1135.0    55.00  0.45     Sequence
             DRB1_0701  358      AWNRKRISNCVADYS  NRKRISNCV  2        0.3029
1887.2    65.00  0.43     Sequence
             DRB1_0701  359      WNRKRISNCVADYSV  NRKRISNCV  1        0.3258
1473.0    60.00  0.31     Sequence
             DRB1_0701  360      NRKRISNCVADYSVL  SNCVADYSV  5        0.3187
1589.2    60.00  0.32     Sequence
             DRB1_0701  361      RKRISNCVADYSVLY  SNCVADYSV  4        0.3110
1728.6    60.00  0.34     Sequence
             DRB1_0701  362      KRISNCVADYSVLYN  SNCVADYSV  3        0.2762
2517.6    70.00  0.38     Sequence
             DRB1_0701  363      RISNCVADYSVLYNS  SNCVADYSV  2        0.2548
3176.0    75.00  0.37     Sequence
             DRB1_0701  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.2373
3836.0    80.00  0.26     Sequence
             DRB1_0701  365      SNCVADYSVLYNSAS  CVADYSVLY  2        0.2181
4722.3    85.00  0.29     Sequence
             DRB1_0701  366      NCVADYSVLYNSASF  SVLYNSASF  6        0.2649
2845.2    75.00  0.51     Sequence
             DRB1_0701  367      CVADYSVLYNSASFS  VLYNSASFS  6        0.3233
1512.6    60.00  0.41     Sequence
             DRB1_0701  368      VADYSVLYNSASFST  LYNSASFST  6        0.4364
445.2    34.00  0.56     Sequence
             DRB1_0701  369      ADYSVLYNSASFSTF  LYNSASFST  5        0.4849
263.2    26.00  0.54     Sequence
             DRB1_0701  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.4862
259.7    25.00  0.56     Sequence
```

```
             DRB1_0701  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.4842
265.4    26.00  0.49     Sequence
             DRB1_0701  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.4661
322.6    29.00  0.45     Sequence
             DRB1_0701  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.4354
449.8    34.00  0.47     Sequence
             DRB1_0701  374      LYNSASFSTFKCYGV  FSTFKCYGV  6        0.5916
83.0    12.00  0.68     Sequence
             DRB1_0701  375      YNSASFSTFKCYGVS  FSTFKCYGV  5        0.5690
105.9    14.00  0.79     Sequence
             DRB1_0701  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.5411
143.4    17.00  0.79     Sequence
             DRB1_0701  377      SASFSTFKCYGVSPT  FSTFKCYGV  3        0.5853
88.8    12.00  0.58     Sequence
             DRB1_0701  378      ASFSTFKCYGVSPTK  FSTFKCYGV  2        0.5734
101.0    14.00  0.56     Sequence
             DRB1_0701  379      SFSTFKCYGVSPTKL  CYGVSPTKL  6        0.7000
25.7     4.00  0.52     Sequence        WB
             DRB1_0701  380      FSTFKCYGVSPTKLN  CYGVSPTKL  5        0.7012
25.4     4.00  0.57     Sequence        WB
             DRB1_0701  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.6624
38.6     6.00  0.64     Sequence        WB
             DRB1_0701  382      TFKCYGVSPTKLNDL  CYGVSPTKL  3        0.6902
28.6     4.50  0.60     Sequence        WB
             DRB1_0701  383      FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.6622
38.6     6.00  0.62     Sequence        WB
             DRB1_0701  384      KCYGVSPTKLNDLCF  CYGVSPTKL  1        0.6163
63.5     9.00  0.60     Sequence        WB
             DRB1_0701  385      CYGVSPTKLNDLCFT  CYGVSPTKL  0        0.5268
167.4    19.00  0.45     Sequence
             DRB1_0701  386      YGVSPTKLNDLCFTN  VSPTKLNDL  2        0.3792
825.9    45.00  0.47     Sequence
             DRB1_0701  387      GVSPTKLNDLCFTNV  VSPTKLNDL  1        0.3345
1339.9    55.00  0.42     Sequence
             DRB1_0701  388      VSPTKLNDLCFTNVY  PTKLNDLCF  2        0.2984
1980.3    65.00  0.41     Sequence
             DRB1_0701  389      SPTKLNDLCFTNVYA  PTKLNDLCF  1        0.2736
2589.6    70.00  0.44     Sequence
             DRB1_0701  390      PTKLNDLCFTNVYAD  LCFTNVYAD  6        0.3430
1223.1    55.00  0.50     Sequence
             DRB1_0701  391      TKLNDLCFTNVYADS  LCFTNVYAD  5        0.3094
1757.4    65.00  0.57     Sequence
             DRB1_0701  392      KLNDLCFTNVYADSF  FTNVYADSF  6        0.3976
677.4    42.00  0.46     Sequence
             DRB1_0701  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.4138
568.4    38.00  0.44     Sequence
             DRB1_0701  394      NDLCFTNVYADSFVI  NVYADSFVI  6        0.4973
230.3    24.00  0.40     Sequence
             DRB1_0701  395      DLCFTNVYADSFVIR  NVYADSFVI  5        0.4891
251.6    25.00  0.41     Sequence
             DRB1_0701  396      LCFTNVYADSFVIRG  NVYADSFVI  4        0.4746
294.3    27.00  0.40     Sequence
             DRB1_0701  397      CFTNVYADSFVIRGD  NVYADSFVI  3        0.4255
500.5    36.00  0.47     Sequence
             DRB1_0701  398      FTNVYADSFVIRGDE  NVYADSFVI  2        0.4003
657.9    41.00  0.53     Sequence
             DRB1_0701  399      TNVYADSFVIRGDEV  NVYADSFVI  1        0.4056
621.0    40.00  0.44     Sequence
             DRB1_0701  400      NVYADSFVIRGDEVR  SFVIRGDEV  5        0.3816
805.3    45.00  0.36     Sequence
             DRB1_0701  401      VYADSFVIRGDEVRQ  SFVIRGDEV  4        0.3085
1775.9    65.00  0.53     Sequence
             DRB1_0701  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.3755
860.3    46.00  0.38     Sequence
             DRB1_0701  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.3603
1013.3    50.00  0.47     Sequence
```

```
             DRB1_0701  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.3390
1277.0    55.00  0.47     Sequence
             DRB1_0701  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.3066
1813.0    65.00  0.44     Sequence
             DRB1_0701  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.2375
3826.6    80.00  0.62     Sequence
             DRB1_0701  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.2471
3449.6    75.00  0.47     Sequence
             DRB1_0701  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.2200
4628.2    80.00  0.44     Sequence
             DRB1_0701  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.1765
7404.5    90.00  0.64     Sequence
             DRB1_0701  410      GDEVRQIAPGQTGTI  IAPGQTGTI  6        0.3197
1573.5    60.00  0.61     Sequence
             DRB1_0701  411      DEVRQIAPGQTGTIA  IAPGQTGTI  5        0.3166
1627.1    60.00  0.64     Sequence
             DRB1_0701  412      EVRQIAPGQTGTIAD  IAPGQTGTI  4        0.3098
1749.9    65.00  0.60     Sequence
             DRB1_0701  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.2916
2131.5    65.00  0.62     Sequence
             DRB1_0701  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.2588
3041.4    75.00  0.73     Sequence
             DRB1_0701  415      QIAPGQTGTIADYNY  IAPGQTGTI  1        0.2212
4565.3    80.00  0.69     Sequence
             DRB1_0701  416      IAPGQTGTIADYNYK  IAPGQTGTI  0        0.1730
7693.6    90.00  0.53     Sequence
             DRB1_0701  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.1651
8381.4    90.00  0.43     Sequence
             DRB1_0701  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.1558
9269.0    95.00  0.42     Sequence
             DRB1_0701  419      GQTGTIADYNYKLPD  TIADYNYKL  4        0.1412
10845.7    95.00  0.48     Sequence
             DRB1_0701  420      QTGTIADYNYKLPDD  TIADYNYKL  3        0.1279
12535.3    95.00  0.48     Sequence
             DRB1_0701  421      TGTIADYNYKLPDDF  TIADYNYKL  2        0.1478
10107.4    95.00  0.35     Sequence
             DRB1_0701  422      GTIADYNYKLPDDFT  YNYKLPDDF  5        0.1438
10552.3    95.00  0.34     Sequence
             DRB1_0701  423      TIADYNYKLPDDFTG  YNYKLPDDF  4        0.1459
10316.9    95.00  0.29     Sequence
             DRB1_0701  424      IADYNYKLPDDFTGC  YKLPDDFTG  5        0.1237
13117.7   100.00  0.38     Sequence
             DRB1_0701  425      ADYNYKLPDDFTGCV  YKLPDDFTG  4        0.1252
12905.8   100.00  0.43     Sequence
             DRB1_0701  426      DYNYKLPDDFTGCVI  PDDFTGCVI  6        0.2655
2826.9    75.00  0.56     Sequence
             DRB1_0701  427      YNYKLPDDFTGCVIA  PDDFTGCVI  5        0.2691
2718.4    70.00  0.54     Sequence
             DRB1_0701  428      NYKLPDDFTGCVIAW  PDDFTGCVI  4        0.2578
3073.1    75.00  0.59     Sequence
             DRB1_0701  429      YKLPDDFTGCVIAWN  PDDFTGCVI  3        0.2619
2941.1    75.00  0.51     Sequence
             DRB1_0701  430      KLPDDFTGCVIAWNS  PDDFTGCVI  2        0.2697
2700.4    70.00  0.40     Sequence
             DRB1_0701  431      LPDDFTGCVIAWNSN  PDDFTGCVI  1        0.2676
2765.1    70.00  0.35     Sequence
             DRB1_0701  432      PDDFTGCVIAWNSNN  TGCVIAWNS  4        0.2576
3078.3    75.00  0.26     Sequence
             DRB1_0701  433      DDFTGCVIAWNSNNL  VIAWNSNNL  6        0.4388
433.7    34.00  0.66     Sequence
             DRB1_0701  434      DFTGCVIAWNSNNLD  VIAWNSNNL  5        0.4521
375.5    31.00  0.59     Sequence
             DRB1_0701  435      FTGCVIAWNSNNLDS  VIAWNSNNL  4        0.4398
429.0    33.00  0.60     Sequence
             DRB1_0701  436      TGCVIAWNSNNLDSK  VIAWNSNNL  3        0.4188
538.5    37.00  0.62     Sequence
```

```
             DRB1_0701  437      GCVIAWNSNNLDSKV  VIAWNSNNL  2        0.4002
658.4    41.00  0.65     Sequence
             DRB1_0701  438      CVIAWNSNNLDSKVG  VIAWNSNNL  1        0.3779
837.8    46.00  0.67     Sequence
             DRB1_0701  439      VIAWNSNNLDSKVGG  VIAWNSNNL  0        0.3359
1320.7    55.00  0.62     Sequence
             DRB1_0701  440      IAWNSNNLDSKVGGN  IAWNSNNLD  0        0.1607
8784.4    95.00  0.47     Sequence
             DRB1_0701  441      AWNSNNLDSKVGGNY  LDSKVGGNY  6        0.1140
14565.5   100.00  0.32     Sequence
             DRB1_0701  442      WNSNNLDSKVGGNYN  DSKVGGNYN  6        0.1269
12664.9   100.00  0.29     Sequence
             DRB1_0701  443      NSNNLDSKVGGNYNY  DSKVGGNYN  5        0.1532
9530.1    95.00  0.29     Sequence
             DRB1_0701  444      SNNLDSKVGGNYNYL  DSKVGGNYN  4        0.1865
6645.6    90.00  0.26     Sequence
             DRB1_0701  445      NNLDSKVGGNYNYLY  DSKVGGNYN  3        0.1956
6021.1    85.00  0.25     Sequence
             DRB1_0701  446      NLDSKVGGNYNYLYR  DSKVGGNYN  2        0.1873
6591.4    90.00  0.23     Sequence
             DRB1_0701  447      LDSKVGGNYNYLYRL  KVGGNYNYL  3        0.2066
5347.8    85.00  0.22     Sequence
             DRB1_0701  448      DSKVGGNYNYLYRLF  NYNYLYRLF  6        0.2332
4008.8    80.00  0.28     Sequence
             DRB1_0701  449      SKVGGNYNYLYRLFR  NYNYLYRLF  5        0.2176
4746.3    85.00  0.29     Sequence
             DRB1_0701  450      KVGGNYNYLYRLFRK  NYNYLYRLF  4        0.2053
5421.2    85.00  0.29     Sequence
             DRB1_0701  451      VGGNYNYLYRLFRKS  YLYRLFRKS  6        0.2891
2191.2    65.00  0.56     Sequence
             DRB1_0701  452      GGNYNYLYRLFRKSN  YLYRLFRKS  5        0.2940
2078.1    65.00  0.53     Sequence
             DRB1_0701  453      GNYNYLYRLFRKSNL  YRLFRKSNL  6        0.5695
105.4    14.00  0.78     Sequence
             DRB1_0701  454      NYNYLYRLFRKSNLK  YRLFRKSNL  5        0.5564
121.4    15.00  0.75     Sequence
             DRB1_0701  455      YNYLYRLFRKSNLKP  YRLFRKSNL  4        0.5347
153.6    18.00  0.73     Sequence
             DRB1_0701  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6        0.7373
17.2     2.50  0.80     Sequence         WB
             DRB1_0701  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.7525
14.5     1.70  0.82     Sequence         SB
             DRB1_0701  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.7419
16.3     2.00  0.84     Sequence         WB
             DRB1_0701  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.7200
20.7     3.00  0.88     Sequence         WB
             DRB1_0701  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.6783
32.5     5.00  0.95     Sequence         WB
             DRB1_0701  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.6262
57.1     8.50  0.94     Sequence         WB
             DRB1_0701  462      FRKSNLKPFERDIST  FRKSNLKPF  0        0.5119
196.6    21.00  0.89     Sequence
             DRB1_0701  463      RKSNLKPFERDISTE  NLKPFERDI  3        0.1192
13761.2   100.00  0.38     Sequence
             DRB1_0701  464      KSNLKPFERDISTEI  FERDISTEI  6        0.6016
74.5    11.00  0.95     Sequence
             DRB1_0701  465      SNLKPFERDISTEIY  FERDISTEI  5        0.6237
58.6     8.50  0.94     Sequence         WB
             DRB1_0701  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.6114
67.0     9.50  0.94     Sequence         WB
             DRB1_0701  467      LKPFERDISTEIYQA  FERDISTEI  3        0.5985
77.0    11.00  0.93     Sequence
             DRB1_0701  468      KPFERDISTEIYQAG  FERDISTEI  2        0.5806
93.5    13.00  0.93     Sequence
             DRB1_0701  469      PFERDISTEIYQAGS  FERDISTEI  1        0.5310
159.9    19.00  0.92     Sequence
```

```
             DRB1_0701  470      FERDISTEIYQAGST  FERDISTEI  0        0.4594
346.9    30.00  0.87     Sequence
             DRB1_0701  471      ERDISTEIYQAGSTP  DISTEIYQA  2        0.1458
10325.6    95.00  0.38     Sequence
             DRB1_0701  472      RDISTEIYQAGSTPC  IYQAGSTPC  6        0.4172
547.9    38.00  0.83     Sequence
             DRB1_0701  473      DISTEIYQAGSTPCN  IYQAGSTPC  5        0.4328
462.8    35.00  0.89     Sequence
             DRB1_0701  474      ISTEIYQAGSTPCNG  IYQAGSTPC  4        0.4082
604.0    39.00  0.88     Sequence
             DRB1_0701  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.4236
511.3    36.00  0.86     Sequence
             DRB1_0701  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.4072
610.1    40.00  0.87     Sequence
             DRB1_0701  477      EIYQAGSTPCNGVKG  IYQAGSTPC  1        0.3813
808.0    45.00  0.86     Sequence
             DRB1_0701  478      IYQAGSTPCNGVKGF  IYQAGSTPC  0        0.3288
1425.5    60.00  0.79     Sequence
             DRB1_0701  479      YQAGSTPCNGVKGFN  AGSTPCNGV  2        0.1088
15414.3   100.00  0.31     Sequence
             DRB1_0701  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.2962
2028.2    65.00  0.81     Sequence
             DRB1_0701  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.3124
1702.2    60.00  0.88     Sequence
             DRB1_0701  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.3408
1252.3    55.00  0.75     Sequence
             DRB1_0701  483      STPCNGVKGFNCYFP  CNGVKGFNC  3        0.3221
1532.1    60.00  0.72     Sequence
             DRB1_0701  484      TPCNGVKGFNCYFPL  CNGVKGFNC  2        0.3491
1143.8    55.00  0.58     Sequence
             DRB1_0701  485      PCNGVKGFNCYFPLQ  CNGVKGFNC  1        0.3316
1382.9    60.00  0.53     Sequence
             DRB1_0701  486      CNGVKGFNCYFPLQS  CNGVKGFNC  0        0.3352
1329.4    55.00  0.34     Sequence
             DRB1_0701  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.2804
2405.6    70.00  0.34     Sequence
             DRB1_0701  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.2633
2896.2    75.00  0.34     Sequence
             DRB1_0701  489      VKGFNCYFPLQSYGF  YFPLQSYGF  6        0.5648
110.9    15.00  0.79     Sequence
             DRB1_0701  490      KGFNCYFPLQSYGFQ  YFPLQSYGF  5        0.5688
106.2    14.00  0.81     Sequence
             DRB1_0701  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.5487
132.0    16.00  0.83     Sequence
             DRB1_0701  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.5364
150.9    18.00  0.81     Sequence
             DRB1_0701  493      NCYFPLQSYGFQPTY  YFPLQSYGF  2        0.5141
191.9    21.00  0.82     Sequence
             DRB1_0701  494      CYFPLQSYGFQPTYG  YFPLQSYGF  1        0.4870
257.3    25.00  0.79     Sequence
             DRB1_0701  495      YFPLQSYGFQPTYGV  YFPLQSYGF  0        0.5162
187.7    21.00  0.44     Sequence
             DRB1_0701  496      FPLQSYGFQPTYGVG  YGFQPTYGV  5        0.3923
717.3    43.00  0.61     Sequence
             DRB1_0701  497      PLQSYGFQPTYGVGY  FQPTYGVGY  6        0.5710
103.7    14.00  0.64     Sequence
             DRB1_0701  498      LQSYGFQPTYGVGYQ  FQPTYGVGY  5        0.5840
90.1    12.00  0.69     Sequence
             DRB1_0701  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4        0.5663
109.1    14.00  0.70     Sequence
             DRB1_0701  500      SYGFQPTYGVGYQPY  FQPTYGVGY  3        0.5611
115.5    15.00  0.73     Sequence
             DRB1_0701  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.5326
157.1    19.00  0.76     Sequence
             DRB1_0701  502      GFQPTYGVGYQPYRV  FQPTYGVGY  1        0.5268
167.4    19.00  0.60     Sequence
```

```
             DRB1_0701  503      FQPTYGVGYQPYRVV  GVGYQPYRV  5        0.4937
239.4    24.00  0.38     Sequence
             DRB1_0701  504      QPTYGVGYQPYRVVV  GVGYQPYRV  4        0.4100
592.0    39.00  0.68     Sequence
             DRB1_0701  505      PTYGVGYQPYRVVVL  YQPYRVVVL  6        0.5052
211.4    22.00  0.45     Sequence
             DRB1_0701  506      TYGVGYQPYRVVVLS  GVGYQPYRV  2        0.4885
253.2    25.00  0.44     Sequence
             DRB1_0701  507      YGVGYQPYRVVVLSF  PYRVVVLSF  6        0.5580
119.3    15.00  0.43     Sequence
             DRB1_0701  508      GVGYQPYRVVVLSFE  PYRVVVLSF  5        0.5355
152.4    18.00  0.38     Sequence
             DRB1_0701  509      VGYQPYRVVVLSFEL  RVVVLSFEL  6        0.7218
20.3     3.00  0.67     Sequence         WB
             DRB1_0701  510      GYQPYRVVVLSFELL  RVVVLSFEL  5        0.7078
23.6     3.50  0.64     Sequence         WB
             DRB1_0701  511      YQPYRVVVLSFELLH  RVVVLSFEL  4        0.6829
30.9     4.50  0.67     Sequence         WB
             DRB1_0701  512      QPYRVVVLSFELLHA  RVVVLSFEL  3        0.6537
42.4     6.50  0.68     Sequence         WB
             DRB1_0701  513      PYRVVVLSFELLHAP  RVVVLSFEL  2        0.6287
55.5     8.00  0.70     Sequence         WB
             DRB1_0701  514      YRVVVLSFELLHAPA  RVVVLSFEL  1        0.5825
91.6    13.00  0.79     Sequence
             DRB1_0701  515      RVVVLSFELLHAPAT  RVVVLSFEL  0        0.5396
145.6    18.00  0.60     Sequence
             DRB1_0701  516      VVVLSFELLHAPATV  FELLHAPAT  5        0.4168
550.2    38.00  0.43     Sequence
             DRB1_0701  517      VVLSFELLHAPATVC  LLHAPATVC  6        0.5725
102.0    14.00  0.68     Sequence
             DRB1_0701  518      VLSFELLHAPATVCG  LLHAPATVC  5        0.5568
121.0    15.00  0.71     Sequence
             DRB1_0701  519      LSFELLHAPATVCGP  LLHAPATVC  4        0.5351
153.0    18.00  0.71     Sequence
             DRB1_0701  520      SFELLHAPATVCGPK  LLHAPATVC  3        0.5205
179.2    20.00  0.74     Sequence
             DRB1_0701  521      FELLHAPATVCGPKK  LLHAPATVC  2        0.4973
230.2    24.00  0.77     Sequence
             DRB1_0701  522      ELLHAPATVCGPKKS  LLHAPATVC  1        0.4398
428.9    33.00  0.87     Sequence
             DRB1_0701  523      LLHAPATVCGPKKST  LLHAPATVC  0        0.3661
952.1    48.00  0.87     Sequence
             DRB1_0701  524      LHAPATVCGPKKSTN  LHAPATVCG  0        0.0866
19588.7   100.00  0.28     Sequence
             DRB1_0701  525      HAPATVCGPKKSTNL  CGPKKSTNL  6        0.2092
5198.6    85.00  0.74     Sequence
             DRB1_0701  526      APATVCGPKKSTNLV  CGPKKSTNL  5        0.2312
4098.0    80.00  0.77     Sequence
             DRB1_0701  527      PATVCGPKKSTNLVK  CGPKKSTNL  4        0.2834
2328.4    70.00  0.50     Sequence
             DRB1_0701  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5        0.2861
2263.0    70.00  0.43     Sequence
             DRB1_0701  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.2770
2497.0    70.00  0.44     Sequence
             DRB1_0701  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3        0.2530
3236.0    75.00  0.44     Sequence
             DRB1_0701  531      CGPKKSTNLVKNKCV  TNLVKNKCV  6        0.5223
175.6    20.00  0.84     Sequence
             DRB1_0701  532      GPKKSTNLVKNKCVN  TNLVKNKCV  5        0.5027
217.1    23.00  0.88     Sequence
             DRB1_0701  533      PKKSTNLVKNKCVNF  TNLVKNKCV  4        0.5108
199.0    22.00  0.81     Sequence
             DRB1_0701  534      KKSTNLVKNKCVNFN  TNLVKNKCV  3        0.4919
244.2    24.00  0.81     Sequence
             DRB1_0701  535      KSTNLVKNKCVNFNF  TNLVKNKCV  2        0.4770
286.9    27.00  0.70     Sequence
```

```
             DRB1_0701  536      STNLVKNKCVNFNFN  TNLVKNKCV  1        0.4403
426.6    33.00  0.62     Sequence
             DRB1_0701  537      TNLVKNKCVNFNFNG  TNLVKNKCV  0        0.3725
888.4    47.00  0.49     Sequence
             DRB1_0701  538      NLVKNKCVNFNFNGL  CVNFNFNGL  6        0.3549
1074.3    55.00  0.44     Sequence
             DRB1_0701  539      LVKNKCVNFNFNGLT  CVNFNFNGL  5        0.3438
1211.9    55.00  0.47     Sequence
             DRB1_0701  540      VKNKCVNFNFNGLTG  CVNFNFNGL  4        0.3117
1714.7    60.00  0.50     Sequence
             DRB1_0701  541      KNKCVNFNFNGLTGT  CVNFNFNGL  3        0.3138
1675.9    60.00  0.46     Sequence
             DRB1_0701  542      NKCVNFNFNGLTGTG  CVNFNFNGL  2        0.2791
2441.7    70.00  0.49     Sequence
             DRB1_0701  543      KCVNFNFNGLTGTGV  FNGLTGTGV  6        0.5380
148.3    18.00  0.78     Sequence
             DRB1_0701  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5        0.5959
79.2    11.00  0.73     Sequence
             DRB1_0701  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.5697
105.1    14.00  0.75     Sequence
             DRB1_0701  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3        0.5513
128.3    16.00  0.73     Sequence
             DRB1_0701  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.5328
156.8    19.00  0.74     Sequence
             DRB1_0701  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.4970
230.9    24.00  0.73     Sequence
             DRB1_0701  549      FNGLTGTGVLTESNK  FNGLTGTGV  0        0.4339
457.3    34.00  0.68     Sequence
             DRB1_0701  550      NGLTGTGVLTESNKK  GVLTESNKK  6        0.2989
1969.6    65.00  0.51     Sequence
             DRB1_0701  551      GLTGTGVLTESNKKF  GVLTESNKK  5        0.3399
1264.7    55.00  0.51     Sequence
             DRB1_0701  552      LTGTGVLTESNKKFL  LTESNKKFL  6        0.4594
346.8    30.00  0.49     Sequence
             DRB1_0701  553      TGTGVLTESNKKFLP  LTESNKKFL  5        0.4306
473.7    35.00  0.51     Sequence
             DRB1_0701  554      GTGVLTESNKKFLPF  LTESNKKFL  4        0.4287
483.9    35.00  0.54     Sequence
             DRB1_0701  555      TGVLTESNKKFLPFQ  LTESNKKFL  3        0.4048
626.4    40.00  0.54     Sequence
             DRB1_0701  556      GVLTESNKKFLPFQQ  LTESNKKFL  2        0.3637
977.6    49.00  0.57     Sequence
             DRB1_0701  557      VLTESNKKFLPFQQF  LTESNKKFL  1        0.3192
1581.8    60.00  0.60     Sequence
             DRB1_0701  558      LTESNKKFLPFQQFG  LTESNKKFL  0        0.2653
2834.9    75.00  0.61     Sequence
             DRB1_0701  559      TESNKKFLPFQQFGR  FLPFQQFGR  6        0.2892
2187.3    65.00  0.73     Sequence
             DRB1_0701  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5        0.3009
1926.8    65.00  0.77     Sequence
             DRB1_0701  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4        0.3334
1356.3    55.00  0.69     Sequence
             DRB1_0701  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.3515
1115.5    55.00  0.57     Sequence
             DRB1_0701  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.3366
1309.8    55.00  0.59     Sequence
             DRB1_0701  564      KFLPFQQFGRDIADT  FLPFQQFGR  1        0.3055
1834.6    65.00  0.57     Sequence
             DRB1_0701  565      FLPFQQFGRDIADTT  FLPFQQFGR  0        0.2520
3270.8    75.00  0.44     Sequence
             DRB1_0701  566      LPFQQFGRDIADTTD  FQQFGRDIA  2        0.1645
8434.8    90.00  0.50     Sequence
             DRB1_0701  567      PFQQFGRDIADTTDA  FQQFGRDIA  1        0.1529
9565.1    95.00  0.47     Sequence
             DRB1_0701  568      FQQFGRDIADTTDAV  FQQFGRDIA  0        0.1420
10755.3    95.00  0.34     Sequence
```

```
             DRB1_0701  569      QQFGRDIADTTDAVR  IADTTDAVR  6        0.1403
10958.7    95.00  0.44     Sequence
             DRB1_0701  570      QFGRDIADTTDAVRD  IADTTDAVR  5        0.1700
7941.9    90.00  0.40     Sequence
             DRB1_0701  571      FGRDIADTTDAVRDP  IADTTDAVR  4        0.1611
8753.5    95.00  0.38     Sequence
             DRB1_0701  572      GRDIADTTDAVRDPQ  IADTTDAVR  3        0.1492
9948.8    95.00  0.40     Sequence
             DRB1_0701  573      RDIADTTDAVRDPQT  IADTTDAVR  2        0.1427
10671.9    95.00  0.41     Sequence
             DRB1_0701  574      DIADTTDAVRDPQTL  IADTTDAVR  1        0.1285
12443.0    95.00  0.38     Sequence
             DRB1_0701  575      IADTTDAVRDPQTLE  ADTTDAVRD  1        0.1091
15360.5   100.00  0.38     Sequence
             DRB1_0701  576      ADTTDAVRDPQTLEI  VRDPQTLEI  6        0.2439
3571.2    75.00  0.81     Sequence
             DRB1_0701  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5        0.2691
2719.3    70.00  0.85     Sequence
             DRB1_0701  578      TTDAVRDPQTLEILD  VRDPQTLEI  4        0.2606
2982.9    75.00  0.82     Sequence
             DRB1_0701  579      TDAVRDPQTLEILDI  VRDPQTLEI  3        0.2875
2229.4    70.00  0.70     Sequence
             DRB1_0701  580      DAVRDPQTLEILDIT  VRDPQTLEI  2        0.2704
2680.4    70.00  0.69     Sequence
             DRB1_0701  581      AVRDPQTLEILDITP  VRDPQTLEI  1        0.2585
3050.7    75.00  0.68     Sequence
             DRB1_0701  582      VRDPQTLEILDITPC  VRDPQTLEI  0        0.2501
3340.1    75.00  0.37     Sequence
             DRB1_0701  583      RDPQTLEILDITPCS  LEILDITPC  5        0.2026
5583.2    85.00  0.58     Sequence
             DRB1_0701  584      DPQTLEILDITPCSF  ILDITPCSF  6        0.3800
818.8    45.00  0.62     Sequence
             DRB1_0701  585      PQTLEILDITPCSFG  ILDITPCSF  5        0.3786
831.9    46.00  0.59     Sequence
             DRB1_0701  586      QTLEILDITPCSFGG  ILDITPCSF  4        0.3676
937.1    48.00  0.54     Sequence
             DRB1_0701  587      TLEILDITPCSFGGV  ILDITPCSF  3        0.3758
857.4    46.00  0.52     Sequence
             DRB1_0701  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.3503
1130.0    55.00  0.52     Sequence
             DRB1_0701  589      EILDITPCSFGGVSV  ILDITPCSF  1        0.3455
1189.6    55.00  0.50     Sequence
             DRB1_0701  590      ILDITPCSFGGVSVI  CSFGGVSVI  6        0.4183
541.3    37.00  0.41     Sequence
             DRB1_0701  591      LDITPCSFGGVSVIT  CSFGGVSVI  5        0.3700
912.4    47.00  0.46     Sequence
             DRB1_0701  592      DITPCSFGGVSVITP  CSFGGVSVI  4        0.3574
1045.9    50.00  0.43     Sequence
             DRB1_0701  593      ITPCSFGGVSVITPG  CSFGGVSVI  3        0.3385
1284.0    55.00  0.35     Sequence
             DRB1_0701  594      TPCSFGGVSVITPGT  CSFGGVSVI  2        0.3274
1447.4    60.00  0.33     Sequence
             DRB1_0701  595      PCSFGGVSVITPGTN  CSFGGVSVI  1        0.3187
1590.7    60.00  0.28     Sequence
             DRB1_0701  596      CSFGGVSVITPGTNT  SVITPGTNT  6        0.3638
976.0    49.00  0.40     Sequence
             DRB1_0701  597      SFGGVSVITPGTNTS  SVITPGTNT  5        0.3345
1339.7    55.00  0.50     Sequence
             DRB1_0701  598      FGGVSVITPGTNTSN  SVITPGTNT  4        0.3054
1837.1    65.00  0.59     Sequence
             DRB1_0701  599      GGVSVITPGTNTSNQ  SVITPGTNT  3        0.2807
2399.6    70.00  0.62     Sequence
             DRB1_0701  600      GVSVITPGTNTSNQV  SVITPGTNT  2        0.2973
2005.3    65.00  0.52     Sequence
             DRB1_0701  601      VSVITPGTNTSNQVA  SVITPGTNT  1        0.2870
2241.5    70.00  0.48     Sequence
```

```
             DRB1_0701  602      SVITPGTNTSNQVAV  SVITPGTNT  0        0.2816
2375.7    70.00  0.29     Sequence
             DRB1_0701  603      VITPGTNTSNQVAVL  TNTSNQVAV  5        0.2595
3017.7    75.00  0.38     Sequence
             DRB1_0701  604      ITPGTNTSNQVAVLY  TNTSNQVAV  4        0.2586
3047.6    75.00  0.35     Sequence
             DRB1_0701  605      TPGTNTSNQVAVLYQ  TNTSNQVAV  3        0.2465
3471.1    75.00  0.35     Sequence
             DRB1_0701  606      PGTNTSNQVAVLYQG  TNTSNQVAV  2        0.2231
4471.9    80.00  0.38     Sequence
             DRB1_0701  607      GTNTSNQVAVLYQGV  QVAVLYQGV  6        0.2652
2835.6    75.00  0.49     Sequence
             DRB1_0701  608      TNTSNQVAVLYQGVN  QVAVLYQGV  5        0.2393
3755.3    80.00  0.53     Sequence
             DRB1_0701  609      NTSNQVAVLYQGVNC  QVAVLYQGV  4        0.2187
4690.2    85.00  0.52     Sequence
             DRB1_0701  610      TSNQVAVLYQGVNCT  QVAVLYQGV  3        0.2282
4233.0    80.00  0.41     Sequence
             DRB1_0701  611      SNQVAVLYQGVNCTE  QVAVLYQGV  2        0.2274
4268.3    80.00  0.41     Sequence
             DRB1_0701  612      NQVAVLYQGVNCTEV  YQGVNCTEV  6        0.3554
1068.6    55.00  0.51     Sequence
             DRB1_0701  613      QVAVLYQGVNCTEVP  YQGVNCTEV  5        0.3427
1226.8    55.00  0.58     Sequence
             DRB1_0701  614      VAVLYQGVNCTEVPV  YQGVNCTEV  4        0.3456
1188.2    55.00  0.62     Sequence
             DRB1_0701  615      AVLYQGVNCTEVPVA  YQGVNCTEV  3        0.3500
1132.7    55.00  0.56     Sequence
             DRB1_0701  616      VLYQGVNCTEVPVAI  YQGVNCTEV  2        0.3589
1029.7    50.00  0.49     Sequence
             DRB1_0701  617      LYQGVNCTEVPVAIH  YQGVNCTEV  1        0.3482
1155.6    55.00  0.45     Sequence
             DRB1_0701  618      YQGVNCTEVPVAIHA  YQGVNCTEV  0        0.2950
2055.2    65.00  0.30     Sequence
             DRB1_0701  619      QGVNCTEVPVAIHAD  CTEVPVAIH  4        0.2432
3598.0    75.00  0.29     Sequence
             DRB1_0701  620      GVNCTEVPVAIHADQ  CTEVPVAIH  3        0.2294
4180.4    80.00  0.28     Sequence
             DRB1_0701  621      VNCTEVPVAIHADQL  PVAIHADQL  6        0.3081
1783.2    65.00  0.44     Sequence
             DRB1_0701  622      NCTEVPVAIHADQLT  PVAIHADQL  5        0.2983
1982.0    65.00  0.44     Sequence
             DRB1_0701  623      CTEVPVAIHADQLTP  PVAIHADQL  4        0.2580
3065.2    75.00  0.47     Sequence
             DRB1_0701  624      TEVPVAIHADQLTPT  PVAIHADQL  3        0.2355
3913.4    80.00  0.47     Sequence
             DRB1_0701  625      EVPVAIHADQLTPTW  PVAIHADQL  2        0.2138
4947.8    85.00  0.47     Sequence
             DRB1_0701  626      VPVAIHADQLTPTWR  PVAIHADQL  1        0.1986
5830.2    85.00  0.43     Sequence
             DRB1_0701  627      PVAIHADQLTPTWRV  DQLTPTWRV  6        0.4510
379.9    31.00  0.85     Sequence
             DRB1_0701  628      VAIHADQLTPTWRVY  DQLTPTWRV  5        0.4782
283.2    27.00  0.85     Sequence
             DRB1_0701  629      AIHADQLTPTWRVYS  DQLTPTWRV  4        0.4927
241.9    24.00  0.76     Sequence
             DRB1_0701  630      IHADQLTPTWRVYST  DQLTPTWRV  3        0.4812
273.9    26.00  0.76     Sequence
             DRB1_0701  631      HADQLTPTWRVYSTG  DQLTPTWRV  2        0.4655
324.7    29.00  0.77     Sequence
             DRB1_0701  632      ADQLTPTWRVYSTGS  DQLTPTWRV  1        0.4627
334.7    29.00  0.68     Sequence
             DRB1_0701  633      DQLTPTWRVYSTGSN  DQLTPTWRV  0        0.4584
350.9    30.00  0.43     Sequence
             DRB1_0701  634      QLTPTWRVYSTGSNV  RVYSTGSNV  6        0.4437
411.0    33.00  0.40     Sequence
```

```
             DRB1_0701  635      LTPTWRVYSTGSNVF  VYSTGSNVF  6        0.6422
48.0     7.00  0.69     Sequence         WB
             DRB1_0701  636      TPTWRVYSTGSNVFQ  VYSTGSNVF  5        0.6321
53.6     8.00  0.68     Sequence         WB
             DRB1_0701  637      PTWRVYSTGSNVFQT  VYSTGSNVF  4        0.6189
61.8     9.00  0.67     Sequence         WB
             DRB1_0701  638      TWRVYSTGSNVFQTR  VYSTGSNVF  3        0.6040
72.6    10.00  0.65     Sequence
             DRB1_0701  639      WRVYSTGSNVFQTRA  VYSTGSNVF  2        0.5719
102.7    14.00  0.70     Sequence
             DRB1_0701  640      RVYSTGSNVFQTRAG  VYSTGSNVF  1        0.5314
159.1    19.00  0.73     Sequence
             DRB1_0701  641      VYSTGSNVFQTRAGC  VYSTGSNVF  0        0.4259
498.7    36.00  0.65     Sequence
             DRB1_0701  642      YSTGSNVFQTRAGCL  VFQTRAGCL  6        0.6379
50.3     7.50  0.88     Sequence         WB
             DRB1_0701  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.7023
25.1     3.50  0.65     Sequence         WB
             DRB1_0701  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.6731
34.4     5.00  0.64     Sequence         WB
             DRB1_0701  645      GSNVFQTRAGCLIGA  VFQTRAGCL  3        0.6573
40.8     6.00  0.63     Sequence         WB
             DRB1_0701  646      SNVFQTRAGCLIGAE  VFQTRAGCL  2        0.6396
49.4     7.50  0.64     Sequence         WB
             DRB1_0701  647      NVFQTRAGCLIGAEY  VFQTRAGCL  1        0.6127
66.1     9.50  0.61     Sequence         WB
             DRB1_0701  648      VFQTRAGCLIGAEYV  VFQTRAGCL  0        0.5659
109.6    14.00  0.50     Sequence
             DRB1_0701  649      FQTRAGCLIGAEYVN  FQTRAGCLI  0        0.4035
635.6    40.00  0.50     Sequence
             DRB1_0701  650      QTRAGCLIGAEYVNN  CLIGAEYVN  5        0.2961
2029.5    65.00  0.34     Sequence
             DRB1_0701  651      TRAGCLIGAEYVNNS  CLIGAEYVN  4        0.2956
2040.9    65.00  0.34     Sequence
             DRB1_0701  652      RAGCLIGAEYVNNSY  CLIGAEYVN  3        0.2904
2158.6    65.00  0.32     Sequence
             DRB1_0701  653      AGCLIGAEYVNNSYE  LIGAEYVNN  3        0.2681
2748.3    70.00  0.28     Sequence
             DRB1_0701  654      GCLIGAEYVNNSYEC  LIGAEYVNN  2        0.2558
3140.5    75.00  0.31     Sequence
             DRB1_0701  655      CLIGAEYVNNSYECD  LIGAEYVNN  1        0.2128
5002.7    85.00  0.35     Sequence
             DRB1_0701  656      LIGAEYVNNSYECDI  VNNSYECDI  6        0.2364
3875.4    80.00  0.39     Sequence
             DRB1_0701  657      IGAEYVNNSYECDIP  VNNSYECDI  5        0.1842
6814.4    90.00  0.49     Sequence
             DRB1_0701  658      GAEYVNNSYECDIPI  VNNSYECDI  4        0.2305
4128.1    80.00  0.41     Sequence
             DRB1_0701  659      AEYVNNSYECDIPIG  VNNSYECDI  3        0.2065
5353.2    85.00  0.40     Sequence
             DRB1_0701  660      EYVNNSYECDIPIGA  VNNSYECDI  2        0.2075
5297.3    85.00  0.32     Sequence
             DRB1_0701  661      YVNNSYECDIPIGAG  VNNSYECDI  1        0.1821
6974.1    90.00  0.37     Sequence
             DRB1_0701  662      VNNSYECDIPIGAGI  CDIPIGAGI  6        0.2631
2903.2    75.00  0.52     Sequence
             DRB1_0701  663      NNSYECDIPIGAGIC  CDIPIGAGI  5        0.2602
2994.4    75.00  0.50     Sequence
             DRB1_0701  664      NSYECDIPIGAGICA  CDIPIGAGI  4        0.2513
3298.6    75.00  0.50     Sequence
             DRB1_0701  665      SYECDIPIGAGICAS  CDIPIGAGI  3        0.2349
3938.2    80.00  0.48     Sequence
             DRB1_0701  666      YECDIPIGAGICASY  CDIPIGAGI  2        0.2232
4469.2    80.00  0.46     Sequence
             DRB1_0701  667      ECDIPIGAGICASYQ  CDIPIGAGI  1        0.1989
5809.2    85.00  0.43     Sequence
```

```
             DRB1_0701  668      CDIPIGAGICASYQT  CDIPIGAGI  0        0.2089
5216.5    85.00  0.28     Sequence
             DRB1_0701  669      DIPIGAGICASYQTQ  AGICASYQT  5        0.1634
8538.0    95.00  0.44     Sequence
             DRB1_0701  670      IPIGAGICASYQTQT  ICASYQTQT  6        0.1942
6118.6    85.00  0.43     Sequence
             DRB1_0701  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.1796
7161.2    90.00  0.43     Sequence
             DRB1_0701  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.1712
7844.7    90.00  0.44     Sequence
             DRB1_0701  673      GAGICASYQTQTNSP  SYQTQTNSP  6        0.1802
7117.9    90.00  0.28     Sequence
             DRB1_0701  674      AGICASYQTQTNSPR  SYQTQTNSP  5        0.1889
6476.5    90.00  0.29     Sequence
             DRB1_0701  675      GICASYQTQTNSPRR  SYQTQTNSP  4        0.1725
7736.1    90.00  0.31     Sequence
             DRB1_0701  676      ICASYQTQTNSPRRA  SYQTQTNSP  3        0.1677
8147.7    90.00  0.31     Sequence
             DRB1_0701  677      CASYQTQTNSPRRAR  SYQTQTNSP  2        0.1544
9401.9    95.00  0.37     Sequence
             DRB1_0701  678      ASYQTQTNSPRRARS  SYQTQTNSP  1        0.1490
9970.3    95.00  0.36     Sequence
             DRB1_0701  679      SYQTQTNSPRRARSV  NSPRRARSV  6        0.1745
7566.8    90.00  0.38     Sequence
             DRB1_0701  680      YQTQTNSPRRARSVA  NSPRRARSV  5        0.1572
9127.6    95.00  0.46     Sequence
             DRB1_0701  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.2933
2094.0    65.00  0.70     Sequence
             DRB1_0701  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.3094
1758.2    65.00  0.75     Sequence
             DRB1_0701  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.3137
1679.1    60.00  0.72     Sequence
             DRB1_0701  684      TNSPRRARSVASQSI  ARSVASQSI  6        0.4439
410.2    33.00  0.56     Sequence
             DRB1_0701  685      NSPRRARSVASQSII  ARSVASQSI  5        0.5392
146.4    18.00  0.41     Sequence
             DRB1_0701  686      SPRRARSVASQSIIA  SVASQSIIA  6        0.6067
70.5    10.00  0.47     Sequence
             DRB1_0701  687      PRRARSVASQSIIAY  SVASQSIIA  5        0.6006
75.3    11.00  0.56     Sequence
             DRB1_0701  688      RRARSVASQSIIAYT  SVASQSIIA  4        0.5825
91.6    13.00  0.58     Sequence
             DRB1_0701  689      RARSVASQSIIAYTM  SVASQSIIA  3        0.5730
101.5    14.00  0.61     Sequence
             DRB1_0701  690      ARSVASQSIIAYTMS  SVASQSIIA  2        0.5350
153.2    18.00  0.60     Sequence
             DRB1_0701  691      RSVASQSIIAYTMSL  SVASQSIIA  1        0.5186
182.8    20.00  0.54     Sequence
             DRB1_0701  692      SVASQSIIAYTMSLG  SVASQSIIA  0        0.4663
321.8    29.00  0.40     Sequence
             DRB1_0701  693      VASQSIIAYTMSLGA  IAYTMSLGA  6        0.8036
8.4     0.70  0.92     Sequence         SB
             DRB1_0701  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.8039
8.3     0.70  0.93     Sequence         SB
             DRB1_0701  695      SQSIIAYTMSLGAEN  IAYTMSLGA  4        0.8086
7.9     0.60  0.88     Sequence         SB
             DRB1_0701  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.8009
8.6     0.80  0.86     Sequence         SB
             DRB1_0701  697      SIIAYTMSLGAENSV  IAYTMSLGA  2        0.7985
8.8     0.80  0.83     Sequence         SB
             DRB1_0701  698      IIAYTMSLGAENSVA  IAYTMSLGA  1        0.7826
10.5     1.00  0.83     Sequence         SB
             DRB1_0701  699      IAYTMSLGAENSVAY  IAYTMSLGA  0        0.7471
15.4     1.90  0.75     Sequence         SB
             DRB1_0701  700      AYTMSLGAENSVAYS  YTMSLGAEN  1        0.4292
481.1    35.00  0.68     Sequence
```

```
             DRB1_0701  701      YTMSLGAENSVAYSN  YTMSLGAEN  0        0.3678
935.1    48.00  0.54     Sequence
             DRB1_0701  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.2237
4446.7    80.00  0.37     Sequence
             DRB1_0701  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.2159
4836.7    85.00  0.34     Sequence
             DRB1_0701  704      SLGAENSVAYSNNSI  SVAYSNNSI  6        0.2664
2800.4    70.00  0.41     Sequence
             DRB1_0701  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.4199
531.8    37.00  0.73     Sequence
             DRB1_0701  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.4929
241.6    24.00  0.64     Sequence
             DRB1_0701  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.4745
294.8    27.00  0.61     Sequence
             DRB1_0701  708      ENSVAYSNNSIAIPT  VAYSNNSIA  3        0.4821
271.5    26.00  0.50     Sequence
             DRB1_0701  709      NSVAYSNNSIAIPTN  VAYSNNSIA  2        0.4781
283.5    27.00  0.48     Sequence
             DRB1_0701  710      SVAYSNNSIAIPTNF  VAYSNNSIA  1        0.4673
318.4    28.00  0.41     Sequence
             DRB1_0701  711      VAYSNNSIAIPTNFT  VAYSNNSIA  0        0.4416
420.8    33.00  0.28     Sequence
             DRB1_0701  712      AYSNNSIAIPTNFTI  IAIPTNFTI  6        0.4465
399.0    32.00  0.31     Sequence
             DRB1_0701  713      YSNNSIAIPTNFTIS  IAIPTNFTI  5        0.4093
596.8    39.00  0.31     Sequence
             DRB1_0701  714      SNNSIAIPTNFTISV  IAIPTNFTI  4        0.3892
741.7    43.00  0.32     Sequence
             DRB1_0701  715      NNSIAIPTNFTISVT  IAIPTNFTI  3        0.3646
967.2    49.00  0.37     Sequence
             DRB1_0701  716      NSIAIPTNFTISVTT  TNFTISVTT  6        0.4762
289.2    27.00  0.58     Sequence
             DRB1_0701  717      SIAIPTNFTISVTTE  TNFTISVTT  5        0.4594
346.8    30.00  0.57     Sequence
             DRB1_0701  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.8280
6.4     0.40  0.91     Sequence         SB
             DRB1_0701  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.8273
6.5     0.40  0.89     Sequence         SB
             DRB1_0701  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.8052
8.2     0.70  0.89     Sequence         SB
             DRB1_0701  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.8083
8.0     0.70  0.83     Sequence         SB
             DRB1_0701  722      TNFTISVTTEILPVS  FTISVTTEI  2        0.8056
8.2     0.70  0.83     Sequence         SB
             DRB1_0701  723      NFTISVTTEILPVSM  FTISVTTEI  1        0.7886
9.8     0.90  0.83     Sequence         SB
             DRB1_0701  724      FTISVTTEILPVSMT  FTISVTTEI  0        0.7548
14.2     1.70  0.77     Sequence         SB
             DRB1_0701  725      TISVTTEILPVSMTK  SVTTEILPV  2        0.4766
288.1    27.00  0.58     Sequence
             DRB1_0701  726      ISVTTEILPVSMTKT  ILPVSMTKT  6        0.5423
141.5    17.00  0.51     Sequence
             DRB1_0701  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.5147
190.7    21.00  0.64     Sequence
             DRB1_0701  728      VTTEILPVSMTKTSV  ILPVSMTKT  4        0.4940
238.5    24.00  0.81     Sequence
             DRB1_0701  729      TTEILPVSMTKTSVD  ILPVSMTKT  3        0.5383
147.8    18.00  0.57     Sequence
             DRB1_0701  730      TEILPVSMTKTSVDC  ILPVSMTKT  2        0.5183
183.4    20.00  0.56     Sequence
             DRB1_0701  731      EILPVSMTKTSVDCT  ILPVSMTKT  1        0.4964
232.6    24.00  0.53     Sequence
             DRB1_0701  732      ILPVSMTKTSVDCTM  VSMTKTSVD  3        0.4665
321.4    29.00  0.42     Sequence
             DRB1_0701  733      LPVSMTKTSVDCTMY  VSMTKTSVD  2        0.3858
769.4    44.00  0.63     Sequence
```

```
             DRB1_0701  734      PVSMTKTSVDCTMYI  VSMTKTSVD  1        0.4072
610.1    40.00  0.47     Sequence
             DRB1_0701  735      VSMTKTSVDCTMYIC  VSMTKTSVD  0        0.3533
1093.4    55.00  0.37     Sequence
             DRB1_0701  736      SMTKTSVDCTMYICG  TSVDCTMYI  4        0.2812
2384.5    70.00  0.34     Sequence
             DRB1_0701  737      MTKTSVDCTMYICGD  TSVDCTMYI  3        0.2572
3093.9    75.00  0.38     Sequence
             DRB1_0701  738      TKTSVDCTMYICGDS  TSVDCTMYI  2        0.2201
4619.7    80.00  0.49     Sequence
             DRB1_0701  739      KTSVDCTMYICGDST  TSVDCTMYI  1        0.1950
6064.1    85.00  0.56     Sequence
             DRB1_0701  740      TSVDCTMYICGDSTE  TSVDCTMYI  0        0.1679
8125.6    90.00  0.45     Sequence
             DRB1_0701  741      SVDCTMYICGDSTEC  YICGDSTEC  6        0.1631
8562.4    95.00  0.45     Sequence
             DRB1_0701  742      VDCTMYICGDSTECS  YICGDSTEC  5        0.1582
9027.2    95.00  0.53     Sequence
             DRB1_0701  743      DCTMYICGDSTECSN  YICGDSTEC  4        0.1454
10365.5    95.00  0.58     Sequence
             DRB1_0701  744      CTMYICGDSTECSNL  YICGDSTEC  3        0.1572
9126.9    95.00  0.56     Sequence
             DRB1_0701  745      TMYICGDSTECSNLL  YICGDSTEC  2        0.2015
5653.9    85.00  0.38     Sequence
             DRB1_0701  746      MYICGDSTECSNLLL  STECSNLLL  6        0.2503
3332.6    75.00  0.40     Sequence
             DRB1_0701  747      YICGDSTECSNLLLQ  STECSNLLL  5        0.2280
4241.0    80.00  0.42     Sequence
             DRB1_0701  748      ICGDSTECSNLLLQY  STECSNLLL  4        0.2048
5452.9    85.00  0.47     Sequence
             DRB1_0701  749      CGDSTECSNLLLQYG  STECSNLLL  3        0.1819
6983.6    90.00  0.47     Sequence
             DRB1_0701  750      GDSTECSNLLLQYGS  STECSNLLL  2        0.1703
7919.2    90.00  0.54     Sequence
             DRB1_0701  751      DSTECSNLLLQYGSF  STECSNLLL  1        0.1695
7989.5    90.00  0.40     Sequence
             DRB1_0701  752      STECSNLLLQYGSFC  STECSNLLL  0        0.1429
10657.5    95.00  0.31     Sequence
             DRB1_0701  753      TECSNLLLQYGSFCT  LLQYGSFCT  6        0.3858
769.2    44.00  0.88     Sequence
             DRB1_0701  754      ECSNLLLQYGSFCTQ  LLQYGSFCT  5        0.3939
705.1    42.00  0.88     Sequence
             DRB1_0701  755      CSNLLLQYGSFCTQL  LLQYGSFCT  4        0.4165
551.7    38.00  0.85     Sequence
             DRB1_0701  756      SNLLLQYGSFCTQLN  LLQYGSFCT  3        0.4343
455.0    34.00  0.73     Sequence
             DRB1_0701  757      NLLLQYGSFCTQLNR  LLQYGSFCT  2        0.4238
509.9    36.00  0.70     Sequence
             DRB1_0701  758      LLLQYGSFCTQLNRA  LLQYGSFCT  1        0.4233
512.7    36.00  0.62     Sequence
             DRB1_0701  759      LLQYGSFCTQLNRAL  FCTQLNRAL  6        0.4965
232.1    24.00  0.41     Sequence
             DRB1_0701  760      LQYGSFCTQLNRALT  FCTQLNRAL  5        0.4171
548.2    38.00  0.54     Sequence
             DRB1_0701  761      QYGSFCTQLNRALTG  FCTQLNRAL  4        0.3808
811.8    45.00  0.52     Sequence
             DRB1_0701  762      YGSFCTQLNRALTGI  FCTQLNRAL  3        0.3800
819.2    45.00  0.57     Sequence
             DRB1_0701  763      GSFCTQLNRALTGIA  LNRALTGIA  6        0.4135
570.2    38.00  0.46     Sequence
             DRB1_0701  764      SFCTQLNRALTGIAV  LNRALTGIA  5        0.4534
370.0    31.00  0.41     Sequence
             DRB1_0701  765      FCTQLNRALTGIAVE  LNRALTGIA  4        0.4239
509.4    36.00  0.46     Sequence
             DRB1_0701  766      CTQLNRALTGIAVEQ  LNRALTGIA  3        0.3855
772.1    44.00  0.52     Sequence
```

```
             DRB1_0701  767      TQLNRALTGIAVEQD  LNRALTGIA  2        0.3848
778.0    44.00  0.56     Sequence
             DRB1_0701  768      QLNRALTGIAVEQDK  LNRALTGIA  1        0.3609
1006.9    49.00  0.54     Sequence
             DRB1_0701  769      LNRALTGIAVEQDKN  LNRALTGIA  0        0.3066
1812.0    65.00  0.46     Sequence
             DRB1_0701  770      NRALTGIAVEQDKNT  NRALTGIAV  0        0.1891
6462.9    90.00  0.51     Sequence
             DRB1_0701  771      RALTGIAVEQDKNTQ  LTGIAVEQD  2        0.1098
15245.3   100.00  0.35     Sequence
             DRB1_0701  772      ALTGIAVEQDKNTQE  LTGIAVEQD  1        0.0931
18250.9   100.00  0.29     Sequence
             DRB1_0701  773      LTGIAVEQDKNTQEV  EQDKNTQEV  6        0.0895
18990.6   100.00  0.22     Sequence
             DRB1_0701  774      TGIAVEQDKNTQEVF  QDKNTQEVF  6        0.1040
16235.5   100.00  0.28     Sequence
             DRB1_0701  775      GIAVEQDKNTQEVFA  DKNTQEVFA  6        0.1342
11702.1    95.00  0.38     Sequence
             DRB1_0701  776      IAVEQDKNTQEVFAQ  DKNTQEVFA  5        0.1366
11408.0    95.00  0.41     Sequence
             DRB1_0701  777      AVEQDKNTQEVFAQV  DKNTQEVFA  4        0.1547
9374.7    95.00  0.36     Sequence
             DRB1_0701  778      VEQDKNTQEVFAQVK  TQEVFAQVK  6        0.1853
6731.8    90.00  0.34     Sequence
             DRB1_0701  779      EQDKNTQEVFAQVKQ  TQEVFAQVK  5        0.1862
6671.7    90.00  0.34     Sequence
             DRB1_0701  780      QDKNTQEVFAQVKQI  EVFAQVKQI  6        0.2795
2430.5    70.00  0.56     Sequence
             DRB1_0701  781      DKNTQEVFAQVKQIY  EVFAQVKQI  5        0.2913
2139.9    65.00  0.47     Sequence
             DRB1_0701  782      KNTQEVFAQVKQIYK  EVFAQVKQI  4        0.3132
1687.7    60.00  0.29     Sequence
             DRB1_0701  783      NTQEVFAQVKQIYKT  FAQVKQIYK  5        0.2985
1979.3    65.00  0.32     Sequence
             DRB1_0701  784      TQEVFAQVKQIYKTP  FAQVKQIYK  4        0.2736
2589.3    70.00  0.34     Sequence
             DRB1_0701  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.2686
2735.4    70.00  0.34     Sequence
             DRB1_0701  786      EVFAQVKQIYKTPPI  KQIYKTPPI  6        0.4731
299.2    27.00  0.68     Sequence
             DRB1_0701  787      VFAQVKQIYKTPPIK  KQIYKTPPI  5        0.4789
281.1    27.00  0.73     Sequence
             DRB1_0701  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6        0.5758
98.5    13.00  0.50     Sequence
             DRB1_0701  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.6077
69.7    10.00  0.56     Sequence
             DRB1_0701  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.5848
89.3    12.00  0.56     Sequence
             DRB1_0701  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.5547
123.8    16.00  0.57     Sequence
             DRB1_0701  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.5229
174.6    20.00  0.64     Sequence
             DRB1_0701  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.4077
607.3    40.00  0.86     Sequence
             DRB1_0701  794      IYKTPPIKDFGGFNF  IYKTPPIKD  0        0.4383
436.1    34.00  0.47     Sequence
             DRB1_0701  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.3406
1254.7    55.00  0.87     Sequence
             DRB1_0701  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.3302
1403.4    60.00  0.93     Sequence
             DRB1_0701  797      TPPIKDFGGFNFSQI  FGGFNFSQI  6        0.5295
162.5    19.00  0.55     Sequence
             DRB1_0701  798      PPIKDFGGFNFSQIL  FGGFNFSQI  5        0.5528
126.4    16.00  0.56     Sequence
             DRB1_0701  799      PIKDFGGFNFSQILP  FGGFNFSQI  4        0.5330
156.5    18.00  0.56     Sequence
```

```
             DRB1_0701  800      IKDFGGFNFSQILPD  FNFSQILPD  6        0.5984
77.1    11.00  0.41     Sequence
             DRB1_0701  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.5558
122.3    16.00  0.51     Sequence
             DRB1_0701  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.5400
145.0    18.00  0.52     Sequence
             DRB1_0701  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.5155
189.1    21.00  0.56     Sequence
             DRB1_0701  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.4104
589.7    39.00  0.74     Sequence
             DRB1_0701  805      GFNFSQILPDPSKPS  FNFSQILPD  1        0.3987
668.8    41.00  0.70     Sequence
             DRB1_0701  806      FNFSQILPDPSKPSK  FNFSQILPD  0        0.3505
1126.8    55.00  0.58     Sequence
             DRB1_0701  807      NFSQILPDPSKPSKR  FSQILPDPS  1        0.1971
5926.8    85.00  0.47     Sequence
             DRB1_0701  808      FSQILPDPSKPSKRS  FSQILPDPS  0        0.1755
7486.2    90.00  0.35     Sequence
             DRB1_0701  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.1516
9700.8    95.00  0.37     Sequence
             DRB1_0701  810      QILPDPSKPSKRSFI  SKPSKRSFI  6        0.2578
3073.6    75.00  0.56     Sequence
             DRB1_0701  811      ILPDPSKPSKRSFIE  SKPSKRSFI  5        0.2549
3170.9    75.00  0.61     Sequence
             DRB1_0701  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.2325
4042.3    80.00  0.65     Sequence
             DRB1_0701  813      PDPSKPSKRSFIEDL  SKPSKRSFI  3        0.2812
2384.8    70.00  0.47     Sequence
             DRB1_0701  814      DPSKPSKRSFIEDLL  SKPSKRSFI  2        0.3046
1851.4    65.00  0.37     Sequence
             DRB1_0701  815      PSKPSKRSFIEDLLF  RSFIEDLLF  6        0.3602
1015.0    50.00  0.32     Sequence
             DRB1_0701  816      SKPSKRSFIEDLLFN  RSFIEDLLF  5        0.3245
1493.6    60.00  0.34     Sequence
             DRB1_0701  817      KPSKRSFIEDLLFNK  RSFIEDLLF  4        0.2865
2251.9    70.00  0.41     Sequence
             DRB1_0701  818      PSKRSFIEDLLFNKV  IEDLLFNKV  6        0.3434
1217.5    55.00  0.42     Sequence
             DRB1_0701  819      SKRSFIEDLLFNKVT  IEDLLFNKV  5        0.3301
1404.8    60.00  0.43     Sequence
             DRB1_0701  820      KRSFIEDLLFNKVTL  IEDLLFNKV  4        0.3407
1252.8    55.00  0.49     Sequence
             DRB1_0701  821      RSFIEDLLFNKVTLA  LLFNKVTLA  6        0.4137
568.9    38.00  0.47     Sequence
             DRB1_0701  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5        0.3786
831.3    46.00  0.53     Sequence
             DRB1_0701  823      FIEDLLFNKVTLADA  FNKVTLADA  6        0.4298
477.8    35.00  0.38     Sequence
             DRB1_0701  824      IEDLLFNKVTLADAG  FNKVTLADA  5        0.4124
576.8    39.00  0.43     Sequence
             DRB1_0701  825      EDLLFNKVTLADAGF  FNKVTLADA  4        0.4245
506.3    36.00  0.45     Sequence
             DRB1_0701  826      DLLFNKVTLADAGFI  VTLADAGFI  6        0.5727
101.8    14.00  0.60     Sequence
             DRB1_0701  827      LLFNKVTLADAGFIK  VTLADAGFI  5        0.5536
125.2    16.00  0.55     Sequence
             DRB1_0701  828      LFNKVTLADAGFIKQ  VTLADAGFI  4        0.5140
192.2    21.00  0.59     Sequence
             DRB1_0701  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.4823
270.9    26.00  0.64     Sequence
             DRB1_0701  830      NKVTLADAGFIKQYG  VTLADAGFI  2        0.4186
539.5    37.00  0.80     Sequence
             DRB1_0701  831      KVTLADAGFIKQYGD  VTLADAGFI  1        0.3884
747.9    44.00  0.81     Sequence
             DRB1_0701  832      VTLADAGFIKQYGDC  VTLADAGFI  0        0.3092
1761.5    65.00  0.75     Sequence
```

```
             DRB1_0701  833      TLADAGFIKQYGDCL  FIKQYGDCL  6        0.2119
5052.1    85.00  0.57     Sequence
             DRB1_0701  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.2181
4720.4    85.00  0.47     Sequence
             DRB1_0701  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4        0.2149
4889.3    85.00  0.45     Sequence
             DRB1_0701  836      DAGFIKQYGDCLGDI  FIKQYGDCL  3        0.2379
3811.7    80.00  0.41     Sequence
             DRB1_0701  837      AGFIKQYGDCLGDIA  FIKQYGDCL  2        0.2513
3296.6    75.00  0.34     Sequence
             DRB1_0701  838      GFIKQYGDCLGDIAA  FIKQYGDCL  1        0.2383
3795.4    80.00  0.34     Sequence
             DRB1_0701  839      FIKQYGDCLGDIAAR  IKQYGDCLG  1        0.2155
4854.4    85.00  0.38     Sequence
             DRB1_0701  840      IKQYGDCLGDIAARD  IKQYGDCLG  0        0.1738
7627.3    90.00  0.38     Sequence
             DRB1_0701  841      KQYGDCLGDIAARDL  LGDIAARDL  6        0.2907
2153.1    65.00  0.74     Sequence
             DRB1_0701  842      QYGDCLGDIAARDLI  LGDIAARDL  5        0.3199
1568.7    60.00  0.76     Sequence
             DRB1_0701  843      YGDCLGDIAARDLIC  LGDIAARDL  4        0.3300
1407.2    60.00  0.58     Sequence
             DRB1_0701  844      GDCLGDIAARDLICA  LGDIAARDL  3        0.3122
1705.4    60.00  0.59     Sequence
             DRB1_0701  845      DCLGDIAARDLICAQ  LGDIAARDL  2        0.3005
1935.1    65.00  0.60     Sequence
             DRB1_0701  846      CLGDIAARDLICAQK  LGDIAARDL  1        0.2888
2197.0    65.00  0.62     Sequence
             DRB1_0701  847      LGDIAARDLICAQKF  RDLICAQKF  6        0.3970
681.5    42.00  0.56     Sequence
             DRB1_0701  848      GDIAARDLICAQKFN  RDLICAQKF  5        0.3569
1051.9    50.00  0.72     Sequence
             DRB1_0701  849      DIAARDLICAQKFNG  RDLICAQKF  4        0.3235
1509.0    60.00  0.68     Sequence
             DRB1_0701  850      IAARDLICAQKFNGL  RDLICAQKF  3        0.3760
855.0    46.00  0.55     Sequence
             DRB1_0701  851      AARDLICAQKFNGLT  RDLICAQKF  2        0.3592
1026.3    50.00  0.54     Sequence
             DRB1_0701  852      ARDLICAQKFNGLTV  AQKFNGLTV  6        0.3985
670.8    41.00  0.31     Sequence
             DRB1_0701  853      RDLICAQKFNGLTVL  AQKFNGLTV  5        0.3992
665.3    41.00  0.40     Sequence
             DRB1_0701  854      DLICAQKFNGLTVLP  AQKFNGLTV  4        0.3501
1131.7    55.00  0.49     Sequence
             DRB1_0701  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.3818
803.2    45.00  0.33     Sequence
             DRB1_0701  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.4128
574.3    39.00  0.38     Sequence
             DRB1_0701  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.4398
428.8    33.00  0.37     Sequence
             DRB1_0701  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.4522
375.1    31.00  0.31     Sequence
             DRB1_0701  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.4207
527.4    37.00  0.35     Sequence
             DRB1_0701  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1        0.3936
707.1    42.00  0.34     Sequence
             DRB1_0701  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.3398
1265.3    55.00  0.37     Sequence
             DRB1_0701  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.2712
2658.2    70.00  0.52     Sequence
             DRB1_0701  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.2946
2063.9    65.00  0.41     Sequence
             DRB1_0701  864      LTVLPPLLTDEMIAQ  PLLTDEMIA  5        0.2711
2662.1    70.00  0.47     Sequence
             DRB1_0701  865      TVLPPLLTDEMIAQY  PLLTDEMIA  4        0.1957
6015.8    85.00  0.74     Sequence
```

```
             DRB1_0701  866      VLPPLLTDEMIAQYT  PLLTDEMIA  3        0.1873
6590.4    90.00  0.69     Sequence
             DRB1_0701  867      LPPLLTDEMIAQYTS  PLLTDEMIA  2        0.1796
7163.7    90.00  0.67     Sequence
             DRB1_0701  868      PPLLTDEMIAQYTSA  PLLTDEMIA  1        0.1819
6985.1    90.00  0.56     Sequence
             DRB1_0701  869      PLLTDEMIAQYTSAL  MIAQYTSAL  6        0.2093
5196.1    85.00  0.42     Sequence
             DRB1_0701  870      LLTDEMIAQYTSALL  IAQYTSALL  6        0.4437
411.0    33.00  0.81     Sequence
             DRB1_0701  871      LTDEMIAQYTSALLA  AQYTSALLA  6        0.5544
124.1    16.00  0.59     Sequence
             DRB1_0701  872      TDEMIAQYTSALLAG  AQYTSALLA  5        0.5263
168.2    19.00  0.63     Sequence
             DRB1_0701  873      DEMIAQYTSALLAGT  AQYTSALLA  4        0.5150
190.1    21.00  0.65     Sequence
             DRB1_0701  874      EMIAQYTSALLAGTI  AQYTSALLA  3        0.5361
151.3    18.00  0.60     Sequence
             DRB1_0701  875      MIAQYTSALLAGTIT  AQYTSALLA  2        0.5316
158.8    19.00  0.59     Sequence
             DRB1_0701  876      IAQYTSALLAGTITS  AQYTSALLA  1        0.5058
210.0    22.00  0.58     Sequence
             DRB1_0701  877      AQYTSALLAGTITSG  AQYTSALLA  0        0.4106
588.3    39.00  0.58     Sequence
             DRB1_0701  878      QYTSALLAGTITSGW  LAGTITSGW  6        0.3525
1102.7    55.00  0.47     Sequence
             DRB1_0701  879      YTSALLAGTITSGWT  LAGTITSGW  5        0.3454
1190.6    55.00  0.54     Sequence
             DRB1_0701  880      TSALLAGTITSGWTF  GTITSGWTF  6        0.4539
368.3    31.00  0.49     Sequence
             DRB1_0701  881      SALLAGTITSGWTFG  GTITSGWTF  5        0.4377
438.6    34.00  0.52     Sequence
             DRB1_0701  882      ALLAGTITSGWTFGA  GTITSGWTF  4        0.4515
378.0    31.00  0.46     Sequence
             DRB1_0701  883      LLAGTITSGWTFGAG  GTITSGWTF  3        0.4197
533.3    37.00  0.45     Sequence
             DRB1_0701  884      LAGTITSGWTFGAGA  GTITSGWTF  2        0.4138
568.3    38.00  0.42     Sequence
             DRB1_0701  885      AGTITSGWTFGAGAA  GTITSGWTF  1        0.3702
910.7    47.00  0.41     Sequence
             DRB1_0701  886      GTITSGWTFGAGAAL  WTFGAGAAL  6        0.4778
284.3    27.00  0.59     Sequence
             DRB1_0701  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.4458
401.8    32.00  0.67     Sequence
             DRB1_0701  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.7539
14.3     1.70  0.83     Sequence         SB
             DRB1_0701  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.7486
15.2     1.80  0.85     Sequence         SB
             DRB1_0701  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.7559
14.0     1.70  0.88     Sequence         SB
             DRB1_0701  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.7448
15.8     1.90  0.87     Sequence         SB
             DRB1_0701  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.7320
18.2     2.50  0.88     Sequence         WB
             DRB1_0701  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.7031
24.8     3.50  0.94     Sequence         WB
             DRB1_0701  894      FGAGAALQIPFAMQM  FGAGAALQI  0        0.6458
46.2     7.00  0.80     Sequence         WB
             DRB1_0701  895      GAGAALQIPFAMQMA  LQIPFAMQM  5        0.3413
1245.3    55.00  0.55     Sequence
             DRB1_0701  896      AGAALQIPFAMQMAY  LQIPFAMQM  4        0.3239
1502.3    60.00  0.55     Sequence
             DRB1_0701  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.3072
1799.8    65.00  0.54     Sequence
             DRB1_0701  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.6682
36.2     5.50  0.87     Sequence         WB
```

```
             DRB1_0701  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5         0.6552
41.7     6.50  0.86     Sequence         WB
             DRB1_0701  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4         0.6172
62.9     9.00  0.84     Sequence         WB
             DRB1_0701  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3         0.6275
56.3     8.00  0.79     Sequence         WB
             DRB1_0701  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2         0.6065
70.7    10.00  0.79     Sequence
             DRB1_0701  903      PFAMQMAYRFNGIGV  FAMQMAYRF  1         0.6278
56.1     8.00  0.62     Sequence         WB
             DRB1_0701  904      FAMQMAYRFNGIGVT  FAMQMAYRF  0         0.5988
76.8    11.00  0.51     Sequence
             DRB1_0701  905      AMQMAYRFNGIGVTQ  AYRFNGIGV  4         0.4547
365.2    31.00  0.44     Sequence
             DRB1_0701  906      MQMAYRFNGIGVTQN  AYRFNGIGV  3         0.4650
326.6    29.00  0.41     Sequence
             DRB1_0701  907      QMAYRFNGIGVTQNV  AYRFNGIGV  2         0.4676
317.6    28.00  0.38     Sequence
             DRB1_0701  908      MAYRFNGIGVTQNVL  GIGVTQNVL  6         0.5073
206.6    22.00  0.32     Sequence
             DRB1_0701  909      AYRFNGIGVTQNVLY  IGVTQNVLY  6         0.5798
94.3    13.00  0.46     Sequence
             DRB1_0701  910      YRFNGIGVTQNVLYE  IGVTQNVLY  5         0.5221
176.1    20.00  0.54     Sequence
             DRB1_0701  911      RFNGIGVTQNVLYEN  IGVTQNVLY  4         0.4905
247.9    25.00  0.58     Sequence
             DRB1_0701  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3         0.4499
384.5    31.00  0.63     Sequence
             DRB1_0701  913      NGIGVTQNVLYENQK  IGVTQNVLY  2         0.4140
566.9    38.00  0.68     Sequence
             DRB1_0701  914      GIGVTQNVLYENQKL  IGVTQNVLY  1         0.4049
625.4    40.00  0.59     Sequence
             DRB1_0701  915      IGVTQNVLYENQKLI  VLYENQKLI  6         0.4581
352.0    30.00  0.47     Sequence
             DRB1_0701  916      GVTQNVLYENQKLIA  VLYENQKLI  5         0.3883
748.7    44.00  0.60     Sequence
             DRB1_0701  917      VTQNVLYENQKLIAN  VLYENQKLI  4         0.3734
879.6    47.00  0.57     Sequence
             DRB1_0701  918      TQNVLYENQKLIANQ  VLYENQKLI  3         0.3554
1068.6    55.00  0.56     Sequence
             DRB1_0701  919      QNVLYENQKLIANQF  NQKLIANQF  6         0.4098
593.4    39.00  0.37     Sequence
             DRB1_0701  920      NVLYENQKLIANQFN  NQKLIANQF  5         0.3876
754.2    44.00  0.38     Sequence
             DRB1_0701  921      VLYENQKLIANQFNS  NQKLIANQF  4         0.3480
1158.6    55.00  0.44     Sequence
             DRB1_0701  922      LYENQKLIANQFNSA  NQKLIANQF  3         0.2890
2192.7    65.00  0.58     Sequence
             DRB1_0701  923      YENQKLIANQFNSAI  NQKLIANQF  2         0.3010
1925.1    65.00  0.47     Sequence
             DRB1_0701  924      ENQKLIANQFNSAIG  ANQFNSAIG  6         0.3200
1568.0    60.00  0.29     Sequence
             DRB1_0701  925      NQKLIANQFNSAIGK  ANQFNSAIG  5         0.3135
1681.4    60.00  0.33     Sequence
             DRB1_0701  926      QKLIANQFNSAIGKI  QFNSAIGKI  6         0.3884
748.3    44.00  0.41     Sequence
             DRB1_0701  927      KLIANQFNSAIGKIQ  FNSAIGKIQ  6         0.4243
507.1    36.00  0.35     Sequence
             DRB1_0701  928      LIANQFNSAIGKIQD  FNSAIGKIQ  5         0.4104
589.4    39.00  0.44     Sequence
             DRB1_0701  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4         0.3957
691.2    42.00  0.49     Sequence
             DRB1_0701  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3         0.3911
726.3    43.00  0.56     Sequence
             DRB1_0701  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2         0.3697
915.8    47.00  0.56     Sequence
```

```
             DRB1_0701  932      QFNSAIGKIQDSLSS  FNSAIGKIQ  1        0.3409
1251.0    55.00  0.59     Sequence
             DRB1_0701  933      FNSAIGKIQDSLSST  FNSAIGKIQ  0        0.2706
2676.8    70.00  0.56     Sequence
             DRB1_0701  934      NSAIGKIQDSLSSTA  IQDSLSSTA  6        0.3434
1216.6    55.00  0.78     Sequence
             DRB1_0701  935      SAIGKIQDSLSSTAS  IQDSLSSTA  5        0.3519
1110.4    55.00  0.79     Sequence
             DRB1_0701  936      AIGKIQDSLSSTASA  IQDSLSSTA  4        0.3491
1143.8    55.00  0.74     Sequence
             DRB1_0701  937      IGKIQDSLSSTASAL  IQDSLSSTA  3        0.4313
470.3    35.00  0.50     Sequence
             DRB1_0701  938      GKIQDSLSSTASALG  LSSTASALG  6        0.4979
228.8    23.00  0.49     Sequence
             DRB1_0701  939      KIQDSLSSTASALGK  LSSTASALG  5        0.5000
223.7    23.00  0.62     Sequence
             DRB1_0701  940      IQDSLSSTASALGKL  LSSTASALG  4        0.5370
149.8    18.00  0.66     Sequence
             DRB1_0701  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.5082
204.5    22.00  0.69     Sequence
             DRB1_0701  942      DSLSSTASALGKLQD  LSSTASALG  2        0.4890
251.8    25.00  0.69     Sequence
             DRB1_0701  943      SLSSTASALGKLQDV  LSSTASALG  1        0.4784
282.4    27.00  0.73     Sequence
             DRB1_0701  944      LSSTASALGKLQDVV  LSSTASALG  0        0.3908
728.5    43.00  0.65     Sequence
             DRB1_0701  945      SSTASALGKLQDVVN  STASALGKL  1        0.2180
4725.3    85.00  0.56     Sequence
             DRB1_0701  946      STASALGKLQDVVNQ  STASALGKL  0        0.1733
7664.1    90.00  0.38     Sequence
             DRB1_0701  947      TASALGKLQDVVNQN  LGKLQDVVN  4        0.1265
12724.3   100.00  0.38     Sequence
             DRB1_0701  948      ASALGKLQDVVNQNA  LQDVVNQNA  6        0.1609
8764.1    95.00  0.50     Sequence
             DRB1_0701  949      SALGKLQDVVNQNAQ  LQDVVNQNA  5        0.1585
9001.9    95.00  0.56     Sequence
             DRB1_0701  950      ALGKLQDVVNQNAQA  LQDVVNQNA  4        0.1624
8626.4    95.00  0.55     Sequence
             DRB1_0701  951      LGKLQDVVNQNAQAL  VVNQNAQAL  6        0.2297
4167.0    80.00  0.44     Sequence
             DRB1_0701  952      GKLQDVVNQNAQALN  VVNQNAQAL  5        0.2304
4133.9    80.00  0.41     Sequence
             DRB1_0701  953      KLQDVVNQNAQALNT  VVNQNAQAL  4        0.2347
3945.7    80.00  0.36     Sequence
             DRB1_0701  954      LQDVVNQNAQALNTL  VVNQNAQAL  3        0.2372
3841.3    80.00  0.40     Sequence
             DRB1_0701  955      QDVVNQNAQALNTLV  NAQALNTLV  6        0.4057
620.3    40.00  0.67     Sequence
             DRB1_0701  956      DVVNQNAQALNTLVK  NAQALNTLV  5        0.3965
685.5    42.00  0.65     Sequence
             DRB1_0701  957      VVNQNAQALNTLVKQ  NAQALNTLV  4        0.3762
853.3    46.00  0.67     Sequence
             DRB1_0701  958      VNQNAQALNTLVKQL  NAQALNTLV  3        0.4208
526.6    37.00  0.55     Sequence
             DRB1_0701  959      NQNAQALNTLVKQLS  NAQALNTLV  2        0.3973
679.4    42.00  0.56     Sequence
             DRB1_0701  960      QNAQALNTLVKQLSS  NAQALNTLV  1        0.3720
893.3    47.00  0.51     Sequence
             DRB1_0701  961      NAQALNTLVKQLSSN  NAQALNTLV  0        0.3138
1677.5    60.00  0.40     Sequence
             DRB1_0701  962      AQALNTLVKQLSSNF  LVKQLSSNF  6        0.3597
1020.0    50.00  0.63     Sequence
             DRB1_0701  963      QALNTLVKQLSSNFG  LVKQLSSNF  5        0.3562
1059.8    50.00  0.54     Sequence
             DRB1_0701  964      ALNTLVKQLSSNFGA  LVKQLSSNF  4        0.3733
880.6    47.00  0.42     Sequence
```

```
             DRB1_0701  965      LNTLVKQLSSNFGAI  LVKQLSSNF  3        0.4244
506.5    36.00  0.37     Sequence
             DRB1_0701  966      NTLVKQLSSNFGAIS  LVKQLSSNF  2        0.4189
537.5    37.00  0.34     Sequence
             DRB1_0701  967      TLVKQLSSNFGAISS  LVKQLSSNF  1        0.4069
612.1    40.00  0.31     Sequence
             DRB1_0701  968      LVKQLSSNFGAISSV  KQLSSNFGA  2        0.3898
736.4    43.00  0.25     Sequence
             DRB1_0701  969      VKQLSSNFGAISSVL  NFGAISSVL  6        0.4972
230.6    24.00  0.56     Sequence
             DRB1_0701  970      KQLSSNFGAISSVLN  NFGAISSVL  5        0.5138
192.5    21.00  0.52     Sequence
             DRB1_0701  971      QLSSNFGAISSVLND  NFGAISSVL  4        0.4968
231.4    24.00  0.52     Sequence
             DRB1_0701  972      LSSNFGAISSVLNDI  NFGAISSVL  3        0.5290
163.4    19.00  0.45     Sequence
             DRB1_0701  973      SSNFGAISSVLNDIL  NFGAISSVL  2        0.5521
127.3    16.00  0.36     Sequence
             DRB1_0701  974      SNFGAISSVLNDILS  NFGAISSVL  1        0.5213
177.5    20.00  0.35     Sequence
             DRB1_0701  975      NFGAISSVLNDILSR  FGAISSVLN  1        0.4743
295.1    27.00  0.32     Sequence
             DRB1_0701  976      FGAISSVLNDILSRL  ISSVLNDIL  3        0.4101
591.5    39.00  0.42     Sequence
             DRB1_0701  977      GAISSVLNDILSRLD  ISSVLNDIL  2        0.3467
1174.6    55.00  0.46     Sequence
             DRB1_0701  978      AISSVLNDILSRLDK  ISSVLNDIL  1        0.3216
1541.3    60.00  0.47     Sequence
             DRB1_0701  979      ISSVLNDILSRLDKV  LNDILSRLD  4        0.2972
2006.7    65.00  0.33     Sequence
             DRB1_0701  980      SSVLNDILSRLDKVE  LNDILSRLD  3        0.2443
3558.2    75.00  0.49     Sequence
             DRB1_0701  981      SVLNDILSRLDKVEA  LNDILSRLD  2        0.2576
3080.5    75.00  0.38     Sequence
             DRB1_0701  982      VLNDILSRLDKVEAE  LNDILSRLD  1        0.2512
3300.7    75.00  0.35     Sequence
             DRB1_0701  983      LNDILSRLDKVEAEV  LSRLDKVEA  4        0.2393
3755.8    80.00  0.35     Sequence
             DRB1_0701  984      NDILSRLDKVEAEVQ  LSRLDKVEA  3        0.2227
4493.9    80.00  0.36     Sequence
             DRB1_0701  985      DILSRLDKVEAEVQI  DKVEAEVQI  6        0.2787
2451.2    70.00  0.29     Sequence
             DRB1_0701  986      ILSRLDKVEAEVQID  DKVEAEVQI  5        0.2609
2970.5    75.00  0.31     Sequence
             DRB1_0701  987      LSRLDKVEAEVQIDR  DKVEAEVQI  4        0.2338
3982.4    80.00  0.34     Sequence
             DRB1_0701  988      SRLDKVEAEVQIDRL  DKVEAEVQI  3        0.2120
5042.8    85.00  0.40     Sequence
             DRB1_0701  989      RLDKVEAEVQIDRLI  DKVEAEVQI  2        0.2288
4204.2    80.00  0.31     Sequence
             DRB1_0701  990      LDKVEAEVQIDRLIT  DKVEAEVQI  1        0.2127
5003.6    85.00  0.29     Sequence
             DRB1_0701  991      DKVEAEVQIDRLITG  AEVQIDRLI  4        0.1728
7709.9    90.00  0.20     Sequence
             DRB1_0701  992      KVEAEVQIDRLITGR  AEVQIDRLI  3        0.1450
10408.5    95.00  0.26     Sequence
             DRB1_0701  993      VEAEVQIDRLITGRL  IDRLITGRL  6        0.4186
539.2    37.00  0.88     Sequence
             DRB1_0701  994      EAEVQIDRLITGRLQ  IDRLITGRL  5        0.4005
656.0    41.00  0.83     Sequence
             DRB1_0701  995      AEVQIDRLITGRLQS  IDRLITGRL  4        0.3838
785.9    44.00  0.81     Sequence
             DRB1_0701  996      EVQIDRLITGRLQSL  IDRLITGRL  3        0.4130
573.4    39.00  0.74     Sequence
             DRB1_0701  997      VQIDRLITGRLQSLQ  IDRLITGRL  2        0.3976
676.9    42.00  0.75     Sequence
```

```
             DRB1_0701  998      QIDRLITGRLQSLQT  IDRLITGRL  1        0.3843
782.0    44.00  0.69     Sequence
             DRB1_0701  999      IDRLITGRLQSLQTY  IDRLITGRL  0        0.3259
1470.7    60.00  0.56     Sequence
             DRB1_0701 1000      DRLITGRLQSLQTYV  RLQSLQTYV  6        0.4180
542.8    37.00  0.68     Sequence
             DRB1_0701 1001      RLITGRLQSLQTYVT  RLQSLQTYV  5        0.4602
343.8    30.00  0.55     Sequence
             DRB1_0701 1002      LITGRLQSLQTYVTQ  RLQSLQTYV  4        0.4601
344.2    30.00  0.56     Sequence
             DRB1_0701 1003      ITGRLQSLQTYVTQQ  RLQSLQTYV  3        0.4444
408.0    32.00  0.52     Sequence
             DRB1_0701 1004      TGRLQSLQTYVTQQL  LQTYVTQQL  6        0.5154
189.4    21.00  0.39     Sequence
             DRB1_0701 1005      GRLQSLQTYVTQQLI  LQTYVTQQL  5        0.5205
179.0    20.00  0.38     Sequence
             DRB1_0701 1006      RLQSLQTYVTQQLIR  LQTYVTQQL  4        0.4789
281.1    27.00  0.43     Sequence
             DRB1_0701 1007      LQSLQTYVTQQLIRA  LQTYVTQQL  3        0.4197
533.3    37.00  0.50     Sequence
             DRB1_0701 1008      QSLQTYVTQQLIRAA  LQTYVTQQL  2        0.3864
764.3    44.00  0.62     Sequence
             DRB1_0701 1009      SLQTYVTQQLIRAAE  LQTYVTQQL  1        0.3577
1043.0    50.00  0.60     Sequence
             DRB1_0701 1010      LQTYVTQQLIRAAEI  QQLIRAAEI  6        0.4470
396.9    32.00  0.70     Sequence
             DRB1_0701 1011      QTYVTQQLIRAAEIR  QQLIRAAEI  5        0.4126
575.7    39.00  0.83     Sequence
             DRB1_0701 1012      TYVTQQLIRAAEIRA  QQLIRAAEI  4        0.4033
636.9    40.00  0.75     Sequence
             DRB1_0701 1013      YVTQQLIRAAEIRAS  QQLIRAAEI  3        0.4089
598.9    39.00  0.63     Sequence
             DRB1_0701 1014      VTQQLIRAAEIRASA  QQLIRAAEI  2        0.3910
727.4    43.00  0.58     Sequence
             DRB1_0701 1015      TQQLIRAAEIRASAN  QQLIRAAEI  1        0.3727
886.5    47.00  0.53     Sequence
             DRB1_0701 1016      QQLIRAAEIRASANL  AEIRASANL  6        0.4311
471.0    35.00  0.41     Sequence
             DRB1_0701 1017      QLIRAAEIRASANLA  AEIRASANL  5        0.4090
598.2    39.00  0.41     Sequence
             DRB1_0701 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.5855
88.7    12.00  0.74     Sequence
             DRB1_0701 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.6378
50.4     7.50  0.84     Sequence         WB
             DRB1_0701 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.6289
55.4     8.00  0.85     Sequence         WB
             DRB1_0701 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.6317
53.8     8.00  0.85     Sequence         WB
             DRB1_0701 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.6120
66.6     9.50  0.86     Sequence         WB
             DRB1_0701 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.5737
100.7    13.00  0.88     Sequence
             DRB1_0701 1024      IRASANLAAIKMSEC  IRASANLAA  0        0.4945
237.2    24.00  0.70     Sequence
             DRB1_0701 1025      RASANLAAIKMSECV  LAAIKMSEC  5        0.3321
1375.5    60.00  0.56     Sequence
             DRB1_0701 1026      ASANLAAIKMSECVL  LAAIKMSEC  4        0.3643
970.3    49.00  0.56     Sequence
             DRB1_0701 1027      SANLAAIKMSECVLG  LAAIKMSEC  3        0.4023
643.6    41.00  0.38     Sequence
             DRB1_0701 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.3951
695.6    42.00  0.41     Sequence
             DRB1_0701 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.3776
841.1    46.00  0.44     Sequence
             DRB1_0701 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.3444
1204.6    55.00  0.52     Sequence
```

```
             DRB1_0701 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.2978
1994.0    65.00  0.68     Sequence
             DRB1_0701 1032      AIKMSECVLGQSKRV  CVLGQSKRV  6        0.4425
416.6    33.00  0.61     Sequence
             DRB1_0701 1033      IKMSECVLGQSKRVD  CVLGQSKRV  5        0.4047
627.2    40.00  0.70     Sequence
             DRB1_0701 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.4429
414.6    33.00  0.59     Sequence
             DRB1_0701 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.4237
510.6    36.00  0.53     Sequence
             DRB1_0701 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.4020
645.9    41.00  0.55     Sequence
             DRB1_0701 1037      ECVLGQSKRVDFCGK  CVLGQSKRV  1        0.3814
806.9    45.00  0.50     Sequence
             DRB1_0701 1038      CVLGQSKRVDFCGKG  LGQSKRVDF  2        0.3401
1260.8    55.00  0.49     Sequence
             DRB1_0701 1039      VLGQSKRVDFCGKGY  LGQSKRVDF  1        0.2802
2411.9    70.00  0.62     Sequence
             DRB1_0701 1040      LGQSKRVDFCGKGYH  LGQSKRVDF  0        0.2343
3963.1    80.00  0.49     Sequence
             DRB1_0701 1041      GQSKRVDFCGKGYHL  DFCGKGYHL  6        0.2481
3411.6    75.00  0.50     Sequence
             DRB1_0701 1042      QSKRVDFCGKGYHLM  FCGKGYHLM  6        0.3568
1052.3    50.00  0.44     Sequence
             DRB1_0701 1043      SKRVDFCGKGYHLMS  FCGKGYHLM  5        0.3528
1099.0    55.00  0.47     Sequence
             DRB1_0701 1044      KRVDFCGKGYHLMSF  FCGKGYHLM  4        0.3552
1071.0    55.00  0.48     Sequence
             DRB1_0701 1045      RVDFCGKGYHLMSFP  FCGKGYHLM  3        0.3323
1372.9    60.00  0.47     Sequence
             DRB1_0701 1046      VDFCGKGYHLMSFPQ  FCGKGYHLM  2        0.3405
1256.3    55.00  0.38     Sequence
             DRB1_0701 1047      DFCGKGYHLMSFPQS  GYHLMSFPQ  5        0.3268
1456.4    60.00  0.40     Sequence
             DRB1_0701 1048      FCGKGYHLMSFPQSA  GYHLMSFPQ  4        0.3217
1539.2    60.00  0.39     Sequence
             DRB1_0701 1049      CGKGYHLMSFPQSAP  GYHLMSFPQ  3        0.2716
2646.7    70.00  0.45     Sequence
             DRB1_0701 1050      GKGYHLMSFPQSAPH  GYHLMSFPQ  2        0.3134
1684.7    60.00  0.35     Sequence
             DRB1_0701 1051      KGYHLMSFPQSAPHG  GYHLMSFPQ  1        0.2909
2147.9    65.00  0.35     Sequence
             DRB1_0701 1052      GYHLMSFPQSAPHGV  FPQSAPHGV  6        0.3756
859.6    46.00  0.49     Sequence
             DRB1_0701 1053      YHLMSFPQSAPHGVV  FPQSAPHGV  5        0.3942
702.7    42.00  0.60     Sequence
             DRB1_0701 1054      HLMSFPQSAPHGVVF  FPQSAPHGV  4        0.4232
513.4    37.00  0.59     Sequence
             DRB1_0701 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.4469
397.1    32.00  0.56     Sequence
             DRB1_0701 1056      MSFPQSAPHGVVFLH  FPQSAPHGV  2        0.4234
512.3    36.00  0.58     Sequence
             DRB1_0701 1057      SFPQSAPHGVVFLHV  FPQSAPHGV  1        0.4600
344.6    30.00  0.40     Sequence
             DRB1_0701 1058      FPQSAPHGVVFLHVT  PHGVVFLHV  5        0.4056
620.8    40.00  0.34     Sequence
             DRB1_0701 1059      PQSAPHGVVFLHVTY  PHGVVFLHV  4        0.3193
1579.9    60.00  0.49     Sequence
             DRB1_0701 1060      QSAPHGVVFLHVTYV  VVFLHVTYV  6        0.3925
715.2    43.00  0.40     Sequence
             DRB1_0701 1061      SAPHGVVFLHVTYVP  VFLHVTYVP  6        0.4165
551.8    38.00  0.35     Sequence
             DRB1_0701 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.6064
70.7    10.00  0.70     Sequence
             DRB1_0701 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.6059
71.1    10.00  0.73     Sequence
```

```
             DRB1_0701 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.5883
86.0    12.00  0.76     Sequence
             DRB1_0701 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.5900
84.4    12.00  0.74     Sequence
             DRB1_0701 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.5827
91.4    13.00  0.75     Sequence
             DRB1_0701 1067      VFLHVTYVPAQEKNF  FLHVTYVPA  1        0.5951
79.9    11.00  0.71     Sequence
             DRB1_0701 1068      FLHVTYVPAQEKNFT  FLHVTYVPA  0        0.5552
123.1    16.00  0.67     Sequence
             DRB1_0701 1069      LHVTYVPAQEKNFTT  YVPAQEKNF  4        0.3329
1363.6    60.00  0.53     Sequence
             DRB1_0701 1070      HVTYVPAQEKNFTTA  YVPAQEKNF  3        0.3042
1859.2    65.00  0.56     Sequence
             DRB1_0701 1071      VTYVPAQEKNFTTAP  YVPAQEKNF  2        0.2665
2796.8    70.00  0.58     Sequence
             DRB1_0701 1072      TYVPAQEKNFTTAPA  YVPAQEKNF  1        0.2331
4013.8    80.00  0.67     Sequence
             DRB1_0701 1073      YVPAQEKNFTTAPAI  KNFTTAPAI  6        0.5518
127.6    16.00  0.89     Sequence
             DRB1_0701 1074      VPAQEKNFTTAPAIC  KNFTTAPAI  5        0.5520
127.4    16.00  0.81     Sequence
             DRB1_0701 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.6411
48.6     7.00  0.52     Sequence        WB
             DRB1_0701 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.6392
49.6     7.50  0.54     Sequence        WB
             DRB1_0701 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.6138
65.3     9.50  0.54     Sequence        WB
             DRB1_0701 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.5938
81.1    11.00  0.58     Sequence
             DRB1_0701 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.5599
117.0    15.00  0.63     Sequence
             DRB1_0701 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.4530
372.0    31.00  0.83     Sequence
             DRB1_0701 1081      FTTAPAICHDGKAHF  FTTAPAICH  0        0.3965
685.3    42.00  0.62     Sequence
             DRB1_0701 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.2669
2785.7    70.00  0.53     Sequence
             DRB1_0701 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.2645
2857.0    75.00  0.52     Sequence
             DRB1_0701 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.2513
3295.3    75.00  0.50     Sequence
             DRB1_0701 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.2355
3912.4    80.00  0.51     Sequence
             DRB1_0701 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.2516
3286.8    75.00  0.44     Sequence
             DRB1_0701 1087      ICHDGKAHFPREGVF  ICHDGKAHF  0        0.2232
4470.3    80.00  0.34     Sequence
             DRB1_0701 1088      CHDGKAHFPREGVFV  HFPREGVFV  6        0.2646
2854.3    75.00  0.54     Sequence
             DRB1_0701 1089      HDGKAHFPREGVFVS  HFPREGVFV  5        0.2721
2634.0    70.00  0.58     Sequence
             DRB1_0701 1090      DGKAHFPREGVFVSN  HFPREGVFV  4        0.2687
2730.8    70.00  0.58     Sequence
             DRB1_0701 1091      GKAHFPREGVFVSNG  HFPREGVFV  3        0.2491
3374.8    75.00  0.54     Sequence
             DRB1_0701 1092      KAHFPREGVFVSNGT  HFPREGVFV  2        0.2630
2904.0    75.00  0.45     Sequence
             DRB1_0701 1093      AHFPREGVFVSNGTH  HFPREGVFV  1        0.2544
3187.7    75.00  0.37     Sequence
             DRB1_0701 1094      HFPREGVFVSNGTHW  VFVSNGTHW  6        0.5113
197.8    21.00  0.76     Sequence
             DRB1_0701 1095      FPREGVFVSNGTHWF  VFVSNGTHW  5        0.6285
55.7     8.00  0.49     Sequence        WB
             DRB1_0701 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.6593
39.9     6.00  0.44     Sequence        WB
```

```
             DRB1_0701 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.6560
41.4     6.00  0.44     Sequence        WB
             DRB1_0701 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.6335
52.7     8.00  0.44     Sequence        WB
             DRB1_0701 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.6225
59.4     8.50  0.45     Sequence        WB
             DRB1_0701 1100      VFVSNGTHWFVTQRN  FVSNGTHWF  1        0.6017
74.4    11.00  0.43     Sequence
             DRB1_0701 1101      FVSNGTHWFVTQRNF  FVSNGTHWF  0        0.5349
153.3    18.00  0.34     Sequence
             DRB1_0701 1102      VSNGTHWFVTQRNFY  WFVTQRNFY  6        0.5021
218.7    23.00  0.38     Sequence
             DRB1_0701 1103      SNGTHWFVTQRNFYE  WFVTQRNFY  5        0.4785
282.1    27.00  0.40     Sequence
             DRB1_0701 1104      NGTHWFVTQRNFYEP  WFVTQRNFY  4        0.4509
380.4    31.00  0.41     Sequence
             DRB1_0701 1105      GTHWFVTQRNFYEPQ  WFVTQRNFY  3        0.4316
468.5    35.00  0.42     Sequence
             DRB1_0701 1106      THWFVTQRNFYEPQI  WFVTQRNFY  2        0.4082
603.9    39.00  0.40     Sequence
             DRB1_0701 1107      HWFVTQRNFYEPQII  RNFYEPQII  6        0.4380
437.5    34.00  0.46     Sequence
             DRB1_0701 1108      WFVTQRNFYEPQIIT  RNFYEPQII  5        0.3845
780.5    44.00  0.56     Sequence
             DRB1_0701 1109      FVTQRNFYEPQIITT  RNFYEPQII  4        0.3418
1238.1    55.00  0.62     Sequence
             DRB1_0701 1110      VTQRNFYEPQIITTD  RNFYEPQII  3        0.3237
1506.3    60.00  0.63     Sequence
             DRB1_0701 1111      TQRNFYEPQIITTDN  RNFYEPQII  2        0.3114
1719.9    60.00  0.67     Sequence
             DRB1_0701 1112      QRNFYEPQIITTDNT  RNFYEPQII  1        0.2888
2197.9    65.00  0.65     Sequence
             DRB1_0701 1113      RNFYEPQIITTDNTF  QIITTDNTF  6        0.3497
1136.6    55.00  0.47     Sequence
             DRB1_0701 1114      NFYEPQIITTDNTFV  IITTDNTFV  6        0.4417
420.3    33.00  0.57     Sequence
             DRB1_0701 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.4138
568.3    38.00  0.57     Sequence
             DRB1_0701 1116      YEPQIITTDNTFVSG  IITTDNTFV  4        0.3699
913.3    47.00  0.58     Sequence
             DRB1_0701 1117      EPQIITTDNTFVSGN  IITTDNTFV  3        0.3468
1173.1    55.00  0.62     Sequence
             DRB1_0701 1118      PQIITTDNTFVSGNC  IITTDNTFV  2        0.3373
1300.6    55.00  0.64     Sequence
             DRB1_0701 1119      QIITTDNTFVSGNCD  IITTDNTFV  1        0.3353
1328.2    55.00  0.62     Sequence
             DRB1_0701 1120      IITTDNTFVSGNCDV  TFVSGNCDV  6        0.3803
816.9    45.00  0.44     Sequence
             DRB1_0701 1121      ITTDNTFVSGNCDVV  TFVSGNCDV  5        0.3568
1053.1    50.00  0.61     Sequence
             DRB1_0701 1122      TTDNTFVSGNCDVVI  TFVSGNCDV  4        0.4280
487.2    36.00  0.45     Sequence
             DRB1_0701 1123      TDNTFVSGNCDVVIG  TFVSGNCDV  3        0.3998
661.5    41.00  0.46     Sequence
             DRB1_0701 1124      DNTFVSGNCDVVIGI  TFVSGNCDV  2        0.3965
685.5    42.00  0.44     Sequence
             DRB1_0701 1125      NTFVSGNCDVVIGIV  TFVSGNCDV  1        0.4023
643.4    41.00  0.41     Sequence
             DRB1_0701 1126      TFVSGNCDVVIGIVN  TFVSGNCDV  0        0.3890
742.8    43.00  0.31     Sequence
             DRB1_0701 1127      FVSGNCDVVIGIVNN  CDVVIGIVN  5        0.3055
1833.5    65.00  0.38     Sequence
             DRB1_0701 1128      VSGNCDVVIGIVNNT  CDVVIGIVN  4        0.2612
2963.1    75.00  0.43     Sequence
             DRB1_0701 1129      SGNCDVVIGIVNNTV  VIGIVNNTV  6        0.3231
1516.9    60.00  0.55     Sequence
```

```
             DRB1_0701 1130      GNCDVVIGIVNNTVY  IGIVNNTVY  6        0.3840
784.8    44.00  0.43     Sequence
             DRB1_0701 1131      NCDVVIGIVNNTVYD  IGIVNNTVY  5        0.3678
935.1    48.00  0.44     Sequence
             DRB1_0701 1132      CDVVIGIVNNTVYDP  IGIVNNTVY  4        0.3369
1305.7    55.00  0.44     Sequence
             DRB1_0701 1133      DVVIGIVNNTVYDPL  IGIVNNTVY  3        0.3747
867.2    46.00  0.40     Sequence
             DRB1_0701 1134      VVIGIVNNTVYDPLQ  IGIVNNTVY  2        0.3669
944.3    48.00  0.40     Sequence
             DRB1_0701 1135      VIGIVNNTVYDPLQP  IGIVNNTVY  1        0.3449
1198.1    55.00  0.47     Sequence
             DRB1_0701 1136      IGIVNNTVYDPLQPE  IGIVNNTVY  0        0.2967
2016.5    65.00  0.51     Sequence
             DRB1_0701 1137      GIVNNTVYDPLQPEL  VNNTVYDPL  2        0.2076
5291.2    85.00  0.58     Sequence
             DRB1_0701 1138      IVNNTVYDPLQPELD  VNNTVYDPL  1        0.1917
6286.1    90.00  0.57     Sequence
             DRB1_0701 1139      VNNTVYDPLQPELDS  VNNTVYDPL  0        0.1600
8857.0    95.00  0.47     Sequence
             DRB1_0701 1140      NNTVYDPLQPELDSF  YDPLQPELD  4        0.1062
15848.3   100.00  0.40     Sequence
             DRB1_0701 1141      NTVYDPLQPELDSFK  YDPLQPELD  3        0.0984
17235.2   100.00  0.42     Sequence
             DRB1_0701 1142      TVYDPLQPELDSFKE  YDPLQPELD  2        0.0843
20082.8   100.00  0.49     Sequence
             DRB1_0701 1143      VYDPLQPELDSFKEE  YDPLQPELD  1        0.0729
22729.5   100.00  0.49     Sequence
             DRB1_0701 1144      YDPLQPELDSFKEEL  ELDSFKEEL  6        0.0804
20950.6   100.00  0.44     Sequence
             DRB1_0701 1145      DPLQPELDSFKEELD  ELDSFKEEL  5        0.0767
21802.3   100.00  0.41     Sequence
             DRB1_0701 1146      PLQPELDSFKEELDK  ELDSFKEEL  4        0.0747
22274.9   100.00  0.38     Sequence
             DRB1_0701 1147      LQPELDSFKEELDKY  ELDSFKEEL  3        0.0736
22549.2   100.00  0.38     Sequence
             DRB1_0701 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.2703
2684.4    70.00  0.83     Sequence
             DRB1_0701 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.2761
2520.1    70.00  0.83     Sequence
             DRB1_0701 1150      ELDSFKEELDKYFKN  FKEELDKYF  4        0.2715
2649.9    70.00  0.80     Sequence
             DRB1_0701 1151      LDSFKEELDKYFKNH  FKEELDKYF  3        0.2567
3111.2    75.00  0.82     Sequence
             DRB1_0701 1152      DSFKEELDKYFKNHT  FKEELDKYF  2        0.2555
3150.5    75.00  0.75     Sequence
             DRB1_0701 1153      SFKEELDKYFKNHTS  FKEELDKYF  1        0.2659
2815.8    75.00  0.61     Sequence
             DRB1_0701 1154      FKEELDKYFKNHTSP  FKEELDKYF  0        0.2248
4393.8    80.00  0.50     Sequence
             DRB1_0701 1155      KEELDKYFKNHTSPD  YFKNHTSPD  6        0.2520
3272.7    75.00  0.57     Sequence
             DRB1_0701 1156      EELDKYFKNHTSPDV  FKNHTSPDV  6        0.4241
508.5    36.00  0.56     Sequence
             DRB1_0701 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.4294
480.0    35.00  0.59     Sequence
             DRB1_0701 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.4681
315.8    28.00  0.56     Sequence
             DRB1_0701 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.4333
460.3    35.00  0.53     Sequence
             DRB1_0701 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.4275
490.2    36.00  0.56     Sequence
             DRB1_0701 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.3735
878.5    47.00  0.55     Sequence
             DRB1_0701 1162      FKNHTSPDVDLGDIS  FKNHTSPDV  0        0.2413
3674.5    80.00  0.56     Sequence
```

```
             DRB1_0701 1163      KNHTSPDVDLGDISG  NHTSPDVDL  1        0.0964
17625.8   100.00  0.66     Sequence
             DRB1_0701 1164      NHTSPDVDLGDISGI  VDLGDISGI  6        0.1098
15233.6   100.00  0.54     Sequence
             DRB1_0701 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.1084
15477.0   100.00  0.62     Sequence
             DRB1_0701 1166      TSPDVDLGDISGINA  LGDISGINA  6        0.1370
11354.8    95.00  0.41     Sequence
             DRB1_0701 1167      SPDVDLGDISGINAS  LGDISGINA  5        0.1390
11110.9    95.00  0.43     Sequence
             DRB1_0701 1168      PDVDLGDISGINASF  LGDISGINA  4        0.1696
7984.2    90.00  0.36     Sequence
             DRB1_0701 1169      DVDLGDISGINASFV  ISGINASFV  6        0.3984
671.3    41.00  0.81     Sequence
             DRB1_0701 1170      VDLGDISGINASFVN  ISGINASFV  5        0.3933
709.2    42.00  0.69     Sequence
             DRB1_0701 1171      DLGDISGINASFVNI  ISGINASFV  4        0.4199
532.0    37.00  0.63     Sequence
             DRB1_0701 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.4123
577.3    39.00  0.60     Sequence
             DRB1_0701 1173      GDISGINASFVNIQK  ISGINASFV  2        0.4017
647.4    41.00  0.60     Sequence
             DRB1_0701 1174      DISGINASFVNIQKE  ISGINASFV  1        0.3810
810.2    45.00  0.61     Sequence
             DRB1_0701 1175      ISGINASFVNIQKEI  ISGINASFV  0        0.3704
908.7    47.00  0.44     Sequence
             DRB1_0701 1176      SGINASFVNIQKEID  FVNIQKEID  6        0.3069
1806.5    65.00  0.25     Sequence
             DRB1_0701 1177      GINASFVNIQKEIDR  FVNIQKEID  5        0.2762
2517.4    70.00  0.34     Sequence
             DRB1_0701 1178      INASFVNIQKEIDRL  FVNIQKEID  4        0.2757
2531.5    70.00  0.42     Sequence
             DRB1_0701 1179      NASFVNIQKEIDRLN  FVNIQKEID  3        0.2664
2800.4    70.00  0.41     Sequence
             DRB1_0701 1180      ASFVNIQKEIDRLNE  FVNIQKEID  2        0.2546
3179.7    75.00  0.41     Sequence
             DRB1_0701 1181      SFVNIQKEIDRLNEV  FVNIQKEID  1        0.2492
3371.2    75.00  0.37     Sequence
             DRB1_0701 1182      FVNIQKEIDRLNEVA  FVNIQKEID  0        0.2126
5012.8    85.00  0.31     Sequence
             DRB1_0701 1183      VNIQKEIDRLNEVAK  IQKEIDRLN  2        0.1567
9171.8    95.00  0.50     Sequence
             DRB1_0701 1184      NIQKEIDRLNEVAKN  IQKEIDRLN  1        0.1511
9749.4    95.00  0.47     Sequence
             DRB1_0701 1185      IQKEIDRLNEVAKNL  RLNEVAKNL  6        0.1586
8989.9    95.00  0.26     Sequence
             DRB1_0701 1186      QKEIDRLNEVAKNLN  LNEVAKNLN  6        0.1734
7660.4    90.00  0.43     Sequence
             DRB1_0701 1187      KEIDRLNEVAKNLNE  LNEVAKNLN  5        0.1701
7935.5    90.00  0.50     Sequence
             DRB1_0701 1188      EIDRLNEVAKNLNES  LNEVAKNLN  4        0.1572
9121.5    95.00  0.54     Sequence
             DRB1_0701 1189      IDRLNEVAKNLNESL  VAKNLNESL  6        0.2016
5648.0    85.00  0.46     Sequence
             DRB1_0701 1190      DRLNEVAKNLNESLI  VAKNLNESL  5        0.2163
4815.8    85.00  0.47     Sequence
             DRB1_0701 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.2128
4999.2    85.00  0.44     Sequence
             DRB1_0701 1192      LNEVAKNLNESLIDL  VAKNLNESL  3        0.2150
4881.1    85.00  0.47     Sequence
             DRB1_0701 1193      NEVAKNLNESLIDLQ  VAKNLNESL  2        0.1927
6212.9    90.00  0.54     Sequence
             DRB1_0701 1194      EVAKNLNESLIDLQE  VAKNLNESL  1        0.1738
7622.2    90.00  0.51     Sequence
             DRB1_0701 1195      VAKNLNESLIDLQEL  VAKNLNESL  0        0.1695
7984.8    90.00  0.31     Sequence
```

```
             DRB1_0701 1196      AKNLNESLIDLQELG  KNLNESLID  1        0.1289
12392.9    95.00  0.31     Sequence
             DRB1_0701 1197      KNLNESLIDLQELGK  KNLNESLID  0        0.1106
15109.7   100.00  0.20     Sequence
             DRB1_0701 1198      NLNESLIDLQELGKY  ESLIDLQEL  3        0.0941
18071.7   100.00  0.26     Sequence
             DRB1_0701 1199      LNESLIDLQELGKYE  ESLIDLQEL  2        0.0818
20631.6   100.00  0.29     Sequence
             DRB1_0701 1200      NESLIDLQELGKYEQ  ESLIDLQEL  1        0.0752
22169.8   100.00  0.28     Sequence
             DRB1_0701 1201      ESLIDLQELGKYEQY  LIDLQELGK  2        0.0718
22982.7   100.00  0.25     Sequence
             DRB1_0701 1202      SLIDLQELGKYEQYI  LQELGKYEQ  4        0.0776
21588.0   100.00  0.16     Sequence
             DRB1_0701 1203      LIDLQELGKYEQYIK  LGKYEQYIK  6        0.0914
18604.0   100.00  0.37     Sequence
             DRB1_0701 1204      IDLQELGKYEQYIKW  GKYEQYIKW  6        0.1239
13077.9   100.00  0.40     Sequence
             DRB1_0701 1205      DLQELGKYEQYIKWP  GKYEQYIKW  5        0.1267
12698.1   100.00  0.44     Sequence
             DRB1_0701 1206      LQELGKYEQYIKWPW  YEQYIKWPW  6        0.2919
2124.1    65.00  0.71     Sequence
             DRB1_0701 1207      QELGKYEQYIKWPWY  YEQYIKWPW  5        0.3150
1654.4    60.00  0.70     Sequence
             DRB1_0701 1208      ELGKYEQYIKWPWYI  YEQYIKWPW  4        0.3933
709.0    42.00  0.54     Sequence
             DRB1_0701 1209      LGKYEQYIKWPWYIW  YEQYIKWPW  3        0.4572
355.2    30.00  0.37     Sequence
             DRB1_0701 1210      GKYEQYIKWPWYIWL  YEQYIKWPW  2        0.4854
261.9    25.00  0.31     Sequence
             DRB1_0701 1211      KYEQYIKWPWYIWLG  YIKWPWYIW  4        0.4580
352.2    30.00  0.29     Sequence
             DRB1_0701 1212      YEQYIKWPWYIWLGF  YIKWPWYIW  3        0.4314
469.8    35.00  0.34     Sequence
             DRB1_0701 1213      EQYIKWPWYIWLGFI  YIKWPWYIW  2        0.3955
693.0    42.00  0.38     Sequence
             DRB1_0701 1214      QYIKWPWYIWLGFIA  YIKWPWYIW  1        0.4091
597.9    39.00  0.34     Sequence
             DRB1_0701 1215      YIKWPWYIWLGFIAG  YIKWPWYIW  0        0.3619
996.8    49.00  0.33     Sequence
             DRB1_0701 1216      IKWPWYIWLGFIAGL  WYIWLGFIA  4        0.2992
1963.1    65.00  0.28     Sequence
             DRB1_0701 1217      KWPWYIWLGFIAGLI  WLGFIAGLI  6        0.5727
101.8    14.00  0.76     Sequence
             DRB1_0701 1218      WPWYIWLGFIAGLIA  WLGFIAGLI  5        0.5755
98.8    13.00  0.64     Sequence
             DRB1_0701 1219      PWYIWLGFIAGLIAI  WLGFIAGLI  4        0.5755
98.7    13.00  0.64     Sequence
             DRB1_0701 1220      WYIWLGFIAGLIAIV  WLGFIAGLI  3        0.5816
92.5    13.00  0.58     Sequence
             DRB1_0701 1221      YIWLGFIAGLIAIVM  WLGFIAGLI  2        0.5734
101.0    14.00  0.58     Sequence
             DRB1_0701 1222      IWLGFIAGLIAIVMV  WLGFIAGLI  1        0.5506
129.3    16.00  0.56     Sequence
             DRB1_0701 1223      WLGFIAGLIAIVMVT  WLGFIAGLI  0        0.5218
176.6    20.00  0.49     Sequence
             DRB1_0701 1224      LGFIAGLIAIVMVTI  LGFIAGLIA  0        0.3780
837.4    46.00  0.38     Sequence
             DRB1_0701 1225      GFIAGLIAIVMVTIM  FIAGLIAIV  1        0.3226
1524.4    60.00  0.50     Sequence
             DRB1_0701 1226      FIAGLIAIVMVTIML  FIAGLIAIV  0        0.2913
2138.5    65.00  0.41     Sequence
             DRB1_0701 1227      IAGLIAIVMVTIMLC  IVMVTIMLC  6        0.2800
2417.6    70.00  0.39     Sequence
             DRB1_0701 1228      AGLIAIVMVTIMLCC  IVMVTIMLC  5        0.2546
3181.3    75.00  0.31     Sequence
```

```
             DRB1_0701 1229      GLIAIVMVTIMLCCM  IVMVTIMLC  4        0.2562
3126.5    75.00  0.29     Sequence
             DRB1_0701 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3        0.2351
3929.9    80.00  0.30     Sequence
             DRB1_0701 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2        0.2244
4410.3    80.00  0.33     Sequence
             DRB1_0701 1232      AIVMVTIMLCCMTSC  IVMVTIMLC  1        0.2435
3587.0    75.00  0.38     Sequence
             DRB1_0701 1233      IVMVTIMLCCMTSCC  IVMVTIMLC  0        0.2361
3886.2    80.00  0.34     Sequence
             DRB1_0701 1234      VMVTIMLCCMTSCCS  LCCMTSCCS  6        0.2298
4159.5    80.00  0.34     Sequence
             DRB1_0701 1235      MVTIMLCCMTSCCSC  LCCMTSCCS  5        0.2466
3468.1    75.00  0.31     Sequence
             DRB1_0701 1236      VTIMLCCMTSCCSCL  CMTSCCSCL  6        0.3241
1499.2    60.00  0.40     Sequence
             DRB1_0701 1237      TIMLCCMTSCCSCLK  CMTSCCSCL  5        0.3152
1651.0    60.00  0.35     Sequence
             DRB1_0701 1238      IMLCCMTSCCSCLKG  CMTSCCSCL  4        0.2885
2204.2    65.00  0.34     Sequence
             DRB1_0701 1239      MLCCMTSCCSCLKGC  CMTSCCSCL  3        0.2660
2812.3    70.00  0.34     Sequence
             DRB1_0701 1240      LCCMTSCCSCLKGCC  CMTSCCSCL  2        0.2398
3733.1    80.00  0.32     Sequence
             DRB1_0701 1241      CCMTSCCSCLKGCCS  CSCLKGCCS  6        0.2418
3654.9    80.00  0.37     Sequence
             DRB1_0701 1242      CMTSCCSCLKGCCSC  CSCLKGCCS  5        0.2044
5476.1    85.00  0.44     Sequence
             DRB1_0701 1243      MTSCCSCLKGCCSCG  CSCLKGCCS  4        0.1653
8362.6    90.00  0.52     Sequence
             DRB1_0701 1244      TSCCSCLKGCCSCGS  CSCLKGCCS  3        0.1800
7129.9    90.00  0.44     Sequence
             DRB1_0701 1245      SCCSCLKGCCSCGSC  CSCLKGCCS  2        0.1731
7685.0    90.00  0.44     Sequence
             DRB1_0701 1246      CCSCLKGCCSCGSCC  CSCLKGCCS  1        0.1690
8032.4    90.00  0.35     Sequence
             DRB1_0701 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.1691
8024.2    90.00  0.30     Sequence
             DRB1_0701 1248      SCLKGCCSCGSCCKF  CSCGSCCKF  6        0.2284
4222.6    80.00  0.41     Sequence
             DRB1_0701 1249      CLKGCCSCGSCCKFD  CSCGSCCKF  5        0.2204
4606.4    80.00  0.43     Sequence
             DRB1_0701 1250      LKGCCSCGSCCKFDE  CSCGSCCKF  4        0.2073
5307.2    85.00  0.44     Sequence
             DRB1_0701 1251      KGCCSCGSCCKFDED  CSCGSCCKF  3        0.1803
7111.1    90.00  0.52     Sequence
             DRB1_0701 1252      GCCSCGSCCKFDEDD  CSCGSCCKF  2        0.1575
9092.0    95.00  0.52     Sequence
             DRB1_0701 1253      CCSCGSCCKFDEDDS  CSCGSCCKF  1        0.1345
11664.2    95.00  0.60     Sequence
             DRB1_0701 1254      CSCGSCCKFDEDDSE  CSCGSCCKF  0        0.1012
16731.8   100.00  0.58     Sequence
             DRB1_0701 1255      SCGSCCKFDEDDSEP  CCKFDEDDS  4        0.0402
32381.1   100.00  0.25     Sequence
             DRB1_0701 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.2313
4091.7    80.00  0.90     Sequence
             DRB1_0701 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.2675
2767.8    70.00  0.90     Sequence
             DRB1_0701 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.2615
2951.1    75.00  0.89     Sequence
             DRB1_0701 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.2369
3852.6    80.00  0.89     Sequence
             DRB1_0701 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.2372
3841.0    80.00  0.87     Sequence
             DRB1_0701 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.2259
4338.5    80.00  0.86     Sequence
```

```
             DRB1_0701 1262      FDEDDSEPVLKGVKL  FDEDDSEPV  0        0.2189
4680.7    85.00  0.48     Sequence
             DRB1_0701 1263      DEDDSEPVLKGVKLH  EPVLKGVKL  5        0.1566
9187.0    95.00  0.70     Sequence
             DRB1_0701 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.2866
2249.8    70.00  0.63     Sequence
             DRB1_0701 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.3716
897.2    47.00  0.43     Sequence
             DRB1_0802    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.2518
3278.1    65.00  0.64     Sequence
             DRB1_0802    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.2481
3414.0    70.00  0.60     Sequence
             DRB1_0802    3      PIKEMFVFLVLLPLV  IKEMFVFLV  1        0.2773
2489.4    60.00  0.47     Sequence
             DRB1_0802    4      IKEMFVFLVLLPLVS  FLVLLPLVS  6        0.3256
1475.8    42.00  0.40     Sequence
             DRB1_0802    5      KEMFVFLVLLPLVSS  LVLLPLVSS  6        0.4669
319.8    11.00  0.56     Sequence
             DRB1_0802    6      EMFVFLVLLPLVSSQ  LVLLPLVSS  5        0.6044
72.3     1.30  0.52     Sequence         SB
             DRB1_0802    7      MFVFLVLLPLVSSQC  LVLLPLVSS  4        0.6131
65.8     1.10  0.46     Sequence         SB
             DRB1_0802    8      FVFLVLLPLVSSQCV  LVLLPLVSS  3        0.6238
58.6     0.80  0.46     Sequence         SB
             DRB1_0802    9      VFLVLLPLVSSQCVN  LVLLPLVSS  2        0.6280
56.0     0.80  0.46     Sequence         SB
             DRB1_0802   10      FLVLLPLVSSQCVNF  LVLLPLVSS  1        0.6080
69.5     1.20  0.44     Sequence         SB
             DRB1_0802   11      LVLLPLVSSQCVNFT  LLPLVSSQC  2        0.5179
184.3     5.50  0.38     Sequence         WB
             DRB1_0802   12      VLLPLVSSQCVNFTN  LLPLVSSQC  1        0.4086
601.0    21.00  0.42     Sequence
             DRB1_0802   13      LLPLVSSQCVNFTNR  LVSSQCVNF  3        0.2885
2204.2    55.00  0.27     Sequence
             DRB1_0802   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.2379
3812.9    70.00  0.37     Sequence
             DRB1_0802   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.2715
2649.4    60.00  0.26     Sequence
             DRB1_0802   16      LVSSQCVNFTNRTQL  VNFTNRTQL  6        0.2884
2206.6    55.00  0.44     Sequence
             DRB1_0802   17      VSSQCVNFTNRTQLP  VNFTNRTQL  5        0.3191
1583.4    44.00  0.49     Sequence
             DRB1_0802   18      SSQCVNFTNRTQLPS  VNFTNRTQL  4        0.3587
1032.0    33.00  0.47     Sequence
             DRB1_0802   19      SQCVNFTNRTQLPSA  VNFTNRTQL  3        0.3999
660.2    23.00  0.45     Sequence
             DRB1_0802   20      QCVNFTNRTQLPSAY  VNFTNRTQL  2        0.4120
579.5    20.00  0.38     Sequence
             DRB1_0802   21      CVNFTNRTQLPSAYT  FTNRTQLPS  3        0.4124
577.2    20.00  0.32     Sequence
             DRB1_0802   22      VNFTNRTQLPSAYTN  FTNRTQLPS  2        0.3726
887.4    29.00  0.41     Sequence
             DRB1_0802   23      NFTNRTQLPSAYTNS  FTNRTQLPS  1        0.3201
1565.6    43.00  0.38     Sequence
             DRB1_0802   24      FTNRTQLPSAYTNSF  RTQLPSAYT  3        0.2533
3225.3    65.00  0.34     Sequence
             DRB1_0802   25      TNRTQLPSAYTNSFT  RTQLPSAYT  2        0.2364
3875.0    70.00  0.37     Sequence
             DRB1_0802   26      NRTQLPSAYTNSFTR  LPSAYTNSF  4        0.2204
4605.5    75.00  0.34     Sequence
             DRB1_0802   27      RTQLPSAYTNSFTRG  LPSAYTNSF  3        0.1985
5839.1    80.00  0.38     Sequence
             DRB1_0802   28      TQLPSAYTNSFTRGV  LPSAYTNSF  2        0.2109
5103.0    80.00  0.31     Sequence
             DRB1_0802   29      QLPSAYTNSFTRGVY  YTNSFTRGV  5        0.1985
5839.1    80.00  0.37     Sequence
```

```
             DRB1_0802   30      LPSAYTNSFTRGVYY  YTNSFTRGV  4        0.2016
5645.3    80.00  0.39     Sequence
             DRB1_0802   31      PSAYTNSFTRGVYYP  YTNSFTRGV  3        0.2104
5132.5    80.00  0.32     Sequence
             DRB1_0802   32      SAYTNSFTRGVYYPD  YTNSFTRGV  2        0.2032
5548.3    80.00  0.32     Sequence
             DRB1_0802   33      AYTNSFTRGVYYPDK  YTNSFTRGV  1        0.2098
5164.9    80.00  0.23     Sequence
             DRB1_0802   34      YTNSFTRGVYYPDKV  FTRGVYYPD  4        0.1933
6173.0    85.00  0.33     Sequence
             DRB1_0802   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.1806
7083.1    85.00  0.30     Sequence
             DRB1_0802   36      NSFTRGVYYPDKVFR  FTRGVYYPD  2        0.2040
5500.6    80.00  0.25     Sequence
             DRB1_0802   37      SFTRGVYYPDKVFRS  VYYPDKVFR  5        0.2213
4559.9    75.00  0.31     Sequence
             DRB1_0802   38      FTRGVYYPDKVFRSS  VYYPDKVFR  4        0.2339
3978.7    70.00  0.31     Sequence
             DRB1_0802   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.2512
3301.2    65.00  0.34     Sequence
             DRB1_0802   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.2724
2623.5    60.00  0.32     Sequence
             DRB1_0802   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.3042
1860.0    48.00  0.25     Sequence
             DRB1_0802   42      VYYPDKVFRSSVLHS  VFRSSVLHS  6        0.3955
692.6    24.00  0.47     Sequence
             DRB1_0802   43      YYPDKVFRSSVLHST  VFRSSVLHS  5        0.4527
373.2    13.00  0.50     Sequence
             DRB1_0802   44      YPDKVFRSSVLHSTQ  VFRSSVLHS  4        0.4844
264.6     9.00  0.50     Sequence         WB
             DRB1_0802   45      PDKVFRSSVLHSTQD  VFRSSVLHS  3        0.4781
283.4     9.50  0.51     Sequence         WB
             DRB1_0802   46      DKVFRSSVLHSTQDL  VFRSSVLHS  2        0.4697
310.5    11.00  0.53     Sequence
             DRB1_0802   47      KVFRSSVLHSTQDLF  VFRSSVLHS  1        0.4596
346.4    12.00  0.49     Sequence
             DRB1_0802   48      VFRSSVLHSTQDLFL  FRSSVLHST  1        0.3425
1229.5    37.00  0.38     Sequence
             DRB1_0802   49      FRSSVLHSTQDLFLP  LHSTQDLFL  5        0.1918
6278.7    85.00  0.38     Sequence
             DRB1_0802   50      RSSVLHSTQDLFLPF  LHSTQDLFL  4        0.1746
7558.2    85.00  0.48     Sequence
             DRB1_0802   51      SSVLHSTQDLFLPFF  LHSTQDLFL  3        0.1766
7401.8    85.00  0.45     Sequence
             DRB1_0802   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2        0.1873
6589.8    85.00  0.43     Sequence
             DRB1_0802   53      VLHSTQDLFLPFFSN  LHSTQDLFL  1        0.1866
6639.5    85.00  0.41     Sequence
             DRB1_0802   54      LHSTQDLFLPFFSNV  FLPFFSNVX  7        0.1880
6538.9    85.00  0.22     Sequence
             DRB1_0802   55      HSTQDLFLPFFSNVT  FLPFFSNVT  6        0.3226
1524.6    43.00  0.41     Sequence
             DRB1_0802   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.3504
1128.4    35.00  0.41     Sequence
             DRB1_0802   57      TQDLFLPFFSNVTWF  FLPFFSNVT  4        0.3766
849.8    28.00  0.36     Sequence
             DRB1_0802   58      QDLFLPFFSNVTWFH  FLPFFSNVT  3        0.4354
449.8    16.00  0.30     Sequence
             DRB1_0802   59      DLFLPFFSNVTWFHA  FSNVTWFHA  6        0.5127
194.9     6.00  0.37     Sequence         WB
             DRB1_0802   60      LFLPFFSNVTWFHAI  FSNVTWFHA  5        0.5214
177.5     5.50  0.41     Sequence         WB
             DRB1_0802   61      FLPFFSNVTWFHAIH  FSNVTWFHA  4        0.5143
191.6     6.00  0.41     Sequence         WB
             DRB1_0802   62      LPFFSNVTWFHAIHV  FSNVTWFHA  3        0.4980
228.5     7.50  0.47     Sequence         WB
```

```
             DRB1_0802   63      PFFSNVTWFHAIHVS  FSNVTWFHA  2        0.5098
201.0     6.50  0.44     Sequence         WB
             DRB1_0802   64      FFSNVTWFHAIHVSG  FSNVTWFHA  1        0.4616
338.8    12.00  0.42     Sequence
             DRB1_0802   65      FSNVTWFHAIHVSGT  VTWFHAIHV  3        0.3999
660.2    23.00  0.26     Sequence
             DRB1_0802   66      SNVTWFHAIHVSGTN  FHAIHVSGT  5        0.4171
548.6    19.00  0.29     Sequence
             DRB1_0802   67      NVTWFHAIHVSGTNG  FHAIHVSGT  4        0.4559
360.5    13.00  0.28     Sequence
             DRB1_0802   68      VTWFHAIHVSGTNGT  IHVSGTNGT  6        0.4774
285.6     9.50  0.22     Sequence         WB
             DRB1_0802   69      TWFHAIHVSGTNGTK  IHVSGTNGT  5        0.4900
249.2     8.00  0.29     Sequence         WB
             DRB1_0802   70      WFHAIHVSGTNGTKR  IHVSGTNGT  4        0.4914
245.5     8.00  0.32     Sequence         WB
             DRB1_0802   71      FHAIHVSGTNGTKRF  IHVSGTNGT  3        0.4770
286.8     9.50  0.38     Sequence         WB
             DRB1_0802   72      HAIHVSGTNGTKRFD  IHVSGTNGT  2        0.4391
432.0    15.00  0.50     Sequence
             DRB1_0802   73      AIHVSGTNGTKRFDN  IHVSGTNGT  1        0.3602
1015.4    32.00  0.58     Sequence
             DRB1_0802   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.2053
5421.6    80.00  0.42     Sequence
             DRB1_0802   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.1084
15467.9   100.00  0.40     Sequence
             DRB1_0802   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.1265
12719.5    95.00  0.53     Sequence
             DRB1_0802   77      SGTNGTKRFDNPVLP  TKRFDNPVL  5        0.1468
10209.5    95.00  0.60     Sequence
             DRB1_0802   78      GTNGTKRFDNPVLPF  TKRFDNPVL  4        0.1810
7053.7    85.00  0.52     Sequence
             DRB1_0802   79      TNGTKRFDNPVLPFN  TKRFDNPVL  3        0.2033
5540.4    80.00  0.44     Sequence
             DRB1_0802   80      NGTKRFDNPVLPFND  TKRFDNPVL  2        0.2075
5294.9    80.00  0.41     Sequence
             DRB1_0802   81      GTKRFDNPVLPFNDG  TKRFDNPVL  1        0.2138
4944.6    80.00  0.34     Sequence
             DRB1_0802   82      TKRFDNPVLPFNDGV  FDNPVLPFN  3        0.2091
5203.1    80.00  0.22     Sequence
             DRB1_0802   83      KRFDNPVLPFNDGVY  VLPFNDGVY  6        0.2196
4648.4    75.00  0.26     Sequence
             DRB1_0802   84      RFDNPVLPFNDGVYF  LPFNDGVYF  6        0.2389
3771.2    70.00  0.30     Sequence
             DRB1_0802   85      FDNPVLPFNDGVYFA  LPFNDGVYF  5        0.2483
3405.6    70.00  0.41     Sequence
             DRB1_0802   86      DNPVLPFNDGVYFAS  LPFNDGVYF  4        0.2570
3099.4    65.00  0.45     Sequence
             DRB1_0802   87      NPVLPFNDGVYFAST  LPFNDGVYF  3        0.2685
2738.0    60.00  0.45     Sequence
             DRB1_0802   88      PVLPFNDGVYFASTE  LPFNDGVYF  2        0.2614
2954.2    65.00  0.44     Sequence
             DRB1_0802   89      VLPFNDGVYFASTEK  LPFNDGVYF  1        0.2508
3314.2    65.00  0.34     Sequence
             DRB1_0802   90      LPFNDGVYFASTEKS  VYFASTEKS  6        0.3706
906.7    30.00  0.62     Sequence
             DRB1_0802   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.4483
391.4    14.00  0.57     Sequence
             DRB1_0802   92      FNDGVYFASTEKSNI  VYFASTEKS  4        0.4769
287.0     9.50  0.56     Sequence         WB
             DRB1_0802   93      NDGVYFASTEKSNII  VYFASTEKS  3        0.4927
241.9     8.00  0.54     Sequence         WB
             DRB1_0802   94      DGVYFASTEKSNIIR  VYFASTEKS  2        0.4951
235.7     7.50  0.51     Sequence         WB
             DRB1_0802   95      GVYFASTEKSNIIRG  VYFASTEKS  1        0.4873
256.6     8.50  0.49     Sequence         WB
```

```
            DRB1_0802   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.3975
677.8    23.00  0.42     Sequence
            DRB1_0802   97      YFASTEKSNIIRGWI  FASTEKSNI  1        0.2462
3483.3    70.00  0.46     Sequence
            DRB1_0802   98      FASTEKSNIIRGWIF  STEKSNIIR  2        0.1906
6360.9    85.00  0.24     Sequence
            DRB1_0802   99      ASTEKSNIIRGWIFG  SNIIRGWIF  5        0.2082
5258.6    80.00  0.23     Sequence
            DRB1_0802  100      STEKSNIIRGWIFGT  IIRGWIFGT  6        0.2578
3073.5    65.00  0.37     Sequence
            DRB1_0802  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5        0.2992
1962.8    50.00  0.41     Sequence
            DRB1_0802  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.3198
1570.6    44.00  0.38     Sequence
            DRB1_0802  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3        0.3233
1512.7    43.00  0.37     Sequence
            DRB1_0802  104      SNIIRGWIFGTTLDS  IIRGWIFGT  2        0.3324
1371.3    40.00  0.32     Sequence
            DRB1_0802  105      NIIRGWIFGTTLDSK  IIRGWIFGT  1        0.3775
841.9    28.00  0.23     Sequence
            DRB1_0802  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.3653
960.7    31.00  0.24     Sequence
            DRB1_0802  107      IRGWIFGTTLDSKTQ  FGTTLDSKT  5        0.3613
1002.8    32.00  0.33     Sequence
            DRB1_0802  108      RGWIFGTTLDSKTQS  FGTTLDSKT  4        0.3679
934.0    30.00  0.36     Sequence
            DRB1_0802  109      GWIFGTTLDSKTQSL  FGTTLDSKT  3        0.3567
1054.0    33.00  0.35     Sequence
            DRB1_0802  110      WIFGTTLDSKTQSLL  FGTTLDSKT  2        0.3235
1509.0    42.00  0.34     Sequence
            DRB1_0802  111      IFGTTLDSKTQSLLI  FGTTLDSKT  1        0.2838
2320.0    55.00  0.34     Sequence
            DRB1_0802  112      FGTTLDSKTQSLLIV  LDSKTQSLL  4        0.2322
4053.7    70.00  0.41     Sequence
            DRB1_0802  113      GTTLDSKTQSLLIVN  LDSKTQSLL  3        0.2247
4395.2    75.00  0.38     Sequence
            DRB1_0802  114      TTLDSKTQSLLIVNN  LDSKTQSLL  2        0.2264
4316.4    75.00  0.38     Sequence
            DRB1_0802  115      TLDSKTQSLLIVNNA  LDSKTQSLL  1        0.2825
2351.6    55.00  0.25     Sequence
            DRB1_0802  116      LDSKTQSLLIVNNAT  LLIVNNATX  7        0.3525
1103.3    34.00  0.35     Sequence
            DRB1_0802  117      DSKTQSLLIVNNATN  LLIVNNATN  6        0.4139
567.5    20.00  0.56     Sequence
            DRB1_0802  118      SKTQSLLIVNNATNV  LLIVNNATN  5        0.4468
397.4    14.00  0.60     Sequence
            DRB1_0802  119      KTQSLLIVNNATNVV  LLIVNNATN  4        0.4866
258.6     8.50  0.53     Sequence         WB
            DRB1_0802  120      TQSLLIVNNATNVVI  LLIVNNATN  3        0.5031
216.3     7.00  0.47     Sequence         WB
            DRB1_0802  121      QSLLIVNNATNVVIK  LLIVNNATN  2        0.5229
174.6     5.00  0.44     Sequence         WB
            DRB1_0802  122      SLLIVNNATNVVIKV  LLIVNNATN  1        0.4925
242.5     8.00  0.38     Sequence         WB
            DRB1_0802  123      LLIVNNATNVVIKVC  VNNATNVVI  3        0.4313
470.1    17.00  0.32     Sequence
            DRB1_0802  124      LIVNNATNVVIKVCE  VNNATNVVI  2        0.3796
822.3    27.00  0.45     Sequence
            DRB1_0802  125      IVNNATNVVIKVCEF  VNNATNVVI  1        0.3253
1480.1    42.00  0.47     Sequence
            DRB1_0802  126      VNNATNVVIKVCEFQ  VVIKVCEFQ  6        0.2715
2649.1    60.00  0.19     Sequence
            DRB1_0802  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.3061
1821.6    48.00  0.28     Sequence
            DRB1_0802  128      NATNVVIKVCEFQFC  VIKVCEFQF  5        0.3145
1663.4    45.00  0.29     Sequence
```

```
             DRB1_0802  129      ATNVVIKVCEFQFCN  IKVCEFQFC  5        0.3266
1459.7    42.00  0.40     Sequence
             DRB1_0802  130      TNVVIKVCEFQFCNY  IKVCEFQFC  4        0.3238
1505.4    42.00  0.40     Sequence
             DRB1_0802  131      NVVIKVCEFQFCNYP  IKVCEFQFC  3        0.3191
1584.0    44.00  0.41     Sequence
             DRB1_0802  132      VVIKVCEFQFCNYPF  IKVCEFQFC  2        0.3308
1395.6    40.00  0.38     Sequence
             DRB1_0802  133      VIKVCEFQFCNYPFL  IKVCEFQFC  1        0.2757
2533.2    60.00  0.37     Sequence
             DRB1_0802  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.2200
4627.0    75.00  0.35     Sequence
             DRB1_0802  135      KVCEFQFCNYPFLGV  FQFCNYPFL  4        0.2410
3687.4    70.00  0.40     Sequence
             DRB1_0802  136      VCEFQFCNYPFLGVY  FCNYPFLGV  5        0.2514
3294.8    65.00  0.31     Sequence
             DRB1_0802  137      CEFQFCNYPFLGVYY  FCNYPFLGV  4        0.2682
2745.7    60.00  0.32     Sequence
             DRB1_0802  138      EFQFCNYPFLGVYYH  FCNYPFLGV  3        0.2692
2717.4    60.00  0.28     Sequence
             DRB1_0802  139      FQFCNYPFLGVYYHK  FCNYPFLGV  2        0.2381
3802.9    70.00  0.32     Sequence
             DRB1_0802  140      QFCNYPFLGVYYHKN  FCNYPFLGV  1        0.2518
3277.8    65.00  0.23     Sequence
             DRB1_0802  141      FCNYPFLGVYYHKNN  YPFLGVYYH  3        0.2385
3786.9    70.00  0.31     Sequence
             DRB1_0802  142      CNYPFLGVYYHKNNK  YPFLGVYYH  2        0.2400
3726.3    70.00  0.25     Sequence
             DRB1_0802  143      NYPFLGVYYHKNNKS  VYYHKNNKS  6        0.3260
1469.2    42.00  0.31     Sequence
             DRB1_0802  144      YPFLGVYYHKNNKSW  VYYHKNNKS  5        0.3584
1034.6    33.00  0.38     Sequence
             DRB1_0802  145      PFLGVYYHKNNKSWM  VYYHKNNKS  4        0.3814
806.6    27.00  0.42     Sequence
             DRB1_0802  146      FLGVYYHKNNKSWME  VYYHKNNKS  3        0.3855
771.9    26.00  0.43     Sequence
             DRB1_0802  147      LGVYYHKNNKSWMES  VYYHKNNKS  2        0.3827
795.8    27.00  0.46     Sequence
             DRB1_0802  148      GVYYHKNNKSWMESE  VYYHKNNKS  1        0.3839
785.0    26.00  0.42     Sequence
             DRB1_0802  149      VYYHKNNKSWMESEF  YYHKNNKSW  1        0.3093
1759.4    47.00  0.37     Sequence
             DRB1_0802  150      YYHKNNKSWMESEFR  YHKNNKSWM  1        0.1536
9484.7    90.00  0.28     Sequence
             DRB1_0802  151      YHKNNKSWMESEFRV  KNNKSWMES  2        0.1036
16304.1   100.00  0.24     Sequence
             DRB1_0802  152      HKNNKSWMESEFRVY  MESEFRVYX  7        0.1398
11012.2    95.00  0.28     Sequence
             DRB1_0802  153      KNNKSWMESEFRVYS  MESEFRVYS  6        0.3129
1693.6    46.00  0.69     Sequence
             DRB1_0802  154      NNKSWMESEFRVYSS  MESEFRVYS  5        0.3685
927.9    30.00  0.71     Sequence
             DRB1_0802  155      NKSWMESEFRVYSSA  MESEFRVYS  4        0.4106
588.5    20.00  0.69     Sequence
             DRB1_0802  156      KSWMESEFRVYSSAN  MESEFRVYS  3        0.4754
291.8    10.00  0.54     Sequence
             DRB1_0802  157      SWMESEFRVYSSANN  FRVYSSANN  6        0.5512
128.6     3.50  0.51     Sequence         WB
             DRB1_0802  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.5610
115.5     3.00  0.54     Sequence         WB
             DRB1_0802  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.5507
129.2     3.50  0.66     Sequence         WB
             DRB1_0802  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.5475
133.7     3.50  0.73     Sequence         WB
             DRB1_0802  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.5524
126.8     3.50  0.71     Sequence         WB
```

```
             DRB1_0802  162      EFRVYSSANNCTFEY  FRVYSSANN  1         0.5279
165.4     5.00  0.69     Sequence         WB
             DRB1_0802  163      FRVYSSANNCTFEYV  FRVYSSANN  0         0.3811
809.9    27.00  0.35     Sequence
             DRB1_0802  164      RVYSSANNCTFEYVS  VYSSANNCT  1         0.2168
4786.3    75.00  0.46     Sequence
             DRB1_0802  165      VYSSANNCTFEYVSQ  YSSANNCTF  1         0.1603
8828.0    90.00  0.40     Sequence
             DRB1_0802  166      YSSANNCTFEYVSQP  NCTFEYVSQ  5         0.1088
15412.5   100.00  0.27     Sequence
             DRB1_0802  167      SSANNCTFEYVSQPF  FEYVSQPFX  7         0.1924
6238.3    85.00  0.35     Sequence
             DRB1_0802  168      SANNCTFEYVSQPFL  FEYVSQPFL  6         0.2403
3714.5    70.00  0.56     Sequence
             DRB1_0802  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5         0.2632
2897.3    65.00  0.55     Sequence
             DRB1_0802  170      NNCTFEYVSQPFLMD  FEYVSQPFL  4         0.2659
2815.7    60.00  0.49     Sequence
             DRB1_0802  171      NCTFEYVSQPFLMDL  FEYVSQPFL  3         0.2642
2868.1    65.00  0.48     Sequence
             DRB1_0802  172      CTFEYVSQPFLMDLE  FEYVSQPFL  2         0.2511
3304.9    65.00  0.49     Sequence
             DRB1_0802  173      TFEYVSQPFLMDLEG  FEYVSQPFL  1         0.2261
4331.7    75.00  0.47     Sequence
             DRB1_0802  174      FEYVSQPFLMDLEGK  YVSQPFLMD  2         0.1693
8008.9    90.00  0.31     Sequence
             DRB1_0802  175      EYVSQPFLMDLEGKQ  FLMDLEGKQ  6         0.2202
4613.9    75.00  0.34     Sequence
             DRB1_0802  176      YVSQPFLMDLEGKQG  FLMDLEGKQ  5         0.2563
3124.4    65.00  0.38     Sequence
             DRB1_0802  177      VSQPFLMDLEGKQGN  LMDLEGKQG  5         0.2705
2678.9    60.00  0.46     Sequence
             DRB1_0802  178      SQPFLMDLEGKQGNF  LMDLEGKQG  4         0.2782
2465.3    60.00  0.48     Sequence
             DRB1_0802  179      QPFLMDLEGKQGNFK  LMDLEGKQG  3         0.2868
2246.5    55.00  0.49     Sequence
             DRB1_0802  180      PFLMDLEGKQGNFKN  LMDLEGKQG  2         0.2797
2425.0    60.00  0.48     Sequence
             DRB1_0802  181      FLMDLEGKQGNFKNL  LMDLEGKQG  1         0.2322
4053.9    70.00  0.50     Sequence
             DRB1_0802  182      LMDLEGKQGNFKNLS  LEGKQGNFK  3         0.1442
10499.7    95.00  0.28     Sequence
             DRB1_0802  183      MDLEGKQGNFKNLSE  LEGKQGNFK  2         0.1129
14742.3   100.00  0.38     Sequence
             DRB1_0802  184      DLEGKQGNFKNLSEF  LEGKQGNFK  1         0.1085
15462.6   100.00  0.34     Sequence
             DRB1_0802  185      LEGKQGNFKNLSEFV  FKNLSEFVX  7         0.1552
9327.6    90.00  0.32     Sequence
             DRB1_0802  186      EGKQGNFKNLSEFVF  FKNLSEFVF  6         0.1945
6096.7    85.00  0.62     Sequence
             DRB1_0802  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5         0.2339
3978.2    70.00  0.63     Sequence
             DRB1_0802  188      KQGNFKNLSEFVFKN  FKNLSEFVF  4         0.2775
2483.6    60.00  0.55     Sequence
             DRB1_0802  189      QGNFKNLSEFVFKNI  FKNLSEFVF  3         0.3016
1913.3    49.00  0.45     Sequence
             DRB1_0802  190      GNFKNLSEFVFKNID  FKNLSEFVF  2         0.2975
2001.0    50.00  0.44     Sequence
             DRB1_0802  191      NFKNLSEFVFKNIDG  LSEFVFKNI  4         0.3023
1898.3    49.00  0.34     Sequence
             DRB1_0802  192      FKNLSEFVFKNIDGY  LSEFVFKNI  3         0.3218
1537.1    43.00  0.34     Sequence
             DRB1_0802  193      KNLSEFVFKNIDGYF  FKNIDGYFX  7         0.4038
632.9    22.00  0.28     Sequence
             DRB1_0802  194      NLSEFVFKNIDGYFK  FKNIDGYFK  6         0.4764
288.5     9.50  0.47     Sequence         WB
```

```
             DRB1_0802  195      LSEFVFKNIDGYFKI  FKNIDGYFK  5        0.4963
232.9     7.50  0.52     Sequence         WB
             DRB1_0802  196      SEFVFKNIDGYFKIY  FKNIDGYFK  4        0.5062
209.2     6.50  0.51     Sequence         WB
             DRB1_0802  197      EFVFKNIDGYFKIYS  FKNIDGYFK  3        0.5445
138.1     4.00  0.48     Sequence         WB
             DRB1_0802  198      FVFKNIDGYFKIYSK  FKNIDGYFK  2        0.5565
121.4     3.00  0.47     Sequence         WB
             DRB1_0802  199      VFKNIDGYFKIYSKH  FKNIDGYFK  1        0.4980
228.4     7.50  0.43     Sequence         WB
             DRB1_0802  200      FKNIDGYFKIYSKHT  IDGYFKIYS  3        0.4585
350.3    12.00  0.41     Sequence
             DRB1_0802  201      KNIDGYFKIYSKHTP  IDGYFKIYS  2        0.4736
297.5    10.00  0.39     Sequence
             DRB1_0802  202      NIDGYFKIYSKHTPI  FKIYSKHTP  5        0.4913
245.6     8.00  0.31     Sequence         WB
             DRB1_0802  203      IDGYFKIYSKHTPIN  FKIYSKHTP  4        0.5166
186.8     5.50  0.31     Sequence         WB
             DRB1_0802  204      DGYFKIYSKHTPINL  FKIYSKHTP  3        0.5343
154.3     4.50  0.31     Sequence         WB
             DRB1_0802  205      GYFKIYSKHTPINLV  FKIYSKHTP  2        0.5521
127.3     3.50  0.31     Sequence         WB
             DRB1_0802  206      YFKIYSKHTPINLVR  IYSKHTPIN  3        0.5516
128.0     3.50  0.38     Sequence         WB
             DRB1_0802  207      FKIYSKHTPINLVRD  IYSKHTPIN  2        0.5019
219.1     7.00  0.44     Sequence         WB
             DRB1_0802  208      KIYSKHTPINLVRDL  IYSKHTPIN  1        0.4522
375.2    13.00  0.43     Sequence
             DRB1_0802  209      IYSKHTPINLVRDLP  YSKHTPINL  1        0.3353
1328.6    39.00  0.37     Sequence
             DRB1_0802  210      YSKHTPINLVRDLPQ  INLVRDLPQ  6        0.2848
2295.7    55.00  0.53     Sequence
             DRB1_0802  211      SKHTPINLVRDLPQG  INLVRDLPQ  5        0.3064
1816.2    48.00  0.56     Sequence
             DRB1_0802  212      KHTPINLVRDLPQGF  INLVRDLPQ  4        0.3302
1404.3    40.00  0.50     Sequence
             DRB1_0802  213      HTPINLVRDLPQGFS  INLVRDLPQ  3        0.3561
1060.9    33.00  0.43     Sequence
             DRB1_0802  214      TPINLVRDLPQGFSA  INLVRDLPQ  2        0.3754
861.1    28.00  0.41     Sequence
             DRB1_0802  215      PINLVRDLPQGFSAL  INLVRDLPQ  1        0.3782
835.1    28.00  0.34     Sequence
             DRB1_0802  216      INLVRDLPQGFSALE  VRDLPQGFS  3        0.3447
1200.1    36.00  0.32     Sequence
             DRB1_0802  217      NLVRDLPQGFSALEP  VRDLPQGFS  2        0.2859
2266.8    55.00  0.41     Sequence
             DRB1_0802  218      LVRDLPQGFSALEPL  VRDLPQGFS  1        0.2379
3812.8    70.00  0.39     Sequence
             DRB1_0802  219      VRDLPQGFSALEPLV  LPQGFSALE  3        0.2315
4083.9    70.00  0.35     Sequence
             DRB1_0802  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.2241
4423.3    75.00  0.40     Sequence
             DRB1_0802  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.2264
4314.7    75.00  0.49     Sequence
             DRB1_0802  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.2466
3468.4    70.00  0.50     Sequence
             DRB1_0802  223      PQGFSALEPLVDLPI  LEPLVDLPI  6        0.2865
2252.9    55.00  0.41     Sequence
             DRB1_0802  224      QGFSALEPLVDLPIG  LEPLVDLPI  5        0.3028
1889.2    49.00  0.50     Sequence
             DRB1_0802  225      GFSALEPLVDLPIGI  LEPLVDLPI  4        0.3000
1947.1    50.00  0.49     Sequence
             DRB1_0802  226      FSALEPLVDLPIGIN  LEPLVDLPI  3        0.3057
1829.5    48.00  0.49     Sequence
             DRB1_0802  227      SALEPLVDLPIGINI  LEPLVDLPI  2        0.3163
1632.6    45.00  0.44     Sequence
```

```
             DRB1_0802  228      ALEPLVDLPIGINIT  LEPLVDLPI  1        0.3398
1265.6    38.00  0.31     Sequence
             DRB1_0802  229      LEPLVDLPIGINITR  LVDLPIGIN  3        0.3195
1577.1    44.00  0.38     Sequence
             DRB1_0802  230      EPLVDLPIGINITRF  LVDLPIGIN  2        0.3402
1260.6    38.00  0.37     Sequence
             DRB1_0802  231      PLVDLPIGINITRFQ  LVDLPIGIN  1        0.3685
927.5    30.00  0.26     Sequence
             DRB1_0802  232      LVDLPIGINITRFQT  IGINITRFQ  5        0.3759
856.5    28.00  0.28     Sequence
             DRB1_0802  233      VDLPIGINITRFQTL  IGINITRFQ  4        0.3928
712.9    24.00  0.28     Sequence
             DRB1_0802  234      DLPIGINITRFQTLL  IGINITRFQ  3        0.4154
558.3    19.00  0.25     Sequence
             DRB1_0802  235      LPIGINITRFQTLLA  ITRFQTLLA  6        0.4759
290.2    10.00  0.29     Sequence
             DRB1_0802  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.5052
211.5     6.50  0.34     Sequence         WB
             DRB1_0802  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.5370
149.8     4.50  0.36     Sequence         WB
             DRB1_0802  238      GINITRFQTLLALHR  ITRFQTLLA  3        0.5410
143.6     4.00  0.37     Sequence         WB
             DRB1_0802  239      INITRFQTLLALHRS  ITRFQTLLA  2        0.5277
165.8     5.00  0.38     Sequence         WB
             DRB1_0802  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.5178
184.4     5.50  0.34     Sequence         WB
             DRB1_0802  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.5048
212.2     6.50  0.35     Sequence         WB
             DRB1_0802  242      TRFQTLLALHRSYLT  FQTLLALHR  2        0.4547
364.9    13.00  0.45     Sequence
             DRB1_0802  243      RFQTLLALHRSYLTP  FQTLLALHR  1        0.4399
428.2    15.00  0.38     Sequence
             DRB1_0802  244      FQTLLALHRSYLTPG  LLALHRSYL  3        0.3856
771.1    26.00  0.46     Sequence
             DRB1_0802  245      QTLLALHRSYLTPGD  LLALHRSYL  2        0.3638
976.5    31.00  0.51     Sequence
             DRB1_0802  246      TLLALHRSYLTPGDS  LLALHRSYL  1        0.3559
1063.3    33.00  0.43     Sequence
             DRB1_0802  247      LLALHRSYLTPGDSS  LALHRSYLT  1        0.2611
2964.7    65.00  0.38     Sequence
             DRB1_0802  248      LALHRSYLTPGDSSS  LHRSYLTPG  2        0.2024
5596.9    80.00  0.34     Sequence
             DRB1_0802  249      ALHRSYLTPGDSSSG  LHRSYLTPG  1        0.1985
5834.8    80.00  0.28     Sequence
             DRB1_0802  250      LHRSYLTPGDSSSGW  LTPGDSSSG  5        0.1702
7930.9    90.00  0.35     Sequence
             DRB1_0802  251      HRSYLTPGDSSSGWT  LTPGDSSSG  4        0.1506
9801.4    90.00  0.50     Sequence
             DRB1_0802  252      RSYLTPGDSSSGWTA  LTPGDSSSG  3        0.1426
10690.2    95.00  0.57     Sequence
             DRB1_0802  253      SYLTPGDSSSGWTAG  LTPGDSSSG  2        0.1248
12953.8    95.00  0.59     Sequence
             DRB1_0802  254      YLTPGDSSSGWTAGA  LTPGDSSSG  1        0.0989
17149.7   100.00  0.54     Sequence
             DRB1_0802  255      LTPGDSSSGWTAGAA  GDSSSGWTA  3        0.0641
24986.5   100.00  0.23     Sequence
             DRB1_0802  256      TPGDSSSGWTAGAAA  GDSSSGWTA  2        0.0727
22764.1   100.00  0.22     Sequence
             DRB1_0802  257      PGDSSSGWTAGAAAY  GWTAGAAAY  6        0.0942
18046.9   100.00  0.22     Sequence
             DRB1_0802  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.1282
12496.5    95.00  0.43     Sequence
             DRB1_0802  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.1435
10586.8    95.00  0.46     Sequence
             DRB1_0802  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.1611
8752.7    90.00  0.47     Sequence
```

```
             DRB1_0802  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.1673
8183.2    90.00  0.47     Sequence
             DRB1_0802  262      SGWTAGAAAYYVGYL  WTAGAAAYY  2        0.1732
7672.1    90.00  0.42     Sequence
             DRB1_0802  263      GWTAGAAAYYVGYLQ  WTAGAAAYY  1        0.1752
7514.0    85.00  0.32     Sequence
             DRB1_0802  264      WTAGAAAYYVGYLQP  AAYYVGYLQ  5        0.1568
9167.2    90.00  0.30     Sequence
             DRB1_0802  265      TAGAAAYYVGYLQPR  AAYYVGYLQ  4        0.1796
7162.9    85.00  0.33     Sequence
             DRB1_0802  266      AGAAAYYVGYLQPRT  YVGYLQPRT  6        0.2509
3309.9    65.00  0.29     Sequence
             DRB1_0802  267      GAAAYYVGYLQPRTF  VGYLQPRTF  6        0.2966
2020.1    55.00  0.33     Sequence
             DRB1_0802  268      AAAYYVGYLQPRTFL  VGYLQPRTF  5        0.3114
1719.9    46.00  0.37     Sequence
             DRB1_0802  269      AAYYVGYLQPRTFLL  VGYLQPRTF  4        0.3337
1351.6    39.00  0.34     Sequence
             DRB1_0802  270      AYYVGYLQPRTFLLK  VGYLQPRTF  3        0.3728
885.5    29.00  0.30     Sequence
             DRB1_0802  271      YYVGYLQPRTFLLKY  LQPRTFLLK  5        0.3853
773.5    26.00  0.31     Sequence
             DRB1_0802  272      YVGYLQPRTFLLKYN  LQPRTFLLK  4        0.3770
846.0    28.00  0.38     Sequence
             DRB1_0802  273      VGYLQPRTFLLKYNE  LQPRTFLLK  3        0.3486
1150.6    35.00  0.46     Sequence
             DRB1_0802  274      GYLQPRTFLLKYNEN  LQPRTFLLK  2        0.3264
1463.0    42.00  0.49     Sequence
             DRB1_0802  275      YLQPRTFLLKYNENG  LQPRTFLLK  1        0.3229
1519.7    43.00  0.38     Sequence
             DRB1_0802  276      LQPRTFLLKYNENGT  FLLKYNENG  5        0.2933
2093.6    55.00  0.36     Sequence
             DRB1_0802  277      QPRTFLLKYNENGTI  FLLKYNENG  4        0.3122
1705.4    46.00  0.34     Sequence
             DRB1_0802  278      PRTFLLKYNENGTIT  LKYNENGTI  5        0.3337
1351.2    39.00  0.32     Sequence
             DRB1_0802  279      RTFLLKYNENGTITD  LKYNENGTI  4        0.3245
1492.7    42.00  0.34     Sequence
             DRB1_0802  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.3155
1646.3    45.00  0.38     Sequence
             DRB1_0802  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.2823
2357.2    55.00  0.47     Sequence
             DRB1_0802  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.2012
5670.6    80.00  0.61     Sequence
             DRB1_0802  283      LKYNENGTITDAVDC  LKYNENGTI  0        0.1451
10401.1    95.00  0.29     Sequence
             DRB1_0802  284      KYNENGTITDAVDCA  GTITDAVDC  5        0.1243
13022.8    95.00  0.25     Sequence
             DRB1_0802  285      YNENGTITDAVDCAL  ITDAVDCAL  6        0.1293
12337.9    95.00  0.38     Sequence
             DRB1_0802  286      NENGTITDAVDCALD  ITDAVDCAL  5        0.1261
12783.0    95.00  0.41     Sequence
             DRB1_0802  287      ENGTITDAVDCALDP  ITDAVDCAL  4        0.1270
12648.2    95.00  0.42     Sequence
             DRB1_0802  288      NGTITDAVDCALDPL  ITDAVDCAL  3        0.1331
11845.4    95.00  0.40     Sequence
             DRB1_0802  289      GTITDAVDCALDPLS  ITDAVDCAL  2        0.1404
10942.8    95.00  0.34     Sequence
             DRB1_0802  290      TITDAVDCALDPLSE  VDCALDPLS  5        0.1374
11302.1    95.00  0.28     Sequence
             DRB1_0802  291      ITDAVDCALDPLSET  VDCALDPLS  4        0.1279
12528.0    95.00  0.37     Sequence
             DRB1_0802  292      TDAVDCALDPLSETK  DCALDPLSE  4        0.1581
9034.0    90.00  0.28     Sequence
             DRB1_0802  293      DAVDCALDPLSETKC  DCALDPLSE  3        0.1699
7953.8    90.00  0.25     Sequence
```

```
             DRB1_0802  294      AVDCALDPLSETKCT  LDPLSETKC  5        0.1812
7039.3    85.00  0.34     Sequence
             DRB1_0802  295      VDCALDPLSETKCTL  LDPLSETKC  4        0.1715
7816.8    90.00  0.37     Sequence
             DRB1_0802  296      DCALDPLSETKCTLK  LDPLSETKC  3        0.1574
9104.6    90.00  0.43     Sequence
             DRB1_0802  297      CALDPLSETKCTLKS  LDPLSETKC  2        0.1689
8045.0    90.00  0.38     Sequence
             DRB1_0802  298      ALDPLSETKCTLKSF  LDPLSETKC  1        0.1683
8094.9    90.00  0.34     Sequence
             DRB1_0802  299      LDPLSETKCTLKSFT  LSETKCTLK  3        0.1457
10334.9    95.00  0.35     Sequence
             DRB1_0802  300      DPLSETKCTLKSFTV  LSETKCTLK  2        0.1517
9683.9    90.00  0.36     Sequence
             DRB1_0802  301      PLSETKCTLKSFTVE  LSETKCTLK  1        0.1562
9228.3    90.00  0.31     Sequence
             DRB1_0802  302      LSETKCTLKSFTVEK  LKSFTVEKX  7        0.2142
4924.7    75.00  0.35     Sequence
             DRB1_0802  303      SETKCTLKSFTVEKG  LKSFTVEKG  6        0.3304
1401.7    40.00  0.70     Sequence
             DRB1_0802  304      ETKCTLKSFTVEKGI  LKSFTVEKG  5        0.3867
761.8    26.00  0.70     Sequence
             DRB1_0802  305      TKCTLKSFTVEKGIY  LKSFTVEKG  4        0.4163
552.9    19.00  0.64     Sequence
             DRB1_0802  306      KCTLKSFTVEKGIYQ  LKSFTVEKG  3        0.4636
331.5    12.00  0.51     Sequence
             DRB1_0802  307      CTLKSFTVEKGIYQT  LKSFTVEKG  2        0.4760
290.0    10.00  0.43     Sequence
             DRB1_0802  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.4804
276.3     9.50  0.44     Sequence         WB
             DRB1_0802  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.4174
546.5    19.00  0.61     Sequence
             DRB1_0802  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.3954
693.2    24.00  0.69     Sequence
             DRB1_0802  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.3957
690.8    24.00  0.54     Sequence
             DRB1_0802  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.4180
543.0    19.00  0.54     Sequence
             DRB1_0802  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.4269
493.2    17.00  0.75     Sequence
             DRB1_0802  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.4518
376.6    13.00  0.71     Sequence
             DRB1_0802  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.4694
311.2    11.00  0.71     Sequence
             DRB1_0802  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.4760
289.9    10.00  0.71     Sequence
             DRB1_0802  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.4700
309.4    11.00  0.59     Sequence
             DRB1_0802  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.3984
671.5    23.00  0.50     Sequence
             DRB1_0802  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.4061
617.8    21.00  0.57     Sequence
             DRB1_0802  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.4357
448.3    16.00  0.57     Sequence
             DRB1_0802  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.4441
409.2    14.00  0.56     Sequence
             DRB1_0802  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.4501
383.6    14.00  0.54     Sequence
             DRB1_0802  323      NFRVQPTESIVRFPN  FRVQPTESI  1        0.4314
469.6    17.00  0.46     Sequence
             DRB1_0802  324      FRVQPTESIVRFPNI  VQPTESIVR  2        0.3450
1196.6    36.00  0.47     Sequence
             DRB1_0802  325      RVQPTESIVRFPNIT  VQPTESIVR  1        0.3122
1705.9    46.00  0.38     Sequence
             DRB1_0802  326      VQPTESIVRFPNITN  IVRFPNITN  6        0.3423
1231.3    37.00  0.54     Sequence
```

```
             DRB1_0802  327      QPTESIVRFPNITNL  IVRFPNITN  5        0.3719
894.3    29.00  0.60     Sequence
             DRB1_0802  328      PTESIVRFPNITNLC  IVRFPNITN  4        0.3781
836.3    28.00  0.55     Sequence
             DRB1_0802  329      TESIVRFPNITNLCP  IVRFPNITN  3        0.3993
664.6    23.00  0.51     Sequence
             DRB1_0802  330      ESIVRFPNITNLCPF  IVRFPNITN  2        0.4063
616.5    21.00  0.50     Sequence
             DRB1_0802  331      SIVRFPNITNLCPFG  IVRFPNITN  1        0.3938
705.9    24.00  0.41     Sequence
             DRB1_0802  332      IVRFPNITNLCPFGE  FPNITNLCP  3        0.3142
1670.1    45.00  0.44     Sequence
             DRB1_0802  333      VRFPNITNLCPFGEV  FPNITNLCP  2        0.2615
2953.5    65.00  0.50     Sequence
             DRB1_0802  334      RFPNITNLCPFGEVF  FPNITNLCP  1        0.2407
3698.3    70.00  0.45     Sequence
             DRB1_0802  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.2085
5240.5    80.00  0.37     Sequence
             DRB1_0802  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.2109
5104.7    80.00  0.37     Sequence
             DRB1_0802  337      NITNLCPFGEVFNAT  LCPFGEVFN  4        0.2250
4383.0    75.00  0.25     Sequence
             DRB1_0802  338      ITNLCPFGEVFNATR  FGEVFNATR  6        0.2587
3042.1    65.00  0.41     Sequence
             DRB1_0802  339      TNLCPFGEVFNATRF  FGEVFNATR  5        0.2762
2518.8    60.00  0.44     Sequence
             DRB1_0802  340      NLCPFGEVFNATRFA  FGEVFNATR  4        0.3466
1175.3    36.00  0.36     Sequence
             DRB1_0802  341      LCPFGEVFNATRFAS  VFNATRFAS  6        0.4075
608.6    21.00  0.35     Sequence
             DRB1_0802  342      CPFGEVFNATRFASV  VFNATRFAS  5        0.4386
434.7    15.00  0.38     Sequence
             DRB1_0802  343      PFGEVFNATRFASVY  VFNATRFAS  4        0.4497
385.5    14.00  0.38     Sequence
             DRB1_0802  344      FGEVFNATRFASVYA  VFNATRFAS  3        0.4623
336.4    12.00  0.38     Sequence
             DRB1_0802  345      GEVFNATRFASVYAW  VFNATRFAS  2        0.4810
274.8     9.00  0.35     Sequence         WB
             DRB1_0802  346      EVFNATRFASVYAWN  FNATRFASV  2        0.4744
294.8    10.00  0.34     Sequence
             DRB1_0802  347      VFNATRFASVYAWNR  FNATRFASV  1        0.4117
581.5    20.00  0.25     Sequence
             DRB1_0802  348      FNATRFASVYAWNRK  TRFASVYAW  3        0.3793
825.0    27.00  0.35     Sequence
             DRB1_0802  349      NATRFASVYAWNRKR  TRFASVYAW  2        0.3666
946.6    31.00  0.35     Sequence
             DRB1_0802  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.3437
1213.7    37.00  0.28     Sequence
             DRB1_0802  351      TRFASVYAWNRKRIS  FASVYAWNR  2        0.3156
1643.9    45.00  0.29     Sequence
             DRB1_0802  352      RFASVYAWNRKRISN  YAWNRKRIS  5        0.3236
1508.4    42.00  0.24     Sequence
             DRB1_0802  353      FASVYAWNRKRISNC  YAWNRKRIS  4        0.3008
1930.0    49.00  0.22     Sequence
             DRB1_0802  354      ASVYAWNRKRISNCV  YAWNRKRIS  3        0.3110
1728.7    46.00  0.20     Sequence
             DRB1_0802  355      SVYAWNRKRISNCVA  YAWNRKRIS  2        0.3263
1464.2    42.00  0.18     Sequence
             DRB1_0802  356      VYAWNRKRISNCVAD  AWNRKRISN  2        0.3056
1832.8    48.00  0.22     Sequence
             DRB1_0802  357      YAWNRKRISNCVADY  RKRISNCVA  4        0.2973
2004.8    50.00  0.22     Sequence
             DRB1_0802  358      AWNRKRISNCVADYS  ISNCVADYS  6        0.3184
1595.5    44.00  0.38     Sequence
             DRB1_0802  359      WNRKRISNCVADYSV  ISNCVADYS  5        0.3212
1547.2    43.00  0.50     Sequence
```

```
             DRB1_0802  360      NRKRISNCVADYSVL  ISNCVADYS  4        0.3147
1659.7    45.00  0.55     Sequence
             DRB1_0802  361      RKRISNCVADYSVLY  ISNCVADYS  3        0.3112
1725.3    46.00  0.55     Sequence
             DRB1_0802  362      KRISNCVADYSVLYN  ISNCVADYS  2        0.3329
1364.3    40.00  0.41     Sequence
             DRB1_0802  363      RISNCVADYSVLYNS  VADYSVLYN  5        0.3461
1181.7    36.00  0.43     Sequence
             DRB1_0802  364      ISNCVADYSVLYNSA  VADYSVLYN  4        0.3271
1452.3    41.00  0.57     Sequence
             DRB1_0802  365      SNCVADYSVLYNSAS  VADYSVLYN  3        0.3450
1195.8    36.00  0.54     Sequence
             DRB1_0802  366      NCVADYSVLYNSASF  VADYSVLYN  2        0.3705
907.6    30.00  0.49     Sequence
             DRB1_0802  367      CVADYSVLYNSASFS  VADYSVLYN  1        0.3883
748.6    25.00  0.35     Sequence
             DRB1_0802  368      VADYSVLYNSASFST  LYNSASFST  6        0.3788
829.6    28.00  0.25     Sequence
             DRB1_0802  369      ADYSVLYNSASFSTF  LYNSASFST  5        0.3802
817.7    27.00  0.36     Sequence
             DRB1_0802  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.4012
651.3    22.00  0.41     Sequence
             DRB1_0802  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.3953
694.3    24.00  0.46     Sequence
             DRB1_0802  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.3732
881.2    29.00  0.57     Sequence
             DRB1_0802  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.3225
1526.4    43.00  0.56     Sequence
             DRB1_0802  374      LYNSASFSTFKCYGV  FSTFKCYGV  6        0.1865
6643.4    85.00  0.34     Sequence
             DRB1_0802  375      YNSASFSTFKCYGVS  FSTFKCYGV  5        0.1782
7271.4    85.00  0.51     Sequence
             DRB1_0802  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.2057
5402.3    80.00  0.45     Sequence
             DRB1_0802  377      SASFSTFKCYGVSPT  FKCYGVSPT  6        0.2738
2583.3    60.00  0.44     Sequence
             DRB1_0802  378      ASFSTFKCYGVSPTK  FKCYGVSPT  5        0.3303
1403.0    40.00  0.45     Sequence
             DRB1_0802  379      SFSTFKCYGVSPTKL  FKCYGVSPT  4        0.3393
1271.8    38.00  0.45     Sequence
             DRB1_0802  380      FSTFKCYGVSPTKLN  FKCYGVSPT  3        0.3378
1293.3    38.00  0.46     Sequence
             DRB1_0802  381      STFKCYGVSPTKLND  FKCYGVSPT  2        0.3256
1475.7    42.00  0.50     Sequence
             DRB1_0802  382      TFKCYGVSPTKLNDL  FKCYGVSPT  1        0.3158
1640.1    45.00  0.46     Sequence
             DRB1_0802  383      FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.2440
3568.6    70.00  0.28     Sequence
             DRB1_0802  384      KCYGVSPTKLNDLCF  YGVSPTKLN  2        0.1863
6660.7    85.00  0.31     Sequence
             DRB1_0802  385      CYGVSPTKLNDLCFT  YGVSPTKLN  1        0.1420
10753.7    95.00  0.29     Sequence
             DRB1_0802  386      YGVSPTKLNDLCFTN  VSPTKLNDL  2        0.1309
12128.8    95.00  0.28     Sequence
             DRB1_0802  387      GVSPTKLNDLCFTNV  LNDLCFTNV  6        0.1390
11113.9    95.00  0.34     Sequence
             DRB1_0802  388      VSPTKLNDLCFTNVY  LNDLCFTNV  5        0.1509
9774.7    90.00  0.40     Sequence
             DRB1_0802  389      SPTKLNDLCFTNVYA  LNDLCFTNV  4        0.1833
6880.1    85.00  0.32     Sequence
             DRB1_0802  390      PTKLNDLCFTNVYAD  LNDLCFTNV  3        0.1911
6326.6    85.00  0.28     Sequence
             DRB1_0802  391      TKLNDLCFTNVYADS  LCFTNVYAD  5        0.2076
5292.3    80.00  0.31     Sequence
             DRB1_0802  392      KLNDLCFTNVYADSF  LCFTNVYAD  4        0.2073
5308.7    80.00  0.32     Sequence
```

```
             DRB1_0802  393      LNDLCFTNVYADSFV  LCFTNVYAD  3        0.1992
5793.7    80.00  0.35     Sequence
             DRB1_0802  394      NDLCFTNVYADSFVI  LCFTNVYAD  2        0.2096
5179.4    80.00  0.36     Sequence
             DRB1_0802  395      DLCFTNVYADSFVIR  LCFTNVYAD  1        0.2222
4515.0    75.00  0.28     Sequence
             DRB1_0802  396      LCFTNVYADSFVIRG  YADSFVIRG  6        0.2393
3755.1    70.00  0.32     Sequence
             DRB1_0802  397      CFTNVYADSFVIRGD  YADSFVIRG  5        0.2356
3908.5    70.00  0.32     Sequence
             DRB1_0802  398      FTNVYADSFVIRGDE  YADSFVIRG  4        0.2389
3771.7    70.00  0.32     Sequence
             DRB1_0802  399      TNVYADSFVIRGDEV  YADSFVIRG  3        0.2317
4074.6    70.00  0.34     Sequence
             DRB1_0802  400      NVYADSFVIRGDEVR  YADSFVIRG  2        0.2337
3988.8    70.00  0.31     Sequence
             DRB1_0802  401      VYADSFVIRGDEVRQ  VIRGDEVRQ  6        0.2448
3539.0    70.00  0.29     Sequence
             DRB1_0802  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.3257
1474.7    42.00  0.41     Sequence
             DRB1_0802  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.3807
813.4    27.00  0.47     Sequence
             DRB1_0802  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.3913
725.0    25.00  0.49     Sequence
             DRB1_0802  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.4081
604.5    21.00  0.47     Sequence
             DRB1_0802  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.4512
379.0    13.00  0.38     Sequence
             DRB1_0802  407      VIRGDEVRQIAPGQT  VRQIAPGQT  6        0.4805
276.0     9.50  0.54     Sequence         WB
             DRB1_0802  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.4959
233.9     7.50  0.66     Sequence         WB
             DRB1_0802  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.4753
292.0    10.00  0.79     Sequence
             DRB1_0802  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.4735
297.7    10.00  0.78     Sequence
             DRB1_0802  411      DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.4660
323.1    11.00  0.73     Sequence
             DRB1_0802  412      EVRQIAPGQTGTIAD  VRQIAPGQT  1        0.4325
464.0    16.00  0.67     Sequence
             DRB1_0802  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.2618
2941.7    65.00  0.38     Sequence
             DRB1_0802  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.1783
7267.2    85.00  0.55     Sequence
             DRB1_0802  415      QIAPGQTGTIADYNY  IAPGQTGTI  1        0.1415
10814.1    95.00  0.48     Sequence
             DRB1_0802  416      IAPGQTGTIADYNYK  IAPGQTGTI  0        0.1138
14593.9   100.00  0.19     Sequence
             DRB1_0802  417      APGQTGTIADYNYKL  IADYNYKLX  7        0.1161
14237.3   100.00  0.22     Sequence
             DRB1_0802  418      PGQTGTIADYNYKLP  IADYNYKLP  6        0.1262
12764.7    95.00  0.41     Sequence
             DRB1_0802  419      GQTGTIADYNYKLPD  IADYNYKLP  5        0.1314
12059.9    95.00  0.44     Sequence
             DRB1_0802  420      QTGTIADYNYKLPDD  IADYNYKLP  4        0.1321
11979.2    95.00  0.44     Sequence
             DRB1_0802  421      TGTIADYNYKLPDDF  IADYNYKLP  3        0.1373
11321.0    95.00  0.46     Sequence
             DRB1_0802  422      GTIADYNYKLPDDFT  IADYNYKLP  2        0.1480
10083.4    95.00  0.39     Sequence
             DRB1_0802  423      TIADYNYKLPDDFTG  YKLPDDFTG  6        0.1525
9604.8    90.00  0.25     Sequence
             DRB1_0802  424      IADYNYKLPDDFTGC  YKLPDDFTG  5        0.1354
11555.7    95.00  0.34     Sequence
             DRB1_0802  425      ADYNYKLPDDFTGCV  YKLPDDFTG  4        0.1421
10740.6    95.00  0.37     Sequence
```

```
             DRB1_0802  426      DYNYKLPDDFTGCVI  YKLPDDFTG  3        0.1462
10281.0    95.00  0.38     Sequence
             DRB1_0802  427      YNYKLPDDFTGCVIA  YKLPDDFTG  2        0.1459
10315.6    95.00  0.44     Sequence
             DRB1_0802  428      NYKLPDDFTGCVIAW  YKLPDDFTG  1        0.1595
8901.9    90.00  0.37     Sequence
             DRB1_0802  429      YKLPDDFTGCVIAWN  FTGCVIAWN  6        0.1739
7619.1    90.00  0.46     Sequence
             DRB1_0802  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.1890
6472.6    85.00  0.50     Sequence
             DRB1_0802  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.2209
4582.9    75.00  0.43     Sequence
             DRB1_0802  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.2726
2619.2    60.00  0.38     Sequence
             DRB1_0802  433      DDFTGCVIAWNSNNL  FTGCVIAWN  2        0.3204
1561.4    43.00  0.25     Sequence
             DRB1_0802  434      DFTGCVIAWNSNNLD  VIAWNSNNL  5        0.3278
1441.3    41.00  0.26     Sequence
             DRB1_0802  435      FTGCVIAWNSNNLDS  IAWNSNNLD  5        0.3366
1309.7    39.00  0.29     Sequence
             DRB1_0802  436      TGCVIAWNSNNLDSK  IAWNSNNLD  4        0.3522
1106.4    34.00  0.33     Sequence
             DRB1_0802  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3        0.3570
1050.7    33.00  0.36     Sequence
             DRB1_0802  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2        0.3285
1429.8    41.00  0.39     Sequence
             DRB1_0802  439      VIAWNSNNLDSKVGG  IAWNSNNLD  1        0.2808
2396.5    55.00  0.44     Sequence
             DRB1_0802  440      IAWNSNNLDSKVGGN  AWNSNNLDS  1        0.2026
5583.3    80.00  0.25     Sequence
             DRB1_0802  441      AWNSNNLDSKVGGNY  LDSKVGGNY  6        0.1746
7561.9    85.00  0.43     Sequence
             DRB1_0802  442      WNSNNLDSKVGGNYN  LDSKVGGNY  5        0.1692
8012.0    90.00  0.53     Sequence
             DRB1_0802  443      NSNNLDSKVGGNYNY  LDSKVGGNY  4        0.1707
7889.2    90.00  0.53     Sequence
             DRB1_0802  444      SNNLDSKVGGNYNYL  LDSKVGGNY  3        0.1696
7979.4    90.00  0.52     Sequence
             DRB1_0802  445      NNLDSKVGGNYNYLY  LDSKVGGNY  2        0.1719
7782.7    90.00  0.47     Sequence
             DRB1_0802  446      NLDSKVGGNYNYLYR  LDSKVGGNY  1        0.1650
8384.4    90.00  0.40     Sequence
             DRB1_0802  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4        0.1296
12304.2    95.00  0.41     Sequence
             DRB1_0802  448      DSKVGGNYNYLYRLF  VGGNYNYLY  3        0.1561
9237.5    90.00  0.38     Sequence
             DRB1_0802  449      SKVGGNYNYLYRLFR  YNYLYRLFR  6        0.2086
5235.5    80.00  0.49     Sequence
             DRB1_0802  450      KVGGNYNYLYRLFRK  YNYLYRLFR  5        0.2522
3264.0    65.00  0.47     Sequence
             DRB1_0802  451      VGGNYNYLYRLFRKS  YNYLYRLFR  4        0.3210
1551.7    43.00  0.42     Sequence
             DRB1_0802  452      GGNYNYLYRLFRKSN  LYRLFRKSN  6        0.4462
400.0    14.00  0.35     Sequence
             DRB1_0802  453      GNYNYLYRLFRKSNL  LYRLFRKSN  5        0.4843
264.9     9.00  0.34     Sequence         WB
             DRB1_0802  454      NYNYLYRLFRKSNLK  YRLFRKSNL  5        0.5148
190.6     6.00  0.37     Sequence         WB
             DRB1_0802  455      YNYLYRLFRKSNLKP  YRLFRKSNL  4        0.5223
175.6     5.50  0.38     Sequence         WB
             DRB1_0802  456      NYLYRLFRKSNLKPF  YRLFRKSNL  3        0.5278
165.5     5.00  0.40     Sequence         WB
             DRB1_0802  457      YLYRLFRKSNLKPFE  YRLFRKSNL  2        0.5175
185.0     5.50  0.37     Sequence         WB
             DRB1_0802  458      LYRLFRKSNLKPFER  YRLFRKSNL  1        0.4742
295.5    10.00  0.34     Sequence
```

```
             DRB1_0802  459      YRLFRKSNLKPFERD  LFRKSNLKP  2        0.3881
750.0    25.00  0.47     Sequence
             DRB1_0802  460      RLFRKSNLKPFERDI  LFRKSNLKP  1        0.3479
1159.3    35.00  0.47     Sequence
             DRB1_0802  461      LFRKSNLKPFERDIS  LKPFERDIS  6        0.2757
2532.8    60.00  0.40     Sequence
             DRB1_0802  462      FRKSNLKPFERDIST  LKPFERDIS  5        0.2598
3008.9    65.00  0.57     Sequence
             DRB1_0802  463      RKSNLKPFERDISTE  LKPFERDIS  4        0.2387
3777.0    70.00  0.63     Sequence
             DRB1_0802  464      KSNLKPFERDISTEI  LKPFERDIS  3        0.2504
3329.3    65.00  0.58     Sequence
             DRB1_0802  465      SNLKPFERDISTEIY  LKPFERDIS  2        0.2470
3452.8    70.00  0.50     Sequence
             DRB1_0802  466      NLKPFERDISTEIYQ  LKPFERDIS  1        0.2433
3596.1    70.00  0.43     Sequence
             DRB1_0802  467      LKPFERDISTEIYQA  FERDISTEI  3        0.2225
4500.7    75.00  0.32     Sequence
             DRB1_0802  468      KPFERDISTEIYQAG  FERDISTEI  2        0.2250
4383.2    75.00  0.34     Sequence
             DRB1_0802  469      PFERDISTEIYQAGS  ISTEIYQAG  5        0.2253
4367.1    75.00  0.29     Sequence
             DRB1_0802  470      FERDISTEIYQAGST  ISTEIYQAG  4        0.2193
4660.7    75.00  0.38     Sequence
             DRB1_0802  471      ERDISTEIYQAGSTP  IYQAGSTPX  7        0.2609
2970.3    65.00  0.28     Sequence
             DRB1_0802  472      RDISTEIYQAGSTPC  IYQAGSTPC  6        0.3020
1905.5    49.00  0.50     Sequence
             DRB1_0802  473      DISTEIYQAGSTPCN  IYQAGSTPC  5        0.3281
1436.7    41.00  0.58     Sequence
             DRB1_0802  474      ISTEIYQAGSTPCNG  IYQAGSTPC  4        0.3578
1041.5    33.00  0.62     Sequence
             DRB1_0802  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.3654
959.5    31.00  0.64     Sequence
             DRB1_0802  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.3730
883.9    29.00  0.62     Sequence
             DRB1_0802  477      EIYQAGSTPCNGVKG  IYQAGSTPC  1        0.3470
1170.9    36.00  0.57     Sequence
             DRB1_0802  478      IYQAGSTPCNGVKGF  YQAGSTPCN  1        0.2185
4702.9    75.00  0.46     Sequence
             DRB1_0802  479      YQAGSTPCNGVKGFN  YQAGSTPCN  0        0.1248
12954.4    95.00  0.28     Sequence
             DRB1_0802  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.0734
22597.5   100.00  0.32     Sequence
             DRB1_0802  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.0964
17623.3   100.00  0.34     Sequence
             DRB1_0802  482      GSTPCNGVKGFNCYF  GVKGFNCYF  6        0.1237
13110.0    95.00  0.28     Sequence
             DRB1_0802  483      STPCNGVKGFNCYFP  VKGFNCYFP  6        0.1481
10067.1    95.00  0.38     Sequence
             DRB1_0802  484      TPCNGVKGFNCYFPL  VKGFNCYFP  5        0.1667
8231.3    90.00  0.43     Sequence
             DRB1_0802  485      PCNGVKGFNCYFPLQ  VKGFNCYFP  4        0.2093
5191.7    80.00  0.37     Sequence
             DRB1_0802  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.2498
3352.8    65.00  0.38     Sequence
             DRB1_0802  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.2587
3044.6    65.00  0.40     Sequence
             DRB1_0802  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.2569
3104.8    65.00  0.46     Sequence
             DRB1_0802  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3        0.2510
3308.8    65.00  0.45     Sequence
             DRB1_0802  490      KGFNCYFPLQSYGFQ  FNCYFPLQS  2        0.2697
2701.6    60.00  0.38     Sequence
             DRB1_0802  491      GFNCYFPLQSYGFQP  FNCYFPLQS  1        0.2695
2706.7    60.00  0.29     Sequence
```

```
              DRB1_0802  492      FNCYFPLQSYGFQPT  FPLQSYGFQ  4        0.2620
2936.9    65.00  0.26     Sequence
              DRB1_0802  493      NCYFPLQSYGFQPTY  LQSYGFQPT  5        0.2599
3003.0    65.00  0.31     Sequence
              DRB1_0802  494      CYFPLQSYGFQPTYG  LQSYGFQPT  4        0.2722
2630.2    60.00  0.32     Sequence
              DRB1_0802  495      YFPLQSYGFQPTYGV  LQSYGFQPT  3        0.2669
2786.2    60.00  0.35     Sequence
              DRB1_0802  496      FPLQSYGFQPTYGVG  LQSYGFQPT  2        0.2394
3751.4    70.00  0.40     Sequence
              DRB1_0802  497      PLQSYGFQPTYGVGY  LQSYGFQPT  1        0.2176
4745.2    75.00  0.40     Sequence
              DRB1_0802  498      LQSYGFQPTYGVGYQ  YGFQPTYGV  3        0.1892
6456.4    85.00  0.34     Sequence
              DRB1_0802  499      QSYGFQPTYGVGYQP  YGFQPTYGV  2        0.1780
7288.0    85.00  0.40     Sequence
              DRB1_0802  500      SYGFQPTYGVGYQPY  YGFQPTYGV  1        0.1715
7814.4    90.00  0.32     Sequence
              DRB1_0802  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.1584
9010.7    90.00  0.32     Sequence
              DRB1_0802  502      GFQPTYGVGYQPYRV  FQPTYGVGY  1        0.1542
9422.5    90.00  0.25     Sequence
              DRB1_0802  503      FQPTYGVGYQPYRVV  VGYQPYRVV  6        0.1764
7411.4    85.00  0.25     Sequence
              DRB1_0802  504      QPTYGVGYQPYRVVV  VGYQPYRVV  5        0.2162
4821.7    75.00  0.26     Sequence
              DRB1_0802  505      PTYGVGYQPYRVVVL  YQPYRVVVL  6        0.2936
2086.9    55.00  0.49     Sequence
              DRB1_0802  506      TYGVGYQPYRVVVLS  YQPYRVVVL  5        0.3346
1339.1    39.00  0.52     Sequence
              DRB1_0802  507      YGVGYQPYRVVVLSF  YQPYRVVVL  4        0.3753
861.9    28.00  0.47     Sequence
              DRB1_0802  508      GVGYQPYRVVVLSFE  YQPYRVVVL  3        0.3962
687.8    24.00  0.43     Sequence
              DRB1_0802  509      VGYQPYRVVVLSFEL  YQPYRVVVL  2        0.3865
763.3    26.00  0.41     Sequence
              DRB1_0802  510      GYQPYRVVVLSFELL  YRVVVLSFE  4        0.3506
1126.3    35.00  0.33     Sequence
              DRB1_0802  511      YQPYRVVVLSFELLH  YRVVVLSFE  3        0.3261
1468.3    42.00  0.38     Sequence
              DRB1_0802  512      QPYRVVVLSFELLHA  YRVVVLSFE  2        0.3369
1306.3    39.00  0.37     Sequence
              DRB1_0802  513      PYRVVVLSFELLHAP  VLSFELLHA  5        0.3388
1278.9    38.00  0.29     Sequence
              DRB1_0802  514      YRVVVLSFELLHAPA  VLSFELLHA  4        0.3341
1346.6    39.00  0.34     Sequence
              DRB1_0802  515      RVVVLSFELLHAPAT  VLSFELLHA  3        0.3658
954.9    31.00  0.29     Sequence
              DRB1_0802  516      VVVLSFELLHAPATV  FELLHAPAT  5        0.4149
561.2    20.00  0.28     Sequence
              DRB1_0802  517      VVLSFELLHAPATVC  LLHAPATVC  6        0.4156
557.5    19.00  0.28     Sequence
              DRB1_0802  518      VLSFELLHAPATVCG  LLHAPATVC  5        0.4128
574.3    20.00  0.41     Sequence
              DRB1_0802  519      LSFELLHAPATVCGP  LLHAPATVC  4        0.4057
620.5    21.00  0.48     Sequence
              DRB1_0802  520      SFELLHAPATVCGPK  LLHAPATVC  3        0.4071
610.8    21.00  0.51     Sequence
              DRB1_0802  521      FELLHAPATVCGPKK  LLHAPATVC  2        0.3507
1124.9    35.00  0.62     Sequence
              DRB1_0802  522      ELLHAPATVCGPKKS  LLHAPATVC  1        0.2665
2797.7    60.00  0.66     Sequence
              DRB1_0802  523      LLHAPATVCGPKKST  LLHAPATVC  0        0.1298
12270.2    95.00  0.22     Sequence
              DRB1_0802  524      LHAPATVCGPKKSTN  PATVCGPKK  3        0.0981
17292.8   100.00  0.27     Sequence
```

```
             DRB1_0802  525      HAPATVCGPKKSTNL  PATVCGPKK  2        0.0935
18187.4   100.00  0.26     Sequence
             DRB1_0802  526      APATVCGPKKSTNLV  CGPKKSTNL  5        0.1010
16769.1   100.00  0.19     Sequence
             DRB1_0802  527      PATVCGPKKSTNLVK  PKKSTNLVK  6        0.1248
12964.3    95.00  0.34     Sequence
             DRB1_0802  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5        0.1504
9822.4    90.00  0.39    Sequence
             DRB1_0802  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.1809
7058.2    85.00  0.41    Sequence
             DRB1_0802  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3        0.1820
6976.7    85.00  0.41    Sequence
             DRB1_0802  531      CGPKKSTNLVKNKCV  PKKSTNLVK  2        0.1880
6543.2    85.00  0.41    Sequence
             DRB1_0802  532      GPKKSTNLVKNKCVN  PKKSTNLVK  1        0.2094
5186.4    80.00  0.36    Sequence
             DRB1_0802  533      PKKSTNLVKNKCVNF  LVKNKCVNF  6        0.2394
3751.5    70.00  0.32    Sequence
             DRB1_0802  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.2922
2117.6    55.00  0.34    Sequence
             DRB1_0802  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.3110
1728.9    46.00  0.31    Sequence
             DRB1_0802  536      STNLVKNKCVNFNFN  VKNKCVNFN  4        0.3257
1473.7    42.00  0.35    Sequence
             DRB1_0802  537      TNLVKNKCVNFNFNG  VKNKCVNFN  3        0.3375
1298.0    38.00  0.34    Sequence
             DRB1_0802  538      NLVKNKCVNFNFNGL  VKNKCVNFN  2        0.3240
1501.9    42.00  0.34    Sequence
             DRB1_0802  539      LVKNKCVNFNFNGLT  VKNKCVNFN  1        0.2764
2513.9    60.00  0.31    Sequence
             DRB1_0802  540      VKNKCVNFNFNGLTG  VNFNFNGLT  5        0.2151
4879.2    75.00  0.19    Sequence
             DRB1_0802  541      KNKCVNFNFNGLTGT  VNFNFNGLT  4        0.1938
6143.1    85.00  0.19    Sequence
             DRB1_0802  542      NKCVNFNFNGLTGTG  VNFNFNGLT  3        0.1957
6020.1    80.00  0.24    Sequence
             DRB1_0802  543      KCVNFNFNGLTGTGV  FNGLTGTGV  6        0.2328
4027.2    70.00  0.38    Sequence
             DRB1_0802  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5        0.2332
4009.2    70.00  0.47    Sequence
             DRB1_0802  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.2518
3278.8    65.00  0.49    Sequence
             DRB1_0802  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3        0.2528
3242.7    65.00  0.43    Sequence
             DRB1_0802  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.2593
3023.5    65.00  0.41    Sequence
             DRB1_0802  548      NFNGLTGTGVLTESN  LTGTGVLTE  4        0.2444
3552.8    70.00  0.37    Sequence
             DRB1_0802  549      FNGLTGTGVLTESNK  LTGTGVLTE  3        0.2243
4416.8    75.00  0.48    Sequence
             DRB1_0802  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.2175
4751.7    75.00  0.46    Sequence
             DRB1_0802  551      GLTGTGVLTESNKKF  VLTESNKKF  6        0.2736
2590.8    60.00  0.41    Sequence
             DRB1_0802  552      LTGTGVLTESNKKFL  VLTESNKKF  5        0.2777
2478.5    60.00  0.50    Sequence
             DRB1_0802  553      TGTGVLTESNKKFLP  VLTESNKKF  4        0.2853
2282.1    55.00  0.53    Sequence
             DRB1_0802  554      GTGVLTESNKKFLPF  VLTESNKKF  3        0.2952
2049.8    55.00  0.52    Sequence
             DRB1_0802  555      TGVLTESNKKFLPFQ  VLTESNKKF  2        0.3072
1801.0    47.00  0.50    Sequence
             DRB1_0802  556      GVLTESNKKFLPFQQ  VLTESNKKF  1        0.3136
1680.4    45.00  0.40    Sequence
             DRB1_0802  557      VLTESNKKFLPFQQF  NKKFLPFQQ  5        0.2613
2960.0    65.00  0.34    Sequence
```

```
             DRB1_0802  558      LTESNKKFLPFQQFG  NKKFLPFQQ  4        0.2291
4190.1    75.00  0.47     Sequence
             DRB1_0802  559      TESNKKFLPFQQFGR  NKKFLPFQQ  3        0.2541
3198.2    65.00  0.41     Sequence
             DRB1_0802  560      ESNKKFLPFQQFGRD  NKKFLPFQQ  2        0.2545
3186.1    65.00  0.40     Sequence
             DRB1_0802  561      SNKKFLPFQQFGRDI  NKKFLPFQQ  1        0.2532
3229.5    65.00  0.34     Sequence
             DRB1_0802  562      NKKFLPFQQFGRDIA  FQQFGRDIA  6        0.2458
3497.7    70.00  0.28     Sequence
             DRB1_0802  563      KKFLPFQQFGRDIAD  FQQFGRDIA  5        0.2176
4749.5    75.00  0.40     Sequence
             DRB1_0802  564      KFLPFQQFGRDIADT  FQQFGRDIA  4        0.2148
4891.2    75.00  0.47     Sequence
             DRB1_0802  565      FLPFQQFGRDIADTT  FQQFGRDIA  3        0.1939
6137.1    85.00  0.51     Sequence
             DRB1_0802  566      LPFQQFGRDIADTTD  FQQFGRDIA  2        0.1790
7207.1    85.00  0.55     Sequence
             DRB1_0802  567      PFQQFGRDIADTTDA  FQQFGRDIA  1        0.1774
7335.6    85.00  0.47     Sequence
             DRB1_0802  568      FQQFGRDIADTTDAV  IADTTDAVX  7        0.1771
7359.0    85.00  0.25     Sequence
             DRB1_0802  569      QQFGRDIADTTDAVR  IADTTDAVR  6        0.2050
5442.6    80.00  0.56     Sequence
             DRB1_0802  570      QFGRDIADTTDAVRD  IADTTDAVR  5        0.2180
4726.8    75.00  0.63     Sequence
             DRB1_0802  571      FGRDIADTTDAVRDP  IADTTDAVR  4        0.2229
4481.8    75.00  0.64     Sequence
             DRB1_0802  572      GRDIADTTDAVRDPQ  IADTTDAVR  3        0.2290
4198.7    75.00  0.63     Sequence
             DRB1_0802  573      RDIADTTDAVRDPQT  IADTTDAVR  2        0.2312
4097.7    75.00  0.54     Sequence
             DRB1_0802  574      DIADTTDAVRDPQTL  IADTTDAVR  1        0.2107
5113.2    80.00  0.50     Sequence
             DRB1_0802  575      IADTTDAVRDPQTLE  TDAVRDPQT  4        0.1587
8974.7    90.00  0.29     Sequence
             DRB1_0802  576      ADTTDAVRDPQTLEI  TDAVRDPQT  3        0.1263
12754.7    95.00  0.40     Sequence
             DRB1_0802  577      DTTDAVRDPQTLEIL  TDAVRDPQT  2        0.1282
12494.0    95.00  0.35     Sequence
             DRB1_0802  578      TTDAVRDPQTLEILD  TDAVRDPQT  1        0.1265
12715.4    95.00  0.34     Sequence
             DRB1_0802  579      TDAVRDPQTLEILDI  VRDPQTLEI  3        0.1196
13707.1    95.00  0.29     Sequence
             DRB1_0802  580      DAVRDPQTLEILDIT  PQTLEILDI  5        0.1020
16590.8   100.00  0.28     Sequence
             DRB1_0802  581      AVRDPQTLEILDITP  LEILDITPX  7        0.1800
7132.7    85.00  0.37     Sequence
             DRB1_0802  582      VRDPQTLEILDITPC  LEILDITPC  6        0.2865
2253.5    55.00  0.70     Sequence
             DRB1_0802  583      RDPQTLEILDITPCS  LEILDITPC  5        0.3663
949.8    31.00  0.58     Sequence
             DRB1_0802  584      DPQTLEILDITPCSF  LEILDITPC  4        0.3859
768.4    26.00  0.57     Sequence
             DRB1_0802  585      PQTLEILDITPCSFG  LEILDITPC  3        0.4064
615.5    21.00  0.56     Sequence
             DRB1_0802  586      QTLEILDITPCSFGG  LEILDITPC  2        0.4110
585.8    20.00  0.56     Sequence
             DRB1_0802  587      TLEILDITPCSFGGV  LEILDITPC  1        0.4089
599.3    21.00  0.49     Sequence
             DRB1_0802  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.3369
1306.5    39.00  0.34     Sequence
             DRB1_0802  589      EILDITPCSFGGVSV  ILDITPCSF  1        0.2544
3189.9    65.00  0.38     Sequence
             DRB1_0802  590      ILDITPCSFGGVSVI  ITPCSFGGV  3        0.1741
7601.2    90.00  0.41     Sequence
```

```
             DRB1_0802  591      LDITPCSFGGVSVIT  ITPCSFGGV  2        0.1739
7614.6    90.00  0.37     Sequence
             DRB1_0802  592      DITPCSFGGVSVITP  FGGVSVITP  6        0.2208
4586.6    75.00  0.60     Sequence
             DRB1_0802  593      ITPCSFGGVSVITPG  FGGVSVITP  5        0.2565
3117.3    65.00  0.58     Sequence
             DRB1_0802  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.3154
1648.0    45.00  0.53     Sequence
             DRB1_0802  595      PCSFGGVSVITPGTN  FGGVSVITP  3        0.3343
1343.0    39.00  0.46     Sequence
             DRB1_0802  596      CSFGGVSVITPGTNT  FGGVSVITP  2        0.3518
1111.0    34.00  0.39     Sequence
             DRB1_0802  597      SFGGVSVITPGTNTS  FGGVSVITP  1        0.3952
695.1    24.00  0.26     Sequence
             DRB1_0802  598      FGGVSVITPGTNTSN  ITPGTNTSN  6        0.4068
612.9    21.00  0.31     Sequence
             DRB1_0802  599      GGVSVITPGTNTSNQ  ITPGTNTSN  5        0.4118
580.4    20.00  0.42     Sequence
             DRB1_0802  600      GVSVITPGTNTSNQV  ITPGTNTSN  4        0.3988
668.2    23.00  0.51     Sequence
             DRB1_0802  601      VSVITPGTNTSNQVA  ITPGTNTSN  3        0.3680
932.6    30.00  0.61     Sequence
             DRB1_0802  602      SVITPGTNTSNQVAV  ITPGTNTSN  2        0.3529
1097.7    34.00  0.64     Sequence
             DRB1_0802  603      VITPGTNTSNQVAVL  ITPGTNTSN  1        0.3015
1915.6    49.00  0.67     Sequence
             DRB1_0802  604      ITPGTNTSNQVAVLY  ITPGTNTSN  0        0.1532
9529.1    90.00  0.20     Sequence
             DRB1_0802  605      TPGTNTSNQVAVLYQ  GTNTSNQVA  2        0.1365
11413.0    95.00  0.28     Sequence
             DRB1_0802  606      PGTNTSNQVAVLYQG  SNQVAVLYQ  5        0.1654
8351.5    90.00  0.28     Sequence
             DRB1_0802  607      GTNTSNQVAVLYQGV  SNQVAVLYQ  4        0.1871
6602.4    85.00  0.28     Sequence
             DRB1_0802  608      TNTSNQVAVLYQGVN  VAVLYQGVN  6        0.2218
4536.2    75.00  0.34     Sequence
             DRB1_0802  609      NTSNQVAVLYQGVNC  VAVLYQGVN  5        0.2457
3501.8    70.00  0.31     Sequence
             DRB1_0802  610      TSNQVAVLYQGVNCT  VAVLYQGVN  4        0.3011
1923.7    49.00  0.23     Sequence
             DRB1_0802  611      SNQVAVLYQGVNCTE  VLYQGVNCT  5        0.3104
1738.5    46.00  0.28     Sequence
             DRB1_0802  612      NQVAVLYQGVNCTEV  VLYQGVNCT  4        0.3088
1770.8    47.00  0.31     Sequence
             DRB1_0802  613      QVAVLYQGVNCTEVP  VLYQGVNCT  3        0.3068
1808.6    47.00  0.31     Sequence
             DRB1_0802  614      VAVLYQGVNCTEVPV  VLYQGVNCT  2        0.2953
2048.4    55.00  0.32     Sequence
             DRB1_0802  615      AVLYQGVNCTEVPVA  VLYQGVNCT  1        0.2768
2500.8    60.00  0.31     Sequence
             DRB1_0802  616      VLYQGVNCTEVPVAI  LYQGVNCTE  1        0.2347
3944.7    70.00  0.29     Sequence
             DRB1_0802  617      LYQGVNCTEVPVAIH  VNCTEVPVA  4        0.1596
8888.1    90.00  0.29     Sequence
             DRB1_0802  618      YQGVNCTEVPVAIHA  VNCTEVPVA  3        0.1688
8046.7    90.00  0.31     Sequence
             DRB1_0802  619      QGVNCTEVPVAIHAD  VNCTEVPVA  2        0.1696
7979.2    90.00  0.29     Sequence
             DRB1_0802  620      GVNCTEVPVAIHADQ  VPVAIHADQ  6        0.1784
7259.3    85.00  0.26     Sequence
             DRB1_0802  621      VNCTEVPVAIHADQL  VPVAIHADQ  5        0.1801
7122.4    85.00  0.31     Sequence
             DRB1_0802  622      NCTEVPVAIHADQLT  VPVAIHADQ  4        0.1881
6533.3    85.00  0.31     Sequence
             DRB1_0802  623      CTEVPVAIHADQLTP  VAIHADQLT  5        0.2038
5511.0    80.00  0.31     Sequence
```

```
              DRB1_0802  624      TEVPVAIHADQLTPT  VAIHADQLT  4        0.2489
3382.6    65.00  0.25     Sequence
              DRB1_0802  625      EVPVAIHADQLTPTW  IHADQLTPT  5        0.2691
2718.5    60.00  0.29     Sequence
              DRB1_0802  626      VPVAIHADQLTPTWR  IHADQLTPT  4        0.2849
2291.2    55.00  0.32     Sequence
              DRB1_0802  627      PVAIHADQLTPTWRV  IHADQLTPT  3        0.2800
2417.4    60.00  0.34     Sequence
              DRB1_0802  628      VAIHADQLTPTWRVY  IHADQLTPT  2        0.2906
2154.4    55.00  0.31     Sequence
              DRB1_0802  629      AIHADQLTPTWRVYS  LTPTWRVYS  6        0.3689
923.8    30.00  0.52    Sequence
              DRB1_0802  630      IHADQLTPTWRVYST  LTPTWRVYS  5        0.3850
776.3    26.00  0.61    Sequence
              DRB1_0802  631      HADQLTPTWRVYSTG  LTPTWRVYS  4        0.3907
729.4    25.00  0.67    Sequence
              DRB1_0802  632      ADQLTPTWRVYSTGS  LTPTWRVYS  3        0.4452
404.6    14.00  0.62    Sequence
              DRB1_0802  633      DQLTPTWRVYSTGSN  LTPTWRVYS  2        0.5291
163.3     5.00  0.38    Sequence        WB
              DRB1_0802  634      QLTPTWRVYSTGSNV  WRVYSTGSN  5        0.5674
107.8     2.50  0.44    Sequence        WB
              DRB1_0802  635      LTPTWRVYSTGSNVF  WRVYSTGSN  4        0.5442
138.6     4.00  0.50    Sequence        WB
              DRB1_0802  636      TPTWRVYSTGSNVFQ  WRVYSTGSN  3        0.5415
142.7     4.00  0.55    Sequence        WB
              DRB1_0802  637      PTWRVYSTGSNVFQT  WRVYSTGSN  2        0.5514
128.2     3.50  0.53    Sequence        WB
              DRB1_0802  638      TWRVYSTGSNVFQTR  WRVYSTGSN  1        0.5408
143.7     4.00  0.49    Sequence        WB
              DRB1_0802  639      WRVYSTGSNVFQTRA  YSTGSNVFQ  3        0.4456
402.8    14.00  0.34    Sequence
              DRB1_0802  640      RVYSTGSNVFQTRAG  YSTGSNVFQ  2        0.3679
934.0    30.00  0.52    Sequence
              DRB1_0802  641      VYSTGSNVFQTRAGC  YSTGSNVFQ  1        0.2861
2262.2    55.00  0.54     Sequence
              DRB1_0802  642      YSTGSNVFQTRAGCL  YSTGSNVFQ  0        0.2518
3279.2    65.00  0.20     Sequence
              DRB1_0802  643      STGSNVFQTRAGCLI  FQTRAGCLI  6        0.2431
3601.8    70.00  0.40     Sequence
              DRB1_0802  644      TGSNVFQTRAGCLIG  FQTRAGCLI  5        0.2733
2599.6    60.00  0.44     Sequence
              DRB1_0802  645      GSNVFQTRAGCLIGA  FQTRAGCLI  4        0.2957
2039.9    55.00  0.46     Sequence
              DRB1_0802  646      SNVFQTRAGCLIGAE  FQTRAGCLI  3        0.2863
2257.9    55.00  0.47     Sequence
              DRB1_0802  647      NVFQTRAGCLIGAEY  FQTRAGCLI  2        0.2602
2994.1    65.00  0.54     Sequence
              DRB1_0802  648      VFQTRAGCLIGAEYV  FQTRAGCLI  1        0.2225
4503.9    75.00  0.57     Sequence
              DRB1_0802  649      FQTRAGCLIGAEYVN  LIGAEYVNX  7        0.1316
12040.6    95.00  0.20     Sequence
              DRB1_0802  650      QTRAGCLIGAEYVNN  LIGAEYVNN  6        0.1431
10633.2    95.00  0.50     Sequence
              DRB1_0802  651      TRAGCLIGAEYVNNS  LIGAEYVNN  5        0.1895
6435.3    85.00  0.50     Sequence
              DRB1_0802  652      RAGCLIGAEYVNNSY  LIGAEYVNN  4        0.2080
5265.4    80.00  0.46     Sequence
              DRB1_0802  653      AGCLIGAEYVNNSYE  LIGAEYVNN  3        0.2134
4969.5    80.00  0.43     Sequence
              DRB1_0802  654      GCLIGAEYVNNSYEC  LIGAEYVNN  2        0.2113
5084.6    80.00  0.43     Sequence
              DRB1_0802  655      CLIGAEYVNNSYECD  LIGAEYVNN  1        0.1889
6474.9    85.00  0.38     Sequence
              DRB1_0802  656      LIGAEYVNNSYECDI  IGAEYVNNS  1        0.1541
9438.2    90.00  0.30     Sequence
```

```
             DRB1_0802  657      IGAEYVNNSYECDIP  AEYVNNSYE  2        0.1145
14481.4   100.00  0.28     Sequence
             DRB1_0802  658      GAEYVNNSYECDIPI  AEYVNNSYE  1        0.0843
20089.7   100.00  0.28     Sequence
             DRB1_0802  659      AEYVNNSYECDIPIG  VNNSYECDI  3        0.0790
21271.3   100.00  0.22     Sequence
             DRB1_0802  660      EYVNNSYECDIPIGA  YECDIPIGA  6        0.0926
18364.6   100.00  0.33     Sequence
             DRB1_0802  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.1057
15929.8   100.00  0.37     Sequence
             DRB1_0802  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.1093
15324.8   100.00  0.38     Sequence
             DRB1_0802  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.1228
13246.8    95.00  0.29     Sequence
             DRB1_0802  664      NSYECDIPIGAGICA  IPIGAGICA  6        0.1493
9942.6    95.00  0.38    Sequence
             DRB1_0802  665      SYECDIPIGAGICAS  IPIGAGICA  5        0.1695
7992.4    90.00  0.44    Sequence
             DRB1_0802  666      YECDIPIGAGICASY  IPIGAGICA  4        0.1935
6162.6    85.00  0.41    Sequence
             DRB1_0802  667      ECDIPIGAGICASYQ  IPIGAGICA  3        0.2088
5224.1    80.00  0.38    Sequence
             DRB1_0802  668      CDIPIGAGICASYQT  IPIGAGICA  2        0.2163
4813.6    75.00  0.35    Sequence
             DRB1_0802  669      DIPIGAGICASYQTQ  IPIGAGICA  1        0.2164
4810.6    75.00  0.30    Sequence
             DRB1_0802  670      IPIGAGICASYQTQT  ICASYQTQT  6        0.2185
4703.7    75.00  0.28    Sequence
             DRB1_0802  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.2228
4488.0    75.00  0.39    Sequence
             DRB1_0802  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.2239
4435.5    75.00  0.50    Sequence
             DRB1_0802  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.2395
3744.5    70.00  0.47    Sequence
             DRB1_0802  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.2593
3024.3    65.00  0.39    Sequence
             DRB1_0802  675      GICASYQTQTNSPRR  YQTQTNSPR  5        0.2700
2693.9    60.00  0.40    Sequence
             DRB1_0802  676      ICASYQTQTNSPRRA  YQTQTNSPR  4        0.2589
3038.3    65.00  0.54    Sequence
             DRB1_0802  677      CASYQTQTNSPRRAR  YQTQTNSPR  3        0.2540
3202.1    65.00  0.63    Sequence
             DRB1_0802  678      ASYQTQTNSPRRARS  YQTQTNSPR  2        0.2590
3033.1    65.00  0.62    Sequence
             DRB1_0802  679      SYQTQTNSPRRARSV  YQTQTNSPR  1        0.2272
4280.3    75.00  0.56    Sequence
             DRB1_0802  680      YQTQTNSPRRARSVA  QTQTNSPRR  1        0.1540
9443.7    90.00  0.22    Sequence
             DRB1_0802  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.1283
12474.5    95.00  0.37     Sequence
             DRB1_0802  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.1762
7428.6    85.00  0.37    Sequence
             DRB1_0802  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.2156
4849.4    75.00  0.33    Sequence
             DRB1_0802  684      TNSPRRARSVASQSI  PRRARSVAS  3        0.2500
3343.2    65.00  0.26    Sequence
             DRB1_0802  685      NSPRRARSVASQSII  ARSVASQSI  5        0.2675
2766.3    60.00  0.31    Sequence
             DRB1_0802  686      SPRRARSVASQSIIA  ARSVASQSI  4        0.3054
1835.8    48.00  0.27    Sequence
             DRB1_0802  687      PRRARSVASQSIIAY  VASQSIIAY  6        0.3653
960.4    31.00  0.46    Sequence
             DRB1_0802  688      RRARSVASQSIIAYT  VASQSIIAY  5        0.3973
679.0    23.00  0.49    Sequence
             DRB1_0802  689      RARSVASQSIIAYTM  VASQSIIAY  4        0.3985
670.3    23.00  0.54    Sequence
```

```
              DRB1_0802  690      ARSVASQSIIAYTMS  VASQSIIAY  3        0.3969
682.1    23.00  0.57     Sequence
              DRB1_0802  691      RSVASQSIIAYTMSL  VASQSIIAY  2        0.3930
711.7    24.00  0.61     Sequence
              DRB1_0802  692      SVASQSIIAYTMSLG  VASQSIIAY  1        0.3670
942.4    30.00  0.48     Sequence
              DRB1_0802  693      VASQSIIAYTMSLGA  IAYTMSLGA  6        0.3386
1282.5    38.00  0.39     Sequence
              DRB1_0802  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.3629
985.3    31.00  0.44     Sequence
              DRB1_0802  695      SQSIIAYTMSLGAEN  IAYTMSLGA  4        0.3822
799.7    27.00  0.47     Sequence
              DRB1_0802  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.4018
647.3    22.00  0.46     Sequence
              DRB1_0802  697      SIIAYTMSLGAENSV  IAYTMSLGA  2        0.3996
662.9    23.00  0.45     Sequence
              DRB1_0802  698      IIAYTMSLGAENSVA  IAYTMSLGA  1        0.3723
890.1    29.00  0.37     Sequence
              DRB1_0802  699      IAYTMSLGAENSVAY  YTMSLGAEN  2        0.3066
1812.8    48.00  0.49     Sequence
              DRB1_0802  700      AYTMSLGAENSVAYS  YTMSLGAEN  1        0.2653
2834.2    60.00  0.40     Sequence
              DRB1_0802  701      YTMSLGAENSVAYSN  LGAENSVAY  4        0.2262
4323.6    75.00  0.41     Sequence
              DRB1_0802  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.2034
5537.2    80.00  0.46     Sequence
              DRB1_0802  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.2045
5468.6    80.00  0.46     Sequence
              DRB1_0802  704      SLGAENSVAYSNNSI  LGAENSVAY  1        0.2478
3426.1    70.00  0.29     Sequence
              DRB1_0802  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.3246
1491.6    42.00  0.56     Sequence
              DRB1_0802  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.3661
952.4    31.00  0.63     Sequence
              DRB1_0802  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.3834
790.0    26.00  0.64     Sequence
              DRB1_0802  708      ENSVAYSNNSIAIPT  VAYSNNSIA  3        0.3999
660.7    23.00  0.62     Sequence
              DRB1_0802  709      NSVAYSNNSIAIPTN  VAYSNNSIA  2        0.4038
633.0    22.00  0.60     Sequence
              DRB1_0802  710      SVAYSNNSIAIPTNF  VAYSNNSIA  1        0.3772
844.5    28.00  0.57     Sequence
              DRB1_0802  711      VAYSNNSIAIPTNFT  YSNNSIAIP  2        0.3296
1413.0    41.00  0.23     Sequence
              DRB1_0802  712      AYSNNSIAIPTNFTI  SIAIPTNFT  5        0.3058
1827.2    48.00  0.31     Sequence
              DRB1_0802  713      YSNNSIAIPTNFTIS  IAIPTNFTI  5        0.3441
1208.1    36.00  0.31     Sequence
              DRB1_0802  714      SNNSIAIPTNFTISV  IPTNFTISV  6        0.3863
765.2    26.00  0.38     Sequence
              DRB1_0802  715      NNSIAIPTNFTISVT  IPTNFTISV  5        0.4036
634.5    22.00  0.44     Sequence
              DRB1_0802  716      NSIAIPTNFTISVTT  IPTNFTISV  4        0.3996
662.4    23.00  0.50     Sequence
              DRB1_0802  717      SIAIPTNFTISVTTE  IPTNFTISV  3        0.3874
755.7    25.00  0.49     Sequence
              DRB1_0802  718      IAIPTNFTISVTTEI  IPTNFTISV  2        0.3730
883.3    29.00  0.49     Sequence
              DRB1_0802  719      AIPTNFTISVTTEIL  IPTNFTISV  1        0.3525
1102.5    34.00  0.35     Sequence
              DRB1_0802  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.3077
1791.5    47.00  0.49     Sequence
              DRB1_0802  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.3236
1507.2    42.00  0.43     Sequence
              DRB1_0802  722      TNFTISVTTEILPVS  FTISVTTEI  2        0.3550
1073.8    34.00  0.31     Sequence
```

```
             DRB1_0802  723      NFTISVTTEILPVSM  FTISVTTEI  1        0.3507
1125.2    35.00  0.26     Sequence
             DRB1_0802  724      FTISVTTEILPVSMT  ISVTTEILP  2        0.3180
1602.6    44.00  0.30     Sequence
             DRB1_0802  725      TISVTTEILPVSMTK  ISVTTEILP  1        0.3572
1048.6    33.00  0.22     Sequence
             DRB1_0802  726      ISVTTEILPVSMTKT  ILPVSMTKT  6        0.4299
477.3    17.00  0.45     Sequence
             DRB1_0802  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.4497
385.5    14.00  0.55     Sequence
             DRB1_0802  728      VTTEILPVSMTKTSV  ILPVSMTKT  4        0.4665
321.2    11.00  0.54     Sequence
             DRB1_0802  729      TTEILPVSMTKTSVD  ILPVSMTKT  3        0.4577
353.2    12.00  0.56     Sequence
             DRB1_0802  730      TEILPVSMTKTSVDC  ILPVSMTKT  2        0.4545
366.0    13.00  0.57     Sequence
             DRB1_0802  731      EILPVSMTKTSVDCT  ILPVSMTKT  1        0.4407
424.8    15.00  0.53     Sequence
             DRB1_0802  732      ILPVSMTKTSVDCTM  VSMTKTSVD  3        0.3720
893.3    29.00  0.36     Sequence
             DRB1_0802  733      LPVSMTKTSVDCTMY  VSMTKTSVD  2        0.2740
2580.3    60.00  0.50     Sequence
             DRB1_0802  734      PVSMTKTSVDCTMYI  VSMTKTSVD  1        0.2415
3664.9    70.00  0.42     Sequence
             DRB1_0802  735      VSMTKTSVDCTMYIC  MTKTSVDCT  2        0.1604
8815.4    90.00  0.35     Sequence
             DRB1_0802  736      SMTKTSVDCTMYICG  TKTSVDCTM  2        0.1311
12109.9    95.00  0.29     Sequence
             DRB1_0802  737      MTKTSVDCTMYICGD  TKTSVDCTM  1        0.1015
16675.8   100.00  0.29     Sequence
             DRB1_0802  738      TKTSVDCTMYICGDS  TSVDCTMYI  2        0.0666
24328.9   100.00  0.28     Sequence
             DRB1_0802  739      KTSVDCTMYICGDST  MYICGDSTX  7        0.1084
15479.5   100.00  0.27     Sequence
             DRB1_0802  740      TSVDCTMYICGDSTE  MYICGDSTE  6        0.1263
12745.4    95.00  0.34     Sequence
             DRB1_0802  741      SVDCTMYICGDSTEC  MYICGDSTE  5        0.1352
11576.1    95.00  0.31     Sequence
             DRB1_0802  742      VDCTMYICGDSTECS  ICGDSTECS  6        0.1775
7323.3    85.00  0.33     Sequence
             DRB1_0802  743      DCTMYICGDSTECSN  ICGDSTECS  5        0.1994
5780.3    80.00  0.38     Sequence
             DRB1_0802  744      CTMYICGDSTECSNL  ICGDSTECS  4        0.2077
5283.2    80.00  0.39     Sequence
             DRB1_0802  745      TMYICGDSTECSNLL  ICGDSTECS  3        0.2018
5630.2    80.00  0.42     Sequence
             DRB1_0802  746      MYICGDSTECSNLLL  ICGDSTECS  2        0.1654
8348.5    90.00  0.50     Sequence
             DRB1_0802  747      YICGDSTECSNLLLQ  ICGDSTECS  1        0.1556
9286.5    90.00  0.44     Sequence
             DRB1_0802  748      ICGDSTECSNLLLQY  ICGDSTECS  0        0.1456
10349.6    95.00  0.19     Sequence
             DRB1_0802  749      CGDSTECSNLLLQYG  CSNLLLQYG  6        0.1370
11356.4    95.00  0.28     Sequence
             DRB1_0802  750      GDSTECSNLLLQYGS  CSNLLLQYG  5        0.1594
8913.0    90.00  0.29     Sequence
             DRB1_0802  751      DSTECSNLLLQYGSF  CSNLLLQYG  4        0.1941
6120.0    85.00  0.19     Sequence
             DRB1_0802  752      STECSNLLLQYGSFC  LLLQYGSFC  6        0.2114
5074.6    80.00  0.28     Sequence
             DRB1_0802  753      TECSNLLLQYGSFCT  LLLQYGSFC  5        0.2293
4182.4    75.00  0.29     Sequence
             DRB1_0802  754      ECSNLLLQYGSFCTQ  LLQYGSFCT  5        0.2359
3896.7    70.00  0.28     Sequence
             DRB1_0802  755      CSNLLLQYGSFCTQL  LLQYGSFCT  4        0.2307
4118.3    75.00  0.29     Sequence
```

```
             DRB1_0802  756      SNLLLQYGSFCTQLN  LLQYGSFCT  3        0.2389
3769.7    70.00  0.28     Sequence
             DRB1_0802  757      NLLLQYGSFCTQLNR  LLQYGSFCT  2        0.2371
3843.7    70.00  0.30     Sequence
             DRB1_0802  758      LLLQYGSFCTQLNRA  LLQYGSFCT  1        0.2262
4323.4    75.00  0.25     Sequence
             DRB1_0802  759      LLQYGSFCTQLNRAL  FCTQLNRAL  6        0.2548
3174.8    65.00  0.39     Sequence
             DRB1_0802  760      LQYGSFCTQLNRALT  FCTQLNRAL  5        0.2744
2568.7    60.00  0.50     Sequence
             DRB1_0802  761      QYGSFCTQLNRALTG  FCTQLNRAL  4        0.2997
1953.6    50.00  0.47     Sequence
             DRB1_0802  762      YGSFCTQLNRALTGI  FCTQLNRAL  3        0.3233
1512.7    43.00  0.44     Sequence
             DRB1_0802  763      GSFCTQLNRALTGIA  LNRALTGIA  6        0.3770
846.4    28.00  0.34     Sequence
             DRB1_0802  764      SFCTQLNRALTGIAV  LNRALTGIA  5        0.3833
790.0    26.00  0.38     Sequence
             DRB1_0802  765      FCTQLNRALTGIAVE  LNRALTGIA  4        0.3608
1008.1    32.00  0.46     Sequence
             DRB1_0802  766      CTQLNRALTGIAVEQ  LNRALTGIA  3        0.3642
971.5    31.00  0.46     Sequence
             DRB1_0802  767      TQLNRALTGIAVEQD  LNRALTGIA  2        0.3582
1037.0    33.00  0.44     Sequence
             DRB1_0802  768      QLNRALTGIAVEQDK  LNRALTGIA  1        0.3349
1334.6    39.00  0.40     Sequence
             DRB1_0802  769      LNRALTGIAVEQDKN  LTGIAVEQD  4        0.3020
1904.1    49.00  0.42     Sequence
             DRB1_0802  770      NRALTGIAVEQDKNT  LTGIAVEQD  3        0.2731
2604.5    60.00  0.50     Sequence
             DRB1_0802  771      RALTGIAVEQDKNTQ  LTGIAVEQD  2        0.2990
1967.9    50.00  0.38     Sequence
             DRB1_0802  772      ALTGIAVEQDKNTQE  VEQDKNTQE  6        0.3047
1849.6    48.00  0.28     Sequence
             DRB1_0802  773      LTGIAVEQDKNTQEV  VEQDKNTQE  5        0.2918
2128.3    55.00  0.41     Sequence
             DRB1_0802  774      TGIAVEQDKNTQEVF  VEQDKNTQE  4        0.3016
1912.2    49.00  0.45     Sequence
             DRB1_0802  775      GIAVEQDKNTQEVFA  VEQDKNTQE  3        0.3057
1829.9    48.00  0.49     Sequence
             DRB1_0802  776      IAVEQDKNTQEVFAQ  VEQDKNTQE  2        0.2731
2604.6    60.00  0.56     Sequence
             DRB1_0802  777      AVEQDKNTQEVFAQV  VEQDKNTQE  1        0.2198
4633.8    75.00  0.52     Sequence
             DRB1_0802  778      VEQDKNTQEVFAQVK  DKNTQEVFA  3        0.1337
11767.0    95.00  0.20     Sequence
             DRB1_0802  779      EQDKNTQEVFAQVKQ  QEVFAQVKQ  6        0.1397
11027.1    95.00  0.29     Sequence
             DRB1_0802  780      QDKNTQEVFAQVKQI  VFAQVKQIX  7        0.2414
3670.5    70.00  0.28     Sequence
             DRB1_0802  781      DKNTQEVFAQVKQIY  VFAQVKQIY  6        0.3541
1084.1    34.00  0.36     Sequence
             DRB1_0802  782      KNTQEVFAQVKQIYK  FAQVKQIYK  6        0.4289
482.4    17.00  0.47     Sequence
             DRB1_0802  783      NTQEVFAQVKQIYKT  FAQVKQIYK  5        0.4640
330.3    12.00  0.51     Sequence
             DRB1_0802  784      TQEVFAQVKQIYKTP  FAQVKQIYK  4        0.4790
280.6     9.50  0.53     Sequence         WB
             DRB1_0802  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.5004
222.7     7.00  0.49     Sequence         WB
             DRB1_0802  786      EVFAQVKQIYKTPPI  FAQVKQIYK  2        0.5046
212.7     7.00  0.44     Sequence         WB
             DRB1_0802  787      VFAQVKQIYKTPPIK  FAQVKQIYK  1        0.4858
260.8     8.50  0.35     Sequence         WB
             DRB1_0802  788      FAQVKQIYKTPPIKD  VKQIYKTPP  3        0.4222
518.9    18.00  0.30     Sequence
```

```
             DRB1_0802  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.4086
600.8    21.00  0.34     Sequence
             DRB1_0802  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.4082
603.9    21.00  0.41     Sequence
             DRB1_0802  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.3779
837.8    28.00  0.47     Sequence
             DRB1_0802  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.3387
1280.9    38.00  0.60     Sequence
             DRB1_0802  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.2767
2505.7    60.00  0.52     Sequence
             DRB1_0802  794      IYKTPPIKDFGGFNF  IKDFGGFNF  6        0.2322
4053.9    70.00  0.59     Sequence
             DRB1_0802  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.2423
3633.1    70.00  0.70     Sequence
             DRB1_0802  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.2655
2829.0    60.00  0.65     Sequence
             DRB1_0802  797      TPPIKDFGGFNFSQI  IKDFGGFNF  3        0.2775
2482.5    60.00  0.57     Sequence
             DRB1_0802  798      PPIKDFGGFNFSQIL  IKDFGGFNF  2        0.2840
2315.6    55.00  0.54     Sequence
             DRB1_0802  799      PIKDFGGFNFSQILP  IKDFGGFNF  1        0.2888
2196.3    55.00  0.42     Sequence
             DRB1_0802  800      IKDFGGFNFSQILPD  FNFSQILPD  6        0.2549
3172.7    65.00  0.34     Sequence
             DRB1_0802  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.2560
3133.7    65.00  0.38     Sequence
             DRB1_0802  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.2871
2237.7    55.00  0.36     Sequence
             DRB1_0802  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.3085
1774.8    47.00  0.39     Sequence
             DRB1_0802  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.3068
1809.5    47.00  0.38     Sequence
             DRB1_0802  805      GFNFSQILPDPSKPS  FNFSQILPD  1        0.3358
1321.1    39.00  0.28     Sequence
             DRB1_0802  806      FNFSQILPDPSKPSK  ILPDPSKPS  5        0.3016
1912.9    49.00  0.38     Sequence
             DRB1_0802  807      NFSQILPDPSKPSKR  ILPDPSKPS  4        0.3020
1904.6    49.00  0.47     Sequence
             DRB1_0802  808      FSQILPDPSKPSKRS  ILPDPSKPS  3        0.2832
2335.8    55.00  0.56     Sequence
             DRB1_0802  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.2576
3078.8    65.00  0.63     Sequence
             DRB1_0802  810      QILPDPSKPSKRSFI  ILPDPSKPS  1        0.2403
3713.3    70.00  0.55     Sequence
             DRB1_0802  811      ILPDPSKPSKRSFIE  ILPDPSKPS  0        0.1747
7552.9    85.00  0.31     Sequence
             DRB1_0802  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.0719
22964.8   100.00  0.31     Sequence
             DRB1_0802  813      PDPSKPSKRSFIEDL  SKPSKRSFI  3        0.0735
22570.6   100.00  0.32     Sequence
             DRB1_0802  814      DPSKPSKRSFIEDLL  SKPSKRSFI  2        0.0725
22826.1   100.00  0.29     Sequence
             DRB1_0802  815      PSKPSKRSFIEDLLF  SKPSKRSFI  1        0.0743
22375.4   100.00  0.25     Sequence
             DRB1_0802  816      SKPSKRSFIEDLLFN  FIEDLLFNX  7        0.1018
16619.6   100.00  0.26     Sequence
             DRB1_0802  817      KPSKRSFIEDLLFNK  FIEDLLFNK  6        0.1590
8953.2    90.00  0.39     Sequence
             DRB1_0802  818      PSKRSFIEDLLFNKV  IEDLLFNKV  6        0.2054
5419.4    80.00  0.32     Sequence
             DRB1_0802  819      SKRSFIEDLLFNKVT  IEDLLFNKV  5        0.2328
4028.6    70.00  0.31     Sequence
             DRB1_0802  820      KRSFIEDLLFNKVTL  IEDLLFNKV  4        0.2564
3120.3    65.00  0.28     Sequence
             DRB1_0802  821      RSFIEDLLFNKVTLA  LLFNKVTLA  6        0.3552
1070.9    33.00  0.22     Sequence
```

```
             DRB1_0802  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5        0.3830
793.0    27.00  0.22     Sequence
             DRB1_0802  823      FIEDLLFNKVTLADA  FNKVTLADA  6        0.4527
373.2    13.00  0.34     Sequence
             DRB1_0802  824      IEDLLFNKVTLADAG  FNKVTLADA  5        0.4842
265.4     9.00  0.38     Sequence         WB
             DRB1_0802  825      EDLLFNKVTLADAGF  FNKVTLADA  4        0.4967
231.8     7.50  0.38     Sequence         WB
             DRB1_0802  826      DLLFNKVTLADAGFI  FNKVTLADA  3        0.4924
242.7     8.00  0.41     Sequence         WB
             DRB1_0802  827      LLFNKVTLADAGFIK  FNKVTLADA  2        0.4802
276.9     9.50  0.42     Sequence         WB
             DRB1_0802  828      LFNKVTLADAGFIKQ  FNKVTLADA  1        0.3832
790.9    26.00  0.41     Sequence
             DRB1_0802  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.3424
1230.4    37.00  0.25     Sequence
             DRB1_0802  830      NKVTLADAGFIKQYG  VTLADAGFI  2        0.2748
2558.1    60.00  0.31     Sequence
             DRB1_0802  831      KVTLADAGFIKQYGD  LADAGFIKQ  3        0.2481
3414.8    70.00  0.43     Sequence
             DRB1_0802  832      VTLADAGFIKQYGDC  LADAGFIKQ  2        0.1925
6232.3    85.00  0.54     Sequence
             DRB1_0802  833      TLADAGFIKQYGDCL  LADAGFIKQ  1        0.1867
6628.9    85.00  0.41     Sequence
             DRB1_0802  834      LADAGFIKQYGDCLG  IKQYGDCLG  6        0.2013
5660.3    80.00  0.47     Sequence
             DRB1_0802  835      ADAGFIKQYGDCLGD  IKQYGDCLG  5        0.2039
5505.8    80.00  0.56     Sequence
             DRB1_0802  836      DAGFIKQYGDCLGDI  IKQYGDCLG  4        0.2148
4894.0    75.00  0.56     Sequence
             DRB1_0802  837      AGFIKQYGDCLGDIA  IKQYGDCLG  3        0.2316
4080.1    70.00  0.55     Sequence
             DRB1_0802  838      GFIKQYGDCLGDIAA  IKQYGDCLG  2        0.2359
3895.9    70.00  0.51     Sequence
             DRB1_0802  839      FIKQYGDCLGDIAAR  IKQYGDCLG  1        0.2243
4415.2    75.00  0.47     Sequence
             DRB1_0802  840      IKQYGDCLGDIAARD  YGDCLGDIA  3        0.1464
10257.6    95.00  0.34     Sequence
             DRB1_0802  841      KQYGDCLGDIAARDL  YGDCLGDIA  2        0.1349
11619.7    95.00  0.32     Sequence
             DRB1_0802  842      QYGDCLGDIAARDLI  LGDIAARDL  5        0.1425
10696.7    95.00  0.35     Sequence
             DRB1_0802  843      YGDCLGDIAARDLIC  LGDIAARDL  4        0.1595
8898.6    90.00  0.27     Sequence
             DRB1_0802  844      GDCLGDIAARDLICA  IAARDLICA  6        0.2220
4525.5    75.00  0.50     Sequence
             DRB1_0802  845      DCLGDIAARDLICAQ  IAARDLICA  5        0.2705
2678.6    60.00  0.51     Sequence
             DRB1_0802  846      CLGDIAARDLICAQK  IAARDLICA  4        0.3059
1826.7    48.00  0.50     Sequence
             DRB1_0802  847      LGDIAARDLICAQKF  IAARDLICA  3        0.3108
1732.3    46.00  0.51     Sequence
             DRB1_0802  848      GDIAARDLICAQKFN  IAARDLICA  2        0.3202
1563.7    43.00  0.49     Sequence
             DRB1_0802  849      DIAARDLICAQKFNG  IAARDLICA  1        0.3174
1612.8    44.00  0.40     Sequence
             DRB1_0802  850      IAARDLICAQKFNGL  LICAQKFNG  5        0.2960
2032.9    55.00  0.44     Sequence
             DRB1_0802  851      AARDLICAQKFNGLT  LICAQKFNG  4        0.3040
1864.8    48.00  0.50     Sequence
             DRB1_0802  852      ARDLICAQKFNGLTV  LICAQKFNG  3        0.3108
1732.7    46.00  0.47     Sequence
             DRB1_0802  853      RDLICAQKFNGLTVL  LICAQKFNG  2        0.3169
1620.7    44.00  0.46     Sequence
             DRB1_0802  854      DLICAQKFNGLTVLP  LICAQKFNG  1        0.3286
1429.2    41.00  0.36     Sequence
```

```
             DRB1_0802  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.3737
876.8    29.00  0.50     Sequence
             DRB1_0802  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.4002
658.6    23.00  0.56     Sequence
             DRB1_0802  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.4140
566.9    20.00  0.56     Sequence
             DRB1_0802  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.4342
455.6    16.00  0.54     Sequence
             DRB1_0802  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.4266
494.8    17.00  0.54     Sequence
             DRB1_0802  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1        0.4052
623.4    22.00  0.45     Sequence
             DRB1_0802  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.3366
1310.1    39.00  0.45     Sequence
             DRB1_0802  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.2837
2322.7    55.00  0.57     Sequence
             DRB1_0802  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.2673
2772.5    60.00  0.50     Sequence
             DRB1_0802  864      LTVLPPLLTDEMIAQ  LLTDEMIAQ  6        0.2390
3766.7    70.00  0.28     Sequence
             DRB1_0802  865      TVLPPLLTDEMIAQY  LTDEMIAQY  6        0.2522
3263.7    65.00  0.31     Sequence
             DRB1_0802  866      VLPPLLTDEMIAQYT  LTDEMIAQY  5        0.2798
2421.8    60.00  0.31     Sequence
             DRB1_0802  867      LPPLLTDEMIAQYTS  LTDEMIAQY  4        0.3051
1841.1    48.00  0.31     Sequence
             DRB1_0802  868      PPLLTDEMIAQYTSA  LTDEMIAQY  3        0.3616
999.4    32.00  0.25     Sequence
             DRB1_0802  869      PLLTDEMIAQYTSAL  IAQYTSALX  7        0.4394
430.9    15.00  0.29     Sequence
             DRB1_0802  870      LLTDEMIAQYTSALL  IAQYTSALL  6        0.4830
268.7     9.00  0.47     Sequence         WB
             DRB1_0802  871      LTDEMIAQYTSALLA  IAQYTSALL  5        0.5246
171.4     5.00  0.56     Sequence         WB
             DRB1_0802  872      TDEMIAQYTSALLAG  IAQYTSALL  4        0.5522
127.1     3.50  0.60     Sequence         WB
             DRB1_0802  873      DEMIAQYTSALLAGT  IAQYTSALL  3        0.5522
127.1     3.50  0.61     Sequence         WB
             DRB1_0802  874      EMIAQYTSALLAGTI  IAQYTSALL  2        0.5474
133.9     3.50  0.63     Sequence         WB
             DRB1_0802  875      MIAQYTSALLAGTIT  IAQYTSALL  1        0.4966
231.9     7.50  0.62     Sequence         WB
             DRB1_0802  876      IAQYTSALLAGTITS  IAQYTSALL  0        0.3059
1826.1    48.00  0.20     Sequence
             DRB1_0802  877      AQYTSALLAGTITSG  LLAGTITSG  6        0.2790
2444.2    60.00  0.29     Sequence
             DRB1_0802  878      QYTSALLAGTITSGW  LLAGTITSG  5        0.2822
2361.2    55.00  0.40     Sequence
             DRB1_0802  879      YTSALLAGTITSGWT  LLAGTITSG  4        0.2924
2114.3    55.00  0.44     Sequence
             DRB1_0802  880      TSALLAGTITSGWTF  LLAGTITSG  3        0.3061
1822.4    48.00  0.41     Sequence
             DRB1_0802  881      SALLAGTITSGWTFG  LLAGTITSG  2        0.3315
1384.2    40.00  0.37     Sequence
             DRB1_0802  882      ALLAGTITSGWTFGA  ITSGWTFGA  6        0.3450
1195.7    36.00  0.31     Sequence
             DRB1_0802  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.3153
1650.4    45.00  0.49     Sequence
             DRB1_0802  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.3287
1426.2    41.00  0.60     Sequence
             DRB1_0802  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.3456
1188.3    36.00  0.58     Sequence
             DRB1_0802  886      GTITSGWTFGAGAAL  ITSGWTFGA  2        0.3357
1323.2    39.00  0.57     Sequence
             DRB1_0802  887      TITSGWTFGAGAALQ  ITSGWTFGA  1        0.3066
1813.0    48.00  0.50     Sequence
```

```
              DRB1_0802  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.2872
2235.5    55.00  0.51     Sequence
              DRB1_0802  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.2832
2333.7    55.00  0.63     Sequence
              DRB1_0802  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.2927
2107.4    55.00  0.64     Sequence
              DRB1_0802  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.3196
1575.5    44.00  0.58     Sequence
              DRB1_0802  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.3254
1478.8    42.00  0.51     Sequence
              DRB1_0802  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.3495
1139.3    35.00  0.38     Sequence
              DRB1_0802  894      FGAGAALQIPFAMQM  GAALQIPFA  3        0.2957
2039.7    55.00  0.22     Sequence
              DRB1_0802  895      GAGAALQIPFAMQMA  AALQIPFAM  3        0.2972
2006.8    50.00  0.25     Sequence
              DRB1_0802  896      AGAALQIPFAMQMAY  AALQIPFAM  2        0.2910
2146.8    55.00  0.24     Sequence
              DRB1_0802  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.3066
1811.6    47.00  0.19     Sequence
              DRB1_0802  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.2807
2399.3    60.00  0.38     Sequence
              DRB1_0802  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.3304
1401.0    40.00  0.34     Sequence
              DRB1_0802  900      LQIPFAMQMAYRFNG  MQMAYRFNG  6        0.4323
465.1    16.00  0.56     Sequence
              DRB1_0802  901      QIPFAMQMAYRFNGI  MQMAYRFNG  5        0.4737
297.3    10.00  0.58     Sequence
              DRB1_0802  902      IPFAMQMAYRFNGIG  MQMAYRFNG  4        0.5189
182.2     5.50  0.52     Sequence         WB
              DRB1_0802  903      PFAMQMAYRFNGIGV  MQMAYRFNG  3        0.5326
157.2     4.50  0.50     Sequence         WB
              DRB1_0802  904      FAMQMAYRFNGIGVT  MQMAYRFNG  2        0.5100
200.7     6.50  0.54     Sequence         WB
              DRB1_0802  905      AMQMAYRFNGIGVTQ  MQMAYRFNG  1        0.4958
234.0     7.50  0.50     Sequence         WB
              DRB1_0802  906      MQMAYRFNGIGVTQN  MAYRFNGIG  2        0.4149
561.4    20.00  0.28     Sequence
              DRB1_0802  907      QMAYRFNGIGVTQNV  FNGIGVTQN  5        0.3910
727.6    25.00  0.33     Sequence
              DRB1_0802  908      MAYRFNGIGVTQNVL  FNGIGVTQN  4        0.3746
868.5    29.00  0.35     Sequence
              DRB1_0802  909      AYRFNGIGVTQNVLY  FNGIGVTQN  3        0.3531
1095.8    34.00  0.38     Sequence
              DRB1_0802  910      YRFNGIGVTQNVLYE  FNGIGVTQN  2        0.3539
1086.1    34.00  0.33     Sequence
              DRB1_0802  911      RFNGIGVTQNVLYEN  IGVTQNVLY  4        0.3533
1093.8    34.00  0.35     Sequence
              DRB1_0802  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.3267
1458.1    42.00  0.41     Sequence
              DRB1_0802  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.3179
1604.5    44.00  0.41     Sequence
              DRB1_0802  914      GIGVTQNVLYENQKL  IGVTQNVLY  1        0.2981
1987.0    50.00  0.34     Sequence
              DRB1_0802  915      IGVTQNVLYENQKLI  VTQNVLYEN  2        0.2551
3162.6    65.00  0.32     Sequence
              DRB1_0802  916      GVTQNVLYENQKLIA  VTQNVLYEN  1        0.2475
3434.8    70.00  0.23     Sequence
              DRB1_0802  917      VTQNVLYENQKLIAN  LYENQKLIA  5        0.2422
3638.2    70.00  0.31     Sequence
              DRB1_0802  918      TQNVLYENQKLIANQ  LYENQKLIA  4        0.2719
2638.5    60.00  0.31     Sequence
              DRB1_0802  919      QNVLYENQKLIANQF  LYENQKLIA  3        0.3013
1919.1    49.00  0.25     Sequence
              DRB1_0802  920      NVLYENQKLIANQFN  YENQKLIAN  3        0.3133
1685.5    45.00  0.26     Sequence
```

```
             DRB1_0802  921      VLYENQKLIANQFNS  YENQKLIAN  2        0.3160
1637.7    45.00  0.25     Sequence
             DRB1_0802  922      LYENQKLIANQFNSA  IANQFNSAX  7        0.3621
993.9    32.00  0.28     Sequence
             DRB1_0802  923      YENQKLIANQFNSAI  IANQFNSAI  6        0.4271
492.3    17.00  0.52     Sequence
             DRB1_0802  924      ENQKLIANQFNSAIG  IANQFNSAI  5        0.4638
330.8    12.00  0.58     Sequence
             DRB1_0802  925      NQKLIANQFNSAIGK  IANQFNSAI  4        0.4863
259.4     8.50  0.62     Sequence        WB
             DRB1_0802  926      QKLIANQFNSAIGKI  IANQFNSAI  3        0.4769
287.2     9.50  0.59     Sequence        WB
             DRB1_0802  927      KLIANQFNSAIGKIQ  IANQFNSAI  2        0.4875
256.0     8.50  0.56     Sequence        WB
             DRB1_0802  928      LIANQFNSAIGKIQD  IANQFNSAI  1        0.4380
437.4    15.00  0.51     Sequence
             DRB1_0802  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4        0.3338
1350.6    39.00  0.51     Sequence
             DRB1_0802  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.2915
2133.9    55.00  0.60     Sequence
             DRB1_0802  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.3291
1420.5    41.00  0.44     Sequence
             DRB1_0802  932      QFNSAIGKIQDSLSS  IGKIQDSLS  5        0.3819
802.0    27.00  0.34     Sequence
             DRB1_0802  933      FNSAIGKIQDSLSST  GKIQDSLSS  5        0.4245
506.0    18.00  0.34     Sequence
             DRB1_0802  934      NSAIGKIQDSLSSTA  GKIQDSLSS  4        0.4629
334.0    12.00  0.39     Sequence
             DRB1_0802  935      SAIGKIQDSLSSTAS  GKIQDSLSS  3        0.4760
289.8    10.00  0.41     Sequence
             DRB1_0802  936      AIGKIQDSLSSTASA  GKIQDSLSS  2        0.4769
287.0     9.50  0.38     Sequence        WB
             DRB1_0802  937      IGKIQDSLSSTASAL  GKIQDSLSS  1        0.4466
398.7    14.00  0.32     Sequence
             DRB1_0802  938      GKIQDSLSSTASALG  IQDSLSSTA  2        0.3637
977.0    31.00  0.39     Sequence
             DRB1_0802  939      KIQDSLSSTASALGK  LSSTASALG  5        0.3395
1270.2    38.00  0.43     Sequence
             DRB1_0802  940      IQDSLSSTASALGKL  LSSTASALG  4        0.3002
1942.9    49.00  0.58     Sequence
             DRB1_0802  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.2824
2354.5    55.00  0.67     Sequence
             DRB1_0802  942      DSLSSTASALGKLQD  LSSTASALG  2        0.2736
2588.9    60.00  0.69     Sequence
             DRB1_0802  943      SLSSTASALGKLQDV  LSSTASALG  1        0.2437
3580.5    70.00  0.67     Sequence
             DRB1_0802  944      LSSTASALGKLQDVV  LSSTASALG  0        0.1664
8264.5    90.00  0.22     Sequence
             DRB1_0802  945      SSTASALGKLQDVVN  LGKLQDVVN  6        0.1570
9142.6    90.00  0.46     Sequence
             DRB1_0802  946      STASALGKLQDVVNQ  LGKLQDVVN  5        0.2278
4251.8    75.00  0.41     Sequence
             DRB1_0802  947      TASALGKLQDVVNQN  LGKLQDVVN  4        0.2983
1981.8    50.00  0.34     Sequence
             DRB1_0802  948      ASALGKLQDVVNQNA  LQDVVNQNA  6        0.3517
1112.8    34.00  0.40     Sequence
             DRB1_0802  949      SALGKLQDVVNQNAQ  LQDVVNQNA  5        0.3795
824.0    27.00  0.43     Sequence
             DRB1_0802  950      ALGKLQDVVNQNAQA  LQDVVNQNA  4        0.3930
711.8    24.00  0.52     Sequence
             DRB1_0802  951      LGKLQDVVNQNAQAL  LQDVVNQNA  3        0.3861
766.6    26.00  0.57     Sequence
             DRB1_0802  952      GKLQDVVNQNAQALN  LQDVVNQNA  2        0.3701
912.0    30.00  0.60     Sequence
             DRB1_0802  953      KLQDVVNQNAQALNT  LQDVVNQNA  1        0.3252
1482.6    42.00  0.52     Sequence
```

```
             DRB1_0802  954      LQDVVNQNAQALNTL  VVNQNAQAL  3        0.2498
3351.4    65.00  0.27     Sequence
             DRB1_0802  955      QDVVNQNAQALNTLV  VVNQNAQAL  2        0.2225
4504.6    75.00  0.26     Sequence
             DRB1_0802  956      DVVNQNAQALNTLVK  AQALNTLVK  6        0.2525
3252.9    65.00  0.23     Sequence
             DRB1_0802  957      VVNQNAQALNTLVKQ  AQALNTLVK  5        0.2698
2700.3    60.00  0.28     Sequence
             DRB1_0802  958      VNQNAQALNTLVKQL  AQALNTLVK  4        0.2983
1982.0    50.00  0.26     Sequence
             DRB1_0802  959      NQNAQALNTLVKQLS  LNTLVKQLS  6        0.4157
556.6    19.00  0.50     Sequence
             DRB1_0802  960      QNAQALNTLVKQLSS  LNTLVKQLS  5        0.4556
361.6    13.00  0.50     Sequence
             DRB1_0802  961      NAQALNTLVKQLSSN  LNTLVKQLS  4        0.5227
175.0     5.50  0.43     Sequence         WB
             DRB1_0802  962      AQALNTLVKQLSSNF  LNTLVKQLS  3        0.5393
146.2     4.00  0.40     Sequence         WB
             DRB1_0802  963      QALNTLVKQLSSNFG  LNTLVKQLS  2        0.5704
104.4     2.50  0.32     Sequence         WB
             DRB1_0802  964      ALNTLVKQLSSNFGA  VKQLSSNFG  5        0.5886
85.8     1.70  0.25     Sequence         SB
             DRB1_0802  965      LNTLVKQLSSNFGAI  VKQLSSNFG  4        0.5784
95.8     2.00  0.26     Sequence         WB
             DRB1_0802  966      NTLVKQLSSNFGAIS  VKQLSSNFG  3        0.5560
122.0     3.00  0.33     Sequence         WB
             DRB1_0802  967      TLVKQLSSNFGAISS  VKQLSSNFG  2        0.5325
157.4     4.50  0.35     Sequence         WB
             DRB1_0802  968      LVKQLSSNFGAISSV  VKQLSSNFG  1        0.4567
357.1    13.00  0.40     Sequence
             DRB1_0802  969      VKQLSSNFGAISSVL  LSSNFGAIS  3        0.4061
617.5    21.00  0.42     Sequence
             DRB1_0802  970      KQLSSNFGAISSVLN  LSSNFGAIS  2        0.3655
958.1    31.00  0.41     Sequence
             DRB1_0802  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.3435
1215.6    37.00  0.47     Sequence
             DRB1_0802  972      LSSNFGAISSVLNDI  FGAISSVLN  4        0.3327
1366.5    40.00  0.55     Sequence
             DRB1_0802  973      SSNFGAISSVLNDIL  FGAISSVLN  3        0.3259
1471.4    42.00  0.56     Sequence
             DRB1_0802  974      SNFGAISSVLNDILS  FGAISSVLN  2        0.3313
1387.7    40.00  0.50     Sequence
             DRB1_0802  975      NFGAISSVLNDILSR  FGAISSVLN  1        0.3257
1473.3    42.00  0.38     Sequence
             DRB1_0802  976      FGAISSVLNDILSRL  ISSVLNDIL  3        0.2802
2410.6    60.00  0.35     Sequence
             DRB1_0802  977      GAISSVLNDILSRLD  ISSVLNDIL  2        0.2517
3282.3    65.00  0.34     Sequence
             DRB1_0802  978      AISSVLNDILSRLDK  ISSVLNDIL  1        0.2661
2810.1    60.00  0.24     Sequence
             DRB1_0802  979      ISSVLNDILSRLDKV  NDILSRLDK  5        0.2848
2293.7    55.00  0.23     Sequence
             DRB1_0802  980      SSVLNDILSRLDKVE  ILSRLDKVE  6        0.3519
1110.3    34.00  0.32     Sequence
             DRB1_0802  981      SVLNDILSRLDKVEA  LSRLDKVEA  6        0.4232
513.5    18.00  0.42     Sequence
             DRB1_0802  982      VLNDILSRLDKVEAE  LSRLDKVEA  5        0.4410
423.4    15.00  0.51     Sequence
             DRB1_0802  983      LNDILSRLDKVEAEV  LSRLDKVEA  4        0.4547
365.0    13.00  0.50     Sequence
             DRB1_0802  984      NDILSRLDKVEAEVQ  LSRLDKVEA  3        0.4573
354.8    12.00  0.55     Sequence
             DRB1_0802  985      DILSRLDKVEAEVQI  LSRLDKVEA  2        0.4454
403.6    14.00  0.54     Sequence
             DRB1_0802  986      ILSRLDKVEAEVQID  LSRLDKVEA  1        0.3774
842.4    28.00  0.50     Sequence
```

```
             DRB1_0802  987      LSRLDKVEAEVQIDR  LDKVEAEVQ  3        0.2691
2719.8    60.00  0.31     Sequence
             DRB1_0802  988      SRLDKVEAEVQIDRL  LDKVEAEVQ  2        0.2344
3956.8    70.00  0.34     Sequence
             DRB1_0802  989      RLDKVEAEVQIDRLI  VEAEVQIDR  4        0.2285
4219.4    75.00  0.35     Sequence
             DRB1_0802  990      LDKVEAEVQIDRLIT  VEAEVQIDR  3        0.2348
3939.5    70.00  0.34     Sequence
             DRB1_0802  991      DKVEAEVQIDRLITG  VQIDRLITG  6        0.2801
2415.4    60.00  0.34     Sequence
             DRB1_0802  992      KVEAEVQIDRLITGR  VQIDRLITG  5        0.3381
1289.7    38.00  0.39     Sequence
             DRB1_0802  993      VEAEVQIDRLITGRL  VQIDRLITG  4        0.3724
889.0    29.00  0.36     Sequence
             DRB1_0802  994      EAEVQIDRLITGRLQ  IDRLITGRL  5        0.3965
685.0    23.00  0.32     Sequence
             DRB1_0802  995      AEVQIDRLITGRLQS  IDRLITGRL  4        0.4142
565.6    20.00  0.31     Sequence
             DRB1_0802  996      EVQIDRLITGRLQSL  IDRLITGRL  3        0.4085
602.0    21.00  0.36     Sequence
             DRB1_0802  997      VQIDRLITGRLQSLQ  IDRLITGRL  2        0.3977
676.6    23.00  0.32     Sequence
             DRB1_0802  998      QIDRLITGRLQSLQT  IDRLITGRL  1        0.3752
863.1    28.00  0.27     Sequence
             DRB1_0802  999      IDRLITGRLQSLQTY  ITGRLQSLQ  4        0.3452
1193.9    36.00  0.23     Sequence
             DRB1_0802 1000      DRLITGRLQSLQTYV  ITGRLQSLQ  3        0.3388
1279.7    38.00  0.25     Sequence
             DRB1_0802 1001      RLITGRLQSLQTYVT  LQSLQTYVT  6        0.3525
1103.4    34.00  0.29     Sequence
             DRB1_0802 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.3535
1090.6    34.00  0.40     Sequence
             DRB1_0802 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.4225
517.4    18.00  0.35     Sequence
             DRB1_0802 1004      TGRLQSLQTYVTQQL  LQTYVTQQL  6        0.4657
324.1    11.00  0.49     Sequence
             DRB1_0802 1005      GRLQSLQTYVTQQLI  LQTYVTQQL  5        0.4688
313.4    11.00  0.55     Sequence
             DRB1_0802 1006      RLQSLQTYVTQQLIR  LQTYVTQQL  4        0.4702
308.8    11.00  0.62     Sequence
             DRB1_0802 1007      LQSLQTYVTQQLIRA  LQTYVTQQL  3        0.4654
325.3    11.00  0.61     Sequence
             DRB1_0802 1008      QSLQTYVTQQLIRAA  LQTYVTQQL  2        0.5210
178.1     5.50  0.47     Sequence         WB
             DRB1_0802 1009      SLQTYVTQQLIRAAE  LQTYVTQQL  1        0.5148
190.5     6.00  0.40     Sequence         WB
             DRB1_0802 1010      LQTYVTQQLIRAAEI  VTQQLIRAA  4        0.4448
406.4    14.00  0.44     Sequence
             DRB1_0802 1011      QTYVTQQLIRAAEIR  VTQQLIRAA  3        0.4564
358.4    13.00  0.48     Sequence
             DRB1_0802 1012      TYVTQQLIRAAEIRA  VTQQLIRAA  2        0.4689
313.1    11.00  0.42     Sequence
             DRB1_0802 1013      YVTQQLIRAAEIRAS  IRAAEIRAS  6        0.5063
208.8     6.50  0.32     Sequence         WB
             DRB1_0802 1014      VTQQLIRAAEIRASA  IRAAEIRAS  5        0.5195
181.2     5.50  0.47     Sequence         WB
             DRB1_0802 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.5048
212.3     6.50  0.60     Sequence         WB
             DRB1_0802 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.5200
180.1     5.50  0.58     Sequence         WB
             DRB1_0802 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.5450
137.5     4.00  0.50     Sequence         WB
             DRB1_0802 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.5455
136.7     3.50  0.35     Sequence         WB
             DRB1_0802 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.5191
181.9     5.50  0.57     Sequence         WB
```

```
             DRB1_0802 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.5122
195.9     6.00  0.80     Sequence         WB
             DRB1_0802 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.5121
196.1     6.00  0.81     Sequence         WB
             DRB1_0802 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.5106
199.5     6.00  0.82     Sequence         WB
             DRB1_0802 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.4808
275.2     9.00  0.75     Sequence         WB
             DRB1_0802 1024      IRASANLAAIKMSEC  IRASANLAA  0        0.3409
1250.6    37.00  0.29     Sequence
             DRB1_0802 1025      RASANLAAIKMSECV  LAAIKMSEC  5        0.2651
2839.0    60.00  0.44     Sequence
             DRB1_0802 1026      ASANLAAIKMSECVL  LAAIKMSEC  4        0.2989
1969.8    50.00  0.42     Sequence
             DRB1_0802 1027      SANLAAIKMSECVLG  IKMSECVLG  6        0.3633
981.8    31.00  0.44     Sequence
             DRB1_0802 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.4052
623.4    22.00  0.52     Sequence
             DRB1_0802 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.4049
626.0    22.00  0.60     Sequence
             DRB1_0802 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.4079
605.6    21.00  0.64     Sequence
             DRB1_0802 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.4160
554.9    19.00  0.63     Sequence
             DRB1_0802 1032      AIKMSECVLGQSKRV  IKMSECVLG  1        0.3835
788.8    26.00  0.57     Sequence
             DRB1_0802 1033      IKMSECVLGQSKRVD  MSECVLGQS  2        0.3052
1841.0    48.00  0.28     Sequence
             DRB1_0802 1034      KMSECVLGQSKRVDF  LGQSKRVDF  6        0.2959
2034.2    55.00  0.40     Sequence
             DRB1_0802 1035      MSECVLGQSKRVDFC  LGQSKRVDF  5        0.2662
2804.9    60.00  0.53     Sequence
             DRB1_0802 1036      SECVLGQSKRVDFCG  LGQSKRVDF  4        0.2756
2534.3    60.00  0.62     Sequence
             DRB1_0802 1037      ECVLGQSKRVDFCGK  LGQSKRVDF  3        0.2871
2239.0    55.00  0.62     Sequence
             DRB1_0802 1038      CVLGQSKRVDFCGKG  LGQSKRVDF  2        0.2916
2131.1    55.00  0.59     Sequence
             DRB1_0802 1039      VLGQSKRVDFCGKGY  LGQSKRVDF  1        0.2664
2800.7    60.00  0.57     Sequence
             DRB1_0802 1040      LGQSKRVDFCGKGYH  VDFCGKGYH  6        0.1939
6134.0    85.00  0.29     Sequence
             DRB1_0802 1041      GQSKRVDFCGKGYHL  VDFCGKGYH  5        0.1600
8850.2    90.00  0.45     Sequence
             DRB1_0802 1042      QSKRVDFCGKGYHLM  VDFCGKGYH  4        0.1681
8110.3    90.00  0.41     Sequence
             DRB1_0802 1043      SKRVDFCGKGYHLMS  VDFCGKGYH  3        0.1773
7342.7    85.00  0.40     Sequence
             DRB1_0802 1044      KRVDFCGKGYHLMSF  VDFCGKGYH  2        0.1762
7427.9    85.00  0.37     Sequence
             DRB1_0802 1045      RVDFCGKGYHLMSFP  VDFCGKGYH  1        0.1680
8119.8    90.00  0.33     Sequence
             DRB1_0802 1046      VDFCGKGYHLMSFPQ  YHLMSFPQX  7        0.2089
5214.2    80.00  0.28     Sequence
             DRB1_0802 1047      DFCGKGYHLMSFPQS  YHLMSFPQS  6        0.2790
2443.4    60.00  0.47     Sequence
             DRB1_0802 1048      FCGKGYHLMSFPQSA  YHLMSFPQS  5        0.3971
680.6    23.00  0.40     Sequence
             DRB1_0802 1049      CGKGYHLMSFPQSAP  YHLMSFPQS  4        0.4302
475.9    17.00  0.34     Sequence
             DRB1_0802 1050      GKGYHLMSFPQSAPH  LMSFPQSAP  5        0.4590
348.6    12.00  0.36     Sequence
             DRB1_0802 1051      KGYHLMSFPQSAPHG  LMSFPQSAP  4        0.4714
304.6    11.00  0.41     Sequence
             DRB1_0802 1052      GYHLMSFPQSAPHGV  LMSFPQSAP  3        0.4506
381.8    13.00  0.44     Sequence
```

```
             DRB1_0802 1053      YHLMSFPQSAPHGVV  LMSFPQSAP  2        0.3832
791.2    26.00  0.54     Sequence
             DRB1_0802 1054      HLMSFPQSAPHGVVF  LMSFPQSAP  1        0.3249
1487.6    42.00  0.57     Sequence
             DRB1_0802 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.1642
8462.5    90.00  0.35     Sequence
             DRB1_0802 1056      MSFPQSAPHGVVFLH  FPQSAPHGV  2        0.1354
11550.5    95.00  0.44     Sequence
             DRB1_0802 1057      SFPQSAPHGVVFLHV  FPQSAPHGV  1        0.1187
13845.9    95.00  0.39     Sequence
             DRB1_0802 1058      FPQSAPHGVVFLHVT  HGVVFLHVT  6        0.1108
15069.5   100.00  0.19     Sequence
             DRB1_0802 1059      PQSAPHGVVFLHVTY  HGVVFLHVT  5        0.1360
11482.4    95.00  0.17     Sequence
             DRB1_0802 1060      QSAPHGVVFLHVTYV  VVFLHVTYV  6        0.2211
4570.9    75.00  0.34     Sequence
             DRB1_0802 1061      SAPHGVVFLHVTYVP  VVFLHVTYV  5        0.2782
2465.5    60.00  0.32     Sequence
             DRB1_0802 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.3905
731.0    25.00  0.41     Sequence
             DRB1_0802 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.4603
343.7    12.00  0.36     Sequence
             DRB1_0802 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.5082
204.7     6.50  0.35     Sequence         WB
             DRB1_0802 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.5504
129.6     3.50  0.32     Sequence         WB
             DRB1_0802 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.5494
131.0     3.50  0.30     Sequence         WB
             DRB1_0802 1067      VFLHVTYVPAQEKNF  FLHVTYVPA  1        0.5259
169.0     5.00  0.28     Sequence         WB
             DRB1_0802 1068      FLHVTYVPAQEKNFT  VTYVPAQEK  3        0.4920
243.8     8.00  0.29     Sequence         WB
             DRB1_0802 1069      LHVTYVPAQEKNFTT  VTYVPAQEK  2        0.4044
628.8    22.00  0.42     Sequence
             DRB1_0802 1070      HVTYVPAQEKNFTTA  VTYVPAQEK  1        0.3281
1436.2    41.00  0.51     Sequence
             DRB1_0802 1071      VTYVPAQEKNFTTAP  VPAQEKNFT  3        0.2351
3927.0    70.00  0.38     Sequence
             DRB1_0802 1072      TYVPAQEKNFTTAPA  VPAQEKNFT  2        0.2290
4198.6    75.00  0.37     Sequence
             DRB1_0802 1073      YVPAQEKNFTTAPAI  EKNFTTAPA  5        0.2509
3311.4    65.00  0.31     Sequence
             DRB1_0802 1074      VPAQEKNFTTAPAIC  FTTAPAICX  7        0.3018
1909.8    49.00  0.31     Sequence
             DRB1_0802 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.3866
762.3    26.00  0.61     Sequence
             DRB1_0802 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.3963
687.1    23.00  0.64     Sequence
             DRB1_0802 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.4097
593.7    21.00  0.69     Sequence
             DRB1_0802 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.4132
572.2    20.00  0.77     Sequence
             DRB1_0802 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.4006
655.3    23.00  0.83     Sequence
             DRB1_0802 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.3382
1287.2    38.00  0.71     Sequence
             DRB1_0802 1081      FTTAPAICHDGKAHF  ICHDGKAHF  6        0.2749
2555.1    60.00  0.53     Sequence
             DRB1_0802 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.2443
3555.1    70.00  0.73     Sequence
             DRB1_0802 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.2666
2795.1    60.00  0.76     Sequence
             DRB1_0802 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.2708
2669.8    60.00  0.76     Sequence
             DRB1_0802 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.2705
2679.0    60.00  0.75     Sequence
```

```
             DRB1_0802 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.2528
3242.6    65.00  0.66     Sequence
             DRB1_0802 1087      ICHDGKAHFPREGVF  ICHDGKAHF  0        0.1649
8392.5    90.00  0.25     Sequence
             DRB1_0802 1088      CHDGKAHFPREGVFV  KAHFPREGV  4        0.1317
12020.1    95.00  0.34     Sequence
             DRB1_0802 1089      HDGKAHFPREGVFVS  FPREGVFVS  6        0.1739
7617.9    90.00  0.39     Sequence
             DRB1_0802 1090      DGKAHFPREGVFVSN  FPREGVFVS  5        0.1925
6227.4    85.00  0.44     Sequence
             DRB1_0802 1091      GKAHFPREGVFVSNG  FPREGVFVS  4        0.2093
5192.9    80.00  0.44     Sequence
             DRB1_0802 1092      KAHFPREGVFVSNGT  FPREGVFVS  3        0.2174
4757.8    75.00  0.44     Sequence
             DRB1_0802 1093      AHFPREGVFVSNGTH  FPREGVFVS  2        0.2378
3817.0    70.00  0.35     Sequence
             DRB1_0802 1094      HFPREGVFVSNGTHW  VFVSNGTHW  6        0.2781
2466.4    60.00  0.28     Sequence
             DRB1_0802 1095      FPREGVFVSNGTHWF  VFVSNGTHW  5        0.2941
2075.0    55.00  0.32     Sequence
             DRB1_0802 1096      PREGVFVSNGTHWFV  VFVSNGTHW  4        0.3219
1535.3    43.00  0.31     Sequence
             DRB1_0802 1097      REGVFVSNGTHWFVT  VFVSNGTHW  3        0.3383
1286.6    38.00  0.31     Sequence
             DRB1_0802 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.3423
1232.0    37.00  0.28     Sequence
             DRB1_0802 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.3348
1336.0    39.00  0.28     Sequence
             DRB1_0802 1100      VFVSNGTHWFVTQRN  VSNGTHWFV  2        0.2868
2245.7    55.00  0.32     Sequence
             DRB1_0802 1101      FVSNGTHWFVTQRNF  VSNGTHWFV  1        0.2444
3552.9    70.00  0.31     Sequence
             DRB1_0802 1102      VSNGTHWFVTQRNFY  FVTQRNFYX  7        0.2531
3234.6    65.00  0.25     Sequence
             DRB1_0802 1103      SNGTHWFVTQRNFYE  FVTQRNFYE  6        0.3084
1778.4    47.00  0.50     Sequence
             DRB1_0802 1104      NGTHWFVTQRNFYEP  FVTQRNFYE  5        0.3452
1193.2    36.00  0.53     Sequence
             DRB1_0802 1105      GTHWFVTQRNFYEPQ  FVTQRNFYE  4        0.3689
923.6    30.00  0.58     Sequence
             DRB1_0802 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3        0.3662
951.6    31.00  0.61     Sequence
             DRB1_0802 1107      HWFVTQRNFYEPQII  FVTQRNFYE  2        0.3706
907.2    30.00  0.62     Sequence
             DRB1_0802 1108      WFVTQRNFYEPQIIT  FVTQRNFYE  1        0.3419
1237.2    37.00  0.60     Sequence
             DRB1_0802 1109      FVTQRNFYEPQIITT  FVTQRNFYE  0        0.2327
4030.4    70.00  0.31     Sequence
             DRB1_0802 1110      VTQRNFYEPQIITTD  QRNFYEPQI  2        0.1317
12022.3    95.00  0.19     Sequence
             DRB1_0802 1111      TQRNFYEPQIITTDN  YEPQIITTD  5        0.1386
11165.0    95.00  0.25     Sequence
             DRB1_0802 1112      QRNFYEPQIITTDNT  YEPQIITTD  4        0.1641
8468.5    90.00  0.20     Sequence
             DRB1_0802 1113      RNFYEPQIITTDNTF  IITTDNTFX  7        0.2852
2284.6    55.00  0.38     Sequence
             DRB1_0802 1114      NFYEPQIITTDNTFV  IITTDNTFV  6        0.4186
539.3    19.00  0.70     Sequence
             DRB1_0802 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.4980
228.5     7.50  0.68     Sequence         WB
             DRB1_0802 1116      YEPQIITTDNTFVSG  IITTDNTFV  4        0.5390
146.6     4.00  0.65     Sequence         WB
             DRB1_0802 1117      EPQIITTDNTFVSGN  IITTDNTFV  3        0.5591
118.0     3.00  0.64     Sequence         WB
             DRB1_0802 1118      PQIITTDNTFVSGNC  IITTDNTFV  2        0.5685
106.5     2.50  0.64     Sequence         WB
```

```
             DRB1_0802 1119      QIITTDNTFVSGNCD  IITTDNTFV  1        0.5409
143.6     4.00  0.64     Sequence         WB
             DRB1_0802 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.3338
1350.4    39.00  0.50     Sequence
             DRB1_0802 1121      ITTDNTFVSGNCDVV  ITTDNTFVS  0        0.1291
12368.4    95.00  0.25     Sequence
             DRB1_0802 1122      TTDNTFVSGNCDVVI  VSGNCDVVI  6        0.1084
15468.8   100.00  0.25     Sequence
             DRB1_0802 1123      TDNTFVSGNCDVVIG  VSGNCDVVI  5        0.1213
13454.4    95.00  0.30     Sequence
             DRB1_0802 1124      DNTFVSGNCDVVIGI  VSGNCDVVI  4        0.1255
12857.5    95.00  0.28     Sequence
             DRB1_0802 1125      NTFVSGNCDVVIGIV  VSGNCDVVI  3        0.1516
9695.3    90.00  0.25     Sequence
             DRB1_0802 1126      TFVSGNCDVVIGIVN  CDVVIGIVN  6        0.1543
9418.0    90.00  0.23     Sequence
             DRB1_0802 1127      FVSGNCDVVIGIVNN  DVVIGIVNN  6        0.1901
6392.5    85.00  0.22     Sequence
             DRB1_0802 1128      VSGNCDVVIGIVNNT  DVVIGIVNN  5        0.2406
3700.3    70.00  0.20     Sequence
             DRB1_0802 1129      SGNCDVVIGIVNNTV  IGIVNNTVX  7        0.3299
1409.2    41.00  0.30     Sequence
             DRB1_0802 1130      GNCDVVIGIVNNTVY  IGIVNNTVY  6        0.3420
1235.8    37.00  0.37     Sequence
             DRB1_0802 1131      NCDVVIGIVNNTVYD  IGIVNNTVY  5        0.3407
1253.1    37.00  0.34     Sequence
             DRB1_0802 1132      CDVVIGIVNNTVYDP  IGIVNNTVY  4        0.3467
1173.9    36.00  0.33     Sequence
             DRB1_0802 1133      DVVIGIVNNTVYDPL  IGIVNNTVY  3        0.3469
1172.1    36.00  0.36     Sequence
             DRB1_0802 1134      VVIGIVNNTVYDPLQ  IGIVNNTVY  2        0.3437
1212.9    37.00  0.35     Sequence
             DRB1_0802 1135      VIGIVNNTVYDPLQP  IGIVNNTVY  1        0.3100
1747.3    46.00  0.35     Sequence
             DRB1_0802 1136      IGIVNNTVYDPLQPE  IVNNTVYDP  2        0.2472
3447.4    70.00  0.34     Sequence
             DRB1_0802 1137      GIVNNTVYDPLQPEL  IVNNTVYDP  1        0.2222
4515.1    75.00  0.37     Sequence
             DRB1_0802 1138      IVNNTVYDPLQPELD  NTVYDPLQP  3        0.1517
9687.8    90.00  0.27     Sequence
             DRB1_0802 1139      VNNTVYDPLQPELDS  NTVYDPLQP  2        0.1464
10252.3    95.00  0.31     Sequence
             DRB1_0802 1140      NNTVYDPLQPELDSF  NTVYDPLQP  1        0.1497
9895.6    90.00  0.23     Sequence
             DRB1_0802 1141      NTVYDPLQPELDSFK  LQPELDSFK  6        0.1689
8044.1    90.00  0.50     Sequence
             DRB1_0802 1142      TVYDPLQPELDSFKE  LQPELDSFK  5        0.1759
7454.0    85.00  0.56     Sequence
             DRB1_0802 1143      VYDPLQPELDSFKEE  LQPELDSFK  4        0.1725
7731.0    90.00  0.60     Sequence
             DRB1_0802 1144      YDPLQPELDSFKEEL  LQPELDSFK  3        0.1811
7046.4    85.00  0.57     Sequence
             DRB1_0802 1145      DPLQPELDSFKEELD  LQPELDSFK  2        0.1800
7128.7    85.00  0.56     Sequence
             DRB1_0802 1146      PLQPELDSFKEELDK  LQPELDSFK  1        0.1805
7093.1    85.00  0.49     Sequence
             DRB1_0802 1147      LQPELDSFKEELDKY  LDSFKEELD  4        0.1493
9944.6    95.00  0.28     Sequence
             DRB1_0802 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.1696
7980.7    90.00  0.48     Sequence
             DRB1_0802 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.2068
5335.4    80.00  0.55     Sequence
             DRB1_0802 1150      ELDSFKEELDKYFKN  FKEELDKYF  4        0.2190
4675.3    75.00  0.56     Sequence
             DRB1_0802 1151      LDSFKEELDKYFKNH  FKEELDKYF  3        0.2496
3359.2    65.00  0.49     Sequence
```

```
             DRB1_0802 1152      DSFKEELDKYFKNHT  LDKYFKNHT  6        0.3030
1885.2    49.00  0.37     Sequence
             DRB1_0802 1153      SFKEELDKYFKNHTS  LDKYFKNHT  5        0.3450
1196.7    36.00  0.35     Sequence
             DRB1_0802 1154      FKEELDKYFKNHTSP  LDKYFKNHT  4        0.3308
1394.2    40.00  0.41     Sequence
             DRB1_0802 1155      KEELDKYFKNHTSPD  LDKYFKNHT  3        0.3294
1415.9    41.00  0.38     Sequence
             DRB1_0802 1156      EELDKYFKNHTSPDV  FKNHTSPDV  6        0.3665
947.8    31.00  0.36     Sequence
             DRB1_0802 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.3636
978.1    31.00  0.42     Sequence
             DRB1_0802 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.3293
1417.7    41.00  0.54     Sequence
             DRB1_0802 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.3127
1697.2    46.00  0.69     Sequence
             DRB1_0802 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.3040
1865.0    48.00  0.75     Sequence
             DRB1_0802 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.2501
3339.8    65.00  0.77     Sequence
             DRB1_0802 1162      FKNHTSPDVDLGDIS  FKNHTSPDV  0        0.1316
12032.6    95.00  0.40     Sequence
             DRB1_0802 1163      KNHTSPDVDLGDISG  DVDLGDISG  6        0.0591
26367.2   100.00  0.28     Sequence
             DRB1_0802 1164      NHTSPDVDLGDISGI  VDLGDISGI  6        0.0824
20511.9   100.00  0.34     Sequence
             DRB1_0802 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.1101
15194.7   100.00  0.34     Sequence
             DRB1_0802 1166      TSPDVDLGDISGINA  LGDISGINA  6        0.1629
8584.2    90.00  0.50     Sequence
             DRB1_0802 1167      SPDVDLGDISGINAS  LGDISGINA  5        0.1982
5857.1    80.00  0.52     Sequence
             DRB1_0802 1168      PDVDLGDISGINASF  LGDISGINA  4        0.2187
4693.4    75.00  0.50     Sequence
             DRB1_0802 1169      DVDLGDISGINASFV  LGDISGINA  3        0.2273
4275.7    75.00  0.47     Sequence
             DRB1_0802 1170      VDLGDISGINASFVN  LGDISGINA  2        0.2304
4133.9    75.00  0.47     Sequence
             DRB1_0802 1171      DLGDISGINASFVNI  LGDISGINA  1        0.2293
4184.2    75.00  0.41     Sequence
             DRB1_0802 1172      LGDISGINASFVNIQ  INASFVNIQ  6        0.2862
2259.0    55.00  0.30     Sequence
             DRB1_0802 1173      GDISGINASFVNIQK  INASFVNIQ  5        0.3289
1423.9    41.00  0.32     Sequence
             DRB1_0802 1174      DISGINASFVNIQKE  INASFVNIQ  4        0.3242
1498.7    42.00  0.34     Sequence
             DRB1_0802 1175      ISGINASFVNIQKEI  INASFVNIQ  3        0.3278
1440.7    41.00  0.34     Sequence
             DRB1_0802 1176      SGINASFVNIQKEID  INASFVNIQ  2        0.3425
1229.3    37.00  0.33     Sequence
             DRB1_0802 1177      GINASFVNIQKEIDR  INASFVNIQ  1        0.3444
1203.8    36.00  0.26     Sequence
             DRB1_0802 1178      INASFVNIQKEIDRL  VNIQKEIDR  5        0.3508
1123.7    35.00  0.27     Sequence
             DRB1_0802 1179      NASFVNIQKEIDRLN  IQKEIDRLN  6        0.3856
770.9    26.00  0.37     Sequence
             DRB1_0802 1180      ASFVNIQKEIDRLNE  IQKEIDRLN  5        0.4046
628.0    22.00  0.41     Sequence
             DRB1_0802 1181      SFVNIQKEIDRLNEV  IQKEIDRLN  4        0.4158
555.9    19.00  0.40     Sequence
             DRB1_0802 1182      FVNIQKEIDRLNEVA  IQKEIDRLN  3        0.4240
508.7    18.00  0.42     Sequence
             DRB1_0802 1183      VNIQKEIDRLNEVAK  IQKEIDRLN  2        0.4016
648.5    22.00  0.46     Sequence
             DRB1_0802 1184      NIQKEIDRLNEVAKN  IQKEIDRLN  1        0.3852
774.1    26.00  0.43     Sequence
```

```
             DRB1_0802 1185      IQKEIDRLNEVAKNL  IDRLNEVAK  4        0.3255
1476.8    42.00  0.31     Sequence
             DRB1_0802 1186      QKEIDRLNEVAKNLN  IDRLNEVAK  3        0.2777
2477.2    60.00  0.44     Sequence
             DRB1_0802 1187      KEIDRLNEVAKNLNE  IDRLNEVAK  2        0.2850
2288.8    55.00  0.38     Sequence
             DRB1_0802 1188      EIDRLNEVAKNLNES  LNEVAKNLN  4        0.2897
2175.4    55.00  0.26     Sequence
             DRB1_0802 1189      IDRLNEVAKNLNESL  VAKNLNESL  6        0.3021
1903.8    49.00  0.35     Sequence
             DRB1_0802 1190      DRLNEVAKNLNESLI  VAKNLNESL  5        0.3122
1705.9    46.00  0.40     Sequence
             DRB1_0802 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.3020
1905.0    49.00  0.42     Sequence
             DRB1_0802 1192      LNEVAKNLNESLIDL  VAKNLNESL  3        0.2749
2553.5    60.00  0.52     Sequence
             DRB1_0802 1193      NEVAKNLNESLIDLQ  VAKNLNESL  2        0.2684
2741.2    60.00  0.51     Sequence
             DRB1_0802 1194      EVAKNLNESLIDLQE  VAKNLNESL  1        0.2605
2984.6    65.00  0.43     Sequence
             DRB1_0802 1195      VAKNLNESLIDLQEL  LNESLIDLQ  4        0.2137
4950.1    80.00  0.32     Sequence
             DRB1_0802 1196      AKNLNESLIDLQELG  LNESLIDLQ  3        0.1938
6140.5    85.00  0.37     Sequence
             DRB1_0802 1197      KNLNESLIDLQELGK  LNESLIDLQ  2        0.2004
5720.4    80.00  0.35     Sequence
             DRB1_0802 1198      NLNESLIDLQELGKY  LNESLIDLQ  1        0.1947
6079.9    85.00  0.33     Sequence
             DRB1_0802 1199      LNESLIDLQELGKYE  NESLIDLQE  1        0.1671
8201.9    90.00  0.22     Sequence
             DRB1_0802 1200      NESLIDLQELGKYEQ  LQELGKYEQ  6        0.1467
10229.4    95.00  0.26     Sequence
             DRB1_0802 1201      ESLIDLQELGKYEQY  LQELGKYEQ  5        0.1510
9761.5    90.00  0.34     Sequence
             DRB1_0802 1202      SLIDLQELGKYEQYI  LQELGKYEQ  4        0.1768
7380.9    85.00  0.31     Sequence
             DRB1_0802 1203      LIDLQELGKYEQYIK  LGKYEQYIK  6        0.1967
5953.4    80.00  0.31     Sequence
             DRB1_0802 1204      IDLQELGKYEQYIKW  LGKYEQYIK  5        0.2067
5339.2    80.00  0.34     Sequence
             DRB1_0802 1205      DLQELGKYEQYIKWP  LGKYEQYIK  4        0.2419
3650.7    70.00  0.31     Sequence
             DRB1_0802 1206      LQELGKYEQYIKWPW  YEQYIKWPW  6        0.2756
2535.0    60.00  0.32     Sequence
             DRB1_0802 1207      QELGKYEQYIKWPWY  YEQYIKWPW  5        0.2972
2007.3    50.00  0.34     Sequence
             DRB1_0802 1208      ELGKYEQYIKWPWYI  YEQYIKWPW  4        0.3173
1615.0    44.00  0.31     Sequence
             DRB1_0802 1209      LGKYEQYIKWPWYIW  YEQYIKWPW  3        0.3114
1720.1    46.00  0.36     Sequence
             DRB1_0802 1210      GKYEQYIKWPWYIWL  YEQYIKWPW  2        0.3207
1555.9    43.00  0.32     Sequence
             DRB1_0802 1211      KYEQYIKWPWYIWLG  YIKWPWYIW  4        0.3189
1586.4    44.00  0.28     Sequence
             DRB1_0802 1212      YEQYIKWPWYIWLGF  YIKWPWYIW  3        0.2974
2002.8    50.00  0.34     Sequence
             DRB1_0802 1213      EQYIKWPWYIWLGFI  YIKWPWYIW  2        0.2941
2074.7    55.00  0.37     Sequence
             DRB1_0802 1214      QYIKWPWYIWLGFIA  YIKWPWYIW  1        0.2933
2094.1    55.00  0.32     Sequence
             DRB1_0802 1215      YIKWPWYIWLGFIAG  WYIWLGFIA  5        0.2586
3048.0    65.00  0.25     Sequence
             DRB1_0802 1216      IKWPWYIWLGFIAGL  WYIWLGFIA  4        0.2518
3277.8    65.00  0.29     Sequence
             DRB1_0802 1217      KWPWYIWLGFIAGLI  WYIWLGFIA  3        0.2556
3148.0    65.00  0.30     Sequence
```

```
             DRB1_0802 1218      WPWYIWLGFIAGLIA  WYIWLGFIA  2        0.2506
3323.3    65.00  0.26     Sequence
             DRB1_0802 1219      PWYIWLGFIAGLIAI  LGFIAGLIA  5        0.2732
2601.7    60.00  0.22     Sequence
             DRB1_0802 1220      WYIWLGFIAGLIAIV  FIAGLIAIV  6        0.2887
2200.7    55.00  0.23     Sequence
             DRB1_0802 1221      YIWLGFIAGLIAIVM  FIAGLIAIV  5        0.2776
2481.6    60.00  0.28     Sequence
             DRB1_0802 1222      IWLGFIAGLIAIVMV  FIAGLIAIV  4        0.2656
2824.2    60.00  0.31     Sequence
             DRB1_0802 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3        0.2600
2999.2    65.00  0.32     Sequence
             DRB1_0802 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.2613
2957.4    65.00  0.31     Sequence
             DRB1_0802 1225      GFIAGLIAIVMVTIM  FIAGLIAIV  1        0.2533
3226.1    65.00  0.31     Sequence
             DRB1_0802 1226      FIAGLIAIVMVTIML  LIAIVMVTI  4        0.2130
4990.9    80.00  0.17     Sequence
             DRB1_0802 1227      IAGLIAIVMVTIMLC  IVMVTIMLC  6        0.1981
5862.5    80.00  0.31     Sequence
             DRB1_0802 1228      AGLIAIVMVTIMLCC  IVMVTIMLC  5        0.1956
6025.8    80.00  0.34     Sequence
             DRB1_0802 1229      GLIAIVMVTIMLCCM  IVMVTIMLC  4        0.1980
5870.4    80.00  0.36     Sequence
             DRB1_0802 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3        0.1632
8554.7    90.00  0.46     Sequence
             DRB1_0802 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2        0.1897
6419.3    85.00  0.40     Sequence
             DRB1_0802 1232      AIVMVTIMLCCMTSC  IVMVTIMLC  1        0.2082
5258.1    80.00  0.33     Sequence
             DRB1_0802 1233      IVMVTIMLCCMTSCC  IMLCCMTSC  5        0.1813
7029.8    85.00  0.27     Sequence
             DRB1_0802 1234      VMVTIMLCCMTSCCS  IMLCCMTSC  4        0.1814
7026.7    85.00  0.34     Sequence
             DRB1_0802 1235      MVTIMLCCMTSCCSC  IMLCCMTSC  3        0.1791
7199.2    85.00  0.35     Sequence
             DRB1_0802 1236      VTIMLCCMTSCCSCL  IMLCCMTSC  2        0.1729
7704.3    90.00  0.38     Sequence
             DRB1_0802 1237      TIMLCCMTSCCSCLK  IMLCCMTSC  1        0.1631
8562.1    90.00  0.34     Sequence
             DRB1_0802 1238      IMLCCMTSCCSCLKG  MTSCCSCLK  5        0.1295
12314.6    95.00  0.31     Sequence
             DRB1_0802 1239      MLCCMTSCCSCLKGC  MTSCCSCLK  4        0.1003
16887.5   100.00  0.35     Sequence
             DRB1_0802 1240      LCCMTSCCSCLKGCC  MTSCCSCLK  3        0.0873
19434.2   100.00  0.47     Sequence
             DRB1_0802 1241      CCMTSCCSCLKGCCS  MTSCCSCLK  2        0.0760
21980.9   100.00  0.50     Sequence
             DRB1_0802 1242      CMTSCCSCLKGCCSC  MTSCCSCLK  1        0.0684
23860.7   100.00  0.47     Sequence
             DRB1_0802 1243      MTSCCSCLKGCCSCG  LKGCCSCGX  7        0.0605
25983.7   100.00  0.28     Sequence
             DRB1_0802 1244      TSCCSCLKGCCSCGS  LKGCCSCGS  6        0.0808
20861.9   100.00  0.54     Sequence
             DRB1_0802 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5        0.0836
20243.8   100.00  0.55     Sequence
             DRB1_0802 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.0782
21446.5   100.00  0.57     Sequence
             DRB1_0802 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.0764
21879.1   100.00  0.64     Sequence
             DRB1_0802 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2        0.0756
22075.3   100.00  0.65     Sequence
             DRB1_0802 1249      CLKGCCSCGSCCKFD  LKGCCSCGS  1        0.0627
25373.1   100.00  0.62     Sequence
             DRB1_0802 1250      LKGCCSCGSCCKFDE  LKGCCSCGS  0        0.0351
34200.0   100.00  0.31     Sequence
```

```
             DRB1_0802 1251      KGCCSCGSCCKFDED  CGSCCKFDE  5        0.0237
38694.7   100.00  0.31     Sequence
             DRB1_0802 1252      GCCSCGSCCKFDEDD  CGSCCKFDE  4        0.0228
39079.7   100.00  0.29     Sequence
             DRB1_0802 1253      CCSCGSCCKFDEDDS  CGSCCKFDE  3        0.0243
38438.5   100.00  0.31     Sequence
             DRB1_0802 1254      CSCGSCCKFDEDDSE  CGSCCKFDE  2        0.0278
37006.9   100.00  0.26     Sequence
             DRB1_0802 1255      SCGSCCKFDEDDSEP  CKFDEDDSE  5        0.0328
35074.7   100.00  0.23     Sequence
             DRB1_0802 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.0447
30841.3   100.00  0.43     Sequence
             DRB1_0802 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.0539
27907.4   100.00  0.42     Sequence
             DRB1_0802 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.0638
25081.3   100.00  0.43     Sequence
             DRB1_0802 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.0728
22745.9   100.00  0.40     Sequence
             DRB1_0802 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.0750
22214.0   100.00  0.39     Sequence
             DRB1_0802 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.0894
18996.6   100.00  0.29     Sequence
             DRB1_0802 1262      FDEDDSEPVLKGVKL  EPVLKGVKL  6        0.0970
17510.6   100.00  0.28     Sequence
             DRB1_0802 1263      DEDDSEPVLKGVKLH  VLKGVKLHX  7        0.1722
7759.9    90.00  0.36     Sequence
             DRB1_0802 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.2756
2534.1    60.00  0.44     Sequence
             DRB1_0802 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.3811
809.8    27.00  0.52     Sequence
             DRB1_0901    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.3228
1521.2    60.00  0.67     Sequence
             DRB1_0901    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.3098
1751.0    65.00  0.57     Sequence
             DRB1_0901    3      PIKEMFVFLVLLPLV  IKEMFVFLV  1        0.2944
2067.7    70.00  0.56     Sequence
             DRB1_0901    4      IKEMFVFLVLLPLVS  IKEMFVFLV  0        0.2672
2777.1    75.00  0.32     Sequence
             DRB1_0901    5      KEMFVFLVLLPLVSS  FLVLLPLVS  5        0.2190
4675.9    85.00  0.34     Sequence
             DRB1_0901    6      EMFVFLVLLPLVSSQ  FLVLLPLVS  4        0.2482
3409.3    80.00  0.28     Sequence
             DRB1_0901    7      MFVFLVLLPLVSSQC  LLPLVSSQC  6        0.3372
1301.5    55.00  0.52     Sequence
             DRB1_0901    8      FVFLVLLPLVSSQCV  LLPLVSSQC  5        0.3957
691.5    40.00  0.51     Sequence
             DRB1_0901    9      VFLVLLPLVSSQCVN  LLPLVSSQC  4        0.4159
555.5    35.00  0.46     Sequence
             DRB1_0901   10      FLVLLPLVSSQCVNF  LVSSQCVNF  6        0.5132
193.8    17.00  0.49     Sequence
             DRB1_0901   11      LVLLPLVSSQCVNFT  LVSSQCVNF  5        0.5359
151.7    14.00  0.54     Sequence
             DRB1_0901   12      VLLPLVSSQCVNFTN  LVSSQCVNF  4        0.5264
168.0    15.00  0.56     Sequence
             DRB1_0901   13      LLPLVSSQCVNFTNR  LVSSQCVNF  3        0.4865
258.7    21.00  0.63     Sequence
             DRB1_0901   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.4534
370.3    27.00  0.75     Sequence
             DRB1_0901   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.4331
461.2    31.00  0.71     Sequence
             DRB1_0901   16      LVSSQCVNFTNRTQL  LVSSQCVNF  0        0.3749
865.3    45.00  0.35     Sequence
             DRB1_0901   17      VSSQCVNFTNRTQLP  VNFTNRTQL  5        0.2891
2191.4    70.00  0.48     Sequence
             DRB1_0901   18      SSQCVNFTNRTQLPS  VNFTNRTQL  4        0.3002
1941.9    65.00  0.47     Sequence
```

```
             DRB1_0901   19      SQCVNFTNRTQLPSA  VNFTNRTQL  3         0.3084
1777.2    65.00  0.46     Sequence
             DRB1_0901   20      QCVNFTNRTQLPSAY  VNFTNRTQL  2         0.3349
1334.3    55.00  0.34     Sequence
             DRB1_0901   21      CVNFTNRTQLPSAYT  NRTQLPSAY  5         0.3337
1351.3    55.00  0.27     Sequence
             DRB1_0901   22      VNFTNRTQLPSAYTN  NRTQLPSAY  4         0.3168
1622.2    60.00  0.29     Sequence
             DRB1_0901   23      NFTNRTQLPSAYTNS  NRTQLPSAY  3         0.3081
1783.8    65.00  0.38     Sequence
             DRB1_0901   24      FTNRTQLPSAYTNSF  RTQLPSAYT  3         0.2975
1999.7    65.00  0.31     Sequence
             DRB1_0901   25      TNRTQLPSAYTNSFT  RTQLPSAYT  2         0.3124
1702.5    65.00  0.30     Sequence
             DRB1_0901   26      NRTQLPSAYTNSFTR  RTQLPSAYT  1         0.2848
2295.8    70.00  0.26     Sequence
             DRB1_0901   27      RTQLPSAYTNSFTRG  SAYTNSFTR  5         0.2660
2811.7    75.00  0.29     Sequence
             DRB1_0901   28      TQLPSAYTNSFTRGV  YTNSFTRGV  6         0.5271
166.9    15.00  0.83     Sequence
             DRB1_0901   29      QLPSAYTNSFTRGVY  YTNSFTRGV  5         0.5749
99.5     9.00  0.87     Sequence         WB
             DRB1_0901   30      LPSAYTNSFTRGVYY  YTNSFTRGV  4         0.5951
79.9     7.00  0.86     Sequence         WB
             DRB1_0901   31      PSAYTNSFTRGVYYP  YTNSFTRGV  3         0.5805
93.6     8.50  0.87     Sequence         WB
             DRB1_0901   32      SAYTNSFTRGVYYPD  YTNSFTRGV  2         0.5638
112.1    10.00  0.77     Sequence
             DRB1_0901   33      AYTNSFTRGVYYPDK  YTNSFTRGV  1         0.5349
153.3    14.00  0.68     Sequence
             DRB1_0901   34      YTNSFTRGVYYPDKV  YTNSFTRGV  0         0.4635
332.0    25.00  0.44     Sequence
             DRB1_0901   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3         0.3864
764.2    42.00  0.41     Sequence
             DRB1_0901   36      NSFTRGVYYPDKVFR  FTRGVYYPD  2         0.4002
658.6    39.00  0.35     Sequence
             DRB1_0901   37      SFTRGVYYPDKVFRS  YYPDKVFRS  6         0.4384
435.5    30.00  0.32     Sequence
             DRB1_0901   38      FTRGVYYPDKVFRSS  YYPDKVFRS  5         0.4307
473.1    32.00  0.47     Sequence
             DRB1_0901   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4         0.4289
482.8    32.00  0.56     Sequence
             DRB1_0901   40      RGVYYPDKVFRSSVL  DKVFRSSVL  6         0.5151
190.0    16.00  0.47     Sequence
             DRB1_0901   41      GVYYPDKVFRSSVLH  DKVFRSSVL  5         0.4784
282.4    22.00  0.48     Sequence
             DRB1_0901   42      VYYPDKVFRSSVLHS  VFRSSVLHS  6         0.5412
143.2    13.00  0.34     Sequence
             DRB1_0901   43      YYPDKVFRSSVLHST  FRSSVLHST  6         0.6110
67.3     6.00  0.41     Sequence         WB
             DRB1_0901   44      YPDKVFRSSVLHSTQ  FRSSVLHST  5         0.6342
52.3     4.50  0.46     Sequence         WB
             DRB1_0901   45      PDKVFRSSVLHSTQD  FRSSVLHST  4         0.6320
53.6     4.50  0.51     Sequence         WB
             DRB1_0901   46      DKVFRSSVLHSTQDL  FRSSVLHST  3         0.6224
59.5     5.00  0.59     Sequence         WB
             DRB1_0901   47      KVFRSSVLHSTQDLF  FRSSVLHST  2         0.6218
59.8     5.00  0.55     Sequence         WB
             DRB1_0901   48      VFRSSVLHSTQDLFL  FRSSVLHST  1         0.5920
82.7     7.50  0.47     Sequence         WB
             DRB1_0901   49      FRSSVLHSTQDLFLP  LHSTQDLFL  5         0.5130
194.3    17.00  0.35     Sequence
             DRB1_0901   50      RSSVLHSTQDLFLPF  LHSTQDLFL  4         0.4417
420.3    29.00  0.49     Sequence
             DRB1_0901   51      SSVLHSTQDLFLPFF  LHSTQDLFL  3         0.4250
503.6    33.00  0.52     Sequence
```

```
             DRB1_0901   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2        0.4255
500.6    33.00  0.46     Sequence
             DRB1_0901   53      VLHSTQDLFLPFFSN  LHSTQDLFL  1        0.3745
869.1    45.00  0.47     Sequence
             DRB1_0901   54      LHSTQDLFLPFFSNV  QDLFLPFFS  4        0.3152
1651.2    60.00  0.28     Sequence
             DRB1_0901   55      HSTQDLFLPFFSNVT  FLPFFSNVT  6        0.4489
388.8    28.00  0.70     Sequence
             DRB1_0901   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.4421
418.4    29.00  0.70     Sequence
             DRB1_0901   57      TQDLFLPFFSNVTWF  FLPFFSNVT  4        0.4501
383.8    28.00  0.66     Sequence
             DRB1_0901   58      QDLFLPFFSNVTWFH  FLPFFSNVT  3        0.4547
365.0    27.00  0.61     Sequence
             DRB1_0901   59      DLFLPFFSNVTWFHA  FLPFFSNVT  2        0.4852
262.4    21.00  0.50     Sequence
             DRB1_0901   60      LFLPFFSNVTWFHAI  FLPFFSNVT  1        0.5078
205.6    17.00  0.38     Sequence
             DRB1_0901   61      FLPFFSNVTWFHAIH  FLPFFSNVT  0        0.4771
286.3    22.00  0.28     Sequence
             DRB1_0901   62      LPFFSNVTWFHAIHV  VTWFHAIHV  6        0.5168
186.4    16.00  0.41     Sequence
             DRB1_0901   63      PFFSNVTWFHAIHVS  VTWFHAIHV  5        0.5176
184.9    16.00  0.40     Sequence
             DRB1_0901   64      FFSNVTWFHAIHVSG  VTWFHAIHV  4        0.5148
190.5    16.00  0.38     Sequence
             DRB1_0901   65      FSNVTWFHAIHVSGT  FHAIHVSGT  6        0.5708
104.0     9.50  0.46     Sequence         WB
             DRB1_0901   66      SNVTWFHAIHVSGTN  FHAIHVSGT  5        0.5757
98.6     9.00  0.54     Sequence         WB
             DRB1_0901   67      NVTWFHAIHVSGTNG  FHAIHVSGT  4        0.5775
96.7     8.50  0.56     Sequence         WB
             DRB1_0901   68      VTWFHAIHVSGTNGT  FHAIHVSGT  3        0.5730
101.5     9.00  0.55     Sequence         WB
             DRB1_0901   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.5324
157.5    14.00  0.66     Sequence
             DRB1_0901   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1        0.4949
236.3    19.00  0.64     Sequence
             DRB1_0901   71      FHAIHVSGTNGTKRF  FHAIHVSGT  0        0.4032
637.0    38.00  0.49     Sequence
             DRB1_0901   72      HAIHVSGTNGTKRFD  IHVSGTNGT  2        0.2841
2312.1    70.00  0.25     Sequence
             DRB1_0901   73      AIHVSGTNGTKRFDN  VSGTNGTKR  3        0.2482
3409.6    80.00  0.32     Sequence
             DRB1_0901   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.1949
6071.7    90.00  0.42     Sequence
             DRB1_0901   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.1676
8156.1    95.00  0.50     Sequence
             DRB1_0901   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.2688
2728.7    75.00  0.63     Sequence
             DRB1_0901   77      SGTNGTKRFDNPVLP  TKRFDNPVL  5        0.2710
2663.9    75.00  0.73     Sequence
             DRB1_0901   78      GTNGTKRFDNPVLPF  TKRFDNPVL  4        0.2761
2520.2    70.00  0.74     Sequence
             DRB1_0901   79      TNGTKRFDNPVLPFN  TKRFDNPVL  3        0.2872
2235.1    70.00  0.67     Sequence
             DRB1_0901   80      NGTKRFDNPVLPFND  TKRFDNPVL  2        0.2910
2145.6    70.00  0.64     Sequence
             DRB1_0901   81      GTKRFDNPVLPFNDG  TKRFDNPVL  1        0.2735
2591.7    75.00  0.62     Sequence
             DRB1_0901   82      TKRFDNPVLPFNDGV  TKRFDNPVL  0        0.2399
3731.6    80.00  0.49     Sequence
             DRB1_0901   83      KRFDNPVLPFNDGVY  VLPFNDGVY  6        0.3074
1796.5    65.00  0.67     Sequence
             DRB1_0901   84      RFDNPVLPFNDGVYF  VLPFNDGVY  5        0.3173
1614.0    60.00  0.61     Sequence
```

```
             DRB1_0901   85      FDNPVLPFNDGVYFA  VLPFNDGVY  4        0.3286
1428.8    60.00  0.56     Sequence
             DRB1_0901   86      DNPVLPFNDGVYFAS  VLPFNDGVY  3        0.3529
1098.2    50.00  0.50     Sequence
             DRB1_0901   87      NPVLPFNDGVYFAST  VLPFNDGVY  2        0.3534
1092.4    50.00  0.51     Sequence
             DRB1_0901   88      PVLPFNDGVYFASTE  VLPFNDGVY  1        0.3495
1139.7    55.00  0.46     Sequence
             DRB1_0901   89      VLPFNDGVYFASTEK  VLPFNDGVY  0        0.3294
1416.8    60.00  0.28     Sequence
             DRB1_0901   90      LPFNDGVYFASTEKS  VYFASTEKS  6        0.3797
821.8    44.00  0.38     Sequence
             DRB1_0901   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.4521
375.3    27.00  0.33     Sequence
             DRB1_0901   92      FNDGVYFASTEKSNI  YFASTEKSN  5        0.5032
216.0    18.00  0.31     Sequence
             DRB1_0901   93      NDGVYFASTEKSNII  YFASTEKSN  4        0.5293
162.8    14.00  0.31     Sequence
             DRB1_0901   94      DGVYFASTEKSNIIR  FASTEKSNI  4        0.5174
185.2    16.00  0.34     Sequence
             DRB1_0901   95      GVYFASTEKSNIIRG  FASTEKSNI  3        0.5010
221.2    19.00  0.38     Sequence
             DRB1_0901   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.4428
415.1    29.00  0.49     Sequence
             DRB1_0901   97      YFASTEKSNIIRGWI  FASTEKSNI  1        0.3703
909.9    46.00  0.62     Sequence
             DRB1_0901   98      FASTEKSNIIRGWIF  SNIIRGWIF  6        0.3490
1145.9    55.00  0.41     Sequence
             DRB1_0901   99      ASTEKSNIIRGWIFG  SNIIRGWIF  5        0.2923
2116.1    70.00  0.49     Sequence
             DRB1_0901  100      STEKSNIIRGWIFGT  IIRGWIFGT  6        0.4624
335.7    25.00  0.69     Sequence
             DRB1_0901  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5        0.5005
222.4    19.00  0.65     Sequence
             DRB1_0901  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.5121
196.2    17.00  0.63     Sequence
             DRB1_0901  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3        0.5095
201.7    17.00  0.65     Sequence
             DRB1_0901  104      SNIIRGWIFGTTLDS  IIRGWIFGT  2        0.5599
117.0    11.00  0.46     Sequence
             DRB1_0901  105      NIIRGWIFGTTLDSK  WIFGTTLDS  5        0.5522
127.1    12.00  0.36     Sequence
             DRB1_0901  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.5185
183.0    16.00  0.47     Sequence
             DRB1_0901  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3        0.4726
300.9    23.00  0.64     Sequence
             DRB1_0901  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2        0.4585
350.3    26.00  0.68     Sequence
             DRB1_0901  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1        0.4256
500.1    33.00  0.58     Sequence
             DRB1_0901  110      WIFGTTLDSKTQSLL  WIFGTTLDS  0        0.3599
1018.2    48.00  0.44     Sequence
             DRB1_0901  111      IFGTTLDSKTQSLLI  DSKTQSLLI  6        0.3316
1382.3    60.00  0.41     Sequence
             DRB1_0901  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5        0.3358
1321.0    55.00  0.55     Sequence
             DRB1_0901  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4        0.3243
1496.4    60.00  0.60     Sequence
             DRB1_0901  114      TTLDSKTQSLLIVNN  DSKTQSLLI  3        0.3128
1694.8    65.00  0.61     Sequence
             DRB1_0901  115      TLDSKTQSLLIVNNA  DSKTQSLLI  2        0.2989
1970.4    65.00  0.57     Sequence
             DRB1_0901  116      LDSKTQSLLIVNNAT  DSKTQSLLI  1        0.2678
2757.5    75.00  0.58     Sequence
             DRB1_0901  117      DSKTQSLLIVNNATN  LLIVNNATN  6        0.2544
3187.5    75.00  0.34     Sequence
```

```
             DRB1_0901  118      SKTQSLLIVNNATNV  LIVNNATNV  6        0.3573
1046.8    49.00  0.71     Sequence
             DRB1_0901  119      KTQSLLIVNNATNVV  LIVNNATNV  5        0.4138
568.3    35.00  0.67     Sequence
             DRB1_0901  120      TQSLLIVNNATNVVI  LIVNNATNV  4        0.4523
374.5    27.00  0.57     Sequence
             DRB1_0901  121      QSLLIVNNATNVVIK  LIVNNATNV  3        0.4515
377.8    27.00  0.56     Sequence
             DRB1_0901  122      SLLIVNNATNVVIKV  LIVNNATNV  2        0.4415
421.2    29.00  0.54     Sequence
             DRB1_0901  123      LLIVNNATNVVIKVC  LIVNNATNV  1        0.4050
625.2    38.00  0.49     Sequence
             DRB1_0901  124      LIVNNATNVVIKVCE  VNNATNVVI  2        0.3506
1126.1    55.00  0.37     Sequence
             DRB1_0901  125      IVNNATNVVIKVCEF  VNNATNVVI  1        0.2937
2083.4    70.00  0.56     Sequence
             DRB1_0901  126      VNNATNVVIKVCEFQ  VNNATNVVI  0        0.2206
4595.9    85.00  0.56     Sequence
             DRB1_0901  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.4254
501.3    33.00  0.80     Sequence
             DRB1_0901  128      NATNVVIKVCEFQFC  VIKVCEFQF  5        0.4121
578.9    36.00  0.73     Sequence
             DRB1_0901  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.4058
619.4    37.00  0.71     Sequence
             DRB1_0901  130      TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.4150
560.9    35.00  0.67     Sequence
             DRB1_0901  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.4082
603.6    37.00  0.64     Sequence
             DRB1_0901  132      VVIKVCEFQFCNYPF  VIKVCEFQF  1        0.4567
357.1    26.00  0.41     Sequence
             DRB1_0901  133      VIKVCEFQFCNYPFL  FQFCNYPFL  6        0.5178
184.5    16.00  0.44     Sequence
             DRB1_0901  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.4740
296.2    23.00  0.51     Sequence
             DRB1_0901  135      KVCEFQFCNYPFLGV  FQFCNYPFL  4        0.4931
241.0    20.00  0.47     Sequence
             DRB1_0901  136      VCEFQFCNYPFLGVY  FQFCNYPFL  3        0.4816
272.8    22.00  0.46     Sequence
             DRB1_0901  137      CEFQFCNYPFLGVYY  FQFCNYPFL  2        0.5216
177.0    15.00  0.35     Sequence
             DRB1_0901  138      EFQFCNYPFLGVYYH  FQFCNYPFL  1        0.5051
211.6    18.00  0.40     Sequence
             DRB1_0901  139      FQFCNYPFLGVYYHK  NYPFLGVYY  4        0.4380
437.2    30.00  0.32     Sequence
             DRB1_0901  140      QFCNYPFLGVYYHKN  NYPFLGVYY  3        0.3962
687.6    40.00  0.37     Sequence
             DRB1_0901  141      FCNYPFLGVYYHKNN  NYPFLGVYY  2        0.3812
808.6    43.00  0.37     Sequence
             DRB1_0901  142      CNYPFLGVYYHKNNK  NYPFLGVYY  1        0.3571
1048.9    49.00  0.44     Sequence
             DRB1_0901  143      NYPFLGVYYHKNNKS  FLGVYYHKN  3        0.3687
925.5    46.00  0.31     Sequence
             DRB1_0901  144      YPFLGVYYHKNNKSW  YYHKNNKSW  6        0.3732
882.0    45.00  0.34     Sequence
             DRB1_0901  145      PFLGVYYHKNNKSWM  YHKNNKSWM  6        0.4545
365.9    27.00  0.35     Sequence
             DRB1_0901  146      FLGVYYHKNNKSWME  YHKNNKSWM  5        0.4730
299.4    23.00  0.43     Sequence
             DRB1_0901  147      LGVYYHKNNKSWMES  YHKNNKSWM  4        0.4861
259.9    21.00  0.46     Sequence
             DRB1_0901  148      GVYYHKNNKSWMESE  YHKNNKSWM  3        0.4921
243.5    20.00  0.50     Sequence
             DRB1_0901  149      VYYHKNNKSWMESEF  YHKNNKSWM  2        0.4717
303.8    23.00  0.49     Sequence
             DRB1_0901  150      YYHKNNKSWMESEFR  YHKNNKSWM  1        0.4300
476.7    32.00  0.51     Sequence
```

```
             DRB1_0901  151      YHKNNKSWMESEFRV  YHKNNKSWM  0        0.3899
736.1    41.00  0.40     Sequence
             DRB1_0901  152      HKNNKSWMESEFRVY  WMESEFRVY  6        0.5129
194.5    17.00  0.64     Sequence
             DRB1_0901  153      KNNKSWMESEFRVYS  WMESEFRVY  5        0.5421
141.8    13.00  0.65     Sequence
             DRB1_0901  154      NNKSWMESEFRVYSS  WMESEFRVY  4        0.5474
133.9    12.00  0.70     Sequence
             DRB1_0901  155      NKSWMESEFRVYSSA  WMESEFRVY  3        0.5388
147.0    13.00  0.73     Sequence
             DRB1_0901  156      KSWMESEFRVYSSAN  WMESEFRVY  2        0.5589
118.2    11.00  0.69     Sequence
             DRB1_0901  157      SWMESEFRVYSSANN  FRVYSSANN  6        0.6674
36.6     2.50  0.60     Sequence        WB
             DRB1_0901  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.6648
37.6     3.00  0.73     Sequence        WB
             DRB1_0901  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.6566
41.1     3.00  0.88     Sequence        WB
             DRB1_0901  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.6747
33.8     2.50  0.74     Sequence        WB
             DRB1_0901  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.6762
33.2     2.50  0.69     Sequence        WB
             DRB1_0901  162      EFRVYSSANNCTFEY  FRVYSSANN  1        0.6451
46.5     3.50  0.63     Sequence        WB
             DRB1_0901  163      FRVYSSANNCTFEYV  FRVYSSANN  0        0.5800
94.1     8.50  0.46     Sequence        WB
             DRB1_0901  164      RVYSSANNCTFEYVS  YSSANNCTF  2        0.4802
276.9    22.00  0.69     Sequence
             DRB1_0901  165      VYSSANNCTFEYVSQ  YSSANNCTF  1        0.4227
516.0    33.00  0.69     Sequence
             DRB1_0901  166      YSSANNCTFEYVSQP  YSSANNCTF  0        0.3299
1409.1    60.00  0.56     Sequence
             DRB1_0901  167      SSANNCTFEYVSQPF  TFEYVSQPF  6        0.3053
1837.2    65.00  0.50     Sequence
             DRB1_0901  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.4537
368.8    27.00  0.62     Sequence
             DRB1_0901  169      ANNCTFEYVSQPFLM  EYVSQPFLM  6        0.6617
38.9     3.00  0.64     Sequence        WB
             DRB1_0901  170      NNCTFEYVSQPFLMD  EYVSQPFLM  5        0.6608
39.2     3.00  0.62     Sequence        WB
             DRB1_0901  171      NCTFEYVSQPFLMDL  EYVSQPFLM  4        0.6566
41.1     3.00  0.61     Sequence        WB
             DRB1_0901  172      CTFEYVSQPFLMDLE  EYVSQPFLM  3        0.6492
44.5     3.50  0.62     Sequence        WB
             DRB1_0901  173      TFEYVSQPFLMDLEG  EYVSQPFLM  2        0.6394
49.5     4.00  0.63     Sequence        WB
             DRB1_0901  174      FEYVSQPFLMDLEGK  EYVSQPFLM  1        0.5954
79.7     7.00  0.67     Sequence        WB
             DRB1_0901  175      EYVSQPFLMDLEGKQ  EYVSQPFLM  0        0.5367
150.3    13.00  0.62     Sequence
             DRB1_0901  176      YVSQPFLMDLEGKQG  FLMDLEGKQ  5        0.3326
1368.4    60.00  0.65     Sequence
             DRB1_0901  177      VSQPFLMDLEGKQGN  FLMDLEGKQ  4        0.3207
1556.2    60.00  0.73     Sequence
             DRB1_0901  178      SQPFLMDLEGKQGNF  FLMDLEGKQ  3        0.3186
1591.5    60.00  0.74     Sequence
             DRB1_0901  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2        0.3028
1888.8    65.00  0.72     Sequence
             DRB1_0901  180      PFLMDLEGKQGNFKN  FLMDLEGKQ  1        0.2786
2452.6    70.00  0.68     Sequence
             DRB1_0901  181      FLMDLEGKQGNFKNL  FLMDLEGKQ  0        0.2104
5130.5    85.00  0.49     Sequence
             DRB1_0901  182      LMDLEGKQGNFKNLS  GKQGNFKNL  5        0.1202
13613.5   100.00  0.22     Sequence
             DRB1_0901  183      MDLEGKQGNFKNLSE  GKQGNFKNL  4        0.1217
13399.4   100.00  0.29     Sequence
```

```
             DRB1_0901  184      DLEGKQGNFKNLSEF  GKQGNFKNL  3        0.1231
13204.6   100.00  0.27     Sequence
             DRB1_0901  185      LEGKQGNFKNLSEFV  NFKNLSEFV  6        0.3064
1815.4    65.00  0.69     Sequence
             DRB1_0901  186      EGKQGNFKNLSEFVF  FKNLSEFVF  6        0.3935
707.5    40.00  0.52     Sequence
             DRB1_0901  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5        0.3885
747.2    41.00  0.48     Sequence
             DRB1_0901  188      KQGNFKNLSEFVFKN  FKNLSEFVF  4        0.3805
815.0    43.00  0.47     Sequence
             DRB1_0901  189      QGNFKNLSEFVFKNI  FKNLSEFVF  3        0.3762
853.1    44.00  0.43     Sequence
             DRB1_0901  190      GNFKNLSEFVFKNID  FKNLSEFVF  2        0.3602
1015.3    48.00  0.43     Sequence
             DRB1_0901  191      NFKNLSEFVFKNIDG  FKNLSEFVF  1        0.3225
1526.0    60.00  0.44     Sequence
             DRB1_0901  192      FKNLSEFVFKNIDGY  FVFKNIDGY  6        0.3295
1414.2    60.00  0.39     Sequence
             DRB1_0901  193      KNLSEFVFKNIDGYF  FVFKNIDGY  5        0.3432
1219.3    55.00  0.41     Sequence
             DRB1_0901  194      NLSEFVFKNIDGYFK  FVFKNIDGY  4        0.3717
896.5    45.00  0.35     Sequence
             DRB1_0901  195      LSEFVFKNIDGYFKI  FKNIDGYFK  5        0.3893
740.5    41.00  0.31     Sequence
             DRB1_0901  196      SEFVFKNIDGYFKIY  FKNIDGYFK  4        0.3888
744.6    41.00  0.33     Sequence
             DRB1_0901  197      EFVFKNIDGYFKIYS  FKNIDGYFK  3        0.3848
777.5    42.00  0.36     Sequence
             DRB1_0901  198      FVFKNIDGYFKIYSK  FKNIDGYFK  2        0.3537
1089.0    50.00  0.39     Sequence
             DRB1_0901  199      VFKNIDGYFKIYSKH  FKNIDGYFK  1        0.2997
1952.4    65.00  0.45     Sequence
             DRB1_0901  200      FKNIDGYFKIYSKHT  YFKIYSKHT  6        0.4583
351.0    26.00  0.77     Sequence
             DRB1_0901  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.4951
235.8    19.00  0.69     Sequence
             DRB1_0901  202      NIDGYFKIYSKHTPI  YFKIYSKHT  4        0.5174
185.2    16.00  0.69     Sequence
             DRB1_0901  203      IDGYFKIYSKHTPIN  YFKIYSKHT  3        0.5142
191.7    16.00  0.65     Sequence
             DRB1_0901  204      DGYFKIYSKHTPINL  YFKIYSKHT  2        0.5816
92.4     8.00  0.47     Sequence         WB
             DRB1_0901  205      GYFKIYSKHTPINLV  YSKHTPINL  5        0.5920
82.7     7.50  0.49     Sequence         WB
             DRB1_0901  206      YFKIYSKHTPINLVR  YSKHTPINL  4        0.5599
117.0    11.00  0.62     Sequence
             DRB1_0901  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.5219
176.4    15.00  0.82     Sequence
             DRB1_0901  208      KIYSKHTPINLVRDL  YSKHTPINL  2        0.5218
176.7    15.00  0.89     Sequence
             DRB1_0901  209      IYSKHTPINLVRDLP  YSKHTPINL  1        0.4750
293.1    23.00  0.90     Sequence
             DRB1_0901  210      YSKHTPINLVRDLPQ  YSKHTPINL  0        0.4094
596.2    37.00  0.69     Sequence
             DRB1_0901  211      SKHTPINLVRDLPQG  INLVRDLPQ  5        0.2212
4567.5    85.00  0.60     Sequence
             DRB1_0901  212      KHTPINLVRDLPQGF  LVRDLPQGF  6        0.3268
1457.3    60.00  0.61     Sequence
             DRB1_0901  213      HTPINLVRDLPQGFS  LVRDLPQGF  5        0.3714
899.3    46.00  0.63     Sequence
             DRB1_0901  214      TPINLVRDLPQGFSA  LVRDLPQGF  4        0.4009
653.4    38.00  0.58     Sequence
             DRB1_0901  215      PINLVRDLPQGFSAL  LVRDLPQGF  3        0.4126
575.6    36.00  0.56     Sequence
             DRB1_0901  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.3985
670.4    39.00  0.49     Sequence
```

```
             DRB1_0901  217      NLVRDLPQGFSALEP  LVRDLPQGF  1        0.3709
903.9    46.00  0.53     Sequence
             DRB1_0901  218      LVRDLPQGFSALEPL  LVRDLPQGF  0        0.3352
1330.5    55.00  0.32     Sequence
             DRB1_0901  219      VRDLPQGFSALEPLV  GFSALEPLV  6        0.4222
518.7    34.00  0.49     Sequence
             DRB1_0901  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.5410
143.5    13.00  0.59     Sequence
             DRB1_0901  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.5701
104.7     9.50  0.69     Sequence         WB
             DRB1_0901  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.5544
124.1    11.00  0.73     Sequence
             DRB1_0901  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.5711
103.6     9.50  0.66     Sequence         WB
             DRB1_0901  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.5441
138.8    13.00  0.64     Sequence
             DRB1_0901  225      GFSALEPLVDLPIGI  FSALEPLVD  1        0.5098
201.1    17.00  0.63     Sequence
             DRB1_0901  226      FSALEPLVDLPIGIN  FSALEPLVD  0        0.4033
636.6    38.00  0.45     Sequence
             DRB1_0901  227      SALEPLVDLPIGINI  LEPLVDLPI  2        0.3518
1111.0    55.00  0.56     Sequence
             DRB1_0901  228      ALEPLVDLPIGINIT  LEPLVDLPI  1        0.3405
1255.5    55.00  0.50     Sequence
             DRB1_0901  229      LEPLVDLPIGINITR  LEPLVDLPI  0        0.2923
2116.7    70.00  0.37     Sequence
             DRB1_0901  230      EPLVDLPIGINITRF  VDLPIGINI  3        0.2369
3853.7    80.00  0.33     Sequence
             DRB1_0901  231      PLVDLPIGINITRFQ  VDLPIGINI  2        0.2486
3394.4    80.00  0.25     Sequence
             DRB1_0901  232      LVDLPIGINITRFQT  IGINITRFQ  5        0.2251
4378.9    85.00  0.39     Sequence
             DRB1_0901  233      VDLPIGINITRFQTL  INITRFQTL  6        0.2774
2486.8    70.00  0.45     Sequence
             DRB1_0901  234      DLPIGINITRFQTLL  INITRFQTL  5        0.2826
2351.0    70.00  0.43     Sequence
             DRB1_0901  235      LPIGINITRFQTLLA  ITRFQTLLA  6        0.4504
382.4    28.00  0.73     Sequence
             DRB1_0901  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.4486
390.1    28.00  0.69     Sequence
             DRB1_0901  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.4437
411.3    29.00  0.66     Sequence
             DRB1_0901  238      GINITRFQTLLALHR  ITRFQTLLA  3        0.4819
271.9    22.00  0.49     Sequence
             DRB1_0901  239      INITRFQTLLALHRS  ITRFQTLLA  2        0.4730
299.4    23.00  0.47     Sequence
             DRB1_0901  240      NITRFQTLLALHRSY  ITRFQTLLA  1        0.4679
316.3    24.00  0.48     Sequence
             DRB1_0901  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.4629
333.9    25.00  0.40     Sequence
             DRB1_0901  242      TRFQTLLALHRSYLT  FQTLLALHR  2        0.4421
418.4    29.00  0.47     Sequence
             DRB1_0901  243      RFQTLLALHRSYLTP  FQTLLALHR  1        0.4163
552.9    35.00  0.44     Sequence
             DRB1_0901  244      FQTLLALHRSYLTPG  LALHRSYLT  4        0.3933
709.7    40.00  0.26     Sequence
             DRB1_0901  245      QTLLALHRSYLTPGD  LHRSYLTPG  5        0.3856
770.9    42.00  0.31     Sequence
             DRB1_0901  246      TLLALHRSYLTPGDS  LHRSYLTPG  4        0.3873
757.2    42.00  0.34     Sequence
             DRB1_0901  247      LLALHRSYLTPGDSS  LHRSYLTPG  3        0.3765
850.5    44.00  0.41     Sequence
             DRB1_0901  248      LALHRSYLTPGDSSS  LHRSYLTPG  2        0.3533
1093.1    50.00  0.49     Sequence
             DRB1_0901  249      ALHRSYLTPGDSSSG  LHRSYLTPG  1        0.3246
1492.1    60.00  0.54     Sequence
```

```
             DRB1_0901  250      LHRSYLTPGDSSSGW  LHRSYLTPG  0        0.2676
2764.5    75.00  0.34     Sequence
             DRB1_0901  251      HRSYLTPGDSSSGWT  LTPGDSSSG  4        0.2159
4834.8    85.00  0.41     Sequence
             DRB1_0901  252      RSYLTPGDSSSGWTA  LTPGDSSSG  3        0.2225
4504.5    85.00  0.43     Sequence
             DRB1_0901  253      SYLTPGDSSSGWTAG  LTPGDSSSG  2        0.2069
5332.6    90.00  0.40     Sequence
             DRB1_0901  254      YLTPGDSSSGWTAGA  GDSSSGWTA  4        0.2130
4989.1    85.00  0.35     Sequence
             DRB1_0901  255      LTPGDSSSGWTAGAA  GDSSSGWTA  3        0.2141
4932.8    85.00  0.32     Sequence
             DRB1_0901  256      TPGDSSSGWTAGAAA  GDSSSGWTA  2        0.2156
4851.9    85.00  0.29     Sequence
             DRB1_0901  257      PGDSSSGWTAGAAAY  GWTAGAAAY  6        0.3468
1173.1    55.00  0.41     Sequence
             DRB1_0901  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.7515
14.7     0.50  0.94     Sequence         SB
             DRB1_0901  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.7794
10.9     0.25  0.91     Sequence         SB
             DRB1_0901  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.7788
11.0     0.25  0.92     Sequence         SB
             DRB1_0901  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.7762
11.3     0.25  0.89     Sequence         SB
             DRB1_0901  262      SGWTAGAAAYYVGYL  WTAGAAAYY  2        0.7614
13.2     0.40  0.86     Sequence         SB
             DRB1_0901  263      GWTAGAAAYYVGYLQ  WTAGAAAYY  1        0.7204
20.6     0.90  0.86     Sequence         SB
             DRB1_0901  264      WTAGAAAYYVGYLQP  WTAGAAAYY  0        0.6091
68.7     6.00  0.67     Sequence         WB
             DRB1_0901  265      TAGAAAYYVGYLQPR  YYVGYLQPR  6        0.4111
585.3    36.00  0.31     Sequence
             DRB1_0901  266      AGAAAYYVGYLQPRT  YVGYLQPRT  6        0.5152
189.8    16.00  0.49     Sequence
             DRB1_0901  267      GAAAYYVGYLQPRTF  VGYLQPRTF  6        0.6188
61.8     5.50  0.49     Sequence         WB
             DRB1_0901  268      AAAYYVGYLQPRTFL  VGYLQPRTF  5        0.6407
48.8     4.00  0.52     Sequence         WB
             DRB1_0901  269      AAYYVGYLQPRTFLL  VGYLQPRTF  4        0.6584
40.3     3.00  0.47     Sequence         WB
             DRB1_0901  270      AYYVGYLQPRTFLLK  VGYLQPRTF  3        0.6444
46.9     3.50  0.52     Sequence         WB
             DRB1_0901  271      YYVGYLQPRTFLLKY  VGYLQPRTF  2        0.6172
62.9     5.50  0.52     Sequence         WB
             DRB1_0901  272      YVGYLQPRTFLLKYN  VGYLQPRTF  1        0.5888
85.5     7.50  0.56     Sequence         WB
             DRB1_0901  273      VGYLQPRTFLLKYNE  VGYLQPRTF  0        0.5085
203.9    17.00  0.57     Sequence
             DRB1_0901  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.3411
1248.1    55.00  0.81     Sequence
             DRB1_0901  275      YLQPRTFLLKYNENG  YLQPRTFLL  0        0.2821
2363.6    70.00  0.56     Sequence
             DRB1_0901  276      LQPRTFLLKYNENGT  LLKYNENGT  6        0.2586
3046.4    75.00  0.34     Sequence
             DRB1_0901  277      QPRTFLLKYNENGTI  LKYNENGTI  6        0.3964
685.6    40.00  0.58     Sequence
             DRB1_0901  278      PRTFLLKYNENGTIT  LKYNENGTI  5        0.4336
458.5    31.00  0.66     Sequence
             DRB1_0901  279      RTFLLKYNENGTITD  LKYNENGTI  4        0.4399
428.6    30.00  0.66     Sequence
             DRB1_0901  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.4384
435.4    30.00  0.69     Sequence
             DRB1_0901  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.4275
489.9    32.00  0.67     Sequence
             DRB1_0901  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.4078
606.6    37.00  0.69     Sequence
```

```
            DRB1_0901  283      LKYNENGTITDAVDC  LKYNENGTI  0        0.3144
1665.6    60.00  0.70     Sequence
            DRB1_0901  284      KYNENGTITDAVDCA  YNENGTITD  1        0.1327
11895.8   100.00  0.55     Sequence
            DRB1_0901  285      YNENGTITDAVDCAL  ITDAVDCAL  6        0.2072
5311.8    90.00  0.74     Sequence
            DRB1_0901  286      NENGTITDAVDCALD  ITDAVDCAL  5        0.2185
4701.4    85.00  0.76     Sequence
            DRB1_0901  287      ENGTITDAVDCALDP  ITDAVDCAL  4        0.2126
5009.6    85.00  0.78     Sequence
            DRB1_0901  288      NGTITDAVDCALDPL  ITDAVDCAL  3        0.2192
4666.9    85.00  0.77     Sequence
            DRB1_0901  289      GTITDAVDCALDPLS  ITDAVDCAL  2        0.2297
4165.3    85.00  0.61     Sequence
            DRB1_0901  290      TITDAVDCALDPLSE  ITDAVDCAL  1        0.2148
4894.7    85.00  0.53     Sequence
            DRB1_0901  291      ITDAVDCALDPLSET  ITDAVDCAL  0        0.1867
6630.1    90.00  0.40     Sequence
            DRB1_0901  292      TDAVDCALDPLSETK  VDCALDPLS  3        0.1444
10478.4    95.00  0.49     Sequence
            DRB1_0901  293      DAVDCALDPLSETKC  VDCALDPLS  2        0.1572
9122.2    95.00  0.37     Sequence
            DRB1_0901  294      AVDCALDPLSETKCT  LDPLSETKC  5        0.1575
9093.2    95.00  0.41     Sequence
            DRB1_0901  295      VDCALDPLSETKCTL  LDPLSETKC  4        0.1525
9604.2    95.00  0.50     Sequence
            DRB1_0901  296      DCALDPLSETKCTLK  LDPLSETKC  3        0.1479
10088.6    95.00  0.52     Sequence
            DRB1_0901  297      CALDPLSETKCTLKS  LDPLSETKC  2        0.1500
9870.5    95.00  0.47     Sequence
            DRB1_0901  298      ALDPLSETKCTLKSF  LDPLSETKC  1        0.1484
10039.6    95.00  0.38     Sequence
            DRB1_0901  299      LDPLSETKCTLKSFT  TKCTLKSFT  6        0.1614
8722.2    95.00  0.34     Sequence
            DRB1_0901  300      DPLSETKCTLKSFTV  KCTLKSFTV  6        0.2702
2687.0    75.00  0.60     Sequence
            DRB1_0901  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.2761
2519.7    70.00  0.64     Sequence
            DRB1_0901  302      LSETKCTLKSFTVEK  KCTLKSFTV  4        0.2876
2227.1    70.00  0.62     Sequence
            DRB1_0901  303      SETKCTLKSFTVEKG  KCTLKSFTV  3        0.3427
1225.9    55.00  0.40     Sequence
            DRB1_0901  304      ETKCTLKSFTVEKGI  LKSFTVEKG  5        0.3701
911.4    46.00  0.52     Sequence
            DRB1_0901  305      TKCTLKSFTVEKGIY  LKSFTVEKG  4        0.4035
635.4    38.00  0.49     Sequence
            DRB1_0901  306      KCTLKSFTVEKGIYQ  LKSFTVEKG  3        0.4534
370.2    27.00  0.36     Sequence
            DRB1_0901  307      CTLKSFTVEKGIYQT  FTVEKGIYQ  5        0.4435
412.2    29.00  0.46     Sequence
            DRB1_0901  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.4409
423.8    29.00  0.49     Sequence
            DRB1_0901  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.4057
620.2    37.00  0.58     Sequence
            DRB1_0901  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.3893
740.6    41.00  0.71     Sequence
            DRB1_0901  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.3538
1088.0    50.00  0.66     Sequence
            DRB1_0901  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.5151
189.9    16.00  0.71     Sequence
            DRB1_0901  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.5449
137.5    12.00  0.75     Sequence
            DRB1_0901  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.5444
138.2    12.00  0.74     Sequence
            DRB1_0901  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.5511
128.6    12.00  0.75     Sequence
```

```
             DRB1_0901  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.5426
141.0    13.00  0.74     Sequence
             DRB1_0901  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.5008
221.7    19.00  0.69     Sequence
             DRB1_0901  318      IYQTSNFRVQPTESI  IYQTSNFRV  0        0.4707
307.1    24.00  0.38     Sequence
             DRB1_0901  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.4469
397.1    28.00  0.60     Sequence
             DRB1_0901  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.4835
267.4    21.00  0.50     Sequence
             DRB1_0901  321      TSNFRVQPTESIVRF  VQPTESIVR  5        0.5020
218.8    18.00  0.38     Sequence
             DRB1_0901  322      SNFRVQPTESIVRFP  VQPTESIVR  4        0.4906
247.5    20.00  0.41     Sequence
             DRB1_0901  323      NFRVQPTESIVRFPN  VQPTESIVR  3        0.4643
329.2    25.00  0.44     Sequence
             DRB1_0901  324      FRVQPTESIVRFPNI  VQPTESIVR  2        0.4052
623.7    37.00  0.52     Sequence
             DRB1_0901  325      RVQPTESIVRFPNIT  VQPTESIVR  1        0.3394
1271.0    55.00  0.71     Sequence
             DRB1_0901  326      VQPTESIVRFPNITN  IVRFPNITN  6        0.2774
2485.0    70.00  0.44     Sequence
             DRB1_0901  327      QPTESIVRFPNITNL  IVRFPNITN  5        0.2782
2465.4    70.00  0.49     Sequence
             DRB1_0901  328      PTESIVRFPNITNLC  IVRFPNITN  4        0.2780
2470.0    70.00  0.49     Sequence
             DRB1_0901  329      TESIVRFPNITNLCP  IVRFPNITN  3        0.2646
2854.7    75.00  0.52     Sequence
             DRB1_0901  330      ESIVRFPNITNLCPF  IVRFPNITN  2        0.2652
2835.1    75.00  0.50     Sequence
             DRB1_0901  331      SIVRFPNITNLCPFG  IVRFPNITN  1        0.2680
2752.9    75.00  0.43     Sequence
             DRB1_0901  332      IVRFPNITNLCPFGE  ITNLCPFGE  6        0.3089
1767.5    65.00  0.43     Sequence
             DRB1_0901  333      VRFPNITNLCPFGEV  ITNLCPFGE  5        0.2953
2047.4    65.00  0.62     Sequence
             DRB1_0901  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.2945
2067.1    70.00  0.61     Sequence
             DRB1_0901  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.3399
1264.4    55.00  0.47     Sequence
             DRB1_0901  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.3574
1046.3    49.00  0.44     Sequence
             DRB1_0901  337      NITNLCPFGEVFNAT  LCPFGEVFN  4        0.3413
1245.6    55.00  0.41     Sequence
             DRB1_0901  338      ITNLCPFGEVFNATR  LCPFGEVFN  3        0.3247
1489.7    60.00  0.43     Sequence
             DRB1_0901  339      TNLCPFGEVFNATRF  LCPFGEVFN  2        0.3345
1340.8    55.00  0.40     Sequence
             DRB1_0901  340      NLCPFGEVFNATRFA  LCPFGEVFN  1        0.3493
1142.1    55.00  0.31     Sequence
             DRB1_0901  341      LCPFGEVFNATRFAS  FGEVFNATR  3        0.3458
1185.9    55.00  0.19     Sequence
             DRB1_0901  342      CPFGEVFNATRFASV  FNATRFASV  6        0.4676
317.5    24.00  0.62     Sequence
             DRB1_0901  343      PFGEVFNATRFASVY  FNATRFASV  5        0.5016
219.8    18.00  0.69     Sequence
             DRB1_0901  344      FGEVFNATRFASVYA  FNATRFASV  4        0.5521
127.2    12.00  0.55     Sequence
             DRB1_0901  345      GEVFNATRFASVYAW  FNATRFASV  3        0.5856
88.6     8.00  0.42     Sequence         WB
             DRB1_0901  346      EVFNATRFASVYAWN  FNATRFASV  2        0.5702
104.6     9.50  0.43     Sequence         WB
             DRB1_0901  347      VFNATRFASVYAWNR  FNATRFASV  1        0.5652
110.5    10.00  0.38     Sequence
             DRB1_0901  348      FNATRFASVYAWNRK  FASVYAWNR  5        0.5343
154.3    14.00  0.22     Sequence
```

```
             DRB1_0901  349      NATRFASVYAWNRKR  FASVYAWNR  4        0.5281
164.9    15.00  0.30     Sequence
             DRB1_0901  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.5250
170.7    15.00  0.31     Sequence
             DRB1_0901  351      TRFASVYAWNRKRIS  FASVYAWNR  2        0.5017
219.5    18.00  0.27     Sequence
             DRB1_0901  352      RFASVYAWNRKRISN  FASVYAWNR  1        0.4694
311.3    24.00  0.27     Sequence
             DRB1_0901  353      FASVYAWNRKRISNC  VYAWNRKRI  3        0.4157
556.6    35.00  0.32     Sequence
             DRB1_0901  354      ASVYAWNRKRISNCV  VYAWNRKRI  2        0.4090
598.7    37.00  0.34     Sequence
             DRB1_0901  355      SVYAWNRKRISNCVA  VYAWNRKRI  1        0.4014
649.8    38.00  0.29     Sequence
             DRB1_0901  356      VYAWNRKRISNCVAD  RKRISNCVA  5        0.3546
1078.8    50.00  0.30     Sequence
             DRB1_0901  357      YAWNRKRISNCVADY  RKRISNCVA  4        0.3266
1459.3    60.00  0.39     Sequence
             DRB1_0901  358      AWNRKRISNCVADYS  RKRISNCVA  3        0.3301
1405.7    60.00  0.43     Sequence
             DRB1_0901  359      WNRKRISNCVADYSV  RKRISNCVA  2        0.3146
1661.7    60.00  0.40     Sequence
             DRB1_0901  360      NRKRISNCVADYSVL  RKRISNCVA  1        0.3224
1527.5    60.00  0.32     Sequence
             DRB1_0901  361      RKRISNCVADYSVLY  CVADYSVLY  6        0.3594
1023.4    49.00  0.41     Sequence
             DRB1_0901  362      KRISNCVADYSVLYN  CVADYSVLY  5        0.3398
1265.2    55.00  0.47     Sequence
             DRB1_0901  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.3324
1371.5    60.00  0.47     Sequence
             DRB1_0901  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.3101
1744.9    65.00  0.54     Sequence
             DRB1_0901  365      SNCVADYSVLYNSAS  YSVLYNSAS  6        0.4142
565.7    35.00  0.56     Sequence
             DRB1_0901  366      NCVADYSVLYNSASF  YSVLYNSAS  5        0.4468
397.5    28.00  0.51     Sequence
             DRB1_0901  367      CVADYSVLYNSASFS  YSVLYNSAS  4        0.4756
291.1    23.00  0.50     Sequence
             DRB1_0901  368      VADYSVLYNSASFST  LYNSASFST  6        0.5514
128.3    12.00  0.43     Sequence
             DRB1_0901  369      ADYSVLYNSASFSTF  LYNSASFST  5        0.6002
75.6     6.50  0.44     Sequence         WB
             DRB1_0901  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.5957
79.4     7.00  0.47     Sequence         WB
             DRB1_0901  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.5750
99.3     9.00  0.47     Sequence         WB
             DRB1_0901  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.5704
104.4     9.50  0.47     Sequence         WB
             DRB1_0901  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.5274
166.2    15.00  0.47     Sequence
             DRB1_0901  374      LYNSASFSTFKCYGV  FSTFKCYGV  6        0.5297
162.1    14.00  0.36     Sequence
             DRB1_0901  375      YNSASFSTFKCYGVS  FSTFKCYGV  5        0.4888
252.5    20.00  0.59     Sequence
             DRB1_0901  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.4456
403.0    29.00  0.70     Sequence
             DRB1_0901  377      SASFSTFKCYGVSPT  FKCYGVSPT  6        0.5839
90.2     8.00  0.50     Sequence         WB
             DRB1_0901  378      ASFSTFKCYGVSPTK  FKCYGVSPT  5        0.6043
72.4     6.50  0.58     Sequence         WB
             DRB1_0901  379      SFSTFKCYGVSPTKL  FKCYGVSPT  4        0.6649
37.6     3.00  0.47     Sequence         WB
             DRB1_0901  380      FSTFKCYGVSPTKLN  FKCYGVSPT  3        0.6676
36.5     2.50  0.46     Sequence         WB
             DRB1_0901  381      STFKCYGVSPTKLND  FKCYGVSPT  2        0.6631
38.3     3.00  0.51     Sequence         WB
```

```
             DRB1_0901  382      TFKCYGVSPTKLNDL  FKCYGVSPT  1        0.6501
44.1     3.50  0.47     Sequence         WB
             DRB1_0901  383      FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.5999
75.9     6.50  0.43     Sequence         WB
             DRB1_0901  384      KCYGVSPTKLNDLCF  CYGVSPTKL  1        0.5075
206.2    18.00  0.63     Sequence
             DRB1_0901  385      CYGVSPTKLNDLCFT  CYGVSPTKL  0        0.4079
605.9    37.00  0.54     Sequence
             DRB1_0901  386      YGVSPTKLNDLCFTN  YGVSPTKLN  0        0.2004
5718.9    90.00  0.34     Sequence
             DRB1_0901  387      GVSPTKLNDLCFTNV  LNDLCFTNV  6        0.2384
3790.5    80.00  0.44     Sequence
             DRB1_0901  388      VSPTKLNDLCFTNVY  LNDLCFTNV  5        0.2485
3396.8    80.00  0.47     Sequence
             DRB1_0901  389      SPTKLNDLCFTNVYA  LNDLCFTNV  4        0.2564
3118.9    75.00  0.46     Sequence
             DRB1_0901  390      PTKLNDLCFTNVYAD  LNDLCFTNV  3        0.2561
3128.7    75.00  0.47     Sequence
             DRB1_0901  391      TKLNDLCFTNVYADS  LNDLCFTNV  2        0.2410
3685.2    80.00  0.47     Sequence
             DRB1_0901  392      KLNDLCFTNVYADSF  FTNVYADSF  6        0.3167
1625.2    60.00  0.55     Sequence
             DRB1_0901  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.3458
1186.5    55.00  0.56     Sequence
             DRB1_0901  394      NDLCFTNVYADSFVI  NVYADSFVI  6        0.4295
479.6    32.00  0.44     Sequence
             DRB1_0901  395      DLCFTNVYADSFVIR  FTNVYADSF  3        0.4059
618.7    37.00  0.38     Sequence
             DRB1_0901  396      LCFTNVYADSFVIRG  FTNVYADSF  2        0.4153
559.4    35.00  0.32     Sequence
             DRB1_0901  397      CFTNVYADSFVIRGD  FTNVYADSF  1        0.4100
592.2    36.00  0.33     Sequence
             DRB1_0901  398      FTNVYADSFVIRGDE  NVYADSFVI  2        0.3885
746.8    41.00  0.29     Sequence
             DRB1_0901  399      TNVYADSFVIRGDEV  NVYADSFVI  1        0.3579
1040.8    49.00  0.35     Sequence
             DRB1_0901  400      NVYADSFVIRGDEVR  YADSFVIRG  2        0.3494
1140.9    55.00  0.34     Sequence
             DRB1_0901  401      VYADSFVIRGDEVRQ  YADSFVIRG  1        0.3206
1557.1    60.00  0.32     Sequence
             DRB1_0901  402      YADSFVIRGDEVRQI  VIRGDEVRQ  5        0.3346
1338.7    55.00  0.25     Sequence
             DRB1_0901  403      ADSFVIRGDEVRQIA  VIRGDEVRQ  4        0.3345
1340.7    55.00  0.31     Sequence
             DRB1_0901  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.3217
1539.2    60.00  0.35     Sequence
             DRB1_0901  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.3146
1662.6    60.00  0.40     Sequence
             DRB1_0901  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.2800
2417.3    70.00  0.46     Sequence
             DRB1_0901  407      VIRGDEVRQIAPGQT  VRQIAPGQT  6        0.3357
1322.5    55.00  0.59     Sequence
             DRB1_0901  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.3578
1041.2    49.00  0.75     Sequence
             DRB1_0901  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.3699
914.0    46.00  0.88     Sequence
             DRB1_0901  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.4420
418.6    29.00  0.61     Sequence
             DRB1_0901  411      DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.4520
376.1    27.00  0.51     Sequence
             DRB1_0901  412      EVRQIAPGQTGTIAD  IAPGQTGTI  4        0.4401
427.4    30.00  0.47     Sequence
             DRB1_0901  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.3964
686.1    40.00  0.62     Sequence
             DRB1_0901  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.3303
1402.6    60.00  0.86     Sequence
```

```
             DRB1_0901  415      QIAPGQTGTIADYNY  IAPGQTGTI  1        0.2918
2127.9    70.00  0.77     Sequence
             DRB1_0901  416      IAPGQTGTIADYNYK  IAPGQTGTI  0        0.2222
4516.8    85.00  0.64     Sequence
             DRB1_0901  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.1411
10858.7   100.00  0.35     Sequence
             DRB1_0901  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.1481
10067.9    95.00  0.34     Sequence
             DRB1_0901  419      GQTGTIADYNYKLPD  TIADYNYKL  4        0.1472
10168.1    95.00  0.41     Sequence
             DRB1_0901  420      QTGTIADYNYKLPDD  TIADYNYKL  3        0.1379
11240.0   100.00  0.43     Sequence
             DRB1_0901  421      TGTIADYNYKLPDDF  YNYKLPDDF  6        0.2797
2425.5    70.00  0.69     Sequence
             DRB1_0901  422      GTIADYNYKLPDDFT  YNYKLPDDF  5        0.3190
1585.2    60.00  0.71     Sequence
             DRB1_0901  423      TIADYNYKLPDDFTG  YNYKLPDDF  4        0.3597
1020.8    49.00  0.60     Sequence
             DRB1_0901  424      IADYNYKLPDDFTGC  YNYKLPDDF  3        0.3576
1043.7    49.00  0.54     Sequence
             DRB1_0901  425      ADYNYKLPDDFTGCV  YNYKLPDDF  2        0.3617
998.5    48.00  0.51     Sequence
             DRB1_0901  426      DYNYKLPDDFTGCVI  YNYKLPDDF  1        0.3715
897.6    45.00  0.39     Sequence
             DRB1_0901  427      YNYKLPDDFTGCVIA  YKLPDDFTG  2        0.3443
1205.8    55.00  0.38     Sequence
             DRB1_0901  428      NYKLPDDFTGCVIAW  YKLPDDFTG  1        0.2978
1994.3    65.00  0.38     Sequence
             DRB1_0901  429      YKLPDDFTGCVIAWN  PDDFTGCVI  3        0.2774
2484.9    70.00  0.25     Sequence
             DRB1_0901  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.2794
2432.8    70.00  0.41     Sequence
             DRB1_0901  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.2688
2729.6    75.00  0.43     Sequence
             DRB1_0901  432      PDDFTGCVIAWNSNN  CVIAWNSNN  6        0.3873
756.6    42.00  0.53     Sequence
             DRB1_0901  433      DDFTGCVIAWNSNNL  CVIAWNSNN  5        0.4625
335.4    25.00  0.42     Sequence
             DRB1_0901  434      DFTGCVIAWNSNNLD  CVIAWNSNN  4        0.4760
290.1    23.00  0.44     Sequence
             DRB1_0901  435      FTGCVIAWNSNNLDS  CVIAWNSNN  3        0.4856
261.4    21.00  0.45     Sequence
             DRB1_0901  436      TGCVIAWNSNNLDSK  CVIAWNSNN  2        0.4881
254.5    21.00  0.48     Sequence
             DRB1_0901  437      GCVIAWNSNNLDSKV  VIAWNSNNL  2        0.4669
319.9    24.00  0.40     Sequence
             DRB1_0901  438      CVIAWNSNNLDSKVG  VIAWNSNNL  1        0.4005
656.4    39.00  0.47     Sequence
             DRB1_0901  439      VIAWNSNNLDSKVGG  VIAWNSNNL  0        0.2968
2014.4    65.00  0.56     Sequence
             DRB1_0901  440      IAWNSNNLDSKVGGN  WNSNNLDSK  2        0.1658
8313.4    95.00  0.24     Sequence
             DRB1_0901  441      AWNSNNLDSKVGGNY  LDSKVGGNY  6        0.1506
9796.7    95.00  0.25     Sequence
             DRB1_0901  442      WNSNNLDSKVGGNYN  LDSKVGGNY  5        0.1269
12661.3   100.00  0.31     Sequence
             DRB1_0901  443      NSNNLDSKVGGNYNY  SKVGGNYNY  6        0.1670
8206.5    95.00  0.39     Sequence
             DRB1_0901  444      SNNLDSKVGGNYNYL  SKVGGNYNY  5        0.1961
5990.8    90.00  0.40     Sequence
             DRB1_0901  445      NNLDSKVGGNYNYLY  SKVGGNYNY  4        0.2322
4052.3    80.00  0.33     Sequence
             DRB1_0901  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.2263
4322.0    85.00  0.34     Sequence
             DRB1_0901  447      LDSKVGGNYNYLYRL  GNYNYLYRL  6        0.2972
2007.5    65.00  0.35     Sequence
```

```
             DRB1_0901  448      DSKVGGNYNYLYRLF  NYNYLYRLF  6        0.3333
1357.6    55.00  0.29     Sequence
             DRB1_0901  449      SKVGGNYNYLYRLFR  GNYNYLYRL  4        0.3031
1882.7    65.00  0.29     Sequence
             DRB1_0901  450      KVGGNYNYLYRLFRK  GNYNYLYRL  3        0.2757
2531.8    70.00  0.33     Sequence
             DRB1_0901  451      VGGNYNYLYRLFRKS  GNYNYLYRL  2        0.2769
2498.5    70.00  0.25     Sequence
             DRB1_0901  452      GGNYNYLYRLFRKSN  GNYNYLYRL  1        0.2955
2044.4    65.00  0.21     Sequence
             DRB1_0901  453      GNYNYLYRLFRKSNL  YRLFRKSNL  6        0.4376
439.4    30.00  0.67     Sequence
             DRB1_0901  454      NYNYLYRLFRKSNLK  YRLFRKSNL  5        0.4230
514.6    33.00  0.69     Sequence
             DRB1_0901  455      YNYLYRLFRKSNLKP  YRLFRKSNL  4        0.4067
613.3    37.00  0.71     Sequence
             DRB1_0901  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6        0.5170
186.0    16.00  0.50     Sequence
             DRB1_0901  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.5376
148.8    13.00  0.65     Sequence
             DRB1_0901  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.5328
156.8    14.00  0.69     Sequence
             DRB1_0901  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.5133
193.7    17.00  0.73     Sequence
             DRB1_0901  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.4822
271.1    22.00  0.88     Sequence
             DRB1_0901  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.4633
332.7    25.00  0.75     Sequence
             DRB1_0901  462      FRKSNLKPFERDIST  FRKSNLKPF  0        0.4089
598.9    37.00  0.59     Sequence
             DRB1_0901  463      RKSNLKPFERDISTE  LKPFERDIS  4        0.2547
3176.3    75.00  0.74     Sequence
             DRB1_0901  464      KSNLKPFERDISTEI  LKPFERDIS  3        0.3390
1275.9    55.00  0.41     Sequence
             DRB1_0901  465      SNLKPFERDISTEIY  FERDISTEI  5        0.3862
765.6    42.00  0.50     Sequence
             DRB1_0901  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.3983
672.0    39.00  0.53     Sequence
             DRB1_0901  467      LKPFERDISTEIYQA  FERDISTEI  3        0.4006
655.2    39.00  0.57     Sequence
             DRB1_0901  468      KPFERDISTEIYQAG  FERDISTEI  2        0.3829
793.8    43.00  0.68     Sequence
             DRB1_0901  469      PFERDISTEIYQAGS  FERDISTEI  1        0.3505
1127.1    55.00  0.63     Sequence
             DRB1_0901  470      FERDISTEIYQAGST  FERDISTEI  0        0.3020
1903.9    65.00  0.44     Sequence
             DRB1_0901  471      ERDISTEIYQAGSTP  TEIYQAGST  5        0.2291
4191.0    85.00  0.32     Sequence
             DRB1_0901  472      RDISTEIYQAGSTPC  IYQAGSTPC  6        0.3377
1293.9    55.00  0.64     Sequence
             DRB1_0901  473      DISTEIYQAGSTPCN  IYQAGSTPC  5        0.3758
857.7    44.00  0.65     Sequence
             DRB1_0901  474      ISTEIYQAGSTPCNG  IYQAGSTPC  4        0.3873
757.2    42.00  0.67     Sequence
             DRB1_0901  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.3991
666.0    39.00  0.64     Sequence
             DRB1_0901  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.3807
812.7    43.00  0.66     Sequence
             DRB1_0901  477      EIYQAGSTPCNGVKG  IYQAGSTPC  1        0.3496
1138.5    55.00  0.62     Sequence
             DRB1_0901  478      IYQAGSTPCNGVKGF  IYQAGSTPC  0        0.2786
2454.2    70.00  0.47     Sequence
             DRB1_0901  479      YQAGSTPCNGVKGFN  YQAGSTPCN  0        0.1666
8244.3    95.00  0.34     Sequence
             DRB1_0901  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.2132
4976.5    85.00  0.61     Sequence
```

```
             DRB1_0901  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.2177
4742.9    85.00  0.71     Sequence
             DRB1_0901  482      GSTPCNGVKGFNCYF  GVKGFNCYF  6        0.2957
2038.3    65.00  0.46     Sequence
             DRB1_0901  483      STPCNGVKGFNCYFP  GVKGFNCYF  5        0.3191
1582.7    60.00  0.35     Sequence
             DRB1_0901  484      TPCNGVKGFNCYFPL  GVKGFNCYF  4        0.3294
1416.2    60.00  0.31     Sequence
             DRB1_0901  485      PCNGVKGFNCYFPLQ  GVKGFNCYF  3        0.3201
1565.5    60.00  0.30     Sequence
             DRB1_0901  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.4384
435.4    30.00  0.55     Sequence
             DRB1_0901  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.4320
466.7    31.00  0.59     Sequence
             DRB1_0901  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.4473
395.4    28.00  0.57     Sequence
             DRB1_0901  489      VKGFNCYFPLQSYGF  YFPLQSYGF  6        0.6276
56.2     4.50  0.75     Sequence         WB
             DRB1_0901  490      KGFNCYFPLQSYGFQ  YFPLQSYGF  5        0.6331
53.0     4.50  0.71     Sequence         WB
             DRB1_0901  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.6196
61.3     5.00  0.73     Sequence         WB
             DRB1_0901  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.6201
61.0     5.00  0.74     Sequence         WB
             DRB1_0901  493      NCYFPLQSYGFQPTY  YFPLQSYGF  2        0.6265
56.9     5.00  0.75     Sequence         WB
             DRB1_0901  494      CYFPLQSYGFQPTYG  YFPLQSYGF  1        0.6085
69.1     6.00  0.72     Sequence         WB
             DRB1_0901  495      YFPLQSYGFQPTYGV  YFPLQSYGF  0        0.5650
110.7    10.00  0.56     Sequence
             DRB1_0901  496      FPLQSYGFQPTYGVG  SYGFQPTYG  4        0.4544
366.4    27.00  0.23     Sequence
             DRB1_0901  497      PLQSYGFQPTYGVGY  FQPTYGVGY  6        0.5762
98.1     9.00  0.57     Sequence         WB
             DRB1_0901  498      LQSYGFQPTYGVGYQ  FQPTYGVGY  5        0.5748
99.6     9.00  0.66     Sequence         WB
             DRB1_0901  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4        0.5595
117.4    11.00  0.71     Sequence
             DRB1_0901  500      SYGFQPTYGVGYQPY  FQPTYGVGY  3        0.5511
128.6    12.00  0.74     Sequence
             DRB1_0901  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.5723
102.3     9.00  0.58     Sequence         WB
             DRB1_0901  502      GFQPTYGVGYQPYRV  FQPTYGVGY  1        0.5835
90.6     8.00  0.47     Sequence         WB
             DRB1_0901  503      FQPTYGVGYQPYRVV  YGVGYQPYR  4        0.5439
139.1    13.00  0.34     Sequence
             DRB1_0901  504      QPTYGVGYQPYRVVV  YGVGYQPYR  3        0.5160
188.0    16.00  0.41     Sequence
             DRB1_0901  505      PTYGVGYQPYRVVVL  YQPYRVVVL  6        0.5841
90.0     8.00  0.34     Sequence         WB
             DRB1_0901  506      TYGVGYQPYRVVVLS  YQPYRVVVL  5        0.5538
124.9    11.00  0.41     Sequence
             DRB1_0901  507      YGVGYQPYRVVVLSF  YQPYRVVVL  4        0.5362
151.2    14.00  0.43     Sequence
             DRB1_0901  508      GVGYQPYRVVVLSFE  YQPYRVVVL  3        0.5205
179.2    16.00  0.42     Sequence
             DRB1_0901  509      VGYQPYRVVVLSFEL  YQPYRVVVL  2        0.5307
160.4    14.00  0.36     Sequence
             DRB1_0901  510      GYQPYRVVVLSFELL  YQPYRVVVL  1        0.5150
190.1    16.00  0.34     Sequence
             DRB1_0901  511      YQPYRVVVLSFELLH  RVVVLSFEL  4        0.4883
253.9    21.00  0.28     Sequence
             DRB1_0901  512      QPYRVVVLSFELLHA  RVVVLSFEL  3        0.4354
449.8    31.00  0.34     Sequence
             DRB1_0901  513      PYRVVVLSFELLHAP  RVVVLSFEL  2        0.4054
622.0    37.00  0.34     Sequence
```

```
             DRB1_0901  514      YRVVVLSFELLHAPA  RVVVLSFEL  1        0.3806
814.0    43.00  0.31     Sequence
             DRB1_0901  515      RVVVLSFELLHAPAT  FELLHAPAT  6        0.5452
137.1    12.00  0.69     Sequence
             DRB1_0901  516      VVVLSFELLHAPATV  FELLHAPAT  5        0.5735
100.9     9.00  0.69     Sequence         WB
             DRB1_0901  517      VVLSFELLHAPATVC  FELLHAPAT  4        0.5775
96.7     8.50  0.64     Sequence         WB
             DRB1_0901  518      VLSFELLHAPATVCG  FELLHAPAT  3        0.5732
101.3     9.00  0.63     Sequence         WB
             DRB1_0901  519      LSFELLHAPATVCGP  FELLHAPAT  2        0.5602
116.5    11.00  0.64     Sequence
             DRB1_0901  520      SFELLHAPATVCGPK  FELLHAPAT  1        0.5439
139.1    13.00  0.62     Sequence
             DRB1_0901  521      FELLHAPATVCGPKK  FELLHAPAT  0        0.4412
422.4    29.00  0.52     Sequence
             DRB1_0901  522      ELLHAPATVCGPKKS  LLHAPATVC  1        0.2836
2324.7    70.00  0.44     Sequence
             DRB1_0901  523      LLHAPATVCGPKKST  LLHAPATVC  0        0.1823
6957.2    90.00  0.47     Sequence
             DRB1_0901  524      LHAPATVCGPKKSTN  ATVCGPKKS  4        0.1013
16715.9   100.00  0.33     Sequence
             DRB1_0901  525      HAPATVCGPKKSTNL  CGPKKSTNL  6        0.1363
11441.7   100.00  0.38     Sequence
             DRB1_0901  526      APATVCGPKKSTNLV  CGPKKSTNL  5        0.1506
9800.6    95.00  0.45     Sequence
             DRB1_0901  527      PATVCGPKKSTNLVK  CGPKKSTNL  4        0.1701
7940.8    95.00  0.40     Sequence
             DRB1_0901  528      ATVCGPKKSTNLVKN  CGPKKSTNL  3        0.1710
7858.8    95.00  0.40     Sequence
             DRB1_0901  529      TVCGPKKSTNLVKNK  CGPKKSTNL  2        0.1618
8686.9    95.00  0.39     Sequence
             DRB1_0901  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3        0.1504
9827.6    95.00  0.39     Sequence
             DRB1_0901  531      CGPKKSTNLVKNKCV  TNLVKNKCV  6        0.2184
4708.3    85.00  0.54     Sequence
             DRB1_0901  532      GPKKSTNLVKNKCVN  TNLVKNKCV  5        0.2141
4929.3    85.00  0.57     Sequence
             DRB1_0901  533      PKKSTNLVKNKCVNF  LVKNKCVNF  6        0.2798
2422.0    70.00  0.54     Sequence
             DRB1_0901  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.2878
2222.1    70.00  0.60     Sequence
             DRB1_0901  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.2868
2244.5    70.00  0.62     Sequence
             DRB1_0901  536      STNLVKNKCVNFNFN  LVKNKCVNF  3        0.2762
2517.4    70.00  0.67     Sequence
             DRB1_0901  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2        0.2599
3004.7    75.00  0.67     Sequence
             DRB1_0901  538      NLVKNKCVNFNFNGL  LVKNKCVNF  1        0.3004
1939.0    65.00  0.46     Sequence
             DRB1_0901  539      LVKNKCVNFNFNGLT  CVNFNFNGL  5        0.3267
1457.8    60.00  0.33     Sequence
             DRB1_0901  540      VKNKCVNFNFNGLTG  CVNFNFNGL  4        0.3049
1845.8    65.00  0.38     Sequence
             DRB1_0901  541      KNKCVNFNFNGLTGT  FNFNGLTGT  6        0.3455
1189.9    55.00  0.28     Sequence
             DRB1_0901  542      NKCVNFNFNGLTGTG  FNFNGLTGT  5        0.3559
1063.3    49.00  0.29     Sequence
             DRB1_0901  543      KCVNFNFNGLTGTGV  FNGLTGTGV  6        0.6982
26.2     1.40  0.87     Sequence         SB
             DRB1_0901  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5        0.7413
16.4     0.60  0.90     Sequence         SB
             DRB1_0901  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.7522
14.6     0.50  0.90     Sequence         SB
             DRB1_0901  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3        0.7540
14.3     0.50  0.90     Sequence         SB
```

```
             DRB1_0901  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.7392
16.8     0.60  0.89     Sequence        SB
             DRB1_0901  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.7238
19.8     0.90  0.88     Sequence        SB
             DRB1_0901  549      FNGLTGTGVLTESNK  FNGLTGTGV  0        0.6236
58.7     5.00  0.84     Sequence        WB
             DRB1_0901  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.2271
4283.6    85.00  0.50     Sequence
             DRB1_0901  551      GLTGTGVLTESNKKF  LTGTGVLTE  1        0.2098
5168.0    85.00  0.40     Sequence
             DRB1_0901  552      LTGTGVLTESNKKFL  LTESNKKFL  6        0.3435
1215.3    55.00  0.72     Sequence
             DRB1_0901  553      TGTGVLTESNKKFLP  LTESNKKFL  5        0.3570
1050.1    49.00  0.81     Sequence
             DRB1_0901  554      GTGVLTESNKKFLPF  LTESNKKFL  4        0.3632
982.7    48.00  0.82     Sequence
             DRB1_0901  555      TGVLTESNKKFLPFQ  LTESNKKFL  3        0.3783
834.7    44.00  0.77     Sequence
             DRB1_0901  556      GVLTESNKKFLPFQQ  LTESNKKFL  2        0.4233
512.9    33.00  0.59     Sequence
             DRB1_0901  557      VLTESNKKFLPFQQF  LTESNKKFL  1        0.4080
604.8    37.00  0.54     Sequence
             DRB1_0901  558      LTESNKKFLPFQQFG  NKKFLPFQQ  4        0.3897
737.3    41.00  0.47     Sequence
             DRB1_0901  559      TESNKKFLPFQQFGR  FLPFQQFGR  6        0.4057
620.5    37.00  0.47     Sequence
             DRB1_0901  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5        0.4090
598.7    37.00  0.54     Sequence
             DRB1_0901  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4        0.4083
603.0    37.00  0.57     Sequence
             DRB1_0901  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.4272
491.6    32.00  0.47     Sequence
             DRB1_0901  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.4162
553.7    35.00  0.50     Sequence
             DRB1_0901  564      KFLPFQQFGRDIADT  FQQFGRDIA  4        0.4053
623.3    37.00  0.47     Sequence
             DRB1_0901  565      FLPFQQFGRDIADTT  FQQFGRDIA  3        0.3841
783.9    42.00  0.51     Sequence
             DRB1_0901  566      LPFQQFGRDIADTTD  FQQFGRDIA  2        0.3635
979.2    48.00  0.68     Sequence
             DRB1_0901  567      PFQQFGRDIADTTDA  FQQFGRDIA  1        0.3680
932.6    46.00  0.63     Sequence
             DRB1_0901  568      FQQFGRDIADTTDAV  FQQFGRDIA  0        0.3280
1437.7    60.00  0.57     Sequence
             DRB1_0901  569      QQFGRDIADTTDAVR  FGRDIADTT  2        0.2111
5090.8    85.00  0.66     Sequence
             DRB1_0901  570      QFGRDIADTTDAVRD  FGRDIADTT  1        0.2000
5743.6    90.00  0.55     Sequence
             DRB1_0901  571      FGRDIADTTDAVRDP  FGRDIADTT  0        0.1590
8946.9    95.00  0.37     Sequence
             DRB1_0901  572      GRDIADTTDAVRDPQ  IADTTDAVR  3        0.1151
14396.9   100.00  0.68     Sequence
             DRB1_0901  573      RDIADTTDAVRDPQT  IADTTDAVR  2        0.1065
15801.7   100.00  0.61     Sequence
             DRB1_0901  574      DIADTTDAVRDPQTL  IADTTDAVR  1        0.0974
17422.6   100.00  0.50     Sequence
             DRB1_0901  575      IADTTDAVRDPQTLE  IADTTDAVR  0        0.0880
19294.2   100.00  0.31     Sequence
             DRB1_0901  576      ADTTDAVRDPQTLEI  VRDPQTLEI  6        0.1418
10786.6   100.00  0.62     Sequence
             DRB1_0901  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5        0.1883
6515.4    90.00  0.57     Sequence
             DRB1_0901  578      TTDAVRDPQTLEILD  VRDPQTLEI  4        0.1952
6052.5    90.00  0.56     Sequence
             DRB1_0901  579      TDAVRDPQTLEILDI  VRDPQTLEI  3        0.2080
5265.3    85.00  0.55     Sequence
```

```
             DRB1_0901  580      DAVRDPQTLEILDIT  VRDPQTLEI  2        0.2037
5517.4    90.00  0.51     Sequence
             DRB1_0901  581      AVRDPQTLEILDITP  VRDPQTLEI  1        0.1863
6658.0    90.00  0.48     Sequence
             DRB1_0901  582      VRDPQTLEILDITPC  LEILDITPC  6        0.1761
7438.1    95.00  0.31     Sequence
             DRB1_0901  583      RDPQTLEILDITPCS  LEILDITPC  5        0.1499
9874.3    95.00  0.47     Sequence
             DRB1_0901  584      DPQTLEILDITPCSF  ILDITPCSF  6        0.2924
2114.4    70.00  0.56     Sequence
             DRB1_0901  585      PQTLEILDITPCSFG  ILDITPCSF  5        0.3096
1754.1    65.00  0.50     Sequence
             DRB1_0901  586      QTLEILDITPCSFGG  ILDITPCSF  4        0.3049
1846.4    65.00  0.47     Sequence
             DRB1_0901  587      TLEILDITPCSFGGV  ILDITPCSF  3        0.3130
1691.6    65.00  0.43     Sequence
             DRB1_0901  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.3108
1731.5    65.00  0.41     Sequence
             DRB1_0901  589      EILDITPCSFGGVSV  ILDITPCSF  1        0.3691
921.9    46.00  0.32     Sequence
             DRB1_0901  590      ILDITPCSFGGVSVI  CSFGGVSVI  6        0.4264
495.6    33.00  0.35     Sequence
             DRB1_0901  591      LDITPCSFGGVSVIT  CSFGGVSVI  5        0.3961
688.5    40.00  0.41     Sequence
             DRB1_0901  592      DITPCSFGGVSVITP  CSFGGVSVI  4        0.3909
728.1    41.00  0.39     Sequence
             DRB1_0901  593      ITPCSFGGVSVITPG  CSFGGVSVI  3        0.3783
834.7    44.00  0.39     Sequence
             DRB1_0901  594      TPCSFGGVSVITPGT  CSFGGVSVI  2        0.3682
931.0    46.00  0.38     Sequence
             DRB1_0901  595      PCSFGGVSVITPGTN  CSFGGVSVI  1        0.3603
1013.5    48.00  0.34     Sequence
             DRB1_0901  596      CSFGGVSVITPGTNT  FGGVSVITP  2        0.3068
1807.7    65.00  0.29     Sequence
             DRB1_0901  597      SFGGVSVITPGTNTS  VSVITPGTN  4        0.2659
2814.5    75.00  0.40     Sequence
             DRB1_0901  598      FGGVSVITPGTNTSN  VSVITPGTN  3        0.2433
3597.0    80.00  0.40     Sequence
             DRB1_0901  599      GGVSVITPGTNTSNQ  VSVITPGTN  2        0.2387
3777.4    80.00  0.43     Sequence
             DRB1_0901  600      GVSVITPGTNTSNQV  VSVITPGTN  1        0.2245
4406.9    85.00  0.37     Sequence
             DRB1_0901  601      VSVITPGTNTSNQVA  ITPGTNTSN  3        0.1928
6211.4    90.00  0.40     Sequence
             DRB1_0901  602      SVITPGTNTSNQVAV  TNTSNQVAV  6        0.2243
4414.9    85.00  0.51     Sequence
             DRB1_0901  603      VITPGTNTSNQVAVL  TNTSNQVAV  5        0.2542
3193.8    80.00  0.50     Sequence
             DRB1_0901  604      ITPGTNTSNQVAVLY  TNTSNQVAV  4        0.2660
2811.5    75.00  0.46     Sequence
             DRB1_0901  605      TPGTNTSNQVAVLYQ  TNTSNQVAV  3        0.2769
2499.2    70.00  0.43     Sequence
             DRB1_0901  606      PGTNTSNQVAVLYQG  TNTSNQVAV  2        0.2700
2691.9    75.00  0.40     Sequence
             DRB1_0901  607      GTNTSNQVAVLYQGV  TNTSNQVAV  1        0.2602
2995.2    75.00  0.31     Sequence
             DRB1_0901  608      TNTSNQVAVLYQGVN  VAVLYQGVN  6        0.2682
2746.7    75.00  0.38     Sequence
             DRB1_0901  609      NTSNQVAVLYQGVNC  AVLYQGVNC  6        0.3205
1559.2    60.00  0.39     Sequence
             DRB1_0901  610      TSNQVAVLYQGVNCT  AVLYQGVNC  5        0.3369
1305.9    55.00  0.34     Sequence
             DRB1_0901  611      SNQVAVLYQGVNCTE  LYQGVNCTE  6        0.3875
755.2    42.00  0.31     Sequence
             DRB1_0901  612      NQVAVLYQGVNCTEV  LYQGVNCTE  5        0.4140
566.9    35.00  0.37     Sequence
```

```
             DRB1_0901  613      QVAVLYQGVNCTEVP  LYQGVNCTE  4        0.4029
639.0    38.00  0.39     Sequence
             DRB1_0901  614      VAVLYQGVNCTEVPV  LYQGVNCTE  3        0.4046
627.4    38.00  0.41     Sequence
             DRB1_0901  615      AVLYQGVNCTEVPVA  LYQGVNCTE  2        0.3957
691.2    40.00  0.41     Sequence
             DRB1_0901  616      VLYQGVNCTEVPVAI  LYQGVNCTE  1        0.3342
1344.0    55.00  0.41     Sequence
             DRB1_0901  617      LYQGVNCTEVPVAIH  YQGVNCTEV  1        0.2757
2532.4    70.00  0.29     Sequence
             DRB1_0901  618      YQGVNCTEVPVAIHA  VNCTEVPVA  3        0.2186
4696.1    85.00  0.26     Sequence
             DRB1_0901  619      QGVNCTEVPVAIHAD  VNCTEVPVA  2        0.1944
6100.3    90.00  0.31     Sequence
             DRB1_0901  620      GVNCTEVPVAIHADQ  VNCTEVPVA  1        0.1859
6689.0    90.00  0.26     Sequence
             DRB1_0901  621      VNCTEVPVAIHADQL  PVAIHADQL  6        0.1911
6326.3    90.00  0.20     Sequence
             DRB1_0901  622      NCTEVPVAIHADQLT  VAIHADQLT  6        0.2372
3842.1    80.00  0.47     Sequence
             DRB1_0901  623      CTEVPVAIHADQLTP  VAIHADQLT  5        0.2418
3653.8    80.00  0.41     Sequence
             DRB1_0901  624      TEVPVAIHADQLTPT  VAIHADQLT  4        0.2580
3066.0    75.00  0.38     Sequence
             DRB1_0901  625      EVPVAIHADQLTPTW  VAIHADQLT  3        0.2503
3334.4    80.00  0.35     Sequence
             DRB1_0901  626      VPVAIHADQLTPTWR  VAIHADQLT  2        0.2443
3556.2    80.00  0.34     Sequence
             DRB1_0901  627      PVAIHADQLTPTWRV  DQLTPTWRV  6        0.2677
2761.7    75.00  0.26     Sequence
             DRB1_0901  628      VAIHADQLTPTWRVY  DQLTPTWRV  5        0.3127
1696.6    65.00  0.31     Sequence
             DRB1_0901  629      AIHADQLTPTWRVYS  LTPTWRVYS  6        0.4933
240.5    20.00  0.68     Sequence
             DRB1_0901  630      IHADQLTPTWRVYST  LTPTWRVYS  5        0.5167
186.5    16.00  0.71     Sequence
             DRB1_0901  631      HADQLTPTWRVYSTG  LTPTWRVYS  4        0.5140
192.2    17.00  0.72     Sequence
             DRB1_0901  632      ADQLTPTWRVYSTGS  LTPTWRVYS  3        0.5225
175.3    15.00  0.66     Sequence
             DRB1_0901  633      DQLTPTWRVYSTGSN  LTPTWRVYS  2        0.5588
118.4    11.00  0.49     Sequence
             DRB1_0901  634      QLTPTWRVYSTGSNV  RVYSTGSNV  6        0.6029
73.4     6.50  0.33     Sequence         WB
             DRB1_0901  635      LTPTWRVYSTGSNVF  VYSTGSNVF  6        0.6668
36.8     2.50  0.34     Sequence         WB
             DRB1_0901  636      TPTWRVYSTGSNVFQ  VYSTGSNVF  5        0.6663
37.0     2.50  0.34     Sequence         WB
             DRB1_0901  637      PTWRVYSTGSNVFQT  VYSTGSNVF  4        0.6702
35.5     2.50  0.34     Sequence         WB
             DRB1_0901  638      TWRVYSTGSNVFQTR  VYSTGSNVF  3        0.6451
46.5     3.50  0.36     Sequence         WB
             DRB1_0901  639      WRVYSTGSNVFQTRA  VYSTGSNVF  2        0.6162
63.6     5.50  0.36     Sequence         WB
             DRB1_0901  640      RVYSTGSNVFQTRAG  VYSTGSNVF  1        0.5743
100.1     9.00  0.35     Sequence         WB
             DRB1_0901  641      VYSTGSNVFQTRAGC  YSTGSNVFQ  1        0.4811
274.4    22.00  0.39     Sequence
             DRB1_0901  642      YSTGSNVFQTRAGCL  VFQTRAGCL  6        0.4758
290.4    23.00  0.55     Sequence
             DRB1_0901  643      STGSNVFQTRAGCLI  FQTRAGCLI  6        0.5588
118.3    11.00  0.47     Sequence
             DRB1_0901  644      TGSNVFQTRAGCLIG  FQTRAGCLI  5        0.5602
116.6    11.00  0.46     Sequence
             DRB1_0901  645      GSNVFQTRAGCLIGA  FQTRAGCLI  4        0.5634
112.6    10.00  0.47     Sequence
```

```
            DRB1_0901  646      SNVFQTRAGCLIGAE  FQTRAGCLI  3        0.5507
129.2    12.00  0.50     Sequence
            DRB1_0901  647      NVFQTRAGCLIGAEY  FQTRAGCLI  2        0.5318
158.5    14.00  0.49     Sequence
            DRB1_0901  648      VFQTRAGCLIGAEYV  FQTRAGCLI  1        0.5139
192.3    17.00  0.46     Sequence
            DRB1_0901  649      FQTRAGCLIGAEYVN  FQTRAGCLI  0        0.4333
459.9    31.00  0.47     Sequence
            DRB1_0901  650      QTRAGCLIGAEYVNN  GCLIGAEYV  4        0.3499
1134.8    55.00  0.36     Sequence
            DRB1_0901  651      TRAGCLIGAEYVNNS  LIGAEYVNN  5        0.3514
1115.9    55.00  0.34     Sequence
            DRB1_0901  652      RAGCLIGAEYVNNSY  LIGAEYVNN  4        0.3465
1177.5    55.00  0.38     Sequence
            DRB1_0901  653      AGCLIGAEYVNNSYE  LIGAEYVNN  3        0.3239
1503.7    60.00  0.43     Sequence
            DRB1_0901  654      GCLIGAEYVNNSYEC  LIGAEYVNN  2        0.2822
2361.3    70.00  0.47     Sequence
            DRB1_0901  655      CLIGAEYVNNSYECD  LIGAEYVNN  1        0.2241
4422.9    85.00  0.51     Sequence
            DRB1_0901  656      LIGAEYVNNSYECDI  VNNSYECDI  6        0.2771
2494.9    70.00  0.51     Sequence
            DRB1_0901  657      IGAEYVNNSYECDIP  VNNSYECDI  5        0.2669
2784.2    75.00  0.65     Sequence
            DRB1_0901  658      GAEYVNNSYECDIPI  VNNSYECDI  4        0.2866
2251.1    70.00  0.66     Sequence
            DRB1_0901  659      AEYVNNSYECDIPIG  VNNSYECDI  3        0.2842
2308.4    70.00  0.69     Sequence
            DRB1_0901  660      EYVNNSYECDIPIGA  VNNSYECDI  2        0.2837
2321.8    70.00  0.60     Sequence
            DRB1_0901  661      YVNNSYECDIPIGAG  VNNSYECDI  1        0.2742
2572.5    75.00  0.56     Sequence
            DRB1_0901  662      VNNSYECDIPIGAGI  VNNSYECDI  0        0.2751
2548.1    70.00  0.35     Sequence
            DRB1_0901  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.2240
4430.6    85.00  0.35     Sequence
            DRB1_0901  664      NSYECDIPIGAGICA  CDIPIGAGI  4        0.2391
3763.8    80.00  0.34     Sequence
            DRB1_0901  665      SYECDIPIGAGICAS  CDIPIGAGI  3        0.2416
3660.7    80.00  0.34     Sequence
            DRB1_0901  666      YECDIPIGAGICASY  IGAGICASY  6        0.2547
3178.7    75.00  0.25     Sequence
            DRB1_0901  667      ECDIPIGAGICASYQ  IGAGICASY  5        0.2533
3225.4    80.00  0.31     Sequence
            DRB1_0901  668      CDIPIGAGICASYQT  IGAGICASY  4        0.2540
3201.8    80.00  0.37     Sequence
            DRB1_0901  669      DIPIGAGICASYQTQ  IGAGICASY  3        0.2441
3564.7    80.00  0.41     Sequence
            DRB1_0901  670      IPIGAGICASYQTQT  ICASYQTQT  6        0.3525
1103.2    50.00  0.56     Sequence
            DRB1_0901  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.3671
941.6    47.00  0.62     Sequence
            DRB1_0901  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.3743
871.2    45.00  0.70     Sequence
            DRB1_0901  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.3589
1028.7    49.00  0.73     Sequence
            DRB1_0901  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.3437
1213.5    55.00  0.69     Sequence
            DRB1_0901  675      GICASYQTQTNSPRR  ICASYQTQT  1        0.3187
1590.0    60.00  0.53     Sequence
            DRB1_0901  676      ICASYQTQTNSPRRA  ICASYQTQT  0        0.2766
2507.7    70.00  0.31     Sequence
            DRB1_0901  677      CASYQTQTNSPRRAR  YQTQTNSPR  3        0.2098
5163.5    85.00  0.37     Sequence
            DRB1_0901  678      ASYQTQTNSPRRARS  YQTQTNSPR  2        0.2091
5205.7    85.00  0.37     Sequence
```

```
             DRB1_0901  679      SYQTQTNSPRRARSV  TQTNSPRRA  3        0.1944
6103.8    90.00  0.27     Sequence
             DRB1_0901  680      YQTQTNSPRRARSVA  TQTNSPRRA  2        0.1689
8045.1    95.00  0.34     Sequence
             DRB1_0901  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.2118
5054.7    85.00  0.46     Sequence
             DRB1_0901  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.2232
4466.5    85.00  0.52     Sequence
             DRB1_0901  683      QTNSPRRARSVASQS  RARSVASQS  6        0.2804
2406.3    70.00  0.41     Sequence
             DRB1_0901  684      TNSPRRARSVASQSI  RARSVASQS  5        0.3561
1061.1    49.00  0.29     Sequence
             DRB1_0901  685      NSPRRARSVASQSII  RSVASQSII  6        0.4706
307.2    24.00  0.46     Sequence
             DRB1_0901  686      SPRRARSVASQSIIA  SVASQSIIA  6        0.5694
105.5     9.50  0.46     Sequence         WB
             DRB1_0901  687      PRRARSVASQSIIAY  SVASQSIIA  5        0.5700
104.9     9.50  0.48     Sequence         WB
             DRB1_0901  688      RRARSVASQSIIAYT  SVASQSIIA  4        0.5795
94.6     8.50  0.44     Sequence         WB
             DRB1_0901  689      RARSVASQSIIAYTM  SVASQSIIA  3        0.5712
103.4     9.50  0.47     Sequence         WB
             DRB1_0901  690      ARSVASQSIIAYTMS  SVASQSIIA  2        0.5494
131.0    12.00  0.41     Sequence
             DRB1_0901  691      RSVASQSIIAYTMSL  SVASQSIIA  1        0.5387
147.1    13.00  0.34     Sequence
             DRB1_0901  692      SVASQSIIAYTMSLG  ASQSIIAYT  2        0.4870
257.4    21.00  0.25     Sequence
             DRB1_0901  693      VASQSIIAYTMSLGA  IAYTMSLGA  6        0.5356
152.1    14.00  0.50     Sequence
             DRB1_0901  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.5776
96.6     8.50  0.51     Sequence         WB
             DRB1_0901  695      SQSIIAYTMSLGAEN  YTMSLGAEN  6        0.7828
10.5     0.20  0.80     Sequence         SB
             DRB1_0901  696      QSIIAYTMSLGAENS  YTMSLGAEN  5        0.8197
7.0     0.05  0.84     Sequence         SB
             DRB1_0901  697      SIIAYTMSLGAENSV  YTMSLGAEN  4        0.8323
6.1     0.03  0.85     Sequence         SB
             DRB1_0901  698      IIAYTMSLGAENSVA  YTMSLGAEN  3        0.8350
6.0     0.03  0.86     Sequence         SB
             DRB1_0901  699      IAYTMSLGAENSVAY  YTMSLGAEN  2        0.8266
6.5     0.04  0.87     Sequence         SB
             DRB1_0901  700      AYTMSLGAENSVAYS  YTMSLGAEN  1        0.7984
8.9     0.12  0.89     Sequence         SB
             DRB1_0901  701      YTMSLGAENSVAYSN  YTMSLGAEN  0        0.6298
54.9     4.50  0.72     Sequence         WB
             DRB1_0901  702      TMSLGAENSVAYSNN  MSLGAENSV  1        0.3705
908.2    46.00  0.51     Sequence
             DRB1_0901  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.3182
1597.9    60.00  0.40     Sequence
             DRB1_0901  704      SLGAENSVAYSNNSI  LGAENSVAY  1        0.2798
2421.2    70.00  0.38     Sequence
             DRB1_0901  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.4790
280.7    22.00  0.79     Sequence
             DRB1_0901  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.5291
163.2    14.00  0.69     Sequence
             DRB1_0901  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.5230
174.4    15.00  0.67     Sequence
             DRB1_0901  708      ENSVAYSNNSIAIPT  VAYSNNSIA  3        0.5360
151.5    14.00  0.61     Sequence
             DRB1_0901  709      NSVAYSNNSIAIPTN  VAYSNNSIA  2        0.5234
173.6    15.00  0.61     Sequence
             DRB1_0901  710      SVAYSNNSIAIPTNF  VAYSNNSIA  1        0.4994
225.1    19.00  0.51     Sequence
             DRB1_0901  711      VAYSNNSIAIPTNFT  VAYSNNSIA  0        0.4245
506.0    33.00  0.36     Sequence
```

```
             DRB1_0901  712      AYSNNSIAIPTNFTI  IAIPTNFTI  6        0.3380
1291.0    55.00  0.33     Sequence
             DRB1_0901  713      YSNNSIAIPTNFTIS  IAIPTNFTI  5        0.3063
1818.1    65.00  0.38     Sequence
             DRB1_0901  714      SNNSIAIPTNFTISV  IAIPTNFTI  4        0.2937
2083.8    70.00  0.47     Sequence
             DRB1_0901  715      NNSIAIPTNFTISVT  IAIPTNFTI  3        0.2998
1950.3    65.00  0.46     Sequence
             DRB1_0901  716      NSIAIPTNFTISVTT  IAIPTNFTI  2        0.2891
2190.2    70.00  0.40     Sequence
             DRB1_0901  717      SIAIPTNFTISVTTE  IAIPTNFTI  1        0.2718
2640.6    75.00  0.41     Sequence
             DRB1_0901  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.7221
20.2     0.90  0.90     Sequence         SB
             DRB1_0901  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.7577
13.8     0.40  0.94     Sequence         SB
             DRB1_0901  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.7500
15.0     0.50  0.94     Sequence         SB
             DRB1_0901  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.7523
14.6     0.50  0.93     Sequence         SB
             DRB1_0901  722      TNFTISVTTEILPVS  FTISVTTEI  2        0.7245
19.7     0.90  0.94     Sequence         SB
             DRB1_0901  723      NFTISVTTEILPVSM  FTISVTTEI  1        0.6977
26.3     1.40  0.90     Sequence         SB
             DRB1_0901  724      FTISVTTEILPVSMT  FTISVTTEI  0        0.5975
77.8     7.00  0.79     Sequence         WB
             DRB1_0901  725      TISVTTEILPVSMTK  TTEILPVSM  4        0.2963
2025.5    65.00  0.40     Sequence
             DRB1_0901  726      ISVTTEILPVSMTKT  ILPVSMTKT  6        0.3884
747.9    41.00  0.54     Sequence
             DRB1_0901  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.4104
589.3    36.00  0.61     Sequence
             DRB1_0901  728      VTTEILPVSMTKTSV  ILPVSMTKT  4        0.4160
554.7    35.00  0.62     Sequence
             DRB1_0901  729      TTEILPVSMTKTSVD  ILPVSMTKT  3        0.4191
536.3    34.00  0.58     Sequence
             DRB1_0901  730      TEILPVSMTKTSVDC  ILPVSMTKT  2        0.3903
732.6    41.00  0.62     Sequence
             DRB1_0901  731      EILPVSMTKTSVDCT  ILPVSMTKT  1        0.3696
916.4    46.00  0.55     Sequence
             DRB1_0901  732      ILPVSMTKTSVDCTM  ILPVSMTKT  0        0.3583
1036.0    49.00  0.33     Sequence
             DRB1_0901  733      LPVSMTKTSVDCTMY  TKTSVDCTM  5        0.2990
1967.5    65.00  0.40     Sequence
             DRB1_0901  734      PVSMTKTSVDCTMYI  TKTSVDCTM  4        0.3269
1454.9    60.00  0.38     Sequence
             DRB1_0901  735      VSMTKTSVDCTMYIC  TKTSVDCTM  3        0.2825
2353.4    70.00  0.45     Sequence
             DRB1_0901  736      SMTKTSVDCTMYICG  TKTSVDCTM  2        0.2571
3098.1    75.00  0.50     Sequence
             DRB1_0901  737      MTKTSVDCTMYICGD  TKTSVDCTM  1        0.2186
4697.6    85.00  0.44     Sequence
             DRB1_0901  738      TKTSVDCTMYICGDS  TSVDCTMYI  2        0.1846
6785.0    90.00  0.31     Sequence
             DRB1_0901  739      KTSVDCTMYICGDST  CTMYICGDS  5        0.1758
7459.9    95.00  0.33     Sequence
             DRB1_0901  740      TSVDCTMYICGDSTE  CTMYICGDS  4        0.1840
6829.9    90.00  0.31     Sequence
             DRB1_0901  741      SVDCTMYICGDSTEC  YICGDSTEC  6        0.2088
5220.3    85.00  0.35     Sequence
             DRB1_0901  742      VDCTMYICGDSTECS  YICGDSTEC  5        0.2226
4499.1    85.00  0.41     Sequence
             DRB1_0901  743      DCTMYICGDSTECSN  YICGDSTEC  4        0.2174
4755.9    85.00  0.43     Sequence
             DRB1_0901  744      CTMYICGDSTECSNL  YICGDSTEC  3        0.2122
5032.4    85.00  0.43     Sequence
```

```
             DRB1_0901  745      TMYICGDSTECSNLL  YICGDSTEC  2        0.2112
5089.8    85.00  0.43     Sequence
             DRB1_0901  746      MYICGDSTECSNLLL  YICGDSTEC  1        0.1895
6431.6    90.00  0.35     Sequence
             DRB1_0901  747      YICGDSTECSNLLLQ  DSTECSNLL  4        0.1522
9633.6    95.00  0.20     Sequence
             DRB1_0901  748      ICGDSTECSNLLLQY  DSTECSNLL  3        0.1364
11427.7   100.00  0.25     Sequence
             DRB1_0901  749      CGDSTECSNLLLQYG  DSTECSNLL  2        0.1357
11513.9   100.00  0.23     Sequence
             DRB1_0901  750      GDSTECSNLLLQYGS  STECSNLLL  2        0.1381
11217.1   100.00  0.26     Sequence
             DRB1_0901  751      DSTECSNLLLQYGSF  NLLLQYGSF  6        0.1376
11277.9   100.00  0.18     Sequence
             DRB1_0901  752      STECSNLLLQYGSFC  LLLQYGSFC  6        0.1813
7035.1    90.00  0.48     Sequence
             DRB1_0901  753      TECSNLLLQYGSFCT  LLQYGSFCT  6        0.2485
3399.5    80.00  0.46     Sequence
             DRB1_0901  754      ECSNLLLQYGSFCTQ  LLQYGSFCT  5        0.2711
2662.2    75.00  0.37     Sequence
             DRB1_0901  755      CSNLLLQYGSFCTQL  QYGSFCTQL  6        0.3241
1499.6    60.00  0.23     Sequence
             DRB1_0901  756      SNLLLQYGSFCTQLN  YGSFCTQLN  6        0.3746
868.8    45.00  0.32     Sequence
             DRB1_0901  757      NLLLQYGSFCTQLNR  YGSFCTQLN  5        0.3655
957.9    47.00  0.38     Sequence
             DRB1_0901  758      LLLQYGSFCTQLNRA  YGSFCTQLN  4        0.3578
1041.9    49.00  0.42     Sequence
             DRB1_0901  759      LLQYGSFCTQLNRAL  FCTQLNRAL  6        0.4724
301.3    23.00  0.55     Sequence
             DRB1_0901  760      LQYGSFCTQLNRALT  FCTQLNRAL  5        0.4905
247.9    20.00  0.57     Sequence
             DRB1_0901  761      QYGSFCTQLNRALTG  FCTQLNRAL  4        0.4778
284.4    22.00  0.60     Sequence
             DRB1_0901  762      YGSFCTQLNRALTGI  FCTQLNRAL  3        0.4618
338.1    25.00  0.71     Sequence
             DRB1_0901  763      GSFCTQLNRALTGIA  LNRALTGIA  6        0.5734
101.1     9.00  0.53     Sequence         WB
             DRB1_0901  764      SFCTQLNRALTGIAV  LNRALTGIA  5        0.5890
85.3     7.50  0.58     Sequence         WB
             DRB1_0901  765      FCTQLNRALTGIAVE  LNRALTGIA  4        0.5759
98.4     9.00  0.65     Sequence         WB
             DRB1_0901  766      CTQLNRALTGIAVEQ  LNRALTGIA  3        0.5520
127.3    12.00  0.75     Sequence
             DRB1_0901  767      TQLNRALTGIAVEQD  LNRALTGIA  2        0.5428
140.7    13.00  0.75     Sequence
             DRB1_0901  768      QLNRALTGIAVEQDK  LNRALTGIA  1        0.5119
196.5    17.00  0.73     Sequence
             DRB1_0901  769      LNRALTGIAVEQDKN  LNRALTGIA  0        0.4311
471.2    32.00  0.58     Sequence
             DRB1_0901  770      NRALTGIAVEQDKNT  NRALTGIAV  0        0.2491
3377.3    80.00  0.35     Sequence
             DRB1_0901  771      RALTGIAVEQDKNTQ  ALTGIAVEQ  1        0.1808
7067.7    90.00  0.28     Sequence
             DRB1_0901  772      ALTGIAVEQDKNTQE  IAVEQDKNT  4        0.1447
10444.6    95.00  0.31     Sequence
             DRB1_0901  773      LTGIAVEQDKNTQEV  IAVEQDKNT  3        0.1152
14378.2   100.00  0.41     Sequence
             DRB1_0901  774      TGIAVEQDKNTQEVF  IAVEQDKNT  2        0.1178
13978.2   100.00  0.44     Sequence
             DRB1_0901  775      GIAVEQDKNTQEVFA  DKNTQEVFA  6        0.1855
6721.9    90.00  0.55     Sequence
             DRB1_0901  776      IAVEQDKNTQEVFAQ  DKNTQEVFA  5        0.1967
5953.9    90.00  0.60     Sequence
             DRB1_0901  777      AVEQDKNTQEVFAQV  DKNTQEVFA  4        0.2110
5101.6    85.00  0.62     Sequence
```

```
             DRB1_0901  778      VEQDKNTQEVFAQVK  DKNTQEVFA  3        0.2099
5162.4    85.00  0.60     Sequence
             DRB1_0901  779      EQDKNTQEVFAQVKQ  DKNTQEVFA  2        0.2311
4100.7    85.00  0.46     Sequence
             DRB1_0901  780      QDKNTQEVFAQVKQI  EVFAQVKQI  6        0.3134
1683.2    65.00  0.49     Sequence
             DRB1_0901  781      DKNTQEVFAQVKQIY  EVFAQVKQI  5        0.3218
1538.1    60.00  0.50     Sequence
             DRB1_0901  782      KNTQEVFAQVKQIYK  EVFAQVKQI  4        0.3380
1289.7    55.00  0.46     Sequence
             DRB1_0901  783      NTQEVFAQVKQIYKT  EVFAQVKQI  3        0.3504
1128.7    55.00  0.43     Sequence
             DRB1_0901  784      TQEVFAQVKQIYKTP  EVFAQVKQI  2        0.3404
1257.1    55.00  0.41     Sequence
             DRB1_0901  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.3305
1399.6    60.00  0.43     Sequence
             DRB1_0901  786      EVFAQVKQIYKTPPI  FAQVKQIYK  2        0.3433
1218.9    55.00  0.35     Sequence
             DRB1_0901  787      VFAQVKQIYKTPPIK  KQIYKTPPI  5        0.3344
1341.0    55.00  0.44     Sequence
             DRB1_0901  788      FAQVKQIYKTPPIKD  KQIYKTPPI  4        0.3410
1249.6    55.00  0.38     Sequence
             DRB1_0901  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.3484
1153.4    55.00  0.39     Sequence
             DRB1_0901  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.3376
1296.6    55.00  0.43     Sequence
             DRB1_0901  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.3245
1493.8    60.00  0.47     Sequence
             DRB1_0901  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.2931
2098.5    70.00  0.57     Sequence
             DRB1_0901  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.2525
3254.0    80.00  0.57     Sequence
             DRB1_0901  794      IYKTPPIKDFGGFNF  IKDFGGFNF  6        0.3660
953.2    47.00  0.73     Sequence
             DRB1_0901  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.3652
961.0    47.00  0.80     Sequence
             DRB1_0901  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.3742
872.2    45.00  0.77     Sequence
             DRB1_0901  797      TPPIKDFGGFNFSQI  FGGFNFSQI  6        0.5107
199.3    17.00  0.52     Sequence
             DRB1_0901  798      PPIKDFGGFNFSQIL  FGGFNFSQI  5        0.5432
140.0    13.00  0.59     Sequence
             DRB1_0901  799      PIKDFGGFNFSQILP  FGGFNFSQI  4        0.5410
143.5    13.00  0.57     Sequence
             DRB1_0901  800      IKDFGGFNFSQILPD  FGGFNFSQI  3        0.5793
94.8     8.50  0.48     Sequence         WB
             DRB1_0901  801      KDFGGFNFSQILPDP  FGGFNFSQI  2        0.5727
101.8     9.00  0.54     Sequence         WB
             DRB1_0901  802      DFGGFNFSQILPDPS  FGGFNFSQI  1        0.5764
97.9     8.50  0.47     Sequence         WB
             DRB1_0901  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.5577
119.7    11.00  0.37     Sequence
             DRB1_0901  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.4839
266.1    21.00  0.62     Sequence
             DRB1_0901  805      GFNFSQILPDPSKPS  FNFSQILPD  1        0.4697
310.4    24.00  0.56     Sequence
             DRB1_0901  806      FNFSQILPDPSKPSK  FNFSQILPD  0        0.4074
608.8    37.00  0.43     Sequence
             DRB1_0901  807      NFSQILPDPSKPSKR  FSQILPDPS  1        0.2849
2291.3    70.00  0.71     Sequence
             DRB1_0901  808      FSQILPDPSKPSKRS  FSQILPDPS  0        0.2149
4889.6    85.00  0.52     Sequence
             DRB1_0901  809      SQILPDPSKPSKRSF  PDPSKPSKR  4        0.1541
9436.9    95.00  0.31     Sequence
             DRB1_0901  810      QILPDPSKPSKRSFI  SKPSKRSFI  6        0.4037
634.0    38.00  0.82     Sequence
```

```
             DRB1_0901  811      ILPDPSKPSKRSFIE  SKPSKRSFI  5        0.4325
464.1    31.00  0.87     Sequence
             DRB1_0901  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.4314
470.0    31.00  0.88     Sequence
             DRB1_0901  813      PDPSKPSKRSFIEDL  SKPSKRSFI  3        0.4715
304.4    24.00  0.74     Sequence
             DRB1_0901  814      DPSKPSKRSFIEDLL  SKPSKRSFI  2        0.4867
258.2    21.00  0.56     Sequence
             DRB1_0901  815      PSKPSKRSFIEDLLF  SKPSKRSFI  1        0.4792
279.9    22.00  0.47     Sequence
             DRB1_0901  816      SKPSKRSFIEDLLFN  SKPSKRSFI  0        0.4266
494.8    33.00  0.29     Sequence
             DRB1_0901  817      KPSKRSFIEDLLFNK  KRSFIEDLL  3        0.3671
941.5    47.00  0.40     Sequence
             DRB1_0901  818      PSKRSFIEDLLFNKV  KRSFIEDLL  2        0.3535
1090.8    50.00  0.38     Sequence
             DRB1_0901  819      SKRSFIEDLLFNKVT  KRSFIEDLL  1        0.3219
1535.4    60.00  0.34     Sequence
             DRB1_0901  820      KRSFIEDLLFNKVTL  KRSFIEDLL  0        0.2816
2375.6    70.00  0.30     Sequence
             DRB1_0901  821      RSFIEDLLFNKVTLA  LLFNKVTLA  6        0.2685
2735.7    75.00  0.33     Sequence
             DRB1_0901  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5        0.2549
3172.2    75.00  0.31     Sequence
             DRB1_0901  823      FIEDLLFNKVTLADA  FNKVTLADA  6        0.3824
798.5    43.00  0.61     Sequence
             DRB1_0901  824      IEDLLFNKVTLADAG  FNKVTLADA  5        0.4269
493.0    32.00  0.67     Sequence
             DRB1_0901  825      EDLLFNKVTLADAGF  FNKVTLADA  4        0.4497
385.5    28.00  0.68     Sequence
             DRB1_0901  826      DLLFNKVTLADAGFI  VTLADAGFI  6        0.5457
136.4    12.00  0.45     Sequence
             DRB1_0901  827      LLFNKVTLADAGFIK  FNKVTLADA  2        0.5378
148.6    13.00  0.44     Sequence
             DRB1_0901  828      LFNKVTLADAGFIKQ  FNKVTLADA  1        0.5270
166.9    15.00  0.41     Sequence
             DRB1_0901  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.4931
240.8    20.00  0.50     Sequence
             DRB1_0901  830      NKVTLADAGFIKQYG  VTLADAGFI  2        0.4239
509.6    33.00  0.73     Sequence
             DRB1_0901  831      KVTLADAGFIKQYGD  VTLADAGFI  1        0.3838
786.4    43.00  0.72     Sequence
             DRB1_0901  832      VTLADAGFIKQYGDC  VTLADAGFI  0        0.2924
2113.3    70.00  0.63     Sequence
             DRB1_0901  833      TLADAGFIKQYGDCL  FIKQYGDCL  6        0.2635
2889.9    75.00  0.62     Sequence
             DRB1_0901  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.3221
1532.5    60.00  0.52     Sequence
             DRB1_0901  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4        0.3267
1457.5    60.00  0.51     Sequence
             DRB1_0901  836      DAGFIKQYGDCLGDI  FIKQYGDCL  3        0.3316
1382.5    60.00  0.55     Sequence
             DRB1_0901  837      AGFIKQYGDCLGDIA  FIKQYGDCL  2        0.3381
1288.7    55.00  0.50     Sequence
             DRB1_0901  838      GFIKQYGDCLGDIAA  FIKQYGDCL  1        0.3189
1587.4    60.00  0.46     Sequence
             DRB1_0901  839      FIKQYGDCLGDIAAR  IKQYGDCLG  1        0.2808
2395.2    70.00  0.39     Sequence
             DRB1_0901  840      IKQYGDCLGDIAARD  IKQYGDCLG  0        0.2243
4415.2    85.00  0.41     Sequence
             DRB1_0901  841      KQYGDCLGDIAARDL  LGDIAARDL  6        0.2128
4999.8    85.00  0.44     Sequence
             DRB1_0901  842      QYGDCLGDIAARDLI  LGDIAARDL  5        0.2442
3560.3    80.00  0.49     Sequence
             DRB1_0901  843      YGDCLGDIAARDLIC  LGDIAARDL  4        0.2377
3820.9    80.00  0.52     Sequence
```

```
             DRB1_0901  844      GDCLGDIAARDLICA  LGDIAARDL  3        0.2413
3673.9    80.00  0.57     Sequence
             DRB1_0901  845      DCLGDIAARDLICAQ  LGDIAARDL  2        0.2290
4196.7    85.00  0.52     Sequence
             DRB1_0901  846      CLGDIAARDLICAQK  LGDIAARDL  1        0.2140
4933.7    85.00  0.50     Sequence
             DRB1_0901  847      LGDIAARDLICAQKF  LGDIAARDL  0        0.2108
5112.8    85.00  0.31     Sequence
             DRB1_0901  848      GDIAARDLICAQKFN  RDLICAQKF  5        0.1658
8311.0    95.00  0.31     Sequence
             DRB1_0901  849      DIAARDLICAQKFNG  LICAQKFNG  6        0.2556
3148.7    75.00  0.61     Sequence
             DRB1_0901  850      IAARDLICAQKFNGL  LICAQKFNG  5        0.2876
2225.4    70.00  0.61     Sequence
             DRB1_0901  851      AARDLICAQKFNGLT  LICAQKFNG  4        0.3036
1872.1    65.00  0.57     Sequence
             DRB1_0901  852      ARDLICAQKFNGLTV  AQKFNGLTV  6        0.4173
547.3    35.00  0.50     Sequence
             DRB1_0901  853      RDLICAQKFNGLTVL  AQKFNGLTV  5        0.4360
447.0    31.00  0.49     Sequence
             DRB1_0901  854      DLICAQKFNGLTVLP  AQKFNGLTV  4        0.4310
471.6    32.00  0.51     Sequence
             DRB1_0901  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.5116
197.3    17.00  0.51     Sequence
             DRB1_0901  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.5337
155.3    14.00  0.58     Sequence
             DRB1_0901  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.5826
91.5     8.00  0.51     Sequence         WB
             DRB1_0901  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.5807
93.4     8.50  0.52     Sequence         WB
             DRB1_0901  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.5407
144.0    13.00  0.56     Sequence
             DRB1_0901  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1        0.5144
191.3    16.00  0.50     Sequence
             DRB1_0901  861      FNGLTVLPPLLTDEM  FNGLTVLPP  0        0.4300
477.0    32.00  0.35     Sequence
             DRB1_0901  862      NGLTVLPPLLTDEMI  GLTVLPPLL  1        0.3513
1117.0    55.00  0.41     Sequence
             DRB1_0901  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.3213
1546.7    60.00  0.46     Sequence
             DRB1_0901  864      LTVLPPLLTDEMIAQ  LTVLPPLLT  0        0.2475
3436.5    80.00  0.37     Sequence
             DRB1_0901  865      TVLPPLLTDEMIAQY  PLLTDEMIA  4        0.2207
4590.4    85.00  0.32     Sequence
             DRB1_0901  866      VLPPLLTDEMIAQYT  PLLTDEMIA  3        0.2258
4345.3    85.00  0.28     Sequence
             DRB1_0901  867      LPPLLTDEMIAQYTS  LTDEMIAQY  4        0.2218
4534.5    85.00  0.23     Sequence
             DRB1_0901  868      PPLLTDEMIAQYTSA  LTDEMIAQY  3        0.2259
4339.1    85.00  0.25     Sequence
             DRB1_0901  869      PLLTDEMIAQYTSAL  MIAQYTSAL  6        0.4046
628.0    38.00  0.73     Sequence
             DRB1_0901  870      LLTDEMIAQYTSALL  IAQYTSALL  6        0.4954
234.9    19.00  0.48     Sequence
             DRB1_0901  871      LTDEMIAQYTSALLA  IAQYTSALL  5        0.5411
143.4    13.00  0.38     Sequence
             DRB1_0901  872      TDEMIAQYTSALLAG  IAQYTSALL  4        0.5338
155.1    14.00  0.41     Sequence
             DRB1_0901  873      DEMIAQYTSALLAGT  IAQYTSALL  3        0.5676
107.6     9.50  0.31     Sequence          WB
             DRB1_0901  874      EMIAQYTSALLAGTI  YTSALLAGT  5        0.5753
99.1     9.00  0.34     Sequence         WB
             DRB1_0901  875      MIAQYTSALLAGTIT  YTSALLAGT  4        0.5608
115.8    11.00  0.40     Sequence
             DRB1_0901  876      IAQYTSALLAGTITS  YTSALLAGT  3        0.5530
126.0    11.00  0.43     Sequence
```

```
             DRB1_0901  877      AQYTSALLAGTITSG  YTSALLAGT  2        0.4847
263.9    21.00 0.56      Sequence
             DRB1_0901  878      QYTSALLAGTITSGW  YTSALLAGT  1        0.4308
473.0    32.00 0.49      Sequence
             DRB1_0901  879      YTSALLAGTITSGWT  YTSALLAGT  0        0.3731
882.5    45.00 0.23      Sequence
             DRB1_0901  880      TSALLAGTITSGWTF  LAGTITSGW  4        0.3561
1061.0    49.00  0.25     Sequence
             DRB1_0901  881      SALLAGTITSGWTFG  LAGTITSGW  3        0.3675
937.3    47.00 0.25      Sequence
             DRB1_0901  882      ALLAGTITSGWTFGA  ITSGWTFGA  6        0.4105
588.7    36.00 0.44      Sequence
             DRB1_0901  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.4153
559.2    35.00 0.56      Sequence
             DRB1_0901  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.4324
464.9    31.00 0.59      Sequence
             DRB1_0901  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.4584
350.9    26.00 0.55      Sequence
             DRB1_0901  886      GTITSGWTFGAGAAL  WTFGAGAAL  6        0.6690
35.9     2.50  0.76     Sequence         WB
             DRB1_0901  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.6659
37.2     2.50  0.74     Sequence         WB
             DRB1_0901  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.7570
13.9     0.40  0.47     Sequence         SB
             DRB1_0901  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.7742
11.5     0.25  0.56     Sequence         SB
             DRB1_0901  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.7782
11.0     0.25  0.57     Sequence         SB
             DRB1_0901  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.7722
11.8     0.30  0.62     Sequence         SB
             DRB1_0901  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.7468
15.5     0.50  0.65     Sequence         SB
             DRB1_0901  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.7057
24.2     1.30  0.73     Sequence         SB
             DRB1_0901  894      FGAGAALQIPFAMQM  FGAGAALQI  0        0.6436
47.3     4.00  0.40     Sequence         WB
             DRB1_0901  895      GAGAALQIPFAMQMA  LQIPFAMQM  5        0.5842
89.9     8.00  0.43     Sequence         WB
             DRB1_0901  896      AGAALQIPFAMQMAY  LQIPFAMQM  4        0.5641
111.8    10.00 0.44      Sequence
             DRB1_0901  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.5496
130.7    12.00 0.49      Sequence
             DRB1_0901  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.5913
83.3     7.50  0.46     Sequence         WB
             DRB1_0901  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.5643
111.5    10.00 0.51      Sequence
             DRB1_0901  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.5420
141.9    13.00 0.51      Sequence
             DRB1_0901  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.5210
178.2    16.00 0.62      Sequence
             DRB1_0901  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.5181
183.9    16.00 0.56      Sequence
             DRB1_0901  903      PFAMQMAYRFNGIGV  AYRFNGIGV  6        0.6070
70.3     6.00  0.41     Sequence         WB
             DRB1_0901  904      FAMQMAYRFNGIGVT  AYRFNGIGV  5        0.6067
70.5     6.00  0.44     Sequence         WB
             DRB1_0901  905      AMQMAYRFNGIGVTQ  AYRFNGIGV  4        0.5798
94.3     8.50  0.51     Sequence         WB
             DRB1_0901  906      MQMAYRFNGIGVTQN  AYRFNGIGV  3        0.5736
100.8     9.00  0.51     Sequence         WB
             DRB1_0901  907      QMAYRFNGIGVTQNV  AYRFNGIGV  2        0.5795
94.6     8.50  0.50     Sequence         WB
             DRB1_0901  908      MAYRFNGIGVTQNVL  AYRFNGIGV  1        0.5637
112.3    10.00 0.49      Sequence
             DRB1_0901  909      AYRFNGIGVTQNVLY  AYRFNGIGV  0        0.5596
117.3    11.00 0.38      Sequence
```

```
             DRB1_0901  910      YRFNGIGVTQNVLYE  IGVTQNVLY  5        0.4291
481.4    32.00  0.38     Sequence
             DRB1_0901  911      RFNGIGVTQNVLYEN  IGVTQNVLY  4        0.3711
902.1    46.00  0.48     Sequence
             DRB1_0901  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.3194
1578.8    60.00  0.63     Sequence
             DRB1_0901  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.2921
2120.9    70.00  0.76     Sequence
             DRB1_0901  914      GIGVTQNVLYENQKL  IGVTQNVLY  1        0.2994
1958.5    65.00  0.54     Sequence
             DRB1_0901  915      IGVTQNVLYENQKLI  VLYENQKLI  6        0.3205
1559.2    60.00  0.34     Sequence
             DRB1_0901  916      GVTQNVLYENQKLIA  LYENQKLIA  6        0.3406
1255.1    55.00  0.46     Sequence
             DRB1_0901  917      VTQNVLYENQKLIAN  LYENQKLIA  5        0.3480
1158.4    55.00  0.50     Sequence
             DRB1_0901  918      TQNVLYENQKLIANQ  LYENQKLIA  4        0.3480
1158.0    55.00  0.52     Sequence
             DRB1_0901  919      QNVLYENQKLIANQF  LYENQKLIA  3        0.3420
1235.3    55.00  0.50     Sequence
             DRB1_0901  920      NVLYENQKLIANQFN  LYENQKLIA  2        0.3212
1547.9    60.00  0.51     Sequence
             DRB1_0901  921      VLYENQKLIANQFNS  LYENQKLIA  1        0.2920
2123.6    70.00  0.47     Sequence
             DRB1_0901  922      LYENQKLIANQFNSA  LYENQKLIA  0        0.2269
4291.5    85.00  0.31     Sequence
             DRB1_0901  923      YENQKLIANQFNSAI  IANQFNSAI  6        0.3022
1900.9    65.00  0.50     Sequence
             DRB1_0901  924      ENQKLIANQFNSAIG  ANQFNSAIG  6        0.4454
403.7    29.00  0.58     Sequence
             DRB1_0901  925      NQKLIANQFNSAIGK  ANQFNSAIG  5        0.4579
352.6    26.00  0.62     Sequence
             DRB1_0901  926      QKLIANQFNSAIGKI  ANQFNSAIG  4        0.5029
216.6    18.00  0.52     Sequence
             DRB1_0901  927      KLIANQFNSAIGKIQ  FNSAIGKIQ  6        0.5712
103.5     9.50  0.41     Sequence         WB
             DRB1_0901  928      LIANQFNSAIGKIQD  FNSAIGKIQ  5        0.5701
104.8     9.50  0.51     Sequence         WB
             DRB1_0901  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4        0.5725
102.1     9.00  0.57     Sequence         WB
             DRB1_0901  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.5517
127.8    12.00  0.66     Sequence
             DRB1_0901  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.5006
222.2    19.00  0.75     Sequence
             DRB1_0901  932      QFNSAIGKIQDSLSS  FNSAIGKIQ  1        0.4545
365.7    27.00  0.71     Sequence
             DRB1_0901  933      FNSAIGKIQDSLSST  FNSAIGKIQ  0        0.3374
1299.1    55.00  0.52     Sequence
             DRB1_0901  934      NSAIGKIQDSLSSTA  IQDSLSSTA  6        0.3437
1213.3    55.00  0.62     Sequence
             DRB1_0901  935      SAIGKIQDSLSSTAS  IQDSLSSTA  5        0.3724
889.0    45.00  0.67     Sequence
             DRB1_0901  936      AIGKIQDSLSSTASA  IQDSLSSTA  4        0.3901
734.7    41.00  0.70     Sequence
             DRB1_0901  937      IGKIQDSLSSTASAL  IQDSLSSTA  3        0.4647
327.5    25.00  0.49     Sequence
             DRB1_0901  938      GKIQDSLSSTASALG  LSSTASALG  6        0.5050
211.8    18.00  0.43     Sequence
             DRB1_0901  939      KIQDSLSSTASALGK  LSSTASALG  5        0.5101
200.6    17.00  0.55     Sequence
             DRB1_0901  940      IQDSLSSTASALGKL  LSSTASALG  4        0.5088
203.2    17.00  0.62     Sequence
             DRB1_0901  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.5022
218.4    18.00  0.64     Sequence
             DRB1_0901  942      DSLSSTASALGKLQD  LSSTASALG  2        0.4735
297.9    23.00  0.63     Sequence
```

```
             DRB1_0901  943      SLSSTASALGKLQDV  LSSTASALG  1        0.4218
521.4    34.00  0.65     Sequence
             DRB1_0901  944      LSSTASALGKLQDVV  LSSTASALG  0        0.3173
1614.8    60.00  0.43     Sequence
             DRB1_0901  945      SSTASALGKLQDVVN  LGKLQDVVN  6        0.2793
2436.1    70.00  0.31     Sequence
             DRB1_0901  946      STASALGKLQDVVNQ  LGKLQDVVN  5        0.2536
3216.4    80.00  0.44     Sequence
             DRB1_0901  947      TASALGKLQDVVNQN  LGKLQDVVN  4        0.2185
4703.1    85.00  0.62     Sequence
             DRB1_0901  948      ASALGKLQDVVNQNA  LGKLQDVVN  3        0.2127
5004.1    85.00  0.67     Sequence
             DRB1_0901  949      SALGKLQDVVNQNAQ  LGKLQDVVN  2        0.1940
6128.2    90.00  0.67     Sequence
             DRB1_0901  950      ALGKLQDVVNQNAQA  LGKLQDVVN  1        0.1806
7085.6    90.00  0.56     Sequence
             DRB1_0901  951      LGKLQDVVNQNAQAL  VVNQNAQAL  6        0.2537
3213.7    80.00  0.50     Sequence
             DRB1_0901  952      GKLQDVVNQNAQALN  VVNQNAQAL  5        0.2905
2157.7    70.00  0.52     Sequence
             DRB1_0901  953      KLQDVVNQNAQALNT  VVNQNAQAL  4        0.3219
1535.1    60.00  0.49     Sequence
             DRB1_0901  954      LQDVVNQNAQALNTL  VVNQNAQAL  3        0.3376
1296.1    55.00  0.47     Sequence
             DRB1_0901  955      QDVVNQNAQALNTLV  VVNQNAQAL  2        0.3849
776.6    42.00  0.36     Sequence
             DRB1_0901  956      DVVNQNAQALNTLVK  VVNQNAQAL  1        0.3756
858.9    44.00  0.28     Sequence
             DRB1_0901  957      VVNQNAQALNTLVKQ  NAQALNTLV  4        0.3478
1160.4    55.00  0.36     Sequence
             DRB1_0901  958      VNQNAQALNTLVKQL  ALNTLVKQL  6        0.3916
722.7    41.00  0.44     Sequence
             DRB1_0901  959      NQNAQALNTLVKQLS  ALNTLVKQL  5        0.4078
606.7    37.00  0.50     Sequence
             DRB1_0901  960      QNAQALNTLVKQLSS  ALNTLVKQL  4        0.4020
645.9    38.00  0.56     Sequence
             DRB1_0901  961      NAQALNTLVKQLSSN  ALNTLVKQL  3        0.3741
873.3    45.00  0.63     Sequence
             DRB1_0901  962      AQALNTLVKQLSSNF  LVKQLSSNF  6        0.4653
325.5    25.00  0.51     Sequence
             DRB1_0901  963      QALNTLVKQLSSNFG  LVKQLSSNF  5        0.5093
202.2    17.00  0.48     Sequence
             DRB1_0901  964      ALNTLVKQLSSNFGA  LVKQLSSNF  4        0.5227
175.0    15.00  0.49     Sequence
             DRB1_0901  965      LNTLVKQLSSNFGAI  LVKQLSSNF  3        0.5331
156.3    14.00  0.47     Sequence
             DRB1_0901  966      NTLVKQLSSNFGAIS  LVKQLSSNF  2        0.5981
77.4     7.00  0.32     Sequence         WB
             DRB1_0901  967      TLVKQLSSNFGAISS  LSSNFGAIS  5        0.5993
76.4     6.50  0.41     Sequence         WB
             DRB1_0901  968      LVKQLSSNFGAISSV  LSSNFGAIS  4        0.5787
95.4     8.50  0.53     Sequence         WB
             DRB1_0901  969      VKQLSSNFGAISSVL  LSSNFGAIS  3        0.5854
88.8     8.00  0.53     Sequence         WB
             DRB1_0901  970      KQLSSNFGAISSVLN  FGAISSVLN  6        0.6225
59.4     5.00  0.44     Sequence         WB
             DRB1_0901  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.6026
73.7     6.50  0.52     Sequence         WB
             DRB1_0901  972      LSSNFGAISSVLNDI  FGAISSVLN  4        0.5778
96.4     8.50  0.66     Sequence         WB
             DRB1_0901  973      SSNFGAISSVLNDIL  FGAISSVLN  3        0.5732
101.3     9.00  0.67     Sequence         WB
             DRB1_0901  974      SNFGAISSVLNDILS  FGAISSVLN  2        0.5546
123.8    11.00  0.64     Sequence
             DRB1_0901  975      NFGAISSVLNDILSR  FGAISSVLN  1        0.5068
207.7    18.00  0.63     Sequence
```

```
             DRB1_0901  976      FGAISSVLNDILSRL  FGAISSVLN  0        0.3991
666.3    39.00  0.44     Sequence
             DRB1_0901  977      GAISSVLNDILSRLD  ISSVLNDIL  2        0.3296
1413.6    60.00  0.63     Sequence
             DRB1_0901  978      AISSVLNDILSRLDK  ISSVLNDIL  1        0.3047
1850.4    65.00  0.60     Sequence
             DRB1_0901  979      ISSVLNDILSRLDKV  ISSVLNDIL  0        0.2716
2646.5    75.00  0.41     Sequence
             DRB1_0901  980      SSVLNDILSRLDKVE  LNDILSRLD  3        0.2205
4598.6    85.00  0.41     Sequence
             DRB1_0901  981      SVLNDILSRLDKVEA  LSRLDKVEA  6        0.2765
2511.5    70.00  0.46     Sequence
             DRB1_0901  982      VLNDILSRLDKVEAE  LSRLDKVEA  5        0.3018
1909.6    65.00  0.58     Sequence
             DRB1_0901  983      LNDILSRLDKVEAEV  LSRLDKVEA  4        0.3028
1889.4    65.00  0.71     Sequence
             DRB1_0901  984      NDILSRLDKVEAEVQ  LSRLDKVEA  3        0.3073
1799.5    65.00  0.74     Sequence
             DRB1_0901  985      DILSRLDKVEAEVQI  LSRLDKVEA  2        0.2944
2069.2    70.00  0.74     Sequence
             DRB1_0901  986      ILSRLDKVEAEVQID  LSRLDKVEA  1        0.2745
2565.2    75.00  0.76     Sequence
             DRB1_0901  987      LSRLDKVEAEVQIDR  LSRLDKVEA  0        0.2205
4599.3    85.00  0.60     Sequence
             DRB1_0901  988      SRLDKVEAEVQIDRL  LDKVEAEVQ  2        0.1421
10745.1   100.00  0.31     Sequence
             DRB1_0901  989      RLDKVEAEVQIDRLI  AEVQIDRLI  6        0.2599
3004.9    75.00  0.61     Sequence
             DRB1_0901  990      LDKVEAEVQIDRLIT  AEVQIDRLI  5        0.2685
2736.5    75.00  0.58     Sequence
             DRB1_0901  991      DKVEAEVQIDRLITG  AEVQIDRLI  4        0.2598
3005.8    75.00  0.59     Sequence
             DRB1_0901  992      KVEAEVQIDRLITGR  AEVQIDRLI  3        0.2458
3499.4    80.00  0.62     Sequence
             DRB1_0901  993      VEAEVQIDRLITGRL  IDRLITGRL  6        0.3600
1016.9    48.00  0.62     Sequence
             DRB1_0901  994      EAEVQIDRLITGRLQ  IDRLITGRL  5        0.4001
658.7    39.00  0.55     Sequence
             DRB1_0901  995      AEVQIDRLITGRLQS  IDRLITGRL  4        0.4020
645.6    38.00  0.57     Sequence
             DRB1_0901  996      EVQIDRLITGRLQSL  IDRLITGRL  3        0.4231
513.9    33.00  0.52     Sequence
             DRB1_0901  997      VQIDRLITGRLQSLQ  IDRLITGRL  2        0.4222
519.1    34.00  0.50     Sequence
             DRB1_0901  998      QIDRLITGRLQSLQT  IDRLITGRL  1        0.4209
526.1    34.00  0.42     Sequence
             DRB1_0901  999      IDRLITGRLQSLQTY  IDRLITGRL  0        0.3944
701.0    40.00  0.34     Sequence
             DRB1_0901 1000      DRLITGRLQSLQTYV  RLQSLQTYV  6        0.4202
530.0    34.00  0.49     Sequence
             DRB1_0901 1001      RLITGRLQSLQTYVT  LQSLQTYVT  6        0.5156
188.8    16.00  0.42     Sequence
             DRB1_0901 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.5197
180.7    16.00  0.50     Sequence
             DRB1_0901 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.5138
192.6    17.00  0.52     Sequence
             DRB1_0901 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.5212
177.7    15.00  0.44     Sequence
             DRB1_0901 1005      GRLQSLQTYVTQQLI  LQSLQTYVT  2        0.5096
201.6    17.00  0.42     Sequence
             DRB1_0901 1006      RLQSLQTYVTQQLIR  LQSLQTYVT  1        0.4556
361.4    27.00  0.38     Sequence
             DRB1_0901 1007      LQSLQTYVTQQLIRA  LQTYVTQQL  3        0.3992
665.3    39.00  0.39     Sequence
             DRB1_0901 1008      QSLQTYVTQQLIRAA  LQTYVTQQL  2        0.3945
700.2    40.00  0.44     Sequence
```

```
             DRB1_0901 1009      SLQTYVTQQLIRAAE  LQTYVTQQL  1        0.3864
764.3    42.00  0.37     Sequence
             DRB1_0901 1010      LQTYVTQQLIRAAEI  YVTQQLIRA  3        0.3787
831.1    44.00  0.29     Sequence
             DRB1_0901 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.3718
894.8    45.00  0.34     Sequence
             DRB1_0901 1012      TYVTQQLIRAAEIRA  LIRAAEIRA  6        0.5066
208.1    18.00  0.61     Sequence
             DRB1_0901 1013      YVTQQLIRAAEIRAS  LIRAAEIRA  5        0.5462
135.6    12.00  0.68     Sequence
             DRB1_0901 1014      VTQQLIRAAEIRASA  LIRAAEIRA  4        0.5615
115.0    11.00  0.69     Sequence
             DRB1_0901 1015      TQQLIRAAEIRASAN  LIRAAEIRA  3        0.5561
121.9    11.00  0.70     Sequence
             DRB1_0901 1016      QQLIRAAEIRASANL  LIRAAEIRA  2        0.5496
130.7    12.00  0.65     Sequence
             DRB1_0901 1017      QLIRAAEIRASANLA  LIRAAEIRA  1        0.5487
132.1    12.00  0.51     Sequence
             DRB1_0901 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.5661
109.3    10.00  0.47     Sequence
             DRB1_0901 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.5689
106.1     9.50  0.69     Sequence         WB
             DRB1_0901 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.5724
102.2     9.00  0.74     Sequence         WB
             DRB1_0901 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.5854
88.7     8.00  0.69     Sequence         WB
             DRB1_0901 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.5654
110.2    10.00  0.58     Sequence
             DRB1_0901 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.5106
199.3    17.00  0.49     Sequence
             DRB1_0901 1024      IRASANLAAIKMSEC  SANLAAIKM  3        0.4243
507.5    33.00  0.38     Sequence
             DRB1_0901 1025      RASANLAAIKMSECV  SANLAAIKM  2        0.3825
797.5    43.00  0.46     Sequence
             DRB1_0901 1026      ASANLAAIKMSECVL  AIKMSECVL  6        0.4612
340.4    25.00  0.28     Sequence
             DRB1_0901 1027      SANLAAIKMSECVLG  IKMSECVLG  6        0.6180
62.4     5.50  0.71     Sequence         WB
             DRB1_0901 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.6099
68.1     6.00  0.75     Sequence         WB
             DRB1_0901 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.6117
66.8     6.00  0.75     Sequence         WB
             DRB1_0901 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.6005
75.3     6.50  0.77     Sequence         WB
             DRB1_0901 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.5998
75.9     6.50  0.80     Sequence         WB
             DRB1_0901 1032      AIKMSECVLGQSKRV  CVLGQSKRV  6        0.6449
46.6     3.50  0.42     Sequence         WB
             DRB1_0901 1033      IKMSECVLGQSKRVD  CVLGQSKRV  5        0.5829
91.2     8.00  0.65     Sequence         WB
             DRB1_0901 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.5494
131.0    12.00  0.84     Sequence
             DRB1_0901 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.5318
158.5    14.00  0.82     Sequence
             DRB1_0901 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.5229
174.5    15.00  0.81     Sequence
             DRB1_0901 1037      ECVLGQSKRVDFCGK  CVLGQSKRV  1        0.4778
284.2    22.00  0.81     Sequence
             DRB1_0901 1038      CVLGQSKRVDFCGKG  CVLGQSKRV  0        0.3840
784.6    42.00  0.70     Sequence
             DRB1_0901 1039      VLGQSKRVDFCGKGY  RVDFCGKGY  6        0.2218
4537.8    85.00  0.45     Sequence
             DRB1_0901 1040      LGQSKRVDFCGKGYH  RVDFCGKGY  5        0.2044
5473.8    90.00  0.50     Sequence
             DRB1_0901 1041      GQSKRVDFCGKGYHL  RVDFCGKGY  4        0.2500
3342.6    80.00  0.41     Sequence
```

```
             DRB1_0901 1042      QSKRVDFCGKGYHLM  FCGKGYHLM  6        0.3459
1185.1    55.00  0.44     Sequence
             DRB1_0901 1043      SKRVDFCGKGYHLMS  FCGKGYHLM  5        0.3636
977.7    48.00  0.44     Sequence
             DRB1_0901 1044      KRVDFCGKGYHLMSF  FCGKGYHLM  4        0.3693
920.2    46.00  0.43     Sequence
             DRB1_0901 1045      RVDFCGKGYHLMSFP  FCGKGYHLM  3        0.3463
1179.5    55.00  0.44     Sequence
             DRB1_0901 1046      VDFCGKGYHLMSFPQ  FCGKGYHLM  2        0.3755
859.6    45.00  0.35     Sequence
             DRB1_0901 1047      DFCGKGYHLMSFPQS  YHLMSFPQS  6        0.4584
350.9    26.00  0.41     Sequence
             DRB1_0901 1048      FCGKGYHLMSFPQSA  YHLMSFPQS  5        0.5212
177.7    15.00  0.34     Sequence
             DRB1_0901 1049      CGKGYHLMSFPQSAP  YHLMSFPQS  4        0.5040
214.1    18.00  0.36     Sequence
             DRB1_0901 1050      GKGYHLMSFPQSAPH  YHLMSFPQS  3        0.4973
230.3    19.00  0.34     Sequence
             DRB1_0901 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.4847
264.0    21.00  0.34     Sequence
             DRB1_0901 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.4735
297.7    23.00  0.26     Sequence
             DRB1_0901 1053      YHLMSFPQSAPHGVV  FPQSAPHGV  5        0.4493
386.9    28.00  0.34     Sequence
             DRB1_0901 1054      HLMSFPQSAPHGVVF  FPQSAPHGV  4        0.4230
514.7    33.00  0.42     Sequence
             DRB1_0901 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.4640
330.1    25.00  0.46     Sequence
             DRB1_0901 1056      MSFPQSAPHGVVFLH  FPQSAPHGV  2        0.4478
393.5    28.00  0.47     Sequence
             DRB1_0901 1057      SFPQSAPHGVVFLHV  FPQSAPHGV  1        0.4284
485.0    32.00  0.45     Sequence
             DRB1_0901 1058      FPQSAPHGVVFLHVT  SAPHGVVFL  3        0.3756
859.1    45.00  0.40     Sequence
             DRB1_0901 1059      PQSAPHGVVFLHVTY  SAPHGVVFL  2        0.3305
1398.9    60.00  0.50     Sequence
             DRB1_0901 1060      QSAPHGVVFLHVTYV  VVFLHVTYV  6        0.3621
994.7    48.00  0.38     Sequence
             DRB1_0901 1061      SAPHGVVFLHVTYVP  VVFLHVTYV  5        0.3057
1829.9    65.00  0.38     Sequence
             DRB1_0901 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.3513
1117.8    55.00  0.50     Sequence
             DRB1_0901 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.3738
875.9    45.00  0.47     Sequence
             DRB1_0901 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.4031
638.2    38.00  0.41     Sequence
             DRB1_0901 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.4117
581.1    36.00  0.40     Sequence
             DRB1_0901 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.4099
592.5    36.00  0.37     Sequence
             DRB1_0901 1067      VFLHVTYVPAQEKNF  YVPAQEKNF  6        0.5049
212.1    18.00  0.50     Sequence
             DRB1_0901 1068      FLHVTYVPAQEKNFT  YVPAQEKNF  5        0.5180
184.1    16.00  0.61     Sequence
             DRB1_0901 1069      LHVTYVPAQEKNFTT  YVPAQEKNF  4        0.5085
203.9    17.00  0.76     Sequence
             DRB1_0901 1070      HVTYVPAQEKNFTTA  YVPAQEKNF  3        0.5026
217.5    18.00  0.83     Sequence
             DRB1_0901 1071      VTYVPAQEKNFTTAP  YVPAQEKNF  2        0.4800
277.7    22.00  0.93     Sequence
             DRB1_0901 1072      TYVPAQEKNFTTAPA  YVPAQEKNF  1        0.4730
299.5    23.00  0.76     Sequence
             DRB1_0901 1073      YVPAQEKNFTTAPAI  YVPAQEKNF  0        0.4589
348.7    26.00  0.39     Sequence
             DRB1_0901 1074      VPAQEKNFTTAPAIC  KNFTTAPAI  5        0.4054
622.4    37.00  0.46     Sequence
```

```
             DRB1_0901 1075      PAQEKNFTTAPAICH  KNFTTAPAI  4        0.4379
437.8    30.00  0.32     Sequence
             DRB1_0901 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.4334
459.8    31.00  0.36     Sequence
             DRB1_0901 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.4068
613.2    37.00  0.38     Sequence
             DRB1_0901 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.3729
884.7    45.00  0.47     Sequence
             DRB1_0901 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.3209
1553.2    60.00  0.62     Sequence
             DRB1_0901 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.2527
3246.6    80.00  0.66     Sequence
             DRB1_0901 1081      FTTAPAICHDGKAHF  ICHDGKAHF  6        0.3113
1721.7    65.00  0.57     Sequence
             DRB1_0901 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.3117
1714.5    65.00  0.65     Sequence
             DRB1_0901 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.3141
1670.7    60.00  0.64     Sequence
             DRB1_0901 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.3213
1545.9    60.00  0.63     Sequence
             DRB1_0901 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.3129
1693.1    65.00  0.56     Sequence
             DRB1_0901 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.2956
2040.8    65.00  0.47     Sequence
             DRB1_0901 1087      ICHDGKAHFPREGVF  ICHDGKAHF  0        0.2886
2201.8    70.00  0.31     Sequence
             DRB1_0901 1088      CHDGKAHFPREGVFV  HFPREGVFV  6        0.3085
1775.0    65.00  0.45     Sequence
             DRB1_0901 1089      HDGKAHFPREGVFVS  HFPREGVFV  5        0.3336
1353.8    55.00  0.43     Sequence
             DRB1_0901 1090      DGKAHFPREGVFVSN  HFPREGVFV  4        0.3325
1368.8    60.00  0.43     Sequence
             DRB1_0901 1091      GKAHFPREGVFVSNG  HFPREGVFV  3        0.3178
1605.2    60.00  0.46     Sequence
             DRB1_0901 1092      KAHFPREGVFVSNGT  HFPREGVFV  2        0.2963
2025.8    65.00  0.42     Sequence
             DRB1_0901 1093      AHFPREGVFVSNGTH  HFPREGVFV  1        0.2792
2438.5    70.00  0.41     Sequence
             DRB1_0901 1094      HFPREGVFVSNGTHW  VFVSNGTHW  6        0.4281
486.9    32.00  0.72     Sequence
             DRB1_0901 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6        0.5326
157.1    14.00  0.49     Sequence
             DRB1_0901 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.5734
101.1     9.00  0.54     Sequence         WB
             DRB1_0901 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.5854
88.8     8.00  0.52     Sequence         WB
             DRB1_0901 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.5752
99.1     9.00  0.56     Sequence         WB
             DRB1_0901 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.5606
116.0    11.00  0.57     Sequence
             DRB1_0901 1100      VFVSNGTHWFVTQRN  FVSNGTHWF  1        0.5115
197.4    17.00  0.61     Sequence
             DRB1_0901 1101      FVSNGTHWFVTQRNF  FVSNGTHWF  0        0.4382
436.6    30.00  0.50     Sequence
             DRB1_0901 1102      VSNGTHWFVTQRNFY  WFVTQRNFY  6        0.3677
936.0    46.00  0.41     Sequence
             DRB1_0901 1103      SNGTHWFVTQRNFYE  WFVTQRNFY  5        0.3619
996.4    48.00  0.47     Sequence
             DRB1_0901 1104      NGTHWFVTQRNFYEP  WFVTQRNFY  4        0.3472
1167.9    55.00  0.44     Sequence
             DRB1_0901 1105      GTHWFVTQRNFYEPQ  WFVTQRNFY  3        0.3402
1260.3    55.00  0.44     Sequence
             DRB1_0901 1106      THWFVTQRNFYEPQI  WFVTQRNFY  2        0.3520
1109.5    50.00  0.36     Sequence
             DRB1_0901 1107      HWFVTQRNFYEPQII  RNFYEPQII  6        0.4232
513.5    33.00  0.44     Sequence
```

```
             DRB1_0901 1108      WFVTQRNFYEPQIIT  RNFYEPQII  5        0.4117
581.0    36.00  0.50     Sequence
             DRB1_0901 1109      FVTQRNFYEPQIITT  RNFYEPQII  4        0.4221
519.5    34.00  0.45     Sequence
             DRB1_0901 1110      VTQRNFYEPQIITTD  RNFYEPQII  3        0.4164
552.6    35.00  0.47     Sequence
             DRB1_0901 1111      TQRNFYEPQIITTDN  RNFYEPQII  2        0.4099
592.8    36.00  0.47     Sequence
             DRB1_0901 1112      QRNFYEPQIITTDNT  RNFYEPQII  1        0.3920
719.4    41.00  0.46     Sequence
             DRB1_0901 1113      RNFYEPQIITTDNTF  FYEPQIITT  2        0.3463
1179.8    55.00  0.47     Sequence
             DRB1_0901 1114      NFYEPQIITTDNTFV  IITTDNTFV  6        0.3762
853.5    44.00  0.56     Sequence
             DRB1_0901 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.3656
956.8    47.00  0.63     Sequence
             DRB1_0901 1116      YEPQIITTDNTFVSG  IITTDNTFV  4        0.3477
1161.9    55.00  0.72     Sequence
             DRB1_0901 1117      EPQIITTDNTFVSGN  IITTDNTFV  3        0.3421
1234.4    55.00  0.72     Sequence
             DRB1_0901 1118      PQIITTDNTFVSGNC  IITTDNTFV  2        0.3311
1390.8    60.00  0.69     Sequence
             DRB1_0901 1119      QIITTDNTFVSGNCD  IITTDNTFV  1        0.2924
2112.6    70.00  0.68     Sequence
             DRB1_0901 1120      IITTDNTFVSGNCDV  TFVSGNCDV  6        0.3259
1470.6    60.00  0.40     Sequence
             DRB1_0901 1121      ITTDNTFVSGNCDVV  FVSGNCDVV  6        0.3743
871.3    45.00  0.54     Sequence
             DRB1_0901 1122      TTDNTFVSGNCDVVI  FVSGNCDVV  5        0.4234
511.9    33.00  0.52     Sequence
             DRB1_0901 1123      TDNTFVSGNCDVVIG  FVSGNCDVV  4        0.4328
462.4    31.00  0.54     Sequence
             DRB1_0901 1124      DNTFVSGNCDVVIGI  FVSGNCDVV  3        0.4355
449.4    31.00  0.55     Sequence
             DRB1_0901 1125      NTFVSGNCDVVIGIV  FVSGNCDVV  2        0.4290
482.0    32.00  0.56     Sequence
             DRB1_0901 1126      TFVSGNCDVVIGIVN  FVSGNCDVV  1        0.3893
740.6    41.00  0.57     Sequence
             DRB1_0901 1127      FVSGNCDVVIGIVNN  FVSGNCDVV  0        0.2822
2359.9    70.00  0.52     Sequence
             DRB1_0901 1128      VSGNCDVVIGIVNNT  VVIGIVNNT  6        0.2116
5065.6    85.00  0.41     Sequence
             DRB1_0901 1129      SGNCDVVIGIVNNTV  VIGIVNNTV  6        0.2476
3432.6    80.00  0.41     Sequence
             DRB1_0901 1130      GNCDVVIGIVNNTVY  IGIVNNTVY  6        0.3042
1861.0    65.00  0.41     Sequence
             DRB1_0901 1131      NCDVVIGIVNNTVYD  IGIVNNTVY  5        0.2946
2062.8    65.00  0.38     Sequence
             DRB1_0901 1132      CDVVIGIVNNTVYDP  IGIVNNTVY  4        0.2727
2614.9    75.00  0.38     Sequence
             DRB1_0901 1133      DVVIGIVNNTVYDPL  IGIVNNTVY  3        0.2914
2135.8    70.00  0.33     Sequence
             DRB1_0901 1134      VVIGIVNNTVYDPLQ  IGIVNNTVY  2        0.2852
2285.9    70.00  0.31     Sequence
             DRB1_0901 1135      VIGIVNNTVYDPLQP  VNNTVYDPL  4        0.2547
3178.0    75.00  0.31     Sequence
             DRB1_0901 1136      IGIVNNTVYDPLQPE  VNNTVYDPL  3        0.2185
4700.1    85.00  0.41     Sequence
             DRB1_0901 1137      GIVNNTVYDPLQPEL  VNNTVYDPL  2        0.2422
3637.1    80.00  0.37     Sequence
             DRB1_0901 1138      IVNNTVYDPLQPELD  YDPLQPELD  6        0.2754
2539.7    70.00  0.46     Sequence
             DRB1_0901 1139      VNNTVYDPLQPELDS  YDPLQPELD  5        0.2995
1957.1    65.00  0.57     Sequence
             DRB1_0901 1140      NNTVYDPLQPELDSF  YDPLQPELD  4        0.2954
2045.7    65.00  0.69     Sequence
```

```
             DRB1_0901 1141      NTVYDPLQPELDSFK  YDPLQPELD  3        0.2937
2084.4    70.00  0.69     Sequence
             DRB1_0901 1142      TVYDPLQPELDSFKE  YDPLQPELD  2        0.2791
2439.4    70.00  0.69     Sequence
             DRB1_0901 1143      VYDPLQPELDSFKEE  YDPLQPELD  1        0.2446
3545.6    80.00  0.69     Sequence
             DRB1_0901 1144      YDPLQPELDSFKEEL  YDPLQPELD  0        0.1658
8312.1    95.00  0.47     Sequence
             DRB1_0901 1145      DPLQPELDSFKEELD  LQPELDSFK  2        0.1353
11569.2   100.00  0.34     Sequence
             DRB1_0901 1146      PLQPELDSFKEELDK  LDSFKEELD  5        0.1343
11692.0   100.00  0.37     Sequence
             DRB1_0901 1147      LQPELDSFKEELDKY  LDSFKEELD  4        0.1292
12350.5   100.00  0.38     Sequence
             DRB1_0901 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.1892
6456.0    90.00  0.56     Sequence
             DRB1_0901 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.1935
6160.1    90.00  0.60     Sequence
             DRB1_0901 1150      ELDSFKEELDKYFKN  FKEELDKYF  4        0.1869
6619.7    90.00  0.65     Sequence
             DRB1_0901 1151      LDSFKEELDKYFKNH  FKEELDKYF  3        0.1738
7626.3    95.00  0.72     Sequence
             DRB1_0901 1152      DSFKEELDKYFKNHT  FKEELDKYF  2        0.2019
5627.5    90.00  0.58     Sequence
             DRB1_0901 1153      SFKEELDKYFKNHTS  FKEELDKYF  1        0.2332
4010.7    80.00  0.38     Sequence
             DRB1_0901 1154      FKEELDKYFKNHTSP  DKYFKNHTS  5        0.2229
4484.6    85.00  0.41     Sequence
             DRB1_0901 1155      KEELDKYFKNHTSPD  YFKNHTSPD  6        0.3014
1918.1    65.00  0.43     Sequence
             DRB1_0901 1156      EELDKYFKNHTSPDV  FKNHTSPDV  6        0.4652
325.7    25.00  0.56     Sequence
             DRB1_0901 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.5019
219.1    18.00  0.64     Sequence
             DRB1_0901 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.5252
170.3    15.00  0.68     Sequence
             DRB1_0901 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.5290
163.4    14.00  0.71     Sequence
             DRB1_0901 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.5161
187.8    16.00  0.75     Sequence
             DRB1_0901 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.4612
340.1    25.00  0.76     Sequence
             DRB1_0901 1162      FKNHTSPDVDLGDIS  FKNHTSPDV  0        0.3565
1056.1    49.00  0.80     Sequence
             DRB1_0901 1163      KNHTSPDVDLGDISG  NHTSPDVDL  1        0.0761
21955.0   100.00  0.40     Sequence
             DRB1_0901 1164      NHTSPDVDLGDISGI  VDLGDISGI  6        0.1009
16775.3   100.00  0.55     Sequence
             DRB1_0901 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.1005
16849.3   100.00  0.60     Sequence
             DRB1_0901 1166      TSPDVDLGDISGINA  LGDISGINA  6        0.1578
9066.8    95.00  0.50     Sequence
             DRB1_0901 1167      SPDVDLGDISGINAS  LGDISGINA  5        0.1773
7346.2    95.00  0.57     Sequence
             DRB1_0901 1168      PDVDLGDISGINASF  LGDISGINA  4        0.1994
5780.5    90.00  0.49     Sequence
             DRB1_0901 1169      DVDLGDISGINASFV  ISGINASFV  6        0.3682
930.8    46.00  0.76     Sequence
             DRB1_0901 1170      VDLGDISGINASFVN  ISGINASFV  5        0.3707
906.0    46.00  0.75     Sequence
             DRB1_0901 1171      DLGDISGINASFVNI  ISGINASFV  4        0.3888
745.0    41.00  0.70     Sequence
             DRB1_0901 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.4355
449.3    31.00  0.54     Sequence
             DRB1_0901 1173      GDISGINASFVNIQK  ISGINASFV  2        0.4400
427.8    30.00  0.51     Sequence
```

```
             DRB1_0901 1174      DISGINASFVNIQKE  ISGINASFV  1        0.4205
528.3    34.00  0.45     Sequence
             DRB1_0901 1175      ISGINASFVNIQKEI  INASFVNIQ  3        0.4063
616.4    37.00  0.51     Sequence
             DRB1_0901 1176      SGINASFVNIQKEID  INASFVNIQ  2        0.3814
806.8    43.00  0.54     Sequence
             DRB1_0901 1177      GINASFVNIQKEIDR  INASFVNIQ  1        0.3645
969.0    47.00  0.47     Sequence
             DRB1_0901 1178      INASFVNIQKEIDRL  FVNIQKEID  4        0.3236
1508.7    60.00  0.52     Sequence
             DRB1_0901 1179      NASFVNIQKEIDRLN  FVNIQKEID  3        0.2858
2269.0    70.00  0.64     Sequence
             DRB1_0901 1180      ASFVNIQKEIDRLNE  FVNIQKEID  2        0.2735
2592.8    75.00  0.65     Sequence
             DRB1_0901 1181      SFVNIQKEIDRLNEV  FVNIQKEID  1        0.2412
3678.0    80.00  0.63     Sequence
             DRB1_0901 1182      FVNIQKEIDRLNEVA  FVNIQKEID  0        0.1799
7136.1    90.00  0.50     Sequence
             DRB1_0901 1183      VNIQKEIDRLNEVAK  IDRLNEVAK  6        0.1331
11838.7   100.00  0.43     Sequence
             DRB1_0901 1184      NIQKEIDRLNEVAKN  IDRLNEVAK  5        0.1458
10323.6    95.00  0.46     Sequence
             DRB1_0901 1185      IQKEIDRLNEVAKNL  IDRLNEVAK  4        0.1581
9035.0    95.00  0.50     Sequence
             DRB1_0901 1186      QKEIDRLNEVAKNLN  IDRLNEVAK  3        0.1650
8388.3    95.00  0.45     Sequence
             DRB1_0901 1187      KEIDRLNEVAKNLNE  IDRLNEVAK  2        0.1676
8155.7    95.00  0.40     Sequence
             DRB1_0901 1188      EIDRLNEVAKNLNES  LNEVAKNLN  4        0.1552
9323.0    95.00  0.28     Sequence
             DRB1_0901 1189      IDRLNEVAKNLNESL  VAKNLNESL  6        0.1895
6432.0    90.00  0.37     Sequence
             DRB1_0901 1190      DRLNEVAKNLNESLI  AKNLNESLI  6        0.3212
1547.6    60.00  0.67     Sequence
             DRB1_0901 1191      RLNEVAKNLNESLID  AKNLNESLI  5        0.3360
1318.9    55.00  0.64     Sequence
             DRB1_0901 1192      LNEVAKNLNESLIDL  AKNLNESLI  4        0.3463
1179.3    55.00  0.69     Sequence
             DRB1_0901 1193      NEVAKNLNESLIDLQ  AKNLNESLI  3        0.3631
983.1    48.00  0.58     Sequence
             DRB1_0901 1194      EVAKNLNESLIDLQE  AKNLNESLI  2        0.3520
1109.3    50.00  0.56     Sequence
             DRB1_0901 1195      VAKNLNESLIDLQEL  AKNLNESLI  1        0.3364
1312.4    55.00  0.56     Sequence
             DRB1_0901 1196      AKNLNESLIDLQELG  AKNLNESLI  0        0.2904
2159.0    70.00  0.47     Sequence
             DRB1_0901 1197      KNLNESLIDLQELGK  LNESLIDLQ  2        0.1787
7234.0    95.00  0.56     Sequence
             DRB1_0901 1198      NLNESLIDLQELGKY  LNESLIDLQ  1        0.1676
8156.1    95.00  0.45     Sequence
             DRB1_0901 1199      LNESLIDLQELGKYE  LIDLQELGK  4        0.1410
10876.5   100.00  0.29     Sequence
             DRB1_0901 1200      NESLIDLQELGKYEQ  LIDLQELGK  3        0.1454
10373.1    95.00  0.29     Sequence
             DRB1_0901 1201      ESLIDLQELGKYEQY  LIDLQELGK  2        0.1496
9909.8    95.00  0.25     Sequence
             DRB1_0901 1202      SLIDLQELGKYEQYI  LQELGKYEQ  4        0.1475
10132.4    95.00  0.25     Sequence
             DRB1_0901 1203      LIDLQELGKYEQYIK  LGKYEQYIK  6        0.1558
9263.0    95.00  0.26     Sequence
             DRB1_0901 1204      IDLQELGKYEQYIKW  GKYEQYIKW  6        0.1864
6652.3    90.00  0.31     Sequence
             DRB1_0901 1205      DLQELGKYEQYIKWP  GKYEQYIKW  5        0.1863
6660.0    90.00  0.30     Sequence
             DRB1_0901 1206      LQELGKYEQYIKWPW  YEQYIKWPW  6        0.2419
3648.3    80.00  0.47     Sequence
```

```
             DRB1_0901 1207      QELGKYEQYIKWPWY  YEQYIKWPW  5        0.2600
3000.1    75.00  0.44     Sequence
             DRB1_0901 1208      ELGKYEQYIKWPWYI  QYIKWPWYI  6        0.4521
375.5    27.00  0.58     Sequence
             DRB1_0901 1209      LGKYEQYIKWPWYIW  QYIKWPWYI  5        0.4832
268.3    21.00  0.50     Sequence
             DRB1_0901 1210      GKYEQYIKWPWYIWL  QYIKWPWYI  4        0.5046
212.8    18.00  0.42     Sequence
             DRB1_0901 1211      KYEQYIKWPWYIWLG  QYIKWPWYI  3        0.4872
256.9    21.00  0.43     Sequence
             DRB1_0901 1212      YEQYIKWPWYIWLGF  QYIKWPWYI  2        0.4712
305.2    24.00  0.43     Sequence
             DRB1_0901 1213      EQYIKWPWYIWLGFI  QYIKWPWYI  1        0.4694
311.2    24.00  0.42     Sequence
             DRB1_0901 1214      QYIKWPWYIWLGFIA  WYIWLGFIA  6        0.4959
233.9    19.00  0.30     Sequence
             DRB1_0901 1215      YIKWPWYIWLGFIAG  WYIWLGFIA  5        0.4231
513.8    33.00  0.40     Sequence
             DRB1_0901 1216      IKWPWYIWLGFIAGL  IWLGFIAGL  6        0.4867
258.2    21.00  0.44     Sequence
             DRB1_0901 1217      KWPWYIWLGFIAGLI  WLGFIAGLI  6        0.5460
136.0    12.00  0.40     Sequence
             DRB1_0901 1218      WPWYIWLGFIAGLIA  WLGFIAGLI  5        0.5336
155.5    14.00  0.37     Sequence
             DRB1_0901 1219      PWYIWLGFIAGLIAI  WLGFIAGLI  4        0.5342
154.4    14.00  0.34     Sequence
             DRB1_0901 1220      WYIWLGFIAGLIAIV  FIAGLIAIV  6        0.6884
29.1     1.70  0.74     Sequence         SB
             DRB1_0901 1221      YIWLGFIAGLIAIVM  FIAGLIAIV  5        0.6666
36.8     2.50  0.70     Sequence         WB
             DRB1_0901 1222      IWLGFIAGLIAIVMV  FIAGLIAIV  4        0.6550
41.8     3.00  0.70     Sequence         WB
             DRB1_0901 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3        0.6358
51.5     4.00  0.79     Sequence         WB
             DRB1_0901 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.6158
63.9     5.50  0.86     Sequence         WB
             DRB1_0901 1225      GFIAGLIAIVMVTIM  FIAGLIAIV  1        0.6137
65.4     5.50  0.86     Sequence         WB
             DRB1_0901 1226      FIAGLIAIVMVTIML  FIAGLIAIV  0        0.5163
187.4    16.00  0.76     Sequence
             DRB1_0901 1227      IAGLIAIVMVTIMLC  IAGLIAIVM  0        0.2250
4380.2    85.00  0.37     Sequence
             DRB1_0901 1228      AGLIAIVMVTIMLCC  LIAIVMVTI  2        0.1675
8164.4    95.00  0.33     Sequence
             DRB1_0901 1229      GLIAIVMVTIMLCCM  LIAIVMVTI  1        0.1652
8366.4    95.00  0.34     Sequence
             DRB1_0901 1230      LIAIVMVTIMLCCMT  IAIVMVTIM  1        0.1538
9464.8    95.00  0.19     Sequence
             DRB1_0901 1231      IAIVMVTIMLCCMTS  TIMLCCMTS  6        0.1679
8130.0    95.00  0.30     Sequence
             DRB1_0901 1232      AIVMVTIMLCCMTSC  TIMLCCMTS  5        0.1613
8732.3    95.00  0.27     Sequence
             DRB1_0901 1233      IVMVTIMLCCMTSCC  TIMLCCMTS  4        0.1478
10106.9    95.00  0.27     Sequence
             DRB1_0901 1234      VMVTIMLCCMTSCCS  LCCMTSCCS  6        0.1628
8590.6    95.00  0.22     Sequence
             DRB1_0901 1235      MVTIMLCCMTSCCSC  TIMLCCMTS  2        0.1651
8375.0    95.00  0.19     Sequence
             DRB1_0901 1236      VTIMLCCMTSCCSCL  CMTSCCSCL  6        0.2598
3008.6    75.00  0.55     Sequence
             DRB1_0901 1237      TIMLCCMTSCCSCLK  CMTSCCSCL  5        0.2508
3314.1    80.00  0.48     Sequence
             DRB1_0901 1238      IMLCCMTSCCSCLKG  CMTSCCSCL  4        0.2356
3908.1    80.00  0.52     Sequence
             DRB1_0901 1239      MLCCMTSCCSCLKGC  CMTSCCSCL  3        0.2191
4671.2    85.00  0.52     Sequence
```

```
             DRB1_0901 1240      LCCMTSCCSCLKGCC  CMTSCCSCL  2        0.2122
5034.9    85.00  0.55     Sequence
             DRB1_0901 1241      CCMTSCCSCLKGCCS  CMTSCCSCL  1        0.2091
5206.1    85.00  0.50     Sequence
             DRB1_0901 1242      CMTSCCSCLKGCCSC  CMTSCCSCL  0        0.1743
7587.8    95.00  0.38     Sequence
             DRB1_0901 1243      MTSCCSCLKGCCSCG  CLKGCCSCG  6        0.1629
8578.9    95.00  0.32     Sequence
             DRB1_0901 1244      TSCCSCLKGCCSCGS  LKGCCSCGS  6        0.2281
4238.8    85.00  0.58     Sequence
             DRB1_0901 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5        0.2296
4167.7    85.00  0.58     Sequence
             DRB1_0901 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.2236
4451.5    85.00  0.57     Sequence
             DRB1_0901 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.2175
4751.2    85.00  0.57     Sequence
             DRB1_0901 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2        0.2541
3198.5    80.00  0.44     Sequence
             DRB1_0901 1249      CLKGCCSCGSCCKFD  CSCGSCCKF  5        0.2394
3750.9    80.00  0.41     Sequence
             DRB1_0901 1250      LKGCCSCGSCCKFDE  CSCGSCCKF  4        0.2185
4703.8    85.00  0.50     Sequence
             DRB1_0901 1251      KGCCSCGSCCKFDED  CSCGSCCKF  3        0.1984
5844.5    90.00  0.58     Sequence
             DRB1_0901 1252      GCCSCGSCCKFDEDD  CSCGSCCKF  2        0.1805
7092.8    90.00  0.59     Sequence
             DRB1_0901 1253      CCSCGSCCKFDEDDS  CSCGSCCKF  1        0.1657
8324.4    95.00  0.51     Sequence
             DRB1_0901 1254      CSCGSCCKFDEDDSE  CSCGSCCKF  0        0.1464
10261.6    95.00  0.41     Sequence
             DRB1_0901 1255      SCGSCCKFDEDDSEP  CCKFDEDDS  4        0.0795
21162.5   100.00  0.33     Sequence
             DRB1_0901 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.1061
15867.1   100.00  0.51     Sequence
             DRB1_0901 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.1175
14018.8   100.00  0.52     Sequence
             DRB1_0901 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.1241
13055.0   100.00  0.52     Sequence
             DRB1_0901 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.1209
13522.5   100.00  0.54     Sequence
             DRB1_0901 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.1149
14428.9   100.00  0.59     Sequence
             DRB1_0901 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.1134
14663.0   100.00  0.53     Sequence
             DRB1_0901 1262      FDEDDSEPVLKGVKL  EPVLKGVKL  6        0.1290
12386.5   100.00  0.43     Sequence
             DRB1_0901 1263      DEDDSEPVLKGVKLH  EPVLKGVKL  5        0.1214
13443.9   100.00  0.49     Sequence
             DRB1_0901 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.2533
3225.2    80.00  0.62     Sequence
             DRB1_0901 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.4165
552.0    35.00  0.64     Sequence
             DRB1_1101    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.3258
1471.9    45.00  0.73     Sequence
             DRB1_1101    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.3371
1303.5    43.00  0.58     Sequence
             DRB1_1101    3      PIKEMFVFLVLLPLV  IKEMFVFLV  1        0.3057
1830.3    50.00  0.43     Sequence
             DRB1_1101    4      IKEMFVFLVLLPLVS  FLVLLPLVS  6        0.3855
771.5    33.00  0.47     Sequence
             DRB1_1101    5      KEMFVFLVLLPLVSS  FLVLLPLVS  5        0.4466
398.6    24.00  0.47     Sequence
             DRB1_1101    6      EMFVFLVLLPLVSSQ  LVLLPLVSS  5        0.4765
288.3    20.00  0.41     Sequence
             DRB1_1101    7      MFVFLVLLPLVSSQC  LVLLPLVSS  4        0.4797
278.5    19.00  0.42     Sequence
```

```
             DRB1_1101    8      FVFLVLLPLVSSQCV  LVLLPLVSS  3        0.4843
265.2    19.00  0.42     Sequence
             DRB1_1101    9      VFLVLLPLVSSQCVN  LVLLPLVSS  2        0.4533
370.5    23.00  0.50     Sequence
             DRB1_1101   10      FLVLLPLVSSQCVNF  LVLLPLVSS  1        0.3848
777.9    33.00  0.44     Sequence
             DRB1_1101   11      LVLLPLVSSQCVNFT  LLPLVSSQC  2        0.2646
2853.6    60.00  0.41     Sequence
             DRB1_1101   12      VLLPLVSSQCVNFTN  LVSSQCVNF  4        0.1794
7181.2    80.00  0.31     Sequence
             DRB1_1101   13      LLPLVSSQCVNFTNR  LVSSQCVNF  3        0.1528
9570.2    90.00  0.47     Sequence
             DRB1_1101   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.1449
10423.5    90.00  0.46     Sequence
             DRB1_1101   15      PLVSSQCVNFTNRTQ  CVNFTNRTQ  6        0.1840
6829.3    80.00  0.23     Sequence
             DRB1_1101   16      LVSSQCVNFTNRTQL  VNFTNRTQL  6        0.2424
3631.0    65.00  0.43     Sequence
             DRB1_1101   17      VSSQCVNFTNRTQLP  VNFTNRTQL  5        0.2788
2448.0    60.00  0.47     Sequence
             DRB1_1101   18      SSQCVNFTNRTQLPS  VNFTNRTQL  4        0.3265
1461.9    45.00  0.45     Sequence
             DRB1_1101   19      SQCVNFTNRTQLPSA  VNFTNRTQL  3        0.3763
852.6    35.00  0.42     Sequence
             DRB1_1101   20      QCVNFTNRTQLPSAY  FTNRTQLPS  4        0.3948
698.1    32.00  0.47     Sequence
             DRB1_1101   21      CVNFTNRTQLPSAYT  FTNRTQLPS  3        0.3800
819.1    34.00  0.60     Sequence
             DRB1_1101   22      VNFTNRTQLPSAYTN  FTNRTQLPS  2        0.3468
1173.1    41.00  0.73     Sequence
             DRB1_1101   23      NFTNRTQLPSAYTNS  FTNRTQLPS  1        0.2837
2321.6    55.00  0.52     Sequence
             DRB1_1101   24      FTNRTQLPSAYTNSF  FTNRTQLPS  0        0.2312
4098.7    70.00  0.37     Sequence
             DRB1_1101   25      TNRTQLPSAYTNSFT  RTQLPSAYT  2        0.1214
13440.8    95.00  0.41     Sequence
             DRB1_1101   26      NRTQLPSAYTNSFTR  LPSAYTNSF  4        0.1348
11624.5    90.00  0.20     Sequence
             DRB1_1101   27      RTQLPSAYTNSFTRG  YTNSFTRGX  7        0.1636
8520.3    85.00  0.27     Sequence
             DRB1_1101   28      TQLPSAYTNSFTRGV  YTNSFTRGV  6        0.2264
4317.3    70.00  0.57     Sequence
             DRB1_1101   29      QLPSAYTNSFTRGVY  YTNSFTRGV  5        0.2863
2258.5    55.00  0.60     Sequence
             DRB1_1101   30      LPSAYTNSFTRGVYY  YTNSFTRGV  4        0.3422
1233.7    42.00  0.56     Sequence
             DRB1_1101   31      PSAYTNSFTRGVYYP  YTNSFTRGV  3        0.3650
963.6    37.00  0.56     Sequence
             DRB1_1101   32      SAYTNSFTRGVYYPD  YTNSFTRGV  2        0.3668
945.2    37.00  0.52     Sequence
             DRB1_1101   33      AYTNSFTRGVYYPDK  FTRGVYYPD  5        0.3552
1071.7    39.00  0.33     Sequence
             DRB1_1101   34      YTNSFTRGVYYPDKV  FTRGVYYPD  4        0.3380
1290.0    43.00  0.43     Sequence
             DRB1_1101   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.3095
1755.8    49.00  0.56     Sequence
             DRB1_1101   36      NSFTRGVYYPDKVFR  FTRGVYYPD  2        0.3582
1036.8    39.00  0.40     Sequence
             DRB1_1101   37      SFTRGVYYPDKVFRS  YYPDKVFRS  6        0.4567
357.3    22.00  0.43     Sequence
             DRB1_1101   38      FTRGVYYPDKVFRSS  YYPDKVFRS  5        0.5087
203.5    16.00  0.53     Sequence
             DRB1_1101   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.5221
176.1    15.00  0.56     Sequence
             DRB1_1101   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.5345
153.9    13.00  0.58     Sequence
```

```
             DRB1_1101   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.5267
167.4    14.00  0.57     Sequence
             DRB1_1101   42      VYYPDKVFRSSVLHS  YYPDKVFRS  1        0.5379
148.5    13.00  0.40     Sequence
             DRB1_1101   43      YYPDKVFRSSVLHST  FRSSVLHST  6        0.5394
146.0    13.00  0.46     Sequence
             DRB1_1101   44      YPDKVFRSSVLHSTQ  FRSSVLHST  5        0.5494
131.0    12.00  0.69     Sequence
             DRB1_1101   45      PDKVFRSSVLHSTQD  FRSSVLHST  4        0.5558
122.3    11.00  0.69     Sequence
             DRB1_1101   46      DKVFRSSVLHSTQDL  FRSSVLHST  3        0.5654
110.2    11.00  0.71     Sequence
             DRB1_1101   47      KVFRSSVLHSTQDLF  FRSSVLHST  2        0.5742
100.2     9.50  0.76     Sequence         WB
             DRB1_1101   48      VFRSSVLHSTQDLFL  FRSSVLHST  1        0.4195
534.2    28.00  0.56     Sequence
             DRB1_1101   49      FRSSVLHSTQDLFLP  FRSSVLHST  0        0.2625
2921.8    60.00  0.37     Sequence
             DRB1_1101   50      RSSVLHSTQDLFLPF  VLHSTQDLF  3        0.1303
12211.0    90.00  0.38     Sequence
             DRB1_1101   51      SSVLHSTQDLFLPFF  VLHSTQDLF  2        0.1246
12984.3    95.00  0.33     Sequence
             DRB1_1101   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2        0.1501
9852.4    90.00  0.23     Sequence
             DRB1_1101   53      VLHSTQDLFLPFFSN  DLFLPFFSN  6        0.1722
7758.1    85.00  0.38     Sequence
             DRB1_1101   54      LHSTQDLFLPFFSNV  DLFLPFFSN  5        0.2038
5510.3    75.00  0.35     Sequence
             DRB1_1101   55      HSTQDLFLPFFSNVT  FLPFFSNVT  6        0.3201
1566.7    47.00  0.49     Sequence
             DRB1_1101   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.3722
891.4    36.00  0.54     Sequence
             DRB1_1101   57      TQDLFLPFFSNVTWF  FLPFFSNVT  4        0.4040
631.7    30.00  0.52     Sequence
             DRB1_1101   58      QDLFLPFFSNVTWFH  FLPFFSNVT  3        0.4375
439.6    25.00  0.43     Sequence
             DRB1_1101   59      DLFLPFFSNVTWFHA  FSNVTWFHA  6        0.4740
296.4    20.00  0.37     Sequence
             DRB1_1101   60      LFLPFFSNVTWFHAI  FSNVTWFHA  5        0.4849
263.2    19.00  0.40     Sequence
             DRB1_1101   61      FLPFFSNVTWFHAIH  FSNVTWFHA  4        0.4588
349.3    22.00  0.49     Sequence
             DRB1_1101   62      LPFFSNVTWFHAIHV  FSNVTWFHA  3        0.4606
342.4    22.00  0.54     Sequence
             DRB1_1101   63      PFFSNVTWFHAIHVS  FSNVTWFHA  2        0.4630
333.5    21.00  0.52     Sequence
             DRB1_1101   64      FFSNVTWFHAIHVSG  WFHAIHVSG  6        0.4600
344.8    22.00  0.36     Sequence
             DRB1_1101   65      FSNVTWFHAIHVSGT  WFHAIHVSG  5        0.4545
365.7    22.00  0.46     Sequence
             DRB1_1101   66      SNVTWFHAIHVSGTN  WFHAIHVSG  4        0.4535
369.9    23.00  0.50     Sequence
             DRB1_1101   67      NVTWFHAIHVSGTNG  WFHAIHVSG  3        0.4700
309.4    20.00  0.51     Sequence
             DRB1_1101   68      VTWFHAIHVSGTNGT  WFHAIHVSG  2        0.4705
307.7    20.00  0.50     Sequence
             DRB1_1101   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.4425
416.4    24.00  0.31     Sequence
             DRB1_1101   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1        0.4143
564.9    28.00  0.25     Sequence
             DRB1_1101   71      FHAIHVSGTNGTKRF  IHVSGTNGT  3        0.2993
1960.4    55.00  0.40     Sequence
             DRB1_1101   72      HAIHVSGTNGTKRFD  IHVSGTNGT  2        0.2420
3645.5    65.00  0.50     Sequence
             DRB1_1101   73      AIHVSGTNGTKRFDN  IHVSGTNGT  1        0.2165
4803.1    75.00  0.34     Sequence
```

```
             DRB1_1101   74      IHVSGTNGTKRFDNP  TNGTKRFDN  5        0.1818
6992.4    80.00  0.26     Sequence
             DRB1_1101   75      HVSGTNGTKRFDNPV  TNGTKRFDN  4        0.1595
8899.8    85.00  0.39     Sequence
             DRB1_1101   76      VSGTNGTKRFDNPVL  TNGTKRFDN  3        0.1689
8043.9    85.00  0.43     Sequence
             DRB1_1101   77      SGTNGTKRFDNPVLP  TNGTKRFDN  2        0.1535
9496.8    85.00  0.44     Sequence
             DRB1_1101   78      GTNGTKRFDNPVLPF  TNGTKRFDN  1        0.1514
9714.2    90.00  0.23     Sequence
             DRB1_1101   79      TNGTKRFDNPVLPFN  RFDNPVLPF  5        0.1509
9773.0    90.00  0.28     Sequence
             DRB1_1101   80      NGTKRFDNPVLPFND  RFDNPVLPF  4        0.1501
9860.1    90.00  0.29     Sequence
             DRB1_1101   81      GTKRFDNPVLPFNDG  RFDNPVLPF  3        0.1577
9077.1    85.00  0.30     Sequence
             DRB1_1101   82      TKRFDNPVLPFNDGV  RFDNPVLPF  2        0.1476
10124.1    90.00  0.31     Sequence
             DRB1_1101   83      KRFDNPVLPFNDGVY  DNPVLPFND  3        0.1235
13141.1    95.00  0.25     Sequence
             DRB1_1101   84      RFDNPVLPFNDGVYF  DNPVLPFND  2        0.1108
15085.0    95.00  0.23     Sequence
             DRB1_1101   85      FDNPVLPFNDGVYFA  LPFNDGVYF  5        0.1093
15332.1    95.00  0.32     Sequence
             DRB1_1101   86      DNPVLPFNDGVYFAS  FNDGVYFAS  6        0.1290
12388.1    90.00  0.38     Sequence
             DRB1_1101   87      NPVLPFNDGVYFAST  FNDGVYFAS  5        0.1547
9378.4    85.00  0.50     Sequence
             DRB1_1101   88      PVLPFNDGVYFASTE  FNDGVYFAS  4        0.1625
8618.4    85.00  0.51     Sequence
             DRB1_1101   89      VLPFNDGVYFASTEK  FNDGVYFAS  3        0.1941
6124.8    80.00  0.52     Sequence
             DRB1_1101   90      LPFNDGVYFASTEKS  VYFASTEKS  6        0.2835
2327.8    55.00  0.33     Sequence
             DRB1_1101   91      PFNDGVYFASTEKSN  YFASTEKSN  6        0.4324
464.8    26.00  0.30     Sequence
             DRB1_1101   92      FNDGVYFASTEKSNI  YFASTEKSN  5        0.5232
174.0    14.00  0.37     Sequence
             DRB1_1101   93      NDGVYFASTEKSNII  FASTEKSNI  5        0.5646
111.1    11.00  0.46     Sequence
             DRB1_1101   94      DGVYFASTEKSNIIR  FASTEKSNI  4        0.6169
63.1     6.50  0.49     Sequence          WB
             DRB1_1101   95      GVYFASTEKSNIIRG  FASTEKSNI  3        0.6432
47.5     5.50  0.49     Sequence          WB
             DRB1_1101   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.5996
76.1     8.00  0.57     Sequence          WB
             DRB1_1101   97      YFASTEKSNIIRGWI  FASTEKSNI  1        0.4530
371.7    23.00  0.44     Sequence
             DRB1_1101   98      FASTEKSNIIRGWIF  EKSNIIRGW  4        0.2788
2447.5    60.00  0.22     Sequence
             DRB1_1101   99      ASTEKSNIIRGWIFG  KSNIIRGWI  4        0.2653
2833.1    60.00  0.28     Sequence
             DRB1_1101  100      STEKSNIIRGWIFGT  KSNIIRGWI  3        0.3003
1939.9    55.00  0.23     Sequence
             DRB1_1101  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5        0.3100
1747.0    49.00  0.28     Sequence
             DRB1_1101  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.3008
1930.8    55.00  0.28     Sequence
             DRB1_1101  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3        0.2695
2707.9    60.00  0.35     Sequence
             DRB1_1101  104      SNIIRGWIFGTTLDS  WIFGTTLDS  6        0.2670
2783.3    60.00  0.32     Sequence
             DRB1_1101  105      NIIRGWIFGTTLDSK  WIFGTTLDS  5        0.2963
2027.2    55.00  0.43     Sequence
             DRB1_1101  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.3013
1919.2    55.00  0.49     Sequence
```

```
             DRB1_1101  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3        0.3094
1758.5    49.00  0.54     Sequence
             DRB1_1101  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2        0.3167
1624.3    47.00  0.50     Sequence
             DRB1_1101  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1        0.2830
2338.8    55.00  0.35     Sequence
             DRB1_1101  110      WIFGTTLDSKTQSLL  GTTLDSKTQ  3        0.2369
3851.4    70.00  0.27     Sequence
             DRB1_1101  111      IFGTTLDSKTQSLLI  GTTLDSKTQ  2        0.1780
7288.0    80.00  0.43     Sequence
             DRB1_1101  112      FGTTLDSKTQSLLIV  TTLDSKTQS  2        0.1557
9279.5    85.00  0.29     Sequence
             DRB1_1101  113      GTTLDSKTQSLLIVN  LDSKTQSLL  3        0.1469
10206.7    90.00  0.17     Sequence
             DRB1_1101  114      TTLDSKTQSLLIVNN  TQSLLIVNN  6        0.1587
8977.0    85.00  0.27     Sequence
             DRB1_1101  115      TLDSKTQSLLIVNNA  TQSLLIVNN  5        0.1976
5897.4    80.00  0.35     Sequence
             DRB1_1101  116      LDSKTQSLLIVNNAT  TQSLLIVNN  4        0.2313
4093.6    70.00  0.31     Sequence
             DRB1_1101  117      DSKTQSLLIVNNATN  TQSLLIVNN  3        0.2617
2947.4    60.00  0.25     Sequence
             DRB1_1101  118      SKTQSLLIVNNATNV  LLIVNNATN  5        0.2926
2109.9    55.00  0.32     Sequence
             DRB1_1101  119      KTQSLLIVNNATNVV  LLIVNNATN  4        0.2963
2026.9    55.00  0.37     Sequence
             DRB1_1101  120      TQSLLIVNNATNVVI  LLIVNNATN  3        0.2727
2614.2    60.00  0.41     Sequence
             DRB1_1101  121      QSLLIVNNATNVVIK  LLIVNNATN  2        0.2867
2248.4    55.00  0.41     Sequence
             DRB1_1101  122      SLLIVNNATNVVIKV  IVNNATNVV  3        0.2465
3471.0    65.00  0.29     Sequence
             DRB1_1101  123      LLIVNNATNVVIKVC  IVNNATNVV  2        0.2388
3774.4    70.00  0.34     Sequence
             DRB1_1101  124      LIVNNATNVVIKVCE  VNNATNVVI  2        0.2142
4923.5    75.00  0.34     Sequence
             DRB1_1101  125      IVNNATNVVIKVCEF  TNVVIKVCE  5        0.2100
5152.7    75.00  0.34     Sequence
             DRB1_1101  126      VNNATNVVIKVCEFQ  TNVVIKVCE  4        0.2235
4454.3    70.00  0.47     Sequence
             DRB1_1101  127      NNATNVVIKVCEFQF  TNVVIKVCE  3        0.2434
3592.3    65.00  0.43     Sequence
             DRB1_1101  128      NATNVVIKVCEFQFC  TNVVIKVCE  2        0.2460
3490.0    65.00  0.42     Sequence
             DRB1_1101  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.2352
3924.4    70.00  0.23     Sequence
             DRB1_1101  130      TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.2073
5306.6    75.00  0.32     Sequence
             DRB1_1101  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.2076
5288.0    75.00  0.34     Sequence
             DRB1_1101  132      VVIKVCEFQFCNYPF  FQFCNYPFX  7        0.2684
2741.5    60.00  0.35     Sequence
             DRB1_1101  133      VIKVCEFQFCNYPFL  FQFCNYPFL  6        0.3034
1876.3    50.00  0.49     Sequence
             DRB1_1101  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.3282
1434.8    45.00  0.60     Sequence
             DRB1_1101  135      KVCEFQFCNYPFLGV  FQFCNYPFL  4        0.3583
1035.6    39.00  0.61     Sequence
             DRB1_1101  136      VCEFQFCNYPFLGVY  FQFCNYPFL  3        0.3696
917.2    36.00  0.56     Sequence
             DRB1_1101  137      CEFQFCNYPFLGVYY  FQFCNYPFL  2        0.3961
688.4    31.00  0.50     Sequence
             DRB1_1101  138      EFQFCNYPFLGVYYH  FQFCNYPFL  1        0.3515
1115.0    40.00  0.28     Sequence
             DRB1_1101  139      FQFCNYPFLGVYYHK  FCNYPFLGV  2        0.3356
1324.1    43.00  0.26     Sequence
```

```
             DRB1_1101  140      QFCNYPFLGVYYHKN  FLGVYYHKN  6        0.3725
888.3    36.00  0.41     Sequence
             DRB1_1101  141      FCNYPFLGVYYHKNN  FLGVYYHKN  5        0.3856
771.0    33.00  0.50     Sequence
             DRB1_1101  142      CNYPFLGVYYHKNNK  FLGVYYHKN  4        0.4335
459.1    25.00  0.53     Sequence
             DRB1_1101  143      NYPFLGVYYHKNNKS  FLGVYYHKN  3        0.4696
310.6    20.00  0.49     Sequence
             DRB1_1101  144      YPFLGVYYHKNNKSW  FLGVYYHKN  2        0.5275
166.0    14.00  0.29     Sequence
             DRB1_1101  145      PFLGVYYHKNNKSWM  YYHKNNKSW  5        0.5692
105.7    10.00  0.25     Sequence
             DRB1_1101  146      FLGVYYHKNNKSWME  YHKNNKSWM  5        0.5727
101.8    10.00  0.31     Sequence
             DRB1_1101  147      LGVYYHKNNKSWMES  YHKNNKSWM  4        0.5837
90.4     9.00  0.39     Sequence         WB
             DRB1_1101  148      GVYYHKNNKSWMESE  YHKNNKSWM  3        0.5862
88.0     9.00  0.41     Sequence         WB
             DRB1_1101  149      VYYHKNNKSWMESEF  YHKNNKSWM  2        0.5538
125.0    12.00  0.45     Sequence
             DRB1_1101  150      YYHKNNKSWMESEFR  HKNNKSWME  2        0.4675
317.9    21.00  0.29     Sequence
             DRB1_1101  151      YHKNNKSWMESEFRV  HKNNKSWME  1        0.2916
2130.7    55.00  0.20     Sequence
             DRB1_1101  152      HKNNKSWMESEFRVY  WMESEFRVY  6        0.2354
3914.6    70.00  0.29     Sequence
             DRB1_1101  153      KNNKSWMESEFRVYS  MESEFRVYS  6        0.3143
1668.3    48.00  0.43     Sequence
             DRB1_1101  154      NNKSWMESEFRVYSS  MESEFRVYS  5        0.3653
960.4    37.00  0.52     Sequence
             DRB1_1101  155      NKSWMESEFRVYSSA  MESEFRVYS  4        0.4052
623.9    30.00  0.58     Sequence
             DRB1_1101  156      KSWMESEFRVYSSAN  MESEFRVYS  3        0.4292
480.9    26.00  0.58     Sequence
             DRB1_1101  157      SWMESEFRVYSSANN  MESEFRVYS  2        0.4045
628.4    30.00  0.54     Sequence
             DRB1_1101  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.3770
846.6    35.00  0.26     Sequence
             DRB1_1101  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.3401
1261.2    42.00  0.38     Sequence
             DRB1_1101  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.3265
1461.7    45.00  0.49     Sequence
             DRB1_1101  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.3477
1162.2    41.00  0.47     Sequence
             DRB1_1101  162      EFRVYSSANNCTFEY  FRVYSSANN  1        0.3248
1489.2    46.00  0.31     Sequence
             DRB1_1101  163      FRVYSSANNCTFEYV  YSSANNCTF  3        0.2764
2511.9    60.00  0.44     Sequence
             DRB1_1101  164      RVYSSANNCTFEYVS  YSSANNCTF  2        0.1948
6077.4    80.00  0.63     Sequence
             DRB1_1101  165      VYSSANNCTFEYVSQ  YSSANNCTF  1        0.1367
11387.9    90.00  0.38     Sequence
             DRB1_1101  166      YSSANNCTFEYVSQP  YSSANNCTF  0        0.1230
13217.4    95.00  0.16     Sequence
             DRB1_1101  167      SSANNCTFEYVSQPF  FEYVSQPFX  7        0.1651
8380.1    85.00  0.44     Sequence
             DRB1_1101  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.2437
3579.2    65.00  0.58     Sequence
             DRB1_1101  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.3155
1646.2    48.00  0.51     Sequence
             DRB1_1101  170      NNCTFEYVSQPFLMD  FEYVSQPFL  4        0.3350
1333.5    43.00  0.50     Sequence
             DRB1_1101  171      NCTFEYVSQPFLMDL  FEYVSQPFL  3        0.3552
1071.0    39.00  0.47     Sequence
             DRB1_1101  172      CTFEYVSQPFLMDLE  FEYVSQPFL  2        0.3568
1052.5    39.00  0.46     Sequence
```

```
             DRB1_1101  173      TFEYVSQPFLMDLEG  YVSQPFLMD  3        0.3133
1685.0    48.00  0.43     Sequence
             DRB1_1101  174      FEYVSQPFLMDLEGK  YVSQPFLMD  2        0.2902
2165.4    55.00  0.47     Sequence
             DRB1_1101  175      EYVSQPFLMDLEGKQ  FLMDLEGKQ  6        0.2605
2986.0    60.00  0.25     Sequence
             DRB1_1101  176      YVSQPFLMDLEGKQG  LMDLEGKQG  6        0.3045
1853.3    50.00  0.38     Sequence
             DRB1_1101  177      VSQPFLMDLEGKQGN  LMDLEGKQG  5        0.3465
1177.1    41.00  0.47     Sequence
             DRB1_1101  178      SQPFLMDLEGKQGNF  LMDLEGKQG  4        0.3715
897.8    36.00  0.47     Sequence
             DRB1_1101  179      QPFLMDLEGKQGNFK  LMDLEGKQG  3        0.3956
692.0    32.00  0.51     Sequence
             DRB1_1101  180      PFLMDLEGKQGNFKN  LMDLEGKQG  2        0.3838
786.1    34.00  0.54     Sequence
             DRB1_1101  181      FLMDLEGKQGNFKNL  LMDLEGKQG  1        0.3241
1500.2    46.00  0.50     Sequence
             DRB1_1101  182      LMDLEGKQGNFKNLS  LMDLEGKQG  0        0.1822
6966.7    80.00  0.27     Sequence
             DRB1_1101  183      MDLEGKQGNFKNLSE  KQGNFKNLS  5        0.1414
10828.5    90.00  0.55     Sequence
             DRB1_1101  184      DLEGKQGNFKNLSEF  KQGNFKNLS  4        0.2126
5013.8    75.00  0.57     Sequence
             DRB1_1101  185      LEGKQGNFKNLSEFV  FKNLSEFVX  7        0.3193
1580.0    47.00  0.47     Sequence
             DRB1_1101  186      EGKQGNFKNLSEFVF  FKNLSEFVF  6        0.4360
446.7    25.00  0.72     Sequence
             DRB1_1101  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5        0.5121
196.2    16.00  0.77     Sequence
             DRB1_1101  188      KQGNFKNLSEFVFKN  FKNLSEFVF  4        0.5348
153.5    13.00  0.81     Sequence
             DRB1_1101  189      QGNFKNLSEFVFKNI  FKNLSEFVF  3        0.5396
145.7    13.00  0.79     Sequence
             DRB1_1101  190      GNFKNLSEFVFKNID  FKNLSEFVF  2        0.5272
166.6    14.00  0.77     Sequence
             DRB1_1101  191      NFKNLSEFVFKNIDG  FKNLSEFVF  1        0.4158
556.1    28.00  0.50     Sequence
             DRB1_1101  192      FKNLSEFVFKNIDGY  SEFVFKNID  4        0.3691
921.7    36.00  0.17     Sequence
             DRB1_1101  193      KNLSEFVFKNIDGYF  FKNIDGYFX  7        0.3785
832.4    35.00  0.34     Sequence
             DRB1_1101  194      NLSEFVFKNIDGYFK  FKNIDGYFK  6        0.4737
297.3    20.00  0.62     Sequence
             DRB1_1101  195      LSEFVFKNIDGYFKI  FKNIDGYFK  5        0.5213
177.5    15.00  0.70     Sequence
             DRB1_1101  196      SEFVFKNIDGYFKIY  FKNIDGYFK  4        0.5397
145.5    13.00  0.74     Sequence
             DRB1_1101  197      EFVFKNIDGYFKIYS  FKNIDGYFK  3        0.5649
110.7    11.00  0.73     Sequence
             DRB1_1101  198      FVFKNIDGYFKIYSK  FKNIDGYFK  2        0.5789
95.3     9.50  0.69     Sequence         WB
             DRB1_1101  199      VFKNIDGYFKIYSKH  FKNIDGYFK  1        0.5811
93.0     9.00  0.33     Sequence         WB
             DRB1_1101  200      FKNIDGYFKIYSKHT  YFKIYSKHT  6        0.6612
39.1     4.50  0.26     Sequence         WB
             DRB1_1101  201      KNIDGYFKIYSKHTP  FKIYSKHTP  6        0.7247
19.7     2.00  0.57     Sequence         WB
             DRB1_1101  202      NIDGYFKIYSKHTPI  FKIYSKHTP  5        0.7684
12.2     1.10  0.63     Sequence         SB
             DRB1_1101  203      IDGYFKIYSKHTPIN  FKIYSKHTP  4        0.7883
9.9     0.80  0.66     Sequence         SB
             DRB1_1101  204      DGYFKIYSKHTPINL  FKIYSKHTP  3        0.7934
9.3     0.70  0.68     Sequence         SB
             DRB1_1101  205      GYFKIYSKHTPINLV  FKIYSKHTP  2        0.8027
8.5     0.60  0.69     Sequence         SB
```

```
             DRB1_1101  206      YFKIYSKHTPINLVR  FKIYSKHTP  1        0.6899
28.7     3.50  0.51     Sequence         WB
             DRB1_1101  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.5504
129.7    12.00  0.34     Sequence
             DRB1_1101  208      KIYSKHTPINLVRDL  YSKHTPINL  2        0.3425
1229.2    42.00  0.51     Sequence
             DRB1_1101  209      IYSKHTPINLVRDLP  KHTPINLVR  3        0.2475
3433.9    65.00  0.25     Sequence
             DRB1_1101  210      YSKHTPINLVRDLPQ  INLVRDLPQ  6        0.2581
3064.3    65.00  0.28     Sequence
             DRB1_1101  211      SKHTPINLVRDLPQG  INLVRDLPQ  5        0.2786
2453.5    60.00  0.40     Sequence
             DRB1_1101  212      KHTPINLVRDLPQGF  INLVRDLPQ  4        0.3013
1919.4    55.00  0.44     Sequence
             DRB1_1101  213      HTPINLVRDLPQGFS  INLVRDLPQ  3        0.3278
1440.7    45.00  0.35     Sequence
             DRB1_1101  214      TPINLVRDLPQGFSA  VRDLPQGFS  5        0.3636
978.5    37.00  0.41     Sequence
             DRB1_1101  215      PINLVRDLPQGFSAL  VRDLPQGFS  4        0.3685
927.6    37.00  0.52     Sequence
             DRB1_1101  216      INLVRDLPQGFSALE  VRDLPQGFS  3        0.3517
1112.8    40.00  0.66     Sequence
             DRB1_1101  217      NLVRDLPQGFSALEP  VRDLPQGFS  2        0.3284
1431.3    45.00  0.72     Sequence
             DRB1_1101  218      LVRDLPQGFSALEPL  VRDLPQGFS  1        0.2622
2929.4    60.00  0.52     Sequence
             DRB1_1101  219      VRDLPQGFSALEPLV  FSALEPLVX  7        0.2395
3746.9    70.00  0.38     Sequence
             DRB1_1101  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.2501
3338.7    65.00  0.75     Sequence
             DRB1_1101  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.3204
1561.1    46.00  0.82     Sequence
             DRB1_1101  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.3488
1147.9    40.00  0.85     Sequence
             DRB1_1101  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.3664
949.3    37.00  0.80     Sequence
             DRB1_1101  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.3619
996.8    38.00  0.75     Sequence
             DRB1_1101  225      GFSALEPLVDLPIGI  FSALEPLVD  1        0.2794
2433.7    60.00  0.52     Sequence
             DRB1_1101  226      FSALEPLVDLPIGIN  LVDLPIGIN  6        0.2086
5234.4    75.00  0.24     Sequence
             DRB1_1101  227      SALEPLVDLPIGINI  LVDLPIGIN  5        0.2084
5243.9    75.00  0.46     Sequence
             DRB1_1101  228      ALEPLVDLPIGINIT  LVDLPIGIN  4        0.2156
4852.1    75.00  0.50     Sequence
             DRB1_1101  229      LEPLVDLPIGINITR  LVDLPIGIN  3        0.2401
3722.0    65.00  0.57     Sequence
             DRB1_1101  230      EPLVDLPIGINITRF  LVDLPIGIN  2        0.2809
2394.3    60.00  0.48     Sequence
             DRB1_1101  231      PLVDLPIGINITRFQ  GINITRFQX  7        0.3336
1353.7    44.00  0.33     Sequence
             DRB1_1101  232      LVDLPIGINITRFQT  GINITRFQT  6        0.3916
722.3    32.00  0.57     Sequence
             DRB1_1101  233      VDLPIGINITRFQTL  GINITRFQT  5        0.4350
451.6    25.00  0.62     Sequence
             DRB1_1101  234      DLPIGINITRFQTLL  GINITRFQT  4        0.4550
363.7    22.00  0.63     Sequence
             DRB1_1101  235      LPIGINITRFQTLLA  GINITRFQT  3        0.4977
229.1    17.00  0.59     Sequence
             DRB1_1101  236      PIGINITRFQTLLAL  GINITRFQT  2        0.5111
198.3    16.00  0.50     Sequence
             DRB1_1101  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.4922
243.3    18.00  0.25     Sequence
             DRB1_1101  238      GINITRFQTLLALHR  FQTLLALHR  6        0.6065
70.6     7.50  0.60     Sequence         WB
```

```
             DRB1_1101  239      INITRFQTLLALHRS  FQTLLALHR  5        0.6690
35.9     4.00  0.63     Sequence         WB
             DRB1_1101  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.6975
26.4     3.00  0.58     Sequence         WB
             DRB1_1101  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.7108
22.9     2.50  0.56     Sequence         WB
             DRB1_1101  242      TRFQTLLALHRSYLT  FQTLLALHR  2        0.7221
20.2     2.50  0.55     Sequence         WB
             DRB1_1101  243      RFQTLLALHRSYLTP  LLALHRSYL  4        0.7001
25.7     3.00  0.28     Sequence         WB
             DRB1_1101  244      FQTLLALHRSYLTPG  LLALHRSYL  3        0.6317
53.8     6.00  0.36     Sequence         WB
             DRB1_1101  245      QTLLALHRSYLTPGD  LLALHRSYL  2        0.5438
139.1    12.00  0.53     Sequence
             DRB1_1101  246      TLLALHRSYLTPGDS  LALHRSYLT  2        0.4161
554.1    28.00  0.27     Sequence
             DRB1_1101  247      LLALHRSYLTPGDSS  LHRSYLTPG  3        0.3187
1589.4    47.00  0.21     Sequence
             DRB1_1101  248      LALHRSYLTPGDSSS  LHRSYLTPG  2        0.2439
3572.0    65.00  0.32     Sequence
             DRB1_1101  249      ALHRSYLTPGDSSSG  LHRSYLTPG  1        0.2539
3204.6    65.00  0.28     Sequence
             DRB1_1101  250      LHRSYLTPGDSSSGW  RSYLTPGDS  2        0.2411
3683.3    65.00  0.23     Sequence
             DRB1_1101  251      HRSYLTPGDSSSGWT  LTPGDSSSG  4        0.2038
5512.0    75.00  0.28     Sequence
             DRB1_1101  252      RSYLTPGDSSSGWTA  LTPGDSSSG  3        0.1828
6921.5    80.00  0.37     Sequence
             DRB1_1101  253      SYLTPGDSSSGWTAG  LTPGDSSSG  2        0.1265
12724.7    95.00  0.51     Sequence
             DRB1_1101  254      YLTPGDSSSGWTAGA  GDSSSGWTA  4        0.0639
25031.9   100.00  0.29     Sequence
             DRB1_1101  255      LTPGDSSSGWTAGAA  GDSSSGWTA  3        0.0629
25309.2   100.00  0.32     Sequence
             DRB1_1101  256      TPGDSSSGWTAGAAA  GDSSSGWTA  2        0.0798
21088.2   100.00  0.25     Sequence
             DRB1_1101  257      PGDSSSGWTAGAAAY  WTAGAAAYX  7        0.1010
16761.5    95.00  0.22     Sequence
             DRB1_1101  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.1345
11669.0    90.00  0.41     Sequence
             DRB1_1101  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.1649
8394.3    85.00  0.50     Sequence
             DRB1_1101  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.1887
6489.2    80.00  0.50     Sequence
             DRB1_1101  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.1990
5802.8    75.00  0.49     Sequence
             DRB1_1101  262      SGWTAGAAAYYVGYL  WTAGAAAYY  2        0.1918
6275.7    80.00  0.51     Sequence
             DRB1_1101  263      GWTAGAAAYYVGYLQ  WTAGAAAYY  1        0.1668
8226.0    85.00  0.22     Sequence
             DRB1_1101  264      WTAGAAAYYVGYLQP  AYYVGYLQP  6        0.1557
9276.7    85.00  0.25     Sequence
             DRB1_1101  265      TAGAAAYYVGYLQPR  AYYVGYLQP  5        0.2424
3630.2    65.00  0.18     Sequence
             DRB1_1101  266      AGAAAYYVGYLQPRT  YVGYLQPRT  6        0.3792
826.4    35.00  0.42     Sequence
             DRB1_1101  267      GAAAYYVGYLQPRTF  YVGYLQPRT  5        0.4707
307.1    20.00  0.44     Sequence
             DRB1_1101  268      AAAYYVGYLQPRTFL  YVGYLQPRT  4        0.5114
197.7    16.00  0.41     Sequence
             DRB1_1101  269      AAYYVGYLQPRTFLL  YVGYLQPRT  3        0.5416
142.6    13.00  0.36     Sequence
             DRB1_1101  270      AYYVGYLQPRTFLLK  YVGYLQPRT  2        0.5733
101.2     9.50  0.31     Sequence         WB
             DRB1_1101  271      YYVGYLQPRTFLLKY  VGYLQPRTF  2        0.5723
102.3    10.00  0.25     Sequence
```

```
             DRB1_1101  272      YVGYLQPRTFLLKYN  GYLQPRTFL  2        0.5387
147.1    13.00  0.24     Sequence
             DRB1_1101  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.4728
300.0    20.00  0.29     Sequence
             DRB1_1101  274      GYLQPRTFLLKYNEN  RTFLLKYNE  5        0.4596
346.0    22.00  0.43     Sequence
             DRB1_1101  275      YLQPRTFLLKYNENG  RTFLLKYNE  4        0.4307
473.2    26.00  0.52     Sequence
             DRB1_1101  276      LQPRTFLLKYNENGT  RTFLLKYNE  3        0.4357
448.4    25.00  0.51     Sequence
             DRB1_1101  277      QPRTFLLKYNENGTI  RTFLLKYNE  2        0.4400
428.2    24.00  0.50     Sequence
             DRB1_1101  278      PRTFLLKYNENGTIT  FLLKYNENG  3        0.4156
557.4    28.00  0.39     Sequence
             DRB1_1101  279      RTFLLKYNENGTITD  FLLKYNENG  2        0.3284
1432.2    45.00  0.44     Sequence
             DRB1_1101  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.2393
3754.4    70.00  0.36     Sequence
             DRB1_1101  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.2190
4677.2    75.00  0.39     Sequence
             DRB1_1101  282      LLKYNENGTITDAVD  YNENGTITD  3        0.1426
10682.5    90.00  0.41     Sequence
             DRB1_1101  283      LKYNENGTITDAVDC  YNENGTITD  2        0.1151
14388.5    95.00  0.50     Sequence
             DRB1_1101  284      KYNENGTITDAVDCA  YNENGTITD  1        0.0762
21935.3   100.00  0.35     Sequence
             DRB1_1101  285      YNENGTITDAVDCAL  GTITDAVDC  4        0.0562
27209.7   100.00  0.31     Sequence
             DRB1_1101  286      NENGTITDAVDCALD  ITDAVDCAL  5        0.0528
28230.8   100.00  0.31     Sequence
             DRB1_1101  287      ENGTITDAVDCALDP  ITDAVDCAL  4        0.0575
26829.0   100.00  0.34     Sequence
             DRB1_1101  288      NGTITDAVDCALDPL  ITDAVDCAL  3        0.0583
26612.8   100.00  0.38     Sequence
             DRB1_1101  289      GTITDAVDCALDPLS  ITDAVDCAL  2        0.0613
25746.9   100.00  0.31     Sequence
             DRB1_1101  290      TITDAVDCALDPLSE  DCALDPLSE  6        0.0556
27382.8   100.00  0.25     Sequence
             DRB1_1101  291      ITDAVDCALDPLSET  DCALDPLSE  5        0.0592
26350.1   100.00  0.33     Sequence
             DRB1_1101  292      TDAVDCALDPLSETK  DCALDPLSE  4        0.0746
22314.2   100.00  0.35     Sequence
             DRB1_1101  293      DAVDCALDPLSETKC  DCALDPLSE  3        0.0784
21419.3   100.00  0.33     Sequence
             DRB1_1101  294      AVDCALDPLSETKCT  DCALDPLSE  2        0.0899
18910.0   100.00  0.31     Sequence
             DRB1_1101  295      VDCALDPLSETKCTL  LDPLSETKC  4        0.0867
19566.9   100.00  0.26     Sequence
             DRB1_1101  296      DCALDPLSETKCTLK  LDPLSETKC  3        0.1020
16582.7    95.00  0.27     Sequence
             DRB1_1101  297      CALDPLSETKCTLKS  LDPLSETKC  2        0.1361
11469.8    90.00  0.20     Sequence
             DRB1_1101  298      ALDPLSETKCTLKSF  PLSETKCTL  3        0.1551
9337.4    85.00  0.20     Sequence
             DRB1_1101  299      LDPLSETKCTLKSFT  TKCTLKSFT  6        0.2040
5499.6    75.00  0.25     Sequence
             DRB1_1101  300      DPLSETKCTLKSFTV  TKCTLKSFT  5        0.2606
2981.3    60.00  0.34     Sequence
             DRB1_1101  301      PLSETKCTLKSFTVE  TKCTLKSFT  4        0.2787
2451.6    60.00  0.37     Sequence
             DRB1_1101  302      LSETKCTLKSFTVEK  TKCTLKSFT  3        0.3237
1505.7    46.00  0.41     Sequence
             DRB1_1101  303      SETKCTLKSFTVEKG  TKCTLKSFT  2        0.3385
1282.9    43.00  0.35     Sequence
             DRB1_1101  304      ETKCTLKSFTVEKGI  LKSFTVEKG  5        0.3661
951.8    37.00  0.34     Sequence
```

```
             DRB1_1101  305      TKCTLKSFTVEKGIY  LKSFTVEKG  4        0.3959
689.8    31.00  0.41     Sequence
             DRB1_1101  306      KCTLKSFTVEKGIYQ  LKSFTVEKG  3        0.4305
474.5    26.00  0.42     Sequence
             DRB1_1101  307      CTLKSFTVEKGIYQT  FTVEKGIYQ  5        0.4491
387.9    23.00  0.40     Sequence
             DRB1_1101  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.4612
340.4    22.00  0.44     Sequence
             DRB1_1101  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.4430
414.2    24.00  0.53     Sequence
             DRB1_1101  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.4106
588.3    29.00  0.55     Sequence
             DRB1_1101  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.3137
1678.2    48.00  0.37     Sequence
             DRB1_1101  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.2976
1997.6    55.00  0.38     Sequence
             DRB1_1101  313      TVEKGIYQTSNFRVQ  YQTSNFRVQ  6        0.3612
1003.5    38.00  0.39     Sequence
             DRB1_1101  314      VEKGIYQTSNFRVQP  YQTSNFRVQ  5        0.3987
669.2    31.00  0.47     Sequence
             DRB1_1101  315      EKGIYQTSNFRVQPT  YQTSNFRVQ  4        0.4211
525.0    27.00  0.51     Sequence
             DRB1_1101  316      KGIYQTSNFRVQPTE  YQTSNFRVQ  3        0.4349
452.4    25.00  0.51     Sequence
             DRB1_1101  317      GIYQTSNFRVQPTES  YQTSNFRVQ  2        0.4098
593.6    29.00  0.51     Sequence
             DRB1_1101  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.3623
992.2    38.00  0.36     Sequence
             DRB1_1101  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.3586
1032.6    38.00  0.63     Sequence
             DRB1_1101  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.3867
762.2    33.00  0.75     Sequence
             DRB1_1101  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.4069
612.5    30.00  0.71     Sequence
             DRB1_1101  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.4161
554.1    28.00  0.69     Sequence
             DRB1_1101  323      NFRVQPTESIVRFPN  FRVQPTESI  1        0.3987
669.1    31.00  0.46     Sequence
             DRB1_1101  324      FRVQPTESIVRFPNI  TESIVRFPN  5        0.3898
736.8    33.00  0.38     Sequence
             DRB1_1101  325      RVQPTESIVRFPNIT  TESIVRFPN  4        0.3580
1039.5    39.00  0.54     Sequence
             DRB1_1101  326      VQPTESIVRFPNITN  TESIVRFPN  3        0.3779
838.2    35.00  0.49     Sequence
             DRB1_1101  327      QPTESIVRFPNITNL  TESIVRFPN  2        0.4007
654.5    31.00  0.47     Sequence
             DRB1_1101  328      PTESIVRFPNITNLC  TESIVRFPN  1        0.3837
786.9    34.00  0.38     Sequence
             DRB1_1101  329      TESIVRFPNITNLCP  IVRFPNITN  3        0.3497
1136.9    40.00  0.37     Sequence
             DRB1_1101  330      ESIVRFPNITNLCPF  IVRFPNITN  2        0.2911
2143.5    55.00  0.49     Sequence
             DRB1_1101  331      SIVRFPNITNLCPFG  FPNITNLCP  4        0.2984
1980.2    55.00  0.37     Sequence
             DRB1_1101  332      IVRFPNITNLCPFGE  FPNITNLCP  3        0.2859
2268.4    55.00  0.42     Sequence
             DRB1_1101  333      VRFPNITNLCPFGEV  FPNITNLCP  2        0.2758
2528.7    60.00  0.44     Sequence
             DRB1_1101  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.2512
3300.5    65.00  0.43     Sequence
             DRB1_1101  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.2155
4856.7    75.00  0.53     Sequence
             DRB1_1101  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.1975
5899.2    80.00  0.52     Sequence
             DRB1_1101  337      NITNLCPFGEVFNAT  ITNLCPFGE  1        0.1595
8903.0    85.00  0.34     Sequence
```

```
             DRB1_1101  338      ITNLCPFGEVFNATR  FGEVFNATR  6        0.1533
9521.0    85.00  0.34     Sequence
             DRB1_1101  339      TNLCPFGEVFNATRF  FGEVFNATR  5        0.2083
5249.6    75.00  0.35     Sequence
             DRB1_1101  340      NLCPFGEVFNATRFA  VFNATRFAX  7        0.3433
1218.5    42.00  0.38     Sequence
             DRB1_1101  341      LCPFGEVFNATRFAS  VFNATRFAS  6        0.5821
92.0     9.00  0.73     Sequence         WB
             DRB1_1101  342      CPFGEVFNATRFASV  VFNATRFAS  5        0.6529
42.7     5.00  0.76     Sequence         WB
             DRB1_1101  343      PFGEVFNATRFASVY  VFNATRFAS  4        0.6770
32.9     4.00  0.77     Sequence         WB
             DRB1_1101  344      FGEVFNATRFASVYA  VFNATRFAS  3        0.6957
26.9     3.00  0.77     Sequence         WB
             DRB1_1101  345      GEVFNATRFASVYAW  VFNATRFAS  2        0.6893
28.8     3.50  0.75     Sequence         WB
             DRB1_1101  346      EVFNATRFASVYAWN  VFNATRFAS  1        0.6195
61.4     6.50  0.59     Sequence         WB
             DRB1_1101  347      VFNATRFASVYAWNR  FASVYAWNR  6        0.5342
154.4    13.00  0.35     Sequence
             DRB1_1101  348      FNATRFASVYAWNRK  FASVYAWNR  5        0.4573
354.9    22.00  0.62     Sequence
             DRB1_1101  349      NATRFASVYAWNRKR  FASVYAWNR  4        0.5653
110.3    11.00  0.53     Sequence
             DRB1_1101  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.6630
38.4     4.50  0.33     Sequence         WB
             DRB1_1101  351      TRFASVYAWNRKRIS  YAWNRKRIS  6        0.7496
15.0     1.40  0.49     Sequence         SB
             DRB1_1101  352      RFASVYAWNRKRISN  YAWNRKRIS  5        0.7656
12.6     1.10  0.56     Sequence         SB
             DRB1_1101  353      FASVYAWNRKRISNC  YAWNRKRIS  4        0.7489
15.1     1.40  0.62     Sequence         SB
             DRB1_1101  354      ASVYAWNRKRISNCV  YAWNRKRIS  3        0.7490
15.1     1.40  0.67     Sequence         SB
             DRB1_1101  355      SVYAWNRKRISNCVA  YAWNRKRIS  2        0.7467
15.5     1.50  0.71     Sequence         SB
             DRB1_1101  356      VYAWNRKRISNCVAD  YAWNRKRIS  1        0.6347
52.1     5.50  0.47     Sequence         WB
             DRB1_1101  357      YAWNRKRISNCVADY  YAWNRKRIS  0        0.5053
211.1    16.00  0.41     Sequence
             DRB1_1101  358      AWNRKRISNCVADYS  RKRISNCVA  3        0.3002
1941.4    55.00  0.43     Sequence
             DRB1_1101  359      WNRKRISNCVADYSV  RKRISNCVA  2        0.2883
2209.9    55.00  0.47     Sequence
             DRB1_1101  360      NRKRISNCVADYSVL  RKRISNCVA  1        0.2802
2411.9    60.00  0.43     Sequence
             DRB1_1101  361      RKRISNCVADYSVLY  ISNCVADYS  3        0.2489
3383.0    65.00  0.26     Sequence
             DRB1_1101  362      KRISNCVADYSVLYN  ISNCVADYS  2        0.1799
7137.0    80.00  0.30     Sequence
             DRB1_1101  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.1573
9116.2    85.00  0.37     Sequence
             DRB1_1101  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.1895
6431.7    80.00  0.31     Sequence
             DRB1_1101  365      SNCVADYSVLYNSAS  YSVLYNSAS  6        0.2704
2680.8    60.00  0.50     Sequence
             DRB1_1101  366      NCVADYSVLYNSASF  YSVLYNSAS  5        0.3246
1491.2    46.00  0.58     Sequence
             DRB1_1101  367      CVADYSVLYNSASFS  YSVLYNSAS  4        0.3705
907.7    36.00  0.62     Sequence
             DRB1_1101  368      VADYSVLYNSASFST  YSVLYNSAS  3        0.4041
631.0    30.00  0.55     Sequence
             DRB1_1101  369      ADYSVLYNSASFSTF  YSVLYNSAS  2        0.4289
482.6    26.00  0.41     Sequence
             DRB1_1101  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.4351
451.2    25.00  0.44     Sequence
```

```
             DRB1_1101  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.4144
564.6    28.00  0.52     Sequence
             DRB1_1101  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.3795
823.9    34.00  0.54     Sequence
             DRB1_1101  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.3681
931.6    37.00  0.32     Sequence
             DRB1_1101  374      LYNSASFSTFKCYGV  SFSTFKCYG  5        0.3717
896.4    36.00  0.32     Sequence
             DRB1_1101  375      YNSASFSTFKCYGVS  FSTFKCYGV  5        0.3912
725.7    32.00  0.40     Sequence
             DRB1_1101  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.3946
699.4    32.00  0.44     Sequence
             DRB1_1101  377      SASFSTFKCYGVSPT  FSTFKCYGV  3        0.4022
644.3    30.00  0.44     Sequence
             DRB1_1101  378      ASFSTFKCYGVSPTK  FSTFKCYGV  2        0.3917
721.4    32.00  0.44     Sequence
             DRB1_1101  379      SFSTFKCYGVSPTKL  FSTFKCYGV  1        0.3636
977.9    37.00  0.25     Sequence
             DRB1_1101  380      FSTFKCYGVSPTKLN  YGVSPTKLN  6        0.3597
1020.5    38.00  0.24     Sequence
             DRB1_1101  381      STFKCYGVSPTKLND  YGVSPTKLN  5        0.3583
1036.1    39.00  0.38     Sequence
             DRB1_1101  382      TFKCYGVSPTKLNDL  YGVSPTKLN  4        0.3779
838.3    35.00  0.43     Sequence
             DRB1_1101  383      FKCYGVSPTKLNDLC  YGVSPTKLN  3        0.3729
884.7    36.00  0.45     Sequence
             DRB1_1101  384      KCYGVSPTKLNDLCF  YGVSPTKLN  2        0.3435
1215.7    42.00  0.52     Sequence
             DRB1_1101  385      CYGVSPTKLNDLCFT  YGVSPTKLN  1        0.2863
2257.3    55.00  0.45     Sequence
             DRB1_1101  386      YGVSPTKLNDLCFTN  YGVSPTKLN  0        0.1874
6582.3    80.00  0.24     Sequence
             DRB1_1101  387      GVSPTKLNDLCFTNV  TKLNDLCFT  4        0.1221
13335.2    95.00  0.28     Sequence
             DRB1_1101  388      VSPTKLNDLCFTNVY  TKLNDLCFT  3        0.1384
11186.8    90.00  0.27     Sequence
             DRB1_1101  389      SPTKLNDLCFTNVYA  KLNDLCFTN  3        0.1723
7753.9    85.00  0.21     Sequence
             DRB1_1101  390      PTKLNDLCFTNVYAD  LNDLCFTNV  3        0.1768
7381.8    80.00  0.20     Sequence
             DRB1_1101  391      TKLNDLCFTNVYADS  LCFTNVYAD  5        0.1911
6326.0    80.00  0.19     Sequence
             DRB1_1101  392      KLNDLCFTNVYADSF  LCFTNVYAD  4        0.2036
5524.8    75.00  0.19     Sequence
             DRB1_1101  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.1999
5747.8    75.00  0.25     Sequence
             DRB1_1101  394      NDLCFTNVYADSFVI  FTNVYADSF  4        0.2147
4896.7    75.00  0.24     Sequence
             DRB1_1101  395      DLCFTNVYADSFVIR  NVYADSFVI  5        0.2390
3765.3    70.00  0.29     Sequence
             DRB1_1101  396      LCFTNVYADSFVIRG  NVYADSFVI  4        0.2825
2352.3    55.00  0.31     Sequence
             DRB1_1101  397      CFTNVYADSFVIRGD  YADSFVIRG  5        0.2874
2231.3    55.00  0.29     Sequence
             DRB1_1101  398      FTNVYADSFVIRGDE  YADSFVIRG  4        0.2928
2104.9    55.00  0.34     Sequence
             DRB1_1101  399      TNVYADSFVIRGDEV  DSFVIRGDE  5        0.2944
2068.3    55.00  0.32     Sequence
             DRB1_1101  400      NVYADSFVIRGDEVR  DSFVIRGDE  4        0.3068
1809.0    50.00  0.41     Sequence
             DRB1_1101  401      VYADSFVIRGDEVRQ  DSFVIRGDE  3        0.3066
1811.6    50.00  0.42     Sequence
             DRB1_1101  402      YADSFVIRGDEVRQI  DSFVIRGDE  2        0.3089
1767.3    49.00  0.44     Sequence
             DRB1_1101  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.2946
2063.8    55.00  0.28     Sequence
```

```
             DRB1_1101  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.2773
2489.7    60.00  0.38     Sequence
             DRB1_1101  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.2731
2603.7    60.00  0.46     Sequence
             DRB1_1101  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.2236
4449.5    70.00  0.54     Sequence
             DRB1_1101  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.2053
5425.9    75.00  0.34     Sequence
             DRB1_1101  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.1980
5866.8    80.00  0.32     Sequence
             DRB1_1101  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.1994
5780.0    75.00  0.41     Sequence
             DRB1_1101  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.2095
5181.8    75.00  0.41     Sequence
             DRB1_1101  411      DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.2096
5177.2    75.00  0.40     Sequence
             DRB1_1101  412      EVRQIAPGQTGTIAD  RQIAPGQTG  2        0.2176
4748.6    75.00  0.43     Sequence
             DRB1_1101  413      VRQIAPGQTGTIADY  RQIAPGQTG  1        0.1673
8184.8    85.00  0.34     Sequence
             DRB1_1101  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.0878
19328.7   100.00  0.51     Sequence
             DRB1_1101  415      QIAPGQTGTIADYNY  IAPGQTGTI  1        0.0534
28064.5   100.00  0.29     Sequence
             DRB1_1101  416      IAPGQTGTIADYNYK  GTIADYNYK  6        0.0675
24081.6   100.00  0.37     Sequence
             DRB1_1101  417      APGQTGTIADYNYKL  GTIADYNYK  5        0.0996
17018.4    95.00  0.35     Sequence
             DRB1_1101  418      PGQTGTIADYNYKLP  IADYNYKLP  6        0.1271
12636.2    90.00  0.32     Sequence
             DRB1_1101  419      GQTGTIADYNYKLPD  IADYNYKLP  5        0.1451
10403.2    90.00  0.34     Sequence
             DRB1_1101  420      QTGTIADYNYKLPDD  IADYNYKLP  4        0.1544
9407.5    85.00  0.34     Sequence
             DRB1_1101  421      TGTIADYNYKLPDDF  IADYNYKLP  3        0.1711
7850.8    85.00  0.31     Sequence
             DRB1_1101  422      GTIADYNYKLPDDFT  IADYNYKLP  2        0.1796
7160.8    80.00  0.28     Sequence
             DRB1_1101  423      TIADYNYKLPDDFTG  YKLPDDFTG  6        0.1741
7599.6    85.00  0.21     Sequence
             DRB1_1101  424      IADYNYKLPDDFTGC  YKLPDDFTG  5        0.1661
8291.1    85.00  0.35     Sequence
             DRB1_1101  425      ADYNYKLPDDFTGCV  YKLPDDFTG  4        0.1632
8549.9    85.00  0.44     Sequence
             DRB1_1101  426      DYNYKLPDDFTGCVI  YKLPDDFTG  3        0.1547
9374.1    85.00  0.55     Sequence
             DRB1_1101  427      YNYKLPDDFTGCVIA  YKLPDDFTG  2        0.1541
9434.0    85.00  0.53     Sequence
             DRB1_1101  428      NYKLPDDFTGCVIAW  YKLPDDFTG  1        0.1384
11182.1    90.00  0.31     Sequence
             DRB1_1101  429      YKLPDDFTGCVIAWN  FTGCVIAWN  6        0.1503
9837.1    90.00  0.38     Sequence
             DRB1_1101  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.1703
7917.0    85.00  0.46     Sequence
             DRB1_1101  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.1828
6921.3    80.00  0.41     Sequence
             DRB1_1101  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.1968
5948.2    80.00  0.37     Sequence
             DRB1_1101  433      DDFTGCVIAWNSNNL  FTGCVIAWN  2        0.2076
5288.7    75.00  0.34     Sequence
             DRB1_1101  434      DFTGCVIAWNSNNLD  FTGCVIAWN  1        0.1973
5915.4    80.00  0.18     Sequence
             DRB1_1101  435      FTGCVIAWNSNNLDS  IAWNSNNLD  5        0.2047
5461.0    75.00  0.34     Sequence
             DRB1_1101  436      TGCVIAWNSNNLDSK  IAWNSNNLD  4        0.2387
3777.3    70.00  0.32     Sequence
```

```
             DRB1_1101  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3        0.2543
3190.1    65.00  0.38     Sequence
             DRB1_1101  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2        0.2460
3492.9    65.00  0.34     Sequence
             DRB1_1101  439      VIAWNSNNLDSKVGG  AWNSNNLDS  2        0.2339
3981.7    70.00  0.25     Sequence
             DRB1_1101  440      IAWNSNNLDSKVGGN  WNSNNLDSK  2        0.2085
5237.6    75.00  0.25     Sequence
             DRB1_1101  441      AWNSNNLDSKVGGNY  SNNLDSKVG  3        0.1803
7108.7    80.00  0.27     Sequence
             DRB1_1101  442      WNSNNLDSKVGGNYN  SNNLDSKVG  2        0.1683
8095.6    85.00  0.28     Sequence
             DRB1_1101  443      NSNNLDSKVGGNYNY  LDSKVGGNY  4        0.1632
8556.6    85.00  0.26     Sequence
             DRB1_1101  444      SNNLDSKVGGNYNYL  LDSKVGGNY  3        0.1545
9393.1    85.00  0.29     Sequence
             DRB1_1101  445      NNLDSKVGGNYNYLY  LDSKVGGNY  2        0.1368
11380.5    90.00  0.29     Sequence
             DRB1_1101  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.1469
10207.1    90.00  0.37     Sequence
             DRB1_1101  447      LDSKVGGNYNYLYRL  YNYLYRLXX  8        0.2670
2781.5    60.00  0.25     Sequence
             DRB1_1101  448      DSKVGGNYNYLYRLF  YNYLYRLFX  7        0.4096
594.7    29.00  0.49     Sequence
             DRB1_1101  449      SKVGGNYNYLYRLFR  YNYLYRLFR  6        0.6527
42.8     5.00  0.83     Sequence         WB
             DRB1_1101  450      KVGGNYNYLYRLFRK  YNYLYRLFR  5        0.7442
15.9     1.50  0.73     Sequence         SB
             DRB1_1101  451      VGGNYNYLYRLFRKS  YNYLYRLFR  4        0.7934
9.4     0.70  0.61     Sequence         SB
             DRB1_1101  452      GGNYNYLYRLFRKSN  YNYLYRLFR  3        0.8362
5.9     0.25  0.47     Sequence         SB
             DRB1_1101  453      GNYNYLYRLFRKSNL  YNYLYRLFR  2        0.8475
5.2     0.17  0.40     Sequence         SB
             DRB1_1101  454      NYNYLYRLFRKSNLK  LYRLFRKSN  4        0.8467
5.3     0.17  0.34     Sequence         SB
             DRB1_1101  455      YNYLYRLFRKSNLKP  LYRLFRKSN  3        0.8403
5.6     0.25  0.38     Sequence         SB
             DRB1_1101  456      NYLYRLFRKSNLKPF  LYRLFRKSN  2        0.8212
6.9     0.40  0.45     Sequence         SB
             DRB1_1101  457      YLYRLFRKSNLKPFE  YRLFRKSNL  2        0.8054
8.2     0.50  0.52     Sequence         SB
             DRB1_1101  458      LYRLFRKSNLKPFER  YRLFRKSNL  1        0.7040
24.6     3.00  0.36     Sequence         WB
             DRB1_1101  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.5699
105.0    10.00  0.44     Sequence
             DRB1_1101  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.5141
192.1    15.00  0.56     Sequence
             DRB1_1101  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.4513
378.6    23.00  0.40     Sequence
             DRB1_1101  462      FRKSNLKPFERDIST  LKPFERDIS  5        0.4070
611.7    30.00  0.36     Sequence
             DRB1_1101  463      RKSNLKPFERDISTE  LKPFERDIS  4        0.3095
1757.1    49.00  0.68     Sequence
             DRB1_1101  464      KSNLKPFERDISTEI  LKPFERDIS  3        0.3242
1498.7    46.00  0.65     Sequence
             DRB1_1101  465      SNLKPFERDISTEIY  LKPFERDIS  2        0.3212
1547.8    46.00  0.56     Sequence
             DRB1_1101  466      NLKPFERDISTEIYQ  LKPFERDIS  1        0.3060
1823.5    50.00  0.38     Sequence
             DRB1_1101  467      LKPFERDISTEIYQA  FERDISTEI  3        0.2934
2091.1    55.00  0.35     Sequence
             DRB1_1101  468      KPFERDISTEIYQAG  FERDISTEI  2        0.2643
2864.6    60.00  0.44     Sequence
             DRB1_1101  469      PFERDISTEIYQAGS  ERDISTEIY  2        0.2411
3682.3    65.00  0.24     Sequence
```

```
             DRB1_1101  470      FERDISTEIYQAGST  ISTEIYQAG  4        0.2251
4376.6    70.00  0.28     Sequence
             DRB1_1101  471      ERDISTEIYQAGSTP  ISTEIYQAG  3        0.1661
8284.7    85.00  0.41     Sequence
             DRB1_1101  472      RDISTEIYQAGSTPC  ISTEIYQAG  2        0.1692
8018.0    85.00  0.45     Sequence
             DRB1_1101  473      DISTEIYQAGSTPCN  YQAGSTPCN  6        0.1555
9299.6    85.00  0.32     Sequence
             DRB1_1101  474      ISTEIYQAGSTPCNG  YQAGSTPCN  5        0.1718
7788.6    85.00  0.46     Sequence
             DRB1_1101  475      STEIYQAGSTPCNGV  YQAGSTPCN  4        0.1861
6672.0    80.00  0.50     Sequence
             DRB1_1101  476      TEIYQAGSTPCNGVK  YQAGSTPCN  3        0.2057
5400.8    75.00  0.56     Sequence
             DRB1_1101  477      EIYQAGSTPCNGVKG  YQAGSTPCN  2        0.1962
5986.8    80.00  0.55     Sequence
             DRB1_1101  478      IYQAGSTPCNGVKGF  YQAGSTPCN  1        0.1679
8132.0    85.00  0.37     Sequence
             DRB1_1101  479      YQAGSTPCNGVKGFN  STPCNGVKG  4        0.1296
12300.0    90.00  0.32     Sequence
             DRB1_1101  480      QAGSTPCNGVKGFNC  STPCNGVKG  3        0.1108
15072.1    95.00  0.35     Sequence
             DRB1_1101  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.1319
12002.5    90.00  0.32     Sequence
             DRB1_1101  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.1490
9970.0    90.00  0.34     Sequence
             DRB1_1101  483      STPCNGVKGFNCYFP  CNGVKGFNC  3        0.1623
8635.5    85.00  0.32     Sequence
             DRB1_1101  484      TPCNGVKGFNCYFPL  VKGFNCYFP  5        0.1925
6230.3    80.00  0.26     Sequence
             DRB1_1101  485      PCNGVKGFNCYFPLQ  VKGFNCYFP  4        0.2172
4768.8    75.00  0.26     Sequence
             DRB1_1101  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.2986
1975.8    55.00  0.44     Sequence
             DRB1_1101  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.3409
1250.8    42.00  0.49     Sequence
             DRB1_1101  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.3789
828.9    35.00  0.47     Sequence
             DRB1_1101  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3        0.4372
441.0    25.00  0.37     Sequence
             DRB1_1101  490      KGFNCYFPLQSYGFQ  YFPLQSYGF  5        0.4599
345.2    22.00  0.38     Sequence
             DRB1_1101  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.4337
458.4    25.00  0.47     Sequence
             DRB1_1101  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.4046
627.6    30.00  0.58     Sequence
             DRB1_1101  493      NCYFPLQSYGFQPTY  YFPLQSYGF  2        0.3701
911.7    36.00  0.63     Sequence
             DRB1_1101  494      CYFPLQSYGFQPTYG  YFPLQSYGF  1        0.3236
1507.4    46.00  0.49     Sequence
             DRB1_1101  495      YFPLQSYGFQPTYGV  YFPLQSYGF  0        0.2595
3016.9    65.00  0.31     Sequence
             DRB1_1101  496      FPLQSYGFQPTYGVG  YGFQPTYGV  5        0.2129
4996.8    75.00  0.38     Sequence
             DRB1_1101  497      PLQSYGFQPTYGVGY  FQPTYGVGY  6        0.3335
1355.0    44.00  0.62     Sequence
             DRB1_1101  498      LQSYGFQPTYGVGYQ  FQPTYGVGY  5        0.3862
766.3    33.00  0.67     Sequence
             DRB1_1101  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4        0.3959
689.6    31.00  0.70     Sequence
             DRB1_1101  500      SYGFQPTYGVGYQPY  FQPTYGVGY  3        0.3925
715.9    32.00  0.74     Sequence
             DRB1_1101  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.3752
862.9    35.00  0.75     Sequence
             DRB1_1101  502      GFQPTYGVGYQPYRV  FQPTYGVGY  1        0.3015
1914.3    55.00  0.47     Sequence
```

```
             DRB1_1101  503      FQPTYGVGYQPYRVV  FQPTYGVGY  0         0.2655
2826.0    60.00  0.25     Sequence
             DRB1_1101  504      QPTYGVGYQPYRVVV  VGYQPYRVV  5         0.2539
3205.3    65.00  0.38     Sequence
             DRB1_1101  505      PTYGVGYQPYRVVVL  VGYQPYRVV  4         0.2994
1958.9    55.00  0.31     Sequence
             DRB1_1101  506      TYGVGYQPYRVVVLS  YQPYRVVVL  5         0.3427
1227.0    42.00  0.35     Sequence
             DRB1_1101  507      YGVGYQPYRVVVLSF  YQPYRVVVL  4         0.3857
769.9    33.00  0.29     Sequence
             DRB1_1101  508      GVGYQPYRVVVLSFE  YRVVVLSFE  6         0.4062
617.0    30.00  0.28     Sequence
             DRB1_1101  509      VGYQPYRVVVLSFEL  YRVVVLSFE  5         0.3966
684.7    31.00  0.39     Sequence
             DRB1_1101  510      GYQPYRVVVLSFELL  YRVVVLSFE  4         0.3751
864.0    35.00  0.47     Sequence
             DRB1_1101  511      YQPYRVVVLSFELLH  YRVVVLSFE  3         0.3575
1045.3    39.00  0.51     Sequence
             DRB1_1101  512      QPYRVVVLSFELLHA  YRVVVLSFE  2         0.3628
987.2    38.00  0.46     Sequence
             DRB1_1101  513      PYRVVVLSFELLHAP  YRVVVLSFE  1         0.3272
1450.0    45.00  0.25     Sequence
             DRB1_1101  514      YRVVVLSFELLHAPA  VVVLSFELL  2         0.3171
1618.3    47.00  0.20     Sequence
             DRB1_1101  515      RVVVLSFELLHAPAT  FELLHAPAT  6         0.3382
1287.7    43.00  0.31     Sequence
             DRB1_1101  516      VVVLSFELLHAPATV  FELLHAPAT  5         0.3714
898.6    36.00  0.44     Sequence
             DRB1_1101  517      VVLSFELLHAPATVC  FELLHAPAT  4         0.3727
886.8    36.00  0.46     Sequence
             DRB1_1101  518      VLSFELLHAPATVCG  FELLHAPAT  3         0.3782
834.9    35.00  0.50     Sequence
             DRB1_1101  519      LSFELLHAPATVCGP  FELLHAPAT  2         0.3804
815.6    34.00  0.47     Sequence
             DRB1_1101  520      SFELLHAPATVCGPK  LLHAPATVC  3         0.3472
1168.7    41.00  0.35     Sequence
             DRB1_1101  521      FELLHAPATVCGPKK  LLHAPATVC  2         0.2830
2338.9    55.00  0.44     Sequence
             DRB1_1101  522      ELLHAPATVCGPKKS  LHAPATVCG  2         0.1946
6091.2    80.00  0.36     Sequence
             DRB1_1101  523      LLHAPATVCGPKKST  LHAPATVCG  1         0.1962
5983.0    80.00  0.23     Sequence
             DRB1_1101  524      LHAPATVCGPKKSTN  ATVCGPKKS  4         0.1888
6482.9    80.00  0.28     Sequence
             DRB1_1101  525      HAPATVCGPKKSTNL  ATVCGPKKS  3         0.1808
7071.8    80.00  0.31     Sequence
             DRB1_1101  526      APATVCGPKKSTNLV  TVCGPKKST  3         0.1869
6621.2    80.00  0.25     Sequence
             DRB1_1101  527      PATVCGPKKSTNLVK  VCGPKKSTN  3         0.1949
6070.9    80.00  0.38     Sequence
             DRB1_1101  528      ATVCGPKKSTNLVKN  VCGPKKSTN  2         0.1819
6987.3    80.00  0.36     Sequence
             DRB1_1101  529      TVCGPKKSTNLVKNK  KKSTNLVKN  5         0.1771
7356.0    80.00  0.19     Sequence
             DRB1_1101  530      VCGPKKSTNLVKNKC  STNLVKNKC  6         0.2103
5136.5    75.00  0.32     Sequence
             DRB1_1101  531      CGPKKSTNLVKNKCV  STNLVKNKC  5         0.2707
2671.5    60.00  0.31     Sequence
             DRB1_1101  532      GPKKSTNLVKNKCVN  STNLVKNKC  4         0.3072
1799.9    49.00  0.29     Sequence
             DRB1_1101  533      PKKSTNLVKNKCVNF  STNLVKNKC  3         0.3319
1378.7    44.00  0.29     Sequence
             DRB1_1101  534      KKSTNLVKNKCVNFN  NLVKNKCVN  4         0.3450
1196.6    41.00  0.31     Sequence
             DRB1_1101  535      KSTNLVKNKCVNFNF  NLVKNKCVN  3         0.3318
1379.7    44.00  0.34     Sequence
```

```
             DRB1_1101  536      STNLVKNKCVNFNFN  NLVKNKCVN  2        0.3054
1836.3    50.00  0.32     Sequence
             DRB1_1101  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2        0.2527
3248.6    65.00  0.32     Sequence
             DRB1_1101  538      NLVKNKCVNFNFNGL  KNKCVNFNF  3        0.2211
4568.9    70.00  0.23     Sequence
             DRB1_1101  539      LVKNKCVNFNFNGLT  VNFNFNGLT  6        0.2143
4918.5    75.00  0.23     Sequence
             DRB1_1101  540      VKNKCVNFNFNGLTG  VNFNFNGLT  5        0.2459
3495.1    65.00  0.31     Sequence
             DRB1_1101  541      KNKCVNFNFNGLTGT  VNFNFNGLT  4        0.2891
2191.0    55.00  0.29     Sequence
             DRB1_1101  542      NKCVNFNFNGLTGTG  VNFNFNGLT  3        0.3143
1668.3    48.00  0.28     Sequence
             DRB1_1101  543      KCVNFNFNGLTGTGV  FNGLTGTGV  6        0.3538
1088.0    39.00  0.35     Sequence
             DRB1_1101  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5        0.3584
1034.6    39.00  0.50     Sequence
             DRB1_1101  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.3632
983.0    38.00  0.61     Sequence
             DRB1_1101  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3        0.3516
1113.3    40.00  0.65     Sequence
             DRB1_1101  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.3284
1430.9    45.00  0.70     Sequence
             DRB1_1101  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.2472
3448.3    65.00  0.52     Sequence
             DRB1_1101  549      FNGLTGTGVLTESNK  GLTGTGVLT  2        0.1912
6314.4    80.00  0.29     Sequence
             DRB1_1101  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.1569
9159.5    85.00  0.26     Sequence
             DRB1_1101  551      GLTGTGVLTESNKKF  LTESNKKFX  7        0.2158
4841.1    75.00  0.32     Sequence
             DRB1_1101  552      LTGTGVLTESNKKFL  LTESNKKFL  6        0.2871
2237.1    55.00  0.50     Sequence
             DRB1_1101  553      TGTGVLTESNKKFLP  LTESNKKFL  5        0.3349
1335.0    43.00  0.55     Sequence
             DRB1_1101  554      GTGVLTESNKKFLPF  LTESNKKFL  4        0.3729
884.9    36.00  0.56     Sequence
             DRB1_1101  555      TGVLTESNKKFLPFQ  LTESNKKFL  3        0.3837
786.6    34.00  0.60     Sequence
             DRB1_1101  556      GVLTESNKKFLPFQQ  LTESNKKFL  2        0.3952
694.9    32.00  0.55     Sequence
             DRB1_1101  557      VLTESNKKFLPFQQF  LTESNKKFL  1        0.3564
1057.9    39.00  0.29     Sequence
             DRB1_1101  558      LTESNKKFLPFQQFG  KKFLPFQQF  5        0.3643
971.0    37.00  0.28     Sequence
             DRB1_1101  559      TESNKKFLPFQQFGR  FLPFQQFGR  6        0.4466
398.4    23.00  0.50     Sequence
             DRB1_1101  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5        0.4654
325.1    21.00  0.54     Sequence
             DRB1_1101  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4        0.4822
271.2    19.00  0.55     Sequence
             DRB1_1101  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.4943
237.9    18.00  0.53     Sequence
             DRB1_1101  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.4851
262.6    19.00  0.54     Sequence
             DRB1_1101  564      KFLPFQQFGRDIADT  FQQFGRDIA  4        0.4358
447.7    25.00  0.43     Sequence
             DRB1_1101  565      FLPFQQFGRDIADTT  FQQFGRDIA  3        0.3946
699.2    32.00  0.56     Sequence
             DRB1_1101  566      LPFQQFGRDIADTTD  FQQFGRDIA  2        0.3528
1099.0    40.00  0.67     Sequence
             DRB1_1101  567      PFQQFGRDIADTTDA  FQQFGRDIA  1        0.3245
1492.8    46.00  0.53     Sequence
             DRB1_1101  568      FQQFGRDIADTTDAV  FQQFGRDIA  0        0.2703
2683.4    60.00  0.41     Sequence
```

```
             DRB1_1101  569      QQFGRDIADTTDAVR  FGRDIADTT  2         0.1083
15493.9    95.00  0.47     Sequence
             DRB1_1101  570      QFGRDIADTTDAVRD  IADTTDAVR  5         0.0854
19850.7   100.00  0.21     Sequence
             DRB1_1101  571      FGRDIADTTDAVRDP  IADTTDAVR  4         0.0698
23492.0   100.00  0.32     Sequence
             DRB1_1101  572      GRDIADTTDAVRDPQ  IADTTDAVR  3         0.0673
24136.2   100.00  0.40     Sequence
             DRB1_1101  573      RDIADTTDAVRDPQT  IADTTDAVR  2         0.0617
25654.6   100.00  0.35     Sequence
             DRB1_1101  574      DIADTTDAVRDPQTL  TTDAVRDPQ  4         0.0528
28227.8   100.00  0.28     Sequence
             DRB1_1101  575      IADTTDAVRDPQTLE  TTDAVRDPQ  3         0.0467
30173.9   100.00  0.34     Sequence
             DRB1_1101  576      ADTTDAVRDPQTLEI  TTDAVRDPQ  2         0.0439
31108.4   100.00  0.36     Sequence
             DRB1_1101  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5         0.0461
30355.6   100.00  0.34     Sequence
             DRB1_1101  578      TTDAVRDPQTLEILD  VRDPQTLEI  4         0.0443
30975.7   100.00  0.40     Sequence
             DRB1_1101  579      TDAVRDPQTLEILDI  VRDPQTLEI  3         0.0455
30575.5   100.00  0.38     Sequence
             DRB1_1101  580      DAVRDPQTLEILDIT  VRDPQTLEI  2         0.0527
28261.7   100.00  0.34     Sequence
             DRB1_1101  581      AVRDPQTLEILDITP  LEILDITPX  7         0.0649
24780.2   100.00  0.28     Sequence
             DRB1_1101  582      VRDPQTLEILDITPC  LEILDITPC  6         0.0937
18142.4    95.00  0.52     Sequence
             DRB1_1101  583      RDPQTLEILDITPCS  LEILDITPC  5         0.1410
10879.1    90.00  0.56     Sequence
             DRB1_1101  584      DPQTLEILDITPCSF  LEILDITPC  4         0.1899
6406.3    80.00  0.44     Sequence
             DRB1_1101  585      PQTLEILDITPCSFG  ILDITPCSF  5         0.2236
4447.3    70.00  0.38     Sequence
             DRB1_1101  586      QTLEILDITPCSFGG  ILDITPCSF  4         0.2531
3235.1    65.00  0.34     Sequence
             DRB1_1101  587      TLEILDITPCSFGGV  ILDITPCSF  3         0.2575
3082.0    65.00  0.36     Sequence
             DRB1_1101  588      LEILDITPCSFGGVS  ILDITPCSF  2         0.2527
3248.8    65.00  0.35     Sequence
             DRB1_1101  589      EILDITPCSFGGVSV  ITPCSFGGV  4         0.2209
4579.5    70.00  0.36     Sequence
             DRB1_1101  590      ILDITPCSFGGVSVI  ITPCSFGGV  3         0.1992
5793.0    75.00  0.40     Sequence
             DRB1_1101  591      LDITPCSFGGVSVIT  ITPCSFGGV  2         0.1854
6724.5    80.00  0.39     Sequence
             DRB1_1101  592      DITPCSFGGVSVITP  FGGVSVITP  6         0.1787
7233.5    80.00  0.50     Sequence
             DRB1_1101  593      ITPCSFGGVSVITPG  FGGVSVITP  5         0.1828
6915.4    80.00  0.64     Sequence
             DRB1_1101  594      TPCSFGGVSVITPGT  FGGVSVITP  4         0.2034
5533.8    75.00  0.62     Sequence
             DRB1_1101  595      PCSFGGVSVITPGTN  FGGVSVITP  3         0.2278
4250.1    70.00  0.50     Sequence
             DRB1_1101  596      CSFGGVSVITPGTNT  FGGVSVITP  2         0.2530
3238.3    65.00  0.40     Sequence
             DRB1_1101  597      SFGGVSVITPGTNTS  VSVITPGTN  4         0.2498
3349.9    65.00  0.39     Sequence
             DRB1_1101  598      FGGVSVITPGTNTSN  VSVITPGTN  3         0.2409
3691.0    65.00  0.49     Sequence
             DRB1_1101  599      GGVSVITPGTNTSNQ  VSVITPGTN  2         0.2275
4267.3    70.00  0.47     Sequence
             DRB1_1101  600      GVSVITPGTNTSNQV  VSVITPGTN  1         0.1990
5807.5    75.00  0.34     Sequence
             DRB1_1101  601      VSVITPGTNTSNQVA  ITPGTNTSN  3         0.1455
10356.7    90.00  0.38     Sequence
```

```
             DRB1_1101  602      SVITPGTNTSNQVAV  ITPGTNTSN  2        0.0973
17448.8    95.00  0.52     Sequence
             DRB1_1101  603      VITPGTNTSNQVAVL  ITPGTNTSN  1        0.0564
27155.3   100.00  0.32     Sequence
             DRB1_1101  604      ITPGTNTSNQVAVLY  GTNTSNQVA  3        0.0562
27219.7   100.00  0.22     Sequence
             DRB1_1101  605      TPGTNTSNQVAVLYQ  SNQVAVLYQ  6        0.0873
19436.3   100.00  0.19     Sequence
             DRB1_1101  606      PGTNTSNQVAVLYQG  NQVAVLYQG  6        0.1230
13206.3    95.00  0.33     Sequence
             DRB1_1101  607      GTNTSNQVAVLYQGV  NQVAVLYQG  5        0.1696
7983.3    85.00  0.34    Sequence
             DRB1_1101  608      TNTSNQVAVLYQGVN  VAVLYQGVN  6        0.2098
5165.8    75.00  0.43    Sequence
             DRB1_1101  609      NTSNQVAVLYQGVNC  VAVLYQGVN  5        0.2292
4188.0    70.00  0.50    Sequence
             DRB1_1101  610      TSNQVAVLYQGVNCT  VAVLYQGVN  4        0.2484
3401.6    65.00  0.49    Sequence
             DRB1_1101  611      SNQVAVLYQGVNCTE  VAVLYQGVN  3        0.2500
3343.9    65.00  0.54    Sequence
             DRB1_1101  612      NQVAVLYQGVNCTEV  VAVLYQGVN  2        0.2442
3560.7    65.00  0.49    Sequence
             DRB1_1101  613      QVAVLYQGVNCTEVP  YQGVNCTEV  5        0.2198
4637.2    70.00  0.34    Sequence
             DRB1_1101  614      VAVLYQGVNCTEVPV  YQGVNCTEV  4        0.1904
6372.5    80.00  0.49    Sequence
             DRB1_1101  615      AVLYQGVNCTEVPVA  YQGVNCTEV  3        0.1950
6060.2    80.00  0.62    Sequence
             DRB1_1101  616      VLYQGVNCTEVPVAI  YQGVNCTEV  2        0.1887
6489.1    80.00  0.62    Sequence
             DRB1_1101  617      LYQGVNCTEVPVAIH  YQGVNCTEV  1        0.1586
8993.8    85.00  0.42    Sequence
             DRB1_1101  618      YQGVNCTEVPVAIHA  GVNCTEVPV  2        0.1440
10528.5    90.00  0.16     Sequence
             DRB1_1101  619      QGVNCTEVPVAIHAD  VPVAIHADX  7        0.1269
12668.1    90.00  0.23     Sequence
             DRB1_1101  620      GVNCTEVPVAIHADQ  VPVAIHADQ  6        0.1539
9460.2    85.00  0.38    Sequence
             DRB1_1101  621      VNCTEVPVAIHADQL  VPVAIHADQ  5        0.1693
8006.3    85.00  0.45    Sequence
             DRB1_1101  622      NCTEVPVAIHADQLT  VPVAIHADQ  4        0.1819
6983.5    80.00  0.46    Sequence
             DRB1_1101  623      CTEVPVAIHADQLTP  VPVAIHADQ  3        0.1840
6832.4    80.00  0.50    Sequence
             DRB1_1101  624      TEVPVAIHADQLTPT  VPVAIHADQ  2        0.1787
7232.0    80.00  0.52    Sequence
             DRB1_1101  625      EVPVAIHADQLTPTW  AIHADQLTP  4        0.1362
11448.8    90.00  0.35     Sequence
             DRB1_1101  626      VPVAIHADQLTPTWR  AIHADQLTP  3        0.1342
11704.5    90.00  0.44     Sequence
             DRB1_1101  627      PVAIHADQLTPTWRV  DQLTPTWRV  6        0.1858
6700.2    80.00  0.31    Sequence
             DRB1_1101  628      VAIHADQLTPTWRVY  LTPTWRVYX  7        0.2554
3154.3    65.00  0.41    Sequence
             DRB1_1101  629      AIHADQLTPTWRVYS  LTPTWRVYS  6        0.3830
792.7    34.00  0.73     Sequence
             DRB1_1101  630      IHADQLTPTWRVYST  LTPTWRVYS  5        0.4417
420.2    24.00  0.76     Sequence
             DRB1_1101  631      HADQLTPTWRVYSTG  LTPTWRVYS  4        0.4705
307.8    20.00  0.76     Sequence
             DRB1_1101  632      ADQLTPTWRVYSTGS  LTPTWRVYS  3        0.4845
264.4    19.00  0.74     Sequence
             DRB1_1101  633      DQLTPTWRVYSTGSN  LTPTWRVYS  2        0.5053
211.1    16.00  0.64     Sequence
             DRB1_1101  634      QLTPTWRVYSTGSNV  LTPTWRVYS  1        0.4614
339.4    22.00  0.44     Sequence
```

```
             DRB1_1101  635      LTPTWRVYSTGSNVF  WRVYSTGSN  4        0.4098
593.4    29.00  0.29     Sequence
             DRB1_1101  636      TPTWRVYSTGSNVFQ  WRVYSTGSN  3        0.3685
927.8    37.00  0.44     Sequence
             DRB1_1101  637      PTWRVYSTGSNVFQT  WRVYSTGSN  2        0.3822
799.6    34.00  0.41     Sequence
             DRB1_1101  638      TWRVYSTGSNVFQTR  YSTGSNVFQ  4        0.3697
916.0    36.00  0.28     Sequence
             DRB1_1101  639      WRVYSTGSNVFQTRA  YSTGSNVFQ  3        0.3441
1207.9    41.00  0.37     Sequence
             DRB1_1101  640      RVYSTGSNVFQTRAG  YSTGSNVFQ  2        0.2684
2740.9    60.00  0.45     Sequence
             DRB1_1101  641      VYSTGSNVFQTRAGC  NVFQTRAGC  6        0.2510
3307.0    65.00  0.25     Sequence
             DRB1_1101  642      YSTGSNVFQTRAGCL  NVFQTRAGC  5        0.2599
3003.9    65.00  0.31     Sequence
             DRB1_1101  643      STGSNVFQTRAGCLI  FQTRAGCLI  6        0.2900
2167.9    55.00  0.34     Sequence
             DRB1_1101  644      TGSNVFQTRAGCLIG  FQTRAGCLI  5        0.3287
1426.7    45.00  0.43     Sequence
             DRB1_1101  645      GSNVFQTRAGCLIGA  FQTRAGCLI  4        0.3584
1034.8    39.00  0.50     Sequence
             DRB1_1101  646      SNVFQTRAGCLIGAE  FQTRAGCLI  3        0.3372
1301.7    43.00  0.55     Sequence
             DRB1_1101  647      NVFQTRAGCLIGAEY  FQTRAGCLI  2        0.3085
1774.7    49.00  0.58     Sequence
             DRB1_1101  648      VFQTRAGCLIGAEYV  FQTRAGCLI  1        0.2499
3348.6    65.00  0.40     Sequence
             DRB1_1101  649      FQTRAGCLIGAEYVN  QTRAGCLIG  1        0.2055
5410.3    75.00  0.19     Sequence
             DRB1_1101  650      QTRAGCLIGAEYVNN  LIGAEYVNN  6        0.1727
7718.0    85.00  0.22     Sequence
             DRB1_1101  651      TRAGCLIGAEYVNNS  LIGAEYVNN  5        0.1714
7824.4    85.00  0.37     Sequence
             DRB1_1101  652      RAGCLIGAEYVNNSY  LIGAEYVNN  4        0.1692
8018.0    85.00  0.43     Sequence
             DRB1_1101  653      AGCLIGAEYVNNSYE  LIGAEYVNN  3        0.1597
8886.3    85.00  0.49     Sequence
             DRB1_1101  654      GCLIGAEYVNNSYEC  LIGAEYVNN  2        0.1681
8110.4    85.00  0.43     Sequence
             DRB1_1101  655      CLIGAEYVNNSYECD  YVNNSYECD  6        0.1432
10619.5    90.00  0.31     Sequence
             DRB1_1101  656      LIGAEYVNNSYECDI  YVNNSYECD  5        0.1446
10458.2    90.00  0.47     Sequence
             DRB1_1101  657      IGAEYVNNSYECDIP  YVNNSYECD  4        0.1440
10532.8    90.00  0.50     Sequence
             DRB1_1101  658      GAEYVNNSYECDIPI  YVNNSYECD  3        0.1539
9454.6    85.00  0.50     Sequence
             DRB1_1101  659      AEYVNNSYECDIPIG  YVNNSYECD  2        0.1595
8900.5    85.00  0.47     Sequence
             DRB1_1101  660      EYVNNSYECDIPIGA  YECDIPIGA  6        0.1877
6559.1    80.00  0.44     Sequence
             DRB1_1101  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.2113
5082.3    75.00  0.55     Sequence
             DRB1_1101  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.2274
4269.7    70.00  0.57     Sequence
             DRB1_1101  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.2376
3823.9    70.00  0.53     Sequence
             DRB1_1101  664      NSYECDIPIGAGICA  YECDIPIGA  2        0.2471
3448.5    65.00  0.47     Sequence
             DRB1_1101  665      SYECDIPIGAGICAS  YECDIPIGA  1        0.2266
4305.1    70.00  0.32     Sequence
             DRB1_1101  666      YECDIPIGAGICASY  IPIGAGICA  4        0.1875
6577.8    80.00  0.25     Sequence
             DRB1_1101  667      ECDIPIGAGICASYQ  IPIGAGICA  3        0.1497
9894.0    90.00  0.31     Sequence
```

```
          DRB1_1101  668      CDIPIGAGICASYQT  IPIGAGICA  2        0.1575
9092.1    85.00  0.31     Sequence
          DRB1_1101  669      DIPIGAGICASYQTQ  IGAGICASY  3        0.1540
9447.3    85.00  0.26     Sequence
          DRB1_1101  670      IPIGAGICASYQTQT  IGAGICASY  2        0.1664
8258.2    85.00  0.22     Sequence
          DRB1_1101  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.1748
7544.0    85.00  0.28     Sequence
          DRB1_1101  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.1759
7451.3    85.00  0.36     Sequence
          DRB1_1101  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.1767
7391.2    85.00  0.41     Sequence
          DRB1_1101  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.1654
8348.3    85.00  0.37     Sequence
          DRB1_1101  675      GICASYQTQTNSPRR  YQTQTNSPR  5        0.1941
6121.7    80.00  0.50     Sequence
          DRB1_1101  676      ICASYQTQTNSPRRA  YQTQTNSPR  4        0.1984
5843.7    75.00  0.60     Sequence
          DRB1_1101  677      CASYQTQTNSPRRAR  YQTQTNSPR  3        0.2504
3328.5    65.00  0.51     Sequence
          DRB1_1101  678      ASYQTQTNSPRRARS  YQTQTNSPR  2        0.2769
2499.9    60.00  0.43     Sequence
          DRB1_1101  679      SYQTQTNSPRRARSV  QTNSPRRAR  4        0.2764
2513.5    60.00  0.29     Sequence
          DRB1_1101  680      YQTQTNSPRRARSVA  QTNSPRRAR  3        0.2779
2473.5    60.00  0.34     Sequence
          DRB1_1101  681      QTQTNSPRRARSVAS  QTNSPRRAR  2        0.2714
2653.5    60.00  0.33     Sequence
          DRB1_1101  682      TQTNSPRRARSVASQ  TNSPRRARS  2        0.2413
3673.7    65.00  0.31     Sequence
          DRB1_1101  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.2139
4943.8    75.00  0.20     Sequence
          DRB1_1101  684      TNSPRRARSVASQSI  PRRARSVAS  3        0.1798
7143.1    80.00  0.29     Sequence
          DRB1_1101  685      NSPRRARSVASQSII  PRRARSVAS  2        0.1786
7243.5    80.00  0.29     Sequence
          DRB1_1101  686      SPRRARSVASQSIIA  RRARSVASQ  2        0.2036
5523.4    75.00  0.14     Sequence
          DRB1_1101  687      PRRARSVASQSIIAY  VASQSIIAY  6        0.2314
4091.1    70.00  0.26     Sequence
          DRB1_1101  688      RRARSVASQSIIAYT  VASQSIIAY  5        0.2473
3442.8    65.00  0.37     Sequence
          DRB1_1101  689      RARSVASQSIIAYTM  VASQSIIAY  4        0.2581
3064.0    65.00  0.42     Sequence
          DRB1_1101  690      ARSVASQSIIAYTMS  VASQSIIAY  3        0.2641
2870.5    60.00  0.41     Sequence
          DRB1_1101  691      RSVASQSIIAYTMSL  VASQSIIAY  2        0.2833
2331.4    55.00  0.35     Sequence
          DRB1_1101  692      SVASQSIIAYTMSLG  QSIIAYTMS  4        0.2654
2830.0    60.00  0.20     Sequence
          DRB1_1101  693      VASQSIIAYTMSLGA  IAYTMSLGA  6        0.3693
919.9    36.00  0.49     Sequence
          DRB1_1101  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.4243
507.3    27.00  0.51     Sequence
          DRB1_1101  695      SQSIIAYTMSLGAEN  IAYTMSLGA  4        0.4722
302.0    20.00  0.46     Sequence
          DRB1_1101  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.5154
189.3    15.00  0.39     Sequence
          DRB1_1101  697      SIIAYTMSLGAENSV  IAYTMSLGA  2        0.5215
177.3    15.00  0.35     Sequence
          DRB1_1101  698      IIAYTMSLGAENSVA  YTMSLGAEN  3        0.5217
176.8    15.00  0.47     Sequence
          DRB1_1101  699      IAYTMSLGAENSVAY  YTMSLGAEN  2        0.4820
271.8    19.00  0.56     Sequence
          DRB1_1101  700      AYTMSLGAENSVAYS  YTMSLGAEN  1        0.3884
747.8    33.00  0.55     Sequence
```

```
             DRB1_1101  701      YTMSLGAENSVAYSN  YTMSLGAEN  0        0.2741
2577.5    60.00  0.40     Sequence
             DRB1_1101  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.0964
17627.9    95.00  0.41     Sequence
             DRB1_1101  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.0980
17311.3    95.00  0.38     Sequence
             DRB1_1101  704      SLGAENSVAYSNNSI  NSVAYSNNS  5        0.0984
17240.3    95.00  0.20     Sequence
             DRB1_1101  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.1156
14316.3    95.00  0.32     Sequence
             DRB1_1101  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.1630
8575.6    85.00  0.40     Sequence
             DRB1_1101  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.2032
5548.5    75.00  0.35     Sequence
             DRB1_1101  708      ENSVAYSNNSIAIPT  YSNNSIAIP  5        0.2383
3793.8    70.00  0.40     Sequence
             DRB1_1101  709      NSVAYSNNSIAIPTN  YSNNSIAIP  4        0.2584
3053.1    65.00  0.43     Sequence
             DRB1_1101  710      SVAYSNNSIAIPTNF  YSNNSIAIP  3        0.2565
3117.1    65.00  0.46     Sequence
             DRB1_1101  711      VAYSNNSIAIPTNFT  YSNNSIAIP  2        0.2427
3619.8    65.00  0.48     Sequence
             DRB1_1101  712      AYSNNSIAIPTNFTI  YSNNSIAIP  1        0.2086
5230.8    75.00  0.32     Sequence
             DRB1_1101  713      YSNNSIAIPTNFTIS  IAIPTNFTI  5        0.1837
6851.9    80.00  0.44     Sequence
             DRB1_1101  714      SNNSIAIPTNFTISV  IAIPTNFTI  4        0.1823
6954.3    80.00  0.51     Sequence
             DRB1_1101  715      NNSIAIPTNFTISVT  IAIPTNFTI  3        0.1861
6674.9    80.00  0.52     Sequence
             DRB1_1101  716      NSIAIPTNFTISVTT  IAIPTNFTI  2        0.1798
7147.7    80.00  0.50     Sequence
             DRB1_1101  717      SIAIPTNFTISVTTE  IAIPTNFTI  1        0.1484
10040.2    90.00  0.23     Sequence
             DRB1_1101  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.1423
10726.7    90.00  0.35     Sequence
             DRB1_1101  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.1576
9085.8    85.00  0.42     Sequence
             DRB1_1101  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.1794
7179.0    80.00  0.38     Sequence
             DRB1_1101  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.1972
5918.3    80.00  0.38     Sequence
             DRB1_1101  722      TNFTISVTTEILPVS  ISVTTEILP  4        0.2138
4947.3    75.00  0.30     Sequence
             DRB1_1101  723      NFTISVTTEILPVSM  ISVTTEILP  3        0.2149
4886.3    75.00  0.36     Sequence
             DRB1_1101  724      FTISVTTEILPVSMT  ISVTTEILP  2        0.2121
5038.2    75.00  0.37     Sequence
             DRB1_1101  725      TISVTTEILPVSMTK  ILPVSMTKX  7        0.2559
3138.2    65.00  0.27     Sequence
             DRB1_1101  726      ISVTTEILPVSMTKT  ILPVSMTKT  6        0.3206
1558.1    46.00  0.42     Sequence
             DRB1_1101  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.3724
889.2    36.00  0.49     Sequence
             DRB1_1101  728      VTTEILPVSMTKTSV  ILPVSMTKT  4        0.4005
656.0    31.00  0.49     Sequence
             DRB1_1101  729      TTEILPVSMTKTSVD  ILPVSMTKT  3        0.3992
665.3    31.00  0.49     Sequence
             DRB1_1101  730      TEILPVSMTKTSVDC  ILPVSMTKT  2        0.3745
869.3    35.00  0.52     Sequence
             DRB1_1101  731      EILPVSMTKTSVDCT  ILPVSMTKT  1        0.3091
1764.7    49.00  0.38     Sequence
             DRB1_1101  732      ILPVSMTKTSVDCTM  PVSMTKTSV  2        0.2283
4230.0    70.00  0.26     Sequence
             DRB1_1101  733      LPVSMTKTSVDCTMY  VSMTKTSVD  2        0.1873
6589.2    80.00  0.32     Sequence
```

```
             DRB1_1101  734      PVSMTKTSVDCTMYI  MTKTSVDCT  3        0.1515
9704.9    90.00  0.20     Sequence
             DRB1_1101  735      VSMTKTSVDCTMYIC  MTKTSVDCT  2        0.1216
13411.2    95.00  0.25     Sequence
             DRB1_1101  736      SMTKTSVDCTMYICG  KTSVDCTMY  3        0.1234
13161.2    95.00  0.25     Sequence
             DRB1_1101  737      MTKTSVDCTMYICGD  SVDCTMYIC  4        0.1215
13422.5    95.00  0.25     Sequence
             DRB1_1101  738      TKTSVDCTMYICGDS  VDCTMYICG  4        0.1269
12672.3    90.00  0.26     Sequence
             DRB1_1101  739      KTSVDCTMYICGDST  VDCTMYICG  3        0.1317
12027.9    90.00  0.24     Sequence
             DRB1_1101  740      TSVDCTMYICGDSTE  VDCTMYICG  2        0.1209
13519.3    95.00  0.25     Sequence
             DRB1_1101  741      SVDCTMYICGDSTEC  CTMYICGDS  3        0.1088
15410.1    95.00  0.25     Sequence
             DRB1_1101  742      VDCTMYICGDSTECS  CTMYICGDS  2        0.1066
15773.2    95.00  0.22     Sequence
             DRB1_1101  743      DCTMYICGDSTECSN  ICGDSTECS  5        0.1020
16586.3    95.00  0.23     Sequence
             DRB1_1101  744      CTMYICGDSTECSNL  ICGDSTECS  4        0.1009
16782.2    95.00  0.28     Sequence
             DRB1_1101  745      TMYICGDSTECSNLL  ICGDSTECS  3        0.0882
19245.0   100.00  0.39     Sequence
             DRB1_1101  746      MYICGDSTECSNLLL  ICGDSTECS  2        0.0768
21791.0   100.00  0.38     Sequence
             DRB1_1101  747      YICGDSTECSNLLLQ  STECSNLLL  5        0.0775
21625.9   100.00  0.25     Sequence
             DRB1_1101  748      ICGDSTECSNLLLQY  STECSNLLL  4        0.0768
21779.9   100.00  0.36     Sequence
             DRB1_1101  749      CGDSTECSNLLLQYG  CSNLLLQYG  6        0.0932
18247.9   100.00  0.26     Sequence
             DRB1_1101  750      GDSTECSNLLLQYGS  CSNLLLQYG  5        0.1349
11622.3    90.00  0.23     Sequence
             DRB1_1101  751      DSTECSNLLLQYGSF  NLLLQYGSF  6        0.1713
7834.8    85.00  0.28     Sequence
             DRB1_1101  752      STECSNLLLQYGSFC  NLLLQYGSF  5        0.1799
7142.5    80.00  0.31     Sequence
             DRB1_1101  753      TECSNLLLQYGSFCT  NLLLQYGSF  4        0.1948
6072.7    80.00  0.31     Sequence
             DRB1_1101  754      ECSNLLLQYGSFCTQ  NLLLQYGSF  3        0.2009
5687.6    75.00  0.31     Sequence
             DRB1_1101  755      CSNLLLQYGSFCTQL  NLLLQYGSF  2        0.2198
4635.0    70.00  0.30     Sequence
             DRB1_1101  756      SNLLLQYGSFCTQLN  LQYGSFCTQ  4        0.2279
4249.2    70.00  0.20     Sequence
             DRB1_1101  757      NLLLQYGSFCTQLNR  GSFCTQLNR  6        0.2694
2712.1    60.00  0.33     Sequence
             DRB1_1101  758      LLLQYGSFCTQLNRA  GSFCTQLNR  5        0.3602
1014.6    38.00  0.34     Sequence
             DRB1_1101  759      LLQYGSFCTQLNRAL  FCTQLNRAL  6        0.4384
435.7    25.00  0.26     Sequence
             DRB1_1101  760      LQYGSFCTQLNRALT  CTQLNRALT  6        0.5113
197.9    16.00  0.44     Sequence
             DRB1_1101  761      QYGSFCTQLNRALTG  CTQLNRALT  5        0.5591
117.9    11.00  0.56     Sequence
             DRB1_1101  762      YGSFCTQLNRALTGI  CTQLNRALT  4        0.5747
99.7     9.50  0.63     Sequence         WB
             DRB1_1101  763      GSFCTQLNRALTGIA  CTQLNRALT  3        0.5780
96.1     9.50  0.64     Sequence         WB
             DRB1_1101  764      SFCTQLNRALTGIAV  CTQLNRALT  2        0.5579
119.6    11.00  0.60     Sequence
             DRB1_1101  765      FCTQLNRALTGIAVE  CTQLNRALT  1        0.4709
306.4    20.00  0.37     Sequence
             DRB1_1101  766      CTQLNRALTGIAVEQ  LNRALTGIA  3        0.4172
547.7    28.00  0.33     Sequence
```

```
             DRB1_1101  767      TQLNRALTGIAVEQD  LNRALTGIA  2        0.3754
861.3    35.00  0.46     Sequence
             DRB1_1101  768      QLNRALTGIAVEQDK  NRALTGIAV  2        0.3412
1247.1    42.00  0.51     Sequence
             DRB1_1101  769      LNRALTGIAVEQDKN  NRALTGIAV  1        0.2738
2586.0    60.00  0.43     Sequence
             DRB1_1101  770      NRALTGIAVEQDKNT  LTGIAVEQD  3        0.1842
6813.4    80.00  0.34     Sequence
             DRB1_1101  771      RALTGIAVEQDKNTQ  LTGIAVEQD  2        0.1525
9600.8    90.00  0.44     Sequence
             DRB1_1101  772      ALTGIAVEQDKNTQE  AVEQDKNTQ  5        0.1270
12657.7    90.00  0.34     Sequence
             DRB1_1101  773      LTGIAVEQDKNTQEV  AVEQDKNTQ  4        0.1233
13171.3    95.00  0.41     Sequence
             DRB1_1101  774      TGIAVEQDKNTQEVF  AVEQDKNTQ  3        0.1249
12941.6    95.00  0.51     Sequence
             DRB1_1101  775      GIAVEQDKNTQEVFA  AVEQDKNTQ  2        0.1246
12983.0    95.00  0.50     Sequence
             DRB1_1101  776      IAVEQDKNTQEVFAQ  AVEQDKNTQ  1        0.0827
20443.6   100.00  0.26     Sequence
             DRB1_1101  777      AVEQDKNTQEVFAQV  DKNTQEVFA  4        0.0752
22164.3   100.00  0.28     Sequence
             DRB1_1101  778      VEQDKNTQEVFAQVK  DKNTQEVFA  3        0.0957
17748.1    95.00  0.27     Sequence
             DRB1_1101  779      EQDKNTQEVFAQVKQ  EVFAQVKQX  7        0.1515
9706.1    90.00  0.17     Sequence
             DRB1_1101  780      QDKNTQEVFAQVKQI  EVFAQVKQI  6        0.2138
4946.3    75.00  0.25     Sequence
             DRB1_1101  781      DKNTQEVFAQVKQIY  VFAQVKQIY  6        0.3016
1912.8    55.00  0.43     Sequence
             DRB1_1101  782      KNTQEVFAQVKQIYK  VFAQVKQIY  5        0.4071
611.2    30.00  0.40     Sequence
             DRB1_1101  783      NTQEVFAQVKQIYKT  VFAQVKQIY  4        0.4444
408.3    24.00  0.38     Sequence
             DRB1_1101  784      TQEVFAQVKQIYKTP  VFAQVKQIY  3        0.4644
328.7    21.00  0.37     Sequence
             DRB1_1101  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.4741
296.0    20.00  0.35     Sequence
             DRB1_1101  786      EVFAQVKQIYKTPPI  VKQIYKTPP  5        0.4769
286.9    20.00  0.30     Sequence
             DRB1_1101  787      VFAQVKQIYKTPPIK  VKQIYKTPP  4        0.4855
261.5    19.00  0.44     Sequence
             DRB1_1101  788      FAQVKQIYKTPPIKD  VKQIYKTPP  3        0.4635
332.0    21.00  0.49     Sequence
             DRB1_1101  789      AQVKQIYKTPPIKDF  VKQIYKTPP  2        0.4649
326.9    21.00  0.47     Sequence
             DRB1_1101  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.4636
331.5    21.00  0.29     Sequence
             DRB1_1101  791      VKQIYKTPPIKDFGG  YKTPPIKDF  4        0.4447
406.6    24.00  0.38     Sequence
             DRB1_1101  792      KQIYKTPPIKDFGGF  YKTPPIKDF  3        0.4108
586.7    29.00  0.50     Sequence
             DRB1_1101  793      QIYKTPPIKDFGGFN  YKTPPIKDF  2        0.3660
952.9    37.00  0.56     Sequence
             DRB1_1101  794      IYKTPPIKDFGGFNF  YKTPPIKDF  1        0.2813
2382.2    55.00  0.42     Sequence
             DRB1_1101  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.2004
5719.5    75.00  0.38     Sequence
             DRB1_1101  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.1675
8164.2    85.00  0.54     Sequence
             DRB1_1101  797      TPPIKDFGGFNFSQI  IKDFGGFNF  3        0.1814
7021.3    80.00  0.47     Sequence
             DRB1_1101  798      PPIKDFGGFNFSQIL  IKDFGGFNF  2        0.1942
6112.7    80.00  0.41     Sequence
             DRB1_1101  799      PIKDFGGFNFSQILP  FNFSQILPX  7        0.2169
4785.4    75.00  0.26     Sequence
```

```
             DRB1_1101  800      IKDFGGFNFSQILPD  FNFSQILPD  6        0.2670
2782.0    60.00  0.47     Sequence
             DRB1_1101  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.3070
1804.8    49.00  0.51     Sequence
             DRB1_1101  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.3508
1123.0    40.00  0.52     Sequence
             DRB1_1101  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.4135
570.0    29.00  0.49     Sequence
             DRB1_1101  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.4178
544.0    28.00  0.47     Sequence
             DRB1_1101  805      GFNFSQILPDPSKPS  FSQILPDPS  3        0.3899
735.8    33.00  0.41     Sequence
             DRB1_1101  806      FNFSQILPDPSKPSK  FSQILPDPS  2        0.3395
1270.2    42.00  0.40     Sequence
             DRB1_1101  807      NFSQILPDPSKPSKR  ILPDPSKPS  4        0.2841
2312.7    55.00  0.39     Sequence
             DRB1_1101  808      FSQILPDPSKPSKRS  ILPDPSKPS  3        0.2606
2981.5    60.00  0.50     Sequence
             DRB1_1101  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.2105
5127.0    75.00  0.67     Sequence
             DRB1_1101  810      QILPDPSKPSKRSFI  ILPDPSKPS  1        0.1770
7365.1    80.00  0.46     Sequence
             DRB1_1101  811      ILPDPSKPSKRSFIE  ILPDPSKPS  0        0.1324
11929.0    90.00  0.26     Sequence
             DRB1_1101  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.0863
19659.6   100.00  0.35     Sequence
             DRB1_1101  813      PDPSKPSKRSFIEDL  SKPSKRSFI  3        0.0953
17822.0    95.00  0.34     Sequence
             DRB1_1101  814      DPSKPSKRSFIEDLL  SKPSKRSFI  2        0.1048
16094.0    95.00  0.28     Sequence
             DRB1_1101  815      PSKPSKRSFIEDLLF  SKRSFIEDL  4        0.1223
13308.1    95.00  0.19     Sequence
             DRB1_1101  816      SKPSKRSFIEDLLFN  RSFIEDLLF  5        0.1389
11122.5    90.00  0.18     Sequence
             DRB1_1101  817      KPSKRSFIEDLLFNK  FIEDLLFNK  6        0.1958
6009.4    80.00  0.34     Sequence
             DRB1_1101  818      PSKRSFIEDLLFNKV  FIEDLLFNK  5        0.2343
3962.6    70.00  0.32     Sequence
             DRB1_1101  819      SKRSFIEDLLFNKVT  FIEDLLFNK  4        0.2672
2774.8    60.00  0.33     Sequence
             DRB1_1101  820      KRSFIEDLLFNKVTL  FIEDLLFNK  3        0.2956
2042.0    55.00  0.29     Sequence
             DRB1_1101  821      RSFIEDLLFNKVTLA  DLLFNKVTL  5        0.3251
1483.2    45.00  0.28     Sequence
             DRB1_1101  822      SFIEDLLFNKVTLAD  DLLFNKVTL  4        0.3208
1554.9    46.00  0.28     Sequence
             DRB1_1101  823      FIEDLLFNKVTLADA  FNKVTLADA  6        0.3521
1107.4    40.00  0.26     Sequence
             DRB1_1101  824      IEDLLFNKVTLADAG  FNKVTLADA  5        0.3655
957.8    37.00  0.38     Sequence
             DRB1_1101  825      EDLLFNKVTLADAGF  FNKVTLADA  4        0.3643
970.4    37.00  0.44     Sequence
             DRB1_1101  826      DLLFNKVTLADAGFI  FNKVTLADA  3        0.3686
927.0    37.00  0.50     Sequence
             DRB1_1101  827      LLFNKVTLADAGFIK  FNKVTLADA  2        0.3745
869.2    35.00  0.56     Sequence
             DRB1_1101  828      LFNKVTLADAGFIKQ  FNKVTLADA  1        0.3504
1128.1    40.00  0.41     Sequence
             DRB1_1101  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.3076
1792.3    49.00  0.30     Sequence
             DRB1_1101  830      NKVTLADAGFIKQYG  VTLADAGFI  2        0.2699
2695.1    60.00  0.34     Sequence
             DRB1_1101  831      KVTLADAGFIKQYGD  LADAGFIKQ  3        0.2400
3727.1    65.00  0.33     Sequence
             DRB1_1101  832      VTLADAGFIKQYGDC  LADAGFIKQ  2        0.2015
5650.4    75.00  0.35     Sequence
```

```
             DRB1_1101  833      TLADAGFIKQYGDCL  DAGFIKQYG  3        0.1764
7414.9    85.00  0.30     Sequence
             DRB1_1101  834      LADAGFIKQYGDCLG  DAGFIKQYG  2        0.1890
6470.3    80.00  0.24     Sequence
             DRB1_1101  835      ADAGFIKQYGDCLGD  IKQYGDCLG  5        0.1948
6073.6    80.00  0.32     Sequence
             DRB1_1101  836      DAGFIKQYGDCLGDI  IKQYGDCLG  4        0.1908
6343.1    80.00  0.38     Sequence
             DRB1_1101  837      AGFIKQYGDCLGDIA  IKQYGDCLG  3        0.1971
5924.0    80.00  0.43     Sequence
             DRB1_1101  838      GFIKQYGDCLGDIAA  IKQYGDCLG  2        0.1975
5899.6    80.00  0.37     Sequence
             DRB1_1101  839      FIKQYGDCLGDIAAR  IKQYGDCLG  1        0.1847
6778.2    80.00  0.28     Sequence
             DRB1_1101  840      IKQYGDCLGDIAARD  YGDCLGDIA  3        0.1614
8723.5    85.00  0.35     Sequence
             DRB1_1101  841      KQYGDCLGDIAARDL  YGDCLGDIA  2        0.1407
10913.9    90.00  0.35     Sequence
             DRB1_1101  842      QYGDCLGDIAARDLI  DCLGDIAAR  3        0.1432
10618.2    90.00  0.17     Sequence
             DRB1_1101  843      YGDCLGDIAARDLIC  GDIAARDLI  5        0.1515
9701.5    90.00  0.15     Sequence
             DRB1_1101  844      GDCLGDIAARDLICA  IAARDLICA  6        0.1721
7770.8    85.00  0.26     Sequence
             DRB1_1101  845      DCLGDIAARDLICAQ  IAARDLICA  5        0.1871
6606.1    80.00  0.34     Sequence
             DRB1_1101  846      CLGDIAARDLICAQK  IAARDLICA  4        0.2205
4602.3    70.00  0.37     Sequence
             DRB1_1101  847      LGDIAARDLICAQKF  IAARDLICA  3        0.2409
3689.1    65.00  0.34     Sequence
             DRB1_1101  848      GDIAARDLICAQKFN  IAARDLICA  2        0.2558
3141.2    65.00  0.29     Sequence
             DRB1_1101  849      DIAARDLICAQKFNG  LICAQKFNG  6        0.3329
1363.0    44.00  0.60     Sequence
             DRB1_1101  850      IAARDLICAQKFNGL  LICAQKFNG  5        0.3960
688.7    31.00  0.70     Sequence
             DRB1_1101  851      AARDLICAQKFNGLT  LICAQKFNG  4        0.4222
518.6    27.00  0.73     Sequence
             DRB1_1101  852      ARDLICAQKFNGLTV  LICAQKFNG  3        0.4381
437.0    25.00  0.73     Sequence
             DRB1_1101  853      RDLICAQKFNGLTVL  LICAQKFNG  2        0.4389
433.2    25.00  0.69     Sequence
             DRB1_1101  854      DLICAQKFNGLTVLP  LICAQKFNG  1        0.4181
542.5    28.00  0.45     Sequence
             DRB1_1101  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.4609
341.2    22.00  0.57     Sequence
             DRB1_1101  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.4762
289.3    20.00  0.74     Sequence
             DRB1_1101  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.5146
191.0    15.00  0.71     Sequence
             DRB1_1101  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.5595
117.5    11.00  0.58     Sequence
             DRB1_1101  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.5734
101.0     9.50  0.49     Sequence         WB
             DRB1_1101  860      KFNGLTVLPPLLTDE  LTVLPPLLT  4        0.5414
142.9    13.00  0.50     Sequence
             DRB1_1101  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.4788
281.3    19.00  0.71     Sequence
             DRB1_1101  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.4265
495.1    26.00  0.89     Sequence
             DRB1_1101  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.3128
1695.3    48.00  0.67     Sequence
             DRB1_1101  864      LTVLPPLLTDEMIAQ  LTVLPPLLT  0        0.1920
6259.8    80.00  0.38     Sequence
             DRB1_1101  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.1233
13166.5    95.00  0.46     Sequence
```

```
             DRB1_1101  866      VLPPLLTDEMIAQYT  LLTDEMIAQ  4        0.1379
11242.4    90.00  0.43     Sequence
             DRB1_1101  867      LPPLLTDEMIAQYTS  LLTDEMIAQ  3        0.1654
8348.3    85.00  0.40     Sequence
             DRB1_1101  868      PPLLTDEMIAQYTSA  LLTDEMIAQ  2        0.1968
5946.9    80.00  0.30     Sequence
             DRB1_1101  869      PLLTDEMIAQYTSAL  DEMIAQYTS  4        0.2024
5594.7    75.00  0.28     Sequence
             DRB1_1101  870      LLTDEMIAQYTSALL  DEMIAQYTS  3        0.2032
5545.8    75.00  0.37     Sequence
             DRB1_1101  871      LTDEMIAQYTSALLA  DEMIAQYTS  2        0.2300
4151.0    70.00  0.28     Sequence
             DRB1_1101  872      TDEMIAQYTSALLAG  AQYTSALLA  5        0.2607
2977.0    60.00  0.25     Sequence
             DRB1_1101  873      DEMIAQYTSALLAGT  YTSALLAGT  6        0.3013
1919.7    55.00  0.30     Sequence
             DRB1_1101  874      EMIAQYTSALLAGTI  YTSALLAGT  5        0.3401
1261.9    42.00  0.41     Sequence
             DRB1_1101  875      MIAQYTSALLAGTIT  YTSALLAGT  4        0.3593
1024.8    38.00  0.50     Sequence
             DRB1_1101  876      IAQYTSALLAGTITS  YTSALLAGT  3        0.3707
906.1    36.00  0.53     Sequence
             DRB1_1101  877      AQYTSALLAGTITSG  YTSALLAGT  2        0.3769
847.3    35.00  0.49     Sequence
             DRB1_1101  878      QYTSALLAGTITSGW  ALLAGTITS  4        0.3496
1138.1    40.00  0.28     Sequence
             DRB1_1101  879      YTSALLAGTITSGWT  ALLAGTITS  3        0.3151
1652.5    48.00  0.41     Sequence
             DRB1_1101  880      TSALLAGTITSGWTF  ALLAGTITS  2        0.2654
2830.9    60.00  0.49     Sequence
             DRB1_1101  881      SALLAGTITSGWTFG  ALLAGTITS  1        0.2305
4128.9    70.00  0.31     Sequence
             DRB1_1101  882      ALLAGTITSGWTFGA  ITSGWTFGA  6        0.2255
4359.8    70.00  0.31     Sequence
             DRB1_1101  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.2303
4136.6    70.00  0.57     Sequence
             DRB1_1101  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.2501
3339.1    65.00  0.61     Sequence
             DRB1_1101  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.2643
2864.1    60.00  0.65     Sequence
             DRB1_1101  886      GTITSGWTFGAGAAL  ITSGWTFGA  2        0.2746
2561.5    60.00  0.58     Sequence
             DRB1_1101  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.2563
3125.0    65.00  0.34     Sequence
             DRB1_1101  888      ITSGWTFGAGAALQI  WTFGAGAAL  4        0.2559
3135.9    65.00  0.38     Sequence
             DRB1_1101  889      TSGWTFGAGAALQIP  WTFGAGAAL  3        0.2525
3255.2    65.00  0.40     Sequence
             DRB1_1101  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.2590
3032.6    65.00  0.37     Sequence
             DRB1_1101  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.2512
3301.6    65.00  0.41     Sequence
             DRB1_1101  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.2354
3914.0    70.00  0.37     Sequence
             DRB1_1101  893      TFGAGAALQIPFAMQ  GAALQIPFA  4        0.2335
3996.5    70.00  0.20     Sequence
             DRB1_1101  894      FGAGAALQIPFAMQM  GAALQIPFA  3        0.2458
3499.3    65.00  0.21     Sequence
             DRB1_1101  895      GAGAALQIPFAMQMA  LQIPFAMQM  5        0.2677
2761.5    60.00  0.26     Sequence
             DRB1_1101  896      AGAALQIPFAMQMAY  LQIPFAMQM  4        0.3007
1932.5    55.00  0.23     Sequence
             DRB1_1101  897      GAALQIPFAMQMAYR  FAMQMAYRX  7        0.3726
887.1    36.00  0.28     Sequence
             DRB1_1101  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.4680
316.2    21.00  0.51     Sequence
```

```
             DRB1_1101  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.5285
164.3    14.00  0.44      Sequence
             DRB1_1101  900      LQIPFAMQMAYRFNG  MQMAYRFNG  6        0.6175
62.7     6.50  0.50     Sequence         WB
             DRB1_1101  901      QIPFAMQMAYRFNGI  MQMAYRFNG  5        0.6548
41.9     4.50  0.59     Sequence         WB
             DRB1_1101  902      IPFAMQMAYRFNGIG  MQMAYRFNG  4        0.6773
32.8     4.00  0.62     Sequence         WB
             DRB1_1101  903      PFAMQMAYRFNGIGV  MQMAYRFNG  3        0.6833
30.8     3.50  0.64     Sequence         WB
             DRB1_1101  904      FAMQMAYRFNGIGVT  MQMAYRFNG  2        0.6813
31.5     3.50  0.64     Sequence         WB
             DRB1_1101  905      AMQMAYRFNGIGVTQ  MQMAYRFNG  1        0.6324
53.4     6.00  0.47     Sequence         WB
             DRB1_1101  906      MQMAYRFNGIGVTQN  YRFNGIGVT  4        0.5724
102.2    10.00  0.40      Sequence
             DRB1_1101  907      QMAYRFNGIGVTQNV  YRFNGIGVT  3        0.5117
197.1    16.00  0.51      Sequence
             DRB1_1101  908      MAYRFNGIGVTQNVL  YRFNGIGVT  2        0.5017
219.5    17.00  0.51      Sequence
             DRB1_1101  909      AYRFNGIGVTQNVLY  FNGIGVTQN  3        0.4213
523.8    27.00  0.38      Sequence
             DRB1_1101  910      YRFNGIGVTQNVLYE  FNGIGVTQN  2        0.3427
1226.0    42.00  0.47     Sequence
             DRB1_1101  911      RFNGIGVTQNVLYEN  FNGIGVTQN  1        0.2529
3240.2    65.00  0.28     Sequence
             DRB1_1101  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.2107
5113.2    75.00  0.41     Sequence
             DRB1_1101  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.1943
6106.9    80.00  0.41     Sequence
             DRB1_1101  914      GIGVTQNVLYENQKL  IGVTQNVLY  1        0.1912
6315.8    80.00  0.28     Sequence
             DRB1_1101  915      IGVTQNVLYENQKLI  VLYENQKLI  6        0.1819
6985.7    80.00  0.22     Sequence
             DRB1_1101  916      GVTQNVLYENQKLIA  LYENQKLIA  6        0.3615
1000.5    38.00  0.55     Sequence
             DRB1_1101  917      VTQNVLYENQKLIAN  LYENQKLIA  5        0.4600
344.7    22.00  0.56      Sequence
             DRB1_1101  918      TQNVLYENQKLIANQ  LYENQKLIA  4        0.5090
202.8    16.00  0.55      Sequence
             DRB1_1101  919      QNVLYENQKLIANQF  LYENQKLIA  3        0.5339
155.0    13.00  0.55      Sequence
             DRB1_1101  920      NVLYENQKLIANQFN  LYENQKLIA  2        0.5354
152.4    13.00  0.53      Sequence
             DRB1_1101  921      VLYENQKLIANQFNS  LYENQKLIA  1        0.5217
176.9    15.00  0.44      Sequence
             DRB1_1101  922      LYENQKLIANQFNSA  KLIANQFNS  5        0.4765
288.2    20.00  0.23      Sequence
             DRB1_1101  923      YENQKLIANQFNSAI  KLIANQFNS  4        0.3765
850.7    35.00  0.49      Sequence
             DRB1_1101  924      ENQKLIANQFNSAIG  KLIANQFNS  3        0.3650
963.4    37.00  0.52      Sequence
             DRB1_1101  925      NQKLIANQFNSAIGK  KLIANQFNS  2        0.3998
661.4    31.00  0.48      Sequence
             DRB1_1101  926      QKLIANQFNSAIGKI  KLIANQFNS  1        0.3881
750.4    33.00  0.34      Sequence
             DRB1_1101  927      KLIANQFNSAIGKIQ  FNSAIGKIQ  6        0.3879
752.1    33.00  0.40      Sequence
             DRB1_1101  928      LIANQFNSAIGKIQD  FNSAIGKIQ  5        0.3738
875.7    36.00  0.63      Sequence
             DRB1_1101  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4        0.4125
576.6    29.00  0.63      Sequence
             DRB1_1101  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.4235
511.8    27.00  0.62      Sequence
             DRB1_1101  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.4179
543.5    28.00  0.61      Sequence
```

```
            DRB1_1101  932      QFNSAIGKIQDSLSS  NSAIGKIQD  2         0.3426
1227.6    42.00  0.36     Sequence
            DRB1_1101  933      FNSAIGKIQDSLSST  NSAIGKIQD  1         0.2607
2977.5    60.00  0.25     Sequence
            DRB1_1101  934      NSAIGKIQDSLSSTA  GKIQDSLSS  4         0.1963
5979.8    80.00  0.43     Sequence
            DRB1_1101  935      SAIGKIQDSLSSTAS  GKIQDSLSS  3         0.1939
6138.1    80.00  0.50     Sequence
            DRB1_1101  936      AIGKIQDSLSSTASA  GKIQDSLSS  2         0.1977
5886.5    80.00  0.47     Sequence
            DRB1_1101  937      IGKIQDSLSSTASAL  GKIQDSLSS  1         0.1741
7601.8    85.00  0.31     Sequence
            DRB1_1101  938      GKIQDSLSSTASALG  LSSTASALG  6         0.1579
9053.0    85.00  0.23     Sequence
            DRB1_1101  939      KIQDSLSSTASALGK  LSSTASALG  5         0.1803
7106.6    80.00  0.56     Sequence
            DRB1_1101  940      IQDSLSSTASALGKL  LSSTASALG  4         0.2060
5382.7    75.00  0.56     Sequence
            DRB1_1101  941      QDSLSSTASALGKLQ  LSSTASALG  3         0.2490
3381.4    65.00  0.54     Sequence
            DRB1_1101  942      DSLSSTASALGKLQD  LSSTASALG  2         0.2473
3442.1    65.00  0.49     Sequence
            DRB1_1101  943      SLSSTASALGKLQDV  ASALGKLQD  5         0.2607
2976.8    60.00  0.38     Sequence
            DRB1_1101  944      LSSTASALGKLQDVV  ASALGKLQD  4         0.2482
3410.3    65.00  0.53     Sequence
            DRB1_1101  945      SSTASALGKLQDVVN  ASALGKLQD  3         0.2363
3878.0    70.00  0.63     Sequence
            DRB1_1101  946      STASALGKLQDVVNQ  ASALGKLQD  2         0.2380
3805.4    70.00  0.54     Sequence
            DRB1_1101  947      TASALGKLQDVVNQN  ASALGKLQD  1         0.1854
6724.7    80.00  0.28     Sequence
            DRB1_1101  948      ASALGKLQDVVNQNA  GKLQDVVNQ  4         0.1836
6855.2    80.00  0.31     Sequence
            DRB1_1101  949      SALGKLQDVVNQNAQ  GKLQDVVNQ  3         0.1926
6222.0    80.00  0.34     Sequence
            DRB1_1101  950      ALGKLQDVVNQNAQA  LQDVVNQNA  4         0.1983
5849.4    75.00  0.38     Sequence
            DRB1_1101  951      LGKLQDVVNQNAQAL  LQDVVNQNA  3         0.1921
6256.6    80.00  0.46     Sequence
            DRB1_1101  952      GKLQDVVNQNAQALN  LQDVVNQNA  2         0.1827
6922.1    80.00  0.46     Sequence
            DRB1_1101  953      KLQDVVNQNAQALNT  LQDVVNQNA  1         0.1459
10310.8    90.00  0.26     Sequence
            DRB1_1101  954      LQDVVNQNAQALNTL  DVVNQNAQA  2         0.1180
13948.9    95.00  0.32     Sequence
            DRB1_1101  955      QDVVNQNAQALNTLV  VNQNAQALN  3         0.1094
15306.9    95.00  0.23     Sequence
            DRB1_1101  956      DVVNQNAQALNTLVK  AQALNTLVK  6         0.1379
11240.4    90.00  0.32     Sequence
            DRB1_1101  957      VVNQNAQALNTLVKQ  AQALNTLVK  5         0.1981
5859.7    80.00  0.41     Sequence
            DRB1_1101  958      VNQNAQALNTLVKQL  AQALNTLVK  4         0.2678
2758.3    60.00  0.32     Sequence
            DRB1_1101  959      NQNAQALNTLVKQLS  LNTLVKQLS  6         0.4558
360.7    22.00  0.73     Sequence
            DRB1_1101  960      QNAQALNTLVKQLSS  LNTLVKQLS  5         0.5767
97.5     9.50  0.75     Sequence         WB
            DRB1_1101  961      NAQALNTLVKQLSSN  LNTLVKQLS  4         0.6196
61.3     6.50  0.73     Sequence         WB
            DRB1_1101  962      AQALNTLVKQLSSNF  LNTLVKQLS  3         0.6446
46.8     5.00  0.73     Sequence         WB
            DRB1_1101  963      QALNTLVKQLSSNFG  LNTLVKQLS  2         0.6517
43.3     5.00  0.70     Sequence         WB
            DRB1_1101  964      ALNTLVKQLSSNFGA  LNTLVKQLS  1         0.6192
61.6     6.50  0.47     Sequence         WB
```

```
             DRB1_1101  965      LNTLVKQLSSNFGAI  VKQLSSNFG  4        0.5642
111.7    11.00  0.25     Sequence
             DRB1_1101  966      NTLVKQLSSNFGAIS  VKQLSSNFG  3        0.4916
245.0    18.00  0.49     Sequence
             DRB1_1101  967      TLVKQLSSNFGAISS  VKQLSSNFG  2        0.5030
216.6    17.00  0.44     Sequence
             DRB1_1101  968      LVKQLSSNFGAISSV  LSSNFGAIS  4        0.4835
267.3    19.00  0.41     Sequence
             DRB1_1101  969      VKQLSSNFGAISSVL  LSSNFGAIS  3        0.4477
393.8    23.00  0.50     Sequence
             DRB1_1101  970      KQLSSNFGAISSVLN  LSSNFGAIS  2        0.3866
762.4    33.00  0.56     Sequence
             DRB1_1101  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.2892
2186.9    55.00  0.54     Sequence
             DRB1_1101  972      LSSNFGAISSVLNDI  FGAISSVLN  4        0.2823
2358.2    55.00  0.65     Sequence
             DRB1_1101  973      SSNFGAISSVLNDIL  FGAISSVLN  3        0.2782
2463.7    60.00  0.70     Sequence
             DRB1_1101  974      SNFGAISSVLNDILS  FGAISSVLN  2        0.2776
2481.8    60.00  0.64     Sequence
             DRB1_1101  975      NFGAISSVLNDILSR  FGAISSVLN  1        0.2689
2724.5    60.00  0.38     Sequence
             DRB1_1101  976      FGAISSVLNDILSRL  SVLNDILSR  5        0.2586
3047.8    65.00  0.25     Sequence
             DRB1_1101  977      GAISSVLNDILSRLD  SVLNDILSR  4        0.2651
2839.7    60.00  0.27     Sequence
             DRB1_1101  978      AISSVLNDILSRLDK  NDILSRLDK  6        0.3227
1522.9    46.00  0.35     Sequence
             DRB1_1101  979      ISSVLNDILSRLDKV  NDILSRLDK  5        0.4017
647.4    30.00  0.44     Sequence
             DRB1_1101  980      SSVLNDILSRLDKVE  NDILSRLDK  4        0.4407
424.5    24.00  0.43     Sequence
             DRB1_1101  981      SVLNDILSRLDKVEA  LSRLDKVEA  6        0.5327
157.0    13.00  0.57     Sequence
             DRB1_1101  982      VLNDILSRLDKVEAE  LSRLDKVEA  5        0.5755
98.8     9.50  0.71     Sequence         WB
             DRB1_1101  983      LNDILSRLDKVEAEV  LSRLDKVEA  4        0.5893
85.1     8.50  0.79     Sequence         WB
             DRB1_1101  984      NDILSRLDKVEAEVQ  LSRLDKVEA  3        0.5883
86.0     8.50  0.88     Sequence         WB
             DRB1_1101  985      DILSRLDKVEAEVQI  LSRLDKVEA  2        0.5854
88.8     9.00  0.92     Sequence         WB
             DRB1_1101  986      ILSRLDKVEAEVQID  LSRLDKVEA  1        0.4502
383.1    23.00  0.66     Sequence
             DRB1_1101  987      LSRLDKVEAEVQIDR  LSRLDKVEA  0        0.3424
1229.8    42.00  0.46     Sequence
             DRB1_1101  988      SRLDKVEAEVQIDRL  VEAEVQIDR  5        0.1015
16670.9    95.00  0.32     Sequence
             DRB1_1101  989      RLDKVEAEVQIDRLI  VEAEVQIDR  4        0.1145
14483.0    95.00  0.31     Sequence
             DRB1_1101  990      LDKVEAEVQIDRLIT  EVQIDRLIT  6        0.1610
8760.3    85.00  0.49     Sequence
             DRB1_1101  991      DKVEAEVQIDRLITG  EVQIDRLIT  5        0.2184
4708.5    75.00  0.49     Sequence
             DRB1_1101  992      KVEAEVQIDRLITGR  EVQIDRLIT  4        0.2935
2087.9    55.00  0.44     Sequence
             DRB1_1101  993      VEAEVQIDRLITGRL  EVQIDRLIT  3        0.3939
704.5    32.00  0.31     Sequence
             DRB1_1101  994      EAEVQIDRLITGRLQ  DRLITGRLQ  6        0.5182
183.6    15.00  0.26     Sequence
             DRB1_1101  995      AEVQIDRLITGRLQS  RLITGRLQS  6        0.6246
58.1     6.50  0.50     Sequence         WB
             DRB1_1101  996      EVQIDRLITGRLQSL  RLITGRLQS  5        0.6832
30.8     3.50  0.63     Sequence         WB
             DRB1_1101  997      VQIDRLITGRLQSLQ  RLITGRLQS  4        0.7225
20.1     2.50  0.64     Sequence         WB
```

```
             DRB1_1101  998      QIDRLITGRLQSLQT  RLITGRLQS  3        0.7356
17.5     1.70  0.65     Sequence         SB
             DRB1_1101  999      IDRLITGRLQSLQTY  RLITGRLQS  2        0.7285
18.9     1.90  0.67     Sequence         SB
             DRB1_1101 1000      DRLITGRLQSLQTYV  RLITGRLQS  1        0.5944
80.5     8.00  0.55     Sequence         WB
             DRB1_1101 1001      RLITGRLQSLQTYVT  RLITGRLQS  0        0.4460
401.0    24.00  0.37     Sequence
             DRB1_1101 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.3390
1276.4    42.00  0.75     Sequence
             DRB1_1101 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.3778
838.8    35.00  0.80     Sequence
             DRB1_1101 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.3865
763.6    33.00  0.82     Sequence
             DRB1_1101 1005      GRLQSLQTYVTQQLI  LQSLQTYVT  2        0.3784
833.4    35.00  0.82     Sequence
             DRB1_1101 1006      RLQSLQTYVTQQLIR  LQSLQTYVT  1        0.3043
1857.8    50.00  0.47     Sequence
             DRB1_1101 1007      LQSLQTYVTQQLIRA  YVTQQLIRA  6        0.3125
1699.8    48.00  0.49     Sequence
             DRB1_1101 1008      QSLQTYVTQQLIRAA  YVTQQLIRA  5        0.3961
688.3    31.00  0.59     Sequence
             DRB1_1101 1009      SLQTYVTQQLIRAAE  YVTQQLIRA  4        0.4244
506.9    27.00  0.57     Sequence
             DRB1_1101 1010      LQTYVTQQLIRAAEI  YVTQQLIRA  3        0.4462
400.3    24.00  0.56     Sequence
             DRB1_1101 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.4682
315.5    21.00  0.50     Sequence
             DRB1_1101 1012      TYVTQQLIRAAEIRA  TQQLIRAAE  3        0.4533
370.5    23.00  0.27     Sequence
             DRB1_1101 1013      YVTQQLIRAAEIRAS  IRAAEIRAS  6        0.4750
292.9    20.00  0.38     Sequence
             DRB1_1101 1014      VTQQLIRAAEIRASA  IRAAEIRAS  5        0.5251
170.5    14.00  0.61     Sequence
             DRB1_1101 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.5464
135.3    12.00  0.65     Sequence
             DRB1_1101 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.5605
116.3    11.00  0.69     Sequence
             DRB1_1101 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.5560
122.0    11.00  0.68     Sequence
             DRB1_1101 1018      LIRAAEIRASANLAA  IRAAEIRAS  1        0.5189
182.3    15.00  0.46     Sequence
             DRB1_1101 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.4958
233.9    17.00  0.62     Sequence
             DRB1_1101 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.5269
167.1    14.00  0.85     Sequence
             DRB1_1101 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.5465
135.2    12.00  0.79     Sequence
             DRB1_1101 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.5645
111.3    11.00  0.72     Sequence
             DRB1_1101 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.5433
139.9    12.00  0.49     Sequence
             DRB1_1101 1024      IRASANLAAIKMSEC  NLAAIKMSE  5        0.4842
265.3    19.00  0.28     Sequence
             DRB1_1101 1025      RASANLAAIKMSECV  NLAAIKMSE  4        0.4230
514.6    27.00  0.50     Sequence
             DRB1_1101 1026      ASANLAAIKMSECVL  NLAAIKMSE  3        0.4176
545.6    28.00  0.51     Sequence
             DRB1_1101 1027      SANLAAIKMSECVLG  NLAAIKMSE  2        0.4319
467.1    26.00  0.46     Sequence
             DRB1_1101 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.4031
638.2    30.00  0.34     Sequence
             DRB1_1101 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.3775
841.8    35.00  0.54     Sequence
             DRB1_1101 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.4113
583.6    29.00  0.57     Sequence
```

```
             DRB1_1101 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.4228
515.7    27.00  0.56     Sequence
             DRB1_1101 1032      AIKMSECVLGQSKRV  IKMSECVLG  1        0.4157
557.0    28.00  0.40     Sequence
             DRB1_1101 1033      IKMSECVLGQSKRVD  MSECVLGQS  2        0.3783
834.3    35.00  0.22     Sequence
             DRB1_1101 1034      KMSECVLGQSKRVDF  VLGQSKRVD  5        0.3264
1463.6    45.00  0.30     Sequence
             DRB1_1101 1035      MSECVLGQSKRVDFC  VLGQSKRVD  4        0.3090
1765.7    49.00  0.34     Sequence
             DRB1_1101 1036      SECVLGQSKRVDFCG  VLGQSKRVD  3        0.3027
1890.5    50.00  0.35     Sequence
             DRB1_1101 1037      ECVLGQSKRVDFCGK  LGQSKRVDF  3        0.3035
1875.1    50.00  0.35     Sequence
             DRB1_1101 1038      CVLGQSKRVDFCGKG  LGQSKRVDF  2        0.3006
1934.7    55.00  0.36     Sequence
             DRB1_1101 1039      VLGQSKRVDFCGKGY  VDFCGKGYX  7        0.2441
3563.3    65.00  0.26     Sequence
             DRB1_1101 1040      LGQSKRVDFCGKGYH  VDFCGKGYH  6        0.2938
2082.0    55.00  0.55     Sequence
             DRB1_1101 1041      GQSKRVDFCGKGYHL  VDFCGKGYH  5        0.3458
1185.7    41.00  0.56     Sequence
             DRB1_1101 1042      QSKRVDFCGKGYHLM  VDFCGKGYH  4        0.3861
766.6    33.00  0.54     Sequence
             DRB1_1101 1043      SKRVDFCGKGYHLMS  VDFCGKGYH  3        0.4146
563.2    28.00  0.51     Sequence
             DRB1_1101 1044      KRVDFCGKGYHLMSF  VDFCGKGYH  2        0.4204
529.1    27.00  0.47     Sequence
             DRB1_1101 1045      RVDFCGKGYHLMSFP  FCGKGYHLM  3        0.4001
658.7    31.00  0.25     Sequence
             DRB1_1101 1046      VDFCGKGYHLMSFPQ  YHLMSFPQX  7        0.4704
308.2    20.00  0.34     Sequence
             DRB1_1101 1047      DFCGKGYHLMSFPQS  YHLMSFPQS  6        0.5273
166.4    14.00  0.54     Sequence
             DRB1_1101 1048      FCGKGYHLMSFPQSA  YHLMSFPQS  5        0.5793
94.8     9.50  0.60     Sequence         WB
             DRB1_1101 1049      CGKGYHLMSFPQSAP  YHLMSFPQS  4        0.5818
92.3     9.00  0.64     Sequence         WB
             DRB1_1101 1050      GKGYHLMSFPQSAPH  YHLMSFPQS  3        0.5878
86.5     8.50  0.67     Sequence         WB
             DRB1_1101 1051      KGYHLMSFPQSAPHG  YHLMSFPQS  2        0.5693
105.6    10.00  0.65     Sequence
             DRB1_1101 1052      GYHLMSFPQSAPHGV  YHLMSFPQS  1        0.4313
470.4    26.00  0.47     Sequence
             DRB1_1101 1053      YHLMSFPQSAPHGVV  LMSFPQSAP  2        0.2895
2181.4    55.00  0.26     Sequence
             DRB1_1101 1054      HLMSFPQSAPHGVVF  FPQSAPHGV  4        0.1694
7995.3    85.00  0.34     Sequence
             DRB1_1101 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.1534
9508.9    85.00  0.41     Sequence
             DRB1_1101 1056      MSFPQSAPHGVVFLH  FPQSAPHGV  2        0.1428
10663.3    90.00  0.46     Sequence
             DRB1_1101 1057      SFPQSAPHGVVFLHV  PQSAPHGVV  2        0.1182
13922.2    95.00  0.20     Sequence
             DRB1_1101 1058      FPQSAPHGVVFLHVT  HGVVFLHVT  6        0.1272
12625.0    90.00  0.22     Sequence
             DRB1_1101 1059      PQSAPHGVVFLHVTY  GVVFLHVTY  6        0.1576
9083.7    85.00  0.26     Sequence
             DRB1_1101 1060      QSAPHGVVFLHVTYV  GVVFLHVTY  5        0.1908
6343.1    80.00  0.25     Sequence
             DRB1_1101 1061      SAPHGVVFLHVTYVP  GVVFLHVTY  4        0.2164
4811.9    75.00  0.26     Sequence
             DRB1_1101 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.3175
1611.2    47.00  0.52     Sequence
             DRB1_1101 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.3710
902.6    36.00  0.56     Sequence
```

```
             DRB1_1101 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.3851
775.2    33.00  0.61     Sequence
             DRB1_1101 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.4170
548.9    28.00  0.58     Sequence
             DRB1_1101 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.4165
552.1    28.00  0.55     Sequence
             DRB1_1101 1067      VFLHVTYVPAQEKNF  FLHVTYVPA  1        0.4132
571.8    29.00  0.42     Sequence
             DRB1_1101 1068      FLHVTYVPAQEKNFT  YVPAQEKNF  5        0.3963
687.0    31.00  0.25     Sequence
             DRB1_1101 1069      LHVTYVPAQEKNFTT  YVPAQEKNF  4        0.3059
1826.6    50.00  0.46     Sequence
             DRB1_1101 1070      HVTYVPAQEKNFTTA  YVPAQEKNF  3        0.2883
2209.7    55.00  0.58     Sequence
             DRB1_1101 1071      VTYVPAQEKNFTTAP  YVPAQEKNF  2        0.2670
2783.0    60.00  0.63     Sequence
             DRB1_1101 1072      TYVPAQEKNFTTAPA  YVPAQEKNF  1        0.2024
5596.9    75.00  0.44     Sequence
             DRB1_1101 1073      YVPAQEKNFTTAPAI  FTTAPAIXX  8        0.1647
8411.3    85.00  0.19     Sequence
             DRB1_1101 1074      VPAQEKNFTTAPAIC  FTTAPAICX  7        0.1899
6405.3    80.00  0.44     Sequence
             DRB1_1101 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.3000
1946.0    55.00  0.75     Sequence
             DRB1_1101 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.3346
1339.2    43.00  0.80     Sequence
             DRB1_1101 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.3668
944.8    37.00  0.80     Sequence
             DRB1_1101 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.3985
670.8    31.00  0.79     Sequence
             DRB1_1101 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.3987
669.4    31.00  0.79     Sequence
             DRB1_1101 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.2883
2209.6    55.00  0.54     Sequence
             DRB1_1101 1081      FTTAPAICHDGKAHF  ICHDGKAHF  6        0.2283
4227.4    70.00  0.35     Sequence
             DRB1_1101 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.1887
6492.1    80.00  0.61     Sequence
             DRB1_1101 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.2308
4115.0    70.00  0.58     Sequence
             DRB1_1101 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.2418
3652.9    65.00  0.58     Sequence
             DRB1_1101 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.2431
3603.5    65.00  0.55     Sequence
             DRB1_1101 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.2188
4687.8    75.00  0.41     Sequence
             DRB1_1101 1087      ICHDGKAHFPREGVF  KAHFPREGV  5        0.1633
8544.1    85.00  0.20     Sequence
             DRB1_1101 1088      CHDGKAHFPREGVFV  KAHFPREGV  4        0.1458
10322.9    90.00  0.25     Sequence
             DRB1_1101 1089      HDGKAHFPREGVFVS  FPREGVFVS  6        0.1769
7374.2    80.00  0.34     Sequence
             DRB1_1101 1090      DGKAHFPREGVFVSN  FPREGVFVS  5        0.1906
6356.6    80.00  0.44     Sequence
             DRB1_1101 1091      GKAHFPREGVFVSNG  FPREGVFVS  4        0.2001
5739.6    75.00  0.47     Sequence
             DRB1_1101 1092      KAHFPREGVFVSNGT  FPREGVFVS  3        0.1923
6244.6    80.00  0.52     Sequence
             DRB1_1101 1093      AHFPREGVFVSNGTH  FPREGVFVS  2        0.2367
3860.3    70.00  0.35     Sequence
             DRB1_1101 1094      HFPREGVFVSNGTHW  FVSNGTHWX  7        0.3047
1849.1    50.00  0.26     Sequence
             DRB1_1101 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6        0.3817
804.4    34.00  0.38     Sequence
             DRB1_1101 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.4280
487.5    26.00  0.43     Sequence
```

```
             DRB1_1101 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.4543
366.4    22.00  0.43     Sequence
             DRB1_1101 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.4558
360.8    22.00  0.43     Sequence
             DRB1_1101 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.4723
301.8    20.00  0.43     Sequence
             DRB1_1101 1100      VFVSNGTHWFVTQRN  VSNGTHWFV  2        0.3841
783.8    34.00  0.34     Sequence
             DRB1_1101 1101      FVSNGTHWFVTQRNF  HWFVTQRNF  6        0.3837
787.1    34.00  0.34     Sequence
             DRB1_1101 1102      VSNGTHWFVTQRNFY  HWFVTQRNF  5        0.4319
467.0    26.00  0.32     Sequence
             DRB1_1101 1103      SNGTHWFVTQRNFYE  WFVTQRNFY  5        0.4586
349.9    22.00  0.36     Sequence
             DRB1_1101 1104      NGTHWFVTQRNFYEP  WFVTQRNFY  4        0.4735
297.8    20.00  0.37     Sequence
             DRB1_1101 1105      GTHWFVTQRNFYEPQ  WFVTQRNFY  3        0.4885
253.3    18.00  0.38     Sequence
             DRB1_1101 1106      THWFVTQRNFYEPQI  WFVTQRNFY  2        0.4341
456.4    25.00  0.43     Sequence
             DRB1_1101 1107      HWFVTQRNFYEPQII  FVTQRNFYE  2        0.3827
795.8    34.00  0.51     Sequence
             DRB1_1101 1108      WFVTQRNFYEPQIIT  FVTQRNFYE  1        0.2560
3133.5    65.00  0.37     Sequence
             DRB1_1101 1109      FVTQRNFYEPQIITT  FYEPQIITT  6        0.2094
5185.7    75.00  0.25     Sequence
             DRB1_1101 1110      VTQRNFYEPQIITTD  FYEPQIITT  5        0.2128
5001.0    75.00  0.32     Sequence
             DRB1_1101 1111      TQRNFYEPQIITTDN  FYEPQIITT  4        0.2323
4050.4    70.00  0.32     Sequence
             DRB1_1101 1112      QRNFYEPQIITTDNT  FYEPQIITT  3        0.2469
3459.1    65.00  0.31     Sequence
             DRB1_1101 1113      RNFYEPQIITTDNTF  YEPQIITTD  3        0.2474
3438.5    65.00  0.36     Sequence
             DRB1_1101 1114      NFYEPQIITTDNTFV  YEPQIITTD  2        0.2269
4291.7    70.00  0.34     Sequence
             DRB1_1101 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.1954
6039.6    80.00  0.25     Sequence
             DRB1_1101 1116      YEPQIITTDNTFVSG  ITTDNTFVS  5        0.1832
6887.2    80.00  0.43     Sequence
             DRB1_1101 1117      EPQIITTDNTFVSGN  ITTDNTFVS  4        0.1918
6274.4    80.00  0.49     Sequence
             DRB1_1101 1118      PQIITTDNTFVSGNC  ITTDNTFVS  3        0.1953
6040.8    80.00  0.49     Sequence
             DRB1_1101 1119      QIITTDNTFVSGNCD  ITTDNTFVS  2        0.1694
8000.0    85.00  0.57     Sequence
             DRB1_1101 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.1397
11034.4    90.00  0.44     Sequence
             DRB1_1101 1121      ITTDNTFVSGNCDVV  TFVSGNCDV  5        0.1144
14497.7    95.00  0.17     Sequence
             DRB1_1101 1122      TTDNTFVSGNCDVVI  TFVSGNCDV  4        0.1128
14750.9    95.00  0.24     Sequence
             DRB1_1101 1123      TDNTFVSGNCDVVIG  FVSGNCDVV  4        0.1211
13488.5    95.00  0.33     Sequence
             DRB1_1101 1124      DNTFVSGNCDVVIGI  FVSGNCDVV  3        0.1217
13392.8    95.00  0.36     Sequence
             DRB1_1101 1125      NTFVSGNCDVVIGIV  FVSGNCDVV  2        0.1325
11917.8    90.00  0.35     Sequence
             DRB1_1101 1126      TFVSGNCDVVIGIVN  CDVVIGIVN  6        0.1255
12861.6    95.00  0.29     Sequence
             DRB1_1101 1127      FVSGNCDVVIGIVNN  CDVVIGIVN  5        0.1271
12642.3    90.00  0.35     Sequence
             DRB1_1101 1128      VSGNCDVVIGIVNNT  CDVVIGIVN  4        0.1328
11879.1    90.00  0.36     Sequence
             DRB1_1101 1129      SGNCDVVIGIVNNTV  CDVVIGIVN  3        0.1479
10095.3    90.00  0.30     Sequence
```

```
             DRB1_1101 1130      GNCDVVIGIVNNTVY  VIGIVNNTV  5        0.1617
8691.7    85.00  0.22     Sequence
             DRB1_1101 1131      NCDVVIGIVNNTVYD  VIGIVNNTV  4        0.1579
9059.5    85.00  0.22     Sequence
             DRB1_1101 1132      CDVVIGIVNNTVYDP  VIGIVNNTV  3        0.1554
9301.1    85.00  0.28     Sequence
             DRB1_1101 1133      DVVIGIVNNTVYDPL  VIGIVNNTV  2        0.1532
9534.2    85.00  0.31     Sequence
             DRB1_1101 1134      VVIGIVNNTVYDPLQ  IVNNTVYDP  4        0.1578
9071.8    85.00  0.37     Sequence
             DRB1_1101 1135      VIGIVNNTVYDPLQP  IVNNTVYDP  3        0.1412
10848.4    90.00  0.43     Sequence
             DRB1_1101 1136      IGIVNNTVYDPLQPE  IVNNTVYDP  2        0.1246
12980.1    95.00  0.53     Sequence
             DRB1_1101 1137      GIVNNTVYDPLQPEL  IVNNTVYDP  1        0.1050
16055.5    95.00  0.34     Sequence
             DRB1_1101 1138      IVNNTVYDPLQPELD  YDPLQPELD  6        0.0747
22288.4   100.00  0.33     Sequence
             DRB1_1101 1139      VNNTVYDPLQPELDS  YDPLQPELD  5        0.0778
21538.3   100.00  0.44     Sequence
             DRB1_1101 1140      NNTVYDPLQPELDSF  YDPLQPELD  4        0.0825
20478.4   100.00  0.52     Sequence
             DRB1_1101 1141      NTVYDPLQPELDSFK  YDPLQPELD  3        0.0937
18135.2    95.00  0.53     Sequence
             DRB1_1101 1142      TVYDPLQPELDSFKE  YDPLQPELD  2        0.0979
17334.6    95.00  0.49     Sequence
             DRB1_1101 1143      VYDPLQPELDSFKEE  YDPLQPELD  1        0.0839
20173.6   100.00  0.32     Sequence
             DRB1_1101 1144      YDPLQPELDSFKEEL  QPELDSFKE  4        0.0699
23467.7   100.00  0.20     Sequence
             DRB1_1101 1145      DPLQPELDSFKEELD  QPELDSFKE  3        0.0653
24675.6   100.00  0.22     Sequence
             DRB1_1101 1146      PLQPELDSFKEELDK  ELDSFKEEL  4        0.0742
22407.9   100.00  0.28     Sequence
             DRB1_1101 1147      LQPELDSFKEELDKY  ELDSFKEEL  3        0.0837
20219.5   100.00  0.30     Sequence
             DRB1_1101 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.1703
7919.8    85.00  0.37     Sequence
             DRB1_1101 1149      PELDSFKEELDKYFK  KEELDKYFK  6        0.2780
2469.3    60.00  0.43     Sequence
             DRB1_1101 1150      ELDSFKEELDKYFKN  KEELDKYFK  5        0.3231
1515.6    46.00  0.44     Sequence
             DRB1_1101 1151      LDSFKEELDKYFKNH  KEELDKYFK  4        0.3440
1208.8    41.00  0.43     Sequence
             DRB1_1101 1152      DSFKEELDKYFKNHT  KEELDKYFK  3        0.3731
883.1    36.00  0.38     Sequence
             DRB1_1101 1153      SFKEELDKYFKNHTS  KEELDKYFK  2        0.4072
610.2    30.00  0.35     Sequence
             DRB1_1101 1154      FKEELDKYFKNHTSP  LDKYFKNHT  4        0.3915
723.4    32.00  0.29     Sequence
             DRB1_1101 1155      KEELDKYFKNHTSPD  LDKYFKNHT  3        0.3407
1253.7    42.00  0.39     Sequence
             DRB1_1101 1156      EELDKYFKNHTSPDV  LDKYFKNHT  2        0.3218
1536.9    46.00  0.39     Sequence
             DRB1_1101 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.3156
1643.8    48.00  0.30     Sequence
             DRB1_1101 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.2994
1960.0    55.00  0.38     Sequence
             DRB1_1101 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.2466
3468.2    65.00  0.51     Sequence
             DRB1_1101 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.2229
4483.3    70.00  0.68     Sequence
             DRB1_1101 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.1350
11599.4    90.00  0.51     Sequence
             DRB1_1101 1162      FKNHTSPDVDLGDIS  FKNHTSPDV  0        0.0623
25472.9   100.00  0.31     Sequence
```

```
             DRB1_1101 1163      KNHTSPDVDLGDISG  DVDLGDISG  6        0.0412
32006.7   100.00  0.26     Sequence
             DRB1_1101 1164      NHTSPDVDLGDISGI  DVDLGDISG  5        0.0451
30705.5   100.00  0.34     Sequence
             DRB1_1101 1165      HTSPDVDLGDISGIN  DVDLGDISG  4        0.0550
27563.2   100.00  0.34     Sequence
             DRB1_1101 1166      TSPDVDLGDISGINA  LGDISGINA  6        0.0738
22508.5   100.00  0.44     Sequence
             DRB1_1101 1167      SPDVDLGDISGINAS  LGDISGINA  5        0.0972
17465.6    95.00  0.47     Sequence
             DRB1_1101 1168      PDVDLGDISGINASF  LGDISGINA  4        0.1115
14956.6    95.00  0.47     Sequence
             DRB1_1101 1169      DVDLGDISGINASFV  LGDISGINA  3        0.1241
13059.1    95.00  0.41     Sequence
             DRB1_1101 1170      VDLGDISGINASFVN  LGDISGINA  2        0.1318
12016.1    90.00  0.37     Sequence
             DRB1_1101 1171      DLGDISGINASFVNI  ISGINASFV  4        0.1367
11398.2    90.00  0.35     Sequence
             DRB1_1101 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.1576
9083.5    85.00  0.34     Sequence
             DRB1_1101 1173      GDISGINASFVNIQK  INASFVNIQ  5        0.2033
5541.5    75.00  0.28     Sequence
             DRB1_1101 1174      DISGINASFVNIQKE  INASFVNIQ  4        0.2635
2888.4    60.00  0.25     Sequence
             DRB1_1101 1175      ISGINASFVNIQKEI  FVNIQKEIX  7        0.3702
910.4    36.00  0.40     Sequence
             DRB1_1101 1176      SGINASFVNIQKEID  FVNIQKEID  6        0.4422
418.0    24.00  0.63     Sequence
             DRB1_1101 1177      GINASFVNIQKEIDR  FVNIQKEID  5        0.5430
140.4    12.00  0.77     Sequence
             DRB1_1101 1178      INASFVNIQKEIDRL  FVNIQKEID  4        0.5711
103.6    10.00  0.81     Sequence
             DRB1_1101 1179      NASFVNIQKEIDRLN  FVNIQKEID  3        0.5844
89.7     9.00  0.80     Sequence         WB
             DRB1_1101 1180      ASFVNIQKEIDRLNE  FVNIQKEID  2        0.5819
92.2     9.00  0.79     Sequence         WB
             DRB1_1101 1181      SFVNIQKEIDRLNEV  FVNIQKEID  1        0.4896
250.2    18.00  0.52     Sequence
             DRB1_1101 1182      FVNIQKEIDRLNEVA  FVNIQKEID  0        0.3662
951.4    37.00  0.34     Sequence
             DRB1_1101 1183      VNIQKEIDRLNEVAK  QKEIDRLNE  3        0.2545
3186.2    65.00  0.43     Sequence
             DRB1_1101 1184      NIQKEIDRLNEVAKN  QKEIDRLNE  2        0.2681
2750.2    60.00  0.42     Sequence
             DRB1_1101 1185      IQKEIDRLNEVAKNL  IDRLNEVAK  4        0.2361
3885.9    70.00  0.34     Sequence
             DRB1_1101 1186      QKEIDRLNEVAKNLN  IDRLNEVAK  3        0.2460
3492.2    65.00  0.37     Sequence
             DRB1_1101 1187      KEIDRLNEVAKNLNE  LNEVAKNLN  5        0.2693
2714.6    60.00  0.40     Sequence
             DRB1_1101 1188      EIDRLNEVAKNLNES  LNEVAKNLN  4        0.2798
2421.7    60.00  0.48     Sequence
             DRB1_1101 1189      IDRLNEVAKNLNESL  LNEVAKNLN  3        0.2851
2288.0    55.00  0.52     Sequence
             DRB1_1101 1190      DRLNEVAKNLNESLI  LNEVAKNLN  2        0.2724
2624.5    60.00  0.55     Sequence
             DRB1_1101 1191      RLNEVAKNLNESLID  LNEVAKNLN  1        0.2678
2757.1    60.00  0.45     Sequence
             DRB1_1101 1192      LNEVAKNLNESLIDL  LNEVAKNLN  0        0.1985
5840.3    75.00  0.34     Sequence
             DRB1_1101 1193      NEVAKNLNESLIDLQ  VAKNLNESL  2        0.1197
13698.9    95.00  0.37     Sequence
             DRB1_1101 1194      EVAKNLNESLIDLQE  KNLNESLID  3        0.1028
16433.8    95.00  0.26     Sequence
             DRB1_1101 1195      VAKNLNESLIDLQEL  KNLNESLID  2        0.1078
15576.1    95.00  0.24     Sequence
```

```
             DRB1_1101 1196      AKNLNESLIDLQELG  LNESLIDLQ  3        0.1051
16043.9    95.00  0.22     Sequence
             DRB1_1101 1197      KNLNESLIDLQELGK  LIDLQELGK  6        0.1313
12078.1    90.00  0.38     Sequence
             DRB1_1101 1198      NLNESLIDLQELGKY  LIDLQELGK  5        0.1630
8573.1    85.00  0.44     Sequence
             DRB1_1101 1199      LNESLIDLQELGKYE  LIDLQELGK  4        0.1823
6958.0    80.00  0.41     Sequence
             DRB1_1101 1200      NESLIDLQELGKYEQ  LQELGKYEQ  6        0.2614
2955.7    60.00  0.55     Sequence
             DRB1_1101 1201      ESLIDLQELGKYEQY  LQELGKYEQ  5        0.3110
1728.9    49.00  0.70     Sequence
             DRB1_1101 1202      SLIDLQELGKYEQYI  LQELGKYEQ  4        0.3323
1372.5    44.00  0.78     Sequence
             DRB1_1101 1203      LIDLQELGKYEQYIK  LQELGKYEQ  3        0.3617
998.8    38.00  0.80     Sequence
             DRB1_1101 1204      IDLQELGKYEQYIKW  LQELGKYEQ  2        0.3810
810.0    34.00  0.70     Sequence
             DRB1_1101 1205      DLQELGKYEQYIKWP  LQELGKYEQ  1        0.3665
947.9    37.00  0.46     Sequence
             DRB1_1101 1206      LQELGKYEQYIKWPW  YEQYIKWPW  6        0.4214
523.5    27.00  0.46     Sequence
             DRB1_1101 1207      QELGKYEQYIKWPWY  YEQYIKWPW  5        0.4031
637.8    30.00  0.63     Sequence
             DRB1_1101 1208      ELGKYEQYIKWPWYI  YEQYIKWPW  4        0.4276
489.3    26.00  0.62     Sequence
             DRB1_1101 1209      LGKYEQYIKWPWYIW  YEQYIKWPW  3        0.4571
355.8    22.00  0.57     Sequence
             DRB1_1101 1210      GKYEQYIKWPWYIWL  YEQYIKWPW  2        0.4641
329.9    21.00  0.56     Sequence
             DRB1_1101 1211      KYEQYIKWPWYIWLG  YEQYIKWPW  1        0.4186
539.4    28.00  0.38     Sequence
             DRB1_1101 1212      YEQYIKWPWYIWLGF  YIKWPWYIW  3        0.3616
1000.0    38.00  0.28     Sequence
             DRB1_1101 1213      EQYIKWPWYIWLGFI  YIKWPWYIW  2        0.2608
2974.2    60.00  0.41     Sequence
             DRB1_1101 1214      QYIKWPWYIWLGFIA  YIKWPWYIW  1        0.2647
2852.9    60.00  0.23     Sequence
             DRB1_1101 1215      YIKWPWYIWLGFIAG  WYIWLGFIA  5        0.2521
3266.9    65.00  0.26     Sequence
             DRB1_1101 1216      IKWPWYIWLGFIAGL  WYIWLGFIA  4        0.2366
3863.4    70.00  0.29     Sequence
             DRB1_1101 1217      KWPWYIWLGFIAGLI  WLGFIAGLI  6        0.2609
2973.1    60.00  0.26     Sequence
             DRB1_1101 1218      WPWYIWLGFIAGLIA  WLGFIAGLI  5        0.2843
2308.0    55.00  0.31     Sequence
             DRB1_1101 1219      PWYIWLGFIAGLIAI  WLGFIAGLI  4        0.3009
1928.4    55.00  0.31     Sequence
             DRB1_1101 1220      WYIWLGFIAGLIAIV  WLGFIAGLI  3        0.3178
1605.0    47.00  0.28     Sequence
             DRB1_1101 1221      YIWLGFIAGLIAIVM  WLGFIAGLI  2        0.3259
1470.3    45.00  0.26     Sequence
             DRB1_1101 1222      IWLGFIAGLIAIVMV  IAGLIAIVM  5        0.3197
1573.0    47.00  0.34     Sequence
             DRB1_1101 1223      WLGFIAGLIAIVMVT  IAGLIAIVM  4        0.3014
1918.0    55.00  0.40     Sequence
             DRB1_1101 1224      LGFIAGLIAIVMVTI  IAGLIAIVM  3        0.2690
2722.8    60.00  0.50     Sequence
             DRB1_1101 1225      GFIAGLIAIVMVTIM  IAGLIAIVM  2        0.2535
3218.7    65.00  0.52     Sequence
             DRB1_1101 1226      FIAGLIAIVMVTIML  IAGLIAIVM  1        0.1897
6418.1    80.00  0.18     Sequence
             DRB1_1101 1227      IAGLIAIVMVTIMLC  IVMVTIMLC  6        0.1821
6972.0    80.00  0.31     Sequence
             DRB1_1101 1228      AGLIAIVMVTIMLCC  IVMVTIMLC  5        0.1820
6979.4    80.00  0.34     Sequence
```

```
             DRB1_1101 1229      GLIAIVMVTIMLCCM  IVMVTIMLC  4        0.1843
6810.2    80.00  0.35     Sequence
             DRB1_1101 1230      LIAIVMVTIMLCCMT  VTIMLCCMT  6        0.2135
4964.1    75.00  0.25     Sequence
             DRB1_1101 1231      IAIVMVTIMLCCMTS  VTIMLCCMT  5        0.2569
3103.6    65.00  0.28     Sequence
             DRB1_1101 1232      AIVMVTIMLCCMTSC  VTIMLCCMT  4        0.2603
2992.4    65.00  0.31     Sequence
             DRB1_1101 1233      IVMVTIMLCCMTSCC  VTIMLCCMT  3        0.2674
2770.7    60.00  0.30     Sequence
             DRB1_1101 1234      VMVTIMLCCMTSCCS  VTIMLCCMT  2        0.2963
2026.1    55.00  0.24     Sequence
             DRB1_1101 1235      MVTIMLCCMTSCCSC  LCCMTSCCS  5        0.3069
1806.7    49.00  0.34     Sequence
             DRB1_1101 1236      VTIMLCCMTSCCSCL  LCCMTSCCS  4        0.2975
2000.4    55.00  0.37     Sequence
             DRB1_1101 1237      TIMLCCMTSCCSCLK  LCCMTSCCS  3        0.2981
1987.0    55.00  0.47     Sequence
             DRB1_1101 1238      IMLCCMTSCCSCLKG  LCCMTSCCS  2        0.2808
2396.1    60.00  0.50     Sequence
             DRB1_1101 1239      MLCCMTSCCSCLKGC  LCCMTSCCS  1        0.2546
3181.6    65.00  0.36     Sequence
             DRB1_1101 1240      LCCMTSCCSCLKGCC  CCSCLKGCC  6        0.2165
4802.1    75.00  0.25     Sequence
             DRB1_1101 1241      CCMTSCCSCLKGCCS  CCSCLKGCC  5        0.1959
6001.7    80.00  0.38     Sequence
             DRB1_1101 1242      CMTSCCSCLKGCCSC  CCSCLKGCC  4        0.1923
6243.8    80.00  0.43     Sequence
             DRB1_1101 1243      MTSCCSCLKGCCSCG  CCSCLKGCC  3        0.1950
6061.1    80.00  0.46     Sequence
             DRB1_1101 1244      TSCCSCLKGCCSCGS  CCSCLKGCC  2        0.2174
4756.0    75.00  0.40     Sequence
             DRB1_1101 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5        0.1950
6062.3    80.00  0.35     Sequence
             DRB1_1101 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.1706
7896.7    85.00  0.45     Sequence
             DRB1_1101 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.1671
8201.3    85.00  0.56     Sequence
             DRB1_1101 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2        0.1773
7345.4    80.00  0.53     Sequence
             DRB1_1101 1249      CLKGCCSCGSCCKFD  LKGCCSCGS  1        0.1672
8191.0    85.00  0.41     Sequence
             DRB1_1101 1250      LKGCCSCGSCCKFDE  CGSCCKFDE  6        0.1479
10095.7    90.00  0.26     Sequence
             DRB1_1101 1251      KGCCSCGSCCKFDED  CGSCCKFDE  5        0.1223
13312.3    95.00  0.38     Sequence
             DRB1_1101 1252      GCCSCGSCCKFDEDD  CGSCCKFDE  4        0.0988
17167.3    95.00  0.51     Sequence
             DRB1_1101 1253      CCSCGSCCKFDEDDS  CGSCCKFDE  3        0.0941
18055.1    95.00  0.58     Sequence
             DRB1_1101 1254      CSCGSCCKFDEDDSE  CGSCCKFDE  2        0.0871
19474.4   100.00  0.62     Sequence
             DRB1_1101 1255      SCGSCCKFDEDDSEP  CGSCCKFDE  1        0.0512
28730.9   100.00  0.44     Sequence
             DRB1_1101 1256      CGSCCKFDEDDSEPV  CCKFDEDDS  3        0.0384
32993.0   100.00  0.22     Sequence
             DRB1_1101 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.0329
35008.7   100.00  0.34     Sequence
             DRB1_1101 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.0398
32508.6   100.00  0.38     Sequence
             DRB1_1101 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.0477
29840.5   100.00  0.34     Sequence
             DRB1_1101 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.0547
27665.4   100.00  0.26     Sequence
             DRB1_1101 1261      KFDEDDSEPVLKGVK  SEPVLKGVK  6        0.0946
17975.2    95.00  0.32     Sequence
```

```
             DRB1_1101 1262      FDEDDSEPVLKGVKL  SEPVLKGVK  5        0.1428
10663.6    90.00  0.35     Sequence
             DRB1_1101 1263      DEDDSEPVLKGVKLH  VLKGVKLHX  7        0.2043
5482.7    75.00  0.25     Sequence
             DRB1_1101 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.3298
1410.3    44.00  0.52     Sequence
             DRB1_1101 1265      DDSEPVLKGVKLHYT  VLKGVKLHY  5        0.4053
623.2    30.00  0.51     Sequence
             DRB1_1201    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.3947
698.6    25.00  0.63     Sequence
             DRB1_1201    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.3783
834.7    29.00  0.61     Sequence
             DRB1_1201    3      PIKEMFVFLVLLPLV  IKEMFVFLV  1        0.2931
2096.8    49.00  0.47     Sequence
             DRB1_1201    4      IKEMFVFLVLLPLVS  FLVLLPLVS  6        0.2625
2919.9    60.00  0.28     Sequence
             DRB1_1201    5      KEMFVFLVLLPLVSS  FLVLLPLVS  5        0.2367
3860.9    65.00  0.33     Sequence
             DRB1_1201    6      EMFVFLVLLPLVSSQ  FLVLLPLVS  4        0.2818
2369.8    55.00  0.26     Sequence
             DRB1_1201    7      MFVFLVLLPLVSSQC  LLPLVSSQC  6        0.4137
568.9    22.00  0.64     Sequence
             DRB1_1201    8      FVFLVLLPLVSSQCV  LLPLVSSQC  5        0.4599
345.1    14.00  0.56     Sequence
             DRB1_1201    9      VFLVLLPLVSSQCVN  LLPLVSSQC  4        0.4639
330.5    14.00  0.54     Sequence
             DRB1_1201   10      FLVLLPLVSSQCVNF  LLPLVSSQC  3        0.5130
194.4     8.00  0.46     Sequence         WB
             DRB1_1201   11      LVLLPLVSSQCVNFT  LLPLVSSQC  2        0.5109
198.7     8.00  0.48     Sequence         WB
             DRB1_1201   12      VLLPLVSSQCVNFTN  LLPLVSSQC  1        0.4856
261.2    11.00  0.45     Sequence
             DRB1_1201   13      LLPLVSSQCVNFTNR  LVSSQCVNF  3        0.4215
522.6    20.00  0.26     Sequence
             DRB1_1201   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.3134
1683.0    44.00  0.49     Sequence
             DRB1_1201   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.2722
2630.1    55.00  0.47     Sequence
             DRB1_1201   16      LVSSQCVNFTNRTQL  VNFTNRTQL  6        0.2560
3132.3    60.00  0.37     Sequence
             DRB1_1201   17      VSSQCVNFTNRTQLP  VNFTNRTQL  5        0.1871
6604.9    80.00  0.62     Sequence
             DRB1_1201   18      SSQCVNFTNRTQLPS  VNFTNRTQL  4        0.1837
6850.1    80.00  0.57     Sequence
             DRB1_1201   19      SQCVNFTNRTQLPSA  VNFTNRTQL  3        0.1814
7026.8    80.00  0.57     Sequence
             DRB1_1201   20      QCVNFTNRTQLPSAY  VNFTNRTQL  2        0.2195
4649.1    70.00  0.38     Sequence
             DRB1_1201   21      CVNFTNRTQLPSAYT  RTQLPSAYT  6        0.2353
3918.7    65.00  0.41     Sequence
             DRB1_1201   22      VNFTNRTQLPSAYTN  RTQLPSAYT  5        0.2261
4330.8    70.00  0.41     Sequence
             DRB1_1201   23      NFTNRTQLPSAYTNS  RTQLPSAYT  4        0.1975
5903.1    75.00  0.51     Sequence
             DRB1_1201   24      FTNRTQLPSAYTNSF  RTQLPSAYT  3        0.2199
4631.9    70.00  0.38     Sequence
             DRB1_1201   25      TNRTQLPSAYTNSFT  RTQLPSAYT  2        0.2114
5076.0    70.00  0.37     Sequence
             DRB1_1201   26      NRTQLPSAYTNSFTR  RTQLPSAYT  1        0.1884
6514.2    75.00  0.28     Sequence
             DRB1_1201   27      RTQLPSAYTNSFTRG  LPSAYTNSF  3        0.1413
10835.3    90.00  0.41     Sequence
             DRB1_1201   28      TQLPSAYTNSFTRGV  LPSAYTNSF  2        0.1181
13927.3    90.00  0.48     Sequence
             DRB1_1201   29      QLPSAYTNSFTRGVY  TNSFTRGVY  6        0.1962
5981.9    75.00  0.48     Sequence
```

```
             DRB1_1201   30      LPSAYTNSFTRGVYY  NSFTRGVYY  6        0.2794
2432.3    55.00  0.31     Sequence
             DRB1_1201   31      PSAYTNSFTRGVYYP  NSFTRGVYY  5        0.2783
2461.7    55.00  0.31     Sequence
             DRB1_1201   32      SAYTNSFTRGVYYPD  FTRGVYYPD  6        0.2965
2021.5    48.00  0.38     Sequence
             DRB1_1201   33      AYTNSFTRGVYYPDK  FTRGVYYPD  5        0.2912
2140.7    49.00  0.37     Sequence
             DRB1_1201   34      YTNSFTRGVYYPDKV  FTRGVYYPD  4        0.2861
2263.1    55.00  0.39     Sequence
             DRB1_1201   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.2761
2522.2    55.00  0.40     Sequence
             DRB1_1201   36      NSFTRGVYYPDKVFR  FTRGVYYPD  2        0.2499
3346.6    60.00  0.39     Sequence
             DRB1_1201   37      SFTRGVYYPDKVFRS  FTRGVYYPD  1        0.1907
6350.9    75.00  0.31     Sequence
             DRB1_1201   38      FTRGVYYPDKVFRSS  VYYPDKVFR  4        0.1477
10115.4    85.00  0.31     Sequence
             DRB1_1201   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.1392
11092.2    90.00  0.29     Sequence
             DRB1_1201   40      RGVYYPDKVFRSSVL  DKVFRSSVL  6        0.1924
6236.1    75.00  0.41     Sequence
             DRB1_1201   41      GVYYPDKVFRSSVLH  DKVFRSSVL  5        0.2210
4574.6    70.00  0.32     Sequence
             DRB1_1201   42      VYYPDKVFRSSVLHS  VFRSSVLHS  6        0.2533
3226.6    60.00  0.45     Sequence
             DRB1_1201   43      YYPDKVFRSSVLHST  VFRSSVLHS  5        0.2652
2835.8    60.00  0.44     Sequence
             DRB1_1201   44      YPDKVFRSSVLHSTQ  VFRSSVLHS  4        0.2626
2919.0    60.00  0.41     Sequence
             DRB1_1201   45      PDKVFRSSVLHSTQD  VFRSSVLHS  3        0.2670
2783.4    60.00  0.34     Sequence
             DRB1_1201   46      DKVFRSSVLHSTQDL  VFRSSVLHS  2        0.2639
2876.4    60.00  0.33     Sequence
             DRB1_1201   47      KVFRSSVLHSTQDLF  VLHSTQDLF  6        0.3318
1379.9    39.00  0.32     Sequence
             DRB1_1201   48      VFRSSVLHSTQDLFL  LHSTQDLFL  6        0.3255
1477.0    41.00  0.31     Sequence
             DRB1_1201   49      FRSSVLHSTQDLFLP  LHSTQDLFL  5        0.2931
2098.3    49.00  0.35     Sequence
             DRB1_1201   50      RSSVLHSTQDLFLPF  LHSTQDLFL  4        0.3042
1859.9    46.00  0.33     Sequence
             DRB1_1201   51      SSVLHSTQDLFLPFF  TQDLFLPFF  6        0.3924
716.2    26.00  0.43     Sequence
             DRB1_1201   52      SVLHSTQDLFLPFFS  TQDLFLPFF  5        0.3691
921.2    31.00  0.41     Sequence
             DRB1_1201   53      VLHSTQDLFLPFFSN  TQDLFLPFF  4        0.3616
999.3    32.00  0.34     Sequence
             DRB1_1201   54      LHSTQDLFLPFFSNV  TQDLFLPFF  3        0.3586
1033.1    33.00  0.38     Sequence
             DRB1_1201   55      HSTQDLFLPFFSNVT  TQDLFLPFF  2        0.3553
1070.3    34.00  0.35     Sequence
             DRB1_1201   56      STQDLFLPFFSNVTW  LPFFSNVTW  6        0.3706
907.0    30.00  0.22     Sequence
             DRB1_1201   57      TQDLFLPFFSNVTWF  LPFFSNVTW  5        0.3505
1126.8    35.00  0.25     Sequence
             DRB1_1201   58      QDLFLPFFSNVTWFH  LPFFSNVTW  4        0.3223
1529.2    41.00  0.30     Sequence
             DRB1_1201   59      DLFLPFFSNVTWFHA  LPFFSNVTW  3        0.3198
1571.8    42.00  0.29     Sequence
             DRB1_1201   60      LFLPFFSNVTWFHAI  LPFFSNVTW  2        0.3150
1655.0    43.00  0.29     Sequence
             DRB1_1201   61      FLPFFSNVTWFHAIH  VTWFHAIHX  7        0.3235
1508.8    41.00  0.25     Sequence
             DRB1_1201   62      LPFFSNVTWFHAIHV  VTWFHAIHV  6        0.4583
351.3    15.00  0.67     Sequence
```

```
             DRB1_1201   63      PFFSNVTWFHAIHVS  VTWFHAIHV  5        0.4507
381.2    16.00  0.66     Sequence
             DRB1_1201   64      FFSNVTWFHAIHVSG  VTWFHAIHV  4        0.4436
411.4    17.00  0.65     Sequence
             DRB1_1201   65      FSNVTWFHAIHVSGT  VTWFHAIHV  3        0.4403
426.6    17.00  0.65     Sequence
             DRB1_1201   66      SNVTWFHAIHVSGTN  VTWFHAIHV  2        0.4270
492.8    19.00  0.67     Sequence
             DRB1_1201   67      NVTWFHAIHVSGTNG  VTWFHAIHV  1        0.3633
980.9    32.00  0.55     Sequence
             DRB1_1201   68      VTWFHAIHVSGTNGT  VTWFHAIHV  0        0.3228
1521.8    41.00  0.44     Sequence
             DRB1_1201   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.1827
6923.8    80.00  0.50     Sequence
             DRB1_1201   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1        0.1311
12109.4    90.00  0.31     Sequence
             DRB1_1201   71      FHAIHVSGTNGTKRF  IHVSGTNGT  3        0.1059
15890.7    95.00  0.28     Sequence
             DRB1_1201   72      HAIHVSGTNGTKRFD  VSGTNGTKR  4        0.1031
16393.3    95.00  0.29     Sequence
             DRB1_1201   73      AIHVSGTNGTKRFDN  VSGTNGTKR  3        0.1000
16941.8    95.00  0.30     Sequence
             DRB1_1201   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.0873
19451.4    95.00  0.32     Sequence
             DRB1_1201   75      HVSGTNGTKRFDNPV  GTKRFDNPV  6        0.0809
20845.2   100.00  0.17     Sequence
             DRB1_1201   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.1201
13634.7    90.00  0.51     Sequence
             DRB1_1201   77      SGTNGTKRFDNPVLP  TKRFDNPVL  5        0.1069
15733.6    95.00  0.53     Sequence
             DRB1_1201   78      GTNGTKRFDNPVLPF  RFDNPVLPF  6        0.1630
8568.8    85.00  0.32     Sequence
             DRB1_1201   79      TNGTKRFDNPVLPFN  RFDNPVLPF  5        0.1654
8355.4    85.00  0.30     Sequence
             DRB1_1201   80      NGTKRFDNPVLPFND  RFDNPVLPF  4        0.1617
8691.2    85.00  0.29     Sequence
             DRB1_1201   81      GTKRFDNPVLPFNDG  RFDNPVLPF  3        0.1507
9789.8    85.00  0.28     Sequence
             DRB1_1201   82      TKRFDNPVLPFNDGV  RFDNPVLPF  2        0.1483
10053.9    85.00  0.32     Sequence
             DRB1_1201   83      KRFDNPVLPFNDGVY  VLPFNDGVY  6        0.2587
3044.7    60.00  0.48     Sequence
             DRB1_1201   84      RFDNPVLPFNDGVYF  LPFNDGVYF  6        0.3554
1068.4    34.00  0.42     Sequence
             DRB1_1201   85      FDNPVLPFNDGVYFA  LPFNDGVYF  5        0.3447
1199.5    36.00  0.43     Sequence
             DRB1_1201   86      DNPVLPFNDGVYFAS  LPFNDGVYF  4        0.3386
1281.8    37.00  0.42     Sequence
             DRB1_1201   87      NPVLPFNDGVYFAST  LPFNDGVYF  3        0.3376
1295.4    38.00  0.41     Sequence
             DRB1_1201   88      PVLPFNDGVYFASTE  LPFNDGVYF  2        0.3254
1479.3    41.00  0.43     Sequence
             DRB1_1201   89      VLPFNDGVYFASTEK  LPFNDGVYF  1        0.3011
1924.0    47.00  0.41     Sequence
             DRB1_1201   90      LPFNDGVYFASTEKS  LPFNDGVYF  0        0.2259
4338.8    70.00  0.44     Sequence
             DRB1_1201   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.0901
18865.9    95.00  0.28     Sequence
             DRB1_1201   92      FNDGVYFASTEKSNI  FASTEKSNI  6        0.0958
17734.1    95.00  0.38     Sequence
             DRB1_1201   93      NDGVYFASTEKSNII  ASTEKSNII  6        0.1159
14275.6    90.00  0.38     Sequence
             DRB1_1201   94      DGVYFASTEKSNIIR  ASTEKSNII  5        0.1248
12952.8    90.00  0.34     Sequence
             DRB1_1201   95      GVYFASTEKSNIIRG  ASTEKSNII  4        0.1202
13612.5    90.00  0.34     Sequence
```

```
             DRB1_1201   96      VYFASTEKSNIIRGW  ASTEKSNII  3        0.1333
11821.4    90.00  0.30     Sequence
             DRB1_1201   97      YFASTEKSNIIRGWI  KSNIIRGWI  6        0.1852
6741.5    80.00  0.44     Sequence
             DRB1_1201   98      FASTEKSNIIRGWIF  SNIIRGWIF  6        0.3037
1871.0    46.00  0.47     Sequence
             DRB1_1201   99      ASTEKSNIIRGWIFG  SNIIRGWIF  5        0.2999
1949.5    47.00  0.41     Sequence
             DRB1_1201  100      STEKSNIIRGWIFGT  SNIIRGWIF  4        0.3394
1271.3    37.00  0.38     Sequence
             DRB1_1201  101      TEKSNIIRGWIFGTT  SNIIRGWIF  3        0.3599
1017.9    33.00  0.34     Sequence
             DRB1_1201  102      EKSNIIRGWIFGTTL  IRGWIFGTT  5        0.3602
1014.5    33.00  0.30     Sequence
             DRB1_1201  103      KSNIIRGWIFGTTLD  IRGWIFGTT  4        0.3506
1125.8    35.00  0.31     Sequence
             DRB1_1201  104      SNIIRGWIFGTTLDS  IRGWIFGTT  3        0.3192
1581.1    42.00  0.34     Sequence
             DRB1_1201  105      NIIRGWIFGTTLDSK  IRGWIFGTT  2        0.2481
3413.2    65.00  0.44     Sequence
             DRB1_1201  106      IIRGWIFGTTLDSKT  IRGWIFGTT  1        0.2063
5365.6    75.00  0.32     Sequence
             DRB1_1201  107      IRGWIFGTTLDSKTQ  GTTLDSKTQ  6        0.1540
9443.2    85.00  0.37     Sequence
             DRB1_1201  108      RGWIFGTTLDSKTQS  GTTLDSKTQ  5        0.1076
15612.4    95.00  0.49     Sequence
             DRB1_1201  109      GWIFGTTLDSKTQSL  GTTLDSKTQ  4        0.1295
12318.1    90.00  0.41     Sequence
             DRB1_1201  110      WIFGTTLDSKTQSLL  LDSKTQSLL  6        0.2155
4855.2    70.00  0.58     Sequence
             DRB1_1201  111      IFGTTLDSKTQSLLI  LDSKTQSLL  5        0.2710
2664.1    55.00  0.44     Sequence
             DRB1_1201  112      FGTTLDSKTQSLLIV  LDSKTQSLL  4        0.3129
1693.0    44.00  0.38     Sequence
             DRB1_1201  113      GTTLDSKTQSLLIVN  LDSKTQSLL  3        0.3238
1504.6    41.00  0.31     Sequence
             DRB1_1201  114      TTLDSKTQSLLIVNN  LDSKTQSLL  2        0.3264
1463.0    40.00  0.29     Sequence
             DRB1_1201  115      TLDSKTQSLLIVNNA  TQSLLIVNN  5        0.3153
1650.0    43.00  0.27     Sequence
             DRB1_1201  116      LDSKTQSLLIVNNAT  TQSLLIVNN  4        0.3069
1807.1    45.00  0.27     Sequence
             DRB1_1201  117      DSKTQSLLIVNNATN  LLIVNNATN  6        0.3253
1480.6    41.00  0.48     Sequence
             DRB1_1201  118      SKTQSLLIVNNATNV  LLIVNNATN  5        0.3514
1116.2    34.00  0.44     Sequence
             DRB1_1201  119      KTQSLLIVNNATNVV  LLIVNNATN  4        0.3670
942.9    31.00  0.42     Sequence
             DRB1_1201  120      TQSLLIVNNATNVVI  LLIVNNATN  3        0.3862
766.2    27.00  0.36     Sequence
             DRB1_1201  121      QSLLIVNNATNVVIK  LLIVNNATN  2        0.3816
805.1    28.00  0.38     Sequence
             DRB1_1201  122      SLLIVNNATNVVIKV  VNNATNVVI  4        0.3714
899.2    30.00  0.29     Sequence
             DRB1_1201  123      LLIVNNATNVVIKVC  VNNATNVVI  3        0.3420
1235.3    37.00  0.33     Sequence
             DRB1_1201  124      LIVNNATNVVIKVCE  VNNATNVVI  2        0.2825
2352.3    55.00  0.40     Sequence
             DRB1_1201  125      IVNNATNVVIKVCEF  NVVIKVCEF  6        0.3117
1715.7    44.00  0.39     Sequence
             DRB1_1201  126      VNNATNVVIKVCEFQ  NVVIKVCEF  5        0.3234
1510.5    41.00  0.41     Sequence
             DRB1_1201  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.5320
158.2     6.50  0.48     Sequence         WB
             DRB1_1201  128      NATNVVIKVCEFQFC  VIKVCEFQF  5        0.5311
159.7     6.50  0.41     Sequence         WB
```

```
             DRB1_1201  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.5312
159.5     6.50  0.41     Sequence         WB
             DRB1_1201  130      TNVVIKVCEFQFCNY  VCEFQFCNY  6        0.5646
111.2     4.00  0.25     Sequence         WB
             DRB1_1201  131      NVVIKVCEFQFCNYP  VCEFQFCNY  5        0.5501
130.1     5.00  0.24     Sequence         WB
             DRB1_1201  132      VVIKVCEFQFCNYPF  VCEFQFCNY  4        0.5457
136.4     5.50  0.28     Sequence         WB
             DRB1_1201  133      VIKVCEFQFCNYPFL  VCEFQFCNY  3        0.5375
149.0     6.00  0.25     Sequence         WB
             DRB1_1201  134      IKVCEFQFCNYPFLG  VCEFQFCNY  2        0.4570
356.1    15.00  0.37     Sequence
             DRB1_1201  135      KVCEFQFCNYPFLGV  FQFCNYPFL  4        0.4280
487.4    19.00  0.37     Sequence
             DRB1_1201  136      VCEFQFCNYPFLGVY  FQFCNYPFL  3        0.4158
556.0    21.00  0.37     Sequence
             DRB1_1201  137      CEFQFCNYPFLGVYY  NYPFLGVYY  6        0.4936
239.7    10.00  0.41     Sequence
             DRB1_1201  138      EFQFCNYPFLGVYYH  NYPFLGVYY  5        0.4653
325.5    14.00  0.38     Sequence
             DRB1_1201  139      FQFCNYPFLGVYYHK  NYPFLGVYY  4        0.4484
390.9    16.00  0.41     Sequence
             DRB1_1201  140      QFCNYPFLGVYYHKN  NYPFLGVYY  3        0.4157
556.5    21.00  0.49     Sequence
             DRB1_1201  141      FCNYPFLGVYYHKNN  NYPFLGVYY  2        0.3990
666.7    24.00  0.49     Sequence
             DRB1_1201  142      CNYPFLGVYYHKNNK  NYPFLGVYY  1        0.3712
901.2    30.00  0.47     Sequence
             DRB1_1201  143      NYPFLGVYYHKNNKS  NYPFLGVYY  0        0.3139
1675.3    44.00  0.39     Sequence
             DRB1_1201  144      YPFLGVYYHKNNKSW  FLGVYYHKN  2        0.2113
5082.6    70.00  0.25     Sequence
             DRB1_1201  145      PFLGVYYHKNNKSWM  YHKNNKSWM  6        0.1923
6240.5    75.00  0.26     Sequence
             DRB1_1201  146      FLGVYYHKNNKSWME  YHKNNKSWM  5        0.1771
7360.0    80.00  0.29     Sequence
             DRB1_1201  147      LGVYYHKNNKSWMES  YHKNNKSWM  4        0.1544
9411.0    85.00  0.37     Sequence
             DRB1_1201  148      GVYYHKNNKSWMESE  YHKNNKSWM  3        0.1393
11082.2    90.00  0.37     Sequence
             DRB1_1201  149      VYYHKNNKSWMESEF  YHKNNKSWM  2        0.1439
10540.1    85.00  0.31     Sequence
             DRB1_1201  150      YYHKNNKSWMESEFR  KSWMESEFR  6        0.1343
11696.8    90.00  0.28     Sequence
             DRB1_1201  151      YHKNNKSWMESEFRV  SWMESEFRV  6        0.1892
6455.6    75.00  0.47     Sequence
             DRB1_1201  152      HKNNKSWMESEFRVY  SWMESEFRV  5        0.2802
2410.7    55.00  0.32     Sequence
             DRB1_1201  153      KNNKSWMESEFRVYS  SWMESEFRV  4        0.2786
2453.1    55.00  0.32     Sequence
             DRB1_1201  154      NNKSWMESEFRVYSS  SWMESEFRV  3        0.2729
2609.9    55.00  0.33     Sequence
             DRB1_1201  155      NKSWMESEFRVYSSA  SWMESEFRV  2        0.2647
2853.3    60.00  0.34     Sequence
             DRB1_1201  156      KSWMESEFRVYSSAN  SWMESEFRV  1        0.2622
2929.3    60.00  0.33     Sequence
             DRB1_1201  157      SWMESEFRVYSSANN  FRVYSSANN  6        0.2467
3464.9    65.00  0.25     Sequence
             DRB1_1201  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.1885
6504.4    75.00  0.31     Sequence
             DRB1_1201  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.1343
11697.3    90.00  0.44     Sequence
             DRB1_1201  160      ESEFRVYSSANNCTF  YSSANNCTF  6        0.1835
6863.4    80.00  0.40     Sequence
             DRB1_1201  161      SEFRVYSSANNCTFE  YSSANNCTF  5        0.1835
6862.4    80.00  0.41     Sequence
```

```
             DRB1_1201  162      EFRVYSSANNCTFEY  YSSANNCTF  4        0.2183
4711.1    70.00  0.29     Sequence
             DRB1_1201  163      FRVYSSANNCTFEYV  YSSANNCTF  3        0.2305
4131.3    65.00  0.26     Sequence
             DRB1_1201  164      RVYSSANNCTFEYVS  YSSANNCTF  2        0.2194
4655.3    70.00  0.27     Sequence
             DRB1_1201  165      VYSSANNCTFEYVSQ  SANNCTFEY  3        0.2042
5487.4    75.00  0.28     Sequence
             DRB1_1201  166      YSSANNCTFEYVSQP  SANNCTFEY  2        0.1833
6881.5    80.00  0.28     Sequence
             DRB1_1201  167      SSANNCTFEYVSQPF  TFEYVSQPF  6        0.2054
5417.7    75.00  0.26     Sequence
             DRB1_1201  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.2694
2711.5    55.00  0.54     Sequence
             DRB1_1201  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.2760
2523.4    55.00  0.49     Sequence
             DRB1_1201  170      NNCTFEYVSQPFLMD  FEYVSQPFL  4        0.2698
2698.8    55.00  0.47     Sequence
             DRB1_1201  171      NCTFEYVSQPFLMDL  FEYVSQPFL  3        0.2793
2434.4    55.00  0.41     Sequence
             DRB1_1201  172      CTFEYVSQPFLMDLE  FEYVSQPFL  2        0.2720
2635.4    55.00  0.37     Sequence
             DRB1_1201  173      TFEYVSQPFLMDLEG  FEYVSQPFL  1        0.2383
3796.3    65.00  0.29     Sequence
             DRB1_1201  174      FEYVSQPFLMDLEGK  EYVSQPFLM  1        0.2150
4882.9    70.00  0.22     Sequence
             DRB1_1201  175      EYVSQPFLMDLEGKQ  SQPFLMDLE  3        0.1654
8352.3    85.00  0.18     Sequence
             DRB1_1201  176      YVSQPFLMDLEGKQG  LMDLEGKQG  6        0.1572
9124.7    85.00  0.47     Sequence
             DRB1_1201  177      VSQPFLMDLEGKQGN  LMDLEGKQG  5        0.1475
10132.4    85.00  0.54     Sequence
             DRB1_1201  178      SQPFLMDLEGKQGNF  LMDLEGKQG  4        0.1659
8305.0    85.00  0.51     Sequence
             DRB1_1201  179      QPFLMDLEGKQGNFK  LMDLEGKQG  3        0.1678
8141.7    80.00  0.46     Sequence
             DRB1_1201  180      PFLMDLEGKQGNFKN  LMDLEGKQG  2        0.1643
8449.8    85.00  0.45     Sequence
             DRB1_1201  181      FLMDLEGKQGNFKNL  LMDLEGKQG  1        0.1588
8968.9    85.00  0.38     Sequence
             DRB1_1201  182      LMDLEGKQGNFKNLS  LEGKQGNFK  3        0.1322
11960.2    90.00  0.25     Sequence
             DRB1_1201  183      MDLEGKQGNFKNLSE  LEGKQGNFK  2        0.1015
16675.8    95.00  0.34     Sequence
             DRB1_1201  184      DLEGKQGNFKNLSEF  GNFKNLSEF  6        0.1255
12861.8    90.00  0.27     Sequence
             DRB1_1201  185      LEGKQGNFKNLSEFV  FKNLSEFVX  7        0.2125
5017.5    70.00  0.37     Sequence
             DRB1_1201  186      EGKQGNFKNLSEFVF  FKNLSEFVF  6        0.4033
636.5    24.00  0.75     Sequence
             DRB1_1201  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5        0.3920
719.3    26.00  0.71     Sequence
             DRB1_1201  188      KQGNFKNLSEFVFKN  FKNLSEFVF  4        0.3977
676.3    25.00  0.68     Sequence
             DRB1_1201  189      QGNFKNLSEFVFKNI  FKNLSEFVF  3        0.4318
467.7    19.00  0.52     Sequence
             DRB1_1201  190      GNFKNLSEFVFKNID  FKNLSEFVF  2        0.4178
544.1    21.00  0.51     Sequence
             DRB1_1201  191      NFKNLSEFVFKNIDG  LSEFVFKNI  4        0.3949
697.3    25.00  0.29     Sequence
             DRB1_1201  192      FKNLSEFVFKNIDGY  LSEFVFKNI  3        0.4077
606.8    23.00  0.28     Sequence
             DRB1_1201  193      KNLSEFVFKNIDGYF  LSEFVFKNI  2        0.4505
382.0    16.00  0.19     Sequence
             DRB1_1201  194      NLSEFVFKNIDGYFK  FKNIDGYFK  6        0.4622
336.4    14.00  0.47     Sequence
```

```
           DRB1_1201  195      LSEFVFKNIDGYFKI  FKNIDGYFK  5        0.4826
269.9    11.00  0.50     Sequence
           DRB1_1201  196      SEFVFKNIDGYFKIY  FKNIDGYFK  4        0.4878
255.1    11.00  0.50     Sequence
           DRB1_1201  197      EFVFKNIDGYFKIYS  FKNIDGYFK  3        0.4765
288.2    12.00  0.50     Sequence
           DRB1_1201  198      FVFKNIDGYFKIYSK  FKNIDGYFK  2        0.4573
355.1    15.00  0.51     Sequence
           DRB1_1201  199      VFKNIDGYFKIYSKH  FKNIDGYFK  1        0.3618
997.8    32.00  0.37     Sequence
           DRB1_1201  200      FKNIDGYFKIYSKHT  IDGYFKIYS  3        0.2770
2495.8    55.00  0.22     Sequence
           DRB1_1201  201      KNIDGYFKIYSKHTP  IDGYFKIYS  2        0.2448
3538.3    65.00  0.19     Sequence
           DRB1_1201  202      NIDGYFKIYSKHTPI  FKIYSKHTP  5        0.2541
3197.7    60.00  0.24     Sequence
           DRB1_1201  203      IDGYFKIYSKHTPIN  IYSKHTPIN  6        0.2533
3226.9    60.00  0.27     Sequence
           DRB1_1201  204      DGYFKIYSKHTPINL  IYSKHTPIN  5        0.2525
3254.1    60.00  0.31     Sequence
           DRB1_1201  205      GYFKIYSKHTPINLV  IYSKHTPIN  4        0.2656
2825.0    60.00  0.31     Sequence
           DRB1_1201  206      YFKIYSKHTPINLVR  IYSKHTPIN  3        0.2501
3339.7    60.00  0.33     Sequence
           DRB1_1201  207      FKIYSKHTPINLVRD  IYSKHTPIN  2        0.2270
4287.7    70.00  0.36     Sequence
           DRB1_1201  208      KIYSKHTPINLVRDL  SKHTPINLV  3        0.2019
5627.2    75.00  0.19     Sequence
           DRB1_1201  209      IYSKHTPINLVRDLP  INLVRDLPX  7        0.2163
4814.3    70.00  0.25     Sequence
           DRB1_1201  210      YSKHTPINLVRDLPQ  INLVRDLPQ  6        0.2691
2718.4    55.00  0.58     Sequence
           DRB1_1201  211      SKHTPINLVRDLPQG  INLVRDLPQ  5        0.2653
2832.7    60.00  0.57     Sequence
           DRB1_1201  212      KHTPINLVRDLPQGF  INLVRDLPQ  4        0.4013
650.4    24.00  0.28     Sequence
           DRB1_1201  213      HTPINLVRDLPQGFS  VRDLPQGFS  6        0.4569
356.6    15.00  0.54     Sequence
           DRB1_1201  214      TPINLVRDLPQGFSA  VRDLPQGFS  5        0.4491
387.8    16.00  0.56     Sequence
           DRB1_1201  215      PINLVRDLPQGFSAL  VRDLPQGFS  4        0.4475
394.7    16.00  0.58     Sequence
           DRB1_1201  216      INLVRDLPQGFSALE  VRDLPQGFS  3        0.4313
470.1    19.00  0.61     Sequence
           DRB1_1201  217      NLVRDLPQGFSALEP  VRDLPQGFS  2        0.3947
698.7    25.00  0.62     Sequence
           DRB1_1201  218      LVRDLPQGFSALEPL  VRDLPQGFS  1        0.3394
1271.0    37.00  0.46     Sequence
           DRB1_1201  219      VRDLPQGFSALEPLV  FSALEPLVX  7        0.2869
2243.8    50.00  0.31     Sequence
           DRB1_1201  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.3053
1838.1    46.00  0.72     Sequence
           DRB1_1201  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.3392
1273.7    37.00  0.68     Sequence
           DRB1_1201  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.3415
1242.8    37.00  0.64     Sequence
           DRB1_1201  223      PQGFSALEPLVDLPI  LEPLVDLPI  6        0.3922
718.1    26.00  0.44     Sequence
           DRB1_1201  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.3712
900.7    30.00  0.45     Sequence
           DRB1_1201  225      GFSALEPLVDLPIGI  LEPLVDLPI  4        0.3462
1180.9    36.00  0.52     Sequence
           DRB1_1201  226      FSALEPLVDLPIGIN  LEPLVDLPI  3        0.3418
1238.9    37.00  0.55     Sequence
           DRB1_1201  227      SALEPLVDLPIGINI  LEPLVDLPI  2        0.3232
1514.8    41.00  0.56     Sequence
```

```
            DRB1_1201  228      ALEPLVDLPIGINIT  LEPLVDLPI  1        0.2854
2280.8    55.00  0.47     Sequence
            DRB1_1201  229      LEPLVDLPIGINITR  LVDLPIGIN  3        0.2553
3156.5    60.00  0.27     Sequence
            DRB1_1201  230      EPLVDLPIGINITRF  PIGINITRF  6        0.3157
1643.3    43.00  0.47     Sequence
            DRB1_1201  231      PLVDLPIGINITRFQ  PIGINITRF  5        0.3241
1500.3    41.00  0.46     Sequence
            DRB1_1201  232      LVDLPIGINITRFQT  PIGINITRF  4        0.3481
1156.6    35.00  0.41     Sequence
            DRB1_1201  233      VDLPIGINITRFQTL  PIGINITRF  3        0.3887
745.6    26.00  0.38     Sequence
            DRB1_1201  234      DLPIGINITRFQTLL  PIGINITRF  2        0.4225
517.4    20.00  0.31     Sequence
            DRB1_1201  235      LPIGINITRFQTLLA  ITRFQTLLA  6        0.4553
362.8    15.00  0.49     Sequence
            DRB1_1201  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.4599
345.0    14.00  0.49     Sequence
            DRB1_1201  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.4579
352.7    15.00  0.49     Sequence
            DRB1_1201  238      GINITRFQTLLALHR  FQTLLALHR  6        0.4753
292.1    12.00  0.41     Sequence
            DRB1_1201  239      INITRFQTLLALHRS  FQTLLALHR  5        0.4763
288.8    12.00  0.38     Sequence
            DRB1_1201  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.5129
194.5     8.00  0.31     Sequence         WB
            DRB1_1201  241      ITRFQTLLALHRSYL  LLALHRSYL  6        0.5716
103.0     4.00  0.47     Sequence         WB
            DRB1_1201  242      TRFQTLLALHRSYLT  LLALHRSYL  5        0.5673
107.9     4.00  0.41     Sequence         WB
            DRB1_1201  243      RFQTLLALHRSYLTP  LLALHRSYL  4        0.5544
124.1     5.00  0.40     Sequence         WB
            DRB1_1201  244      FQTLLALHRSYLTPG  LLALHRSYL  3        0.5238
172.8     7.00  0.43     Sequence         WB
            DRB1_1201  245      QTLLALHRSYLTPGD  LLALHRSYL  2        0.4927
241.9    10.00  0.47     Sequence
            DRB1_1201  246      TLLALHRSYLTPGDS  LALHRSYLT  2        0.4261
497.6    20.00  0.41     Sequence
            DRB1_1201  247      LLALHRSYLTPGDSS  LALHRSYLT  1        0.3240
1502.2    41.00  0.35     Sequence
            DRB1_1201  248      LALHRSYLTPGDSSS  LHRSYLTPG  2        0.2258
4342.6    70.00  0.37     Sequence
            DRB1_1201  249      ALHRSYLTPGDSSSG  LHRSYLTPG  1        0.1242
13048.8    90.00  0.34     Sequence
            DRB1_1201  250      LHRSYLTPGDSSSGW  LTPGDSSSG  5        0.0786
21368.6   100.00  0.43     Sequence
            DRB1_1201  251      HRSYLTPGDSSSGWT  LTPGDSSSG  4        0.0654
24636.1   100.00  0.52     Sequence
            DRB1_1201  252      RSYLTPGDSSSGWTA  LTPGDSSSG  3        0.0622
25507.7   100.00  0.56     Sequence
            DRB1_1201  253      SYLTPGDSSSGWTAG  LTPGDSSSG  2        0.0500
29101.7   100.00  0.65     Sequence
            DRB1_1201  254      YLTPGDSSSGWTAGA  LTPGDSSSG  1        0.0357
33996.4   100.00  0.50     Sequence
            DRB1_1201  255      LTPGDSSSGWTAGAA  LTPGDSSSG  0        0.0257
37862.3   100.00  0.27     Sequence
            DRB1_1201  256      TPGDSSSGWTAGAAA  SSGWTAGAA  5        0.0221
39372.9   100.00  0.21     Sequence
            DRB1_1201  257      PGDSSSGWTAGAAAY  GWTAGAAAY  6        0.1181
13925.2    90.00  0.63     Sequence
            DRB1_1201  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.2759
2526.4    55.00  0.45     Sequence
            DRB1_1201  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.3224
1527.5    41.00  0.34     Sequence
            DRB1_1201  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.3062
1821.3    45.00  0.34     Sequence
```

```
             DRB1_1201  261      SSGWTAGAAAYYVGY  TAGAAAYYV  4        0.3375
1297.3    38.00  0.25     Sequence
             DRB1_1201  262      SGWTAGAAAYYVGYL  TAGAAAYYV  3        0.3368
1307.8    38.00  0.23     Sequence
             DRB1_1201  263      GWTAGAAAYYVGYLQ  TAGAAAYYV  2        0.3163
1631.3    43.00  0.25     Sequence
             DRB1_1201  264      WTAGAAAYYVGYLQP  TAGAAAYYV  1        0.2822
2359.7    55.00  0.28     Sequence
             DRB1_1201  265      TAGAAAYYVGYLQPR  GAAAYYVGY  2        0.1985
5835.6    75.00  0.22     Sequence
             DRB1_1201  266      AGAAAYYVGYLQPRT  VGYLQPRTX  7        0.1961
5990.3    75.00  0.31     Sequence
             DRB1_1201  267      GAAAYYVGYLQPRTF  VGYLQPRTF  6        0.4297
478.6    19.00  0.76     Sequence
             DRB1_1201  268      AAAYYVGYLQPRTFL  VGYLQPRTF  5        0.4404
425.9    17.00  0.77     Sequence
             DRB1_1201  269      AAYYVGYLQPRTFLL  VGYLQPRTF  4        0.4669
319.8    13.00  0.68     Sequence
             DRB1_1201  270      AYYVGYLQPRTFLLK  VGYLQPRTF  3        0.4737
297.1    13.00  0.61     Sequence
             DRB1_1201  271      YYVGYLQPRTFLLKY  VGYLQPRTF  2        0.4730
299.5    13.00  0.56     Sequence
             DRB1_1201  272      YVGYLQPRTFLLKYN  VGYLQPRTF  1        0.4560
359.9    15.00  0.46     Sequence
             DRB1_1201  273      VGYLQPRTFLLKYNE  LQPRTFLLK  3        0.4248
504.7    20.00  0.28     Sequence
             DRB1_1201  274      GYLQPRTFLLKYNEN  LQPRTFLLK  2        0.3378
1293.8    38.00  0.34     Sequence
             DRB1_1201  275      YLQPRTFLLKYNENG  LQPRTFLLK  1        0.3102
1743.0    44.00  0.29     Sequence
             DRB1_1201  276      LQPRTFLLKYNENGT  RTFLLKYNE  3        0.2871
2238.1    50.00  0.25     Sequence
             DRB1_1201  277      QPRTFLLKYNENGTI  LKYNENGTI  6        0.3121
1707.0    44.00  0.46     Sequence
             DRB1_1201  278      PRTFLLKYNENGTIT  LKYNENGTI  5        0.2924
2113.2    49.00  0.52     Sequence
             DRB1_1201  279      RTFLLKYNENGTITD  LKYNENGTI  4        0.2715
2648.3    55.00  0.60     Sequence
             DRB1_1201  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.2450
3528.5    65.00  0.64     Sequence
             DRB1_1201  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.2239
4433.9    70.00  0.71     Sequence
             DRB1_1201  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.1858
6694.9    80.00  0.65     Sequence
             DRB1_1201  283      LKYNENGTITDAVDC  LKYNENGTI  0        0.1423
10725.8    90.00  0.47     Sequence
             DRB1_1201  284      KYNENGTITDAVDCA  GTITDAVDC  5        0.0872
19468.5    95.00  0.46     Sequence
             DRB1_1201  285      YNENGTITDAVDCAL  ITDAVDCAL  6        0.1694
8000.9    80.00  0.38     Sequence
             DRB1_1201  286      NENGTITDAVDCALD  ITDAVDCAL  5        0.1846
6787.5    80.00  0.37     Sequence
             DRB1_1201  287      ENGTITDAVDCALDP  TDAVDCALD  5        0.1944
6100.1    75.00  0.36     Sequence
             DRB1_1201  288      NGTITDAVDCALDPL  TDAVDCALD  4        0.2200
4624.0    70.00  0.31     Sequence
             DRB1_1201  289      GTITDAVDCALDPLS  TDAVDCALD  3        0.2302
4141.9    65.00  0.25     Sequence
             DRB1_1201  290      TITDAVDCALDPLSE  DCALDPLSE  6        0.2245
4404.3    70.00  0.32     Sequence
             DRB1_1201  291      ITDAVDCALDPLSET  DCALDPLSE  5        0.2143
4922.1    70.00  0.37     Sequence
             DRB1_1201  292      TDAVDCALDPLSETK  DCALDPLSE  4        0.1894
6442.8    75.00  0.41     Sequence
             DRB1_1201  293      DAVDCALDPLSETKC  LDPLSETKC  6        0.2301
4147.2    65.00  0.52     Sequence
```

```
             DRB1_1201  294      AVDCALDPLSETKCT  LDPLSETKC  5        0.2264
4315.2    70.00  0.55     Sequence
             DRB1_1201  295      VDCALDPLSETKCTL  LDPLSETKC  4        0.2190
4676.8    70.00  0.54     Sequence
             DRB1_1201  296      DCALDPLSETKCTLK  LDPLSETKC  3        0.2001
5735.9    75.00  0.60     Sequence
             DRB1_1201  297      CALDPLSETKCTLKS  LDPLSETKC  2        0.1994
5778.6    75.00  0.60     Sequence
             DRB1_1201  298      ALDPLSETKCTLKSF  ETKCTLKSF  6        0.2372
3839.4    65.00  0.23     Sequence
             DRB1_1201  299      LDPLSETKCTLKSFT  ETKCTLKSF  5        0.2399
3730.7    65.00  0.23     Sequence
             DRB1_1201  300      DPLSETKCTLKSFTV  KCTLKSFTV  6        0.3194
1578.4    42.00  0.62     Sequence
             DRB1_1201  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.3266
1459.0    40.00  0.58     Sequence
             DRB1_1201  302      LSETKCTLKSFTVEK  KCTLKSFTV  4        0.3338
1350.2    39.00  0.56     Sequence
             DRB1_1201  303      SETKCTLKSFTVEKG  KCTLKSFTV  3        0.3235
1509.8    41.00  0.51     Sequence
             DRB1_1201  304      ETKCTLKSFTVEKGI  KCTLKSFTV  2        0.3211
1549.6    42.00  0.47     Sequence
             DRB1_1201  305      TKCTLKSFTVEKGIY  LKSFTVEKG  4        0.3242
1498.6    41.00  0.34     Sequence
             DRB1_1201  306      KCTLKSFTVEKGIYQ  FTVEKGIYQ  6        0.3542
1082.9    34.00  0.33     Sequence
             DRB1_1201  307      CTLKSFTVEKGIYQT  FTVEKGIYQ  5        0.3393
1272.0    37.00  0.35     Sequence
             DRB1_1201  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.3100
1746.6    44.00  0.37     Sequence
             DRB1_1201  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.3009
1928.6    47.00  0.39     Sequence
             DRB1_1201  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.2836
2324.2    55.00  0.38     Sequence
             DRB1_1201  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.2743
2571.9    55.00  0.36     Sequence
             DRB1_1201  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.3961
688.0    25.00  0.56     Sequence
             DRB1_1201  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.3647
966.9    31.00  0.64     Sequence
             DRB1_1201  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.3468
1172.8    36.00  0.68     Sequence
             DRB1_1201  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.3393
1272.5    37.00  0.70     Sequence
             DRB1_1201  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.3308
1394.5    39.00  0.68     Sequence
             DRB1_1201  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.2995
1956.2    47.00  0.61     Sequence
             DRB1_1201  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.2823
2358.7    55.00  0.31     Sequence
             DRB1_1201  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.2439
3571.4    65.00  0.55     Sequence
             DRB1_1201  320      QTSNFRVQPTESIVR  VQPTESIVR  6        0.2787
2452.4    55.00  0.43     Sequence
             DRB1_1201  321      TSNFRVQPTESIVRF  VQPTESIVR  5        0.3104
1739.2    44.00  0.44     Sequence
             DRB1_1201  322      SNFRVQPTESIVRFP  VQPTESIVR  4        0.3039
1866.4    46.00  0.40     Sequence
             DRB1_1201  323      NFRVQPTESIVRFPN  VQPTESIVR  3        0.3032
1881.0    46.00  0.38     Sequence
             DRB1_1201  324      FRVQPTESIVRFPNI  VQPTESIVR  2        0.3002
1942.7    47.00  0.33     Sequence
             DRB1_1201  325      RVQPTESIVRFPNIT  TESIVRFPN  4        0.2757
2532.4    55.00  0.19     Sequence
             DRB1_1201  326      VQPTESIVRFPNITN  IVRFPNITN  6        0.3383
1286.9    38.00  0.64     Sequence
```

```
             DRB1_1201  327      QPTESIVRFPNITNL  IVRFPNITN  5        0.3398
1266.1    37.00  0.72     Sequence
             DRB1_1201  328      PTESIVRFPNITNLC  IVRFPNITN  4        0.3160
1637.8    43.00  0.75     Sequence
             DRB1_1201  329      TESIVRFPNITNLCP  IVRFPNITN  3        0.3078
1789.9    45.00  0.74     Sequence
             DRB1_1201  330      ESIVRFPNITNLCPF  IVRFPNITN  2        0.3498
1135.3    35.00  0.54     Sequence
             DRB1_1201  331      SIVRFPNITNLCPFG  IVRFPNITN  1        0.3318
1380.5    39.00  0.38     Sequence
             DRB1_1201  332      IVRFPNITNLCPFGE  ITNLCPFGE  6        0.3483
1154.7    35.00  0.54     Sequence
             DRB1_1201  333      VRFPNITNLCPFGEV  ITNLCPFGE  5        0.3524
1104.4    34.00  0.60     Sequence
             DRB1_1201  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.3708
904.7    30.00  0.53     Sequence
             DRB1_1201  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.3693
919.6    30.00  0.52     Sequence
             DRB1_1201  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.3540
1084.7    34.00  0.50     Sequence
             DRB1_1201  337      NITNLCPFGEVFNAT  ITNLCPFGE  1        0.2976
1997.1    48.00  0.47     Sequence
             DRB1_1201  338      ITNLCPFGEVFNATR  LCPFGEVFN  3        0.2473
3441.3    65.00  0.32     Sequence
             DRB1_1201  339      TNLCPFGEVFNATRF  GEVFNATRF  6        0.2445
3547.6    65.00  0.41     Sequence
             DRB1_1201  340      NLCPFGEVFNATRFA  GEVFNATRF  5        0.2463
3478.8    65.00  0.38     Sequence
             DRB1_1201  341      LCPFGEVFNATRFAS  VFNATRFAS  6        0.3163
1631.3    43.00  0.31     Sequence
             DRB1_1201  342      CPFGEVFNATRFASV  FNATRFASV  6        0.3543
1081.5    34.00  0.38     Sequence
             DRB1_1201  343      PFGEVFNATRFASVY  FNATRFASV  5        0.3776
840.3    29.00  0.36     Sequence
             DRB1_1201  344      FGEVFNATRFASVYA  FNATRFASV  4        0.3865
763.3    27.00  0.30     Sequence
             DRB1_1201  345      GEVFNATRFASVYAW  FNATRFASV  3        0.3727
886.3    30.00  0.31     Sequence
             DRB1_1201  346      EVFNATRFASVYAWN  FNATRFASV  2        0.3411
1247.2    37.00  0.38     Sequence
             DRB1_1201  347      VFNATRFASVYAWNR  ATRFASVYA  3        0.2975
1999.6    48.00  0.33     Sequence
             DRB1_1201  348      FNATRFASVYAWNRK  ATRFASVYA  2        0.2361
3885.3    65.00  0.38     Sequence
             DRB1_1201  349      NATRFASVYAWNRKR  FASVYAWNR  4        0.1905
6368.2    75.00  0.28     Sequence
             DRB1_1201  350      ATRFASVYAWNRKRI  VYAWNRKRI  6        0.2317
4075.2    65.00  0.46     Sequence
             DRB1_1201  351      TRFASVYAWNRKRIS  VYAWNRKRI  5        0.2235
4456.4    70.00  0.50     Sequence
             DRB1_1201  352      RFASVYAWNRKRISN  VYAWNRKRI  4        0.2135
4964.9    70.00  0.55     Sequence
             DRB1_1201  353      FASVYAWNRKRISNC  VYAWNRKRI  3        0.1990
5809.1    75.00  0.52     Sequence
             DRB1_1201  354      ASVYAWNRKRISNCV  VYAWNRKRI  2        0.2093
5195.6    70.00  0.41     Sequence
             DRB1_1201  355      SVYAWNRKRISNCVA  RKRISNCVA  6        0.2231
4474.4    70.00  0.28     Sequence
             DRB1_1201  356      VYAWNRKRISNCVAD  RKRISNCVA  5        0.2218
4534.5    70.00  0.29     Sequence
             DRB1_1201  357      YAWNRKRISNCVADY  RKRISNCVA  4        0.3215
1543.4    42.00  0.27     Sequence
             DRB1_1201  358      AWNRKRISNCVADYS  ISNCVADYS  6        0.3293
1417.4    40.00  0.28     Sequence
             DRB1_1201  359      WNRKRISNCVADYSV  ISNCVADYS  5        0.3394
1271.1    37.00  0.34     Sequence
```

```
             DRB1_1201  360      NRKRISNCVADYSVL  ISNCVADYS  4        0.3389
1277.5    37.00  0.34     Sequence
             DRB1_1201  361      RKRISNCVADYSVLY  CVADYSVLY  6        0.4604
343.4    14.00  0.41     Sequence
             DRB1_1201  362      KRISNCVADYSVLYN  CVADYSVLY  5        0.4419
419.1    17.00  0.41     Sequence
             DRB1_1201  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.3985
670.2    24.00  0.45     Sequence
             DRB1_1201  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.3511
1119.6    35.00  0.50     Sequence
             DRB1_1201  365      SNCVADYSVLYNSAS  CVADYSVLY  2        0.3326
1367.4    39.00  0.48     Sequence
             DRB1_1201  366      NCVADYSVLYNSASF  CVADYSVLY  1        0.3598
1018.7    33.00  0.38     Sequence
             DRB1_1201  367      CVADYSVLYNSASFS  CVADYSVLY  0        0.3554
1069.2    34.00  0.31     Sequence
             DRB1_1201  368      VADYSVLYNSASFST  LYNSASFST  6        0.3150
1654.8    43.00  0.46     Sequence
             DRB1_1201  369      ADYSVLYNSASFSTF  LYNSASFST  5        0.3337
1351.5    39.00  0.47     Sequence
             DRB1_1201  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.3310
1392.1    39.00  0.50     Sequence
             DRB1_1201  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.3288
1424.9    40.00  0.47     Sequence
             DRB1_1201  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.3206
1558.4    42.00  0.44     Sequence
             DRB1_1201  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.2819
2368.9    55.00  0.38     Sequence
             DRB1_1201  374      LYNSASFSTFKCYGV  FSTFKCYGV  6        0.3175
1611.5    43.00  0.62     Sequence
             DRB1_1201  375      YNSASFSTFKCYGVS  FSTFKCYGV  5        0.3031
1881.4    46.00  0.69     Sequence
             DRB1_1201  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.2946
2062.7    48.00  0.67     Sequence
             DRB1_1201  377      SASFSTFKCYGVSPT  FSTFKCYGV  3        0.2887
2199.2    50.00  0.67     Sequence
             DRB1_1201  378      ASFSTFKCYGVSPTK  FSTFKCYGV  2        0.2682
2746.4    55.00  0.73     Sequence
             DRB1_1201  379      SFSTFKCYGVSPTKL  FSTFKCYGV  1        0.2288
4205.9    65.00  0.37     Sequence
             DRB1_1201  380      FSTFKCYGVSPTKLN  CYGVSPTKL  5        0.1950
6062.2    75.00  0.31     Sequence
             DRB1_1201  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.1414
10826.4    90.00  0.54     Sequence
             DRB1_1201  382      TFKCYGVSPTKLNDL  VSPTKLNDL  6        0.1865
6643.6    80.00  0.34     Sequence
             DRB1_1201  383      FKCYGVSPTKLNDLC  VSPTKLNDL  5        0.1934
6166.6    75.00  0.28     Sequence
             DRB1_1201  384      KCYGVSPTKLNDLCF  PTKLNDLCF  6        0.2852
2285.6    55.00  0.63     Sequence
             DRB1_1201  385      CYGVSPTKLNDLCFT  PTKLNDLCF  5        0.2889
2195.0    50.00  0.61     Sequence
             DRB1_1201  386      YGVSPTKLNDLCFTN  PTKLNDLCF  4        0.2983
1983.6    48.00  0.57     Sequence
             DRB1_1201  387      GVSPTKLNDLCFTNV  LNDLCFTNV  6        0.3543
1081.5    34.00  0.41     Sequence
             DRB1_1201  388      VSPTKLNDLCFTNVY  LNDLCFTNV  5        0.3848
777.6    27.00  0.42     Sequence
             DRB1_1201  389      SPTKLNDLCFTNVYA  LNDLCFTNV  4        0.3727
886.7    30.00  0.44     Sequence
             DRB1_1201  390      PTKLNDLCFTNVYAD  LNDLCFTNV  3        0.3631
983.1    32.00  0.44     Sequence
             DRB1_1201  391      TKLNDLCFTNVYADS  LNDLCFTNV  2        0.3305
1400.0    39.00  0.49     Sequence
             DRB1_1201  392      KLNDLCFTNVYADSF  FTNVYADSF  6        0.3396
1268.1    37.00  0.25     Sequence
```

```
             DRB1_1201  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.3144
1666.3    43.00  0.30     Sequence
             DRB1_1201  394      NDLCFTNVYADSFVI  FTNVYADSF  4        0.2800
2416.7    55.00  0.36     Sequence
             DRB1_1201  395      DLCFTNVYADSFVIR  FTNVYADSF  3        0.2713
2656.8    55.00  0.32     Sequence
             DRB1_1201  396      LCFTNVYADSFVIRG  FTNVYADSF  2        0.2472
3445.2    65.00  0.41     Sequence
             DRB1_1201  397      CFTNVYADSFVIRGD  VYADSFVIR  4        0.2218
4535.1    70.00  0.37     Sequence
             DRB1_1201  398      FTNVYADSFVIRGDE  VYADSFVIR  3        0.1975
5901.1    75.00  0.40     Sequence
             DRB1_1201  399      TNVYADSFVIRGDEV  VYADSFVIR  2        0.1762
7433.7    80.00  0.43     Sequence
             DRB1_1201  400      NVYADSFVIRGDEVR  VYADSFVIR  1        0.1697
7972.6    80.00  0.32     Sequence
             DRB1_1201  401      VYADSFVIRGDEVRQ  VIRGDEVRQ  6        0.1934
6171.7    75.00  0.28     Sequence
             DRB1_1201  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.2588
3038.7    60.00  0.56     Sequence
             DRB1_1201  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.2702
2687.8    55.00  0.57     Sequence
             DRB1_1201  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.2685
2736.4    55.00  0.58     Sequence
             DRB1_1201  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.2620
2936.8    60.00  0.56     Sequence
             DRB1_1201  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.2659
2814.1    60.00  0.53     Sequence
             DRB1_1201  407      VIRGDEVRQIAPGQT  VRQIAPGQT  6        0.2657
2821.8    60.00  0.34     Sequence
             DRB1_1201  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.2251
4378.8    70.00  0.47     Sequence
             DRB1_1201  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.1718
7795.6    80.00  0.74     Sequence
             DRB1_1201  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.2123
5026.5    70.00  0.47     Sequence
             DRB1_1201  411      DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.2083
5251.8    75.00  0.47     Sequence
             DRB1_1201  412      EVRQIAPGQTGTIAD  IAPGQTGTI  4        0.1785
7249.9    80.00  0.46     Sequence
             DRB1_1201  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.1701
7940.6    80.00  0.51     Sequence
             DRB1_1201  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.1513
9730.1    85.00  0.57     Sequence
             DRB1_1201  415      QIAPGQTGTIADYNY  TGTIADYNY  6        0.1779
7295.2    80.00  0.36     Sequence
             DRB1_1201  416      IAPGQTGTIADYNYK  TGTIADYNY  5        0.1639
8488.0    85.00  0.41     Sequence
             DRB1_1201  417      APGQTGTIADYNYKL  TGTIADYNY  4        0.1771
7359.4    80.00  0.39     Sequence
             DRB1_1201  418      PGQTGTIADYNYKLP  TGTIADYNY  3        0.1850
6757.9    80.00  0.31     Sequence
             DRB1_1201  419      GQTGTIADYNYKLPD  TGTIADYNY  2        0.1865
6647.2    80.00  0.30     Sequence
             DRB1_1201  420      QTGTIADYNYKLPDD  TGTIADYNY  1        0.1820
6975.9    80.00  0.28     Sequence
             DRB1_1201  421      TGTIADYNYKLPDDF  IADYNYKLP  3        0.1899
6407.2    75.00  0.22     Sequence
             DRB1_1201  422      GTIADYNYKLPDDFT  IADYNYKLP  2        0.1703
7924.2    80.00  0.23     Sequence
             DRB1_1201  423      TIADYNYKLPDDFTG  NYKLPDDFT  5        0.1449
10424.2    85.00  0.20     Sequence
             DRB1_1201  424      IADYNYKLPDDFTGC  NYKLPDDFT  4        0.1149
14429.8    95.00  0.32     Sequence
             DRB1_1201  425      ADYNYKLPDDFTGCV  NYKLPDDFT  3        0.0953
17831.0    95.00  0.40     Sequence
```

```
             DRB1_1201  426      DYNYKLPDDFTGCVI  NYKLPDDFT  2        0.1015
16669.5    95.00  0.32     Sequence
             DRB1_1201  427      YNYKLPDDFTGCVIA  PDDFTGCVI  5        0.0862
19681.4    95.00  0.31     Sequence
             DRB1_1201  428      NYKLPDDFTGCVIAW  FTGCVIAWX  7        0.1226
13272.3    90.00  0.23     Sequence
             DRB1_1201  429      YKLPDDFTGCVIAWN  FTGCVIAWN  6        0.1345
11666.7    90.00  0.34     Sequence
             DRB1_1201  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.1352
11583.0    90.00  0.35     Sequence
             DRB1_1201  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.1344
11684.5    90.00  0.35     Sequence
             DRB1_1201  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.1501
9852.2    85.00  0.31     Sequence
             DRB1_1201  433      DDFTGCVIAWNSNNL  VIAWNSNNL  6        0.2735
2592.2    55.00  0.50     Sequence
             DRB1_1201  434      DFTGCVIAWNSNNLD  VIAWNSNNL  5        0.2873
2233.8    50.00  0.43     Sequence
             DRB1_1201  435      FTGCVIAWNSNNLDS  VIAWNSNNL  4        0.2814
2379.6    55.00  0.45     Sequence
             DRB1_1201  436      TGCVIAWNSNNLDSK  VIAWNSNNL  3        0.2822
2360.1    55.00  0.45     Sequence
             DRB1_1201  437      GCVIAWNSNNLDSKV  VIAWNSNNL  2        0.2792
2438.5    55.00  0.42     Sequence
             DRB1_1201  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2        0.2727
2616.8    55.00  0.39     Sequence
             DRB1_1201  439      VIAWNSNNLDSKVGG  IAWNSNNLD  1        0.2094
5188.4    70.00  0.31     Sequence
             DRB1_1201  440      IAWNSNNLDSKVGGN  SNNLDSKVG  4        0.1134
14658.1    95.00  0.40     Sequence
             DRB1_1201  441      AWNSNNLDSKVGGNY  LDSKVGGNY  6        0.2343
3964.8    65.00  0.56     Sequence
             DRB1_1201  442      WNSNNLDSKVGGNYN  LDSKVGGNY  5        0.2449
3534.7    65.00  0.57     Sequence
             DRB1_1201  443      NSNNLDSKVGGNYNY  LDSKVGGNY  4        0.2761
2520.6    55.00  0.46     Sequence
             DRB1_1201  444      SNNLDSKVGGNYNYL  LDSKVGGNY  3        0.2964
2023.5    48.00  0.42     Sequence
             DRB1_1201  445      NNLDSKVGGNYNYLY  VGGNYNYLY  6        0.3674
938.6    31.00  0.41     Sequence
             DRB1_1201  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.3600
1017.1    33.00  0.43     Sequence
             DRB1_1201  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4        0.3742
872.5    29.00  0.43     Sequence
             DRB1_1201  448      DSKVGGNYNYLYRLF  VGGNYNYLY  3        0.3912
725.9    26.00  0.46     Sequence
             DRB1_1201  449      SKVGGNYNYLYRLFR  VGGNYNYLY  2        0.3903
732.6    26.00  0.42     Sequence
             DRB1_1201  450      KVGGNYNYLYRLFRK  VGGNYNYLY  1        0.3799
819.8    28.00  0.40     Sequence
             DRB1_1201  451      VGGNYNYLYRLFRKS  YNYLYRLFR  4        0.3596
1021.7    33.00  0.23     Sequence
             DRB1_1201  452      GGNYNYLYRLFRKSN  LYRLFRKSN  6        0.3625
989.4    32.00  0.61     Sequence
             DRB1_1201  453      GNYNYLYRLFRKSNL  LYRLFRKSN  5        0.4189
537.6    21.00  0.47     Sequence
             DRB1_1201  454      NYNYLYRLFRKSNLK  LYRLFRKSN  4        0.4097
594.2    22.00  0.49     Sequence
             DRB1_1201  455      YNYLYRLFRKSNLKP  LYRLFRKSN  3        0.4136
569.2    22.00  0.45     Sequence
             DRB1_1201  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6        0.4922
243.4    10.00  0.37     Sequence
             DRB1_1201  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.4796
278.9    12.00  0.41     Sequence
             DRB1_1201  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.4605
343.0    14.00  0.41     Sequence
```

```
             DRB1_1201  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.4321
466.1    18.00  0.50     Sequence
             DRB1_1201  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.4123
577.4    22.00  0.50     Sequence
             DRB1_1201  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.3691
921.4    31.00  0.49     Sequence
             DRB1_1201  462      FRKSNLKPFERDIST  FRKSNLKPF  0        0.3089
1768.8    45.00  0.44     Sequence
             DRB1_1201  463      RKSNLKPFERDISTE  LKPFERDIS  4        0.1305
12184.8    90.00  0.33     Sequence
             DRB1_1201  464      KSNLKPFERDISTEI  LKPFERDIS  3        0.1287
12422.9    90.00  0.37     Sequence
             DRB1_1201  465      SNLKPFERDISTEIY  ERDISTEIY  6        0.1685
8071.9    80.00  0.32     Sequence
             DRB1_1201  466      NLKPFERDISTEIYQ  ERDISTEIY  5        0.1637
8503.8    85.00  0.28     Sequence
             DRB1_1201  467      LKPFERDISTEIYQA  ERDISTEIY  4        0.1671
8200.7    80.00  0.23     Sequence
             DRB1_1201  468      KPFERDISTEIYQAG  ISTEIYQAG  6        0.1764
7411.8    80.00  0.32     Sequence
             DRB1_1201  469      PFERDISTEIYQAGS  ISTEIYQAG  5        0.1724
7739.1    80.00  0.35     Sequence
             DRB1_1201  470      FERDISTEIYQAGST  ISTEIYQAG  4        0.1701
7940.1    80.00  0.34     Sequence
             DRB1_1201  471      ERDISTEIYQAGSTP  ISTEIYQAG  3        0.1588
8969.4    85.00  0.34     Sequence
             DRB1_1201  472      RDISTEIYQAGSTPC  IYQAGSTPC  6        0.2154
4864.1    70.00  0.60     Sequence
             DRB1_1201  473      DISTEIYQAGSTPCN  IYQAGSTPC  5        0.2080
5265.3    75.00  0.68     Sequence
             DRB1_1201  474      ISTEIYQAGSTPCNG  IYQAGSTPC  4        0.1866
6641.8    80.00  0.73     Sequence
             DRB1_1201  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.1781
7283.0    80.00  0.82     Sequence
             DRB1_1201  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.1679
8131.1    80.00  0.83     Sequence
             DRB1_1201  477      EIYQAGSTPCNGVKG  IYQAGSTPC  1        0.1356
11530.1    90.00  0.64     Sequence
             DRB1_1201  478      IYQAGSTPCNGVKGF  IYQAGSTPC  0        0.1083
15492.2    95.00  0.46     Sequence
             DRB1_1201  479      YQAGSTPCNGVKGFN  PCNGVKGFN  6        0.0437
31151.5   100.00  0.20     Sequence
             DRB1_1201  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.0987
17194.5    95.00  0.57     Sequence
             DRB1_1201  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.1309
12134.5    90.00  0.47     Sequence
             DRB1_1201  482      GSTPCNGVKGFNCYF  GVKGFNCYF  6        0.2477
3428.2    65.00  0.41     Sequence
             DRB1_1201  483      STPCNGVKGFNCYFP  VKGFNCYFP  6        0.2790
2442.3    55.00  0.48     Sequence
             DRB1_1201  484      TPCNGVKGFNCYFPL  VKGFNCYFP  5        0.2901
2167.4    50.00  0.46     Sequence
             DRB1_1201  485      PCNGVKGFNCYFPLQ  VKGFNCYFP  4        0.2836
2325.2    55.00  0.47     Sequence
             DRB1_1201  486      CNGVKGFNCYFPLQS  VKGFNCYFP  3        0.2747
2560.7    55.00  0.47     Sequence
             DRB1_1201  487      NGVKGFNCYFPLQSY  VKGFNCYFP  2        0.2957
2039.5    48.00  0.40     Sequence
             DRB1_1201  488      GVKGFNCYFPLQSYG  VKGFNCYFP  1        0.2870
2241.4    50.00  0.29     Sequence
             DRB1_1201  489      VKGFNCYFPLQSYGF  YFPLQSYGF  6        0.5541
124.6     5.00  0.71     Sequence          WB
             DRB1_1201  490      KGFNCYFPLQSYGFQ  YFPLQSYGF  5        0.5456
136.6     5.50  0.69     Sequence          WB
             DRB1_1201  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.5321
158.0     6.50  0.69     Sequence          WB
```

```
             DRB1_1201  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.5278
165.6     6.50  0.69     Sequence         WB
             DRB1_1201  493      NCYFPLQSYGFQPTY  YFPLQSYGF  2        0.5185
183.1     7.50  0.67     Sequence         WB
             DRB1_1201  494      CYFPLQSYGFQPTYG  YFPLQSYGF  1        0.4654
325.1    14.00  0.56     Sequence
             DRB1_1201  495      YFPLQSYGFQPTYGV  YFPLQSYGF  0        0.4004
657.0    24.00  0.50     Sequence
             DRB1_1201  496      FPLQSYGFQPTYGVG  LQSYGFQPT  2        0.1801
7124.3    80.00  0.39     Sequence
             DRB1_1201  497      PLQSYGFQPTYGVGY  FQPTYGVGY  6        0.1803
7105.0    80.00  0.36     Sequence
             DRB1_1201  498      LQSYGFQPTYGVGYQ  FQPTYGVGY  5        0.1653
8364.5    85.00  0.38     Sequence
             DRB1_1201  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4        0.1497
9896.2    85.00  0.45     Sequence
             DRB1_1201  500      SYGFQPTYGVGYQPY  TYGVGYQPY  6        0.2054
5415.7    75.00  0.41     Sequence
             DRB1_1201  501      YGFQPTYGVGYQPYR  TYGVGYQPY  5        0.1987
5823.2    75.00  0.43     Sequence
             DRB1_1201  502      GFQPTYGVGYQPYRV  TYGVGYQPY  4        0.2083
5251.4    75.00  0.35     Sequence
             DRB1_1201  503      FQPTYGVGYQPYRVV  TYGVGYQPY  3        0.2200
4624.0    70.00  0.32     Sequence
             DRB1_1201  504      QPTYGVGYQPYRVVV  TYGVGYQPY  2        0.2150
4883.8    70.00  0.34     Sequence
             DRB1_1201  505      PTYGVGYQPYRVVVL  VGYQPYRVV  4        0.2241
4424.6    70.00  0.26     Sequence
             DRB1_1201  506      TYGVGYQPYRVVVLS  VGYQPYRVV  3        0.2143
4918.0    70.00  0.26     Sequence
             DRB1_1201  507      YGVGYQPYRVVVLSF  PYRVVVLSF  6        0.2804
2405.6    55.00  0.47     Sequence
             DRB1_1201  508      GVGYQPYRVVVLSFE  PYRVVVLSF  5        0.2795
2429.1    55.00  0.43     Sequence
             DRB1_1201  509      VGYQPYRVVVLSFEL  PYRVVVLSF  4        0.2962
2027.7    48.00  0.41     Sequence
             DRB1_1201  510      GYQPYRVVVLSFELL  PYRVVVLSF  3        0.3002
1942.1    47.00  0.37     Sequence
             DRB1_1201  511      YQPYRVVVLSFELLH  PYRVVVLSF  2        0.3139
1674.9    44.00  0.31     Sequence
             DRB1_1201  512      QPYRVVVLSFELLHA  VLSFELLHA  6        0.3454
1191.1    36.00  0.34     Sequence
             DRB1_1201  513      PYRVVVLSFELLHAP  VLSFELLHA  5        0.3611
1004.6    32.00  0.31     Sequence
             DRB1_1201  514      YRVVVLSFELLHAPA  SFELLHAPA  6        0.4383
435.9    18.00  0.28     Sequence
             DRB1_1201  515      RVVVLSFELLHAPAT  FELLHAPAT  6        0.4430
414.4    17.00  0.42     Sequence
             DRB1_1201  516      VVVLSFELLHAPATV  FELLHAPAT  5        0.4460
401.2    16.00  0.44     Sequence
             DRB1_1201  517      VVLSFELLHAPATVC  FELLHAPAT  4        0.4410
423.5    17.00  0.40     Sequence
             DRB1_1201  518      VLSFELLHAPATVCG  FELLHAPAT  3        0.4067
613.8    23.00  0.41     Sequence
             DRB1_1201  519      LSFELLHAPATVCGP  FELLHAPAT  2        0.3597
1020.6    33.00  0.50     Sequence
             DRB1_1201  520      SFELLHAPATVCGPK  FELLHAPAT  1        0.2627
2913.9    60.00  0.36     Sequence
             DRB1_1201  521      FELLHAPATVCGPKK  LLHAPATVC  2        0.1955
6028.9    75.00  0.47     Sequence
             DRB1_1201  522      ELLHAPATVCGPKKS  LLHAPATVC  1        0.1375
11296.1    90.00  0.48     Sequence
             DRB1_1201  523      LLHAPATVCGPKKST  LLHAPATVC  0        0.1029
16428.3    95.00  0.37     Sequence
             DRB1_1201  524      LHAPATVCGPKKSTN  VCGPKKSTN  6        0.0499
29133.8   100.00  0.24     Sequence
```

```
             DRB1_1201  525      HAPATVCGPKKSTNL  CGPKKSTNL  6        0.0960
17693.8    95.00  0.46     Sequence
             DRB1_1201  526      APATVCGPKKSTNLV  CGPKKSTNL  5        0.1108
15072.1    95.00  0.38     Sequence
             DRB1_1201  527      PATVCGPKKSTNLVK  CGPKKSTNL  4        0.1142
14526.8    95.00  0.38     Sequence
             DRB1_1201  528      ATVCGPKKSTNLVKN  CGPKKSTNL  3        0.1184
13892.5    90.00  0.37     Sequence
             DRB1_1201  529      TVCGPKKSTNLVKNK  CGPKKSTNL  2        0.1139
14585.2    95.00  0.36     Sequence
             DRB1_1201  530      VCGPKKSTNLVKNKC  STNLVKNKC  6        0.1356
11524.3    90.00  0.44     Sequence
             DRB1_1201  531      CGPKKSTNLVKNKCV  STNLVKNKC  5        0.1777
7310.1    80.00  0.34     Sequence
             DRB1_1201  532      GPKKSTNLVKNKCVN  LVKNKCVNX  7        0.2159
4836.8    70.00  0.31     Sequence
             DRB1_1201  533      PKKSTNLVKNKCVNF  LVKNKCVNF  6        0.4793
279.9    12.00  0.62     Sequence
             DRB1_1201  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.4813
273.8    12.00  0.60     Sequence
             DRB1_1201  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.5052
211.3     9.00  0.56     Sequence         WB
             DRB1_1201  536      STNLVKNKCVNFNFN  LVKNKCVNF  3        0.4954
235.0    10.00  0.57     Sequence
             DRB1_1201  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2        0.4787
281.5    12.00  0.58     Sequence
             DRB1_1201  538      NLVKNKCVNFNFNGL  LVKNKCVNF  1        0.4713
305.0    13.00  0.41     Sequence
             DRB1_1201  539      LVKNKCVNFNFNGLT  LVKNKCVNF  0        0.4166
551.4    21.00  0.34     Sequence
             DRB1_1201  540      VKNKCVNFNFNGLTG  CVNFNFNGL  4        0.2675
2766.8    60.00  0.33     Sequence
             DRB1_1201  541      KNKCVNFNFNGLTGT  CVNFNFNGL  3        0.2507
3318.3    60.00  0.34     Sequence
             DRB1_1201  542      NKCVNFNFNGLTGTG  CVNFNFNGL  2        0.2264
4318.5    70.00  0.41     Sequence
             DRB1_1201  543      KCVNFNFNGLTGTGV  FNGLTGTGV  6        0.3017
1910.3    47.00  0.50     Sequence
             DRB1_1201  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5        0.2937
2083.5    49.00  0.57     Sequence
             DRB1_1201  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.2716
2645.8    55.00  0.69     Sequence
             DRB1_1201  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3        0.2641
2869.5    60.00  0.73     Sequence
             DRB1_1201  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.2510
3306.2    60.00  0.74     Sequence
             DRB1_1201  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.2204
4606.9    70.00  0.55     Sequence
             DRB1_1201  549      FNGLTGTGVLTESNK  FNGLTGTGV  0        0.1858
6695.0    80.00  0.44     Sequence
             DRB1_1201  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.0968
17534.1    95.00  0.51     Sequence
             DRB1_1201  551      GLTGTGVLTESNKKF  VLTESNKKF  6        0.2892
2187.1    50.00  0.57     Sequence
             DRB1_1201  552      LTGTGVLTESNKKFL  VLTESNKKF  5        0.3226
1524.4    41.00  0.46     Sequence
             DRB1_1201  553      TGTGVLTESNKKFLP  VLTESNKKF  4        0.3126
1699.4    44.00  0.47     Sequence
             DRB1_1201  554      GTGVLTESNKKFLPF  VLTESNKKF  3        0.3413
1245.4    37.00  0.38     Sequence
             DRB1_1201  555      TGVLTESNKKFLPFQ  VLTESNKKF  2        0.3463
1179.2    36.00  0.37     Sequence
             DRB1_1201  556      GVLTESNKKFLPFQQ  VLTESNKKF  1        0.3415
1241.9    37.00  0.34     Sequence
             DRB1_1201  557      VLTESNKKFLPFQQF  KKFLPFQQF  6        0.4143
565.1    22.00  0.44     Sequence
```

```
             DRB1_1201  558      LTESNKKFLPFQQFG  KKFLPFQQF  5        0.3725
888.3    30.00  0.52     Sequence
             DRB1_1201  559      TESNKKFLPFQQFGR  KKFLPFQQF  4        0.3748
866.8    29.00  0.51     Sequence
             DRB1_1201  560      ESNKKFLPFQQFGRD  KKFLPFQQF  3        0.3687
925.2    31.00  0.51     Sequence
             DRB1_1201  561      SNKKFLPFQQFGRDI  KKFLPFQQF  2        0.3634
980.3    32.00  0.49     Sequence
             DRB1_1201  562      NKKFLPFQQFGRDIA  KKFLPFQQF  1        0.3391
1274.9    37.00  0.43     Sequence
             DRB1_1201  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.3022
1900.6    47.00  0.40     Sequence
             DRB1_1201  564      KFLPFQQFGRDIADT  FLPFQQFGR  1        0.1761
7438.3    80.00  0.49     Sequence
             DRB1_1201  565      FLPFQQFGRDIADTT  FQQFGRDIA  3        0.1358
11499.5    90.00  0.31     Sequence
             DRB1_1201  566      LPFQQFGRDIADTTD  FQQFGRDIA  2        0.0908
18723.3    95.00  0.49     Sequence
             DRB1_1201  567      PFQQFGRDIADTTDA  FQQFGRDIA  1        0.0538
27948.5   100.00  0.29     Sequence
             DRB1_1201  568      FQQFGRDIADTTDAV  FGRDIADTT  3        0.0597
26195.4   100.00  0.18     Sequence
             DRB1_1201  569      QQFGRDIADTTDAVR  ADTTDAVRX  7        0.0749
22227.5   100.00  0.30     Sequence
             DRB1_1201  570      QFGRDIADTTDAVRD  ADTTDAVRD  6        0.0835
20266.8    95.00  0.43     Sequence
             DRB1_1201  571      FGRDIADTTDAVRDP  ADTTDAVRD  5        0.0816
20668.5   100.00  0.43     Sequence
             DRB1_1201  572      GRDIADTTDAVRDPQ  ADTTDAVRD  4        0.0792
21219.3   100.00  0.44     Sequence
             DRB1_1201  573      RDIADTTDAVRDPQT  ADTTDAVRD  3        0.0808
20849.5   100.00  0.43     Sequence
             DRB1_1201  574      DIADTTDAVRDPQTL  ADTTDAVRD  2        0.0784
21410.7   100.00  0.38     Sequence
             DRB1_1201  575      IADTTDAVRDPQTLE  ADTTDAVRD  1        0.0630
25282.6   100.00  0.19     Sequence
             DRB1_1201  576      ADTTDAVRDPQTLEI  VRDPQTLEI  6        0.1055
15974.6    95.00  0.47     Sequence
             DRB1_1201  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5        0.1247
12971.8    90.00  0.44     Sequence
             DRB1_1201  578      TTDAVRDPQTLEILD  VRDPQTLEI  4        0.1414
10824.5    90.00  0.39     Sequence
             DRB1_1201  579      TDAVRDPQTLEILDI  PQTLEILDI  6        0.2465
3472.1    65.00  0.62     Sequence
             DRB1_1201  580      DAVRDPQTLEILDIT  PQTLEILDI  5        0.2782
2463.7    55.00  0.51     Sequence
             DRB1_1201  581      AVRDPQTLEILDITP  PQTLEILDI  4        0.3266
1459.5    40.00  0.40     Sequence
             DRB1_1201  582      VRDPQTLEILDITPC  LEILDITPC  6        0.3592
1025.5    33.00  0.55     Sequence
             DRB1_1201  583      RDPQTLEILDITPCS  LEILDITPC  5        0.3531
1096.1    34.00  0.57     Sequence
             DRB1_1201  584      DPQTLEILDITPCSF  ILDITPCSF  6        0.5343
154.3     6.00  0.46     Sequence         WB
             DRB1_1201  585      PQTLEILDITPCSFG  ILDITPCSF  5        0.5169
186.2     7.50  0.48     Sequence         WB
             DRB1_1201  586      QTLEILDITPCSFGG  ILDITPCSF  4        0.4963
232.8     9.50  0.48     Sequence         WB
             DRB1_1201  587      TLEILDITPCSFGGV  ILDITPCSF  3        0.4885
253.2    11.00  0.46     Sequence
             DRB1_1201  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.4629
333.9    14.00  0.50     Sequence
             DRB1_1201  589      EILDITPCSFGGVSV  ILDITPCSF  1        0.4276
489.3    19.00  0.49     Sequence
             DRB1_1201  590      ILDITPCSFGGVSVI  ILDITPCSF  0        0.3845
780.0    27.00  0.42     Sequence
```

```
             DRB1_1201  591      LDITPCSFGGVSVIT  ITPCSFGGV  2        0.2246
4401.8    70.00  0.47     Sequence
             DRB1_1201  592      DITPCSFGGVSVITP  FGGVSVITP  6        0.2056
5404.2    75.00  0.24     Sequence
             DRB1_1201  593      ITPCSFGGVSVITPG  FGGVSVITP  5        0.1772
7347.9    80.00  0.30     Sequence
             DRB1_1201  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.1405
10935.4    90.00  0.40     Sequence
             DRB1_1201  595      PCSFGGVSVITPGTN  VSVITPGTN  6        0.2027
5577.5    75.00  0.54     Sequence
             DRB1_1201  596      CSFGGVSVITPGTNT  VSVITPGTN  5        0.2005
5713.1    75.00  0.56     Sequence
             DRB1_1201  597      SFGGVSVITPGTNTS  VSVITPGTN  4        0.1729
7696.8    80.00  0.63     Sequence
             DRB1_1201  598      FGGVSVITPGTNTSN  VSVITPGTN  3        0.1717
7799.9    80.00  0.63     Sequence
             DRB1_1201  599      GGVSVITPGTNTSNQ  VSVITPGTN  2        0.1664
8264.9    80.00  0.64     Sequence
             DRB1_1201  600      GVSVITPGTNTSNQV  VSVITPGTN  1        0.1572
9128.9    85.00  0.50     Sequence
             DRB1_1201  601      VSVITPGTNTSNQVA  VSVITPGTN  0        0.1383
11191.8    90.00  0.38     Sequence
             DRB1_1201  602      SVITPGTNTSNQVAV  ITPGTNTSN  2        0.0940
18077.8    95.00  0.43     Sequence
             DRB1_1201  603      VITPGTNTSNQVAVL  TNTSNQVAV  5        0.0915
18575.8    95.00  0.29     Sequence
             DRB1_1201  604      ITPGTNTSNQVAVLY  TSNQVAVLY  6        0.2358
3899.3    65.00  0.57     Sequence
             DRB1_1201  605      TPGTNTSNQVAVLYQ  TSNQVAVLY  5        0.2370
3848.5    65.00  0.49     Sequence
             DRB1_1201  606      PGTNTSNQVAVLYQG  TSNQVAVLY  4        0.2538
3210.2    60.00  0.44     Sequence
             DRB1_1201  607      GTNTSNQVAVLYQGV  TSNQVAVLY  3        0.3132
1687.3    44.00  0.32     Sequence
             DRB1_1201  608      TNTSNQVAVLYQGVN  VAVLYQGVN  6        0.3822
799.5    28.00  0.58     Sequence
             DRB1_1201  609      NTSNQVAVLYQGVNC  VAVLYQGVN  5        0.3614
1001.4    32.00  0.58     Sequence
             DRB1_1201  610      TSNQVAVLYQGVNCT  VAVLYQGVN  4        0.3523
1105.0    34.00  0.61     Sequence
             DRB1_1201  611      SNQVAVLYQGVNCTE  VAVLYQGVN  3        0.3327
1366.5    39.00  0.63     Sequence
             DRB1_1201  612      NQVAVLYQGVNCTEV  VAVLYQGVN  2        0.3239
1503.5    41.00  0.61     Sequence
             DRB1_1201  613      QVAVLYQGVNCTEVP  VAVLYQGVN  1        0.2842
2309.4    55.00  0.44     Sequence
             DRB1_1201  614      VAVLYQGVNCTEVPV  LYQGVNCTE  3        0.2495
3360.4    60.00  0.35     Sequence
             DRB1_1201  615      AVLYQGVNCTEVPVA  LYQGVNCTE  2        0.1769
7377.2    80.00  0.42     Sequence
             DRB1_1201  616      VLYQGVNCTEVPVAI  LYQGVNCTE  1        0.1530
9554.5    85.00  0.34     Sequence
             DRB1_1201  617      LYQGVNCTEVPVAIH  CTEVPVAIH  6        0.1258
12824.0    90.00  0.19     Sequence
             DRB1_1201  618      YQGVNCTEVPVAIHA  CTEVPVAIH  5        0.0976
17398.4    95.00  0.31     Sequence
             DRB1_1201  619      QGVNCTEVPVAIHAD  CTEVPVAIH  4        0.0893
19016.5    95.00  0.29     Sequence
             DRB1_1201  620      GVNCTEVPVAIHADQ  CTEVPVAIH  3        0.1024
16512.4    95.00  0.22     Sequence
             DRB1_1201  621      VNCTEVPVAIHADQL  PVAIHADQL  6        0.1343
11698.0    90.00  0.38     Sequence
             DRB1_1201  622      NCTEVPVAIHADQLT  PVAIHADQL  5        0.1562
9227.9    85.00  0.34     Sequence
             DRB1_1201  623      CTEVPVAIHADQLTP  PVAIHADQL  4        0.1930
6197.3    75.00  0.26     Sequence
```

```
             DRB1_1201  624      TEVPVAIHADQLTPT  IHADQLTPT  6        0.2204
4606.3    70.00  0.42     Sequence
             DRB1_1201  625      EVPVAIHADQLTPTW  IHADQLTPT  5        0.2348
3941.6    65.00  0.46     Sequence
             DRB1_1201  626      VPVAIHADQLTPTWR  IHADQLTPT  4        0.2359
3896.6    65.00  0.44     Sequence
             DRB1_1201  627      PVAIHADQLTPTWRV  IHADQLTPT  3        0.2634
2892.2    60.00  0.38     Sequence
             DRB1_1201  628      VAIHADQLTPTWRVY  IHADQLTPT  2        0.3085
1776.1    45.00  0.26     Sequence
             DRB1_1201  629      AIHADQLTPTWRVYS  LTPTWRVYS  6        0.2968
2014.6    48.00  0.31     Sequence
             DRB1_1201  630      IHADQLTPTWRVYST  LTPTWRVYS  5        0.2818
2371.2    55.00  0.37     Sequence
             DRB1_1201  631      HADQLTPTWRVYSTG  LTPTWRVYS  4        0.2354
3916.2    65.00  0.41     Sequence
             DRB1_1201  632      ADQLTPTWRVYSTGS  LTPTWRVYS  3        0.2230
4477.0    70.00  0.44     Sequence
             DRB1_1201  633      DQLTPTWRVYSTGSN  LTPTWRVYS  2        0.1988
5815.8    75.00  0.47     Sequence
             DRB1_1201  634      QLTPTWRVYSTGSNV  LTPTWRVYS  1        0.1517
9683.0    85.00  0.38     Sequence
             DRB1_1201  635      LTPTWRVYSTGSNVF  VYSTGSNVF  6        0.2245
4406.4    70.00  0.58     Sequence
             DRB1_1201  636      TPTWRVYSTGSNVFQ  VYSTGSNVF  5        0.2092
5200.3    70.00  0.61     Sequence
             DRB1_1201  637      PTWRVYSTGSNVFQT  VYSTGSNVF  4        0.2046
5462.0    75.00  0.61     Sequence
             DRB1_1201  638      TWRVYSTGSNVFQTR  VYSTGSNVF  3        0.1981
5860.7    75.00  0.63     Sequence
             DRB1_1201  639      WRVYSTGSNVFQTRA  VYSTGSNVF  2        0.1884
6508.0    75.00  0.64     Sequence
             DRB1_1201  640      RVYSTGSNVFQTRAG  VYSTGSNVF  1        0.1639
8489.3    85.00  0.55     Sequence
             DRB1_1201  641      VYSTGSNVFQTRAGC  VYSTGSNVF  0        0.1276
12565.1    90.00  0.41     Sequence
             DRB1_1201  642      YSTGSNVFQTRAGCL  VFQTRAGCL  6        0.1167
14142.0    90.00  0.52     Sequence
             DRB1_1201  643      STGSNVFQTRAGCLI  FQTRAGCLI  6        0.2087
5224.9    70.00  0.52     Sequence
             DRB1_1201  644      TGSNVFQTRAGCLIG  FQTRAGCLI  5        0.1956
6023.9    75.00  0.51     Sequence
             DRB1_1201  645      GSNVFQTRAGCLIGA  FQTRAGCLI  4        0.1985
5836.3    75.00  0.46     Sequence
             DRB1_1201  646      SNVFQTRAGCLIGAE  FQTRAGCLI  3        0.2037
5520.2    75.00  0.47     Sequence
             DRB1_1201  647      NVFQTRAGCLIGAEY  FQTRAGCLI  2        0.2585
3050.2    60.00  0.30     Sequence
             DRB1_1201  648      VFQTRAGCLIGAEYV  AGCLIGAEY  5        0.2793
2434.3    55.00  0.30     Sequence
             DRB1_1201  649      FQTRAGCLIGAEYVN  AGCLIGAEY  4        0.3004
1937.5    47.00  0.27     Sequence
             DRB1_1201  650      QTRAGCLIGAEYVNN  AGCLIGAEY  3        0.2937
2084.5    49.00  0.31     Sequence
             DRB1_1201  651      TRAGCLIGAEYVNNS  IGAEYVNNS  6        0.2930
2100.1    49.00  0.20     Sequence
             DRB1_1201  652      RAGCLIGAEYVNNSY  IGAEYVNNS  5        0.3006
1933.9    47.00  0.23     Sequence
             DRB1_1201  653      AGCLIGAEYVNNSYE  IGAEYVNNS  4        0.2781
2468.4    55.00  0.26     Sequence
             DRB1_1201  654      GCLIGAEYVNNSYEC  IGAEYVNNS  3        0.2423
3632.6    65.00  0.32     Sequence
             DRB1_1201  655      CLIGAEYVNNSYECD  IGAEYVNNS  2        0.2224
4506.3    70.00  0.38     Sequence
             DRB1_1201  656      LIGAEYVNNSYECDI  EYVNNSYEC  4        0.1567
9174.4    85.00  0.25     Sequence
```

```
             DRB1_1201  657      IGAEYVNNSYECDIP  EYVNNSYEC  3        0.1117
14936.5    95.00  0.29     Sequence
             DRB1_1201  658      GAEYVNNSYECDIPI  VNNSYECDI  4        0.1126
14788.6    95.00  0.26     Sequence
             DRB1_1201  659      AEYVNNSYECDIPIG  VNNSYECDI  3        0.1081
15526.3    95.00  0.29     Sequence
             DRB1_1201  660      EYVNNSYECDIPIGA  VNNSYECDI  2        0.0980
17313.0    95.00  0.35     Sequence
             DRB1_1201  661      YVNNSYECDIPIGAG  VNNSYECDI  1        0.0716
23032.0   100.00  0.32     Sequence
             DRB1_1201  662      VNNSYECDIPIGAGI  NSYECDIPI  2        0.0733
22612.9   100.00  0.25     Sequence
             DRB1_1201  663      NNSYECDIPIGAGIC  DIPIGAGIC  6        0.1005
16852.1    95.00  0.38     Sequence
             DRB1_1201  664      NSYECDIPIGAGICA  IPIGAGICA  6        0.1277
12557.9    90.00  0.39     Sequence
             DRB1_1201  665      SYECDIPIGAGICAS  IPIGAGICA  5        0.1351
11589.7    90.00  0.38     Sequence
             DRB1_1201  666      YECDIPIGAGICASY  IGAGICASY  6        0.2597
3009.8    60.00  0.47     Sequence
             DRB1_1201  667      ECDIPIGAGICASYQ  IGAGICASY  5        0.2807
2399.2    55.00  0.38     Sequence
             DRB1_1201  668      CDIPIGAGICASYQT  IGAGICASY  4        0.2929
2101.0    49.00  0.36     Sequence
             DRB1_1201  669      DIPIGAGICASYQTQ  IGAGICASY  3        0.2986
1976.5    47.00  0.34     Sequence
             DRB1_1201  670      IPIGAGICASYQTQT  IGAGICASY  2        0.3001
1944.2    47.00  0.37     Sequence
             DRB1_1201  671      PIGAGICASYQTQTN  IGAGICASY  1        0.2675
2766.2    60.00  0.34     Sequence
             DRB1_1201  672      IGAGICASYQTQTNS  AGICASYQT  2        0.2426
3623.1    65.00  0.22     Sequence
             DRB1_1201  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.1463
10266.3    85.00  0.35     Sequence
             DRB1_1201  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.1251
12919.9    90.00  0.42     Sequence
             DRB1_1201  675      GICASYQTQTNSPRR  ICASYQTQT  1        0.0610
25839.0   100.00  0.34     Sequence
             DRB1_1201  676      ICASYQTQTNSPRRA  TQTNSPRRA  6        0.0451
30708.8   100.00  0.23     Sequence
             DRB1_1201  677      CASYQTQTNSPRRAR  TQTNSPRRA  5        0.0326
35156.8   100.00  0.29     Sequence
             DRB1_1201  678      ASYQTQTNSPRRARS  TQTNSPRRA  4        0.0313
35618.9   100.00  0.28     Sequence
             DRB1_1201  679      SYQTQTNSPRRARSV  NSPRRARSV  6        0.0550
27575.1   100.00  0.37     Sequence
             DRB1_1201  680      YQTQTNSPRRARSVA  NSPRRARSV  5        0.0606
25964.3   100.00  0.33     Sequence
             DRB1_1201  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.0722
22888.9   100.00  0.48     Sequence
             DRB1_1201  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.0731
22661.7   100.00  0.44     Sequence
             DRB1_1201  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.0740
22440.9   100.00  0.43     Sequence
             DRB1_1201  684      TNSPRRARSVASQSI  ARSVASQSI  6        0.1677
8142.2    80.00  0.56     Sequence
             DRB1_1201  685      NSPRRARSVASQSII  ARSVASQSI  5        0.1935
6161.1    75.00  0.54     Sequence
             DRB1_1201  686      SPRRARSVASQSIIA  ARSVASQSI  4        0.2309
4113.4    65.00  0.44     Sequence
             DRB1_1201  687      PRRARSVASQSIIAY  VASQSIIAY  6        0.4777
284.6    12.00  0.64     Sequence
             DRB1_1201  688      RRARSVASQSIIAYT  VASQSIIAY  5        0.4803
276.7    12.00  0.64     Sequence
             DRB1_1201  689      RARSVASQSIIAYTM  VASQSIIAY  4        0.5119
196.6     8.00  0.48     Sequence         WB
```

```
             DRB1_1201  690      ARSVASQSIIAYTMS  VASQSIIAY  3        0.4986
227.0     9.50  0.47     Sequence         WB
             DRB1_1201  691      RSVASQSIIAYTMSL  VASQSIIAY  2        0.4897
249.8    11.00  0.43     Sequence
             DRB1_1201  692      SVASQSIIAYTMSLG  SQSIIAYTM  3        0.4612
340.3    14.00  0.38     Sequence
             DRB1_1201  693      VASQSIIAYTMSLGA  SQSIIAYTM  2        0.4328
462.7    18.00  0.36     Sequence
             DRB1_1201  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.3353
1329.2    38.00  0.25     Sequence
             DRB1_1201  695      SQSIIAYTMSLGAEN  IAYTMSLGA  4        0.3131
1689.0    44.00  0.34     Sequence
             DRB1_1201  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.2935
2087.5    49.00  0.41     Sequence
             DRB1_1201  697      SIIAYTMSLGAENSV  IAYTMSLGA  2        0.2885
2204.0    50.00  0.39     Sequence
             DRB1_1201  698      IIAYTMSLGAENSVA  IAYTMSLGA  1        0.2814
2380.2    55.00  0.37     Sequence
             DRB1_1201  699      IAYTMSLGAENSVAY  LGAENSVAY  6        0.4211
525.2    20.00  0.59     Sequence
             DRB1_1201  700      AYTMSLGAENSVAYS  LGAENSVAY  5        0.3996
662.7    24.00  0.64     Sequence
             DRB1_1201  701      YTMSLGAENSVAYSN  LGAENSVAY  4        0.3950
696.6    25.00  0.66     Sequence
             DRB1_1201  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.3890
742.8    26.00  0.67     Sequence
             DRB1_1201  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.3726
887.8    30.00  0.69     Sequence
             DRB1_1201  704      SLGAENSVAYSNNSI  LGAENSVAY  1        0.3292
1418.9    40.00  0.56     Sequence
             DRB1_1201  705      LGAENSVAYSNNSIA  LGAENSVAY  0        0.2879
2219.8    50.00  0.51     Sequence
             DRB1_1201  706      GAENSVAYSNNSIAI  AYSNNSIAI  6        0.2258
4345.6    70.00  0.56     Sequence
             DRB1_1201  707      AENSVAYSNNSIAIP  AYSNNSIAI  5        0.2201
4619.7    70.00  0.56     Sequence
             DRB1_1201  708      ENSVAYSNNSIAIPT  AYSNNSIAI  4        0.2188
4688.1    70.00  0.51     Sequence
             DRB1_1201  709      NSVAYSNNSIAIPTN  AYSNNSIAI  3        0.2151
4876.1    70.00  0.51     Sequence
             DRB1_1201  710      SVAYSNNSIAIPTNF  AYSNNSIAI  2        0.2163
4816.6    70.00  0.48     Sequence
             DRB1_1201  711      VAYSNNSIAIPTNFT  AYSNNSIAI  1        0.2118
5052.7    70.00  0.38     Sequence
             DRB1_1201  712      AYSNNSIAIPTNFTI  IAIPTNFTI  6        0.2395
3747.3    65.00  0.41     Sequence
             DRB1_1201  713      YSNNSIAIPTNFTIS  IAIPTNFTI  5        0.2186
4696.4    70.00  0.49     Sequence
             DRB1_1201  714      SNNSIAIPTNFTISV  IAIPTNFTI  4        0.2401
3723.0    65.00  0.44     Sequence
             DRB1_1201  715      NNSIAIPTNFTISVT  IAIPTNFTI  3        0.2372
3840.8    65.00  0.46     Sequence
             DRB1_1201  716      NSIAIPTNFTISVTT  IAIPTNFTI  2        0.2279
4246.3    70.00  0.44     Sequence
             DRB1_1201  717      SIAIPTNFTISVTTE  IAIPTNFTI  1        0.2111
5091.6    70.00  0.39     Sequence
             DRB1_1201  718      IAIPTNFTISVTTEI  IPTNFTISV  2        0.1862
6667.9    80.00  0.25     Sequence
             DRB1_1201  719      AIPTNFTISVTTEIL  ISVTTEILX  7        0.1552
9321.2    85.00  0.19     Sequence
             DRB1_1201  720      IPTNFTISVTTEILP  ISVTTEILP  6        0.1666
8241.8    80.00  0.56     Sequence
             DRB1_1201  721      PTNFTISVTTEILPV  ISVTTEILP  5        0.1723
7753.4    80.00  0.56     Sequence
             DRB1_1201  722      TNFTISVTTEILPVS  ISVTTEILP  4        0.1885
6502.2    75.00  0.47     Sequence
```

```
             DRB1_1201  723      NFTISVTTEILPVSM  TTEILPVSM  6        0.2407
3698.3    65.00  0.31     Sequence
             DRB1_1201  724      FTISVTTEILPVSMT  TEILPVSMT  6        0.2581
3063.6    60.00  0.31     Sequence
             DRB1_1201  725      TISVTTEILPVSMTK  TEILPVSMT  5        0.2568
3106.1    60.00  0.33     Sequence
             DRB1_1201  726      ISVTTEILPVSMTKT  ILPVSMTKT  6        0.2746
2563.3    55.00  0.28     Sequence
             DRB1_1201  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.2515
3289.6    60.00  0.40     Sequence
             DRB1_1201  728      VTTEILPVSMTKTSV  ILPVSMTKT  4        0.2752
2546.8    55.00  0.30     Sequence
             DRB1_1201  729      TTEILPVSMTKTSVD  ILPVSMTKT  3        0.2559
3135.4    60.00  0.32     Sequence
             DRB1_1201  730      TEILPVSMTKTSVDC  ILPVSMTKT  2        0.2241
4424.2    70.00  0.41     Sequence
             DRB1_1201  731      EILPVSMTKTSVDCT  PVSMTKTSV  3        0.2026
5583.3    75.00  0.38     Sequence
             DRB1_1201  732      ILPVSMTKTSVDCTM  PVSMTKTSV  2        0.1897
6417.9    75.00  0.39     Sequence
             DRB1_1201  733      LPVSMTKTSVDCTMY  PVSMTKTSV  1        0.1753
7506.4    80.00  0.29     Sequence
             DRB1_1201  734      PVSMTKTSVDCTMYI  KTSVDCTMY  5        0.1632
8554.4    85.00  0.25     Sequence
             DRB1_1201  735      VSMTKTSVDCTMYIC  KTSVDCTMY  4        0.1652
8371.2    85.00  0.22     Sequence
             DRB1_1201  736      SMTKTSVDCTMYICG  KTSVDCTMY  3        0.1518
9670.7    85.00  0.25     Sequence
             DRB1_1201  737      MTKTSVDCTMYICGD  KTSVDCTMY  2        0.1443
10490.8    85.00  0.25     Sequence
             DRB1_1201  738      TKTSVDCTMYICGDS  SVDCTMYIC  3        0.1368
11377.4    90.00  0.23     Sequence
             DRB1_1201  739      KTSVDCTMYICGDST  DCTMYICGD  4        0.1447
10443.5    85.00  0.17     Sequence
             DRB1_1201  740      TSVDCTMYICGDSTE  MYICGDSTE  6        0.1383
11200.7    90.00  0.26     Sequence
             DRB1_1201  741      SVDCTMYICGDSTEC  MYICGDSTE  5        0.1262
12756.4    90.00  0.28     Sequence
             DRB1_1201  742      VDCTMYICGDSTECS  MYICGDSTE  4        0.1121
14872.8    95.00  0.38     Sequence
             DRB1_1201  743      DCTMYICGDSTECSN  MYICGDSTE  3        0.1005
16860.3    95.00  0.40     Sequence
             DRB1_1201  744      CTMYICGDSTECSNL  MYICGDSTE  2        0.1018
16614.5    95.00  0.40     Sequence
             DRB1_1201  745      TMYICGDSTECSNLL  DSTECSNLL  6        0.0972
17469.2    95.00  0.23     Sequence
             DRB1_1201  746      MYICGDSTECSNLLL  STECSNLLL  6        0.1226
13271.7    90.00  0.44     Sequence
             DRB1_1201  747      YICGDSTECSNLLLQ  STECSNLLL  5        0.1106
15108.7    95.00  0.46     Sequence
             DRB1_1201  748      ICGDSTECSNLLLQY  ECSNLLLQY  6        0.2502
3336.5    60.00  0.32     Sequence
             DRB1_1201  749      CGDSTECSNLLLQYG  CSNLLLQYG  6        0.3066
1812.4    45.00  0.43     Sequence
             DRB1_1201  750      GDSTECSNLLLQYGS  SNLLLQYGS  6        0.3224
1526.9    41.00  0.39     Sequence
             DRB1_1201  751      DSTECSNLLLQYGSF  NLLLQYGSF  6        0.3994
664.2    24.00  0.29     Sequence
             DRB1_1201  752      STECSNLLLQYGSFC  SNLLLQYGS  4        0.3830
793.4    28.00  0.25     Sequence
             DRB1_1201  753      TECSNLLLQYGSFCT  SNLLLQYGS  3        0.3769
847.3    29.00  0.25     Sequence
             DRB1_1201  754      ECSNLLLQYGSFCTQ  SNLLLQYGS  2        0.3603
1013.8    32.00  0.22     Sequence
             DRB1_1201  755      CSNLLLQYGSFCTQL  NLLLQYGSF  2        0.3040
1863.5    46.00  0.31     Sequence
```

```
             DRB1_1201  756      SNLLLQYGSFCTQLN  NLLLQYGSF  1        0.2686
2733.6    55.00  0.30     Sequence
             DRB1_1201  757      NLLLQYGSFCTQLNR  LQYGSFCTQ  3        0.2377
3818.1    65.00  0.25     Sequence
             DRB1_1201  758      LLLQYGSFCTQLNRA  LQYGSFCTQ  2        0.1581
9035.4    85.00  0.46     Sequence
             DRB1_1201  759      LLQYGSFCTQLNRAL  FCTQLNRAL  6        0.1793
7185.8    80.00  0.28     Sequence
             DRB1_1201  760      LQYGSFCTQLNRALT  CTQLNRALT  6        0.3060
1824.5    46.00  0.62     Sequence
             DRB1_1201  761      QYGSFCTQLNRALTG  CTQLNRALT  5        0.2996
1954.5    47.00  0.55     Sequence
             DRB1_1201  762      YGSFCTQLNRALTGI  CTQLNRALT  4        0.3265
1460.9    40.00  0.50     Sequence
             DRB1_1201  763      GSFCTQLNRALTGIA  CTQLNRALT  3        0.3314
1386.1    39.00  0.42     Sequence
             DRB1_1201  764      SFCTQLNRALTGIAV  NRALTGIAV  6        0.4411
422.9    17.00  0.51     Sequence
             DRB1_1201  765      FCTQLNRALTGIAVE  NRALTGIAV  5        0.4218
521.1    20.00  0.55     Sequence
             DRB1_1201  766      CTQLNRALTGIAVEQ  NRALTGIAV  4        0.4240
508.7    20.00  0.56     Sequence
             DRB1_1201  767      TQLNRALTGIAVEQD  NRALTGIAV  3        0.4039
632.8    23.00  0.58     Sequence
             DRB1_1201  768      QLNRALTGIAVEQDK  NRALTGIAV  2        0.3891
742.4    26.00  0.58     Sequence
             DRB1_1201  769      LNRALTGIAVEQDKN  NRALTGIAV  1        0.3563
1058.3    33.00  0.47     Sequence
             DRB1_1201  770      NRALTGIAVEQDKNT  LTGIAVEQD  3        0.3097
1753.0    45.00  0.47     Sequence
             DRB1_1201  771      RALTGIAVEQDKNTQ  LTGIAVEQD  2        0.2312
4098.2    65.00  0.72     Sequence
             DRB1_1201  772      ALTGIAVEQDKNTQE  LTGIAVEQD  1        0.1816
7010.4    80.00  0.50     Sequence
             DRB1_1201  773      LTGIAVEQDKNTQEV  IAVEQDKNT  3        0.1213
13460.5    90.00  0.28     Sequence
             DRB1_1201  774      TGIAVEQDKNTQEVF  VEQDKNTQE  4        0.1107
15101.2    95.00  0.25     Sequence
             DRB1_1201  775      GIAVEQDKNTQEVFA  VEQDKNTQE  3        0.1075
15620.1    95.00  0.27     Sequence
             DRB1_1201  776      IAVEQDKNTQEVFAQ  VEQDKNTQE  2        0.1011
16751.9    95.00  0.28     Sequence
             DRB1_1201  777      AVEQDKNTQEVFAQV  NTQEVFAQV  6        0.0820
20588.4   100.00  0.26     Sequence
             DRB1_1201  778      VEQDKNTQEVFAQVK  TQEVFAQVK  6        0.0817
20651.7   100.00  0.25     Sequence
             DRB1_1201  779      EQDKNTQEVFAQVKQ  TQEVFAQVK  5        0.0849
19946.8    95.00  0.25     Sequence
             DRB1_1201  780      QDKNTQEVFAQVKQI  TQEVFAQVK  4        0.1236
13130.1    90.00  0.16     Sequence
             DRB1_1201  781      DKNTQEVFAQVKQIY  VFAQVKQIY  6        0.3727
886.2    30.00  0.56     Sequence
             DRB1_1201  782      KNTQEVFAQVKQIYK  FAQVKQIYK  6        0.3801
818.7    28.00  0.47     Sequence
             DRB1_1201  783      NTQEVFAQVKQIYKT  FAQVKQIYK  5        0.3907
729.7    26.00  0.44     Sequence
             DRB1_1201  784      TQEVFAQVKQIYKTP  FAQVKQIYK  4        0.4070
611.9    23.00  0.34     Sequence
             DRB1_1201  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.4110
585.9    22.00  0.28     Sequence
             DRB1_1201  786      EVFAQVKQIYKTPPI  VKQIYKTPP  5        0.4145
563.8    22.00  0.37     Sequence
             DRB1_1201  787      VFAQVKQIYKTPPIK  VKQIYKTPP  4        0.3974
678.9    25.00  0.40     Sequence
             DRB1_1201  788      FAQVKQIYKTPPIKD  VKQIYKTPP  3        0.3459
1185.3    36.00  0.49     Sequence
```

```
             DRB1_1201  789      AQVKQIYKTPPIKDF  VKQIYKTPP  2        0.3448
1198.5    36.00  0.43     Sequence
             DRB1_1201  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.2932
2095.1    49.00  0.43     Sequence
             DRB1_1201  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.2484
3400.7    60.00  0.55     Sequence
             DRB1_1201  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.2195
4648.6    70.00  0.60     Sequence
             DRB1_1201  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.1714
7829.7    80.00  0.42     Sequence
             DRB1_1201  794      IYKTPPIKDFGGFNF  IKDFGGFNF  6        0.3946
699.2    25.00  0.64     Sequence
             DRB1_1201  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.3818
803.0    28.00  0.64     Sequence
             DRB1_1201  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.3703
910.0    30.00  0.65     Sequence
             DRB1_1201  797      TPPIKDFGGFNFSQI  IKDFGGFNF  3        0.3876
754.6    27.00  0.55     Sequence
             DRB1_1201  798      PPIKDFGGFNFSQIL  IKDFGGFNF  2        0.3814
806.4    28.00  0.51     Sequence
             DRB1_1201  799      PIKDFGGFNFSQILP  IKDFGGFNF  1        0.3786
831.9    29.00  0.44     Sequence
             DRB1_1201  800      IKDFGGFNFSQILPD  IKDFGGFNF  0        0.3381
1288.4    38.00  0.34     Sequence
             DRB1_1201  801      KDFGGFNFSQILPDP  FGGFNFSQI  2        0.2181
4721.1    70.00  0.41     Sequence
             DRB1_1201  802      DFGGFNFSQILPDPS  FGGFNFSQI  1        0.2165
4806.9    70.00  0.33     Sequence
             DRB1_1201  803      FGGFNFSQILPDPSK  FSQILPDPS  5        0.2156
4850.8    70.00  0.22     Sequence
             DRB1_1201  804      GGFNFSQILPDPSKP  FSQILPDPS  4        0.1809
7063.2    80.00  0.28     Sequence
             DRB1_1201  805      GFNFSQILPDPSKPS  FSQILPDPS  3        0.1935
6164.1    75.00  0.28     Sequence
             DRB1_1201  806      FNFSQILPDPSKPSK  FSQILPDPS  2        0.1857
6706.5    80.00  0.31     Sequence
             DRB1_1201  807      NFSQILPDPSKPSKR  SQILPDPSK  2        0.1522
9635.5    85.00  0.37     Sequence
             DRB1_1201  808      FSQILPDPSKPSKRS  ILPDPSKPS  3        0.1176
14013.9    90.00  0.42     Sequence
             DRB1_1201  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.1057
15939.8    95.00  0.41     Sequence
             DRB1_1201  810      QILPDPSKPSKRSFI  ILPDPSKPS  1        0.1013
16701.0    95.00  0.25     Sequence
             DRB1_1201  811      ILPDPSKPSKRSFIE  PSKRSFIEX  7        0.1098
15244.0    95.00  0.22     Sequence
             DRB1_1201  812      LPDPSKPSKRSFIED  PSKRSFIED  6        0.0967
17560.7    95.00  0.32     Sequence
             DRB1_1201  813      PDPSKPSKRSFIEDL  PSKRSFIED  5        0.1097
15261.3    95.00  0.30     Sequence
             DRB1_1201  814      DPSKPSKRSFIEDLL  KRSFIEDLL  6        0.1408
10901.2    90.00  0.28     Sequence
             DRB1_1201  815      PSKPSKRSFIEDLLF  RSFIEDLLF  6        0.1835
6868.7    80.00  0.40     Sequence
             DRB1_1201  816      SKPSKRSFIEDLLFN  RSFIEDLLF  5        0.2043
5483.4    75.00  0.34     Sequence
             DRB1_1201  817      KPSKRSFIEDLLFNK  IEDLLFNKX  7        0.2457
3502.6    65.00  0.26     Sequence
             DRB1_1201  818      PSKRSFIEDLLFNKV  IEDLLFNKV  6        0.4024
643.0    24.00  0.68     Sequence
             DRB1_1201  819      SKRSFIEDLLFNKVT  IEDLLFNKV  5        0.4075
608.4    23.00  0.65     Sequence
             DRB1_1201  820      KRSFIEDLLFNKVTL  IEDLLFNKV  4        0.4325
464.0    18.00  0.60     Sequence
             DRB1_1201  821      RSFIEDLLFNKVTLA  IEDLLFNKV  3        0.4311
471.1    19.00  0.55     Sequence
```

```
            DRB1_1201  822      SFIEDLLFNKVTLAD  IEDLLFNKV  2        0.4320
466.6    19.00  0.50     Sequence
            DRB1_1201  823      FIEDLLFNKVTLADA  IEDLLFNKV  1        0.4136
569.5    22.00  0.35     Sequence
            DRB1_1201  824      IEDLLFNKVTLADAG  FNKVTLADA  5        0.3771
845.4    29.00  0.30     Sequence
            DRB1_1201  825      EDLLFNKVTLADAGF  FNKVTLADA  4        0.3649
964.1    31.00  0.29     Sequence
            DRB1_1201  826      DLLFNKVTLADAGFI  FNKVTLADA  3        0.3776
840.9    29.00  0.25     Sequence
            DRB1_1201  827      LLFNKVTLADAGFIK  FNKVTLADA  2        0.3629
986.0    32.00  0.27     Sequence
            DRB1_1201  828      LFNKVTLADAGFIKQ  VTLADAGFI  4        0.3315
1384.6    39.00  0.32     Sequence
            DRB1_1201  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.3097
1752.7    45.00  0.32     Sequence
            DRB1_1201  830      NKVTLADAGFIKQYG  VTLADAGFI  2        0.2940
2078.0    49.00  0.32     Sequence
            DRB1_1201  831      KVTLADAGFIKQYGD  VTLADAGFI  1        0.2707
2673.9    55.00  0.29     Sequence
            DRB1_1201  832      VTLADAGFIKQYGDC  LADAGFIKQ  2        0.2067
5342.8    75.00  0.24     Sequence
            DRB1_1201  833      TLADAGFIKQYGDCL  AGFIKQYGD  4        0.1761
7442.5    80.00  0.26     Sequence
            DRB1_1201  834      LADAGFIKQYGDCLG  AGFIKQYGD  3        0.1716
7810.6    80.00  0.28     Sequence
            DRB1_1201  835      ADAGFIKQYGDCLGD  AGFIKQYGD  2        0.1535
9501.8    85.00  0.29     Sequence
            DRB1_1201  836      DAGFIKQYGDCLGDI  IKQYGDCLG  4        0.1528
9568.5    85.00  0.23     Sequence
            DRB1_1201  837      AGFIKQYGDCLGDIA  IKQYGDCLG  3        0.1462
10279.7    85.00  0.26     Sequence
            DRB1_1201  838      GFIKQYGDCLGDIAA  IKQYGDCLG  2        0.1426
10690.8    85.00  0.28     Sequence
            DRB1_1201  839      FIKQYGDCLGDIAAR  GDCLGDIAA  5        0.1281
12506.8    90.00  0.17     Sequence
            DRB1_1201  840      IKQYGDCLGDIAARD  LGDIAARDX  7        0.1447
10443.9    85.00  0.21     Sequence
            DRB1_1201  841      KQYGDCLGDIAARDL  LGDIAARDL  6        0.1989
5810.3    75.00  0.61     Sequence
            DRB1_1201  842      QYGDCLGDIAARDLI  LGDIAARDL  5        0.2066
5345.7    75.00  0.61     Sequence
            DRB1_1201  843      YGDCLGDIAARDLIC  LGDIAARDL  4        0.2021
5617.2    75.00  0.56     Sequence
            DRB1_1201  844      GDCLGDIAARDLICA  LGDIAARDL  3        0.2204
4604.9    70.00  0.41     Sequence
            DRB1_1201  845      DCLGDIAARDLICAQ  LGDIAARDL  2        0.2220
4525.2    70.00  0.39     Sequence
            DRB1_1201  846      CLGDIAARDLICAQK  IAARDLICA  4        0.2126
5011.5    70.00  0.31     Sequence
            DRB1_1201  847      LGDIAARDLICAQKF  RDLICAQKF  6        0.2738
2584.1    55.00  0.41     Sequence
            DRB1_1201  848      GDIAARDLICAQKFN  RDLICAQKF  5        0.3200
1568.2    42.00  0.40     Sequence
            DRB1_1201  849      DIAARDLICAQKFNG  ICAQKFNGX  7        0.3699
914.2    30.00  0.29     Sequence
            DRB1_1201  850      IAARDLICAQKFNGL  ICAQKFNGL  6        0.4242
507.6    20.00  0.47     Sequence
            DRB1_1201  851      AARDLICAQKFNGLT  ICAQKFNGL  5        0.4276
489.6    19.00  0.48     Sequence
            DRB1_1201  852      ARDLICAQKFNGLTV  ICAQKFNGL  4        0.4953
235.4    10.00  0.41     Sequence
            DRB1_1201  853      RDLICAQKFNGLTVL  ICAQKFNGL  3        0.5009
221.5     9.00  0.37     Sequence         WB
            DRB1_1201  854      DLICAQKFNGLTVLP  ICAQKFNGL  2        0.4898
249.7    11.00  0.34     Sequence
```

```
             DRB1_1201  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.4681
315.8    13.00  0.34     Sequence
             DRB1_1201  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.4363
445.6    18.00  0.44     Sequence
             DRB1_1201  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.4680
316.0    13.00  0.37     Sequence
             DRB1_1201  858      AQKFNGLTVLPPLLT  LTVLPPLLT  6        0.5321
158.0     6.50  0.62     Sequence         WB
             DRB1_1201  859      QKFNGLTVLPPLLTD  LTVLPPLLT  5        0.5179
184.3     7.50  0.67     Sequence         WB
             DRB1_1201  860      KFNGLTVLPPLLTDE  LTVLPPLLT  4        0.4960
233.4     9.50  0.73     Sequence         WB
             DRB1_1201  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.4816
273.0    12.00  0.79     Sequence
             DRB1_1201  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.4576
353.9    15.00  0.77     Sequence
             DRB1_1201  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.3917
721.8    26.00  0.62     Sequence
             DRB1_1201  864      LTVLPPLLTDEMIAQ  LTVLPPLLT  0        0.3273
1448.2    40.00  0.43     Sequence
             DRB1_1201  865      TVLPPLLTDEMIAQY  LTDEMIAQY  6        0.3556
1066.9    34.00  0.44     Sequence
             DRB1_1201  866      VLPPLLTDEMIAQYT  LTDEMIAQY  5        0.3662
951.0    31.00  0.40     Sequence
             DRB1_1201  867      LPPLLTDEMIAQYTS  LTDEMIAQY  4        0.3588
1030.7    33.00  0.39     Sequence
             DRB1_1201  868      PPLLTDEMIAQYTSA  LTDEMIAQY  3        0.3510
1121.1    35.00  0.41     Sequence
             DRB1_1201  869      PLLTDEMIAQYTSAL  LTDEMIAQY  2        0.3625
990.1    32.00  0.39     Sequence
             DRB1_1201  870      LLTDEMIAQYTSALL  IAQYTSALL  6        0.3945
700.5    25.00  0.35     Sequence
             DRB1_1201  871      LTDEMIAQYTSALLA  IAQYTSALL  5        0.3593
1024.7    33.00  0.39     Sequence
             DRB1_1201  872      TDEMIAQYTSALLAG  IAQYTSALL  4        0.2988
1972.7    47.00  0.51     Sequence
             DRB1_1201  873      DEMIAQYTSALLAGT  IAQYTSALL  3        0.3027
1891.5    46.00  0.49     Sequence
             DRB1_1201  874      EMIAQYTSALLAGTI  TSALLAGTI  6        0.4016
648.2    24.00  0.60     Sequence
             DRB1_1201  875      MIAQYTSALLAGTIT  TSALLAGTI  5        0.3891
742.5    26.00  0.60     Sequence
             DRB1_1201  876      IAQYTSALLAGTITS  TSALLAGTI  4        0.3680
932.2    31.00  0.62     Sequence
             DRB1_1201  877      AQYTSALLAGTITSG  TSALLAGTI  3        0.3349
1334.2    38.00  0.70     Sequence
             DRB1_1201  878      QYTSALLAGTITSGW  TSALLAGTI  2        0.3173
1614.5    43.00  0.67     Sequence
             DRB1_1201  879      YTSALLAGTITSGWT  TSALLAGTI  1        0.2618
2942.1    60.00  0.47     Sequence
             DRB1_1201  880      TSALLAGTITSGWTF  TSALLAGTI  0        0.2750
2551.5    55.00  0.29     Sequence
             DRB1_1201  881      SALLAGTITSGWTFG  AGTITSGWT  4        0.2186
4696.1    70.00  0.26     Sequence
             DRB1_1201  882      ALLAGTITSGWTFGA  ITSGWTFGA  6        0.2163
4813.3    70.00  0.28     Sequence
             DRB1_1201  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.2001
5736.7    75.00  0.29     Sequence
             DRB1_1201  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.1813
7032.9    80.00  0.37     Sequence
             DRB1_1201  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.1589
8960.0    85.00  0.43     Sequence
             DRB1_1201  886      GTITSGWTFGAGAAL  ITSGWTFGA  2        0.1512
9735.7    85.00  0.35     Sequence
             DRB1_1201  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.1270
12646.5    90.00  0.25     Sequence
```

```
             DRB1_1201  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.1656
8329.0    85.00  0.55      Sequence
             DRB1_1201  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.1599
8866.7    85.00  0.51      Sequence
             DRB1_1201  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.2642
2868.1    60.00  0.25      Sequence
             DRB1_1201  891      GWTFGAGAALQIPFA  GAALQIPFA  6        0.2952
2049.3    48.00  0.50      Sequence
             DRB1_1201  892      WTFGAGAALQIPFAM  GAALQIPFA  5        0.3045
1854.0    46.00  0.47      Sequence
             DRB1_1201  893      TFGAGAALQIPFAMQ  GAALQIPFA  4        0.3007
1931.4    47.00  0.41      Sequence
             DRB1_1201  894      FGAGAALQIPFAMQM  GAALQIPFA  3        0.3089
1767.8    45.00  0.38      Sequence
             DRB1_1201  895      GAGAALQIPFAMQMA  GAALQIPFA  2        0.3154
1648.6    43.00  0.34      Sequence
             DRB1_1201  896      AGAALQIPFAMQMAY  IPFAMQMAY  6        0.4564
358.5    15.00  0.41     Sequence
             DRB1_1201  897      GAALQIPFAMQMAYR  PFAMQMAYR  6        0.4357
448.2    18.00  0.35     Sequence
             DRB1_1201  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.5383
147.8     6.00  0.47     Sequence         WB
             DRB1_1201  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.5505
129.4     5.00  0.43     Sequence         WB
             DRB1_1201  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.5300
161.7     6.50  0.43     Sequence         WB
             DRB1_1201  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.5177
184.6     7.50  0.45     Sequence         WB
             DRB1_1201  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.4902
248.6    11.00  0.46     Sequence
             DRB1_1201  903      PFAMQMAYRFNGIGV  AYRFNGIGV  6        0.4619
337.9    14.00  0.28     Sequence
             DRB1_1201  904      FAMQMAYRFNGIGVT  AYRFNGIGV  5        0.4417
420.3    17.00  0.31     Sequence
             DRB1_1201  905      AMQMAYRFNGIGVTQ  AYRFNGIGV  4        0.3505
1127.6    35.00  0.54      Sequence
             DRB1_1201  906      MQMAYRFNGIGVTQN  AYRFNGIGV  3        0.3226
1523.8    41.00  0.57      Sequence
             DRB1_1201  907      QMAYRFNGIGVTQNV  AYRFNGIGV  2        0.3083
1779.5    45.00  0.57      Sequence
             DRB1_1201  908      MAYRFNGIGVTQNVL  AYRFNGIGV  1        0.2883
2210.5    50.00  0.38      Sequence
             DRB1_1201  909      AYRFNGIGVTQNVLY  IGVTQNVLY  6        0.4204
529.2    20.00  0.61     Sequence
             DRB1_1201  910      YRFNGIGVTQNVLYE  IGVTQNVLY  5        0.4034
635.9    24.00  0.61     Sequence
             DRB1_1201  911      RFNGIGVTQNVLYEN  IGVTQNVLY  4        0.3869
760.2    27.00  0.58     Sequence
             DRB1_1201  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.3776
840.3    29.00  0.58     Sequence
             DRB1_1201  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.3678
934.3    31.00  0.57     Sequence
             DRB1_1201  914      GIGVTQNVLYENQKL  IGVTQNVLY  1        0.3551
1071.9    34.00  0.53      Sequence
             DRB1_1201  915      IGVTQNVLYENQKLI  IGVTQNVLY  0        0.4241
508.5    20.00  0.31     Sequence
             DRB1_1201  916      GVTQNVLYENQKLIA  LYENQKLIA  6        0.4252
502.6    20.00  0.56     Sequence
             DRB1_1201  917      VTQNVLYENQKLIAN  LYENQKLIA  5        0.4149
561.4    21.00  0.61     Sequence
             DRB1_1201  918      TQNVLYENQKLIANQ  LYENQKLIA  4        0.4095
595.2    22.00  0.61     Sequence
             DRB1_1201  919      QNVLYENQKLIANQF  NQKLIANQF  6        0.5349
153.3     6.00  0.49     Sequence         WB
             DRB1_1201  920      NVLYENQKLIANQFN  NQKLIANQF  5        0.5303
161.1     6.50  0.47     Sequence         WB
```

```
             DRB1_1201  921      VLYENQKLIANQFNS  NQKLIANQF  4        0.5137
192.8     8.00  0.51     Sequence         WB
             DRB1_1201  922      LYENQKLIANQFNSA  NQKLIANQF  3        0.4907
247.2    11.00  0.50     Sequence
             DRB1_1201  923      YENQKLIANQFNSAI  NQKLIANQF  2        0.4945
237.4    10.00  0.49     Sequence
             DRB1_1201  924      ENQKLIANQFNSAIG  NQKLIANQF  1        0.4749
293.3    12.00  0.44     Sequence
             DRB1_1201  925      NQKLIANQFNSAIGK  NQKLIANQF  0        0.4417
420.1    17.00  0.38     Sequence
             DRB1_1201  926      QKLIANQFNSAIGKI  IANQFNSAI  3        0.3401
1262.0    37.00  0.40     Sequence
             DRB1_1201  927      KLIANQFNSAIGKIQ  IANQFNSAI  2        0.3156
1645.1    43.00  0.42     Sequence
             DRB1_1201  928      LIANQFNSAIGKIQD  IANQFNSAI  1        0.2691
2720.6    55.00  0.40     Sequence
             DRB1_1201  929      IANQFNSAIGKIQDS  NSAIGKIQD  5        0.1539
9460.4    85.00  0.24     Sequence
             DRB1_1201  930      ANQFNSAIGKIQDSL  IGKIQDSLX  7        0.1719
7786.1    80.00  0.25     Sequence
             DRB1_1201  931      NQFNSAIGKIQDSLS  IGKIQDSLS  6        0.2142
4925.1    70.00  0.55     Sequence
             DRB1_1201  932      QFNSAIGKIQDSLSS  IGKIQDSLS  5        0.2271
4286.1    70.00  0.51     Sequence
             DRB1_1201  933      FNSAIGKIQDSLSST  IGKIQDSLS  4        0.2272
4276.9    70.00  0.51     Sequence
             DRB1_1201  934      NSAIGKIQDSLSSTA  IGKIQDSLS  3        0.2420
3647.0    65.00  0.41     Sequence
             DRB1_1201  935      SAIGKIQDSLSSTAS  IGKIQDSLS  2        0.2436
3585.0    65.00  0.38     Sequence
             DRB1_1201  936      AIGKIQDSLSSTASA  IQDSLSSTA  4        0.2250
4380.7    70.00  0.28     Sequence
             DRB1_1201  937      IGKIQDSLSSTASAL  IQDSLSSTA  3        0.2043
5484.5    75.00  0.37     Sequence
             DRB1_1201  938      GKIQDSLSSTASALG  IQDSLSSTA  2        0.1891
6459.1    75.00  0.37     Sequence
             DRB1_1201  939      KIQDSLSSTASALGK  LSSTASALG  5        0.1717
7798.8    80.00  0.34     Sequence
             DRB1_1201  940      IQDSLSSTASALGKL  LSSTASALG  4        0.1718
7793.1    80.00  0.39     Sequence
             DRB1_1201  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.1635
8524.1    85.00  0.44     Sequence
             DRB1_1201  942      DSLSSTASALGKLQD  ASALGKLQD  6        0.2049
5447.9    75.00  0.60     Sequence
             DRB1_1201  943      SLSSTASALGKLQDV  ASALGKLQD  5        0.2202
4618.2    70.00  0.59     Sequence
             DRB1_1201  944      LSSTASALGKLQDVV  ASALGKLQD  4        0.2865
2253.9    55.00  0.49     Sequence
             DRB1_1201  945      SSTASALGKLQDVVN  LGKLQDVVN  6        0.3272
1450.1    40.00  0.55     Sequence
             DRB1_1201  946      STASALGKLQDVVNQ  LGKLQDVVN  5        0.3231
1516.7    41.00  0.59     Sequence
             DRB1_1201  947      TASALGKLQDVVNQN  LGKLQDVVN  4        0.3079
1786.7    45.00  0.64     Sequence
             DRB1_1201  948      ASALGKLQDVVNQNA  LGKLQDVVN  3        0.2919
2125.3    49.00  0.69     Sequence
             DRB1_1201  949      SALGKLQDVVNQNAQ  LGKLQDVVN  2        0.2715
2650.0    55.00  0.70     Sequence
             DRB1_1201  950      ALGKLQDVVNQNAQA  LGKLQDVVN  1        0.2174
4758.2    70.00  0.54     Sequence
             DRB1_1201  951      LGKLQDVVNQNAQAL  VVNQNAQAL  6        0.2877
2224.3    50.00  0.39     Sequence
             DRB1_1201  952      GKLQDVVNQNAQALN  VVNQNAQAL  5        0.2763
2515.9    55.00  0.50     Sequence
             DRB1_1201  953      KLQDVVNQNAQALNT  VVNQNAQAL  4        0.2763
2514.3    55.00  0.50     Sequence
```

```
             DRB1_1201  954      LQDVVNQNAQALNTL  VVNQNAQAL  3        0.3018
1910.0    47.00  0.44     Sequence
             DRB1_1201  955      QDVVNQNAQALNTLV  VVNQNAQAL  2        0.3111
1725.8    44.00  0.38     Sequence
             DRB1_1201  956      DVVNQNAQALNTLVK  AQALNTLVK  6        0.3796
823.1    28.00  0.50     Sequence
             DRB1_1201  957      VVNQNAQALNTLVKQ  AQALNTLVK  5        0.3680
932.4    31.00  0.54     Sequence
             DRB1_1201  958      VNQNAQALNTLVKQL  AQALNTLVK  4        0.3935
707.9    25.00  0.50     Sequence
             DRB1_1201  959      NQNAQALNTLVKQLS  LNTLVKQLS  6        0.4347
453.3    18.00  0.50     Sequence
             DRB1_1201  960      QNAQALNTLVKQLSS  LNTLVKQLS  5        0.4305
474.1    19.00  0.50     Sequence
             DRB1_1201  961      NAQALNTLVKQLSSN  LNTLVKQLS  4        0.4382
436.2    18.00  0.47     Sequence
             DRB1_1201  962      AQALNTLVKQLSSNF  LVKQLSSNF  6        0.6093
68.5     2.00  0.37     Sequence         WB
             DRB1_1201  963      QALNTLVKQLSSNFG  VKQLSSNFG  6        0.6077
69.8     2.50  0.50     Sequence         WB
             DRB1_1201  964      ALNTLVKQLSSNFGA  VKQLSSNFG  5        0.5990
76.6     2.50  0.51     Sequence         WB
             DRB1_1201  965      LNTLVKQLSSNFGAI  VKQLSSNFG  4        0.6062
70.9     2.50  0.54     Sequence         WB
             DRB1_1201  966      NTLVKQLSSNFGAIS  VKQLSSNFG  3        0.5891
85.3     3.00  0.58     Sequence         WB
             DRB1_1201  967      TLVKQLSSNFGAISS  VKQLSSNFG  2        0.5671
108.2     4.00  0.58     Sequence         WB
             DRB1_1201  968      LVKQLSSNFGAISSV  VKQLSSNFG  1        0.4537
369.1    15.00  0.43     Sequence
             DRB1_1201  969      VKQLSSNFGAISSVL  VKQLSSNFG  0        0.2904
2159.0    50.00  0.37     Sequence
             DRB1_1201  970      KQLSSNFGAISSVLN  FGAISSVLN  6        0.2932
2095.1    49.00  0.62     Sequence
             DRB1_1201  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.2859
2267.3    55.00  0.69     Sequence
             DRB1_1201  972      LSSNFGAISSVLNDI  FGAISSVLN  4        0.2954
2045.7    48.00  0.65     Sequence
             DRB1_1201  973      SSNFGAISSVLNDIL  FGAISSVLN  3        0.3143
1667.2    43.00  0.55     Sequence
             DRB1_1201  974      SNFGAISSVLNDILS  FGAISSVLN  2        0.3112
1723.7    44.00  0.46     Sequence
             DRB1_1201  975      NFGAISSVLNDILSR  FGAISSVLN  1        0.2928
2105.5    49.00  0.38     Sequence
             DRB1_1201  976      FGAISSVLNDILSRL  SSVLNDILS  4        0.3021
1903.2    47.00  0.24     Sequence
             DRB1_1201  977      GAISSVLNDILSRLD  LNDILSRLD  6        0.3185
1592.9    42.00  0.38     Sequence
             DRB1_1201  978      AISSVLNDILSRLDK  LNDILSRLD  5        0.3440
1209.6    36.00  0.38     Sequence
             DRB1_1201  979      ISSVLNDILSRLDKV  LNDILSRLD  4        0.4174
546.4    21.00  0.34     Sequence
             DRB1_1201  980      SSVLNDILSRLDKVE  LNDILSRLD  3        0.4882
254.0    11.00  0.22     Sequence
             DRB1_1201  981      SVLNDILSRLDKVEA  LSRLDKVEA  6        0.5464
135.4     5.50  0.63     Sequence         WB
             DRB1_1201  982      VLNDILSRLDKVEAE  LSRLDKVEA  5        0.5434
139.8     5.50  0.64     Sequence         WB
             DRB1_1201  983      LNDILSRLDKVEAEV  LSRLDKVEA  4        0.5401
145.0     6.00  0.69     Sequence         WB
             DRB1_1201  984      NDILSRLDKVEAEVQ  LSRLDKVEA  3        0.5206
179.0     7.50  0.74     Sequence         WB
             DRB1_1201  985      DILSRLDKVEAEVQI  LSRLDKVEA  2        0.4896
250.2    11.00  0.81     Sequence
             DRB1_1201  986      ILSRLDKVEAEVQID  LSRLDKVEA  1        0.4021
645.0    24.00  0.61     Sequence
```

```
             DRB1_1201  987      LSRLDKVEAEVQIDR  LSRLDKVEA  0        0.2984
1980.6    47.00  0.45     Sequence
             DRB1_1201  988      SRLDKVEAEVQIDRL  LDKVEAEVQ  2        0.1969
5940.7    75.00  0.35     Sequence
             DRB1_1201  989      RLDKVEAEVQIDRLI  VEAEVQIDR  4        0.1979
5878.5    75.00  0.31     Sequence
             DRB1_1201  990      LDKVEAEVQIDRLIT  EVQIDRLIT  6        0.2205
4602.3    70.00  0.29     Sequence
             DRB1_1201  991      DKVEAEVQIDRLITG  VQIDRLITG  6        0.2254
4363.4    70.00  0.26     Sequence
             DRB1_1201  992      KVEAEVQIDRLITGR  VQIDRLITG  5        0.2301
4147.9    65.00  0.26     Sequence
             DRB1_1201  993      VEAEVQIDRLITGRL  IDRLITGRL  6        0.3774
842.2    29.00  0.63     Sequence
             DRB1_1201  994      EAEVQIDRLITGRLQ  IDRLITGRL  5        0.3925
715.6    26.00  0.57     Sequence
             DRB1_1201  995      AEVQIDRLITGRLQS  IDRLITGRL  4        0.3908
729.1    26.00  0.57     Sequence
             DRB1_1201  996      EVQIDRLITGRLQSL  IDRLITGRL  3        0.4343
455.2    18.00  0.43     Sequence
             DRB1_1201  997      VQIDRLITGRLQSLQ  IDRLITGRL  2        0.4498
384.9    16.00  0.39     Sequence
             DRB1_1201  998      QIDRLITGRLQSLQT  TGRLQSLQT  6        0.4456
402.9    16.00  0.30     Sequence
             DRB1_1201  999      IDRLITGRLQSLQTY  TGRLQSLQT  5        0.4818
272.4    12.00  0.31     Sequence
             DRB1_1201 1000      DRLITGRLQSLQTYV  TGRLQSLQT  4        0.5325
157.3     6.50  0.24     Sequence         WB
             DRB1_1201 1001      RLITGRLQSLQTYVT  LQSLQTYVT  6        0.5977
77.7     2.50  0.69     Sequence         WB
             DRB1_1201 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.5835
90.6     3.00  0.70     Sequence         WB
             DRB1_1201 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.5583
119.1     4.50  0.79     Sequence         WB
             DRB1_1201 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.5383
147.7     6.00  0.85     Sequence         WB
             DRB1_1201 1005      GRLQSLQTYVTQQLI  LQSLQTYVT  2        0.5182
183.6     7.50  0.82     Sequence         WB
             DRB1_1201 1006      RLQSLQTYVTQQLIR  LQSLQTYVT  1        0.4288
483.1    19.00  0.63     Sequence
             DRB1_1201 1007      LQSLQTYVTQQLIRA  LQSLQTYVT  0        0.3189
1586.7    42.00  0.43     Sequence
             DRB1_1201 1008      QSLQTYVTQQLIRAA  LQTYVTQQL  2        0.2723
2626.3    55.00  0.20     Sequence
             DRB1_1201 1009      SLQTYVTQQLIRAAE  TQQLIRAAE  6        0.2878
2222.1    50.00  0.38     Sequence
             DRB1_1201 1010      LQTYVTQQLIRAAEI  TQQLIRAAE  5        0.3386
1282.3    37.00  0.41     Sequence
             DRB1_1201 1011      QTYVTQQLIRAAEIR  TQQLIRAAE  4        0.3390
1276.1    37.00  0.40     Sequence
             DRB1_1201 1012      TYVTQQLIRAAEIRA  LIRAAEIRA  6        0.3935
707.5    25.00  0.33     Sequence
             DRB1_1201 1013      YVTQQLIRAAEIRAS  LIRAAEIRA  5        0.4014
649.6    24.00  0.37     Sequence
             DRB1_1201 1014      VTQQLIRAAEIRASA  LIRAAEIRA  4        0.3845
779.9    27.00  0.38     Sequence
             DRB1_1201 1015      TQQLIRAAEIRASAN  LIRAAEIRA  3        0.3633
981.6    32.00  0.44     Sequence
             DRB1_1201 1016      QQLIRAAEIRASANL  LIRAAEIRA  2        0.3573
1047.2    33.00  0.43     Sequence
             DRB1_1201 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.3406
1254.2    37.00  0.31     Sequence
             DRB1_1201 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.3370
1305.0    38.00  0.45     Sequence
             DRB1_1201 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.3225
1525.2    41.00  0.69     Sequence
```

```
             DRB1_1201 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.3123
1704.2    44.00  0.70     Sequence
             DRB1_1201 1021      AAEIRASANLAAIKM  SANLAAIKM  6        0.3899
735.9    26.00  0.42     Sequence
             DRB1_1201 1022      AEIRASANLAAIKMS  SANLAAIKM  5        0.3895
739.2    26.00  0.41     Sequence
             DRB1_1201 1023      EIRASANLAAIKMSE  SANLAAIKM  4        0.4168
550.4    21.00  0.38     Sequence
             DRB1_1201 1024      IRASANLAAIKMSEC  LAAIKMSEC  6        0.4442
409.1    17.00  0.57     Sequence
             DRB1_1201 1025      RASANLAAIKMSECV  LAAIKMSEC  5        0.4534
370.4    15.00  0.69     Sequence
             DRB1_1201 1026      ASANLAAIKMSECVL  LAAIKMSEC  4        0.4931
241.0    10.00  0.57     Sequence
             DRB1_1201 1027      SANLAAIKMSECVLG  LAAIKMSEC  3        0.4741
296.0    13.00  0.60     Sequence
             DRB1_1201 1028      ANLAAIKMSECVLGQ  LAAIKMSEC  2        0.4546
365.5    15.00  0.61     Sequence
             DRB1_1201 1029      NLAAIKMSECVLGQS  LAAIKMSEC  1        0.4011
652.3    24.00  0.44     Sequence
             DRB1_1201 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.3380
1290.6    38.00  0.34     Sequence
             DRB1_1201 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.2653
2832.4    60.00  0.40     Sequence
             DRB1_1201 1032      AIKMSECVLGQSKRV  CVLGQSKRV  6        0.2881
2214.6    50.00  0.28     Sequence
             DRB1_1201 1033      IKMSECVLGQSKRVD  CVLGQSKRV  5        0.2863
2256.6    55.00  0.32     Sequence
             DRB1_1201 1034      KMSECVLGQSKRVDF  LGQSKRVDF  6        0.3341
1345.4    39.00  0.44     Sequence
             DRB1_1201 1035      MSECVLGQSKRVDFC  LGQSKRVDF  5        0.3172
1616.1    43.00  0.44     Sequence
             DRB1_1201 1036      SECVLGQSKRVDFCG  LGQSKRVDF  4        0.2976
1997.5    48.00  0.43     Sequence
             DRB1_1201 1037      ECVLGQSKRVDFCGK  LGQSKRVDF  3        0.2911
2143.7    49.00  0.43     Sequence
             DRB1_1201 1038      CVLGQSKRVDFCGKG  LGQSKRVDF  2        0.2673
2774.3    60.00  0.46     Sequence
             DRB1_1201 1039      VLGQSKRVDFCGKGY  LGQSKRVDF  1        0.2534
3223.1    60.00  0.29     Sequence
             DRB1_1201 1040      LGQSKRVDFCGKGYH  VDFCGKGYH  6        0.2638
2879.1    60.00  0.35     Sequence
             DRB1_1201 1041      GQSKRVDFCGKGYHL  VDFCGKGYH  5        0.2758
2528.5    55.00  0.40     Sequence
             DRB1_1201 1042      QSKRVDFCGKGYHLM  VDFCGKGYH  4        0.3112
1724.4    44.00  0.29     Sequence
             DRB1_1201 1043      SKRVDFCGKGYHLMS  FCGKGYHLM  5        0.3121
1708.3    44.00  0.23     Sequence
             DRB1_1201 1044      KRVDFCGKGYHLMSF  FCGKGYHLM  4        0.3517
1113.0    34.00  0.22     Sequence
             DRB1_1201 1045      RVDFCGKGYHLMSFP  FCGKGYHLM  3        0.3503
1130.0    35.00  0.19     Sequence
             DRB1_1201 1046      VDFCGKGYHLMSFPQ  GYHLMSFPQ  6        0.3893
740.9    26.00  0.43     Sequence
             DRB1_1201 1047      DFCGKGYHLMSFPQS  GYHLMSFPQ  5        0.3633
981.5    32.00  0.48     Sequence
             DRB1_1201 1048      FCGKGYHLMSFPQSA  GYHLMSFPQ  4        0.3553
1070.2    34.00  0.50     Sequence
             DRB1_1201 1049      CGKGYHLMSFPQSAP  GYHLMSFPQ  3        0.3478
1160.9    35.00  0.49     Sequence
             DRB1_1201 1050      GKGYHLMSFPQSAPH  GYHLMSFPQ  2        0.3357
1322.3    38.00  0.45     Sequence
             DRB1_1201 1051      KGYHLMSFPQSAPHG  GYHLMSFPQ  1        0.2875
2229.1    50.00  0.42     Sequence
             DRB1_1201 1052      GYHLMSFPQSAPHGV  LMSFPQSAP  3        0.2492
3373.1    60.00  0.37     Sequence
```

```
             DRB1_1201 1053      YHLMSFPQSAPHGVV  LMSFPQSAP  2        0.1872
6596.4    80.00  0.50     Sequence
             DRB1_1201 1054      HLMSFPQSAPHGVVF  LMSFPQSAP  1        0.1696
7978.8    80.00  0.38     Sequence
             DRB1_1201 1055      LMSFPQSAPHGVVFL  PQSAPHGVV  4        0.1557
9274.1    85.00  0.20     Sequence
             DRB1_1201 1056      MSFPQSAPHGVVFLH  PQSAPHGVV  3        0.1517
9688.5    85.00  0.18     Sequence
             DRB1_1201 1057      SFPQSAPHGVVFLHV  PHGVVFLHV  6        0.2071
5317.1    75.00  0.50     Sequence
             DRB1_1201 1058      FPQSAPHGVVFLHVT  PHGVVFLHV  5        0.2210
4576.2    70.00  0.49     Sequence
             DRB1_1201 1059      PQSAPHGVVFLHVTY  GVVFLHVTY  6        0.3462
1180.6    36.00  0.36     Sequence
             DRB1_1201 1060      QSAPHGVVFLHVTYV  VVFLHVTYV  6        0.3496
1138.6    35.00  0.31     Sequence
             DRB1_1201 1061      SAPHGVVFLHVTYVP  VVFLHVTYV  5        0.3416
1241.1    37.00  0.28     Sequence
             DRB1_1201 1062      APHGVVFLHVTYVPA  VVFLHVTYV  4        0.3706
907.0    30.00  0.23     Sequence
             DRB1_1201 1063      PHGVVFLHVTYVPAQ  VVFLHVTYV  3        0.3603
1013.5    32.00  0.23     Sequence
             DRB1_1201 1064      HGVVFLHVTYVPAQE  VVFLHVTYV  2        0.3403
1258.9    37.00  0.23     Sequence
             DRB1_1201 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.3181
1600.6    42.00  0.31     Sequence
             DRB1_1201 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.2751
2547.8    55.00  0.42     Sequence
             DRB1_1201 1067      VFLHVTYVPAQEKNF  VTYVPAQEK  4        0.2645
2858.4    60.00  0.26     Sequence
             DRB1_1201 1068      FLHVTYVPAQEKNFT  VTYVPAQEK  3        0.2336
3994.2    65.00  0.32     Sequence
             DRB1_1201 1069      LHVTYVPAQEKNFTT  VTYVPAQEK  2        0.1795
7172.8    80.00  0.35     Sequence
             DRB1_1201 1070      HVTYVPAQEKNFTTA  VTYVPAQEK  1        0.1440
10532.6    85.00  0.24     Sequence
             DRB1_1201 1071      VTYVPAQEKNFTTAP  YVPAQEKNF  2        0.1232
13186.1    90.00  0.31     Sequence
             DRB1_1201 1072      TYVPAQEKNFTTAPA  PAQEKNFTT  3        0.1019
16594.0    95.00  0.23     Sequence
             DRB1_1201 1073      YVPAQEKNFTTAPAI  KNFTTAPAI  6        0.1208
13525.0    90.00  0.24     Sequence
             DRB1_1201 1074      VPAQEKNFTTAPAIC  FTTAPAICX  7        0.1228
13239.6    90.00  0.34     Sequence
             DRB1_1201 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.1562
9230.1    85.00  0.59     Sequence
             DRB1_1201 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.1553
9316.8    85.00  0.56     Sequence
             DRB1_1201 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.1474
10144.2    85.00  0.56     Sequence
             DRB1_1201 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.1447
10447.6    85.00  0.57     Sequence
             DRB1_1201 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.1376
11286.3    90.00  0.56     Sequence
             DRB1_1201 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.1101
15185.4    95.00  0.38     Sequence
             DRB1_1201 1081      FTTAPAICHDGKAHF  ICHDGKAHF  6        0.2845
2301.8    55.00  0.61     Sequence
             DRB1_1201 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.2942
2071.8    49.00  0.56     Sequence
             DRB1_1201 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.2923
2116.9    49.00  0.56     Sequence
             DRB1_1201 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.2893
2186.6    50.00  0.56     Sequence
             DRB1_1201 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.2762
2517.6    55.00  0.56     Sequence
```

```
             DRB1_1201 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.2649
2847.2    60.00  0.50     Sequence
             DRB1_1201 1087      ICHDGKAHFPREGVF  ICHDGKAHF  0        0.2205
4599.0    70.00  0.42     Sequence
             DRB1_1201 1088      CHDGKAHFPREGVFV  HFPREGVFV  6        0.1264
12735.1    90.00  0.31     Sequence
             DRB1_1201 1089      HDGKAHFPREGVFVS  HFPREGVFV  5        0.1229
13222.6    90.00  0.29     Sequence
             DRB1_1201 1090      DGKAHFPREGVFVSN  HFPREGVFV  4        0.1215
13425.4    90.00  0.31     Sequence
             DRB1_1201 1091      GKAHFPREGVFVSNG  HFPREGVFV  3        0.1109
15067.4    95.00  0.31     Sequence
             DRB1_1201 1092      KAHFPREGVFVSNGT  HFPREGVFV  2        0.1085
15463.4    95.00  0.33     Sequence
             DRB1_1201 1093      AHFPREGVFVSNGTH  HFPREGVFV  1        0.1028
16435.9    95.00  0.29     Sequence
             DRB1_1201 1094      HFPREGVFVSNGTHW  VFVSNGTHW  6        0.1528
9569.5    85.00  0.41     Sequence
             DRB1_1201 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6        0.3281
1436.4    40.00  0.54     Sequence
             DRB1_1201 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.3524
1104.5    34.00  0.50     Sequence
             DRB1_1201 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.3497
1137.3    35.00  0.48     Sequence
             DRB1_1201 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.3402
1260.1    37.00  0.49     Sequence
             DRB1_1201 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.3326
1368.0    39.00  0.49     Sequence
             DRB1_1201 1100      VFVSNGTHWFVTQRN  FVSNGTHWF  1        0.3119
1711.6    44.00  0.46     Sequence
             DRB1_1201 1101      FVSNGTHWFVTQRNF  HWFVTQRNF  6        0.2742
2573.1    55.00  0.28     Sequence
             DRB1_1201 1102      VSNGTHWFVTQRNFY  HWFVTQRNF  5        0.2804
2406.5    55.00  0.31     Sequence
             DRB1_1201 1103      SNGTHWFVTQRNFYE  FVTQRNFYE  6        0.2984
1981.0    47.00  0.25     Sequence
             DRB1_1201 1104      NGTHWFVTQRNFYEP  FVTQRNFYE  5        0.2902
2165.1    50.00  0.24     Sequence
             DRB1_1201 1105      GTHWFVTQRNFYEPQ  FVTQRNFYE  4        0.2845
2302.4    55.00  0.25     Sequence
             DRB1_1201 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3        0.2898
2173.6    50.00  0.24     Sequence
             DRB1_1201 1107      HWFVTQRNFYEPQII  FVTQRNFYE  2        0.2730
2607.5    55.00  0.26     Sequence
             DRB1_1201 1108      WFVTQRNFYEPQIIT  VTQRNFYEP  2        0.2430
3606.3    65.00  0.26     Sequence
             DRB1_1201 1109      FVTQRNFYEPQIITT  FYEPQIITT  6        0.1802
7111.9    80.00  0.25     Sequence
             DRB1_1201 1110      VTQRNFYEPQIITTD  FYEPQIITT  5        0.1292
12357.7    90.00  0.40     Sequence
             DRB1_1201 1111      TQRNFYEPQIITTDN  FYEPQIITT  4        0.1069
15735.5    95.00  0.51     Sequence
             DRB1_1201 1112      QRNFYEPQIITTDNT  FYEPQIITT  3        0.1058
15918.7    95.00  0.44     Sequence
             DRB1_1201 1113      RNFYEPQIITTDNTF  FYEPQIITT  2        0.1301
12237.6    90.00  0.28     Sequence
             DRB1_1201 1114      NFYEPQIITTDNTFV  IITTDNTFV  6        0.1876
6571.0    80.00  0.44     Sequence
             DRB1_1201 1115      FYEPQIITTDNTFVS  ITTDNTFVS  6        0.1979
5876.5    75.00  0.43     Sequence
             DRB1_1201 1116      YEPQIITTDNTFVSG  ITTDNTFVS  5        0.1830
6900.0    80.00  0.42     Sequence
             DRB1_1201 1117      EPQIITTDNTFVSGN  ITTDNTFVS  4        0.1790
7208.6    80.00  0.42     Sequence
             DRB1_1201 1118      PQIITTDNTFVSGNC  ITTDNTFVS  3        0.1736
7643.3    80.00  0.43     Sequence
```

```
             DRB1_1201 1119      QIITTDNTFVSGNCD  ITTDNTFVS  2        0.1602
8839.2    85.00  0.41     Sequence
             DRB1_1201 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.1302
12222.4    90.00  0.29     Sequence
             DRB1_1201 1121      ITTDNTFVSGNCDVV  TFVSGNCDV  5        0.1079
15557.2    95.00  0.25     Sequence
             DRB1_1201 1122      TTDNTFVSGNCDVVI  VSGNCDVVI  6        0.1639
8490.8    85.00  0.38     Sequence
             DRB1_1201 1123      TDNTFVSGNCDVVIG  VSGNCDVVI  5        0.1591
8944.1    85.00  0.38     Sequence
             DRB1_1201 1124      DNTFVSGNCDVVIGI  VSGNCDVVI  4        0.1772
7350.0    80.00  0.37     Sequence
             DRB1_1201 1125      NTFVSGNCDVVIGIV  VSGNCDVVI  3        0.1874
6585.0    80.00  0.36     Sequence
             DRB1_1201 1126      TFVSGNCDVVIGIVN  VSGNCDVVI  2        0.2050
5442.5    75.00  0.27     Sequence
             DRB1_1201 1127      FVSGNCDVVIGIVNN  CDVVIGIVN  5        0.2006
5704.3    75.00  0.32     Sequence
             DRB1_1201 1128      VSGNCDVVIGIVNNT  CDVVIGIVN  4        0.2110
5096.5    70.00  0.28     Sequence
             DRB1_1201 1129      SGNCDVVIGIVNNTV  VIGIVNNTV  6        0.3878
752.8    27.00  0.64     Sequence
             DRB1_1201 1130      GNCDVVIGIVNNTVY  IGIVNNTVY  6        0.5123
195.8     8.00  0.51     Sequence         WB
             DRB1_1201 1131      NCDVVIGIVNNTVYD  IGIVNNTVY  5        0.5147
190.7     8.00  0.48     Sequence         WB
             DRB1_1201 1132      CDVVIGIVNNTVYDP  IGIVNNTVY  4        0.5129
194.5     8.00  0.46     Sequence         WB
             DRB1_1201 1133      DVVIGIVNNTVYDPL  IGIVNNTVY  3        0.5122
195.9     8.00  0.46     Sequence         WB
             DRB1_1201 1134      VVIGIVNNTVYDPLQ  IGIVNNTVY  2        0.4979
228.7     9.50  0.49     Sequence         WB
             DRB1_1201 1135      VIGIVNNTVYDPLQP  IGIVNNTVY  1        0.4486
389.9    16.00  0.44     Sequence
             DRB1_1201 1136      IGIVNNTVYDPLQPE  IGIVNNTVY  0        0.3789
829.2    28.00  0.38     Sequence
             DRB1_1201 1137      GIVNNTVYDPLQPEL  VNNTVYDPL  2        0.2046
5466.9    75.00  0.31     Sequence
             DRB1_1201 1138      IVNNTVYDPLQPELD  YDPLQPELD  6        0.1680
8120.3    80.00  0.28     Sequence
             DRB1_1201 1139      VNNTVYDPLQPELDS  YDPLQPELD  5        0.1359
11487.7    90.00  0.40     Sequence
             DRB1_1201 1140      NNTVYDPLQPELDSF  YDPLQPELD  4        0.1445
10470.2    85.00  0.37     Sequence
             DRB1_1201 1141      NTVYDPLQPELDSFK  YDPLQPELD  3        0.1577
9079.1    85.00  0.32     Sequence
             DRB1_1201 1142      TVYDPLQPELDSFKE  YDPLQPELD  2        0.1604
8817.1    85.00  0.33     Sequence
             DRB1_1201 1143      VYDPLQPELDSFKEE  QPELDSFKE  5        0.1397
11029.8    90.00  0.27     Sequence
             DRB1_1201 1144      YDPLQPELDSFKEEL  QPELDSFKE  4        0.1206
13556.8    90.00  0.35     Sequence
             DRB1_1201 1145      DPLQPELDSFKEELD  QPELDSFKE  3        0.1211
13482.3    90.00  0.33     Sequence
             DRB1_1201 1146      PLQPELDSFKEELDK  QPELDSFKE  2        0.1142
14536.8    95.00  0.35     Sequence
             DRB1_1201 1147      LQPELDSFKEELDKY  LDSFKEELD  4        0.1322
11959.5    90.00  0.17     Sequence
             DRB1_1201 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.2773
2487.9    55.00  0.47     Sequence
             DRB1_1201 1149      PELDSFKEELDKYFK  KEELDKYFK  6        0.3097
1752.7    45.00  0.49     Sequence
             DRB1_1201 1150      ELDSFKEELDKYFKN  KEELDKYFK  5        0.3084
1778.1    45.00  0.49     Sequence
             DRB1_1201 1151      LDSFKEELDKYFKNH  KEELDKYFK  4        0.3064
1816.9    45.00  0.47     Sequence
```

```
             DRB1_1201 1152      DSFKEELDKYFKNHT  KEELDKYFK  3        0.2935
2087.6    49.00  0.47     Sequence
             DRB1_1201 1153      SFKEELDKYFKNHTS  KEELDKYFK  2        0.2851
2287.4    55.00  0.44     Sequence
             DRB1_1201 1154      FKEELDKYFKNHTSP  KEELDKYFK  1        0.2292
4185.9    65.00  0.34     Sequence
             DRB1_1201 1155      KEELDKYFKNHTSPD  LDKYFKNHT  3        0.1306
12164.7    90.00  0.35     Sequence
             DRB1_1201 1156      EELDKYFKNHTSPDV  FKNHTSPDV  6        0.1251
12917.3    90.00  0.49     Sequence
             DRB1_1201 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.1132
14689.4    95.00  0.50     Sequence
             DRB1_1201 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.1094
15305.5    95.00  0.52     Sequence
             DRB1_1201 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.0917
18543.9    95.00  0.57     Sequence
             DRB1_1201 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.0890
19080.0    95.00  0.65     Sequence
             DRB1_1201 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.0769
21755.4   100.00  0.55     Sequence
             DRB1_1201 1162      FKNHTSPDVDLGDIS  FKNHTSPDV  0        0.0611
25826.7   100.00  0.38     Sequence
             DRB1_1201 1163      KNHTSPDVDLGDISG  DVDLGDISG  6        0.0419
31783.8   100.00  0.33     Sequence
             DRB1_1201 1164      NHTSPDVDLGDISGI  VDLGDISGI  6        0.0650
24751.3   100.00  0.44     Sequence
             DRB1_1201 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.0837
20208.3    95.00  0.36     Sequence
             DRB1_1201 1166      TSPDVDLGDISGINA  LGDISGINA  6        0.1355
11536.1    90.00  0.63     Sequence
             DRB1_1201 1167      SPDVDLGDISGINAS  LGDISGINA  5        0.1429
10656.1    85.00  0.59     Sequence
             DRB1_1201 1168      PDVDLGDISGINASF  LGDISGINA  4        0.2208
4587.0    70.00  0.35     Sequence
             DRB1_1201 1169      DVDLGDISGINASFV  ISGINASFV  6        0.4188
538.3    21.00  0.74     Sequence
             DRB1_1201 1170      VDLGDISGINASFVN  ISGINASFV  5        0.4212
524.7    20.00  0.74     Sequence
             DRB1_1201 1171      DLGDISGINASFVNI  ISGINASFV  4        0.4376
439.1    18.00  0.69     Sequence
             DRB1_1201 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.4362
445.9    18.00  0.69     Sequence
             DRB1_1201 1173      GDISGINASFVNIQK  ISGINASFV  2        0.4113
584.0    22.00  0.66     Sequence
             DRB1_1201 1174      DISGINASFVNIQKE  ISGINASFV  1        0.3874
756.5    27.00  0.56     Sequence
             DRB1_1201 1175      ISGINASFVNIQKEI  ISGINASFV  0        0.3424
1230.9    37.00  0.47     Sequence
             DRB1_1201 1176      SGINASFVNIQKEID  FVNIQKEID  6        0.2084
5243.9    75.00  0.25     Sequence
             DRB1_1201 1177      GINASFVNIQKEIDR  VNIQKEIDR  6        0.2278
4252.1    70.00  0.40     Sequence
             DRB1_1201 1178      INASFVNIQKEIDRL  VNIQKEIDR  5        0.2355
3913.3    65.00  0.44     Sequence
             DRB1_1201 1179      NASFVNIQKEIDRLN  VNIQKEIDR  4        0.2501
3339.5    60.00  0.36     Sequence
             DRB1_1201 1180      ASFVNIQKEIDRLNE  VNIQKEIDR  3        0.2582
3058.7    60.00  0.34     Sequence
             DRB1_1201 1181      SFVNIQKEIDRLNEV  VNIQKEIDR  2        0.2740
2578.9    55.00  0.29     Sequence
             DRB1_1201 1182      FVNIQKEIDRLNEVA  IQKEIDRLN  3        0.2827
2348.1    55.00  0.24     Sequence
             DRB1_1201 1183      VNIQKEIDRLNEVAK  IDRLNEVAK  6        0.3438
1212.4    36.00  0.55     Sequence
             DRB1_1201 1184      NIQKEIDRLNEVAKN  IDRLNEVAK  5        0.3329
1363.0    39.00  0.64     Sequence
```

```
             DRB1_1201 1185      IQKEIDRLNEVAKNL  IDRLNEVAK  4        0.3389
1278.2    37.00  0.67     Sequence
             DRB1_1201 1186      QKEIDRLNEVAKNLN  IDRLNEVAK  3        0.3349
1333.8    38.00  0.62     Sequence
             DRB1_1201 1187      KEIDRLNEVAKNLNE  IDRLNEVAK  2        0.3204
1560.9    42.00  0.62     Sequence
             DRB1_1201 1188      EIDRLNEVAKNLNES  IDRLNEVAK  1        0.2677
2760.5    55.00  0.45     Sequence
             DRB1_1201 1189      IDRLNEVAKNLNESL  VAKNLNESL  6        0.2934
2091.0    49.00  0.25     Sequence
             DRB1_1201 1190      DRLNEVAKNLNESLI  AKNLNESLI  6        0.3187
1589.8    42.00  0.46     Sequence
             DRB1_1201 1191      RLNEVAKNLNESLID  AKNLNESLI  5        0.3127
1697.3    44.00  0.44     Sequence
             DRB1_1201 1192      LNEVAKNLNESLIDL  AKNLNESLI  4        0.3155
1646.4    43.00  0.44     Sequence
             DRB1_1201 1193      NEVAKNLNESLIDLQ  AKNLNESLI  3        0.3004
1938.7    47.00  0.43     Sequence
             DRB1_1201 1194      EVAKNLNESLIDLQE  AKNLNESLI  2        0.2884
2207.4    50.00  0.41     Sequence
             DRB1_1201 1195      VAKNLNESLIDLQEL  AKNLNESLI  1        0.2711
2660.4    55.00  0.27     Sequence
             DRB1_1201 1196      AKNLNESLIDLQELG  ESLIDLQEL  5        0.2199
4631.4    70.00  0.20     Sequence
             DRB1_1201 1197      KNLNESLIDLQELGK  LIDLQELGK  6        0.2597
3010.3    60.00  0.57     Sequence
             DRB1_1201 1198      NLNESLIDLQELGKY  LIDLQELGK  5        0.3444
1204.6    36.00  0.38     Sequence
             DRB1_1201 1199      LNESLIDLQELGKYE  LIDLQELGK  4        0.3578
1041.7    33.00  0.31     Sequence
             DRB1_1201 1200      NESLIDLQELGKYEQ  LQELGKYEQ  6        0.3994
664.2    24.00  0.48     Sequence
             DRB1_1201 1201      ESLIDLQELGKYEQY  LQELGKYEQ  5        0.4096
594.5    22.00  0.51     Sequence
             DRB1_1201 1202      SLIDLQELGKYEQYI  LQELGKYEQ  4        0.4103
590.2    22.00  0.55     Sequence
             DRB1_1201 1203      LIDLQELGKYEQYIK  LQELGKYEQ  3        0.3955
692.6    25.00  0.59     Sequence
             DRB1_1201 1204      IDLQELGKYEQYIKW  LQELGKYEQ  2        0.3610
1006.3    32.00  0.63     Sequence
             DRB1_1201 1205      DLQELGKYEQYIKWP  LQELGKYEQ  1        0.2636
2887.7    60.00  0.54     Sequence
             DRB1_1201 1206      LQELGKYEQYIKWPW  LQELGKYEQ  0        0.2189
4681.9    70.00  0.37     Sequence
             DRB1_1201 1207      QELGKYEQYIKWPWY  EQYIKWPWY  6        0.1847
6774.9    80.00  0.31     Sequence
             DRB1_1201 1208      ELGKYEQYIKWPWYI  QYIKWPWYI  6        0.2422
3637.5    65.00  0.26     Sequence
             DRB1_1201 1209      LGKYEQYIKWPWYIW  IKWPWYIWX  7        0.2769
2499.0    55.00  0.25     Sequence
             DRB1_1201 1210      GKYEQYIKWPWYIWL  IKWPWYIWL  6        0.3068
1809.0    45.00  0.42     Sequence
             DRB1_1201 1211      KYEQYIKWPWYIWLG  IKWPWYIWL  5        0.2921
2119.2    49.00  0.41     Sequence
             DRB1_1201 1212      YEQYIKWPWYIWLGF  IKWPWYIWL  4        0.2962
2027.6    48.00  0.38     Sequence
             DRB1_1201 1213      EQYIKWPWYIWLGFI  IKWPWYIWL  3        0.2948
2060.0    48.00  0.37     Sequence
             DRB1_1201 1214      QYIKWPWYIWLGFIA  IKWPWYIWL  2        0.2838
2319.2    55.00  0.34     Sequence
             DRB1_1201 1215      YIKWPWYIWLGFIAG  YIWLGFIAG  6        0.2278
4252.9    70.00  0.22     Sequence
             DRB1_1201 1216      IKWPWYIWLGFIAGL  IWLGFIAGL  6        0.2277
4256.0    70.00  0.28     Sequence
             DRB1_1201 1217      KWPWYIWLGFIAGLI  WLGFIAGLI  6        0.3481
1157.4    35.00  0.38     Sequence
```

```
             DRB1_1201 1218      WPWYIWLGFIAGLIA  LGFIAGLIA  6        0.3840
784.4    27.00  0.44     Sequence
             DRB1_1201 1219      PWYIWLGFIAGLIAI  LGFIAGLIA  5        0.4235
511.9    20.00  0.38     Sequence
             DRB1_1201 1220      WYIWLGFIAGLIAIV  LGFIAGLIA  4        0.4640
330.2    14.00  0.36     Sequence
             DRB1_1201 1221      YIWLGFIAGLIAIVM  IAGLIAIVM  6        0.5379
148.4     6.00  0.54     Sequence         WB
             DRB1_1201 1222      IWLGFIAGLIAIVMV  IAGLIAIVM  5        0.5428
140.8     5.50  0.56     Sequence         WB
             DRB1_1201 1223      WLGFIAGLIAIVMVT  IAGLIAIVM  4        0.5213
177.5     7.50  0.62     Sequence         WB
             DRB1_1201 1224      LGFIAGLIAIVMVTI  IAGLIAIVM  3        0.5069
207.5     8.50  0.70     Sequence         WB
             DRB1_1201 1225      GFIAGLIAIVMVTIM  IAGLIAIVM  2        0.4800
277.6    12.00  0.75     Sequence
             DRB1_1201 1226      FIAGLIAIVMVTIML  IAGLIAIVM  1        0.4169
549.5    21.00  0.61     Sequence
             DRB1_1201 1227      IAGLIAIVMVTIMLC  IAGLIAIVM  0        0.3506
1125.7    35.00  0.49     Sequence
             DRB1_1201 1228      AGLIAIVMVTIMLCC  LIAIVMVTI  2        0.1691
8025.8    80.00  0.49     Sequence
             DRB1_1201 1229      GLIAIVMVTIMLCCM  LIAIVMVTI  1        0.1510
9757.1    85.00  0.30     Sequence
             DRB1_1201 1230      LIAIVMVTIMLCCMT  VTIMLCCMT  6        0.1437
10564.3    85.00  0.32     Sequence
             DRB1_1201 1231      IAIVMVTIMLCCMTS  VTIMLCCMT  5        0.1330
11861.6    90.00  0.31     Sequence
             DRB1_1201 1232      AIVMVTIMLCCMTSC  VTIMLCCMT  4        0.1337
11773.5    90.00  0.29     Sequence
             DRB1_1201 1233      IVMVTIMLCCMTSCC  VTIMLCCMT  3        0.1298
12278.4    90.00  0.28     Sequence
             DRB1_1201 1234      VMVTIMLCCMTSCCS  VTIMLCCMT  2        0.1338
11761.0    90.00  0.23     Sequence
             DRB1_1201 1235      MVTIMLCCMTSCCSC  LCCMTSCCS  5        0.1278
12541.4    90.00  0.26     Sequence
             DRB1_1201 1236      VTIMLCCMTSCCSCL  LCCMTSCCS  4        0.1435
10582.3    85.00  0.22     Sequence
             DRB1_1201 1237      TIMLCCMTSCCSCLK  MTSCCSCLK  6        0.1686
8070.8    80.00  0.35     Sequence
             DRB1_1201 1238      IMLCCMTSCCSCLKG  MTSCCSCLK  5        0.1591
8936.5    85.00  0.37     Sequence
             DRB1_1201 1239      MLCCMTSCCSCLKGC  MTSCCSCLK  4        0.1418
10786.6    90.00  0.43     Sequence
             DRB1_1201 1240      LCCMTSCCSCLKGCC  MTSCCSCLK  3        0.1351
11593.0    90.00  0.40     Sequence
             DRB1_1201 1241      CCMTSCCSCLKGCCS  CSCLKGCCS  6        0.1439
10534.9    85.00  0.30     Sequence
             DRB1_1201 1242      CMTSCCSCLKGCCSC  CSCLKGCCS  5        0.1306
12174.4    90.00  0.31     Sequence
             DRB1_1201 1243      MTSCCSCLKGCCSCG  CSCLKGCCS  4        0.1289
12391.9    90.00  0.29     Sequence
             DRB1_1201 1244      TSCCSCLKGCCSCGS  LKGCCSCGS  6        0.1465
10242.8    85.00  0.44     Sequence
             DRB1_1201 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5        0.1374
11305.0    90.00  0.43     Sequence
             DRB1_1201 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.1260
12795.7    90.00  0.46     Sequence
             DRB1_1201 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.1174
14042.3    90.00  0.55     Sequence
             DRB1_1201 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2        0.1348
11630.1    90.00  0.46     Sequence
             DRB1_1201 1249      CLKGCCSCGSCCKFD  LKGCCSCGS  1        0.1186
13853.8    90.00  0.34     Sequence
             DRB1_1201 1250      LKGCCSCGSCCKFDE  CGSCCKFDE  6        0.1047
16102.5    95.00  0.25     Sequence
```

```
             DRB1_1201 1251      KGCCSCGSCCKFDED  CGSCCKFDE  5        0.0948
17921.8    95.00  0.34     Sequence
             DRB1_1201 1252      GCCSCGSCCKFDEDD  CGSCCKFDE  4        0.0918
18515.4    95.00  0.34     Sequence
             DRB1_1201 1253      CCSCGSCCKFDEDDS  CGSCCKFDE  3        0.0917
18533.7    95.00  0.34     Sequence
             DRB1_1201 1254      CSCGSCCKFDEDDSE  CGSCCKFDE  2        0.0830
20361.5   100.00  0.34     Sequence
             DRB1_1201 1255      SCGSCCKFDEDDSEP  CGSCCKFDE  1        0.0518
28554.6   100.00  0.35     Sequence
             DRB1_1201 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.0743
22370.8   100.00  0.56     Sequence
             DRB1_1201 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.0772
21693.6   100.00  0.64     Sequence
             DRB1_1201 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.0756
22068.6   100.00  0.67     Sequence
             DRB1_1201 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.0711
23165.9   100.00  0.64     Sequence
             DRB1_1201 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.0723
22864.9   100.00  0.58     Sequence
             DRB1_1201 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.0713
23124.9   100.00  0.38     Sequence
             DRB1_1201 1262      FDEDDSEPVLKGVKL  EPVLKGVKL  6        0.1784
7257.9    80.00  0.64     Sequence
             DRB1_1201 1263      DEDDSEPVLKGVKLH  EPVLKGVKL  5        0.2199
4629.8    70.00  0.50     Sequence
             DRB1_1201 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.5651
110.5     4.00  0.52     Sequence          WB
             DRB1_1201 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.6238
58.6     1.60  0.46     Sequence          SB
             DRB1_1302    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.2717
2644.3    65.00  0.68     Sequence
             DRB1_1302    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.2938
2082.4    60.00  0.50     Sequence
             DRB1_1302    3      PIKEMFVFLVLLPLV  IKEMFVFLV  1        0.2519
3275.0    70.00  0.40     Sequence
             DRB1_1302    4      IKEMFVFLVLLPLVS  FVFLVLLPL  4        0.1978
5883.1    85.00  0.32     Sequence
             DRB1_1302    5      KEMFVFLVLLPLVSS  FVFLVLLPL  3        0.1846
6782.2    85.00  0.31     Sequence
             DRB1_1302    6      EMFVFLVLLPLVSSQ  LVLLPLVSS  5        0.1740
7610.0    90.00  0.29     Sequence
             DRB1_1302    7      MFVFLVLLPLVSSQC  LLPLVSSQC  6        0.1940
6127.1    85.00  0.29     Sequence
             DRB1_1302    8      FVFLVLLPLVSSQCV  LPLVSSQCV  6        0.3263
1465.3    55.00  0.56     Sequence
             DRB1_1302    9      VFLVLLPLVSSQCVN  LPLVSSQCV  5        0.3323
1372.0    55.00  0.55     Sequence
             DRB1_1302   10      FLVLLPLVSSQCVNF  LVSSQCVNF  6        0.4897
250.0    24.00  0.60     Sequence
             DRB1_1302   11      LVLLPLVSSQCVNFT  LVSSQCVNF  5        0.5142
191.8    21.00  0.54     Sequence
             DRB1_1302   12      VLLPLVSSQCVNFTN  LVSSQCVNF  4        0.5154
189.2    20.00  0.56     Sequence
             DRB1_1302   13      LLPLVSSQCVNFTNR  LVSSQCVNF  3        0.5019
219.1    22.00  0.58     Sequence
             DRB1_1302   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.5007
221.9    22.00  0.47     Sequence
             DRB1_1302   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.4601
344.5    28.00  0.34     Sequence
             DRB1_1302   16      LVSSQCVNFTNRTQL  QCVNFTNRT  4        0.4875
256.0    24.00  0.31     Sequence
             DRB1_1302   17      VSSQCVNFTNRTQLP  NFTNRTQLP  6        0.5312
159.5    18.00  0.42     Sequence
             DRB1_1302   18      SSQCVNFTNRTQLPS  NFTNRTQLP  5        0.5270
167.0    19.00  0.46     Sequence
```

```
             DRB1_1302   19      SQCVNFTNRTQLPSA  NFTNRTQLP  4        0.5188
182.4    20.00  0.49     Sequence
             DRB1_1302   20      QCVNFTNRTQLPSAY  NFTNRTQLP  3        0.5034
215.5    22.00  0.52     Sequence
             DRB1_1302   21      CVNFTNRTQLPSAYT  NFTNRTQLP  2        0.4490
388.1    30.00  0.56     Sequence
             DRB1_1302   22      VNFTNRTQLPSAYTN  NFTNRTQLP  1        0.3908
728.7    39.00  0.57     Sequence
             DRB1_1302   23      NFTNRTQLPSAYTNS  NFTNRTQLP  0        0.2728
2612.6    65.00  0.44     Sequence
             DRB1_1302   24      FTNRTQLPSAYTNSF  LPSAYTNSF  6        0.2292
4186.0    75.00  0.44     Sequence
             DRB1_1302   25      TNRTQLPSAYTNSFT  LPSAYTNSF  5        0.2340
3977.6    75.00  0.49     Sequence
             DRB1_1302   26      NRTQLPSAYTNSFTR  LPSAYTNSF  4        0.2268
4299.3    75.00  0.50     Sequence
             DRB1_1302   27      RTQLPSAYTNSFTRG  AYTNSFTRG  6        0.2902
2164.4    60.00  0.43     Sequence
             DRB1_1302   28      TQLPSAYTNSFTRGV  AYTNSFTRG  5        0.3229
1519.3    55.00  0.38     Sequence
             DRB1_1302   29      QLPSAYTNSFTRGVY  AYTNSFTRG  4        0.3238
1505.4    55.00  0.43     Sequence
             DRB1_1302   30      LPSAYTNSFTRGVYY  AYTNSFTRG  3        0.3602
1014.7    45.00  0.38     Sequence
             DRB1_1302   31      PSAYTNSFTRGVYYP  AYTNSFTRG  2        0.3334
1356.3    55.00  0.37     Sequence
             DRB1_1302   32      SAYTNSFTRGVYYPD  NSFTRGVYY  4        0.3119
1712.3    60.00  0.34     Sequence
             DRB1_1302   33      AYTNSFTRGVYYPDK  NSFTRGVYY  3        0.2652
2837.0    70.00  0.44     Sequence
             DRB1_1302   34      YTNSFTRGVYYPDKV  NSFTRGVYY  2        0.2256
4353.1    75.00  0.44     Sequence
             DRB1_1302   35      TNSFTRGVYYPDKVF  NSFTRGVYY  1        0.2259
4340.8    75.00  0.31     Sequence
             DRB1_1302   36      NSFTRGVYYPDKVFR  RGVYYPDKV  4        0.2341
3972.2    75.00  0.22     Sequence
             DRB1_1302   37      SFTRGVYYPDKVFRS  YYPDKVFRS  6        0.3462
1180.2    48.00  0.65     Sequence
             DRB1_1302   38      FTRGVYYPDKVFRSS  YYPDKVFRS  5        0.3616
999.3    45.00  0.70     Sequence
             DRB1_1302   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.3821
800.9    41.00  0.72     Sequence
             DRB1_1302   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.4458
402.2    30.00  0.57     Sequence
             DRB1_1302   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.4358
447.9    32.00  0.47     Sequence
             DRB1_1302   42      VYYPDKVFRSSVLHS  VFRSSVLHS  6        0.6260
57.2     9.50  0.65     Sequence         WB
             DRB1_1302   43      YYPDKVFRSSVLHST  VFRSSVLHS  5        0.6424
47.9     8.50  0.68     Sequence         WB
             DRB1_1302   44      YPDKVFRSSVLHSTQ  VFRSSVLHS  4        0.6376
50.5     9.00  0.72     Sequence         WB
             DRB1_1302   45      PDKVFRSSVLHSTQD  VFRSSVLHS  3        0.6283
55.8     9.50  0.72     Sequence         WB
             DRB1_1302   46      DKVFRSSVLHSTQDL  VFRSSVLHS  2        0.6155
64.1    11.00  0.68     Sequence
             DRB1_1302   47      KVFRSSVLHSTQDLF  VFRSSVLHS  1        0.5966
78.6    12.00  0.56     Sequence
             DRB1_1302   48      VFRSSVLHSTQDLFL  VFRSSVLHS  0        0.5128
194.6    21.00  0.37     Sequence
             DRB1_1302   49      FRSSVLHSTQDLFLP  VLHSTQDLF  4        0.3939
704.7    39.00  0.36     Sequence
             DRB1_1302   50      RSSVLHSTQDLFLPF  VLHSTQDLF  3        0.3933
709.4    39.00  0.40     Sequence
             DRB1_1302   51      SSVLHSTQDLFLPFF  VLHSTQDLF  2        0.3631
983.5    45.00  0.38     Sequence
```

```
             DRB1_1302   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2        0.3094
1757.9    60.00  0.34     Sequence
             DRB1_1302   53      VLHSTQDLFLPFFSN  LHSTQDLFL  1        0.2339
3978.2    75.00  0.31     Sequence
             DRB1_1302   54      LHSTQDLFLPFFSNV  LFLPFFSNV  6        0.2388
3775.3    75.00  0.48     Sequence
             DRB1_1302   55      HSTQDLFLPFFSNVT  LFLPFFSNV  5        0.2634
2891.5    70.00  0.42     Sequence
             DRB1_1302   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.2701
2690.4    65.00  0.29     Sequence
             DRB1_1302   57      TQDLFLPFFSNVTWF  PFFSNVTWF  6        0.4628
334.2    27.00  0.54     Sequence
             DRB1_1302   58      QDLFLPFFSNVTWFH  FFSNVTWFH  6        0.5162
187.7    20.00  0.37     Sequence
             DRB1_1302   59      DLFLPFFSNVTWFHA  FFSNVTWFH  5        0.5296
162.4    19.00  0.37     Sequence
             DRB1_1302   60      LFLPFFSNVTWFHAI  FFSNVTWFH  4        0.5492
131.3    17.00  0.41     Sequence
             DRB1_1302   61      FLPFFSNVTWFHAIH  FFSNVTWFH  3        0.5293
162.8    19.00  0.45     Sequence
             DRB1_1302   62      LPFFSNVTWFHAIHV  FFSNVTWFH  2        0.5303
161.1    19.00  0.37     Sequence
             DRB1_1302   63      PFFSNVTWFHAIHVS  FFSNVTWFH  1        0.4875
256.0    24.00  0.34     Sequence
             DRB1_1302   64      FFSNVTWFHAIHVSG  VTWFHAIHV  4        0.3715
898.0    43.00  0.38     Sequence
             DRB1_1302   65      FSNVTWFHAIHVSGT  VTWFHAIHV  3        0.3253
1480.2    55.00  0.54     Sequence
             DRB1_1302   66      SNVTWFHAIHVSGTN  VTWFHAIHV  2        0.3087
1772.3    60.00  0.56     Sequence
             DRB1_1302   67      NVTWFHAIHVSGTNG  VTWFHAIHV  1        0.3180
1601.5    55.00  0.47     Sequence
             DRB1_1302   68      VTWFHAIHVSGTNGT  IHVSGTNGT  6        0.5036
215.0    22.00  0.75     Sequence
             DRB1_1302   69      TWFHAIHVSGTNGTK  IHVSGTNGT  5        0.5081
204.8    21.00  0.82     Sequence
             DRB1_1302   70      WFHAIHVSGTNGTKR  IHVSGTNGT  4        0.5215
177.2    20.00  0.77     Sequence
             DRB1_1302   71      FHAIHVSGTNGTKRF  IHVSGTNGT  3        0.5350
153.0    18.00  0.75     Sequence
             DRB1_1302   72      HAIHVSGTNGTKRFD  IHVSGTNGT  2        0.5052
211.5    22.00  0.71     Sequence
             DRB1_1302   73      AIHVSGTNGTKRFDN  IHVSGTNGT  1        0.4417
420.3    31.00  0.61     Sequence
             DRB1_1302   74      IHVSGTNGTKRFDNP  IHVSGTNGT  0        0.3025
1894.4    60.00  0.42     Sequence
             DRB1_1302   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.1832
6885.6    85.00  0.50     Sequence
             DRB1_1302   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.2001
5738.3    85.00  0.19     Sequence
             DRB1_1302   77      SGTNGTKRFDNPVLP  KRFDNPVLP  6        0.3425
1228.4    49.00  0.69     Sequence
             DRB1_1302   78      GTNGTKRFDNPVLPF  RFDNPVLPF  6        0.5479
133.2    17.00  0.57     Sequence
             DRB1_1302   79      TNGTKRFDNPVLPFN  RFDNPVLPF  5        0.5498
130.5    16.00  0.53     Sequence
             DRB1_1302   80      NGTKRFDNPVLPFND  RFDNPVLPF  4        0.5459
136.1    17.00  0.55     Sequence
             DRB1_1302   81      GTKRFDNPVLPFNDG  RFDNPVLPF  3        0.5228
174.7    20.00  0.56     Sequence
             DRB1_1302   82      TKRFDNPVLPFNDGV  RFDNPVLPF  2        0.4917
244.6    23.00  0.56     Sequence
             DRB1_1302   83      KRFDNPVLPFNDGVY  RFDNPVLPF  1        0.4754
291.8    26.00  0.49     Sequence
             DRB1_1302   84      RFDNPVLPFNDGVYF  LPFNDGVYF  6        0.5584
118.8    16.00  0.62     Sequence
```

```
             DRB1_1302   85      FDNPVLPFNDGVYFA  LPFNDGVYF  5        0.5550
123.3    16.00  0.77     Sequence
             DRB1_1302   86      DNPVLPFNDGVYFAS  LPFNDGVYF  4        0.5621
114.2    15.00  0.78     Sequence
             DRB1_1302   87      NPVLPFNDGVYFAST  LPFNDGVYF  3        0.5616
114.8    15.00  0.77     Sequence
             DRB1_1302   88      PVLPFNDGVYFASTE  LPFNDGVYF  2        0.5286
164.0    19.00  0.79     Sequence
             DRB1_1302   89      VLPFNDGVYFASTEK  LPFNDGVYF  1        0.4753
292.3    26.00  0.74     Sequence
             DRB1_1302   90      LPFNDGVYFASTEKS  VYFASTEKS  6        0.4235
511.6    34.00  0.47     Sequence
             DRB1_1302   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.3475
1164.6    48.00  0.81     Sequence
             DRB1_1302   92      FNDGVYFASTEKSNI  VYFASTEKS  4        0.3809
811.5    41.00  0.78     Sequence
             DRB1_1302   93      NDGVYFASTEKSNII  VYFASTEKS  3        0.4402
426.9    31.00  0.60     Sequence
             DRB1_1302   94      DGVYFASTEKSNIIR  VYFASTEKS  2        0.4223
518.2    34.00  0.56     Sequence
             DRB1_1302   95      GVYFASTEKSNIIRG  VYFASTEKS  1        0.4047
627.1    37.00  0.46     Sequence
             DRB1_1302   96      VYFASTEKSNIIRGW  ASTEKSNII  3        0.3583
1036.2    46.00  0.32     Sequence
             DRB1_1302   97      YFASTEKSNIIRGWI  ASTEKSNII  2        0.3294
1416.8    55.00  0.34     Sequence
             DRB1_1302   98      FASTEKSNIIRGWIF  TEKSNIIRG  3        0.3427
1226.0    49.00  0.31     Sequence
             DRB1_1302   99      ASTEKSNIIRGWIFG  EKSNIIRGW  3        0.3150
1654.8    55.00  0.31     Sequence
             DRB1_1302  100      STEKSNIIRGWIFGT  IIRGWIFGT  6        0.3402
1259.6    49.00  0.33     Sequence
             DRB1_1302  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5        0.3238
1504.6    55.00  0.43     Sequence
             DRB1_1302  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.3236
1507.3    55.00  0.44     Sequence
             DRB1_1302  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3        0.3009
1927.1    60.00  0.47     Sequence
             DRB1_1302  104      SNIIRGWIFGTTLDS  IIRGWIFGT  2        0.2698
2699.2    65.00  0.43     Sequence
             DRB1_1302  105      NIIRGWIFGTTLDSK  IIRGWIFGT  1        0.2416
3662.1    75.00  0.34     Sequence
             DRB1_1302  106      IIRGWIFGTTLDSKT  IFGTTLDSK  5        0.1882
6522.7    85.00  0.22     Sequence
             DRB1_1302  107      IRGWIFGTTLDSKTQ  IFGTTLDSK  4        0.1483
10043.8    95.00  0.32     Sequence
             DRB1_1302  108      RGWIFGTTLDSKTQS  IFGTTLDSK  3        0.1310
12119.0    95.00  0.39     Sequence
             DRB1_1302  109      GWIFGTTLDSKTQSL  TLDSKTQSL  6        0.2022
5606.1    80.00  0.55     Sequence
             DRB1_1302  110      WIFGTTLDSKTQSLL  TLDSKTQSL  5        0.2060
5381.0    80.00  0.54     Sequence
             DRB1_1302  111      IFGTTLDSKTQSLLI  DSKTQSLLI  6        0.3385
1283.7    50.00  0.54     Sequence
             DRB1_1302  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5        0.3761
854.3    42.00  0.46     Sequence
             DRB1_1302  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4        0.3632
982.6    45.00  0.47     Sequence
             DRB1_1302  114      TTLDSKTQSLLIVNN  DSKTQSLLI  3        0.3430
1222.7    49.00  0.50     Sequence
             DRB1_1302  115      TLDSKTQSLLIVNNA  DSKTQSLLI  2        0.3281
1436.2    55.00  0.49     Sequence
             DRB1_1302  116      LDSKTQSLLIVNNAT  DSKTQSLLI  1        0.3332
1359.6    55.00  0.34     Sequence
             DRB1_1302  117      DSKTQSLLIVNNATN  LLIVNNATN  6        0.4012
651.5    38.00  0.41     Sequence
```

```
            DRB1_1302  118      SKTQSLLIVNNATNV  LIVNNATNV  6        0.9306
2.1     0.05  0.81     Sequence         SB
            DRB1_1302  119      KTQSLLIVNNATNVV  IVNNATNVV  6        0.9653
1.5     0.01  0.49     Sequence         SB
            DRB1_1302  120      TQSLLIVNNATNVVI  IVNNATNVV  5        0.9716
1.4     0.01  0.46     Sequence         SB
            DRB1_1302  121      QSLLIVNNATNVVIK  IVNNATNVV  4        0.9717
1.4     0.01  0.44     Sequence         SB
            DRB1_1302  122      SLLIVNNATNVVIKV  IVNNATNVV  3        0.9700
1.4     0.01  0.50     Sequence         SB
            DRB1_1302  123      LLIVNNATNVVIKVC  IVNNATNVV  2        0.9630
1.5     0.01  0.51     Sequence         SB
            DRB1_1302  124      LIVNNATNVVIKVCE  IVNNATNVV  1        0.9465
1.8     0.02  0.60     Sequence         SB
            DRB1_1302  125      IVNNATNVVIKVCEF  IVNNATNVV  0        0.8533
4.9     0.70  0.67     Sequence         SB
            DRB1_1302  126      VNNATNVVIKVCEFQ  NATNVVIKV  2        0.4845
264.6    24.00  0.69     Sequence
            DRB1_1302  127      NNATNVVIKVCEFQF  NATNVVIKV  1        0.4141
566.3    35.00  0.58     Sequence
            DRB1_1302  128      NATNVVIKVCEFQFC  NATNVVIKV  0        0.3377
1294.0    50.00  0.33     Sequence
            DRB1_1302  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.2725
2620.1    65.00  0.38     Sequence
            DRB1_1302  130      TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.2699
2697.2    65.00  0.40     Sequence
            DRB1_1302  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.2535
3218.4    70.00  0.38     Sequence
            DRB1_1302  132      VVIKVCEFQFCNYPF  IKVCEFQFC  2        0.2755
2537.6    65.00  0.28     Sequence
            DRB1_1302  133      VIKVCEFQFCNYPFL  FQFCNYPFL  6        0.3302
1403.7    55.00  0.41     Sequence
            DRB1_1302  134      IKVCEFQFCNYPFLG  QFCNYPFLG  6        0.3592
1025.4    45.00  0.37     Sequence
            DRB1_1302  135      KVCEFQFCNYPFLGV  QFCNYPFLG  5        0.3906
730.8    40.00  0.32     Sequence
            DRB1_1302  136      VCEFQFCNYPFLGVY  QFCNYPFLG  4        0.3879
752.3    40.00  0.34     Sequence
            DRB1_1302  137      CEFQFCNYPFLGVYY  QFCNYPFLG  3        0.3820
802.0    41.00  0.35     Sequence
            DRB1_1302  138      EFQFCNYPFLGVYYH  QFCNYPFLG  2        0.3546
1078.7    46.00  0.39     Sequence
            DRB1_1302  139      FQFCNYPFLGVYYHK  QFCNYPFLG  1        0.2463
3482.0    70.00  0.39     Sequence
            DRB1_1302  140      QFCNYPFLGVYYHKN  FLGVYYHKN  6        0.2064
5361.4    80.00  0.23     Sequence
            DRB1_1302  141      FCNYPFLGVYYHKNN  FLGVYYHKN  5        0.1546
9390.1    90.00  0.37     Sequence
            DRB1_1302  142      CNYPFLGVYYHKNNK  FLGVYYHKN  4        0.1622
8642.1    90.00  0.44     Sequence
            DRB1_1302  143      NYPFLGVYYHKNNKS  VYYHKNNKS  6        0.3043
1857.9    60.00  0.63     Sequence
            DRB1_1302  144      YPFLGVYYHKNNKSW  VYYHKNNKS  5        0.3457
1187.0    48.00  0.58     Sequence
            DRB1_1302  145      PFLGVYYHKNNKSWM  VYYHKNNKS  4        0.4056
620.9    37.00  0.49     Sequence
            DRB1_1302  146      FLGVYYHKNNKSWME  VYYHKNNKS  3        0.4218
521.0    34.00  0.44     Sequence
            DRB1_1302  147      LGVYYHKNNKSWMES  VYYHKNNKS  2        0.4131
572.7    35.00  0.40     Sequence
            DRB1_1302  148      GVYYHKNNKSWMESE  VYYHKNNKS  1        0.3952
695.2    39.00  0.36     Sequence
            DRB1_1302  149      VYYHKNNKSWMESEF  HKNNKSWME  3        0.3446
1201.6    48.00  0.31     Sequence
            DRB1_1302  150      YYHKNNKSWMESEFR  HKNNKSWME  2        0.2502
3336.0    70.00  0.41     Sequence
```

```
            DRB1_1302  151      YHKNNKSWMESEFRV  HKNNKSWME  1        0.1824
6949.6    85.00  0.36    Sequence
            DRB1_1302  152      HKNNKSWMESEFRVY  WMESEFRVY  6        0.1691
8024.7    90.00  0.34    Sequence
            DRB1_1302  153      KNNKSWMESEFRVYS  WMESEFRVY  5        0.1546
9389.0    90.00  0.40    Sequence
            DRB1_1302  154      NNKSWMESEFRVYSS  WMESEFRVY  4        0.1437
10562.2    95.00  0.42    Sequence
            DRB1_1302  155      NKSWMESEFRVYSSA  WMESEFRVY  3        0.1391
11104.7    95.00  0.47    Sequence
            DRB1_1302  156      KSWMESEFRVYSSAN  WMESEFRVY  2        0.1770
7369.3    85.00  0.36    Sequence
            DRB1_1302  157      SWMESEFRVYSSANN  FRVYSSANN  6        0.2072
5312.9    80.00  0.38    Sequence
            DRB1_1302  158      WMESEFRVYSSANNC  RVYSSANNC  6        0.2905
2157.8    60.00  0.51    Sequence
            DRB1_1302  159      MESEFRVYSSANNCT  VYSSANNCT  6        0.4593
347.3    28.00  0.57    Sequence
            DRB1_1302  160      ESEFRVYSSANNCTF  VYSSANNCT  5        0.4986
227.1    23.00  0.54    Sequence
            DRB1_1302  161      SEFRVYSSANNCTFE  VYSSANNCT  4        0.4974
230.0    23.00  0.56    Sequence
            DRB1_1302  162      EFRVYSSANNCTFEY  VYSSANNCT  3        0.4917
244.7    23.00  0.55    Sequence
            DRB1_1302  163      FRVYSSANNCTFEYV  VYSSANNCT  2        0.4435
412.0    30.00  0.54    Sequence
            DRB1_1302  164      RVYSSANNCTFEYVS  VYSSANNCT  1        0.3755
860.0    42.00  0.51    Sequence
            DRB1_1302  165      VYSSANNCTFEYVSQ  VYSSANNCT  0        0.2481
3413.4    70.00  0.35    Sequence
            DRB1_1302  166      YSSANNCTFEYVSQP  SANNCTFEY  2        0.1364
11428.6    95.00  0.41    Sequence
            DRB1_1302  167      SSANNCTFEYVSQPF  TFEYVSQPF  6        0.1567
9171.4    90.00  0.38    Sequence
            DRB1_1302  168      SANNCTFEYVSQPFL  TFEYVSQPF  5        0.1990
5809.1    85.00  0.36    Sequence
            DRB1_1302  169      ANNCTFEYVSQPFLM  EYVSQPFLM  6        0.3582
1036.9    46.00  0.61    Sequence
            DRB1_1302  170      NNCTFEYVSQPFLMD  EYVSQPFLM  5        0.3507
1124.2    47.00  0.54    Sequence
            DRB1_1302  171      NCTFEYVSQPFLMDL  EYVSQPFLM  4        0.3550
1073.3    46.00  0.56    Sequence
            DRB1_1302  172      CTFEYVSQPFLMDLE  EYVSQPFLM  3        0.3353
1328.7    50.00  0.57    Sequence
            DRB1_1302  173      TFEYVSQPFLMDLEG  EYVSQPFLM  2        0.3108
1732.2    60.00  0.58    Sequence
            DRB1_1302  174      FEYVSQPFLMDLEGK  EYVSQPFLM  1        0.2449
3535.2    75.00  0.55    Sequence
            DRB1_1302  175      EYVSQPFLMDLEGKQ  EYVSQPFLM  0        0.1863
6659.2    85.00  0.39    Sequence
            DRB1_1302  176      YVSQPFLMDLEGKQG  FLMDLEGKQ  5        0.1046
16130.9   100.00  0.40    Sequence
            DRB1_1302  177      VSQPFLMDLEGKQGN  FLMDLEGKQ  4        0.0946
17973.0   100.00  0.55    Sequence
            DRB1_1302  178      SQPFLMDLEGKQGNF  FLMDLEGKQ  3        0.1108
15078.5   100.00  0.49    Sequence
            DRB1_1302  179      QPFLMDLEGKQGNFK  LEGKQGNFK  6        0.1287
12418.0    95.00  0.38    Sequence
            DRB1_1302  180      PFLMDLEGKQGNFKN  LEGKQGNFK  5        0.1237
13116.1    95.00  0.49    Sequence
            DRB1_1302  181      FLMDLEGKQGNFKNL  LEGKQGNFK  4        0.1362
11449.3    95.00  0.50    Sequence
            DRB1_1302  182      LMDLEGKQGNFKNLS  LEGKQGNFK  3        0.1494
9931.6    90.00  0.45    Sequence
            DRB1_1302  183      MDLEGKQGNFKNLSE  LEGKQGNFK  2        0.1371
11340.9    95.00  0.44    Sequence
```

```
             DRB1_1302  184      DLEGKQGNFKNLSEF  LEGKQGNFK  1        0.1407
10907.3    95.00  0.31     Sequence
             DRB1_1302  185      LEGKQGNFKNLSEFV  NFKNLSEFV  6        0.4859
260.4    24.00  0.75     Sequence
             DRB1_1302  186      EGKQGNFKNLSEFVF  NFKNLSEFV  5        0.5262
168.4    19.00  0.69     Sequence
             DRB1_1302  187      GKQGNFKNLSEFVFK  NFKNLSEFV  4        0.5300
161.5    19.00  0.70     Sequence
             DRB1_1302  188      KQGNFKNLSEFVFKN  NFKNLSEFV  3        0.5288
163.8    19.00  0.69     Sequence
             DRB1_1302  189      QGNFKNLSEFVFKNI  NFKNLSEFV  2        0.5165
187.1    20.00  0.58     Sequence
             DRB1_1302  190      GNFKNLSEFVFKNID  NFKNLSEFV  1        0.4652
325.7    27.00  0.56     Sequence
             DRB1_1302  191      NFKNLSEFVFKNIDG  NFKNLSEFV  0        0.3728
885.1    43.00  0.40     Sequence
             DRB1_1302  192      FKNLSEFVFKNIDGY  FVFKNIDGY  6        0.3354
1327.7    50.00  0.31     Sequence
             DRB1_1302  193      KNLSEFVFKNIDGYF  VFKNIDGYF  6        0.5275
166.0    19.00  0.61     Sequence
             DRB1_1302  194      NLSEFVFKNIDGYFK  VFKNIDGYF  5        0.5398
145.3    18.00  0.59     Sequence
             DRB1_1302  195      LSEFVFKNIDGYFKI  VFKNIDGYF  4        0.5809
93.2    13.00  0.55     Sequence
             DRB1_1302  196      SEFVFKNIDGYFKIY  VFKNIDGYF  3        0.5871
87.1    13.00  0.57     Sequence
             DRB1_1302  197      EFVFKNIDGYFKIYS  VFKNIDGYF  2        0.5636
112.4    15.00  0.58     Sequence
             DRB1_1302  198      FVFKNIDGYFKIYSK  VFKNIDGYF  1        0.5038
214.5    22.00  0.52     Sequence
             DRB1_1302  199      VFKNIDGYFKIYSKH  VFKNIDGYF  0        0.3514
1116.5    47.00  0.41     Sequence
             DRB1_1302  200      FKNIDGYFKIYSKHT  KNIDGYFKI  1        0.2461
3489.5    70.00  0.31     Sequence
             DRB1_1302  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.2031
5552.1    80.00  0.38     Sequence
             DRB1_1302  202      NIDGYFKIYSKHTPI  KIYSKHTPI  6        0.4589
348.8    28.00  0.67     Sequence
             DRB1_1302  203      IDGYFKIYSKHTPIN  KIYSKHTPI  5        0.4891
251.6    24.00  0.60     Sequence
             DRB1_1302  204      DGYFKIYSKHTPINL  KIYSKHTPI  4        0.5549
123.5    16.00  0.47     Sequence
             DRB1_1302  205      GYFKIYSKHTPINLV  KIYSKHTPI  3        0.6416
48.3     8.50  0.37     Sequence        WB
             DRB1_1302  206      YFKIYSKHTPINLVR  KIYSKHTPI  2        0.6141
65.1    11.00  0.31     Sequence
             DRB1_1302  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.5868
87.5    13.00  0.32     Sequence
             DRB1_1302  208      KIYSKHTPINLVRDL  SKHTPINLV  3        0.5408
143.8    17.00  0.33     Sequence
             DRB1_1302  209      IYSKHTPINLVRDLP  SKHTPINLV  2        0.3769
847.2    42.00  0.39     Sequence
             DRB1_1302  210      YSKHTPINLVRDLPQ  SKHTPINLV  1        0.3510
1121.1    47.00  0.33     Sequence
             DRB1_1302  211      SKHTPINLVRDLPQG  INLVRDLPQ  5        0.3182
1598.5    55.00  0.35     Sequence
             DRB1_1302  212      KHTPINLVRDLPQGF  LVRDLPQGF  6        0.5621
114.2    15.00  0.78     Sequence
             DRB1_1302  213      HTPINLVRDLPQGFS  LVRDLPQGF  5        0.5855
88.6    13.00  0.80     Sequence
             DRB1_1302  214      TPINLVRDLPQGFSA  LVRDLPQGF  4        0.5970
78.3    12.00  0.81     Sequence
             DRB1_1302  215      PINLVRDLPQGFSAL  LVRDLPQGF  3        0.6150
64.5    11.00  0.79     Sequence
             DRB1_1302  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.5884
85.9    13.00  0.81     Sequence
```

```
             DRB1_1302  217      NLVRDLPQGFSALEP  LVRDLPQGF  1        0.5063
208.9    22.00  0.79     Sequence
             DRB1_1302  218      LVRDLPQGFSALEPL  LVRDLPQGF  0        0.3632
982.4    45.00  0.60     Sequence
             DRB1_1302  219      VRDLPQGFSALEPLV  GFSALEPLV  6        0.2065
5352.7    80.00  0.28     Sequence
             DRB1_1302  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.2100
5152.8    80.00  0.32     Sequence
             DRB1_1302  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.2136
4956.7    80.00  0.36     Sequence
             DRB1_1302  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.1868
6622.1    85.00  0.41     Sequence
             DRB1_1302  223      PQGFSALEPLVDLPI  LEPLVDLPI  6        0.2557
3144.4    70.00  0.38     Sequence
             DRB1_1302  224      QGFSALEPLVDLPIG  LEPLVDLPI  5        0.2445
3549.1    75.00  0.44     Sequence
             DRB1_1302  225      GFSALEPLVDLPIGI  PLVDLPIGI  6        0.5790
95.1    14.00  0.78     Sequence
             DRB1_1302  226      FSALEPLVDLPIGIN  PLVDLPIGI  5        0.5867
87.5    13.00  0.79     Sequence
             DRB1_1302  227      SALEPLVDLPIGINI  PLVDLPIGI  4        0.6171
63.0    11.00  0.74     Sequence
             DRB1_1302  228      ALEPLVDLPIGINIT  PLVDLPIGI  3        0.6400
49.1     8.50  0.69     Sequence         WB
             DRB1_1302  229      LEPLVDLPIGINITR  PLVDLPIGI  2        0.6187
61.9    10.00  0.68     Sequence
             DRB1_1302  230      EPLVDLPIGINITRF  PLVDLPIGI  1        0.6475
45.3     8.00  0.45     Sequence         WB
             DRB1_1302  231      PLVDLPIGINITRFQ  IGINITRFQ  6        0.6426
47.8     8.50  0.34     Sequence         WB
             DRB1_1302  232      LVDLPIGINITRFQT  IGINITRFQ  5        0.5906
83.9    13.00  0.50     Sequence
             DRB1_1302  233      VDLPIGINITRFQTL  IGINITRFQ  4        0.6570
40.9     7.50  0.41     Sequence         WB
             DRB1_1302  234      DLPIGINITRFQTLL  IGINITRFQ  3        0.6594
39.9     7.50  0.43     Sequence         WB
             DRB1_1302  235      LPIGINITRFQTLLA  IGINITRFQ  2        0.6472
45.5     8.00  0.38     Sequence         WB
             DRB1_1302  236      PIGINITRFQTLLAL  IGINITRFQ  1        0.6320
53.6     9.00  0.28     Sequence         WB
             DRB1_1302  237      IGINITRFQTLLALH  INITRFQTL  2        0.5672
108.0    15.00  0.33     Sequence
             DRB1_1302  238      GINITRFQTLLALHR  ITRFQTLLA  3        0.5059
209.7    22.00  0.32     Sequence
             DRB1_1302  239      INITRFQTLLALHRS  ITRFQTLLA  2        0.4450
405.5    30.00  0.35     Sequence
             DRB1_1302  240      NITRFQTLLALHRSY  TRFQTLLAL  2        0.3737
876.6    43.00  0.32     Sequence
             DRB1_1302  241      ITRFQTLLALHRSYL  LLALHRSYL  6        0.4003
657.5    38.00  0.38     Sequence
             DRB1_1302  242      TRFQTLLALHRSYLT  LALHRSYLT  6        0.4331
461.1    32.00  0.41     Sequence
             DRB1_1302  243      RFQTLLALHRSYLTP  LALHRSYLT  5        0.4431
413.7    30.00  0.51     Sequence
             DRB1_1302  244      FQTLLALHRSYLTPG  LALHRSYLT  4        0.4487
389.4    30.00  0.52     Sequence
             DRB1_1302  245      QTLLALHRSYLTPGD  LALHRSYLT  3        0.4391
432.1    31.00  0.58     Sequence
             DRB1_1302  246      TLLALHRSYLTPGDS  LALHRSYLT  2        0.4083
603.1    36.00  0.56     Sequence
             DRB1_1302  247      LLALHRSYLTPGDSS  LALHRSYLT  1        0.3685
927.3    44.00  0.51     Sequence
             DRB1_1302  248      LALHRSYLTPGDSSS  LALHRSYLT  0        0.2769
2500.2    65.00  0.42     Sequence
             DRB1_1302  249      ALHRSYLTPGDSSSG  LHRSYLTPG  1        0.1621
8656.0    90.00  0.47     Sequence
```

```
             DRB1_1302  250      LHRSYLTPGDSSSGW  LTPGDSSSG  5        0.1054
15978.1   100.00  0.28     Sequence
             DRB1_1302  251      HRSYLTPGDSSSGWT  LTPGDSSSG  4        0.0864
19629.3   100.00  0.43     Sequence
             DRB1_1302  252      RSYLTPGDSSSGWTA  LTPGDSSSG  3        0.0931
18250.1   100.00  0.40     Sequence
             DRB1_1302  253      SYLTPGDSSSGWTAG  LTPGDSSSG  2        0.0820
20600.6   100.00  0.38     Sequence
             DRB1_1302  254      YLTPGDSSSGWTAGA  GDSSSGWTA  4        0.0658
24525.2   100.00  0.32     Sequence
             DRB1_1302  255      LTPGDSSSGWTAGAA  GDSSSGWTA  3        0.0495
29279.8   100.00  0.41     Sequence
             DRB1_1302  256      TPGDSSSGWTAGAAA  GDSSSGWTA  2        0.0477
29827.9   100.00  0.31     Sequence
             DRB1_1302  257      PGDSSSGWTAGAAAY  GWTAGAAAY  6        0.0738
22494.8   100.00  0.44     Sequence
             DRB1_1302  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.1217
13405.4    95.00  0.47     Sequence
             DRB1_1302  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.1717
7800.1    90.00  0.37    Sequence
             DRB1_1302  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.1677
8145.4    90.00  0.41    Sequence
             DRB1_1302  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.1726
7725.2    90.00  0.39    Sequence
             DRB1_1302  262      SGWTAGAAAYYVGYL  TAGAAAYYV  3        0.1728
7704.7    90.00  0.34    Sequence
             DRB1_1302  263      GWTAGAAAYYVGYLQ  TAGAAAYYV  2        0.1493
9937.1    90.00  0.32    Sequence
             DRB1_1302  264      WTAGAAAYYVGYLQP  TAGAAAYYV  1        0.1174
14037.3    95.00  0.28     Sequence
             DRB1_1302  265      TAGAAAYYVGYLQPR  YYVGYLQPR  6        0.1398
11017.4    95.00  0.35     Sequence
             DRB1_1302  266      AGAAAYYVGYLQPRT  YYVGYLQPR  5        0.1514
9722.4    90.00  0.43    Sequence
             DRB1_1302  267      GAAAYYVGYLQPRTF  VGYLQPRTF  6        0.2284
4221.9    75.00  0.42    Sequence
             DRB1_1302  268      AAAYYVGYLQPRTFL  VGYLQPRTF  5        0.2835
2327.5    65.00  0.39    Sequence
             DRB1_1302  269      AAYYVGYLQPRTFLL  VGYLQPRTF  4        0.3409
1249.9    49.00  0.32    Sequence
             DRB1_1302  270      AYYVGYLQPRTFLLK  VGYLQPRTF  3        0.3427
1226.1    49.00  0.34    Sequence
             DRB1_1302  271      YYVGYLQPRTFLLKY  VGYLQPRTF  2        0.3336
1353.5    55.00  0.32    Sequence
             DRB1_1302  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.3036
1873.3    60.00  0.34    Sequence
             DRB1_1302  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.2441
3565.0    75.00  0.38    Sequence
             DRB1_1302  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.2036
5521.2    80.00  0.37    Sequence
             DRB1_1302  275      YLQPRTFLLKYNENG  FLLKYNENG  6        0.1899
6405.3    85.00  0.25    Sequence
             DRB1_1302  276      LQPRTFLLKYNENGT  FLLKYNENG  5        0.2256
4353.3    75.00  0.30    Sequence
             DRB1_1302  277      QPRTFLLKYNENGTI  LKYNENGTI  6        0.7333
17.9     4.00  0.87     Sequence         WB
             DRB1_1302  278      PRTFLLKYNENGTIT  LKYNENGTI  5        0.7574
13.8     3.00  0.86     Sequence         WB
             DRB1_1302  279      RTFLLKYNENGTITD  LKYNENGTI  4        0.7577
13.8     3.00  0.86     Sequence         WB
             DRB1_1302  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.7568
13.9     3.00  0.87     Sequence         WB
             DRB1_1302  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.7338
17.8     4.00  0.86     Sequence         WB
             DRB1_1302  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.6793
32.1     6.50  0.81     Sequence         WB
```

```
             DRB1_1302  283      LKYNENGTITDAVDC  LKYNENGTI  0        0.5505
129.5    16.00  0.72     Sequence
             DRB1_1302  284      KYNENGTITDAVDCA  YNENGTITD  1        0.1503
9830.6    90.00  0.29     Sequence
             DRB1_1302  285      YNENGTITDAVDCAL  ITDAVDCAL  6        0.1555
9291.8    90.00  0.31     Sequence
             DRB1_1302  286      NENGTITDAVDCALD  ITDAVDCAL  5        0.1545
9393.8    90.00  0.34     Sequence
             DRB1_1302  287      ENGTITDAVDCALDP  DAVDCALDP  6        0.1741
7603.8    90.00  0.31     Sequence
             DRB1_1302  288      NGTITDAVDCALDPL  DAVDCALDP  5        0.1893
6450.5    85.00  0.34     Sequence
             DRB1_1302  289      GTITDAVDCALDPLS  DAVDCALDP  4        0.1740
7608.8    90.00  0.43     Sequence
             DRB1_1302  290      TITDAVDCALDPLSE  DAVDCALDP  3        0.1612
8740.4    90.00  0.44     Sequence
             DRB1_1302  291      ITDAVDCALDPLSET  DAVDCALDP  2        0.1422
10736.5    95.00  0.45     Sequence
             DRB1_1302  292      TDAVDCALDPLSETK  DAVDCALDP  1        0.1045
16136.5   100.00  0.35     Sequence
             DRB1_1302  293      DAVDCALDPLSETKC  DCALDPLSE  3        0.0924
18390.5   100.00  0.19     Sequence
             DRB1_1302  294      AVDCALDPLSETKCT  DCALDPLSE  2        0.0804
20946.3   100.00  0.23     Sequence
             DRB1_1302  295      VDCALDPLSETKCTL  LDPLSETKC  4        0.0886
19174.8   100.00  0.21     Sequence
             DRB1_1302  296      DCALDPLSETKCTLK  LSETKCTLK  6        0.1176
14005.9    95.00  0.46     Sequence
             DRB1_1302  297      CALDPLSETKCTLKS  LSETKCTLK  5        0.1191
13781.1    95.00  0.52     Sequence
             DRB1_1302  298      ALDPLSETKCTLKSF  LSETKCTLK  4        0.1293
12337.4    95.00  0.56     Sequence
             DRB1_1302  299      LDPLSETKCTLKSFT  LSETKCTLK  3        0.1207
13548.1    95.00  0.57     Sequence
             DRB1_1302  300      DPLSETKCTLKSFTV  KCTLKSFTV  6        0.1646
8423.7    90.00  0.35     Sequence
             DRB1_1302  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.1494
9928.5    90.00  0.35     Sequence
             DRB1_1302  302      LSETKCTLKSFTVEK  KCTLKSFTV  4        0.1303
12212.2    95.00  0.41     Sequence
             DRB1_1302  303      SETKCTLKSFTVEKG  KCTLKSFTV  3        0.1393
11076.6    95.00  0.35     Sequence
             DRB1_1302  304      ETKCTLKSFTVEKGI  KCTLKSFTV  2        0.1566
9183.5    90.00  0.25     Sequence
             DRB1_1302  305      TKCTLKSFTVEKGIY  LKSFTVEKG  4        0.1620
8667.1    90.00  0.30     Sequence
             DRB1_1302  306      KCTLKSFTVEKGIYQ  LKSFTVEKG  3        0.1660
8299.7    90.00  0.28     Sequence
             DRB1_1302  307      CTLKSFTVEKGIYQT  FTVEKGIYQ  5        0.1511
9748.8    90.00  0.37     Sequence
             DRB1_1302  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.1474
10148.1    95.00  0.38     Sequence
             DRB1_1302  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.1278
12538.9    95.00  0.46     Sequence
             DRB1_1302  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.1290
12385.7    95.00  0.38     Sequence
             DRB1_1302  311      SFTVEKGIYQTSNFR  GIYQTSNFR  6        0.1591
8939.0    90.00  0.31     Sequence
             DRB1_1302  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.5556
122.5    16.00  0.79     Sequence
             DRB1_1302  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.5749
99.4    14.00  0.73     Sequence
             DRB1_1302  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.5723
102.3    14.00  0.74     Sequence
             DRB1_1302  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.5722
102.4    14.00  0.73     Sequence
```

```
             DRB1_1302  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.5415
142.7    17.00  0.71     Sequence
             DRB1_1302  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.4769
287.0    25.00  0.67     Sequence
             DRB1_1302  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.5791
95.0    14.00  0.66     Sequence
             DRB1_1302  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.6409
48.7     8.50  0.77     Sequence         WB
             DRB1_1302  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.6693
35.8     7.00  0.72     Sequence         WB
             DRB1_1302  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.6857
30.0     6.00  0.69     Sequence         WB
             DRB1_1302  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.6631
38.3     7.50  0.68     Sequence         WB
             DRB1_1302  323      NFRVQPTESIVRFPN  FRVQPTESI  1        0.6234
58.8    10.00  0.64     Sequence
             DRB1_1302  324      FRVQPTESIVRFPNI  FRVQPTESI  0        0.5170
186.1    20.00  0.44     Sequence
             DRB1_1302  325      RVQPTESIVRFPNIT  VQPTESIVR  1        0.3369
1306.0    50.00  0.43     Sequence
             DRB1_1302  326      VQPTESIVRFPNITN  IVRFPNITN  6        0.3076
1792.0    60.00  0.31     Sequence
             DRB1_1302  327      QPTESIVRFPNITNL  VRFPNITNL  6        0.4798
278.1    25.00  0.55     Sequence
             DRB1_1302  328      PTESIVRFPNITNLC  VRFPNITNL  5        0.5397
145.6    18.00  0.43     Sequence
             DRB1_1302  329      TESIVRFPNITNLCP  VRFPNITNL  4        0.5339
155.0    18.00  0.44     Sequence
             DRB1_1302  330      ESIVRFPNITNLCPF  VRFPNITNL  3        0.5544
124.1    16.00  0.41     Sequence
             DRB1_1302  331      SIVRFPNITNLCPFG  RFPNITNLC  3        0.5396
145.7    18.00  0.32     Sequence
             DRB1_1302  332      IVRFPNITNLCPFGE  RFPNITNLC  2        0.4949
236.2    23.00  0.34     Sequence
             DRB1_1302  333      VRFPNITNLCPFGEV  RFPNITNLC  1        0.4186
539.3    34.00  0.28     Sequence
             DRB1_1302  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.3456
1188.9    48.00  0.32     Sequence
             DRB1_1302  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.2771
2494.6    65.00  0.43     Sequence
             DRB1_1302  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.2420
3647.3    75.00  0.46     Sequence
             DRB1_1302  337      NITNLCPFGEVFNAT  ITNLCPFGE  1        0.1717
7801.6    90.00  0.42     Sequence
             DRB1_1302  338      ITNLCPFGEVFNATR  ITNLCPFGE  0        0.1098
15245.5   100.00  0.32     Sequence
             DRB1_1302  339      TNLCPFGEVFNATRF  GEVFNATRF  6        0.1769
7377.0    85.00  0.54     Sequence
             DRB1_1302  340      NLCPFGEVFNATRFA  EVFNATRFA  6        0.3073
1798.3    60.00  0.55     Sequence
             DRB1_1302  341      LCPFGEVFNATRFAS  EVFNATRFA  5        0.3277
1443.0    55.00  0.48     Sequence
             DRB1_1302  342      CPFGEVFNATRFASV  FNATRFASV  6        0.4783
282.6    25.00  0.47     Sequence
             DRB1_1302  343      PFGEVFNATRFASVY  FNATRFASV  5        0.4910
246.6    23.00  0.46     Sequence
             DRB1_1302  344      FGEVFNATRFASVYA  FNATRFASV  4        0.4855
261.5    24.00  0.49     Sequence
             DRB1_1302  345      GEVFNATRFASVYAW  FNATRFASV  3        0.4748
293.8    26.00  0.49     Sequence
             DRB1_1302  346      EVFNATRFASVYAWN  FNATRFASV  2        0.4249
504.0    33.00  0.49     Sequence
             DRB1_1302  347      VFNATRFASVYAWNR  FNATRFASV  1        0.3311
1390.2    55.00  0.47     Sequence
             DRB1_1302  348      FNATRFASVYAWNRK  TRFASVYAW  3        0.2541
3199.0    70.00  0.26     Sequence
```

```
             DRB1_1302  349      NATRFASVYAWNRKR  TRFASVYAW  2        0.2173
4762.4    80.00  0.29     Sequence
             DRB1_1302  350      ATRFASVYAWNRKRI  VYAWNRKRI  6        0.3065
1814.6    60.00  0.42     Sequence
             DRB1_1302  351      TRFASVYAWNRKRIS  VYAWNRKRI  5        0.3135
1682.7    55.00  0.38     Sequence
             DRB1_1302  352      RFASVYAWNRKRISN  VYAWNRKRI  4        0.3053
1837.3    60.00  0.40     Sequence
             DRB1_1302  353      FASVYAWNRKRISNC  VYAWNRKRI  3        0.2878
2220.8    65.00  0.40     Sequence
             DRB1_1302  354      ASVYAWNRKRISNCV  NRKRISNCV  6        0.3868
761.0    40.00  0.34     Sequence
             DRB1_1302  355      SVYAWNRKRISNCVA  NRKRISNCV  5        0.4010
652.7    38.00  0.37     Sequence
             DRB1_1302  356      VYAWNRKRISNCVAD  NRKRISNCV  4        0.4004
656.9    38.00  0.38     Sequence
             DRB1_1302  357      YAWNRKRISNCVADY  RISNCVADY  6        0.5427
140.9    17.00  0.52     Sequence
             DRB1_1302  358      AWNRKRISNCVADYS  RISNCVADY  5        0.5430
140.5    17.00  0.52     Sequence
             DRB1_1302  359      WNRKRISNCVADYSV  RISNCVADY  4        0.5493
131.2    17.00  0.55     Sequence
             DRB1_1302  360      NRKRISNCVADYSVL  RISNCVADY  3        0.5474
133.9    17.00  0.58     Sequence
             DRB1_1302  361      RKRISNCVADYSVLY  RISNCVADY  2        0.5717
102.9    14.00  0.40     Sequence
             DRB1_1302  362      KRISNCVADYSVLYN  CVADYSVLY  5        0.5275
166.1    19.00  0.36     Sequence
             DRB1_1302  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.4667
320.7    27.00  0.50     Sequence
             DRB1_1302  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.3901
734.7    40.00  0.71     Sequence
             DRB1_1302  365      SNCVADYSVLYNSAS  CVADYSVLY  2        0.3764
851.8    42.00  0.65     Sequence
             DRB1_1302  366      NCVADYSVLYNSASF  CVADYSVLY  1        0.4600
344.6    28.00  0.42     Sequence
             DRB1_1302  367      CVADYSVLYNSASFS  VLYNSASFS  6        0.6114
67.0    11.00  0.75     Sequence
             DRB1_1302  368      VADYSVLYNSASFST  VLYNSASFS  5        0.6631
38.3     7.50  0.71     Sequence        WB
             DRB1_1302  369      ADYSVLYNSASFSTF  VLYNSASFS  4        0.6856
30.0     6.00  0.71     Sequence        WB
             DRB1_1302  370      DYSVLYNSASFSTFK  VLYNSASFS  3        0.6869
29.6     6.00  0.71     Sequence        WB
             DRB1_1302  371      YSVLYNSASFSTFKC  VLYNSASFS  2        0.6696
35.7     7.00  0.70     Sequence        WB
             DRB1_1302  372      SVLYNSASFSTFKCY  VLYNSASFS  1        0.5857
88.5    13.00  0.61     Sequence
             DRB1_1302  373      VLYNSASFSTFKCYG  VLYNSASFS  0        0.4299
477.4    33.00  0.48     Sequence
             DRB1_1302  374      LYNSASFSTFKCYGV  LYNSASFST  0        0.2076
5287.6    80.00  0.28     Sequence
             DRB1_1302  375      YNSASFSTFKCYGVS  ASFSTFKCY  3        0.1603
8826.4    90.00  0.39     Sequence
             DRB1_1302  376      NSASFSTFKCYGVSP  ASFSTFKCY  2        0.1491
9961.5    90.00  0.38     Sequence
             DRB1_1302  377      SASFSTFKCYGVSPT  FSTFKCYGV  3        0.1477
10110.2    95.00  0.28     Sequence
             DRB1_1302  378      ASFSTFKCYGVSPTK  FSTFKCYGV  2        0.1331
11845.2    95.00  0.30     Sequence
             DRB1_1302  379      SFSTFKCYGVSPTKL  CYGVSPTKL  6        0.3036
1872.6    60.00  0.66     Sequence
             DRB1_1302  380      FSTFKCYGVSPTKLN  CYGVSPTKL  5        0.3003
1939.3    60.00  0.64     Sequence
             DRB1_1302  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.2850
2288.5    65.00  0.66     Sequence
```

```
             DRB1_1302  382      TFKCYGVSPTKLNDL  CYGVSPTKL  3        0.3288
1425.9    55.00  0.50     Sequence
             DRB1_1302  383      FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.3009
1928.1    60.00  0.50     Sequence
             DRB1_1302  384      KCYGVSPTKLNDLCF  CYGVSPTKL  1        0.2813
2382.8    65.00  0.39     Sequence
             DRB1_1302  385      CYGVSPTKLNDLCFT  VSPTKLNDL  3        0.2417
3658.3    75.00  0.37     Sequence
             DRB1_1302  386      YGVSPTKLNDLCFTN  VSPTKLNDL  2        0.2056
5406.5    80.00  0.44     Sequence
             DRB1_1302  387      GVSPTKLNDLCFTNV  LNDLCFTNV  6        0.2425
3627.6    75.00  0.28     Sequence
             DRB1_1302  388      VSPTKLNDLCFTNVY  LNDLCFTNV  5        0.2693
2714.0    65.00  0.27     Sequence
             DRB1_1302  389      SPTKLNDLCFTNVYA  LNDLCFTNV  4        0.2901
2167.7    60.00  0.28     Sequence
             DRB1_1302  390      PTKLNDLCFTNVYAD  LCFTNVYAD  6        0.3219
1536.7    55.00  0.33     Sequence
             DRB1_1302  391      TKLNDLCFTNVYADS  LCFTNVYAD  5        0.3234
1510.6    55.00  0.35     Sequence
             DRB1_1302  392      KLNDLCFTNVYADSF  LCFTNVYAD  4        0.3238
1505.3    55.00  0.45     Sequence
             DRB1_1302  393      LNDLCFTNVYADSFV  LCFTNVYAD  3        0.3178
1605.9    55.00  0.47     Sequence
             DRB1_1302  394      NDLCFTNVYADSFVI  NVYADSFVI  6        0.4163
553.0    35.00  0.43     Sequence
             DRB1_1302  395      DLCFTNVYADSFVIR  VYADSFVIR  6        0.4704
308.1    26.00  0.38     Sequence
             DRB1_1302  396      LCFTNVYADSFVIRG  VYADSFVIR  5        0.4294
480.0    33.00  0.42     Sequence
             DRB1_1302  397      CFTNVYADSFVIRGD  VYADSFVIR  4        0.4016
648.2    37.00  0.50     Sequence
             DRB1_1302  398      FTNVYADSFVIRGDE  VYADSFVIR  3        0.3879
751.8    40.00  0.52     Sequence
             DRB1_1302  399      TNVYADSFVIRGDEV  VYADSFVIR  2        0.3881
750.5    40.00  0.43     Sequence
             DRB1_1302  400      NVYADSFVIRGDEVR  VYADSFVIR  1        0.3324
1371.4    55.00  0.37     Sequence
             DRB1_1302  401      VYADSFVIRGDEVRQ  VIRGDEVRQ  6        0.3013
1919.1    60.00  0.22     Sequence
             DRB1_1302  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.5813
92.8    13.00  0.74     Sequence
             DRB1_1302  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.5865
87.7    13.00  0.74     Sequence
             DRB1_1302  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.5784
95.7    14.00  0.76     Sequence
             DRB1_1302  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.5653
110.3    15.00  0.76     Sequence
             DRB1_1302  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.5335
155.6    18.00  0.79     Sequence
             DRB1_1302  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.5144
191.3    21.00  0.55     Sequence
             DRB1_1302  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.4329
462.0    32.00  0.44     Sequence
             DRB1_1302  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.3487
1149.0    48.00  0.72     Sequence
             DRB1_1302  410      GDEVRQIAPGQTGTI  IAPGQTGTI  6        0.4891
251.5    24.00  0.50     Sequence
             DRB1_1302  411      DEVRQIAPGQTGTIA  IAPGQTGTI  5        0.4713
304.9    26.00  0.55     Sequence
             DRB1_1302  412      EVRQIAPGQTGTIAD  IAPGQTGTI  4        0.4407
424.8    31.00  0.62     Sequence
             DRB1_1302  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.4033
636.7    37.00  0.77     Sequence
             DRB1_1302  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.3322
1374.6    55.00  0.86     Sequence
```

```
             DRB1_1302  415      QIAPGQTGTIADYNY  IAPGQTGTI  1        0.2532
3230.1    70.00  0.78     Sequence
             DRB1_1302  416      IAPGQTGTIADYNYK  IAPGQTGTI  0        0.1512
9734.6    90.00  0.61     Sequence
             DRB1_1302  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.3811
809.4    41.00  0.81     Sequence
             DRB1_1302  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.3914
724.1    39.00  0.79     Sequence
             DRB1_1302  419      GQTGTIADYNYKLPD  TIADYNYKL  4        0.3913
725.2    39.00  0.76     Sequence
             DRB1_1302  420      QTGTIADYNYKLPDD  TIADYNYKL  3        0.3801
818.2    41.00  0.76     Sequence
             DRB1_1302  421      TGTIADYNYKLPDDF  TIADYNYKL  2        0.3498
1135.9    47.00  0.74     Sequence
             DRB1_1302  422      GTIADYNYKLPDDFT  TIADYNYKL  1        0.3026
1892.0    60.00  0.68     Sequence
             DRB1_1302  423      TIADYNYKLPDDFTG  TIADYNYKL  0        0.2006
5704.6    80.00  0.50     Sequence
             DRB1_1302  424      IADYNYKLPDDFTGC  YNYKLPDDF  3        0.0956
17767.5   100.00  0.22     Sequence
             DRB1_1302  425      ADYNYKLPDDFTGCV  LPDDFTGCV  6        0.1321
11971.2    95.00  0.44     Sequence
             DRB1_1302  426      DYNYKLPDDFTGCVI  LPDDFTGCV  5        0.1564
9209.2    90.00  0.39     Sequence
             DRB1_1302  427      YNYKLPDDFTGCVIA  LPDDFTGCV  4        0.1647
8416.1    90.00  0.36     Sequence
             DRB1_1302  428      NYKLPDDFTGCVIAW  LPDDFTGCV  3        0.1808
7066.5    85.00  0.31     Sequence
             DRB1_1302  429      YKLPDDFTGCVIAWN  LPDDFTGCV  2        0.1733
7664.0    90.00  0.26     Sequence
             DRB1_1302  430      KLPDDFTGCVIAWNS  DFTGCVIAW  4        0.1549
9356.0    90.00  0.24     Sequence
             DRB1_1302  431      LPDDFTGCVIAWNSN  DFTGCVIAW  3        0.1429
10655.0    95.00  0.24     Sequence
             DRB1_1302  432      PDDFTGCVIAWNSNN  CVIAWNSNN  6        0.2058
5396.0    80.00  0.29     Sequence
             DRB1_1302  433      DDFTGCVIAWNSNNL  VIAWNSNNL  6        0.5301
161.5    19.00  0.66     Sequence
             DRB1_1302  434      DFTGCVIAWNSNNLD  IAWNSNNLD  6        0.7015
25.3     5.50  0.68     Sequence        WB
             DRB1_1302  435      FTGCVIAWNSNNLDS  IAWNSNNLD  5        0.7223
20.2     4.50  0.69     Sequence        WB
             DRB1_1302  436      TGCVIAWNSNNLDSK  IAWNSNNLD  4        0.7281
19.0     4.00  0.68     Sequence        WB
             DRB1_1302  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3        0.7368
17.2     4.00  0.70     Sequence        WB
             DRB1_1302  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2        0.7151
21.8     4.50  0.70     Sequence        WB
             DRB1_1302  439      VIAWNSNNLDSKVGG  IAWNSNNLD  1        0.6418
48.2     8.50  0.69     Sequence        WB
             DRB1_1302  440      IAWNSNNLDSKVGGN  IAWNSNNLD  0        0.4624
335.9    28.00  0.62     Sequence
             DRB1_1302  441      AWNSNNLDSKVGGNY  NSNNLDSKV  2        0.1895
6431.6    85.00  0.32     Sequence
             DRB1_1302  442      WNSNNLDSKVGGNYN  LDSKVGGNY  5        0.1742
7594.9    90.00  0.35     Sequence
             DRB1_1302  443      NSNNLDSKVGGNYNY  LDSKVGGNY  4        0.1680
8119.8    90.00  0.41     Sequence
             DRB1_1302  444      SNNLDSKVGGNYNYL  KVGGNYNYL  6        0.2386
3781.2    75.00  0.38     Sequence
             DRB1_1302  445      NNLDSKVGGNYNYLY  VGGNYNYLY  6        0.3906
730.1    39.00  0.63     Sequence
             DRB1_1302  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.3948
698.2    39.00  0.64     Sequence
             DRB1_1302  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4        0.4385
435.1    31.00  0.61     Sequence
```

```
             DRB1_1302  448      DSKVGGNYNYLYRLF  VGGNYNYLY  3        0.4504
382.5    29.00  0.64     Sequence
             DRB1_1302  449      SKVGGNYNYLYRLFR  VGGNYNYLY  2        0.4420
419.0    31.00  0.63     Sequence
             DRB1_1302  450      KVGGNYNYLYRLFRK  VGGNYNYLY  1        0.4245
505.9    33.00  0.50     Sequence
             DRB1_1302  451      VGGNYNYLYRLFRKS  VGGNYNYLY  0        0.3296
1413.9    55.00  0.34     Sequence
             DRB1_1302  452      GGNYNYLYRLFRKSN  NYLYRLFRK  4        0.2507
3318.0    70.00  0.37     Sequence
             DRB1_1302  453      GNYNYLYRLFRKSNL  NYLYRLFRK  3        0.2688
2729.2    65.00  0.28     Sequence
             DRB1_1302  454      NYNYLYRLFRKSNLK  NYLYRLFRK  2        0.2780
2470.9    65.00  0.22     Sequence
             DRB1_1302  455      YNYLYRLFRKSNLKP  RLFRKSNLK  5        0.2894
2182.4    65.00  0.20     Sequence
             DRB1_1302  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6        0.4334
459.7    32.00  0.52     Sequence
             DRB1_1302  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.4347
453.3    32.00  0.55     Sequence
             DRB1_1302  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.4294
479.9    33.00  0.62     Sequence
             DRB1_1302  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.4090
598.3    36.00  0.67     Sequence
             DRB1_1302  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.3631
983.8    45.00  0.67     Sequence
             DRB1_1302  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.2870
2240.1    65.00  0.68     Sequence
             DRB1_1302  462      FRKSNLKPFERDIST  FRKSNLKPF  0        0.1908
6344.4    85.00  0.52     Sequence
             DRB1_1302  463      RKSNLKPFERDISTE  LKPFERDIS  4        0.0821
20561.0   100.00  0.18     Sequence
             DRB1_1302  464      KSNLKPFERDISTEI  FERDISTEI  6        0.3386
1281.7    50.00  0.78     Sequence
             DRB1_1302  465      SNLKPFERDISTEIY  FERDISTEI  5        0.3810
810.4    41.00  0.76     Sequence
             DRB1_1302  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.3857
770.1    40.00  0.77     Sequence
             DRB1_1302  467      LKPFERDISTEIYQA  FERDISTEI  3        0.3985
670.5    38.00  0.69     Sequence
             DRB1_1302  468      KPFERDISTEIYQAG  FERDISTEI  2        0.3705
907.5    43.00  0.68     Sequence
             DRB1_1302  469      PFERDISTEIYQAGS  FERDISTEI  1        0.3151
1653.1    55.00  0.60     Sequence
             DRB1_1302  470      FERDISTEIYQAGST  FERDISTEI  0        0.2274
4270.4    75.00  0.44     Sequence
             DRB1_1302  471      ERDISTEIYQAGSTP  DISTEIYQA  2        0.1269
12666.5    95.00  0.38     Sequence
             DRB1_1302  472      RDISTEIYQAGSTPC  IYQAGSTPC  6        0.1749
7531.9    90.00  0.53     Sequence
             DRB1_1302  473      DISTEIYQAGSTPCN  IYQAGSTPC  5        0.1816
7007.6    85.00  0.60     Sequence
             DRB1_1302  474      ISTEIYQAGSTPCNG  IYQAGSTPC  4        0.1803
7111.0    85.00  0.61     Sequence
             DRB1_1302  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.1947
6081.4    85.00  0.60     Sequence
             DRB1_1302  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.1777
7314.5    85.00  0.55     Sequence
             DRB1_1302  477      EIYQAGSTPCNGVKG  IYQAGSTPC  1        0.1566
9188.9    90.00  0.40     Sequence
             DRB1_1302  478      IYQAGSTPCNGVKGF  STPCNGVKG  5        0.1244
13016.2    95.00  0.28     Sequence
             DRB1_1302  479      YQAGSTPCNGVKGFN  STPCNGVKG  4        0.0969
17516.3   100.00  0.41     Sequence
             DRB1_1302  480      QAGSTPCNGVKGFNC  STPCNGVKG  3        0.0959
17719.5   100.00  0.38     Sequence
```

```
             DRB1_1302  481      AGSTPCNGVKGFNCY  STPCNGVKG  2        0.1030
16397.2   100.00  0.32     Sequence
             DRB1_1302  482      GSTPCNGVKGFNCYF  GVKGFNCYF  6        0.1248
12959.7    95.00  0.27     Sequence
             DRB1_1302  483      STPCNGVKGFNCYFP  VKGFNCYFP  6        0.1396
11041.8    95.00  0.29     Sequence
             DRB1_1302  484      TPCNGVKGFNCYFPL  KGFNCYFPL  6        0.2413
3675.0    75.00  0.56     Sequence
             DRB1_1302  485      PCNGVKGFNCYFPLQ  KGFNCYFPL  5        0.2501
3340.4    70.00  0.52     Sequence
             DRB1_1302  486      CNGVKGFNCYFPLQS  KGFNCYFPL  4        0.2520
3270.5    70.00  0.54     Sequence
             DRB1_1302  487      NGVKGFNCYFPLQSY  KGFNCYFPL  3        0.2564
3119.2    70.00  0.51     Sequence
             DRB1_1302  488      GVKGFNCYFPLQSYG  KGFNCYFPL  2        0.2241
4425.8    75.00  0.51     Sequence
             DRB1_1302  489      VKGFNCYFPLQSYGF  KGFNCYFPL  1        0.2029
5566.3    80.00  0.42     Sequence
             DRB1_1302  490      KGFNCYFPLQSYGFQ  KGFNCYFPL  0        0.1554
9301.9    90.00  0.28     Sequence
             DRB1_1302  491      GFNCYFPLQSYGFQP  PLQSYGFQP  6        0.1396
11036.2    95.00  0.33     Sequence
             DRB1_1302  492      FNCYFPLQSYGFQPT  PLQSYGFQP  5        0.1425
10694.6    95.00  0.35     Sequence
             DRB1_1302  493      NCYFPLQSYGFQPTY  PLQSYGFQP  4        0.1412
10848.0    95.00  0.37     Sequence
             DRB1_1302  494      CYFPLQSYGFQPTYG  PLQSYGFQP  3        0.1342
11709.6    95.00  0.41     Sequence
             DRB1_1302  495      YFPLQSYGFQPTYGV  YGFQPTYGV  6        0.2029
5565.0    80.00  0.46     Sequence
             DRB1_1302  496      FPLQSYGFQPTYGVG  YGFQPTYGV  5        0.1982
5858.5    85.00  0.56     Sequence
             DRB1_1302  497      PLQSYGFQPTYGVGY  YGFQPTYGV  4        0.2428
3613.1    75.00  0.46     Sequence
             DRB1_1302  498      LQSYGFQPTYGVGYQ  YGFQPTYGV  3        0.2403
3714.4    75.00  0.48     Sequence
             DRB1_1302  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4        0.2320
4061.0    75.00  0.41     Sequence
             DRB1_1302  500      SYGFQPTYGVGYQPY  FQPTYGVGY  3        0.2267
4303.8    75.00  0.39     Sequence
             DRB1_1302  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.1896
6430.8    85.00  0.41     Sequence
             DRB1_1302  502      GFQPTYGVGYQPYRV  GVGYQPYRV  6        0.2980
1988.4    60.00  0.58     Sequence
             DRB1_1302  503      FQPTYGVGYQPYRVV  GVGYQPYRV  5        0.3632
982.5    45.00  0.47     Sequence
             DRB1_1302  504      QPTYGVGYQPYRVVV  GVGYQPYRV  4        0.3884
747.8    40.00  0.42     Sequence
             DRB1_1302  505      PTYGVGYQPYRVVVL  GVGYQPYRV  3        0.4336
458.9    32.00  0.37     Sequence
             DRB1_1302  506      TYGVGYQPYRVVVLS  GVGYQPYRV  2        0.4273
490.8    33.00  0.33     Sequence
             DRB1_1302  507      YGVGYQPYRVVVLSF  GVGYQPYRV  1        0.4248
504.3    33.00  0.28     Sequence
             DRB1_1302  508      GVGYQPYRVVVLSFE  YQPYRVVVL  3        0.3739
874.7    43.00  0.29     Sequence
             DRB1_1302  509      VGYQPYRVVVLSFEL  RVVVLSFEL  6        0.3488
1148.4    48.00  0.28     Sequence
             DRB1_1302  510      GYQPYRVVVLSFELL  RVVVLSFEL  5        0.3273
1448.4    55.00  0.28     Sequence
             DRB1_1302  511      YQPYRVVVLSFELLH  VVLSFELLH  6        0.3350
1333.0    55.00  0.29     Sequence
             DRB1_1302  512      QPYRVVVLSFELLHA  VVLSFELLH  5        0.3354
1326.8    50.00  0.26     Sequence
             DRB1_1302  513      PYRVVVLSFELLHAP  VVLSFELLH  4        0.3050
1843.1    60.00  0.27     Sequence
```

```
             DRB1_1302  514      YRVVVLSFELLHAPA  VVLSFELLH  3        0.2798
2423.4    65.00  0.33     Sequence
             DRB1_1302  515      RVVVLSFELLHAPAT  VVLSFELLH  2        0.2594
3021.3    70.00  0.31     Sequence
             DRB1_1302  516      VVVLSFELLHAPATV  ELLHAPATV  6        0.4013
650.5    38.00  0.47     Sequence
             DRB1_1302  517      VVLSFELLHAPATVC  LLHAPATVC  6        0.4745
294.5    26.00  0.46     Sequence
             DRB1_1302  518      VLSFELLHAPATVCG  LLHAPATVC  5        0.4712
305.3    26.00  0.47     Sequence
             DRB1_1302  519      LSFELLHAPATVCGP  LLHAPATVC  4        0.4630
333.8    27.00  0.49     Sequence
             DRB1_1302  520      SFELLHAPATVCGPK  LLHAPATVC  3        0.4493
387.0    30.00  0.51     Sequence
             DRB1_1302  521      FELLHAPATVCGPKK  LLHAPATVC  2        0.4110
585.5    36.00  0.55     Sequence
             DRB1_1302  522      ELLHAPATVCGPKKS  LLHAPATVC  1        0.3406
1254.8    49.00  0.55     Sequence
             DRB1_1302  523      LLHAPATVCGPKKST  LLHAPATVC  0        0.1980
5866.3    85.00  0.51     Sequence
             DRB1_1302  524      LHAPATVCGPKKSTN  PATVCGPKK  3        0.0644
24919.8   100.00  0.34     Sequence
             DRB1_1302  525      HAPATVCGPKKSTNL  CGPKKSTNL  6        0.0756
22067.2   100.00  0.31     Sequence
             DRB1_1302  526      APATVCGPKKSTNLV  PKKSTNLVX  7        0.1287
12420.2    95.00  0.16     Sequence
             DRB1_1302  527      PATVCGPKKSTNLVK  PKKSTNLVK  6        0.2087
5226.0    80.00  0.63     Sequence
             DRB1_1302  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5        0.2344
3957.3    75.00  0.62     Sequence
             DRB1_1302  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.2618
2943.9    70.00  0.52     Sequence
             DRB1_1302  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3        0.2514
3293.0    70.00  0.52     Sequence
             DRB1_1302  531      CGPKKSTNLVKNKCV  PKKSTNLVK  2        0.3080
1785.5    60.00  0.26     Sequence
             DRB1_1302  532      GPKKSTNLVKNKCVN  TNLVKNKCV  5        0.3361
1316.7    50.00  0.32     Sequence
             DRB1_1302  533      PKKSTNLVKNKCVNF  LVKNKCVNF  6        0.7034
24.8     5.00  0.81     Sequence        WB
             DRB1_1302  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.7354
17.5     4.00  0.79     Sequence        WB
             DRB1_1302  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.7517
14.7     3.00  0.80     Sequence        WB
             DRB1_1302  536      STNLVKNKCVNFNFN  LVKNKCVNF  3        0.7573
13.8     3.00  0.78     Sequence        WB
             DRB1_1302  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2        0.7439
16.0     3.50  0.75     Sequence        WB
             DRB1_1302  538      NLVKNKCVNFNFNGL  LVKNKCVNF  1        0.7062
24.0     5.00  0.73     Sequence        WB
             DRB1_1302  539      LVKNKCVNFNFNGLT  LVKNKCVNF  0        0.6073
70.1    11.00  0.43     Sequence
             DRB1_1302  540      VKNKCVNFNFNGLTG  VNFNFNGLT  5        0.4379
437.7    31.00  0.58     Sequence
             DRB1_1302  541      KNKCVNFNFNGLTGT  VNFNFNGLT  4        0.4315
469.4    32.00  0.60     Sequence
             DRB1_1302  542      NKCVNFNFNGLTGTG  VNFNFNGLT  3        0.4147
562.8    35.00  0.66     Sequence
             DRB1_1302  543      KCVNFNFNGLTGTGV  VNFNFNGLT  2        0.4233
512.9    34.00  0.49     Sequence
             DRB1_1302  544      CVNFNFNGLTGTGVL  VNFNFNGLT  1        0.4079
605.7    36.00  0.35     Sequence
             DRB1_1302  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.3723
890.4    43.00  0.29     Sequence
             DRB1_1302  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3        0.3120
1709.5    55.00  0.40     Sequence
```

```
             DRB1_1302  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.2612
2961.4    70.00  0.43     Sequence
             DRB1_1302  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.2260
4336.5    75.00  0.44     Sequence
             DRB1_1302  549      FNGLTGTGVLTESNK  LTGTGVLTE  3        0.1683
8091.3    90.00  0.33     Sequence
             DRB1_1302  550      NGLTGTGVLTESNKK  GVLTESNKK  6        0.1387
11143.2    95.00  0.37     Sequence
             DRB1_1302  551      GLTGTGVLTESNKKF  VLTESNKKF  6        0.2498
3350.2    70.00  0.56     Sequence
             DRB1_1302  552      LTGTGVLTESNKKFL  VLTESNKKF  5        0.3434
1217.0    49.00  0.41     Sequence
             DRB1_1302  553      TGTGVLTESNKKFLP  VLTESNKKF  4        0.3653
960.7    44.00  0.40     Sequence
             DRB1_1302  554      GTGVLTESNKKFLPF  LTESNKKFL  4        0.3818
802.9    41.00  0.39     Sequence
             DRB1_1302  555      TGVLTESNKKFLPFQ  LTESNKKFL  3        0.3632
982.8    45.00  0.42     Sequence
             DRB1_1302  556      GVLTESNKKFLPFQQ  LTESNKKFL  2        0.3295
1414.9    55.00  0.42     Sequence
             DRB1_1302  557      VLTESNKKFLPFQQF  LTESNKKFL  1        0.2776
2480.3    65.00  0.37     Sequence
             DRB1_1302  558      LTESNKKFLPFQQFG  KKFLPFQQF  5        0.1749
7532.5    90.00  0.26     Sequence
             DRB1_1302  559      TESNKKFLPFQQFGR  KKFLPFQQF  4        0.1365
11421.4    95.00  0.37     Sequence
             DRB1_1302  560      ESNKKFLPFQQFGRD  KKFLPFQQF  3        0.1318
12018.7    95.00  0.36     Sequence
             DRB1_1302  561      SNKKFLPFQQFGRDI  KKFLPFQQF  2        0.1431
10630.6    95.00  0.26     Sequence
             DRB1_1302  562      NKKFLPFQQFGRDIA  PFQQFGRDI  5        0.1438
10555.0    95.00  0.24     Sequence
             DRB1_1302  563      KKFLPFQQFGRDIAD  PFQQFGRDI  4        0.1357
11515.0    95.00  0.28     Sequence
             DRB1_1302  564      KFLPFQQFGRDIADT  PFQQFGRDI  3        0.1307
12160.1    95.00  0.31     Sequence
             DRB1_1302  565      FLPFQQFGRDIADTT  FGRDIADTT  6        0.1409
10880.9    95.00  0.35     Sequence
             DRB1_1302  566      LPFQQFGRDIADTTD  FGRDIADTT  5        0.1314
12065.3    95.00  0.44     Sequence
             DRB1_1302  567      PFQQFGRDIADTTDA  FGRDIADTT  4        0.1299
12262.0    95.00  0.50     Sequence
             DRB1_1302  568      FQQFGRDIADTTDAV  DIADTTDAV  6        0.3999
660.2    38.00  0.76     Sequence
             DRB1_1302  569      QQFGRDIADTTDAVR  DIADTTDAV  5        0.3957
691.5    39.00  0.73     Sequence
             DRB1_1302  570      QFGRDIADTTDAVRD  DIADTTDAV  4        0.3878
752.9    40.00  0.74     Sequence
             DRB1_1302  571      FGRDIADTTDAVRDP  DIADTTDAV  3        0.3757
858.6    42.00  0.75     Sequence
             DRB1_1302  572      GRDIADTTDAVRDPQ  DIADTTDAV  2        0.3498
1135.1    47.00  0.73     Sequence
             DRB1_1302  573      RDIADTTDAVRDPQT  DIADTTDAV  1        0.3070
1805.6    60.00  0.69     Sequence
             DRB1_1302  574      DIADTTDAVRDPQTL  DIADTTDAV  0        0.2133
4974.1    80.00  0.50     Sequence
             DRB1_1302  575      IADTTDAVRDPQTLE  DAVRDPQTL  5        0.1143
14519.9   100.00  0.34     Sequence
             DRB1_1302  576      ADTTDAVRDPQTLEI  VRDPQTLEI  6        0.2067
5339.3    80.00  0.56     Sequence
             DRB1_1302  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5        0.2335
3995.8    75.00  0.54     Sequence
             DRB1_1302  578      TTDAVRDPQTLEILD  VRDPQTLEI  4        0.2302
4143.4    75.00  0.52     Sequence
             DRB1_1302  579      TDAVRDPQTLEILDI  VRDPQTLEI  3        0.2678
2756.6    65.00  0.41     Sequence
```

```
             DRB1_1302  580      DAVRDPQTLEILDIT  VRDPQTLEI  2        0.2402
3718.5    75.00  0.41     Sequence
             DRB1_1302  581      AVRDPQTLEILDITP  VRDPQTLEI  1        0.2064
5357.8    80.00  0.38     Sequence
             DRB1_1302  582      VRDPQTLEILDITPC  PQTLEILDI  3        0.1938
6141.9    85.00  0.31     Sequence
             DRB1_1302  583      RDPQTLEILDITPCS  EILDITPCS  6        0.2286
4213.3    75.00  0.32     Sequence
             DRB1_1302  584      DPQTLEILDITPCSF  ILDITPCSF  6        0.4941
238.5    23.00  0.72     Sequence
             DRB1_1302  585      PQTLEILDITPCSFG  ILDITPCSF  5        0.4878
255.3    24.00  0.73     Sequence
             DRB1_1302  586      QTLEILDITPCSFGG  ILDITPCSF  4        0.4755
291.4    26.00  0.73     Sequence
             DRB1_1302  587      TLEILDITPCSFGGV  ILDITPCSF  3        0.4830
268.7    25.00  0.73     Sequence
             DRB1_1302  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.4482
391.7    30.00  0.71     Sequence
             DRB1_1302  589      EILDITPCSFGGVSV  ILDITPCSF  1        0.3924
716.3    39.00  0.61     Sequence
             DRB1_1302  590      ILDITPCSFGGVSVI  ILDITPCSF  0        0.3126
1699.2    55.00  0.52     Sequence
             DRB1_1302  591      LDITPCSFGGVSVIT  ITPCSFGGV  2        0.1432
10613.7    95.00  0.36     Sequence
             DRB1_1302  592      DITPCSFGGVSVITP  ITPCSFGGV  1        0.1203
13610.7    95.00  0.29     Sequence
             DRB1_1302  593      ITPCSFGGVSVITPG  CSFGGVSVI  3        0.1033
16347.6   100.00  0.22     Sequence
             DRB1_1302  594      TPCSFGGVSVITPGT  SFGGVSVIT  3        0.1066
15773.5   100.00  0.20     Sequence
             DRB1_1302  595      PCSFGGVSVITPGTN  VSVITPGTN  6        0.1816
7006.0    85.00  0.56     Sequence
             DRB1_1302  596      CSFGGVSVITPGTNT  VSVITPGTN  5        0.2043
5484.4    80.00  0.47     Sequence
             DRB1_1302  597      SFGGVSVITPGTNTS  VSVITPGTN  4        0.2296
4169.6    75.00  0.46     Sequence
             DRB1_1302  598      FGGVSVITPGTNTSN  ITPGTNTSN  6        0.2623
2926.2    70.00  0.34     Sequence
             DRB1_1302  599      GGVSVITPGTNTSNQ  ITPGTNTSN  5        0.2672
2774.5    70.00  0.35     Sequence
             DRB1_1302  600      GVSVITPGTNTSNQV  PGTNTSNQV  6        0.4955
234.8    23.00  0.62     Sequence
             DRB1_1302  601      VSVITPGTNTSNQVA  PGTNTSNQV  5        0.4794
279.4    25.00  0.67     Sequence
             DRB1_1302  602      SVITPGTNTSNQVAV  PGTNTSNQV  4        0.4905
247.9    24.00  0.66     Sequence
             DRB1_1302  603      VITPGTNTSNQVAVL  PGTNTSNQV  3        0.5440
138.9    17.00  0.52     Sequence
             DRB1_1302  604      ITPGTNTSNQVAVLY  PGTNTSNQV  2        0.5119
196.5    21.00  0.47     Sequence
             DRB1_1302  605      TPGTNTSNQVAVLYQ  NTSNQVAVL  4        0.4733
298.5    26.00  0.34     Sequence
             DRB1_1302  606      PGTNTSNQVAVLYQG  NTSNQVAVL  3        0.4039
632.4    37.00  0.45     Sequence
             DRB1_1302  607      GTNTSNQVAVLYQGV  NTSNQVAVL  2        0.3674
938.3    44.00  0.49     Sequence
             DRB1_1302  608      TNTSNQVAVLYQGVN  NTSNQVAVL  1        0.2889
2194.6    65.00  0.41     Sequence
             DRB1_1302  609      NTSNQVAVLYQGVNC  QVAVLYQGV  4        0.2491
3378.1    70.00  0.25     Sequence
             DRB1_1302  610      TSNQVAVLYQGVNCT  VLYQGVNCT  6        0.2864
2254.0    65.00  0.50     Sequence
             DRB1_1302  611      SNQVAVLYQGVNCTE  VLYQGVNCT  5        0.2853
2281.1    65.00  0.49     Sequence
             DRB1_1302  612      NQVAVLYQGVNCTEV  VLYQGVNCT  4        0.3132
1686.7    55.00  0.48     Sequence
```

```
             DRB1_1302  613      QVAVLYQGVNCTEVP  VLYQGVNCT  3        0.3025
1895.2    60.00  0.50     Sequence
             DRB1_1302  614      VAVLYQGVNCTEVPV  VLYQGVNCT  2        0.3023
1899.1    60.00  0.41     Sequence
             DRB1_1302  615      AVLYQGVNCTEVPVA  VLYQGVNCT  1        0.2854
2279.9    65.00  0.28     Sequence
             DRB1_1302  616      VLYQGVNCTEVPVAI  GVNCTEVPV  4        0.2681
2748.8    65.00  0.19     Sequence
             DRB1_1302  617      LYQGVNCTEVPVAIH  GVNCTEVPV  3        0.2387
3779.9    75.00  0.22     Sequence
             DRB1_1302  618      YQGVNCTEVPVAIHA  VNCTEVPVA  3        0.2171
4774.9    80.00  0.27     Sequence
             DRB1_1302  619      QGVNCTEVPVAIHAD  NCTEVPVAI  3        0.1805
7094.2    85.00  0.29     Sequence
             DRB1_1302  620      GVNCTEVPVAIHADQ  NCTEVPVAI  2        0.1457
10335.9    95.00  0.29     Sequence
             DRB1_1302  621      VNCTEVPVAIHADQL  PVAIHADQL  6        0.3067
1810.2    60.00  0.64     Sequence
             DRB1_1302  622      NCTEVPVAIHADQLT  PVAIHADQL  5        0.3303
1402.9    55.00  0.53     Sequence
             DRB1_1302  623      CTEVPVAIHADQLTP  PVAIHADQL  4        0.3383
1286.9    50.00  0.49     Sequence
             DRB1_1302  624      TEVPVAIHADQLTPT  IHADQLTPT  6        0.4108
587.1    36.00  0.38     Sequence
             DRB1_1302  625      EVPVAIHADQLTPTW  IHADQLTPT  5        0.4043
629.8    37.00  0.43     Sequence
             DRB1_1302  626      VPVAIHADQLTPTWR  IHADQLTPT  4        0.3908
729.0    39.00  0.48     Sequence
             DRB1_1302  627      PVAIHADQLTPTWRV  DQLTPTWRV  6        0.5780
96.2    14.00  0.58     Sequence
             DRB1_1302  628      VAIHADQLTPTWRVY  DQLTPTWRV  5        0.5564
121.5    16.00  0.64     Sequence
             DRB1_1302  629      AIHADQLTPTWRVYS  DQLTPTWRV  4        0.5249
170.7    19.00  0.63     Sequence
             DRB1_1302  630      IHADQLTPTWRVYST  DQLTPTWRV  3        0.4873
256.5    24.00  0.68     Sequence
             DRB1_1302  631      HADQLTPTWRVYSTG  DQLTPTWRV  2        0.4395
430.4    31.00  0.73     Sequence
             DRB1_1302  632      ADQLTPTWRVYSTGS  DQLTPTWRV  1        0.3950
696.7    39.00  0.69     Sequence
             DRB1_1302  633      DQLTPTWRVYSTGSN  DQLTPTWRV  0        0.2991
1966.3    60.00  0.57     Sequence
             DRB1_1302  634      QLTPTWRVYSTGSNV  RVYSTGSNV  6        0.5305
160.8    19.00  0.77     Sequence
             DRB1_1302  635      LTPTWRVYSTGSNVF  VYSTGSNVF  6        0.6659
37.1     7.00  0.44     Sequence         WB
             DRB1_1302  636      TPTWRVYSTGSNVFQ  VYSTGSNVF  5        0.6721
34.7     7.00  0.44     Sequence         WB
             DRB1_1302  637      PTWRVYSTGSNVFQT  VYSTGSNVF  4        0.6761
33.3     6.50  0.44     Sequence         WB
             DRB1_1302  638      TWRVYSTGSNVFQTR  VYSTGSNVF  3        0.6646
37.7     7.00  0.46     Sequence         WB
             DRB1_1302  639      WRVYSTGSNVFQTRA  VYSTGSNVF  2        0.6292
55.2     9.50  0.49     Sequence         WB
             DRB1_1302  640      RVYSTGSNVFQTRAG  VYSTGSNVF  1        0.5353
152.6    18.00  0.52     Sequence
             DRB1_1302  641      VYSTGSNVFQTRAGC  VYSTGSNVF  0        0.3228
1520.5    55.00  0.57     Sequence
             DRB1_1302  642      YSTGSNVFQTRAGCL  VFQTRAGCL  6        0.4406
425.0    31.00  0.79     Sequence
             DRB1_1302  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.5004
222.6    22.00  0.71     Sequence
             DRB1_1302  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.4894
250.9    24.00  0.70     Sequence
             DRB1_1302  645      GSNVFQTRAGCLIGA  VFQTRAGCL  3        0.4898
249.7    24.00  0.69     Sequence
```

```
             DRB1_1302  646      SNVFQTRAGCLIGAE  VFQTRAGCL  2        0.4624
335.9    28.00  0.68     Sequence
             DRB1_1302  647      NVFQTRAGCLIGAEY  VFQTRAGCL  1        0.4136
569.4    35.00  0.62     Sequence
             DRB1_1302  648      VFQTRAGCLIGAEYV  VFQTRAGCL  0        0.2907
2152.8    60.00  0.50     Sequence
             DRB1_1302  649      FQTRAGCLIGAEYVN  FQTRAGCLI  0        0.1236
13126.9    95.00  0.30     Sequence
             DRB1_1302  650      QTRAGCLIGAEYVNN  LIGAEYVNN  6        0.1265
12727.9    95.00  0.44     Sequence
             DRB1_1302  651      TRAGCLIGAEYVNNS  LIGAEYVNN  5        0.1411
10862.7    95.00  0.43     Sequence
             DRB1_1302  652      RAGCLIGAEYVNNSY  LIGAEYVNN  4        0.1680
8117.5    90.00  0.37     Sequence
             DRB1_1302  653      AGCLIGAEYVNNSYE  LIGAEYVNN  3        0.1761
7437.6    85.00  0.35     Sequence
             DRB1_1302  654      GCLIGAEYVNNSYEC  EYVNNSYEC  6        0.2686
2735.0    65.00  0.49     Sequence
             DRB1_1302  655      CLIGAEYVNNSYECD  EYVNNSYEC  5        0.2885
2205.3    65.00  0.46     Sequence
             DRB1_1302  656      LIGAEYVNNSYECDI  EYVNNSYEC  4        0.3310
1392.0    55.00  0.38     Sequence
             DRB1_1302  657      IGAEYVNNSYECDIP  EYVNNSYEC  3        0.3207
1556.1    55.00  0.38     Sequence
             DRB1_1302  658      GAEYVNNSYECDIPI  EYVNNSYEC  2        0.3291
1421.3    55.00  0.29     Sequence
             DRB1_1302  659      AEYVNNSYECDIPIG  VNNSYECDI  3        0.3003
1939.4    60.00  0.25     Sequence
             DRB1_1302  660      EYVNNSYECDIPIGA  YECDIPIGA  6        0.2778
2475.1    65.00  0.20     Sequence
             DRB1_1302  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.2164
4809.0    80.00  0.35     Sequence
             DRB1_1302  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.1965
5963.1    85.00  0.43     Sequence
             DRB1_1302  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.2254
4363.3    75.00  0.41     Sequence
             DRB1_1302  664      NSYECDIPIGAGICA  IPIGAGICA  6        0.2730
2607.5    65.00  0.38     Sequence
             DRB1_1302  665      SYECDIPIGAGICAS  IPIGAGICA  5        0.2671
2778.2    70.00  0.46     Sequence
             DRB1_1302  666      YECDIPIGAGICASY  IPIGAGICA  4        0.2859
2268.3    65.00  0.37     Sequence
             DRB1_1302  667      ECDIPIGAGICASYQ  IPIGAGICA  3        0.2665
2796.4    70.00  0.43     Sequence
             DRB1_1302  668      CDIPIGAGICASYQT  IPIGAGICA  2        0.2491
3376.6    70.00  0.41     Sequence
             DRB1_1302  669      DIPIGAGICASYQTQ  IPIGAGICA  1        0.2411
3680.3    75.00  0.37     Sequence
             DRB1_1302  670      IPIGAGICASYQTQT  ICASYQTQT  6        0.1951
6058.0    85.00  0.40     Sequence
             DRB1_1302  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.1704
7915.5    90.00  0.55     Sequence
             DRB1_1302  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.1590
8950.2    90.00  0.58     Sequence
             DRB1_1302  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.1547
9379.0    90.00  0.61     Sequence
             DRB1_1302  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.1692
8012.1    90.00  0.47     Sequence
             DRB1_1302  675      GICASYQTQTNSPRR  ICASYQTQT  1        0.1907
6354.7    85.00  0.28     Sequence
             DRB1_1302  676      ICASYQTQTNSPRRA  TQTNSPRRA  6        0.3298
1409.8    55.00  0.80     Sequence
             DRB1_1302  677      CASYQTQTNSPRRAR  TQTNSPRRA  5        0.3416
1240.6    49.00  0.80     Sequence
             DRB1_1302  678      ASYQTQTNSPRRARS  TQTNSPRRA  4        0.3489
1147.3    48.00  0.79     Sequence
```

```
             DRB1_1302  679      SYQTQTNSPRRARSV  TQTNSPRRA  3        0.3787
830.5    42.00  0.69     Sequence
             DRB1_1302  680      YQTQTNSPRRARSVA  TQTNSPRRA  2        0.3673
939.5    44.00  0.65     Sequence
             DRB1_1302  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.3517
1112.5    47.00  0.40     Sequence
             DRB1_1302  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.3290
1421.7    55.00  0.54     Sequence
             DRB1_1302  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.3174
1613.4    55.00  0.56     Sequence
             DRB1_1302  684      TNSPRRARSVASQSI  PRRARSVAS  3        0.3869
759.9    40.00  0.40     Sequence
             DRB1_1302  685      NSPRRARSVASQSII  PRRARSVAS  2        0.4045
628.3    37.00  0.35     Sequence
             DRB1_1302  686      SPRRARSVASQSIIA  SVASQSIIA  6        0.4406
425.4    31.00  0.36     Sequence
             DRB1_1302  687      PRRARSVASQSIIAY  SVASQSIIA  5        0.4498
384.9    29.00  0.38     Sequence
             DRB1_1302  688      RRARSVASQSIIAYT  SVASQSIIA  4        0.4345
454.0    32.00  0.38     Sequence
             DRB1_1302  689      RARSVASQSIIAYTM  SVASQSIIA  3        0.4233
512.8    34.00  0.41     Sequence
             DRB1_1302  690      ARSVASQSIIAYTMS  SVASQSIIA  2        0.3834
789.5    41.00  0.40     Sequence
             DRB1_1302  691      RSVASQSIIAYTMSL  SIIAYTMSL  6        0.4992
225.6    22.00  0.47     Sequence
             DRB1_1302  692      SVASQSIIAYTMSLG  SIIAYTMSL  5        0.4609
341.3    28.00  0.47     Sequence
             DRB1_1302  693      VASQSIIAYTMSLGA  SIIAYTMSL  4        0.4707
307.1    26.00  0.43     Sequence
             DRB1_1302  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.4679
316.6    27.00  0.31     Sequence
             DRB1_1302  695      SQSIIAYTMSLGAEN  IAYTMSLGA  4        0.4595
346.4    28.00  0.38     Sequence
             DRB1_1302  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.4329
462.3    32.00  0.44     Sequence
             DRB1_1302  697      SIIAYTMSLGAENSV  IAYTMSLGA  2        0.3994
663.7    38.00  0.34     Sequence
             DRB1_1302  698      IIAYTMSLGAENSVA  IAYTMSLGA  1        0.3439
1211.2    49.00  0.35     Sequence
             DRB1_1302  699      IAYTMSLGAENSVAY  LGAENSVAY  6        0.3325
1369.3    55.00  0.34     Sequence
             DRB1_1302  700      AYTMSLGAENSVAYS  LGAENSVAY  5        0.3190
1584.0    55.00  0.37     Sequence
             DRB1_1302  701      YTMSLGAENSVAYSN  LGAENSVAY  4        0.3053
1838.4    60.00  0.43     Sequence
             DRB1_1302  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.2897
2175.8    60.00  0.50     Sequence
             DRB1_1302  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.2709
2668.4    65.00  0.50     Sequence
             DRB1_1302  704      SLGAENSVAYSNNSI  SVAYSNNSI  6        0.4682
315.6    27.00  0.54     Sequence
             DRB1_1302  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.5691
105.9    15.00  0.47     Sequence
             DRB1_1302  706      GAENSVAYSNNSIAI  AYSNNSIAI  6        0.8406
5.6     0.80  0.65     Sequence         SB
             DRB1_1302  707      AENSVAYSNNSIAIP  AYSNNSIAI  5        0.8456
5.3     0.80  0.67     Sequence         SB
             DRB1_1302  708      ENSVAYSNNSIAIPT  AYSNNSIAI  4        0.8457
5.3     0.80  0.68     Sequence         SB
             DRB1_1302  709      NSVAYSNNSIAIPTN  AYSNNSIAI  3        0.8423
5.5     0.80  0.69     Sequence         SB
             DRB1_1302  710      SVAYSNNSIAIPTNF  AYSNNSIAI  2        0.8030
8.4     1.50  0.70     Sequence         SB
             DRB1_1302  711      VAYSNNSIAIPTNFT  AYSNNSIAI  1        0.7358
17.4     4.00  0.69     Sequence         WB
```

```
             DRB1_1302  712      AYSNNSIAIPTNFTI  AYSNNSIAI  0        0.6133
65.6    11.00  0.60     Sequence
             DRB1_1302  713      YSNNSIAIPTNFTIS  IAIPTNFTI  5        0.3647
967.1    44.00  0.41     Sequence
             DRB1_1302  714      SNNSIAIPTNFTISV  IPTNFTISV  6        0.5254
169.9    19.00  0.60     Sequence
             DRB1_1302  715      NNSIAIPTNFTISVT  IPTNFTISV  5        0.5396
145.6    18.00  0.62     Sequence
             DRB1_1302  716      NSIAIPTNFTISVTT  IPTNFTISV  4        0.5303
161.0    19.00  0.67     Sequence
             DRB1_1302  717      SIAIPTNFTISVTTE  IPTNFTISV  3        0.5090
202.9    21.00  0.70     Sequence
             DRB1_1302  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.6475
45.3     8.00  0.63     Sequence         WB
             DRB1_1302  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.6836
30.7     6.00  0.64     Sequence         WB
             DRB1_1302  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.6569
40.9     7.50  0.69     Sequence         WB
             DRB1_1302  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.6791
32.2     6.50  0.65     Sequence         WB
             DRB1_1302  722      TNFTISVTTEILPVS  FTISVTTEI  2        0.6449
46.6     8.50  0.64     Sequence         WB
             DRB1_1302  723      NFTISVTTEILPVSM  FTISVTTEI  1        0.5910
83.5    13.00  0.60     Sequence
             DRB1_1302  724      FTISVTTEILPVSMT  FTISVTTEI  0        0.4464
399.3    30.00  0.39     Sequence
             DRB1_1302  725      TISVTTEILPVSMTK  SVTTEILPV  2        0.3019
1906.2    60.00  0.41     Sequence
             DRB1_1302  726      ISVTTEILPVSMTKT  ILPVSMTKT  6        0.3417
1239.6    49.00  0.48     Sequence
             DRB1_1302  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.3200
1567.2    55.00  0.53     Sequence
             DRB1_1302  728      VTTEILPVSMTKTSV  ILPVSMTKT  4        0.3658
955.5    44.00  0.47     Sequence
             DRB1_1302  729      TTEILPVSMTKTSVD  ILPVSMTKT  3        0.3684
928.7    44.00  0.44     Sequence
             DRB1_1302  730      TEILPVSMTKTSVDC  ILPVSMTKT  2        0.3534
1092.0    47.00  0.41     Sequence
             DRB1_1302  731      EILPVSMTKTSVDCT  ILPVSMTKT  1        0.3233
1512.7    55.00  0.35     Sequence
             DRB1_1302  732      ILPVSMTKTSVDCTM  VSMTKTSVD  3        0.2583
3057.9    70.00  0.26     Sequence
             DRB1_1302  733      LPVSMTKTSVDCTMY  VSMTKTSVD  2        0.2020
5621.3    80.00  0.34     Sequence
             DRB1_1302  734      PVSMTKTSVDCTMYI  TSVDCTMYI  6        0.3707
905.4    43.00  0.62     Sequence
             DRB1_1302  735      VSMTKTSVDCTMYIC  TSVDCTMYI  5        0.3344
1342.3    55.00  0.68     Sequence
             DRB1_1302  736      SMTKTSVDCTMYICG  TSVDCTMYI  4        0.3168
1623.6    55.00  0.70     Sequence
             DRB1_1302  737      MTKTSVDCTMYICGD  TSVDCTMYI  3        0.3025
1895.6    60.00  0.72     Sequence
             DRB1_1302  738      TKTSVDCTMYICGDS  TSVDCTMYI  2        0.2768
2502.2    65.00  0.75     Sequence
             DRB1_1302  739      KTSVDCTMYICGDST  TSVDCTMYI  1        0.2427
3620.4    75.00  0.64     Sequence
             DRB1_1302  740      TSVDCTMYICGDSTE  TSVDCTMYI  0        0.1670
8205.2    90.00  0.48     Sequence
             DRB1_1302  741      SVDCTMYICGDSTEC  MYICGDSTE  5        0.0859
19728.9   100.00  0.19     Sequence
             DRB1_1302  742      VDCTMYICGDSTECS  ICGDSTECS  6        0.1238
13093.9    95.00  0.44     Sequence
             DRB1_1302  743      DCTMYICGDSTECSN  ICGDSTECS  5        0.1245
13002.4    95.00  0.55     Sequence
             DRB1_1302  744      CTMYICGDSTECSNL  ICGDSTECS  4        0.1347
11641.1    95.00  0.60     Sequence
```

```
             DRB1_1302  745      TMYICGDSTECSNLL  ICGDSTECS  3        0.1854
6723.0    85.00  0.46     Sequence
             DRB1_1302  746      MYICGDSTECSNLLL  ICGDSTECS  2        0.1838
6841.8    85.00  0.39     Sequence
             DRB1_1302  747      YICGDSTECSNLLLQ  DSTECSNLL  4        0.1795
7169.4    85.00  0.38     Sequence
             DRB1_1302  748      ICGDSTECSNLLLQY  DSTECSNLL  3        0.1934
6170.2    85.00  0.32     Sequence
             DRB1_1302  749      CGDSTECSNLLLQYG  ECSNLLLQY  5        0.1738
7627.4    90.00  0.31     Sequence
             DRB1_1302  750      GDSTECSNLLLQYGS  ECSNLLLQY  4        0.1705
7904.5    90.00  0.29     Sequence
             DRB1_1302  751      DSTECSNLLLQYGSF  ECSNLLLQY  3        0.1948
6076.2    85.00  0.28     Sequence
             DRB1_1302  752      STECSNLLLQYGSFC  LLLQYGSFC  6        0.2504
3329.3    70.00  0.48     Sequence
             DRB1_1302  753      TECSNLLLQYGSFCT  LLLQYGSFC  5        0.2615
2951.0    70.00  0.47     Sequence
             DRB1_1302  754      ECSNLLLQYGSFCTQ  LLLQYGSFC  4        0.2549
3171.3    70.00  0.50     Sequence
             DRB1_1302  755      CSNLLLQYGSFCTQL  LLLQYGSFC  3        0.2858
2269.2    65.00  0.41     Sequence
             DRB1_1302  756      SNLLLQYGSFCTQLN  LLLQYGSFC  2        0.2844
2304.6    65.00  0.41     Sequence
             DRB1_1302  757      NLLLQYGSFCTQLNR  LLLQYGSFC  1        0.2529
3240.6    70.00  0.34     Sequence
             DRB1_1302  758      LLLQYGSFCTQLNRA  QYGSFCTQL  3        0.2148
4891.4    80.00  0.20     Sequence
             DRB1_1302  759      LLQYGSFCTQLNRAL  FCTQLNRAL  6        0.2195
4649.5    80.00  0.31     Sequence
             DRB1_1302  760      LQYGSFCTQLNRALT  FCTQLNRAL  5        0.2250
4383.8    75.00  0.35     Sequence
             DRB1_1302  761      QYGSFCTQLNRALTG  TQLNRALTG  6        0.3276
1444.5    55.00  0.58     Sequence
             DRB1_1302  762      YGSFCTQLNRALTGI  TQLNRALTG  5        0.3916
722.6    39.00  0.60     Sequence
             DRB1_1302  763      GSFCTQLNRALTGIA  TQLNRALTG  4        0.4337
458.2    32.00  0.52     Sequence
             DRB1_1302  764      SFCTQLNRALTGIAV  TQLNRALTG  3        0.5283
164.6    19.00  0.31     Sequence
             DRB1_1302  765      FCTQLNRALTGIAVE  TQLNRALTG  2        0.5130
194.2    21.00  0.33     Sequence
             DRB1_1302  766      CTQLNRALTGIAVEQ  NRALTGIAV  4        0.4900
249.1    24.00  0.29     Sequence
             DRB1_1302  767      TQLNRALTGIAVEQD  NRALTGIAV  3        0.4561
359.6    29.00  0.33     Sequence
             DRB1_1302  768      QLNRALTGIAVEQDK  NRALTGIAV  2        0.3819
802.5    41.00  0.47     Sequence
             DRB1_1302  769      LNRALTGIAVEQDKN  NRALTGIAV  1        0.2894
2183.9    65.00  0.50     Sequence
             DRB1_1302  770      NRALTGIAVEQDKNT  NRALTGIAV  0        0.2047
5461.1    80.00  0.34     Sequence
             DRB1_1302  771      RALTGIAVEQDKNTQ  LTGIAVEQD  2        0.1274
12599.2    95.00  0.37     Sequence
             DRB1_1302  772      ALTGIAVEQDKNTQE  VEQDKNTQE  6        0.1591
8937.2    90.00  0.43     Sequence
             DRB1_1302  773      LTGIAVEQDKNTQEV  VEQDKNTQE  5        0.1988
5817.3    85.00  0.41     Sequence
             DRB1_1302  774      TGIAVEQDKNTQEVF  VEQDKNTQE  4        0.2159
4835.2    80.00  0.46     Sequence
             DRB1_1302  775      GIAVEQDKNTQEVFA  VEQDKNTQE  3        0.2297
4166.4    75.00  0.42     Sequence
             DRB1_1302  776      IAVEQDKNTQEVFAQ  VEQDKNTQE  2        0.2166
4796.9    80.00  0.39     Sequence
             DRB1_1302  777      AVEQDKNTQEVFAQV  VEQDKNTQE  1        0.2083
5250.7    80.00  0.31     Sequence
```

```
             DRB1_1302  778      VEQDKNTQEVFAQVK  DKNTQEVFA  3        0.1644
8444.4    90.00  0.23     Sequence
             DRB1_1302  779      EQDKNTQEVFAQVKQ  DKNTQEVFA  2        0.1369
11367.1    95.00  0.24     Sequence
             DRB1_1302  780      QDKNTQEVFAQVKQI  EVFAQVKQI  6        0.3770
846.3    42.00  0.71     Sequence
             DRB1_1302  781      DKNTQEVFAQVKQIY  EVFAQVKQI  5        0.4044
628.9    37.00  0.54     Sequence
             DRB1_1302  782      KNTQEVFAQVKQIYK  EVFAQVKQI  4        0.4061
617.9    37.00  0.50     Sequence
             DRB1_1302  783      NTQEVFAQVKQIYKT  EVFAQVKQI  3        0.4042
630.6    37.00  0.50     Sequence
             DRB1_1302  784      TQEVFAQVKQIYKTP  EVFAQVKQI  2        0.3807
812.7    41.00  0.47     Sequence
             DRB1_1302  785      QEVFAQVKQIYKTPP  VFAQVKQIY  2        0.3506
1125.8    47.00  0.37     Sequence
             DRB1_1302  786      EVFAQVKQIYKTPPI  KQIYKTPPI  6        0.4088
599.7    36.00  0.44     Sequence
             DRB1_1302  787      VFAQVKQIYKTPPIK  KQIYKTPPI  5        0.4196
533.9    34.00  0.54     Sequence
             DRB1_1302  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6        0.6415
48.4     8.50  0.71     Sequence         WB
             DRB1_1302  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.6820
31.2     6.00  0.75     Sequence         WB
             DRB1_1302  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.6708
35.2     7.00  0.77     Sequence         WB
             DRB1_1302  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.6586
40.2     7.50  0.80     Sequence         WB
             DRB1_1302  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.6159
63.8    11.00  0.81     Sequence
             DRB1_1302  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.4883
253.8    24.00  0.77     Sequence
             DRB1_1302  794      IYKTPPIKDFGGFNF  IYKTPPIKD  0        0.3506
1126.1    47.00  0.63     Sequence
             DRB1_1302  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.1457
10336.9    95.00  0.56     Sequence
             DRB1_1302  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.1538
9463.9    90.00  0.51     Sequence
             DRB1_1302  797      TPPIKDFGGFNFSQI  IKDFGGFNF  3        0.1978
5882.3    85.00  0.33     Sequence
             DRB1_1302  798      PPIKDFGGFNFSQIL  GGFNFSQIL  6        0.2745
2564.3    65.00  0.39     Sequence
             DRB1_1302  799      PIKDFGGFNFSQILP  GGFNFSQIL  5        0.2790
2443.4    65.00  0.40     Sequence
             DRB1_1302  800      IKDFGGFNFSQILPD  GGFNFSQIL  4        0.2834
2330.6    65.00  0.31     Sequence
             DRB1_1302  801      KDFGGFNFSQILPDP  GGFNFSQIL  3        0.2771
2493.8    65.00  0.32     Sequence
             DRB1_1302  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.2666
2793.8    70.00  0.35     Sequence
             DRB1_1302  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.2484
3400.3    70.00  0.41     Sequence
             DRB1_1302  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.2268
4300.0    75.00  0.41     Sequence
             DRB1_1302  805      GFNFSQILPDPSKPS  ILPDPSKPS  6        0.3747
867.5    42.00  0.68     Sequence
             DRB1_1302  806      FNFSQILPDPSKPSK  ILPDPSKPS  5        0.3679
933.7    44.00  0.77     Sequence
             DRB1_1302  807      NFSQILPDPSKPSKR  ILPDPSKPS  4        0.3755
859.6    42.00  0.79     Sequence
             DRB1_1302  808      FSQILPDPSKPSKRS  ILPDPSKPS  3        0.3718
895.5    43.00  0.81     Sequence
             DRB1_1302  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.3465
1176.7    48.00  0.80     Sequence
             DRB1_1302  810      QILPDPSKPSKRSFI  ILPDPSKPS  1        0.3270
1453.6    55.00  0.66     Sequence
```

```
             DRB1_1302  811      ILPDPSKPSKRSFIE  ILPDPSKPS  0        0.2260
4336.7    75.00  0.49     Sequence
             DRB1_1302  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.1132
14696.6   100.00  0.40     Sequence
             DRB1_1302  813      PDPSKPSKRSFIEDL  SKPSKRSFI  3        0.1319
12002.1    95.00  0.37     Sequence
             DRB1_1302  814      DPSKPSKRSFIEDLL  SKRSFIEDL  5        0.1453
10380.1    95.00  0.37     Sequence
             DRB1_1302  815      PSKPSKRSFIEDLLF  RSFIEDLLF  6        0.1801
7120.8    85.00  0.29     Sequence
             DRB1_1302  816      SKPSKRSFIEDLLFN  RSFIEDLLF  5        0.1872
6593.4    85.00  0.28     Sequence
             DRB1_1302  817      KPSKRSFIEDLLFNK  RSFIEDLLF  4        0.1939
6134.3    85.00  0.25     Sequence
             DRB1_1302  818      PSKRSFIEDLLFNKV  IEDLLFNKV  6        0.3981
673.7    38.00  0.54     Sequence
             DRB1_1302  819      SKRSFIEDLLFNKVT  IEDLLFNKV  5        0.4096
594.4    36.00  0.56     Sequence
             DRB1_1302  820      KRSFIEDLLFNKVTL  IEDLLFNKV  4        0.4657
324.1    27.00  0.50     Sequence
             DRB1_1302  821      RSFIEDLLFNKVTLA  LLFNKVTLA  6        0.7628
13.0     3.00  0.82     Sequence        WB
             DRB1_1302  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5        0.7643
12.8     3.00  0.84     Sequence        WB
             DRB1_1302  823      FIEDLLFNKVTLADA  LLFNKVTLA  4        0.7642
12.8     3.00  0.85     Sequence        WB
             DRB1_1302  824      IEDLLFNKVTLADAG  LLFNKVTLA  3        0.7519
14.6     3.00  0.87     Sequence        WB
             DRB1_1302  825      EDLLFNKVTLADAGF  LLFNKVTLA  2        0.7126
22.4     5.00  0.87     Sequence        WB
             DRB1_1302  826      DLLFNKVTLADAGFI  LLFNKVTLA  1        0.6852
30.1     6.00  0.71     Sequence        WB
             DRB1_1302  827      LLFNKVTLADAGFIK  LLFNKVTLA  0        0.6137
65.4    11.00  0.59     Sequence
             DRB1_1302  828      LFNKVTLADAGFIKQ  VTLADAGFI  4        0.3974
678.9    38.00  0.61     Sequence
             DRB1_1302  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.4000
660.1    38.00  0.59     Sequence
             DRB1_1302  830      NKVTLADAGFIKQYG  VTLADAGFI  2        0.3758
857.4    42.00  0.57     Sequence
             DRB1_1302  831      KVTLADAGFIKQYGD  VTLADAGFI  1        0.3090
1765.3    60.00  0.51     Sequence
             DRB1_1302  832      VTLADAGFIKQYGDC  VTLADAGFI  0        0.2011
5673.6    80.00  0.38     Sequence
             DRB1_1302  833      TLADAGFIKQYGDCL  FIKQYGDCL  6        0.2259
4341.5    75.00  0.53     Sequence
             DRB1_1302  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.2162
4821.3    80.00  0.67     Sequence
             DRB1_1302  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4        0.2135
4962.7    80.00  0.71     Sequence
             DRB1_1302  836      DAGFIKQYGDCLGDI  FIKQYGDCL  3        0.2696
2705.1    65.00  0.52     Sequence
             DRB1_1302  837      AGFIKQYGDCLGDIA  FIKQYGDCL  2        0.2625
2920.5    70.00  0.50     Sequence
             DRB1_1302  838      GFIKQYGDCLGDIAA  FIKQYGDCL  1        0.2397
3735.9    75.00  0.46     Sequence
             DRB1_1302  839      FIKQYGDCLGDIAAR  QYGDCLGDI  3        0.1895
6437.1    85.00  0.32     Sequence
             DRB1_1302  840      IKQYGDCLGDIAARD  CLGDIAARD  6        0.1625
8613.3    90.00  0.42     Sequence
             DRB1_1302  841      KQYGDCLGDIAARDL  CLGDIAARD  5        0.1825
6937.2    85.00  0.47     Sequence
             DRB1_1302  842      QYGDCLGDIAARDLI  CLGDIAARD  4        0.2082
5254.2    80.00  0.44     Sequence
             DRB1_1302  843      YGDCLGDIAARDLIC  CLGDIAARD  3        0.2142
4925.0    80.00  0.37     Sequence
```

```
             DRB1_1302  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.2305
4127.7    75.00  0.27     Sequence
             DRB1_1302  845      DCLGDIAARDLICAQ  IAARDLICA  5        0.2202
4616.3    80.00  0.25     Sequence
             DRB1_1302  846      CLGDIAARDLICAQK  IAARDLICA  4        0.1995
5772.9    85.00  0.29     Sequence
             DRB1_1302  847      LGDIAARDLICAQKF  RDLICAQKF  6        0.2530
3236.7    70.00  0.35     Sequence
             DRB1_1302  848      GDIAARDLICAQKFN  RDLICAQKF  5        0.2470
3455.1    70.00  0.37     Sequence
             DRB1_1302  849      DIAARDLICAQKFNG  RDLICAQKF  4        0.2498
3350.1    70.00  0.34     Sequence
             DRB1_1302  850      IAARDLICAQKFNGL  ICAQKFNGL  6        0.3873
757.3    40.00  0.52     Sequence
             DRB1_1302  851      AARDLICAQKFNGLT  ICAQKFNGL  5        0.3717
896.3    43.00  0.57     Sequence
             DRB1_1302  852      ARDLICAQKFNGLTV  ICAQKFNGL  4        0.4106
588.6    36.00  0.49     Sequence
             DRB1_1302  853      RDLICAQKFNGLTVL  ICAQKFNGL  3        0.4727
300.4    26.00  0.31     Sequence
             DRB1_1302  854      DLICAQKFNGLTVLP  QKFNGLTVL  5        0.4384
435.6    31.00  0.38     Sequence
             DRB1_1302  855      LICAQKFNGLTVLPP  QKFNGLTVL  4        0.4123
577.5    36.00  0.41     Sequence
             DRB1_1302  856      ICAQKFNGLTVLPPL  QKFNGLTVL  3        0.3883
748.7    40.00  0.49     Sequence
             DRB1_1302  857      CAQKFNGLTVLPPLL  QKFNGLTVL  2        0.3999
660.2    38.00  0.38     Sequence
             DRB1_1302  858      AQKFNGLTVLPPLLT  GLTVLPPLL  5        0.3993
664.8    38.00  0.25     Sequence
             DRB1_1302  859      QKFNGLTVLPPLLTD  GLTVLPPLL  4        0.3423
1232.3    49.00  0.31     Sequence
             DRB1_1302  860      KFNGLTVLPPLLTDE  GLTVLPPLL  3        0.3070
1804.7    60.00  0.41     Sequence
             DRB1_1302  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.2831
2336.6    65.00  0.48     Sequence
             DRB1_1302  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.2457
3502.4    70.00  0.45     Sequence
             DRB1_1302  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.2175
4753.6    80.00  0.38     Sequence
             DRB1_1302  864      LTVLPPLLTDEMIAQ  LLTDEMIAQ  6        0.2513
3298.2    70.00  0.57     Sequence
             DRB1_1302  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.2606
2980.6    70.00  0.63     Sequence
             DRB1_1302  866      VLPPLLTDEMIAQYT  LLTDEMIAQ  4        0.2685
2737.4    65.00  0.62     Sequence
             DRB1_1302  867      LPPLLTDEMIAQYTS  LLTDEMIAQ  3        0.2681
2748.8    65.00  0.63     Sequence
             DRB1_1302  868      PPLLTDEMIAQYTSA  LLTDEMIAQ  2        0.2645
2857.2    70.00  0.54     Sequence
             DRB1_1302  869      PLLTDEMIAQYTSAL  MIAQYTSAL  6        0.4598
345.3    28.00  0.68     Sequence
             DRB1_1302  870      LLTDEMIAQYTSALL  MIAQYTSAL  5        0.5594
117.6    15.00  0.53     Sequence
             DRB1_1302  871      LTDEMIAQYTSALLA  MIAQYTSAL  4        0.5745
99.9    14.00  0.50     Sequence
             DRB1_1302  872      TDEMIAQYTSALLAG  MIAQYTSAL  3        0.5612
115.3    15.00  0.49     Sequence
             DRB1_1302  873      DEMIAQYTSALLAGT  MIAQYTSAL  2        0.5394
145.9    18.00  0.46     Sequence
             DRB1_1302  874      EMIAQYTSALLAGTI  IAQYTSALL  2        0.5000
223.6    22.00  0.42     Sequence
             DRB1_1302  875      MIAQYTSALLAGTIT  IAQYTSALL  1        0.3895
738.9    40.00  0.48     Sequence
             DRB1_1302  876      IAQYTSALLAGTITS  IAQYTSALL  0        0.2396
3740.6    75.00  0.38     Sequence
```

```
             DRB1_1302  877      AQYTSALLAGTITSG  LLAGTITSG  6        0.1692
8015.1    90.00  0.32     Sequence
             DRB1_1302  878      QYTSALLAGTITSGW  LAGTITSGW  6        0.1796
7161.8    85.00  0.29     Sequence
             DRB1_1302  879      YTSALLAGTITSGWT  LAGTITSGW  5        0.1795
7171.0    85.00  0.31     Sequence
             DRB1_1302  880      TSALLAGTITSGWTF  GTITSGWTF  6        0.2373
3834.4    75.00  0.34     Sequence
             DRB1_1302  881      SALLAGTITSGWTFG  GTITSGWTF  5        0.2296
4170.2    75.00  0.34     Sequence
             DRB1_1302  882      ALLAGTITSGWTFGA  ITSGWTFGA  6        0.2601
2996.2    70.00  0.31     Sequence
             DRB1_1302  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.2381
3801.2    75.00  0.37     Sequence
             DRB1_1302  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.2167
4792.7    80.00  0.44     Sequence
             DRB1_1302  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.2030
5558.9    80.00  0.54     Sequence
             DRB1_1302  886      GTITSGWTFGAGAAL  WTFGAGAAL  6        0.2296
4169.4    75.00  0.38     Sequence
             DRB1_1302  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.2184
4704.3    80.00  0.41     Sequence
             DRB1_1302  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.3362
1315.7    50.00  0.52     Sequence
             DRB1_1302  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.3399
1264.3    49.00  0.56     Sequence
             DRB1_1302  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.3445
1203.3    49.00  0.60     Sequence
             DRB1_1302  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.3323
1372.5    55.00  0.65     Sequence
             DRB1_1302  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.3088
1770.0    60.00  0.57     Sequence
             DRB1_1302  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.2575
3084.1    70.00  0.54     Sequence
             DRB1_1302  894      FGAGAALQIPFAMQM  LQIPFAMQM  6        0.2257
4351.2    75.00  0.32     Sequence
             DRB1_1302  895      GAGAALQIPFAMQMA  LQIPFAMQM  5        0.2136
4958.0    80.00  0.43     Sequence
             DRB1_1302  896      AGAALQIPFAMQMAY  LQIPFAMQM  4        0.2492
3371.4    70.00  0.39     Sequence
             DRB1_1302  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.2720
2636.5    65.00  0.35     Sequence
             DRB1_1302  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.5218
176.6    20.00  0.74     Sequence
             DRB1_1302  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.5469
134.7    17.00  0.79     Sequence
             DRB1_1302  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.5372
149.5    18.00  0.79     Sequence
             DRB1_1302  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.5743
100.1    14.00  0.69     Sequence
             DRB1_1302  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.5221
176.1    20.00  0.67     Sequence
             DRB1_1302  903      PFAMQMAYRFNGIGV  FAMQMAYRF  1        0.5214
177.3    20.00  0.53     Sequence
             DRB1_1302  904      FAMQMAYRFNGIGVT  YRFNGIGVT  6        0.5489
131.8    17.00  0.47     Sequence
             DRB1_1302  905      AMQMAYRFNGIGVTQ  YRFNGIGVT  5        0.5212
177.8    20.00  0.58     Sequence
             DRB1_1302  906      MQMAYRFNGIGVTQN  YRFNGIGVT  4        0.5178
184.4    20.00  0.63     Sequence
             DRB1_1302  907      QMAYRFNGIGVTQNV  YRFNGIGVT  3        0.5247
171.1    19.00  0.65     Sequence
             DRB1_1302  908      MAYRFNGIGVTQNVL  YRFNGIGVT  2        0.4965
232.1    23.00  0.59     Sequence
             DRB1_1302  909      AYRFNGIGVTQNVLY  IGVTQNVLY  6        0.5834
90.7    13.00  0.50     Sequence
```

```
             DRB1_1302  910      YRFNGIGVTQNVLYE  IGVTQNVLY  5        0.5355
152.2    18.00  0.59     Sequence
             DRB1_1302  911      RFNGIGVTQNVLYEN  IGVTQNVLY  4        0.5168
186.3    20.00  0.62     Sequence
             DRB1_1302  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.5074
206.3    21.00  0.62     Sequence
             DRB1_1302  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.4841
265.7    24.00  0.61     Sequence
             DRB1_1302  914      GIGVTQNVLYENQKL  IGVTQNVLY  1        0.4907
247.2    24.00  0.42     Sequence
             DRB1_1302  915      IGVTQNVLYENQKLI  VLYENQKLI  6        0.5535
125.4    16.00  0.39     Sequence
             DRB1_1302  916      GVTQNVLYENQKLIA  LYENQKLIA  6        0.6373
50.6     9.00  0.50     Sequence        WB
             DRB1_1302  917      VTQNVLYENQKLIAN  LYENQKLIA  5        0.6443
46.9     8.50  0.56     Sequence        WB
             DRB1_1302  918      TQNVLYENQKLIANQ  LYENQKLIA  4        0.6419
48.2     8.50  0.57     Sequence        WB
             DRB1_1302  919      QNVLYENQKLIANQF  LYENQKLIA  3        0.6454
46.4     8.50  0.59     Sequence        WB
             DRB1_1302  920      NVLYENQKLIANQFN  LYENQKLIA  2        0.6063
70.8    11.00  0.56     Sequence
             DRB1_1302  921      VLYENQKLIANQFNS  LYENQKLIA  1        0.5566
121.2    16.00  0.52     Sequence
             DRB1_1302  922      LYENQKLIANQFNSA  LIANQFNSA  6        0.7792
10.9     2.50  0.82     Sequence        WB
             DRB1_1302  923      YENQKLIANQFNSAI  LIANQFNSA  5        0.8203
7.0     1.20  0.78     Sequence        SB
             DRB1_1302  924      ENQKLIANQFNSAIG  LIANQFNSA  4        0.8189
7.1     1.20  0.80     Sequence        SB
             DRB1_1302  925      NQKLIANQFNSAIGK  LIANQFNSA  3        0.8183
7.1     1.20  0.77     Sequence        SB
             DRB1_1302  926      QKLIANQFNSAIGKI  LIANQFNSA  2        0.8013
8.6     1.60  0.72     Sequence        SB
             DRB1_1302  927      KLIANQFNSAIGKIQ  LIANQFNSA  1        0.7424
16.2     3.50  0.64     Sequence        WB
             DRB1_1302  928      LIANQFNSAIGKIQD  LIANQFNSA  0        0.6307
54.3     9.50  0.49     Sequence        WB
             DRB1_1302  929      IANQFNSAIGKIQDS  QFNSAIGKI  3        0.4113
583.6    36.00  0.31     Sequence
             DRB1_1302  930      ANQFNSAIGKIQDSL  QFNSAIGKI  2        0.3288
1425.9    55.00  0.35     Sequence
             DRB1_1302  931      NQFNSAIGKIQDSLS  QFNSAIGKI  1        0.2774
2486.8    65.00  0.32     Sequence
             DRB1_1302  932      QFNSAIGKIQDSLSS  IGKIQDSLS  5        0.2049
5448.7    80.00  0.23     Sequence
             DRB1_1302  933      FNSAIGKIQDSLSST  IGKIQDSLS  4        0.1908
6345.5    85.00  0.31     Sequence
             DRB1_1302  934      NSAIGKIQDSLSSTA  IQDSLSSTA  6        0.2356
3908.4    75.00  0.47     Sequence
             DRB1_1302  935      SAIGKIQDSLSSTAS  IQDSLSSTA  5        0.2387
3779.0    75.00  0.49     Sequence
             DRB1_1302  936      AIGKIQDSLSSTASA  IQDSLSSTA  4        0.2883
2209.5    65.00  0.40     Sequence
             DRB1_1302  937      IGKIQDSLSSTASAL  SLSSTASAL  6        0.4011
651.7    38.00  0.46     Sequence
             DRB1_1302  938      GKIQDSLSSTASALG  SLSSTASAL  5        0.4180
542.9    35.00  0.32     Sequence
             DRB1_1302  939      KIQDSLSSTASALGK  LSSTASALG  5        0.3955
692.5    39.00  0.34     Sequence
             DRB1_1302  940      IQDSLSSTASALGKL  LSSTASALG  4        0.4038
633.2    37.00  0.46     Sequence
             DRB1_1302  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.3788
829.5    42.00  0.51     Sequence
             DRB1_1302  942      DSLSSTASALGKLQD  LSSTASALG  2        0.3191
1583.9    55.00  0.51     Sequence
```

```
             DRB1_1302  943      SLSSTASALGKLQDV  LSSTASALG  1         0.2489
3385.5    70.00  0.56     Sequence
             DRB1_1302  944      LSSTASALGKLQDVV  LSSTASALG  0         0.1532
9526.5    90.00  0.38     Sequence
             DRB1_1302  945      SSTASALGKLQDVVN  LGKLQDVVN  6         0.1232
13187.4    95.00  0.22     Sequence
             DRB1_1302  946      STASALGKLQDVVNQ  LGKLQDVVN  5         0.1288
12410.2    95.00  0.20     Sequence
             DRB1_1302  947      TASALGKLQDVVNQN  KLQDVVNQN  6         0.1842
6811.3    85.00  0.49     Sequence
             DRB1_1302  948      ASALGKLQDVVNQNA  KLQDVVNQN  5         0.2441
3565.7    75.00  0.43     Sequence
             DRB1_1302  949      SALGKLQDVVNQNAQ  KLQDVVNQN  4         0.2623
2926.1    70.00  0.43     Sequence
             DRB1_1302  950      ALGKLQDVVNQNAQA  DVVNQNAQA  6         0.4989
226.3    22.00  0.67     Sequence
             DRB1_1302  951      LGKLQDVVNQNAQAL  VVNQNAQAL  6         0.6943
27.3     5.50  0.58     Sequence        WB
             DRB1_1302  952      GKLQDVVNQNAQALN  VVNQNAQAL  5         0.7240
19.8     4.50  0.61     Sequence        WB
             DRB1_1302  953      KLQDVVNQNAQALNT  VVNQNAQAL  4         0.7303
18.5     4.00  0.60     Sequence        WB
             DRB1_1302  954      LQDVVNQNAQALNTL  VVNQNAQAL  3         0.7393
16.8     3.50  0.63     Sequence        WB
             DRB1_1302  955      QDVVNQNAQALNTLV  VVNQNAQAL  2         0.7163
21.5     4.50  0.61     Sequence        WB
             DRB1_1302  956      DVVNQNAQALNTLVK  VVNQNAQAL  1         0.6566
41.1     7.50  0.62     Sequence        WB
             DRB1_1302  957      VVNQNAQALNTLVKQ  VVNQNAQAL  0         0.5541
124.5    16.00  0.48     Sequence
             DRB1_1302  958      VNQNAQALNTLVKQL  QALNTLVKQ  5         0.4314
469.6    32.00  0.37     Sequence
             DRB1_1302  959      NQNAQALNTLVKQLS  QALNTLVKQ  4         0.4028
640.1    37.00  0.44     Sequence
             DRB1_1302  960      QNAQALNTLVKQLSS  QALNTLVKQ  3         0.3805
814.9    41.00  0.48     Sequence
             DRB1_1302  961      NAQALNTLVKQLSSN  QALNTLVKQ  2         0.3409
1251.1    49.00  0.46     Sequence
             DRB1_1302  962      AQALNTLVKQLSSNF  LVKQLSSNF  6         0.4281
486.6    33.00  0.52     Sequence
             DRB1_1302  963      QALNTLVKQLSSNFG  LVKQLSSNF  5         0.4542
367.1    29.00  0.58     Sequence
             DRB1_1302  964      ALNTLVKQLSSNFGA  LVKQLSSNF  4         0.4783
282.7    25.00  0.60     Sequence
             DRB1_1302  965      LNTLVKQLSSNFGAI  LVKQLSSNF  3         0.6086
69.0    11.00  0.40     Sequence
             DRB1_1302  966      NTLVKQLSSNFGAIS  LSSNFGAIS  6         0.6552
41.7     7.50  0.40     Sequence        WB
             DRB1_1302  967      TLVKQLSSNFGAISS  LSSNFGAIS  5         0.6429
47.7     8.50  0.46     Sequence        WB
             DRB1_1302  968      LVKQLSSNFGAISSV  LSSNFGAIS  4         0.6366
51.0     9.00  0.55     Sequence        WB
             DRB1_1302  969      VKQLSSNFGAISSVL  LSSNFGAIS  3         0.6313
54.0     9.50  0.62     Sequence        WB
             DRB1_1302  970      KQLSSNFGAISSVLN  LSSNFGAIS  2         0.5878
86.5    13.00  0.60     Sequence
             DRB1_1302  971      QLSSNFGAISSVLND  LSSNFGAIS  1         0.5049
212.2    22.00  0.54     Sequence
             DRB1_1302  972      LSSNFGAISSVLNDI  AISSVLNDI  6         0.5744
100.0    14.00  0.56     Sequence
             DRB1_1302  973      SSNFGAISSVLNDIL  AISSVLNDI  5         0.5687
106.3    15.00  0.55     Sequence
             DRB1_1302  974      SNFGAISSVLNDILS  AISSVLNDI  4         0.5555
122.6    16.00  0.56     Sequence
             DRB1_1302  975      NFGAISSVLNDILSR  AISSVLNDI  3         0.5446
138.0    17.00  0.51     Sequence
```

```
            DRB1_1302  976      FGAISSVLNDILSRL  VLNDILSRL  6        0.6417
48.3     8.50  0.48     Sequence         WB
            DRB1_1302  977      GAISSVLNDILSRLD  VLNDILSRL  5        0.6240
58.5    10.00  0.51     Sequence
            DRB1_1302  978      AISSVLNDILSRLDK  VLNDILSRL  4        0.5991
76.5    12.00  0.62     Sequence
            DRB1_1302  979      ISSVLNDILSRLDKV  VLNDILSRL  3        0.6290
55.4     9.50  0.50     Sequence         WB
            DRB1_1302  980      SSVLNDILSRLDKVE  VLNDILSRL  2        0.5949
80.1    12.00  0.49     Sequence
            DRB1_1302  981      SVLNDILSRLDKVEA  VLNDILSRL  1        0.5607
115.9    15.00  0.47     Sequence
            DRB1_1302  982      VLNDILSRLDKVEAE  DILSRLDKV  3        0.4668
320.3    27.00  0.38     Sequence
            DRB1_1302  983      LNDILSRLDKVEAEV  DILSRLDKV  2        0.3674
938.8    44.00  0.50     Sequence
            DRB1_1302  984      NDILSRLDKVEAEVQ  DILSRLDKV  1        0.3557
1065.5    46.00  0.40     Sequence
            DRB1_1302  985      DILSRLDKVEAEVQI  DKVEAEVQI  6        0.3582
1036.7    46.00  0.26     Sequence
            DRB1_1302  986      ILSRLDKVEAEVQID  LDKVEAEVQ  4        0.3254
1478.1    55.00  0.25     Sequence
            DRB1_1302  987      LSRLDKVEAEVQIDR  LDKVEAEVQ  3        0.3048
1848.0    60.00  0.25     Sequence
            DRB1_1302  988      SRLDKVEAEVQIDRL  DKVEAEVQI  3        0.2959
2035.3    60.00  0.37     Sequence
            DRB1_1302  989      RLDKVEAEVQIDRLI  DKVEAEVQI  2        0.2882
2211.5    65.00  0.31     Sequence
            DRB1_1302  990      LDKVEAEVQIDRLIT  DKVEAEVQI  1        0.2581
3063.7    70.00  0.28     Sequence
            DRB1_1302  991      DKVEAEVQIDRLITG  VQIDRLITG  6        0.3431
1221.1    49.00  0.65     Sequence
            DRB1_1302  992      KVEAEVQIDRLITGR  VQIDRLITG  5        0.3616
999.9    45.00  0.68     Sequence
            DRB1_1302  993      VEAEVQIDRLITGRL  IDRLITGRL  6        0.5107
199.1    21.00  0.44     Sequence
            DRB1_1302  994      EAEVQIDRLITGRLQ  IDRLITGRL  5        0.5286
164.2    19.00  0.41     Sequence
            DRB1_1302  995      AEVQIDRLITGRLQS  IDRLITGRL  4        0.5219
176.4    20.00  0.41     Sequence
            DRB1_1302  996      EVQIDRLITGRLQSL  IDRLITGRL  3        0.5645
111.2    15.00  0.32     Sequence
            DRB1_1302  997      VQIDRLITGRLQSLQ  IDRLITGRL  2        0.5281
165.0    19.00  0.34     Sequence
            DRB1_1302  998      QIDRLITGRLQSLQT  LITGRLQSL  4        0.4827
269.6    25.00  0.38     Sequence
            DRB1_1302  999      IDRLITGRLQSLQTY  LITGRLQSL  3        0.4199
531.8    34.00  0.49     Sequence
            DRB1_1302 1000      DRLITGRLQSLQTYV  LITGRLQSL  2        0.3597
1020.4    45.00  0.47     Sequence
            DRB1_1302 1001      RLITGRLQSLQTYVT  LITGRLQSL  1        0.3474
1166.1    48.00  0.40     Sequence
            DRB1_1302 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.2899
2172.2    60.00  0.30     Sequence
            DRB1_1302 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.2589
3038.3    70.00  0.42     Sequence
            DRB1_1302 1004      TGRLQSLQTYVTQQL  LQTYVTQQL  6        0.3381
1288.9    50.00  0.41     Sequence
            DRB1_1302 1005      GRLQSLQTYVTQQLI  LQTYVTQQL  5        0.3516
1113.7    47.00  0.49     Sequence
            DRB1_1302 1006      RLQSLQTYVTQQLIR  LQTYVTQQL  4        0.3298
1410.6    55.00  0.52     Sequence
            DRB1_1302 1007      LQSLQTYVTQQLIRA  LQTYVTQQL  3        0.3479
1159.4    48.00  0.50     Sequence
            DRB1_1302 1008      QSLQTYVTQQLIRAA  LQTYVTQQL  2        0.3422
1233.4    49.00  0.44     Sequence
```

```
             DRB1_1302 1009      SLQTYVTQQLIRAAE  YVTQQLIRA  4        0.3102
1743.1    60.00  0.38     Sequence
             DRB1_1302 1010      LQTYVTQQLIRAAEI  QQLIRAAEI  6        0.5078
205.5    21.00  0.56     Sequence
             DRB1_1302 1011      QTYVTQQLIRAAEIR  QQLIRAAEI  5        0.4944
237.6    23.00  0.57     Sequence
             DRB1_1302 1012      TYVTQQLIRAAEIRA  QQLIRAAEI  4        0.5397
145.5    18.00  0.44     Sequence
             DRB1_1302 1013      YVTQQLIRAAEIRAS  QQLIRAAEI  3        0.5501
130.0    16.00  0.41     Sequence
             DRB1_1302 1014      VTQQLIRAAEIRASA  QQLIRAAEI  2        0.5398
145.4    18.00  0.35     Sequence
             DRB1_1302 1015      TQQLIRAAEIRASAN  LIRAAEIRA  3        0.5210
178.1    20.00  0.37     Sequence
             DRB1_1302 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.4840
266.0    24.00  0.37     Sequence
             DRB1_1302 1017      QLIRAAEIRASANLA  EIRASANLA  6        0.5881
86.2    13.00  0.44     Sequence
             DRB1_1302 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.7352
17.6     4.00  0.71     Sequence        WB
             DRB1_1302 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.7808
10.7     2.50  0.76     Sequence        WB
             DRB1_1302 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.7888
9.8     1.90  0.75     Sequence        SB
             DRB1_1302 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.7896
9.7     1.90  0.77     Sequence        SB
             DRB1_1302 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.7637
12.9     3.00  0.77     Sequence        WB
             DRB1_1302 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.6898
28.7     6.00  0.73     Sequence        WB
             DRB1_1302 1024      IRASANLAAIKMSEC  IRASANLAA  0        0.4730
299.4    26.00  0.55     Sequence
             DRB1_1302 1025      RASANLAAIKMSECV  ASANLAAIK  1        0.2813
2384.2    65.00  0.41     Sequence
             DRB1_1302 1026      ASANLAAIKMSECVL  AAIKMSECV  5        0.2796
2426.4    65.00  0.31     Sequence
             DRB1_1302 1027      SANLAAIKMSECVLG  IKMSECVLG  6        0.4145
564.1    35.00  0.69     Sequence
             DRB1_1302 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.4294
480.2    33.00  0.69     Sequence
             DRB1_1302 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.4254
501.1    33.00  0.75     Sequence
             DRB1_1302 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.4168
550.3    35.00  0.78     Sequence
             DRB1_1302 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.3912
725.7    39.00  0.82     Sequence
             DRB1_1302 1032      AIKMSECVLGQSKRV  CVLGQSKRV  6        0.4520
375.9    29.00  0.44     Sequence
             DRB1_1302 1033      IKMSECVLGQSKRVD  CVLGQSKRV  5        0.3831
792.2    41.00  0.55     Sequence
             DRB1_1302 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.3711
901.9    43.00  0.67     Sequence
             DRB1_1302 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.3525
1103.3    47.00  0.67     Sequence
             DRB1_1302 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.3233
1513.6    55.00  0.68     Sequence
             DRB1_1302 1037      ECVLGQSKRVDFCGK  CVLGQSKRV  1        0.2787
2450.2    65.00  0.63     Sequence
             DRB1_1302 1038      CVLGQSKRVDFCGKG  CVLGQSKRV  0        0.1830
6904.1    85.00  0.42     Sequence
             DRB1_1302 1039      VLGQSKRVDFCGKGY  LGQSKRVDF  1        0.1249
12949.3    95.00  0.31     Sequence
             DRB1_1302 1040      LGQSKRVDFCGKGYH  KRVDFCGKG  4        0.1350
11600.9    95.00  0.27     Sequence
             DRB1_1302 1041      GQSKRVDFCGKGYHL  DFCGKGYHL  6        0.2434
3589.3    75.00  0.56     Sequence
```

```
             DRB1_1302 1042      QSKRVDFCGKGYHLM  DFCGKGYHL  5        0.2504
3328.7    70.00  0.51     Sequence
             DRB1_1302 1043      SKRVDFCGKGYHLMS  DFCGKGYHL  4        0.2413
3672.6    75.00  0.51     Sequence
             DRB1_1302 1044      KRVDFCGKGYHLMSF  DFCGKGYHL  3        0.2372
3840.1    75.00  0.49     Sequence
             DRB1_1302 1045      RVDFCGKGYHLMSFP  DFCGKGYHL  2        0.2055
5413.3    80.00  0.50     Sequence
             DRB1_1302 1046      VDFCGKGYHLMSFPQ  DFCGKGYHL  1        0.1754
7495.1    90.00  0.46     Sequence
             DRB1_1302 1047      DFCGKGYHLMSFPQS  YHLMSFPQS  6        0.1722
7761.7    90.00  0.33     Sequence
             DRB1_1302 1048      FCGKGYHLMSFPQSA  HLMSFPQSA  6        0.2618
2942.2    70.00  0.60     Sequence
             DRB1_1302 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.2727
2615.5    65.00  0.59     Sequence
             DRB1_1302 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.2853
2282.9    65.00  0.55     Sequence
             DRB1_1302 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.2842
2309.4    65.00  0.51     Sequence
             DRB1_1302 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.3031
1881.9    60.00  0.37     Sequence
             DRB1_1302 1053      YHLMSFPQSAPHGVV  FPQSAPHGV  5        0.3047
1850.7    60.00  0.29     Sequence
             DRB1_1302 1054      HLMSFPQSAPHGVVF  FPQSAPHGV  4        0.2810
2391.1    65.00  0.38     Sequence
             DRB1_1302 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.2679
2755.9    65.00  0.46     Sequence
             DRB1_1302 1056      MSFPQSAPHGVVFLH  FPQSAPHGV  2        0.2387
3779.4    75.00  0.47     Sequence
             DRB1_1302 1057      SFPQSAPHGVVFLHV  FPQSAPHGV  1        0.2297
4165.0    75.00  0.36     Sequence
             DRB1_1302 1058      FPQSAPHGVVFLHVT  PHGVVFLHV  5        0.1715
7816.2    90.00  0.23     Sequence
             DRB1_1302 1059      PQSAPHGVVFLHVTY  PHGVVFLHV  4        0.1307
12162.6    95.00  0.35     Sequence
             DRB1_1302 1060      QSAPHGVVFLHVTYV  VVFLHVTYV  6        0.3313
1387.5    55.00  0.70     Sequence
             DRB1_1302 1061      SAPHGVVFLHVTYVP  VVFLHVTYV  5        0.3275
1445.7    55.00  0.65     Sequence
             DRB1_1302 1062      APHGVVFLHVTYVPA  VVFLHVTYV  4        0.3564
1057.1    46.00  0.47     Sequence
             DRB1_1302 1063      PHGVVFLHVTYVPAQ  VVFLHVTYV  3        0.3685
928.1    44.00  0.46     Sequence
             DRB1_1302 1064      HGVVFLHVTYVPAQE  VVFLHVTYV  2        0.3590
1027.8    46.00  0.40     Sequence
             DRB1_1302 1065      GVVFLHVTYVPAQEK  VVFLHVTYV  1        0.3400
1263.2    49.00  0.34     Sequence
             DRB1_1302 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.2992
1963.7    60.00  0.22     Sequence
             DRB1_1302 1067      VFLHVTYVPAQEKNF  LHVTYVPAQ  2        0.2483
3405.3    70.00  0.30     Sequence
             DRB1_1302 1068      FLHVTYVPAQEKNFT  VTYVPAQEK  3        0.2014
5654.2    80.00  0.31     Sequence
             DRB1_1302 1069      LHVTYVPAQEKNFTT  VTYVPAQEK  2        0.1456
10351.4    95.00  0.40     Sequence
             DRB1_1302 1070      HVTYVPAQEKNFTTA  VTYVPAQEK  1        0.1253
12892.0    95.00  0.36     Sequence
             DRB1_1302 1071      VTYVPAQEKNFTTAP  YVPAQEKNF  2        0.1041
16211.6   100.00  0.19     Sequence
             DRB1_1302 1072      TYVPAQEKNFTTAPA  EKNFTTAPA  6        0.1125
14800.4   100.00  0.24     Sequence
             DRB1_1302 1073      YVPAQEKNFTTAPAI  KNFTTAPAI  6        0.3348
1335.5    55.00  0.68     Sequence
             DRB1_1302 1074      VPAQEKNFTTAPAIC  KNFTTAPAI  5        0.3519
1109.9    47.00  0.66     Sequence
```

```
             DRB1_1302 1075      PAQEKNFTTAPAICH  KNFTTAPAI  4        0.4041
630.9    37.00  0.43     Sequence
             DRB1_1302 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.4090
598.5    36.00  0.43     Sequence
             DRB1_1302 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.3901
734.6    40.00  0.49     Sequence
             DRB1_1302 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.3671
941.5    44.00  0.54     Sequence
             DRB1_1302 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.2997
1953.0    60.00  0.63     Sequence
             DRB1_1302 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.2207
4590.7    80.00  0.63     Sequence
             DRB1_1302 1081      FTTAPAICHDGKAHF  ICHDGKAHF  6        0.3179
1603.3    55.00  0.60     Sequence
             DRB1_1302 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.3196
1575.1    55.00  0.74     Sequence
             DRB1_1302 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.3283
1433.5    55.00  0.73     Sequence
             DRB1_1302 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.3262
1466.6    55.00  0.75     Sequence
             DRB1_1302 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.3059
1826.0    60.00  0.69     Sequence
             DRB1_1302 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.2719
2638.5    65.00  0.68     Sequence
             DRB1_1302 1087      ICHDGKAHFPREGVF  ICHDGKAHF  0        0.1689
8042.6    90.00  0.50     Sequence
             DRB1_1302 1088      CHDGKAHFPREGVFV  HFPREGVFV  6        0.1796
7164.7    85.00  0.54     Sequence
             DRB1_1302 1089      HDGKAHFPREGVFVS  HFPREGVFV  5        0.1793
7183.8    85.00  0.51     Sequence
             DRB1_1302 1090      DGKAHFPREGVFVSN  HFPREGVFV  4        0.1766
7394.5    85.00  0.49     Sequence
             DRB1_1302 1091      GKAHFPREGVFVSNG  HFPREGVFV  3        0.1677
8147.9    90.00  0.52     Sequence
             DRB1_1302 1092      KAHFPREGVFVSNGT  HFPREGVFV  2        0.1770
7370.1    85.00  0.46     Sequence
             DRB1_1302 1093      AHFPREGVFVSNGTH  HFPREGVFV  1        0.2270
4288.9    75.00  0.37     Sequence
             DRB1_1302 1094      HFPREGVFVSNGTHW  VFVSNGTHW  6        0.7386
16.9     3.50  0.79     Sequence         WB
             DRB1_1302 1095      FPREGVFVSNGTHWF  VFVSNGTHW  5        0.7945
9.2     1.70  0.62     Sequence         SB
             DRB1_1302 1096      PREGVFVSNGTHWFV  VFVSNGTHW  4        0.8151
7.4     1.30  0.60     Sequence         SB
             DRB1_1302 1097      REGVFVSNGTHWFVT  VFVSNGTHW  3        0.8148
7.4     1.30  0.58     Sequence         SB
             DRB1_1302 1098      EGVFVSNGTHWFVTQ  VFVSNGTHW  2        0.7978
8.9     1.70  0.56     Sequence         SB
             DRB1_1302 1099      GVFVSNGTHWFVTQR  VFVSNGTHW  1        0.7640
12.8     3.00  0.56     Sequence         WB
             DRB1_1302 1100      VFVSNGTHWFVTQRN  VFVSNGTHW  0        0.6317
53.8     9.00  0.44     Sequence         WB
             DRB1_1302 1101      FVSNGTHWFVTQRNF  FVSNGTHWF  0        0.2957
2038.4    60.00  0.63     Sequence
             DRB1_1302 1102      VSNGTHWFVTQRNFY  WFVTQRNFY  6        0.1995
5777.1    85.00  0.52     Sequence
             DRB1_1302 1103      SNGTHWFVTQRNFYE  WFVTQRNFY  5        0.2102
5141.9    80.00  0.43     Sequence
             DRB1_1302 1104      NGTHWFVTQRNFYEP  WFVTQRNFY  4        0.2133
4971.7    80.00  0.40     Sequence
             DRB1_1302 1105      GTHWFVTQRNFYEPQ  WFVTQRNFY  3        0.2159
4834.7    80.00  0.37     Sequence
             DRB1_1302 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3        0.2201
4618.6    80.00  0.38     Sequence
             DRB1_1302 1107      HWFVTQRNFYEPQII  RNFYEPQII  6        0.2734
2596.7    65.00  0.37     Sequence
```

```
             DRB1_1302 1108      WFVTQRNFYEPQIIT  RNFYEPQII  5        0.2534
3224.0    70.00  0.40     Sequence
             DRB1_1302 1109      FVTQRNFYEPQIITT  RNFYEPQII  4        0.2288
4206.3    75.00  0.44     Sequence
             DRB1_1302 1110      VTQRNFYEPQIITTD  RNFYEPQII  3        0.2138
4947.1    80.00  0.49     Sequence
             DRB1_1302 1111      TQRNFYEPQIITTDN  RNFYEPQII  2        0.1919
6268.7    85.00  0.49     Sequence
             DRB1_1302 1112      QRNFYEPQIITTDNT  RNFYEPQII  1        0.1799
7142.4    85.00  0.41     Sequence
             DRB1_1302 1113      RNFYEPQIITTDNTF  QIITTDNTF  6        0.2407
3698.9    75.00  0.40     Sequence
             DRB1_1302 1114      NFYEPQIITTDNTFV  IITTDNTFV  6        0.5907
83.8    13.00  0.76     Sequence
             DRB1_1302 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.6394
49.5     8.50  0.54     Sequence         WB
             DRB1_1302 1116      YEPQIITTDNTFVSG  IITTDNTFV  4        0.6427
47.7     8.50  0.48     Sequence         WB
             DRB1_1302 1117      EPQIITTDNTFVSGN  IITTDNTFV  3        0.6475
45.3     8.00  0.46     Sequence         WB
             DRB1_1302 1118      PQIITTDNTFVSGNC  ITTDNTFVS  3        0.6256
57.4     9.50  0.47     Sequence         WB
             DRB1_1302 1119      QIITTDNTFVSGNCD  ITTDNTFVS  2        0.5824
91.6    13.00  0.47     Sequence
             DRB1_1302 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.4786
281.8    25.00  0.50     Sequence
             DRB1_1302 1121      ITTDNTFVSGNCDVV  FVSGNCDVV  6        0.3967
683.5    38.00  0.23     Sequence
             DRB1_1302 1122      TTDNTFVSGNCDVVI  VSGNCDVVI  6        0.5727
101.8    14.00  0.65     Sequence
             DRB1_1302 1123      TDNTFVSGNCDVVIG  VSGNCDVVI  5        0.5632
112.8    15.00  0.67     Sequence
             DRB1_1302 1124      DNTFVSGNCDVVIGI  VSGNCDVVI  4        0.5880
86.3    13.00  0.64     Sequence
             DRB1_1302 1125      NTFVSGNCDVVIGIV  VSGNCDVVI  3        0.5925
82.2    12.00  0.68     Sequence
             DRB1_1302 1126      TFVSGNCDVVIGIVN  VSGNCDVVI  2        0.5405
144.3    17.00  0.68     Sequence
             DRB1_1302 1127      FVSGNCDVVIGIVNN  VSGNCDVVI  1        0.4754
291.9    26.00  0.63     Sequence
             DRB1_1302 1128      VSGNCDVVIGIVNNT  VVIGIVNNT  6        0.4342
455.7    32.00  0.38     Sequence
             DRB1_1302 1129      SGNCDVVIGIVNNTV  VIGIVNNTV  6        0.7867
10.1     2.00  0.77     Sequence         WB
             DRB1_1302 1130      GNCDVVIGIVNNTVY  VIGIVNNTV  5        0.8182
7.2     1.20  0.69     Sequence         SB
             DRB1_1302 1131      NCDVVIGIVNNTVYD  VIGIVNNTV  4        0.8220
6.9     1.20  0.68     Sequence         SB
             DRB1_1302 1132      CDVVIGIVNNTVYDP  VIGIVNNTV  3        0.8307
6.2     1.00  0.63     Sequence         SB
             DRB1_1302 1133      DVVIGIVNNTVYDPL  VIGIVNNTV  2        0.8376
5.8     0.90  0.57     Sequence         SB
             DRB1_1302 1134      VVIGIVNNTVYDPLQ  VIGIVNNTV  1        0.8215
6.9     1.20  0.52     Sequence         SB
             DRB1_1302 1135      VIGIVNNTVYDPLQP  IVNNTVYDP  3        0.7606
13.3     3.00  0.35     Sequence         WB
             DRB1_1302 1136      IGIVNNTVYDPLQPE  IVNNTVYDP  2        0.5528
126.3    16.00  0.69     Sequence
             DRB1_1302 1137      GIVNNTVYDPLQPEL  IVNNTVYDP  1        0.4402
427.0    31.00  0.67     Sequence
             DRB1_1302 1138      IVNNTVYDPLQPELD  IVNNTVYDP  0        0.2894
2182.9    65.00  0.53     Sequence
             DRB1_1302 1139      VNNTVYDPLQPELDS  TVYDPLQPE  3        0.1248
12961.5    95.00  0.46     Sequence
             DRB1_1302 1140      NNTVYDPLQPELDSF  TVYDPLQPE  2        0.1122
14851.5   100.00  0.47     Sequence
```

```
             DRB1_1302 1141      NTVYDPLQPELDSFK  TVYDPLQPE  1        0.0970
17512.1   100.00  0.35     Sequence
             DRB1_1302 1142      TVYDPLQPELDSFKE  YDPLQPELD  2        0.0757
22050.7   100.00  0.31     Sequence
             DRB1_1302 1143      VYDPLQPELDSFKEE  YDPLQPELD  1        0.0613
25763.1   100.00  0.29     Sequence
             DRB1_1302 1144      YDPLQPELDSFKEEL  ELDSFKEEL  6        0.0703
23367.1   100.00  0.33     Sequence
             DRB1_1302 1145      DPLQPELDSFKEELD  ELDSFKEEL  5        0.0782
21464.3   100.00  0.29     Sequence
             DRB1_1302 1146      PLQPELDSFKEELDK  LDSFKEELD  5        0.0826
20463.1   100.00  0.26     Sequence
             DRB1_1302 1147      LQPELDSFKEELDKY  LDSFKEELD  4        0.0824
20493.0   100.00  0.28     Sequence
             DRB1_1302 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.0998
16981.5   100.00  0.34     Sequence
             DRB1_1302 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.0977
17371.9   100.00  0.38     Sequence
             DRB1_1302 1150      ELDSFKEELDKYFKN  EELDKYFKN  6        0.1171
14086.1    95.00  0.32     Sequence
             DRB1_1302 1151      LDSFKEELDKYFKNH  EELDKYFKN  5        0.1073
15651.4   100.00  0.37     Sequence
             DRB1_1302 1152      DSFKEELDKYFKNHT  EELDKYFKN  4        0.1160
14250.1    95.00  0.34     Sequence
             DRB1_1302 1153      SFKEELDKYFKNHTS  EELDKYFKN  3        0.1356
11525.8    95.00  0.27     Sequence
             DRB1_1302 1154      FKEELDKYFKNHTSP  EELDKYFKN  2        0.1478
10103.5    95.00  0.22     Sequence
             DRB1_1302 1155      KEELDKYFKNHTSPD  YFKNHTSPD  6        0.2742
2574.0    65.00  0.56     Sequence
             DRB1_1302 1156      EELDKYFKNHTSPDV  YFKNHTSPD  5        0.3912
725.6    39.00  0.38     Sequence
             DRB1_1302 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.3950
696.4    39.00  0.41     Sequence
             DRB1_1302 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.4169
549.6    35.00  0.41     Sequence
             DRB1_1302 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.3986
670.0    38.00  0.46     Sequence
             DRB1_1302 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.3723
890.4    43.00  0.46     Sequence
             DRB1_1302 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.2824
2354.5    65.00  0.46     Sequence
             DRB1_1302 1162      FKNHTSPDVDLGDIS  FKNHTSPDV  0        0.1460
10300.9    95.00  0.46     Sequence
             DRB1_1302 1163      KNHTSPDVDLGDISG  NHTSPDVDL  1        0.0617
25635.8   100.00  0.41     Sequence
             DRB1_1302 1164      NHTSPDVDLGDISGI  VDLGDISGI  6        0.0956
17770.4   100.00  0.52     Sequence
             DRB1_1302 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.1082
15504.5   100.00  0.41     Sequence
             DRB1_1302 1166      TSPDVDLGDISGINA  VDLGDISGI  4        0.1230
13213.6    95.00  0.36     Sequence
             DRB1_1302 1167      SPDVDLGDISGINAS  VDLGDISGI  3        0.1335
11789.6    95.00  0.32     Sequence
             DRB1_1302 1168      PDVDLGDISGINASF  DISGINASF  6        0.2233
4463.5    75.00  0.49     Sequence
             DRB1_1302 1169      DVDLGDISGINASFV  ISGINASFV  6        0.6091
68.7    11.00  0.76     Sequence
             DRB1_1302 1170      VDLGDISGINASFVN  ISGINASFV  5        0.6234
58.8    10.00  0.78     Sequence
             DRB1_1302 1171      DLGDISGINASFVNI  ISGINASFV  4        0.6599
39.6     7.50  0.74     Sequence         WB
             DRB1_1302 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.7017
25.2     5.50  0.58     Sequence         WB
             DRB1_1302 1173      GDISGINASFVNIQK  ISGINASFV  2        0.6868
29.6     6.00  0.56     Sequence         WB
```

```
             DRB1_1302 1174      DISGINASFVNIQKE  ISGINASFV  1        0.6426
47.8     8.50  0.48     Sequence         WB
             DRB1_1302 1175      ISGINASFVNIQKEI  INASFVNIQ  3        0.5991
76.5    12.00  0.50     Sequence
             DRB1_1302 1176      SGINASFVNIQKEID  INASFVNIQ  2        0.4792
280.1    25.00  0.65     Sequence
             DRB1_1302 1177      GINASFVNIQKEIDR  INASFVNIQ  1        0.4325
464.0    32.00  0.50     Sequence
             DRB1_1302 1178      INASFVNIQKEIDRL  INASFVNIQ  0        0.3736
877.5    43.00  0.34     Sequence
             DRB1_1302 1179      NASFVNIQKEIDRLN  SFVNIQKEI  2        0.2784
2458.3    65.00  0.43     Sequence
             DRB1_1302 1180      ASFVNIQKEIDRLNE  SFVNIQKEI  1        0.2472
3447.4    70.00  0.35     Sequence
             DRB1_1302 1181      SFVNIQKEIDRLNEV  KEIDRLNEV  6        0.3693
919.6    43.00  0.59     Sequence
             DRB1_1302 1182      FVNIQKEIDRLNEVA  KEIDRLNEV  5        0.3854
772.8    40.00  0.61     Sequence
             DRB1_1302 1183      VNIQKEIDRLNEVAK  KEIDRLNEV  4        0.4222
518.7    34.00  0.54     Sequence
             DRB1_1302 1184      NIQKEIDRLNEVAKN  DRLNEVAKN  6        0.5208
178.6    20.00  0.43     Sequence
             DRB1_1302 1185      IQKEIDRLNEVAKNL  DRLNEVAKN  5        0.5370
149.8    18.00  0.44     Sequence
             DRB1_1302 1186      QKEIDRLNEVAKNLN  DRLNEVAKN  4        0.5227
174.8    20.00  0.49     Sequence
             DRB1_1302 1187      KEIDRLNEVAKNLNE  DRLNEVAKN  3        0.4938
239.1    23.00  0.50     Sequence
             DRB1_1302 1188      EIDRLNEVAKNLNES  DRLNEVAKN  2        0.4603
343.5    28.00  0.49     Sequence
             DRB1_1302 1189      IDRLNEVAKNLNESL  VAKNLNESL  6        0.6309
54.3     9.50  0.64     Sequence         WB
             DRB1_1302 1190      DRLNEVAKNLNESLI  VAKNLNESL  5        0.6684
36.2     7.00  0.78     Sequence         WB
             DRB1_1302 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.6668
36.8     7.00  0.81     Sequence         WB
             DRB1_1302 1192      LNEVAKNLNESLIDL  VAKNLNESL  3        0.6839
30.6     6.00  0.81     Sequence         WB
             DRB1_1302 1193      NEVAKNLNESLIDLQ  VAKNLNESL  2        0.6552
41.7     7.50  0.79     Sequence         WB
             DRB1_1302 1194      EVAKNLNESLIDLQE  VAKNLNESL  1        0.5760
98.3    14.00  0.71     Sequence
             DRB1_1302 1195      VAKNLNESLIDLQEL  VAKNLNESL  0        0.4148
561.9    35.00  0.54     Sequence
             DRB1_1302 1196      AKNLNESLIDLQELG  LNESLIDLQ  3        0.2062
5371.9    80.00  0.40     Sequence
             DRB1_1302 1197      KNLNESLIDLQELGK  LNESLIDLQ  2        0.1512
9737.9    90.00  0.43     Sequence
             DRB1_1302 1198      NLNESLIDLQELGKY  IDLQELGKY  6        0.1786
7242.9    85.00  0.46     Sequence
             DRB1_1302 1199      LNESLIDLQELGKYE  IDLQELGKY  5        0.1547
9380.7    90.00  0.51     Sequence
             DRB1_1302 1200      NESLIDLQELGKYEQ  IDLQELGKY  4        0.1437
10566.6    95.00  0.57     Sequence
             DRB1_1302 1201      ESLIDLQELGKYEQY  IDLQELGKY  3        0.1438
10549.2    95.00  0.58     Sequence
             DRB1_1302 1202      SLIDLQELGKYEQYI  ELGKYEQYI  6        0.1995
5775.2    85.00  0.31     Sequence
             DRB1_1302 1203      LIDLQELGKYEQYIK  ELGKYEQYI  5        0.1898
6410.5    85.00  0.34     Sequence
             DRB1_1302 1204      IDLQELGKYEQYIKW  ELGKYEQYI  4        0.1724
7739.2    90.00  0.38     Sequence
             DRB1_1302 1205      DLQELGKYEQYIKWP  ELGKYEQYI  3        0.1556
9288.5    90.00  0.45     Sequence
             DRB1_1302 1206      LQELGKYEQYIKWPW  ELGKYEQYI  2        0.1562
9229.1    90.00  0.41     Sequence
```

```
             DRB1_1302 1207      QELGKYEQYIKWPWY  ELGKYEQYI  1        0.1538
9470.7    90.00  0.37     Sequence
             DRB1_1302 1208      ELGKYEQYIKWPWYI  QYIKWPWYI  6        0.2265
4314.0    75.00  0.51     Sequence
             DRB1_1302 1209      LGKYEQYIKWPWYIW  QYIKWPWYI  5        0.2136
4955.0    80.00  0.52     Sequence
             DRB1_1302 1210      GKYEQYIKWPWYIWL  QYIKWPWYI  4        0.2364
3874.1    75.00  0.49     Sequence
             DRB1_1302 1211      KYEQYIKWPWYIWLG  QYIKWPWYI  3        0.2270
4288.3    75.00  0.50     Sequence
             DRB1_1302 1212      YEQYIKWPWYIWLGF  QYIKWPWYI  2        0.2176
4749.6    80.00  0.46     Sequence
             DRB1_1302 1213      EQYIKWPWYIWLGFI  QYIKWPWYI  1        0.2202
4615.3    80.00  0.36     Sequence
             DRB1_1302 1214      QYIKWPWYIWLGFIA  QYIKWPWYI  0        0.1958
6009.2    85.00  0.25     Sequence
             DRB1_1302 1215      YIKWPWYIWLGFIAG  PWYIWLGFI  4        0.1605
8810.4    90.00  0.18     Sequence
             DRB1_1302 1216      IKWPWYIWLGFIAGL  IWLGFIAGL  6        0.2457
3503.9    70.00  0.58     Sequence
             DRB1_1302 1217      KWPWYIWLGFIAGLI  WLGFIAGLI  6        0.3658
955.0    44.00  0.45     Sequence
             DRB1_1302 1218      WPWYIWLGFIAGLIA  WLGFIAGLI  5        0.4003
657.4    38.00  0.34     Sequence
             DRB1_1302 1219      PWYIWLGFIAGLIAI  WLGFIAGLI  4        0.4351
451.1    32.00  0.32     Sequence
             DRB1_1302 1220      WYIWLGFIAGLIAIV  FIAGLIAIV  6        0.5171
185.8    20.00  0.35     Sequence
             DRB1_1302 1221      YIWLGFIAGLIAIVM  FIAGLIAIV  5        0.5305
160.8    19.00  0.35     Sequence
             DRB1_1302 1222      IWLGFIAGLIAIVMV  FIAGLIAIV  4        0.5173
185.4    20.00  0.40     Sequence
             DRB1_1302 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3        0.4876
255.7    24.00  0.44     Sequence
             DRB1_1302 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.4543
366.7    29.00  0.40     Sequence
             DRB1_1302 1225      GFIAGLIAIVMVTIM  IAGLIAIVM  2        0.4076
607.7    36.00  0.30     Sequence
             DRB1_1302 1226      FIAGLIAIVMVTIML  IAGLIAIVM  1        0.3401
1261.6    49.00  0.27     Sequence
             DRB1_1302 1227      IAGLIAIVMVTIMLC  IAIVMVTIM  4        0.2697
2700.5    65.00  0.26     Sequence
             DRB1_1302 1228      AGLIAIVMVTIMLCC  IAIVMVTIM  3        0.2118
5054.2    80.00  0.38     Sequence
             DRB1_1302 1229      GLIAIVMVTIMLCCM  IAIVMVTIM  2        0.1960
5994.8    85.00  0.33     Sequence
             DRB1_1302 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3        0.1401
10978.0    95.00  0.25     Sequence
             DRB1_1302 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2        0.1232
13179.6    95.00  0.26     Sequence
             DRB1_1302 1232      AIVMVTIMLCCMTSC  IMLCCMTSC  6        0.1269
12667.6    95.00  0.34     Sequence
             DRB1_1302 1233      IVMVTIMLCCMTSCC  IMLCCMTSC  5        0.1271
12642.5    95.00  0.32     Sequence
             DRB1_1302 1234      VMVTIMLCCMTSCCS  IMLCCMTSC  4        0.1165
14181.1    95.00  0.40     Sequence
             DRB1_1302 1235      MVTIMLCCMTSCCSC  IMLCCMTSC  3        0.1056
15951.7   100.00  0.43     Sequence
             DRB1_1302 1236      VTIMLCCMTSCCSCL  IMLCCMTSC  2        0.1152
14369.5    95.00  0.32     Sequence
             DRB1_1302 1237      TIMLCCMTSCCSCLK  IMLCCMTSC  1        0.1084
15467.4   100.00  0.24     Sequence
             DRB1_1302 1238      IMLCCMTSCCSCLKG  MTSCCSCLK  5        0.0835
20266.8   100.00  0.26     Sequence
             DRB1_1302 1239      MLCCMTSCCSCLKGC  MTSCCSCLK  4        0.0644
24908.5   100.00  0.34     Sequence
```

```
             DRB1_1302 1240      LCCMTSCCSCLKGCC  MTSCCSCLK  3        0.0486
29539.8   100.00  0.40     Sequence
             DRB1_1302 1241      CCMTSCCSCLKGCCS  MTSCCSCLK  2        0.0424
31613.6   100.00  0.40     Sequence
             DRB1_1302 1242      CMTSCCSCLKGCCSC  MTSCCSCLK  1        0.0358
33925.1   100.00  0.37     Sequence
             DRB1_1302 1243      MTSCCSCLKGCCSCG  MTSCCSCLK  0        0.0307
35887.0   100.00  0.23     Sequence
             DRB1_1302 1244      TSCCSCLKGCCSCGS  LKGCCSCGS  6        0.0399
32482.6   100.00  0.56     Sequence
             DRB1_1302 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5        0.0403
32338.8   100.00  0.56     Sequence
             DRB1_1302 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.0424
31610.6   100.00  0.56     Sequence
             DRB1_1302 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.0427
31490.4   100.00  0.52     Sequence
             DRB1_1302 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2        0.0479
29790.5   100.00  0.47     Sequence
             DRB1_1302 1249      CLKGCCSCGSCCKFD  LKGCCSCGS  1        0.0392
32727.4   100.00  0.34     Sequence
             DRB1_1302 1250      LKGCCSCGSCCKFDE  GCCSCGSCC  2        0.0280
36941.6   100.00  0.19     Sequence
             DRB1_1302 1251      KGCCSCGSCCKFDED  CSCGSCCKF  3        0.0220
39408.7   100.00  0.30     Sequence
             DRB1_1302 1252      GCCSCGSCCKFDEDD  CSCGSCCKF  2        0.0181
41106.8   100.00  0.28     Sequence
             DRB1_1302 1253      CCSCGSCCKFDEDDS  SCGSCCKFD  2        0.0145
42718.3   100.00  0.32     Sequence
             DRB1_1302 1254      CSCGSCCKFDEDDSE  CKFDEDDSE  6        0.0227
39095.7   100.00  0.44     Sequence
             DRB1_1302 1255      SCGSCCKFDEDDSEP  CKFDEDDSE  5        0.0284
36759.8   100.00  0.50     Sequence
             DRB1_1302 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.2342
3966.8    75.00  0.80     Sequence
             DRB1_1302 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.2749
2554.1    65.00  0.74     Sequence
             DRB1_1302 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.2829
2343.4    65.00  0.69     Sequence
             DRB1_1302 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.2784
2458.4    65.00  0.69     Sequence
             DRB1_1302 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.2770
2495.4    65.00  0.66     Sequence
             DRB1_1302 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.2605
2984.3    70.00  0.63     Sequence
             DRB1_1302 1262      FDEDDSEPVLKGVKL  FDEDDSEPV  0        0.2348
3941.1    75.00  0.35     Sequence
             DRB1_1302 1263      DEDDSEPVLKGVKLH  EPVLKGVKL  5        0.1687
8057.2    90.00  0.47     Sequence
             DRB1_1302 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.2618
2944.5    70.00  0.53     Sequence
             DRB1_1302 1265      DDSEPVLKGVKLHYT  VLKGVKLHY  5        0.3013
1919.6    60.00  0.46     Sequence
             DRB1_1501    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.3820
801.5    39.00  0.50     Sequence
             DRB1_1501    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.3537
1088.3    44.00  0.56     Sequence
             DRB1_1501    3      PIKEMFVFLVLLPLV  IKEMFVFLV  1        0.3203
1562.3    55.00  0.49     Sequence
             DRB1_1501    4      IKEMFVFLVLLPLVS  IKEMFVFLV  0        0.2525
3253.2    70.00  0.22     Sequence
             DRB1_1501    5      KEMFVFLVLLPLVSS  FLVLLPLVS  5        0.2502
3335.6    70.00  0.31     Sequence
             DRB1_1501    6      EMFVFLVLLPLVSSQ  LVLLPLVSS  5        0.2921
2120.9    60.00  0.20     Sequence
             DRB1_1501    7      MFVFLVLLPLVSSQC  LLPLVSSQC  6        0.4168
549.8    32.00  0.47     Sequence
```

```
             DRB1_1501    8      FVFLVLLPLVSSQCV  LLPLVSSQC  5        0.5082
204.6    17.00  0.50     Sequence
             DRB1_1501    9      VFLVLLPLVSSQCVN  LLPLVSSQC  4        0.5420
142.0    13.00  0.49     Sequence
             DRB1_1501    10     FLVLLPLVSSQCVNF  LLPLVSSQC  3        0.5674
107.8    10.00  0.49     Sequence
             DRB1_1501    11     LVLLPLVSSQCVNFT  LLPLVSSQC  2        0.5711
103.7    10.00  0.46     Sequence
             DRB1_1501    12     VLLPLVSSQCVNFTN  LPLVSSQCV  2        0.5440
138.9    13.00  0.43     Sequence
             DRB1_1501    13     LLPLVSSQCVNFTNR  LPLVSSQCV  1        0.4667
320.6    23.00  0.39     Sequence
             DRB1_1501   14      LPLVSSQCVNFTNRT  VSSQCVNFT  3        0.3331
1361.4    49.00  0.36     Sequence
             DRB1_1501   15      PLVSSQCVNFTNRTQ  VSSQCVNFT  2        0.3195
1576.8    55.00  0.37     Sequence
             DRB1_1501   16      LVSSQCVNFTNRTQL  CVNFTNRTQ  5        0.3365
1311.8    48.00  0.34     Sequence
             DRB1_1501   17      VSSQCVNFTNRTQLP  CVNFTNRTQ  4        0.3255
1477.0    55.00  0.40     Sequence
             DRB1_1501   18      SSQCVNFTNRTQLPS  CVNFTNRTQ  3        0.3107
1734.6    55.00  0.47     Sequence
             DRB1_1501   19      SQCVNFTNRTQLPSA  CVNFTNRTQ  2        0.3029
1886.1    60.00  0.41     Sequence
             DRB1_1501   20      QCVNFTNRTQLPSAY  CVNFTNRTQ  1        0.2423
3634.5    70.00  0.29     Sequence
             DRB1_1501   21      CVNFTNRTQLPSAYT  FTNRTQLPS  3        0.2219
4531.7    75.00  0.24     Sequence
             DRB1_1501   22      VNFTNRTQLPSAYTN  RTQLPSAYT  5        0.2169
4785.1    75.00  0.36     Sequence
             DRB1_1501   23      NFTNRTQLPSAYTNS  RTQLPSAYT  4        0.1976
5891.7    80.00  0.44     Sequence
             DRB1_1501   24      FTNRTQLPSAYTNSF  RTQLPSAYT  3        0.2310
4106.6    75.00  0.45     Sequence
             DRB1_1501   25      TNRTQLPSAYTNSFT  PSAYTNSFT  6        0.2688
2727.1    65.00  0.32     Sequence
             DRB1_1501   26      NRTQLPSAYTNSFTR  PSAYTNSFT  5        0.3050
1843.5    55.00  0.47     Sequence
             DRB1_1501   27      RTQLPSAYTNSFTRG  PSAYTNSFT  4        0.2921
2121.4    60.00  0.52     Sequence
             DRB1_1501   28      TQLPSAYTNSFTRGV  PSAYTNSFT  3        0.2931
2097.8    60.00  0.56     Sequence
             DRB1_1501   29      QLPSAYTNSFTRGVY  PSAYTNSFT  2        0.3058
1827.9    55.00  0.44     Sequence
             DRB1_1501   30      LPSAYTNSFTRGVYY  PSAYTNSFT  1        0.3093
1760.0    55.00  0.31     Sequence
             DRB1_1501   31      PSAYTNSFTRGVYYP  YTNSFTRGV  3        0.2953
2048.4    60.00  0.22     Sequence
             DRB1_1501   32      SAYTNSFTRGVYYPD  FTRGVYYPD  6        0.3014
1918.3    60.00  0.23     Sequence
             DRB1_1501   33      AYTNSFTRGVYYPDK  FTRGVYYPD  5        0.3190
1584.1    55.00  0.31     Sequence
             DRB1_1501   34      YTNSFTRGVYYPDKV  FTRGVYYPD  4        0.3337
1351.9    49.00  0.35     Sequence
             DRB1_1501   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.3896
738.5    37.00  0.32     Sequence
             DRB1_1501   36      NSFTRGVYYPDKVFR  GVYYPDKVF  5        0.4259
498.7    30.00  0.40     Sequence
             DRB1_1501   37      SFTRGVYYPDKVFRS  GVYYPDKVF  4        0.4356
449.1    28.00  0.44     Sequence
             DRB1_1501   38      FTRGVYYPDKVFRSS  GVYYPDKVF  3        0.4279
488.1    30.00  0.43     Sequence
             DRB1_1501   39      TRGVYYPDKVFRSSV  GVYYPDKVF  2        0.4065
614.8    34.00  0.44     Sequence
             DRB1_1501   40      RGVYYPDKVFRSSVL  DKVFRSSVL  6        0.4517
377.0    26.00  0.31     Sequence
```

```
             DRB1_1501   41      GVYYPDKVFRSSVLH  DKVFRSSVL  5        0.4289
482.7    30.00  0.46     Sequence
             DRB1_1501   42      VYYPDKVFRSSVLHS  DKVFRSSVL  4        0.4239
509.2    31.00  0.54     Sequence
             DRB1_1501   43      YYPDKVFRSSVLHST  DKVFRSSVL  3        0.4312
470.7    29.00  0.50     Sequence
             DRB1_1501   44      YPDKVFRSSVLHSTQ  DKVFRSSVL  2        0.4437
411.4    27.00  0.47     Sequence
             DRB1_1501   45      PDKVFRSSVLHSTQD  DKVFRSSVL  1        0.4248
504.4    30.00  0.44     Sequence
             DRB1_1501   46      DKVFRSSVLHSTQDL  FRSSVLHST  3        0.3827
795.8    38.00  0.34     Sequence
             DRB1_1501   47      KVFRSSVLHSTQDLF  FRSSVLHST  2        0.3017
1910.1    60.00  0.44     Sequence
             DRB1_1501   48      VFRSSVLHSTQDLFL  FRSSVLHST  1        0.3009
1927.4    60.00  0.22     Sequence
             DRB1_1501   49      FRSSVLHSTQDLFLP  LHSTQDLFL  5        0.3000
1946.2    60.00  0.26     Sequence
             DRB1_1501   50      RSSVLHSTQDLFLPF  LHSTQDLFL  4        0.3121
1707.4    55.00  0.34     Sequence
             DRB1_1501   51      SSVLHSTQDLFLPFF  LHSTQDLFL  3        0.3145
1664.7    55.00  0.36     Sequence
             DRB1_1501   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2        0.3331
1360.8    49.00  0.25     Sequence
             DRB1_1501   53      VLHSTQDLFLPFFSN  QDLFLPFFS  5        0.3318
1380.2    49.00  0.31     Sequence
             DRB1_1501   54      LHSTQDLFLPFFSNV  QDLFLPFFS  4        0.3653
960.2    42.00  0.37     Sequence
             DRB1_1501   55      HSTQDLFLPFFSNVT  FLPFFSNVT  6        0.5331
156.3    14.00  0.62     Sequence
             DRB1_1501   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.5863
87.9     8.50  0.63     Sequence         WB
             DRB1_1501   57      TQDLFLPFFSNVTWF  FLPFFSNVT  4        0.6137
65.3     6.50  0.64     Sequence         WB
             DRB1_1501   58      QDLFLPFFSNVTWFH  FLPFFSNVT  3        0.6398
49.3     5.00  0.62     Sequence         WB
             DRB1_1501   59      DLFLPFFSNVTWFHA  FLPFFSNVT  2        0.6338
52.6     5.00  0.63     Sequence         WB
             DRB1_1501   60      LFLPFFSNVTWFHAI  FLPFFSNVT  1        0.6264
57.0     5.50  0.58     Sequence         WB
             DRB1_1501   61      FLPFFSNVTWFHAIH  FLPFFSNVT  0        0.5787
95.4     9.00  0.45     Sequence         WB
             DRB1_1501   62      LPFFSNVTWFHAIHV  VTWFHAIHV  6        0.5593
117.7    11.00  0.54     Sequence
             DRB1_1501   63      PFFSNVTWFHAIHVS  VTWFHAIHV  5        0.5926
82.1     8.00  0.64     Sequence         WB
             DRB1_1501   64      FFSNVTWFHAIHVSG  VTWFHAIHV  4        0.5765
97.8     9.50  0.69     Sequence         WB
             DRB1_1501   65      FSNVTWFHAIHVSGT  VTWFHAIHV  3        0.5724
102.1    10.00  0.76     Sequence
             DRB1_1501   66      SNVTWFHAIHVSGTN  VTWFHAIHV  2        0.5714
103.2    10.00  0.75     Sequence
             DRB1_1501   67      NVTWFHAIHVSGTNG  VTWFHAIHV  1        0.5167
186.6    16.00  0.65     Sequence
             DRB1_1501   68      VTWFHAIHVSGTNGT  VTWFHAIHV  0        0.4217
521.6    31.00  0.44     Sequence
             DRB1_1501   69      TWFHAIHVSGTNGTK  IHVSGTNGT  5        0.3325
1369.8    49.00  0.44     Sequence
             DRB1_1501   70      WFHAIHVSGTNGTKR  IHVSGTNGT  4        0.3619
996.6    43.00  0.52     Sequence
             DRB1_1501   71      FHAIHVSGTNGTKRF  IHVSGTNGT  3        0.3704
908.3    41.00  0.59     Sequence
             DRB1_1501   72      HAIHVSGTNGTKRFD  IHVSGTNGT  2        0.3476
1163.4    46.00  0.68     Sequence
             DRB1_1501   73      AIHVSGTNGTKRFDN  IHVSGTNGT  1        0.2983
1982.7    60.00  0.59     Sequence
```

```
             DRB1_1501   74      IHVSGTNGTKRFDNP  IHVSGTNGT  0        0.1918
6279.3    80.00  0.47     Sequence
             DRB1_1501   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.1080
15536.5    95.00  0.34     Sequence
             DRB1_1501   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.2209
4582.8    75.00  0.68     Sequence
             DRB1_1501   77      SGTNGTKRFDNPVLP  TKRFDNPVL  5        0.2602
2993.9    65.00  0.73     Sequence
             DRB1_1501   78      GTNGTKRFDNPVLPF  TKRFDNPVL  4        0.3085
1775.3    55.00  0.65     Sequence
             DRB1_1501   79      TNGTKRFDNPVLPFN  TKRFDNPVL  3        0.3230
1517.9    55.00  0.62     Sequence
             DRB1_1501   80      NGTKRFDNPVLPFND  TKRFDNPVL  2        0.3179
1603.3    55.00  0.59     Sequence
             DRB1_1501   81      GTKRFDNPVLPFNDG  TKRFDNPVL  1        0.2882
2211.2    60.00  0.55     Sequence
             DRB1_1501   82      TKRFDNPVLPFNDGV  TKRFDNPVL  0        0.2491
3375.3    70.00  0.40     Sequence
             DRB1_1501   83      KRFDNPVLPFNDGVY  VLPFNDGVY  6        0.3436
1214.6    47.00  0.60     Sequence
             DRB1_1501   84      RFDNPVLPFNDGVYF  VLPFNDGVY  5        0.4454
403.9    27.00  0.62     Sequence
             DRB1_1501   85      FDNPVLPFNDGVYFA  VLPFNDGVY  4        0.4858
260.6    20.00  0.60     Sequence
             DRB1_1501   86      DNPVLPFNDGVYFAS  VLPFNDGVY  3        0.4954
235.0    19.00  0.59     Sequence
             DRB1_1501   87      NPVLPFNDGVYFAST  VLPFNDGVY  2        0.4958
234.1    19.00  0.58     Sequence
             DRB1_1501   88      PVLPFNDGVYFASTE  VLPFNDGVY  1        0.4579
352.7    25.00  0.54     Sequence
             DRB1_1501   89      VLPFNDGVYFASTEK  VLPFNDGVY  0        0.3816
805.3    39.00  0.34     Sequence
             DRB1_1501   90      LPFNDGVYFASTEKS  GVYFASTEK  5        0.2889
2194.3    60.00  0.34     Sequence
             DRB1_1501   91      PFNDGVYFASTEKSN  GVYFASTEK  4        0.2411
3682.2    70.00  0.46     Sequence
             DRB1_1501   92      FNDGVYFASTEKSNI  GVYFASTEK  3        0.2748
2557.4    65.00  0.43     Sequence
             DRB1_1501   93      NDGVYFASTEKSNII  VYFASTEKS  3        0.2893
2185.3    60.00  0.35     Sequence
             DRB1_1501   94      DGVYFASTEKSNIIR  VYFASTEKS  2        0.2789
2445.6    65.00  0.31     Sequence
             DRB1_1501   95      GVYFASTEKSNIIRG  ASTEKSNII  4        0.2421
3642.6    70.00  0.28     Sequence
             DRB1_1501   96      VYFASTEKSNIIRGW  ASTEKSNII  3        0.2017
5639.9    80.00  0.41     Sequence
             DRB1_1501   97      YFASTEKSNIIRGWI  ASTEKSNII  2        0.2430
3607.8    70.00  0.33     Sequence
             DRB1_1501   98      FASTEKSNIIRGWIF  SNIIRGWIF  6        0.4623
336.1    24.00  0.64     Sequence
             DRB1_1501   99      ASTEKSNIIRGWIFG  SNIIRGWIF  5        0.5468
134.8    13.00  0.64     Sequence
             DRB1_1501  100      STEKSNIIRGWIFGT  SNIIRGWIF  4        0.6307
54.4     5.50  0.50     Sequence         WB
             DRB1_1501  101      TEKSNIIRGWIFGTT  SNIIRGWIF  3        0.6850
30.2     3.00  0.35     Sequence         WB
             DRB1_1501  102      EKSNIIRGWIFGTTL  IRGWIFGTT  5        0.7130
22.3     1.80  0.44     Sequence         SB
             DRB1_1501  103      KSNIIRGWIFGTTLD  IRGWIFGTT  4        0.7059
24.1     2.00  0.47     Sequence         WB
             DRB1_1501  104      SNIIRGWIFGTTLDS  IRGWIFGTT  3        0.6605
39.4     4.00  0.52     Sequence         WB
             DRB1_1501  105      NIIRGWIFGTTLDSK  IRGWIFGTT  2        0.6034
73.0     7.00  0.58     Sequence         WB
             DRB1_1501  106      IIRGWIFGTTLDSKT  IRGWIFGTT  1        0.4845
264.5    21.00  0.53     Sequence
```

```
             DRB1_1501  107      IRGWIFGTTLDSKTQ  IRGWIFGTT  0        0.3201
1565.7    55.00  0.34     Sequence
             DRB1_1501  108      RGWIFGTTLDSKTQS  GWIFGTTLD  1        0.2176
4747.9    75.00  0.25     Sequence
             DRB1_1501  109      GWIFGTTLDSKTQSL  FGTTLDSKT  3        0.1537
9478.2    90.00  0.31     Sequence
             DRB1_1501  110      WIFGTTLDSKTQSLL  FGTTLDSKT  2        0.1424
10711.3    90.00  0.28     Sequence
             DRB1_1501  111      IFGTTLDSKTQSLLI  LDSKTQSLL  5        0.1960
5996.1    80.00  0.34     Sequence
             DRB1_1501  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5        0.2280
4243.0    75.00  0.34     Sequence
             DRB1_1501  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4        0.2410
3686.4    70.00  0.40     Sequence
             DRB1_1501  114      TTLDSKTQSLLIVNN  DSKTQSLLI  3        0.2422
3637.5    70.00  0.39     Sequence
             DRB1_1501  115      TLDSKTQSLLIVNNA  DSKTQSLLI  2        0.2354
3916.5    75.00  0.37     Sequence
             DRB1_1501  116      LDSKTQSLLIVNNAT  SLLIVNNAT  6        0.2852
2284.7    60.00  0.28     Sequence
             DRB1_1501  117      DSKTQSLLIVNNATN  LLIVNNATN  6        0.3722
891.3    41.00  0.52     Sequence
             DRB1_1501  118      SKTQSLLIVNNATNV  LLIVNNATN  5        0.4576
353.7    25.00  0.63     Sequence
             DRB1_1501  119      KTQSLLIVNNATNVV  LLIVNNATN  4        0.5136
193.1    16.00  0.58     Sequence
             DRB1_1501  120      TQSLLIVNNATNVVI  LLIVNNATN  3        0.5364
150.8    14.00  0.53     Sequence
             DRB1_1501  121      QSLLIVNNATNVVIK  LLIVNNATN  2        0.5323
157.7    14.00  0.46     Sequence
             DRB1_1501  122      SLLIVNNATNVVIKV  IVNNATNVV  3        0.4992
225.7    18.00  0.38     Sequence
             DRB1_1501  123      LLIVNNATNVVIKVC  IVNNATNVV  2        0.4313
470.1    29.00  0.47     Sequence
             DRB1_1501  124      LIVNNATNVVIKVCE  IVNNATNVV  1        0.3805
814.8    39.00  0.44     Sequence
             DRB1_1501  125      IVNNATNVVIKVCEF  IVNNATNVV  0        0.3197
1573.0    55.00  0.28     Sequence
             DRB1_1501  126      VNNATNVVIKVCEFQ  NATNVVIKV  2        0.2175
4752.8    75.00  0.25     Sequence
             DRB1_1501  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.3016
1912.4    60.00  0.41     Sequence
             DRB1_1501  128      NATNVVIKVCEFQFC  VIKVCEFQF  5        0.3173
1615.2    55.00  0.44     Sequence
             DRB1_1501  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.3295
1414.4    50.00  0.46     Sequence
             DRB1_1501  130      TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.3486
1150.4    46.00  0.47     Sequence
             DRB1_1501  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.3403
1258.6    47.00  0.44     Sequence
             DRB1_1501  132      VVIKVCEFQFCNYPF  EFQFCNYPF  6        0.4401
427.6    28.00  0.47     Sequence
             DRB1_1501  133      VIKVCEFQFCNYPFL  EFQFCNYPF  5        0.4815
273.3    21.00  0.59     Sequence
             DRB1_1501  134      IKVCEFQFCNYPFLG  EFQFCNYPF  4        0.4787
281.7    21.00  0.64     Sequence
             DRB1_1501  135      KVCEFQFCNYPFLGV  EFQFCNYPF  3        0.5127
194.9    17.00  0.59     Sequence
             DRB1_1501  136      VCEFQFCNYPFLGVY  EFQFCNYPF  2        0.5060
209.5    17.00  0.52     Sequence
             DRB1_1501  137      CEFQFCNYPFLGVYY  NYPFLGVYY  6        0.5728
101.7    10.00  0.29     Sequence
             DRB1_1501  138      EFQFCNYPFLGVYYH  NYPFLGVYY  5        0.5497
130.6    12.00  0.40     Sequence
             DRB1_1501  139      FQFCNYPFLGVYYHK  NYPFLGVYY  4        0.5376
148.8    14.00  0.49     Sequence
```

```
             DRB1_1501  140      QFCNYPFLGVYYHKN  NYPFLGVYY  3        0.5479
133.2    12.00  0.48     Sequence
             DRB1_1501  141      FCNYPFLGVYYHKNN  NYPFLGVYY  2        0.5148
190.5    16.00  0.49     Sequence
             DRB1_1501  142      CNYPFLGVYYHKNNK  NYPFLGVYY  1        0.5096
201.6    17.00  0.46     Sequence
             DRB1_1501  143      NYPFLGVYYHKNNKS  VYYHKNNKS  6        0.5255
169.7    15.00  0.28     Sequence
             DRB1_1501  144      YPFLGVYYHKNNKSW  VYYHKNNKS  5        0.5002
223.0    18.00  0.55     Sequence
             DRB1_1501  145      PFLGVYYHKNNKSWM  VYYHKNNKS  4        0.5325
157.2    14.00  0.61     Sequence
             DRB1_1501  146      FLGVYYHKNNKSWME  VYYHKNNKS  3        0.5278
165.5    15.00  0.62     Sequence
             DRB1_1501  147      LGVYYHKNNKSWMES  VYYHKNNKS  2        0.5066
208.1    17.00  0.66     Sequence
             DRB1_1501  148      GVYYHKNNKSWMESE  VYYHKNNKS  1        0.4681
315.6    23.00  0.57     Sequence
             DRB1_1501  149      VYYHKNNKSWMESEF  VYYHKNNKS  0        0.3503
1129.6    45.00  0.43     Sequence
             DRB1_1501  150      YYHKNNKSWMESEFR  HKNNKSWME  2        0.2128
5002.7    80.00  0.38     Sequence
             DRB1_1501  151      YHKNNKSWMESEFRV  HKNNKSWME  1        0.2090
5211.8    80.00  0.29     Sequence
             DRB1_1501  152      HKNNKSWMESEFRVY  SWMESEFRV  5        0.2142
4924.8    75.00  0.34     Sequence
             DRB1_1501  153      KNNKSWMESEFRVYS  SWMESEFRV  4        0.2448
3537.8    70.00  0.29     Sequence
             DRB1_1501  154      NNKSWMESEFRVYSS  SWMESEFRV  3        0.2582
3060.3    70.00  0.26     Sequence
             DRB1_1501  155      NKSWMESEFRVYSSA  MESEFRVYS  4        0.2763
2515.1    65.00  0.33     Sequence
             DRB1_1501  156      KSWMESEFRVYSSAN  FRVYSSANX  7        0.4022
644.5    35.00  0.28     Sequence
             DRB1_1501  157      SWMESEFRVYSSANN  FRVYSSANN  6        0.5869
87.3     8.50  0.80     Sequence        WB
             DRB1_1501  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.6386
49.9     5.00  0.86     Sequence        WB
             DRB1_1501  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.6644
37.8     3.50  0.85     Sequence        WB
             DRB1_1501  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.6857
30.0     3.00  0.83     Sequence        WB
             DRB1_1501  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.6737
34.1     3.00  0.81     Sequence        WB
             DRB1_1501  162      EFRVYSSANNCTFEY  FRVYSSANN  1        0.5873
87.0     8.50  0.69     Sequence        WB
             DRB1_1501  163      FRVYSSANNCTFEYV  FRVYSSANN  0        0.3700
912.7    41.00  0.44     Sequence
             DRB1_1501  164      RVYSSANNCTFEYVS  VYSSANNCT  1        0.2045
5469.7    80.00  0.56     Sequence
             DRB1_1501  165      VYSSANNCTFEYVSQ  VYSSANNCT  0        0.1367
11388.6    95.00  0.38     Sequence
             DRB1_1501  166      YSSANNCTFEYVSQP  SANNCTFEY  2        0.0863
19647.5   100.00  0.25     Sequence
             DRB1_1501  167      SSANNCTFEYVSQPF  TFEYVSQPF  6        0.2090
5210.9    80.00  0.53     Sequence
             DRB1_1501  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.3185
1592.9    55.00  0.37     Sequence
             DRB1_1501  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.3982
672.7    35.00  0.37     Sequence
             DRB1_1501  170      NNCTFEYVSQPFLMD  FEYVSQPFL  4        0.4025
642.3    35.00  0.35     Sequence
             DRB1_1501  171      NCTFEYVSQPFLMDL  FEYVSQPFL  3        0.4144
564.5    32.00  0.37     Sequence
             DRB1_1501  172      CTFEYVSQPFLMDLE  FEYVSQPFL  2        0.3941
703.1    36.00  0.38     Sequence
```

```
            DRB1_1501  173      TFEYVSQPFLMDLEG  FEYVSQPFL  1        0.3386
1281.6    48.00  0.32     Sequence
            DRB1_1501  174      FEYVSQPFLMDLEGK  YVSQPFLMD  2        0.2654
2830.6    65.00  0.22     Sequence
            DRB1_1501  175      EYVSQPFLMDLEGKQ  SQPFLMDLE  3        0.1829
6913.9    85.00  0.22     Sequence
            DRB1_1501  176      YVSQPFLMDLEGKQG  LMDLEGKQG  6        0.1679
8126.9    85.00  0.19     Sequence
            DRB1_1501  177      VSQPFLMDLEGKQGN  LMDLEGKQG  5        0.1816
7011.4    85.00  0.31     Sequence
            DRB1_1501  178      SQPFLMDLEGKQGNF  LMDLEGKQG  4        0.1906
6357.3    85.00  0.38     Sequence
            DRB1_1501  179      QPFLMDLEGKQGNFK  LMDLEGKQG  3        0.2153
4865.1    75.00  0.34     Sequence
            DRB1_1501  180      PFLMDLEGKQGNFKN  LEGKQGNFK  5        0.2299
4157.5    75.00  0.37     Sequence
            DRB1_1501  181      FLMDLEGKQGNFKNL  LEGKQGNFK  4        0.2229
4482.9    75.00  0.47     Sequence
            DRB1_1501  182      LMDLEGKQGNFKNLS  LEGKQGNFK  3        0.2133
4973.8    80.00  0.56     Sequence
            DRB1_1501  183      MDLEGKQGNFKNLSE  LEGKQGNFK  2        0.2007
5700.7    80.00  0.59     Sequence
            DRB1_1501  184      DLEGKQGNFKNLSEF  LEGKQGNFK  1        0.1946
6092.0    80.00  0.52     Sequence
            DRB1_1501  185      LEGKQGNFKNLSEFV  FKNLSEFVX  7        0.2265
4310.3    75.00  0.25     Sequence
            DRB1_1501  186      EGKQGNFKNLSEFVF  FKNLSEFVF  6        0.3195
1576.9    55.00  0.64     Sequence
            DRB1_1501  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5        0.3798
820.9    39.00  0.67     Sequence
            DRB1_1501  188      KQGNFKNLSEFVFKN  FKNLSEFVF  4        0.4223
518.2    31.00  0.59     Sequence
            DRB1_1501  189      QGNFKNLSEFVFKNI  FKNLSEFVF  3        0.4525
373.8    25.00  0.51     Sequence
            DRB1_1501  190      GNFKNLSEFVFKNID  FKNLSEFVF  2        0.4480
392.5    26.00  0.47     Sequence
            DRB1_1501  191      NFKNLSEFVFKNIDG  FKNLSEFVF  1        0.4373
440.8    28.00  0.32     Sequence
            DRB1_1501  192      FKNLSEFVFKNIDGY  EFVFKNIDG  5        0.4202
530.1    31.00  0.43     Sequence
            DRB1_1501  193      KNLSEFVFKNIDGYF  EFVFKNIDG  4        0.4876
255.7    20.00  0.38     Sequence
            DRB1_1501  194      NLSEFVFKNIDGYFK  FKNIDGYFK  6        0.5645
111.3    11.00  0.32     Sequence
            DRB1_1501  195      LSEFVFKNIDGYFKI  FKNIDGYFK  5        0.5991
76.5     7.50  0.40     Sequence         WB
            DRB1_1501  196      SEFVFKNIDGYFKIY  FKNIDGYFK  4        0.6182
62.2     6.00  0.43     Sequence         WB
            DRB1_1501  197      EFVFKNIDGYFKIYS  FKNIDGYFK  3        0.6394
49.5     5.00  0.38     Sequence         WB
            DRB1_1501  198      FVFKNIDGYFKIYSK  FKNIDGYFK  2        0.6501
44.1     4.50  0.38     Sequence         WB
            DRB1_1501  199      VFKNIDGYFKIYSKH  IDGYFKIYS  4        0.6404
48.9     5.00  0.38     Sequence         WB
            DRB1_1501  200      FKNIDGYFKIYSKHT  IDGYFKIYS  3        0.6304
54.5     5.50  0.41     Sequence         WB
            DRB1_1501  201      KNIDGYFKIYSKHTP  IDGYFKIYS  2        0.6389
49.8     5.00  0.39     Sequence         WB
            DRB1_1501  202      NIDGYFKIYSKHTPI  YFKIYSKHT  4        0.6541
42.2     4.00  0.32     Sequence         WB
            DRB1_1501  203      IDGYFKIYSKHTPIN  YFKIYSKHT  3        0.6246
58.1     5.50  0.34     Sequence         WB
            DRB1_1501  204      DGYFKIYSKHTPINL  FKIYSKHTP  3        0.5816
92.5     9.00  0.38     Sequence         WB
            DRB1_1501  205      GYFKIYSKHTPINLV  FKIYSKHTP  2        0.5802
93.9     9.00  0.37     Sequence         WB
```

```
             DRB1_1501  206      YFKIYSKHTPINLVR  FKIYSKHTP  1        0.5110
198.5    17.00  0.28     Sequence
             DRB1_1501  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.4057
620.0    34.00  0.32     Sequence
             DRB1_1501  208      KIYSKHTPINLVRDL  YSKHTPINL  2        0.3599
1018.6    43.00  0.38     Sequence
             DRB1_1501  209      IYSKHTPINLVRDLP  YSKHTPINL  1        0.2882
2211.0    60.00  0.34     Sequence
             DRB1_1501  210      YSKHTPINLVRDLPQ  INLVRDLPQ  6        0.3033
1879.0    60.00  0.45     Sequence
             DRB1_1501  211      SKHTPINLVRDLPQG  INLVRDLPQ  5        0.2924
2113.0    60.00  0.62     Sequence
             DRB1_1501  212      KHTPINLVRDLPQGF  INLVRDLPQ  4        0.3409
1250.6    47.00  0.56     Sequence
             DRB1_1501  213      HTPINLVRDLPQGFS  INLVRDLPQ  3        0.3619
996.6    43.00  0.50     Sequence
             DRB1_1501  214      TPINLVRDLPQGFSA  INLVRDLPQ  2        0.3686
926.3    41.00  0.44     Sequence
             DRB1_1501  215      PINLVRDLPQGFSAL  INLVRDLPQ  1        0.3655
958.4    42.00  0.33     Sequence
             DRB1_1501  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.3271
1451.2    50.00  0.32     Sequence
             DRB1_1501  217      NLVRDLPQGFSALEP  VRDLPQGFS  2        0.3128
1695.3    55.00  0.26     Sequence
             DRB1_1501  218      LVRDLPQGFSALEPL  PQGFSALEP  5        0.3002
1943.4    60.00  0.40     Sequence
             DRB1_1501  219      VRDLPQGFSALEPLV  PQGFSALEP  4        0.3099
1748.4    55.00  0.52     Sequence
             DRB1_1501  220      RDLPQGFSALEPLVD  PQGFSALEP  3        0.3172
1615.7    55.00  0.48     Sequence
             DRB1_1501  221      DLPQGFSALEPLVDL  PQGFSALEP  2        0.3068
1809.4    55.00  0.41     Sequence
             DRB1_1501  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.2687
2730.3    65.00  0.30     Sequence
             DRB1_1501  223      PQGFSALEPLVDLPI  LEPLVDLPI  6        0.3283
1433.0    50.00  0.48     Sequence
             DRB1_1501  224      QGFSALEPLVDLPIG  LEPLVDLPI  5        0.3346
1338.4    49.00  0.54     Sequence
             DRB1_1501  225      GFSALEPLVDLPIGI  LEPLVDLPI  4        0.3487
1149.7    46.00  0.55     Sequence
             DRB1_1501  226      FSALEPLVDLPIGIN  LEPLVDLPI  3        0.3311
1390.2    49.00  0.57     Sequence
             DRB1_1501  227      SALEPLVDLPIGINI  LEPLVDLPI  2        0.3456
1189.1    46.00  0.49     Sequence
             DRB1_1501  228      ALEPLVDLPIGINIT  LEPLVDLPI  1        0.3351
1331.8    48.00  0.37     Sequence
             DRB1_1501  229      LEPLVDLPIGINITR  VDLPIGINI  4        0.3140
1673.5    55.00  0.20     Sequence
             DRB1_1501  230      EPLVDLPIGINITRF  VDLPIGINI  3        0.2942
2073.7    60.00  0.26     Sequence
             DRB1_1501  231      PLVDLPIGINITRFQ  LPIGINITR  4        0.2806
2402.3    65.00  0.24     Sequence
             DRB1_1501  232      LVDLPIGINITRFQT  LPIGINITR  3        0.2584
3053.4    70.00  0.29     Sequence
             DRB1_1501  233      VDLPIGINITRFQTL  LPIGINITR  2        0.2588
3038.6    70.00  0.28     Sequence
             DRB1_1501  234      DLPIGINITRFQTLL  ITRFQTLLX  7        0.3124
1702.6    55.00  0.22     Sequence
             DRB1_1501  235      LPIGINITRFQTLLA  ITRFQTLLA  6        0.5107
199.2    17.00  0.75     Sequence
             DRB1_1501  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.5913
83.3     8.00  0.77     Sequence         WB
             DRB1_1501  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.6346
52.1     5.00  0.73     Sequence         WB
             DRB1_1501  238      GINITRFQTLLALHR  ITRFQTLLA  3        0.7027
24.9     2.50  0.56     Sequence         WB
```

```
             DRB1_1501  239      INITRFQTLLALHRS  ITRFQTLLA  2        0.7040
24.6     2.00  0.49     Sequence         WB
             DRB1_1501  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.7032
24.8     2.00  0.38     Sequence         WB
             DRB1_1501  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.7076
23.6     1.90  0.43     Sequence         SB
             DRB1_1501  242      TRFQTLLALHRSYLT  LALHRSYLT  6        0.7154
21.8     1.70  0.39     Sequence         SB
             DRB1_1501  243      RFQTLLALHRSYLTP  LALHRSYLT  5        0.7317
18.2     1.30  0.55     Sequence         SB
             DRB1_1501  244      FQTLLALHRSYLTPG  LALHRSYLT  4        0.7164
21.5     1.70  0.64     Sequence         SB
             DRB1_1501  245      QTLLALHRSYLTPGD  LALHRSYLT  3        0.7001
25.7     2.50  0.71     Sequence         WB
             DRB1_1501  246      TLLALHRSYLTPGDS  LALHRSYLT  2        0.6833
30.8     3.00  0.69     Sequence         WB
             DRB1_1501  247      LLALHRSYLTPGDSS  LALHRSYLT  1        0.6004
75.5     7.50  0.62     Sequence         WB
             DRB1_1501  248      LALHRSYLTPGDSSS  LALHRSYLT  0        0.4713
304.9    23.00  0.50     Sequence
             DRB1_1501  249      ALHRSYLTPGDSSSG  HRSYLTPGD  2        0.2838
2319.8    60.00  0.56     Sequence
             DRB1_1501  250      LHRSYLTPGDSSSGW  HRSYLTPGD  1        0.2367
3863.1    75.00  0.48     Sequence
             DRB1_1501  251      HRSYLTPGDSSSGWT  LTPGDSSSG  4        0.1322
11959.7    95.00  0.54     Sequence
             DRB1_1501  252      RSYLTPGDSSSGWTA  LTPGDSSSG  3        0.1187
13846.2    95.00  0.68     Sequence
             DRB1_1501  253      SYLTPGDSSSGWTAG  LTPGDSSSG  2        0.1024
16517.7   100.00  0.63     Sequence
             DRB1_1501  254      YLTPGDSSSGWTAGA  LTPGDSSSG  1        0.0832
20332.2   100.00  0.52     Sequence
             DRB1_1501  255      LTPGDSSSGWTAGAA  SSGWTAGAA  6        0.0735
22577.2   100.00  0.32     Sequence
             DRB1_1501  256      TPGDSSSGWTAGAAA  SSGWTAGAA  5        0.0791
21251.5   100.00  0.42     Sequence
             DRB1_1501  257      PGDSSSGWTAGAAAY  SSGWTAGAA  4        0.1069
15724.6    95.00  0.41     Sequence
             DRB1_1501  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.1906
6360.9    85.00  0.38     Sequence
             DRB1_1501  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.2816
2375.4    60.00  0.34     Sequence
             DRB1_1501  260      SSSGWTAGAAAYYVG  TAGAAAYYV  5        0.3146
1661.6    55.00  0.45     Sequence
             DRB1_1501  261      SSGWTAGAAAYYVGY  TAGAAAYYV  4        0.3601
1015.4    43.00  0.50     Sequence
             DRB1_1501  262      SGWTAGAAAYYVGYL  TAGAAAYYV  3        0.4772
286.1    22.00  0.33     Sequence
             DRB1_1501  263      GWTAGAAAYYVGYLQ  AAYYVGYLQ  6        0.5397
145.6    13.00  0.45     Sequence
             DRB1_1501  264      WTAGAAAYYVGYLQP  AAYYVGYLQ  5        0.5522
127.1    12.00  0.55     Sequence
             DRB1_1501  265      TAGAAAYYVGYLQPR  AAYYVGYLQ  4        0.5804
93.7     9.00  0.65     Sequence         WB
             DRB1_1501  266      AGAAAYYVGYLQPRT  AAYYVGYLQ  3        0.6642
37.8     3.50  0.46     Sequence         WB
             DRB1_1501  267      GAAAYYVGYLQPRTF  AAYYVGYLQ  2        0.7048
24.4     2.00  0.34     Sequence         WB
             DRB1_1501  268      AAAYYVGYLQPRTFL  YVGYLQPRT  4        0.7109
22.8     1.80  0.52     Sequence         SB
             DRB1_1501  269      AAYYVGYLQPRTFLL  YVGYLQPRT  3        0.6950
27.1     2.50  0.54     Sequence         WB
             DRB1_1501  270      AYYVGYLQPRTFLLK  YVGYLQPRT  2        0.6858
30.0     3.00  0.51     Sequence         WB
             DRB1_1501  271      YYVGYLQPRTFLLKY  YVGYLQPRT  1        0.6832
30.8     3.00  0.44     Sequence         WB
```

```
              DRB1_1501  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.6355
51.6     5.00  0.25     Sequence         WB
              DRB1_1501  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.5135
193.2    16.00  0.41     Sequence
              DRB1_1501  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.4937
239.5    19.00  0.41     Sequence
              DRB1_1501  275      YLQPRTFLLKYNENG  PRTFLLKYN  3        0.4732
298.7    22.00  0.26     Sequence
              DRB1_1501  276      LQPRTFLLKYNENGT  LLKYNENGT  6        0.5067
208.0    17.00  0.43     Sequence
              DRB1_1501  277      QPRTFLLKYNENGTI  LLKYNENGT  5        0.6085
69.1     7.00  0.54     Sequence         WB
              DRB1_1501  278      PRTFLLKYNENGTIT  LLKYNENGT  4        0.6457
46.2     4.50  0.51     Sequence         WB
              DRB1_1501  279      RTFLLKYNENGTITD  LLKYNENGT  3        0.6437
47.2     4.50  0.52     Sequence         WB
              DRB1_1501  280      TFLLKYNENGTITDA  LLKYNENGT  2        0.6113
67.1     6.50  0.50     Sequence         WB
              DRB1_1501  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.5476
133.7    12.00  0.43     Sequence
              DRB1_1501  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.3923
717.1    37.00  0.56     Sequence
              DRB1_1501  283      LKYNENGTITDAVDC  LKYNENGTI  0        0.2198
4635.6    75.00  0.56     Sequence
              DRB1_1501  284      KYNENGTITDAVDCA  GTITDAVDC  5        0.0431
31371.0   100.00  0.19     Sequence
              DRB1_1501  285      YNENGTITDAVDCAL  ITDAVDCAL  6        0.0744
22348.1   100.00  0.36     Sequence
              DRB1_1501  286      NENGTITDAVDCALD  ITDAVDCAL  5        0.0919
18504.2   100.00  0.35     Sequence
              DRB1_1501  287      ENGTITDAVDCALDP  ITDAVDCAL  4        0.0999
16968.8   100.00  0.35     Sequence
              DRB1_1501  288      NGTITDAVDCALDPL  ITDAVDCAL  3        0.1192
13761.6    95.00  0.36     Sequence
              DRB1_1501  289      GTITDAVDCALDPLS  ITDAVDCAL  2        0.1220
13356.2    95.00  0.31     Sequence
              DRB1_1501  290      TITDAVDCALDPLSE  ITDAVDCAL  1        0.1144
14502.7    95.00  0.26     Sequence
              DRB1_1501  291      ITDAVDCALDPLSET  DAVDCALDP  2        0.1007
16813.6   100.00  0.22     Sequence
              DRB1_1501  292      TDAVDCALDPLSETK  VDCALDPLS  3        0.0766
21827.3   100.00  0.23     Sequence
              DRB1_1501  293      DAVDCALDPLSETKC  LDPLSETKC  6        0.0795
21161.5   100.00  0.31     Sequence
              DRB1_1501  294      AVDCALDPLSETKCT  LDPLSETKC  5        0.0877
19365.1   100.00  0.44     Sequence
              DRB1_1501  295      VDCALDPLSETKCTL  LDPLSETKC  4        0.0966
17575.0   100.00  0.54     Sequence
              DRB1_1501  296      DCALDPLSETKCTLK  LDPLSETKC  3        0.1105
15131.1    95.00  0.48     Sequence
              DRB1_1501  297      CALDPLSETKCTLKS  LDPLSETKC  2        0.1242
13042.7    95.00  0.40     Sequence
              DRB1_1501  298      ALDPLSETKCTLKSF  SETKCTLKS  5        0.1375
11290.0    95.00  0.34     Sequence
              DRB1_1501  299      LDPLSETKCTLKSFT  SETKCTLKS  4        0.1407
10910.8    90.00  0.39     Sequence
              DRB1_1501  300      DPLSETKCTLKSFTV  KCTLKSFTV  6        0.3040
1865.0    55.00  0.59     Sequence
              DRB1_1501  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.3451
1195.0    46.00  0.65     Sequence
              DRB1_1501  302      LSETKCTLKSFTVEK  KCTLKSFTV  4        0.4220
519.8    31.00  0.60     Sequence
              DRB1_1501  303      SETKCTLKSFTVEKG  KCTLKSFTV  3        0.4637
331.0    24.00  0.46     Sequence
              DRB1_1501  304      ETKCTLKSFTVEKGI  LKSFTVEKG  5        0.5059
209.9    18.00  0.56     Sequence
```

```
             DRB1_1501  305      TKCTLKSFTVEKGIY  LKSFTVEKG  4        0.5246
171.3    15.00  0.65     Sequence
             DRB1_1501  306      KCTLKSFTVEKGIYQ  LKSFTVEKG  3        0.5138
192.6    16.00  0.68     Sequence
             DRB1_1501  307      CTLKSFTVEKGIYQT  LKSFTVEKG  2        0.4671
319.3    23.00  0.68     Sequence
             DRB1_1501  308      TLKSFTVEKGIYQTS  LKSFTVEKG  1        0.4142
565.5    32.00  0.52     Sequence
             DRB1_1501  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.3207
1556.3    55.00  0.55     Sequence
             DRB1_1501  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.2954
2044.9    60.00  0.65     Sequence
             DRB1_1501  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.2841
2312.8    60.00  0.44     Sequence
             DRB1_1501  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.4665
321.2    23.00  0.70     Sequence
             DRB1_1501  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.5425
141.2    13.00  0.79     Sequence
             DRB1_1501  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.5600
116.8    11.00  0.79     Sequence
             DRB1_1501  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.5718
102.9    10.00  0.80     Sequence
             DRB1_1501  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.5567
121.1    12.00  0.77     Sequence
             DRB1_1501  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.4914
245.5    19.00  0.71     Sequence
             DRB1_1501  318      IYQTSNFRVQPTESI  IYQTSNFRV  0        0.3656
957.7    42.00  0.51     Sequence
             DRB1_1501  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.2659
2814.1    65.00  0.63     Sequence
             DRB1_1501  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.3350
1333.3    48.00  0.53     Sequence
             DRB1_1501  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.3786
831.5    39.00  0.47     Sequence
             DRB1_1501  322      SNFRVQPTESIVRFP  VQPTESIVR  4        0.3765
851.0    40.00  0.46     Sequence
             DRB1_1501  323      NFRVQPTESIVRFPN  VQPTESIVR  3        0.3581
1037.8    44.00  0.49     Sequence
             DRB1_1501  324      FRVQPTESIVRFPNI  VQPTESIVR  2        0.3523
1105.4    45.00  0.48     Sequence
             DRB1_1501  325      RVQPTESIVRFPNIT  IVRFPNITX  7        0.4367
443.5    28.00  0.29     Sequence
             DRB1_1501  326      VQPTESIVRFPNITN  IVRFPNITN  6        0.6602
39.5     4.00  0.86     Sequence         WB
             DRB1_1501  327      QPTESIVRFPNITNL  IVRFPNITN  5        0.7454
15.7     1.10  0.88     Sequence         SB
             DRB1_1501  328      PTESIVRFPNITNLC  IVRFPNITN  4        0.7482
15.2     1.00  0.88     Sequence         SB
             DRB1_1501  329      TESIVRFPNITNLCP  IVRFPNITN  3        0.7455
15.7     1.10  0.90     Sequence         SB
             DRB1_1501  330      ESIVRFPNITNLCPF  IVRFPNITN  2        0.7266
19.3     1.50  0.88     Sequence         SB
             DRB1_1501  331      SIVRFPNITNLCPFG  IVRFPNITN  1        0.6582
40.4     4.00  0.81     Sequence         WB
             DRB1_1501  332      IVRFPNITNLCPFGE  IVRFPNITN  0        0.4295
479.6    29.00  0.54     Sequence
             DRB1_1501  333      VRFPNITNLCPFGEV  ITNLCPFGE  5        0.2511
3304.4    70.00  0.48     Sequence
             DRB1_1501  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.2594
3019.1    65.00  0.50     Sequence
             DRB1_1501  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.2669
2786.1    65.00  0.49     Sequence
             DRB1_1501  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.2802
2411.9    65.00  0.48     Sequence
             DRB1_1501  337      NITNLCPFGEVFNAT  LCPFGEVFN  4        0.2543
3190.7    70.00  0.44     Sequence
```

```
             DRB1_1501  338      ITNLCPFGEVFNATR  LCPFGEVFN  3        0.2517
3281.6    70.00  0.48     Sequence
             DRB1_1501  339      TNLCPFGEVFNATRF  LCPFGEVFN  2        0.2703
2685.7    65.00  0.39     Sequence
             DRB1_1501  340      NLCPFGEVFNATRFA  GEVFNATRF  5        0.2872
2236.9    60.00  0.39     Sequence
             DRB1_1501  341      LCPFGEVFNATRFAS  GEVFNATRF  4        0.2683
2744.3    65.00  0.43     Sequence
             DRB1_1501  342      CPFGEVFNATRFASV  GEVFNATRF  3        0.2623
2928.2    65.00  0.43     Sequence
             DRB1_1501  343      PFGEVFNATRFASVY  GEVFNATRF  2        0.2943
2071.2    60.00  0.34     Sequence
             DRB1_1501  344      FGEVFNATRFASVYA  ATRFASVYA  6        0.5203
179.5    16.00  0.64    Sequence
             DRB1_1501  345      GEVFNATRFASVYAW  ATRFASVYA  5        0.5913
83.3     8.00  0.73    Sequence        WB
             DRB1_1501  346      EVFNATRFASVYAWN  ATRFASVYA  4        0.6182
62.2     6.00  0.74    Sequence        WB
             DRB1_1501  347      VFNATRFASVYAWNR  ATRFASVYA  3        0.6727
34.5     3.50  0.67    Sequence        WB
             DRB1_1501  348      FNATRFASVYAWNRK  ATRFASVYA  2        0.6822
31.1     3.00  0.61    Sequence        WB
             DRB1_1501  349      NATRFASVYAWNRKR  ATRFASVYA  1        0.6714
35.0     3.50  0.50    Sequence        WB
             DRB1_1501  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.6327
53.2     5.00  0.35    Sequence        WB
             DRB1_1501  351      TRFASVYAWNRKRIS  FASVYAWNR  2        0.5458
136.3    13.00  0.47    Sequence
             DRB1_1501  352      RFASVYAWNRKRISN  FASVYAWNR  1        0.5140
192.2    16.00  0.37    Sequence
             DRB1_1501  353      FASVYAWNRKRISNC  VYAWNRKRI  3        0.4102
590.9    33.00  0.41    Sequence
             DRB1_1501  354      ASVYAWNRKRISNCV  VYAWNRKRI  2        0.3752
863.1    40.00  0.49    Sequence
             DRB1_1501  355      SVYAWNRKRISNCVA  VYAWNRKRI  1        0.3353
1329.2    48.00  0.42     Sequence
             DRB1_1501  356      VYAWNRKRISNCVAD  NRKRISNCV  4        0.2535
3218.5    70.00  0.33     Sequence
             DRB1_1501  357      YAWNRKRISNCVADY  NRKRISNCV  3        0.2447
3541.6    70.00  0.46     Sequence
             DRB1_1501  358      AWNRKRISNCVADYS  NRKRISNCV  2        0.2843
2307.2    60.00  0.34     Sequence
             DRB1_1501  359      WNRKRISNCVADYSV  ISNCVADYS  5        0.3128
1695.7    55.00  0.54     Sequence
             DRB1_1501  360      NRKRISNCVADYSVL  ISNCVADYS  4        0.3280
1437.5    50.00  0.60     Sequence
             DRB1_1501  361      RKRISNCVADYSVLY  ISNCVADYS  3        0.3399
1264.0    47.00  0.65     Sequence
             DRB1_1501  362      KRISNCVADYSVLYN  ISNCVADYS  2        0.3407
1252.6    47.00  0.50     Sequence
             DRB1_1501  363      RISNCVADYSVLYNS  ISNCVADYS  1        0.3360
1318.3    48.00  0.37     Sequence
             DRB1_1501  364      ISNCVADYSVLYNSA  VADYSVLYN  4        0.2967
2018.1    60.00  0.41     Sequence
             DRB1_1501  365      SNCVADYSVLYNSAS  VADYSVLYN  3        0.3152
1651.7    55.00  0.36     Sequence
             DRB1_1501  366      NCVADYSVLYNSASF  SVLYNSASF  6        0.3915
723.6    37.00  0.26    Sequence
             DRB1_1501  367      CVADYSVLYNSASFS  SVLYNSASF  5        0.4355
449.3    28.00  0.31    Sequence
             DRB1_1501  368      VADYSVLYNSASFST  SVLYNSASF  4        0.4558
360.7    25.00  0.34    Sequence
             DRB1_1501  369      ADYSVLYNSASFSTF  SVLYNSASF  3        0.4837
266.8    21.00  0.31    Sequence
             DRB1_1501  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.4828
269.3    21.00  0.31    Sequence
```

```
             DRB1_1501  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.4865
258.8    20.00  0.29     Sequence
             DRB1_1501  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.4617
338.3    24.00  0.32     Sequence
             DRB1_1501  373      VLYNSASFSTFKCYG  SASFSTFKC  4        0.4102
590.8    33.00  0.41     Sequence
             DRB1_1501  374      LYNSASFSTFKCYGV  FSTFKCYGV  6        0.4973
230.2    19.00  0.51     Sequence
             DRB1_1501  375      YNSASFSTFKCYGVS  FSTFKCYGV  5        0.5170
186.1    16.00  0.63     Sequence
             DRB1_1501  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.5187
182.7    16.00  0.67     Sequence
             DRB1_1501  377      SASFSTFKCYGVSPT  FSTFKCYGV  3        0.5131
194.1    17.00  0.68     Sequence
             DRB1_1501  378      ASFSTFKCYGVSPTK  FSTFKCYGV  2        0.5011
221.0    18.00  0.60     Sequence
             DRB1_1501  379      SFSTFKCYGVSPTKL  FSTFKCYGV  1        0.4552
363.0    25.00  0.44     Sequence
             DRB1_1501  380      FSTFKCYGVSPTKLN  FKCYGVSPT  3        0.3867
762.0    38.00  0.44     Sequence
             DRB1_1501  381      STFKCYGVSPTKLND  FKCYGVSPT  2        0.3049
1846.8    55.00  0.56     Sequence
             DRB1_1501  382      TFKCYGVSPTKLNDL  FKCYGVSPT  1        0.2619
2940.1    65.00  0.49     Sequence
             DRB1_1501  383      FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.1708
7874.6    85.00  0.35     Sequence
             DRB1_1501  384      KCYGVSPTKLNDLCF  PTKLNDLCF  6        0.1438
10550.7    90.00  0.31     Sequence
             DRB1_1501  385      CYGVSPTKLNDLCFT  PTKLNDLCF  5        0.1429
10654.1    90.00  0.41     Sequence
             DRB1_1501  386      YGVSPTKLNDLCFTN  PTKLNDLCF  4        0.1440
10525.6    90.00  0.51     Sequence
             DRB1_1501  387      GVSPTKLNDLCFTNV  PTKLNDLCF  3        0.1577
9077.4    90.00  0.47     Sequence
             DRB1_1501  388      VSPTKLNDLCFTNVY  PTKLNDLCF  2        0.1713
7837.7    85.00  0.38     Sequence
             DRB1_1501  389      SPTKLNDLCFTNVYA  DLCFTNVYA  6        0.2656
2824.3    65.00  0.50     Sequence
             DRB1_1501  390      PTKLNDLCFTNVYAD  DLCFTNVYA  5        0.2804
2407.1    65.00  0.59     Sequence
             DRB1_1501  391      TKLNDLCFTNVYADS  DLCFTNVYA  4        0.2861
2261.5    60.00  0.61     Sequence
             DRB1_1501  392      KLNDLCFTNVYADSF  DLCFTNVYA  3        0.3259
1470.7    50.00  0.51     Sequence
             DRB1_1501  393      LNDLCFTNVYADSFV  DLCFTNVYA  2        0.3402
1260.6    47.00  0.43     Sequence
             DRB1_1501  394      NDLCFTNVYADSFVI  NVYADSFVI  6        0.4500
384.2    26.00  0.31     Sequence
             DRB1_1501  395      DLCFTNVYADSFVIR  NVYADSFVI  5        0.4992
225.6    18.00  0.41     Sequence
             DRB1_1501  396      LCFTNVYADSFVIRG  NVYADSFVI  4        0.4865
258.7    20.00  0.45     Sequence
             DRB1_1501  397      CFTNVYADSFVIRGD  NVYADSFVI  3        0.4737
297.4    22.00  0.47     Sequence
             DRB1_1501  398      FTNVYADSFVIRGDE  NVYADSFVI  2        0.4376
439.3    28.00  0.50     Sequence
             DRB1_1501  399      TNVYADSFVIRGDEV  NVYADSFVI  1        0.3885
747.1    37.00  0.47     Sequence
             DRB1_1501  400      NVYADSFVIRGDEVR  NVYADSFVI  0        0.3251
1484.4    55.00  0.37     Sequence
             DRB1_1501  401      VYADSFVIRGDEVRQ  VIRGDEVRQ  6        0.2336
3992.6    75.00  0.26     Sequence
             DRB1_1501  402      YADSFVIRGDEVRQI  VIRGDEVRQ  5        0.3122
1706.6    55.00  0.28     Sequence
             DRB1_1501  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.3558
1063.9    44.00  0.40     Sequence
```

```
             DRB1_1501  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.3553
1069.9    44.00  0.43     Sequence
             DRB1_1501  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.3384
1284.5    48.00  0.47     Sequence
             DRB1_1501  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.3001
1943.6    60.00  0.50     Sequence
             DRB1_1501  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.2726
2618.8    65.00  0.37     Sequence
             DRB1_1501  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.2504
3328.4    70.00  0.51     Sequence
             DRB1_1501  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.2387
3777.7    70.00  0.58     Sequence
             DRB1_1501  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.2622
2930.9    65.00  0.50     Sequence
             DRB1_1501  411      DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.2775
2484.5    65.00  0.38     Sequence
             DRB1_1501  412      EVRQIAPGQTGTIAD  IAPGQTGTI  4        0.2601
2999.1    65.00  0.40     Sequence
             DRB1_1501  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.2314
4090.7    75.00  0.57     Sequence
             DRB1_1501  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.2119
5051.0    80.00  0.66     Sequence
             DRB1_1501  415      QIAPGQTGTIADYNY  IAPGQTGTI  1        0.1605
8802.6    90.00  0.52     Sequence
             DRB1_1501  416      IAPGQTGTIADYNYK  IAPGQTGTI  0        0.1343
11687.3    95.00  0.34     Sequence
             DRB1_1501  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.2890
2193.1    60.00  0.56     Sequence
             DRB1_1501  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.3948
697.7    36.00  0.49     Sequence
             DRB1_1501  419      GQTGTIADYNYKLPD  IADYNYKLP  5        0.4216
522.4    31.00  0.46     Sequence
             DRB1_1501  420      QTGTIADYNYKLPDD  IADYNYKLP  4        0.4218
520.9    31.00  0.46     Sequence
             DRB1_1501  421      TGTIADYNYKLPDDF  IADYNYKLP  3        0.4230
514.3    31.00  0.46     Sequence
             DRB1_1501  422      GTIADYNYKLPDDFT  IADYNYKLP  2        0.4023
643.4    35.00  0.46     Sequence
             DRB1_1501  423      TIADYNYKLPDDFTG  IADYNYKLP  1        0.3125
1699.7    55.00  0.41     Sequence
             DRB1_1501  424      IADYNYKLPDDFTGC  IADYNYKLP  0        0.1842
6811.3    85.00  0.22     Sequence
             DRB1_1501  425      ADYNYKLPDDFTGCV  YNYKLPDDF  2        0.1332
11830.8    95.00  0.28     Sequence
             DRB1_1501  426      DYNYKLPDDFTGCVI  YNYKLPDDF  1        0.1477
10117.6    90.00  0.19     Sequence
             DRB1_1501  427      YNYKLPDDFTGCVIA  PDDFTGCVI  5        0.1542
9428.2    90.00  0.22     Sequence
             DRB1_1501  428      NYKLPDDFTGCVIAW  PDDFTGCVI  4        0.1610
8762.8    90.00  0.24     Sequence
             DRB1_1501  429      YKLPDDFTGCVIAWN  PDDFTGCVI  3        0.1643
8452.7    90.00  0.25     Sequence
             DRB1_1501  430      KLPDDFTGCVIAWNS  PDDFTGCVI  2        0.1678
8139.0    85.00  0.22     Sequence
             DRB1_1501  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.1613
8728.1    90.00  0.22     Sequence
             DRB1_1501  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.1861
6674.9    85.00  0.22     Sequence
             DRB1_1501  433      DDFTGCVIAWNSNNL  VIAWNSNNL  6        0.4810
274.7    21.00  0.69     Sequence
             DRB1_1501  434      DFTGCVIAWNSNNLD  VIAWNSNNL  5        0.5368
150.2    14.00  0.67     Sequence
             DRB1_1501  435      FTGCVIAWNSNNLDS  VIAWNSNNL  4        0.5634
112.6    11.00  0.65     Sequence
             DRB1_1501  436      TGCVIAWNSNNLDSK  VIAWNSNNL  3        0.5881
86.2     8.50  0.65     Sequence          WB
```

```
             DRB1_1501  437      GCVIAWNSNNLDSKV  VIAWNSNNL  2        0.5748
99.5     9.50  0.63     Sequence         WB
             DRB1_1501  438      CVIAWNSNNLDSKVG  VIAWNSNNL  1        0.5231
174.1    15.00  0.59     Sequence
             DRB1_1501  439      VIAWNSNNLDSKVGG  VIAWNSNNL  0        0.4042
630.2    34.00  0.51     Sequence
             DRB1_1501  440      IAWNSNNLDSKVGGN  IAWNSNNLD  0        0.1057
15925.4    95.00  0.35     Sequence
             DRB1_1501  441      AWNSNNLDSKVGGNY  LDSKVGGNY  6        0.1094
15310.6    95.00  0.35     Sequence
             DRB1_1501  442      WNSNNLDSKVGGNYN  LDSKVGGNY  5        0.1472
10167.2    90.00  0.44     Sequence
             DRB1_1501  443      NSNNLDSKVGGNYNY  LDSKVGGNY  4        0.1854
6728.0    85.00  0.43     Sequence
             DRB1_1501  444      SNNLDSKVGGNYNYL  LDSKVGGNY  3        0.2232
4469.5    75.00  0.38     Sequence
             DRB1_1501  445      NNLDSKVGGNYNYLY  LDSKVGGNY  2        0.2626
2918.6    65.00  0.26     Sequence
             DRB1_1501  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.2885
2204.7    60.00  0.25     Sequence
             DRB1_1501  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4        0.3444
1204.5    46.00  0.26     Sequence
             DRB1_1501  448      DSKVGGNYNYLYRLF  NYNYLYRLF  6        0.4070
611.4    34.00  0.30     Sequence
             DRB1_1501  449      SKVGGNYNYLYRLFR  NYNYLYRLF  5        0.4830
268.7    21.00  0.30     Sequence
             DRB1_1501  450      KVGGNYNYLYRLFRK  NYNYLYRLF  4        0.5312
159.6    14.00  0.28     Sequence
             DRB1_1501  451      VGGNYNYLYRLFRKS  NYLYRLFRK  5        0.5312
159.6    14.00  0.31     Sequence
             DRB1_1501  452      GGNYNYLYRLFRKSN  NYLYRLFRK  4        0.5275
166.0    15.00  0.31     Sequence
             DRB1_1501  453      GNYNYLYRLFRKSNL  YRLFRKSNL  6        0.5882
86.1     8.50  0.34     Sequence         WB
             DRB1_1501  454      NYNYLYRLFRKSNLK  YRLFRKSNL  5        0.5997
76.0     7.50  0.44     Sequence         WB
             DRB1_1501  455      YNYLYRLFRKSNLKP  YRLFRKSNL  4        0.5787
95.5     9.00  0.55     Sequence         WB
             DRB1_1501  456      NYLYRLFRKSNLKPF  YRLFRKSNL  3        0.5737
100.7     9.50  0.61     Sequence         WB
             DRB1_1501  457      YLYRLFRKSNLKPFE  YRLFRKSNL  2        0.5390
146.6    13.00  0.68     Sequence
             DRB1_1501  458      LYRLFRKSNLKPFER  YRLFRKSNL  1        0.4928
241.7    19.00  0.58     Sequence
             DRB1_1501  459      YRLFRKSNLKPFERD  YRLFRKSNL  0        0.3798
820.7    39.00  0.38     Sequence
             DRB1_1501  460      RLFRKSNLKPFERDI  LFRKSNLKP  1        0.2631
2900.5    65.00  0.41     Sequence
             DRB1_1501  461      LFRKSNLKPFERDIS  LKPFERDIS  6        0.2703
2683.1    65.00  0.49     Sequence
             DRB1_1501  462      FRKSNLKPFERDIST  LKPFERDIS  5        0.2898
2172.6    60.00  0.72     Sequence
             DRB1_1501  463      RKSNLKPFERDISTE  LKPFERDIS  4        0.2995
1956.4    60.00  0.77     Sequence
             DRB1_1501  464      KSNLKPFERDISTEI  LKPFERDIS  3        0.3375
1296.9    48.00  0.68     Sequence
             DRB1_1501  465      SNLKPFERDISTEIY  LKPFERDIS  2        0.3427
1226.9    47.00  0.57     Sequence
             DRB1_1501  466      NLKPFERDISTEIYQ  LKPFERDIS  1        0.3245
1493.0    55.00  0.42     Sequence
             DRB1_1501  467      LKPFERDISTEIYQA  FERDISTEI  3        0.3070
1804.1    55.00  0.39     Sequence
             DRB1_1501  468      KPFERDISTEIYQAG  FERDISTEI  2        0.2716
2647.8    65.00  0.49     Sequence
             DRB1_1501  469      PFERDISTEIYQAGS  FERDISTEI  1        0.2670
2782.2    65.00  0.41     Sequence
```

```
             DRB1_1501  470      FERDISTEIYQAGST  ISTEIYQAG  4        0.2694
2710.3    65.00  0.30     Sequence
             DRB1_1501  471      ERDISTEIYQAGSTP  TEIYQAGST  5        0.2703
2683.3    65.00  0.41     Sequence
             DRB1_1501  472      RDISTEIYQAGSTPC  IYQAGSTPC  6        0.3526
1102.4    45.00  0.47     Sequence
             DRB1_1501  473      DISTEIYQAGSTPCN  IYQAGSTPC  5        0.4010
652.4    35.00  0.63     Sequence
             DRB1_1501  474      ISTEIYQAGSTPCNG  IYQAGSTPC  4        0.4001
659.1    35.00  0.67     Sequence
             DRB1_1501  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.4118
580.4    33.00  0.70     Sequence
             DRB1_1501  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.3778
838.5    39.00  0.77     Sequence
             DRB1_1501  477      EIYQAGSTPCNGVKG  IYQAGSTPC  1        0.3148
1659.2    55.00  0.67     Sequence
             DRB1_1501  478      IYQAGSTPCNGVKGF  IYQAGSTPC  0        0.2247
4397.4    75.00  0.53     Sequence
             DRB1_1501  479      YQAGSTPCNGVKGFN  STPCNGVKG  4        0.0921
18458.8   100.00  0.50     Sequence
             DRB1_1501  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.1356
11535.1    95.00  0.46     Sequence
             DRB1_1501  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.1931
6186.4    80.00  0.51     Sequence
             DRB1_1501  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.3693
919.7    41.00  0.32     Sequence
             DRB1_1501  483      STPCNGVKGFNCYFP  VKGFNCYFP  6        0.4805
276.1    21.00  0.56     Sequence
             DRB1_1501  484      TPCNGVKGFNCYFPL  VKGFNCYFP  5        0.5446
138.1    13.00  0.59     Sequence
             DRB1_1501  485      PCNGVKGFNCYFPLQ  VKGFNCYFP  4        0.5638
112.1    11.00  0.58     Sequence
             DRB1_1501  486      CNGVKGFNCYFPLQS  VKGFNCYFP  3        0.5904
84.1     8.00  0.54     Sequence         WB
             DRB1_1501  487      NGVKGFNCYFPLQSY  VKGFNCYFP  2        0.5871
87.1     8.50  0.50     Sequence         WB
             DRB1_1501  488      GVKGFNCYFPLQSYG  VKGFNCYFP  1        0.5290
163.4    15.00  0.41     Sequence
             DRB1_1501  489      VKGFNCYFPLQSYGF  YFPLQSYGF  6        0.5252
170.2    15.00  0.39     Sequence
             DRB1_1501  490      KGFNCYFPLQSYGFQ  YFPLQSYGF  5        0.5339
155.0    14.00  0.53     Sequence
             DRB1_1501  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.5491
131.4    12.00  0.52     Sequence
             DRB1_1501  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.5581
119.3    11.00  0.50     Sequence
             DRB1_1501  493      NCYFPLQSYGFQPTY  YFPLQSYGF  2        0.5656
109.9    11.00  0.47     Sequence
             DRB1_1501  494      CYFPLQSYGFQPTYG  YFPLQSYGF  1        0.5273
166.4    15.00  0.41     Sequence
             DRB1_1501  495      YFPLQSYGFQPTYGV  LQSYGFQPT  3        0.4845
264.5    21.00  0.41     Sequence
             DRB1_1501  496      FPLQSYGFQPTYGVG  LQSYGFQPT  2        0.4417
420.1    27.00  0.46     Sequence
             DRB1_1501  497      PLQSYGFQPTYGVGY  YGFQPTYGV  4        0.4166
551.3    32.00  0.29     Sequence
             DRB1_1501  498      LQSYGFQPTYGVGYQ  YGFQPTYGV  3        0.3545
1078.9    44.00  0.43     Sequence
             DRB1_1501  499      QSYGFQPTYGVGYQP  YGFQPTYGV  2        0.3366
1309.7    48.00  0.43     Sequence
             DRB1_1501  500      SYGFQPTYGVGYQPY  YGFQPTYGV  1        0.3304
1400.4    49.00  0.33     Sequence
             DRB1_1501  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.3383
1285.9    48.00  0.28     Sequence
             DRB1_1501  502      GFQPTYGVGYQPYRV  GVGYQPYRV  6        0.4023
643.4    35.00  0.47     Sequence
```

```
             DRB1_1501  503      FQPTYGVGYQPYRVV  GVGYQPYRV  5        0.4571
355.9    25.00  0.56     Sequence
             DRB1_1501  504      QPTYGVGYQPYRVVV  GVGYQPYRV  4        0.5045
212.9    18.00  0.57     Sequence
             DRB1_1501  505      PTYGVGYQPYRVVVL  GVGYQPYRV  3        0.5366
150.6    14.00  0.53     Sequence
             DRB1_1501  506      TYGVGYQPYRVVVLS  GVGYQPYRV  2        0.5297
162.1    14.00  0.49     Sequence
             DRB1_1501  507      YGVGYQPYRVVVLSF  GVGYQPYRV  1        0.5060
209.5    17.00  0.35     Sequence
             DRB1_1501  508      GVGYQPYRVVVLSFE  YQPYRVVVL  3        0.4453
403.9    27.00  0.38     Sequence
             DRB1_1501  509      VGYQPYRVVVLSFEL  RVVVLSFEL  6        0.5063
209.0    17.00  0.38     Sequence
             DRB1_1501  510      GYQPYRVVVLSFELL  RVVVLSFEL  5        0.5458
136.2    13.00  0.46     Sequence
             DRB1_1501  511      YQPYRVVVLSFELLH  RVVVLSFEL  4        0.5685
106.6    10.00  0.46     Sequence
             DRB1_1501  512      QPYRVVVLSFELLHA  RVVVLSFEL  3        0.6194
61.4     6.00  0.43     Sequence         WB
             DRB1_1501  513      PYRVVVLSFELLHAP  VLSFELLHA  5        0.6213
60.2     6.00  0.34     Sequence         WB
             DRB1_1501  514      YRVVVLSFELLHAPA  VLSFELLHA  4        0.6089
68.8     7.00  0.41     Sequence         WB
             DRB1_1501  515      RVVVLSFELLHAPAT  VLSFELLHA  3        0.5978
77.6     7.50  0.47     Sequence         WB
             DRB1_1501  516      VVVLSFELLHAPATV  VLSFELLHA  2        0.5886
85.7     8.50  0.44     Sequence         WB
             DRB1_1501  517      VVLSFELLHAPATVC  FELLHAPAT  4        0.5918
82.8     8.00  0.37     Sequence         WB
             DRB1_1501  518      VLSFELLHAPATVCG  FELLHAPAT  3        0.5495
131.0    12.00  0.40     Sequence
             DRB1_1501  519      LSFELLHAPATVCGP  FELLHAPAT  2        0.5174
185.2    16.00  0.44     Sequence
             DRB1_1501  520      SFELLHAPATVCGPK  LLHAPATVC  3        0.5106
199.4    17.00  0.51     Sequence
             DRB1_1501  521      FELLHAPATVCGPKK  LLHAPATVC  2        0.4419
419.1    27.00  0.60     Sequence
             DRB1_1501  522      ELLHAPATVCGPKKS  LLHAPATVC  1        0.3688
925.1    41.00  0.64     Sequence
             DRB1_1501  523      LLHAPATVCGPKKST  LLHAPATVC  0        0.2594
3021.6    65.00  0.44     Sequence
             DRB1_1501  524      LHAPATVCGPKKSTN  PATVCGPKK  3        0.1310
12123.3    95.00  0.44     Sequence
             DRB1_1501  525      HAPATVCGPKKSTNL  PATVCGPKK  2        0.1437
10558.0    90.00  0.38     Sequence
             DRB1_1501  526      APATVCGPKKSTNLV  CGPKKSTNL  5        0.1542
9423.9    90.00  0.22     Sequence
             DRB1_1501  527      PATVCGPKKSTNLVK  CGPKKSTNL  4        0.1768
7385.0    85.00  0.20     Sequence
             DRB1_1501  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5        0.1884
6514.8    85.00  0.43     Sequence
             DRB1_1501  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.1988
5820.2    80.00  0.46     Sequence
             DRB1_1501  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3        0.1947
6080.5    80.00  0.43     Sequence
             DRB1_1501  531      CGPKKSTNLVKNKCV  TNLVKNKCV  6        0.2289
4203.4    75.00  0.35     Sequence
             DRB1_1501  532      GPKKSTNLVKNKCVN  TNLVKNKCV  5        0.2477
3427.6    70.00  0.47     Sequence
             DRB1_1501  533      PKKSTNLVKNKCVNF  TNLVKNKCV  4        0.2972
2006.2    60.00  0.47     Sequence
             DRB1_1501  534      KKSTNLVKNKCVNFN  TNLVKNKCV  3        0.3236
1508.2    55.00  0.41     Sequence
             DRB1_1501  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.3659
954.5    42.00  0.28     Sequence
```

```
             DRB1_1501  536      STNLVKNKCVNFNFN  KNKCVNFNF  5        0.3811
809.5    39.00  0.30     Sequence
             DRB1_1501  537      TNLVKNKCVNFNFNG  KNKCVNFNF  4        0.3585
1033.9    43.00  0.34     Sequence
             DRB1_1501  538      NLVKNKCVNFNFNGL  KNKCVNFNF  3        0.3589
1028.9    43.00  0.40     Sequence
             DRB1_1501  539      LVKNKCVNFNFNGLT  KNKCVNFNF  2        0.3571
1049.8    44.00  0.37     Sequence
             DRB1_1501  540      VKNKCVNFNFNGLTG  KNKCVNFNF  1        0.3465
1177.3    46.00  0.29     Sequence
             DRB1_1501  541      KNKCVNFNFNGLTGT  NFNFNGLTG  5        0.3412
1246.9    47.00  0.29     Sequence
             DRB1_1501  542      NKCVNFNFNGLTGTG  NFNFNGLTG  4        0.3120
1709.2    55.00  0.34     Sequence
             DRB1_1501  543      KCVNFNFNGLTGTGV  NFNFNGLTG  3        0.3233
1512.6    55.00  0.31     Sequence
             DRB1_1501  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5        0.3158
1641.6    55.00  0.34     Sequence
             DRB1_1501  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.2915
2133.4    60.00  0.42     Sequence
             DRB1_1501  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3        0.2498
3350.0    70.00  0.54     Sequence
             DRB1_1501  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.2269
4294.2    75.00  0.56     Sequence
             DRB1_1501  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.2033
5543.1    80.00  0.49     Sequence
             DRB1_1501  549      FNGLTGTGVLTESNK  FNGLTGTGV  0        0.1552
9320.8    90.00  0.35     Sequence
             DRB1_1501  550      NGLTGTGVLTESNKK  GVLTESNKK  6        0.1260
12785.3    95.00  0.28     Sequence
             DRB1_1501  551      GLTGTGVLTESNKKF  VLTESNKKF  6        0.2270
4290.0    75.00  0.67     Sequence
             DRB1_1501  552      LTGTGVLTESNKKFL  VLTESNKKF  5        0.3285
1429.9    50.00  0.73     Sequence
             DRB1_1501  553      TGTGVLTESNKKFLP  VLTESNKKF  4        0.3532
1094.5    45.00  0.69     Sequence
             DRB1_1501  554      GTGVLTESNKKFLPF  VLTESNKKF  3        0.3755
859.7    40.00  0.66     Sequence
             DRB1_1501  555      TGVLTESNKKFLPFQ  VLTESNKKF  2        0.3531
1096.0    45.00  0.59     Sequence
             DRB1_1501  556      GVLTESNKKFLPFQQ  VLTESNKKF  1        0.3368
1308.0    48.00  0.40     Sequence
             DRB1_1501  557      VLTESNKKFLPFQQF  NKKFLPFQQ  5        0.3140
1672.3    55.00  0.44     Sequence
             DRB1_1501  558      LTESNKKFLPFQQFG  NKKFLPFQQ  4        0.3253
1480.3    55.00  0.54     Sequence
             DRB1_1501  559      TESNKKFLPFQQFGR  FLPFQQFGR  6        0.5048
212.2    18.00  0.64     Sequence
             DRB1_1501  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5        0.5234
173.5    15.00  0.68     Sequence
             DRB1_1501  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4        0.5448
137.7    13.00  0.75     Sequence
             DRB1_1501  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.5552
123.0    12.00  0.73     Sequence
             DRB1_1501  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.5415
142.7    13.00  0.70     Sequence
             DRB1_1501  564      KFLPFQQFGRDIADT  FLPFQQFGR  1        0.4736
297.5    22.00  0.60     Sequence
             DRB1_1501  565      FLPFQQFGRDIADTT  FQQFGRDIA  3        0.3549
1074.5    44.00  0.38     Sequence
             DRB1_1501  566      LPFQQFGRDIADTTD  FQQFGRDIA  2        0.2486
3393.0    70.00  0.63     Sequence
             DRB1_1501  567      PFQQFGRDIADTTDA  FQQFGRDIA  1        0.2285
4217.7    75.00  0.58     Sequence
             DRB1_1501  568      FQQFGRDIADTTDAV  FQQFGRDIA  0        0.1687
8055.4    85.00  0.37     Sequence
```

```
             DRB1_1501  569      QQFGRDIADTTDAVR  FGRDIADTT  2        0.1022
16545.3   100.00  0.31     Sequence
             DRB1_1501  570      QFGRDIADTTDAVRD  IADTTDAVR  5        0.1057
15929.9    95.00  0.40     Sequence
             DRB1_1501  571      FGRDIADTTDAVRDP  IADTTDAVR  4        0.1028
16440.5   100.00  0.46     Sequence
             DRB1_1501  572      GRDIADTTDAVRDPQ  IADTTDAVR  3        0.0991
17109.1   100.00  0.56     Sequence
             DRB1_1501  573      RDIADTTDAVRDPQT  IADTTDAVR  2        0.0953
17835.5   100.00  0.52     Sequence
             DRB1_1501  574      DIADTTDAVRDPQTL  IADTTDAVR  1        0.0886
19173.5   100.00  0.35     Sequence
             DRB1_1501  575      IADTTDAVRDPQTLE  DAVRDPQTL  5        0.0805
20920.2   100.00  0.17     Sequence
             DRB1_1501  576      ADTTDAVRDPQTLEI  AVRDPQTLE  5        0.0797
21100.7   100.00  0.24     Sequence
             DRB1_1501  577      DTTDAVRDPQTLEIL  AVRDPQTLE  4        0.0949
17906.5   100.00  0.26     Sequence
             DRB1_1501  578      TTDAVRDPQTLEILD  VRDPQTLEI  4        0.0963
17642.2   100.00  0.26     Sequence
             DRB1_1501  579      TDAVRDPQTLEILDI  PQTLEILDI  6        0.1080
15542.1    95.00  0.31     Sequence
             DRB1_1501  580      DAVRDPQTLEILDIT  PQTLEILDI  5        0.1060
15887.1    95.00  0.38     Sequence
             DRB1_1501  581      AVRDPQTLEILDITP  PQTLEILDI  4        0.1125
14804.8    95.00  0.37     Sequence
             DRB1_1501  582      VRDPQTLEILDITPC  LEILDITPC  6        0.1416
10808.3    90.00  0.38     Sequence
             DRB1_1501  583      RDPQTLEILDITPCS  LEILDITPC  5        0.1663
8267.9    85.00  0.42     Sequence
             DRB1_1501  584      DPQTLEILDITPCSF  LEILDITPC  4        0.2019
5627.8    80.00  0.40     Sequence
             DRB1_1501  585      PQTLEILDITPCSFG  LEILDITPC  3        0.2160
4830.7    75.00  0.32     Sequence
             DRB1_1501  586      QTLEILDITPCSFGG  LEILDITPC  2        0.2225
4502.4    75.00  0.31     Sequence
             DRB1_1501  587      TLEILDITPCSFGGV  ILDITPCSF  3        0.2257
4350.6    75.00  0.19     Sequence
             DRB1_1501  588      LEILDITPCSFGGVS  ITPCSFGGV  5        0.2138
4947.5    80.00  0.23     Sequence
             DRB1_1501  589      EILDITPCSFGGVSV  PCSFGGVSV  6        0.2434
3593.0    70.00  0.25     Sequence
             DRB1_1501  590      ILDITPCSFGGVSVI  PCSFGGVSV  5        0.2471
3450.0    70.00  0.35     Sequence
             DRB1_1501  591      LDITPCSFGGVSVIT  PCSFGGVSV  4        0.2340
3975.6    75.00  0.38     Sequence
             DRB1_1501  592      DITPCSFGGVSVITP  PCSFGGVSV  3        0.2146
4906.0    75.00  0.43     Sequence
             DRB1_1501  593      ITPCSFGGVSVITPG  PCSFGGVSV  2        0.2046
5463.7    80.00  0.47     Sequence
             DRB1_1501  594      TPCSFGGVSVITPGT  PCSFGGVSV  1        0.1966
5958.8    80.00  0.35     Sequence
             DRB1_1501  595      PCSFGGVSVITPGTN  SFGGVSVIT  2        0.1734
7655.9    85.00  0.26     Sequence
             DRB1_1501  596      CSFGGVSVITPGTNT  VSVITPGTN  5        0.1633
8541.0    90.00  0.38     Sequence
             DRB1_1501  597      SFGGVSVITPGTNTS  VSVITPGTN  4        0.1781
7282.5    85.00  0.39     Sequence
             DRB1_1501  598      FGGVSVITPGTNTSN  VSVITPGTN  3        0.1930
6192.4    80.00  0.38     Sequence
             DRB1_1501  599      GGVSVITPGTNTSNQ  ITPGTNTSN  5        0.2016
5647.1    80.00  0.34     Sequence
             DRB1_1501  600      GVSVITPGTNTSNQV  ITPGTNTSN  4        0.1886
6496.3    85.00  0.46     Sequence
             DRB1_1501  601      VSVITPGTNTSNQVA  ITPGTNTSN  3        0.1758
7459.4    85.00  0.56     Sequence
```

```
             DRB1_1501  602      SVITPGTNTSNQVAV  ITPGTNTSN  2         0.1654
8349.8    90.00  0.56     Sequence
             DRB1_1501  603      VITPGTNTSNQVAVL  ITPGTNTSN  1         0.1487
10005.3    90.00  0.36     Sequence
             DRB1_1501  604      ITPGTNTSNQVAVLY  TSNQVAVLY  6         0.1659
8305.0    85.00  0.34     Sequence
             DRB1_1501  605      TPGTNTSNQVAVLYQ  TSNQVAVLY  5         0.2072
5314.5    80.00  0.37     Sequence
             DRB1_1501  606      PGTNTSNQVAVLYQG  TSNQVAVLY  4         0.2153
4864.8    75.00  0.32     Sequence
             DRB1_1501  607      GTNTSNQVAVLYQGV  TSNQVAVLY  3         0.2532
3229.2    70.00  0.29     Sequence
             DRB1_1501  608      TNTSNQVAVLYQGVN  VAVLYQGVN  6         0.3283
1433.8    50.00  0.23     Sequence
             DRB1_1501  609      NTSNQVAVLYQGVNC  AVLYQGVNC  6         0.4166
551.5    32.00  0.44     Sequence
             DRB1_1501  610      TSNQVAVLYQGVNCT  AVLYQGVNC  5         0.4775
285.3    22.00  0.47     Sequence
             DRB1_1501  611      SNQVAVLYQGVNCTE  AVLYQGVNC  4         0.4987
226.7    18.00  0.49     Sequence
             DRB1_1501  612      NQVAVLYQGVNCTEV  AVLYQGVNC  3         0.5047
212.5    18.00  0.48     Sequence
             DRB1_1501  613      QVAVLYQGVNCTEVP  AVLYQGVNC  2         0.4741
296.1    22.00  0.47     Sequence
             DRB1_1501  614      VAVLYQGVNCTEVPV  VLYQGVNCT  2         0.4109
586.6    33.00  0.40     Sequence
             DRB1_1501  615      AVLYQGVNCTEVPVA  VLYQGVNCT  1         0.2759
2527.0    65.00  0.44     Sequence
             DRB1_1501  616      VLYQGVNCTEVPVAI  VLYQGVNCT  0         0.1479
10089.2    90.00  0.33     Sequence
             DRB1_1501  617      LYQGVNCTEVPVAIH  NCTEVPVAI  5         0.0938
18127.1   100.00  0.28     Sequence
             DRB1_1501  618      YQGVNCTEVPVAIHA  NCTEVPVAI  4         0.1025
16496.8   100.00  0.32     Sequence
             DRB1_1501  619      QGVNCTEVPVAIHAD  NCTEVPVAI  3         0.1022
16540.8   100.00  0.35     Sequence
             DRB1_1501  620      GVNCTEVPVAIHADQ  NCTEVPVAI  2         0.1009
16781.5   100.00  0.33     Sequence
             DRB1_1501  621      VNCTEVPVAIHADQL  PVAIHADQL  6         0.1264
12732.5    95.00  0.37     Sequence
             DRB1_1501  622      NCTEVPVAIHADQLT  PVAIHADQL  5         0.1587
8978.6    90.00  0.40     Sequence
             DRB1_1501  623      CTEVPVAIHADQLTP  PVAIHADQL  4         0.1745
7566.4    85.00  0.37     Sequence
             DRB1_1501  624      TEVPVAIHADQLTPT  VAIHADQLT  4         0.2046
5464.7    80.00  0.35     Sequence
             DRB1_1501  625      EVPVAIHADQLTPTW  IHADQLTPT  5         0.2309
4110.4    75.00  0.34     Sequence
             DRB1_1501  626      VPVAIHADQLTPTWR  IHADQLTPT  4         0.2551
3163.8    70.00  0.40     Sequence
             DRB1_1501  627      PVAIHADQLTPTWRV  IHADQLTPT  3         0.2686
2732.7    65.00  0.41     Sequence
             DRB1_1501  628      VAIHADQLTPTWRVY  IHADQLTPT  2         0.2766
2508.2    65.00  0.44     Sequence
             DRB1_1501  629      AIHADQLTPTWRVYS  LTPTWRVYS  6         0.3511
1120.3    45.00  0.29     Sequence
             DRB1_1501  630      IHADQLTPTWRVYST  LTPTWRVYS  5         0.3780
837.2    39.00  0.44     Sequence
             DRB1_1501  631      HADQLTPTWRVYSTG  LTPTWRVYS  4         0.3651
962.5    42.00  0.51     Sequence
             DRB1_1501  632      ADQLTPTWRVYSTGS  LTPTWRVYS  3         0.3811
809.7    39.00  0.48     Sequence
             DRB1_1501  633      DQLTPTWRVYSTGSN  LTPTWRVYS  2         0.3828
794.8    38.00  0.40     Sequence
             DRB1_1501  634      QLTPTWRVYSTGSNV  LTPTWRVYS  1         0.3940
704.4    36.00  0.35     Sequence
```

```
             DRB1_1501  635      LTPTWRVYSTGSNVF  VYSTGSNVF  6        0.4457
402.6    27.00  0.30     Sequence
             DRB1_1501  636      TPTWRVYSTGSNVFQ  VYSTGSNVF  5        0.4776
284.9    22.00  0.48     Sequence
             DRB1_1501  637      PTWRVYSTGSNVFQT  VYSTGSNVF  4        0.4919
244.0    19.00  0.51     Sequence
             DRB1_1501  638      TWRVYSTGSNVFQTR  VYSTGSNVF  3        0.4927
242.0    19.00  0.57     Sequence
             DRB1_1501  639      WRVYSTGSNVFQTRA  VYSTGSNVF  2        0.4555
361.7    25.00  0.62     Sequence
             DRB1_1501  640      RVYSTGSNVFQTRAG  VYSTGSNVF  1        0.4205
528.4    31.00  0.62     Sequence
             DRB1_1501  641      VYSTGSNVFQTRAGC  VYSTGSNVF  0        0.2970
2011.2    60.00  0.46     Sequence
             DRB1_1501  642      YSTGSNVFQTRAGCL  VFQTRAGCL  6        0.2344
3960.6    75.00  0.40     Sequence
             DRB1_1501  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.3146
1662.5    55.00  0.46     Sequence
             DRB1_1501  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.3261
1467.6    50.00  0.49     Sequence
             DRB1_1501  645      GSNVFQTRAGCLIGA  VFQTRAGCL  3        0.3432
1220.4    47.00  0.50     Sequence
             DRB1_1501  646      SNVFQTRAGCLIGAE  VFQTRAGCL  2        0.3112
1724.0    55.00  0.51     Sequence
             DRB1_1501  647      NVFQTRAGCLIGAEY  VFQTRAGCL  1        0.2784
2460.1    65.00  0.45     Sequence
             DRB1_1501  648      VFQTRAGCLIGAEYV  GCLIGAEYV  6        0.2713
2655.3    65.00  0.22     Sequence
             DRB1_1501  649      FQTRAGCLIGAEYVN  GCLIGAEYV  5        0.2537
3213.5    70.00  0.46     Sequence
             DRB1_1501  650      QTRAGCLIGAEYVNN  GCLIGAEYV  4        0.2614
2957.0    65.00  0.47     Sequence
             DRB1_1501  651      TRAGCLIGAEYVNNS  GCLIGAEYV  3        0.2796
2427.4    65.00  0.47     Sequence
             DRB1_1501  652      RAGCLIGAEYVNNSY  GCLIGAEYV  2        0.2940
2078.0    60.00  0.35     Sequence
             DRB1_1501  653      AGCLIGAEYVNNSYE  GCLIGAEYV  1        0.2736
2590.0    65.00  0.27     Sequence
             DRB1_1501  654      GCLIGAEYVNNSYEC  GAEYVNNSY  4        0.2393
3755.0    70.00  0.25     Sequence
             DRB1_1501  655      CLIGAEYVNNSYECD  GAEYVNNSY  3        0.1870
6608.3    85.00  0.35     Sequence
             DRB1_1501  656      LIGAEYVNNSYECDI  GAEYVNNSY  2        0.1701
7936.1    85.00  0.38     Sequence
             DRB1_1501  657      IGAEYVNNSYECDIP  GAEYVNNSY  1        0.1317
12029.1    95.00  0.31     Sequence
             DRB1_1501  658      GAEYVNNSYECDIPI  NSYECDIPI  6        0.1446
10458.0    90.00  0.34     Sequence
             DRB1_1501  659      AEYVNNSYECDIPIG  NSYECDIPI  5        0.1491
9959.4    90.00  0.51     Sequence
             DRB1_1501  660      EYVNNSYECDIPIGA  NSYECDIPI  4        0.1676
8157.0    85.00  0.55     Sequence
             DRB1_1501  661      YVNNSYECDIPIGAG  NSYECDIPI  3        0.1648
8404.8    90.00  0.54     Sequence
             DRB1_1501  662      VNNSYECDIPIGAGI  NSYECDIPI  2        0.1732
7674.8    85.00  0.51     Sequence
             DRB1_1501  663      NNSYECDIPIGAGIC  NSYECDIPI  1        0.1804
7097.0    85.00  0.37     Sequence
             DRB1_1501  664      NSYECDIPIGAGICA  IPIGAGICA  6        0.1980
5870.8    80.00  0.31     Sequence
             DRB1_1501  665      SYECDIPIGAGICAS  IPIGAGICA  5        0.1942
6117.5    80.00  0.46     Sequence
             DRB1_1501  666      YECDIPIGAGICASY  IPIGAGICA  4        0.2206
4594.6    75.00  0.46     Sequence
             DRB1_1501  667      ECDIPIGAGICASYQ  IPIGAGICA  3        0.2398
3731.9    70.00  0.44     Sequence
```

```
             DRB1_1501  668      CDIPIGAGICASYQT  IPIGAGICA  2        0.2538
3207.3    70.00  0.37     Sequence
             DRB1_1501  669      DIPIGAGICASYQTQ  AGICASYQT  5        0.2558
3139.7    70.00  0.27     Sequence
             DRB1_1501  670      IPIGAGICASYQTQT  ICASYQTQT  6        0.3718
895.3    41.00  0.34     Sequence
             DRB1_1501  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.4362
445.9    28.00  0.46     Sequence
             DRB1_1501  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.4574
354.7    25.00  0.49     Sequence
             DRB1_1501  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.4436
411.6    27.00  0.52     Sequence
             DRB1_1501  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.3977
676.6    36.00  0.52     Sequence
             DRB1_1501  675      GICASYQTQTNSPRR  ICASYQTQT  1        0.3580
1038.9    44.00  0.50     Sequence
             DRB1_1501  676      ICASYQTQTNSPRRA  ICASYQTQT  0        0.2464
3477.8    70.00  0.32     Sequence
             DRB1_1501  677      CASYQTQTNSPRRAR  YQTQTNSPR  3        0.1546
9390.3    90.00  0.58     Sequence
             DRB1_1501  678      ASYQTQTNSPRRARS  YQTQTNSPR  2        0.1482
10060.7    90.00  0.61     Sequence
             DRB1_1501  679      SYQTQTNSPRRARSV  YQTQTNSPR  1        0.1298
12270.9    95.00  0.43     Sequence
             DRB1_1501  680      YQTQTNSPRRARSVA  NSPRRARSV  5        0.1083
15495.7    95.00  0.17     Sequence
             DRB1_1501  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.1333
11815.7    95.00  0.47     Sequence
             DRB1_1501  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.1580
9048.2    90.00  0.57     Sequence
             DRB1_1501  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.1729
7697.7    85.00  0.60     Sequence
             DRB1_1501  684      TNSPRRARSVASQSI  PRRARSVAS  3        0.1975
5900.0    80.00  0.54     Sequence
             DRB1_1501  685      NSPRRARSVASQSII  PRRARSVAS  2        0.2326
4038.5    75.00  0.42     Sequence
             DRB1_1501  686      SPRRARSVASQSIIA  SVASQSIIA  6        0.3117
1714.5    55.00  0.31     Sequence
             DRB1_1501  687      PRRARSVASQSIIAY  SVASQSIIA  5        0.3728
885.8    40.00  0.43     Sequence
             DRB1_1501  688      RRARSVASQSIIAYT  SVASQSIIA  4        0.4207
527.2    31.00  0.40     Sequence
             DRB1_1501  689      RARSVASQSIIAYTM  SQSIIAYTM  6        0.4941
238.2    19.00  0.28     Sequence
             DRB1_1501  690      ARSVASQSIIAYTMS  SQSIIAYTM  5        0.5043
213.5    18.00  0.41     Sequence
             DRB1_1501  691      RSVASQSIIAYTMSL  SQSIIAYTM  4        0.5623
114.0    11.00  0.38     Sequence
             DRB1_1501  692      SVASQSIIAYTMSLG  IIAYTMSLG  6        0.5914
83.2     8.00  0.33     Sequence         WB
             DRB1_1501  693      VASQSIIAYTMSLGA  IIAYTMSLG  5        0.6492
44.5     4.50  0.38     Sequence         WB
             DRB1_1501  694      ASQSIIAYTMSLGAE  IIAYTMSLG  4        0.6819
31.2     3.00  0.37     Sequence         WB
             DRB1_1501  695      SQSIIAYTMSLGAEN  IAYTMSLGA  4        0.6908
28.4     2.50  0.38     Sequence         WB
             DRB1_1501  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.6859
29.9     3.00  0.40     Sequence         WB
             DRB1_1501  697      SIIAYTMSLGAENSV  IAYTMSLGA  2        0.6611
39.1     4.00  0.43     Sequence         WB
             DRB1_1501  698      IIAYTMSLGAENSVA  IAYTMSLGA  1        0.5630
113.1    11.00  0.47     Sequence
             DRB1_1501  699      IAYTMSLGAENSVAY  IAYTMSLGA  0        0.4384
435.4    28.00  0.35     Sequence
             DRB1_1501  700      AYTMSLGAENSVAYS  LGAENSVAY  5        0.3384
1284.7    48.00  0.30     Sequence
```

```
             DRB1_1501  701      YTMSLGAENSVAYSN  LGAENSVAY  4        0.2906
2155.4    60.00  0.47     Sequence
             DRB1_1501  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.2579
3070.2    70.00  0.62     Sequence
             DRB1_1501  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.2400
3723.8    70.00  0.62     Sequence
             DRB1_1501  704      SLGAENSVAYSNNSI  SVAYSNNSI  6        0.2824
2353.9    60.00  0.32     Sequence
             DRB1_1501  705      LGAENSVAYSNNSIA  SVAYSNNSI  5        0.3657
956.4    42.00  0.37     Sequence
             DRB1_1501  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.4794
279.4    21.00  0.46     Sequence
             DRB1_1501  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.5014
220.3    18.00  0.49     Sequence
             DRB1_1501  708      ENSVAYSNNSIAIPT  VAYSNNSIA  3        0.5085
203.9    17.00  0.49     Sequence
             DRB1_1501  709      NSVAYSNNSIAIPTN  VAYSNNSIA  2        0.4986
227.1    18.00  0.50     Sequence
             DRB1_1501  710      SVAYSNNSIAIPTNF  VAYSNNSIA  1        0.4429
414.8    27.00  0.46     Sequence
             DRB1_1501  711      VAYSNNSIAIPTNFT  VAYSNNSIA  0        0.3478
1160.7    46.00  0.29     Sequence
             DRB1_1501  712      AYSNNSIAIPTNFTI  IAIPTNFTI  6        0.3482
1155.1    46.00  0.43     Sequence
             DRB1_1501  713      YSNNSIAIPTNFTIS  IAIPTNFTI  5        0.3939
704.7    36.00  0.55     Sequence
             DRB1_1501  714      SNNSIAIPTNFTISV  IAIPTNFTI  4        0.4346
453.6    29.00  0.57     Sequence
             DRB1_1501  715      NNSIAIPTNFTISVT  IAIPTNFTI  3        0.4319
467.0    29.00  0.57     Sequence
             DRB1_1501  716      NSIAIPTNFTISVTT  IAIPTNFTI  2        0.4089
599.2    33.00  0.53     Sequence
             DRB1_1501  717      SIAIPTNFTISVTTE  IAIPTNFTI  1        0.3439
1211.0    47.00  0.38     Sequence
             DRB1_1501  718      IAIPTNFTISVTTEI  PTNFTISVT  3        0.2895
2181.6    60.00  0.24     Sequence
             DRB1_1501  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.3000
1947.0    60.00  0.26     Sequence
             DRB1_1501  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.3009
1928.3    60.00  0.24     Sequence
             DRB1_1501  721      PTNFTISVTTEILPV  ISVTTEILP  5        0.3255
1477.5    55.00  0.32     Sequence
             DRB1_1501  722      TNFTISVTTEILPVS  ISVTTEILP  4        0.3307
1396.2    49.00  0.34     Sequence
             DRB1_1501  723      NFTISVTTEILPVSM  ISVTTEILP  3        0.3156
1645.1    55.00  0.38     Sequence
             DRB1_1501  724      FTISVTTEILPVSMT  ISVTTEILP  2        0.2855
2276.6    60.00  0.40     Sequence
             DRB1_1501  725      TISVTTEILPVSMTK  ISVTTEILP  1        0.2682
2745.5    65.00  0.33     Sequence
             DRB1_1501  726      ISVTTEILPVSMTKT  ILPVSMTKT  6        0.2608
2975.7    65.00  0.38     Sequence
             DRB1_1501  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.2757
2532.0    65.00  0.55     Sequence
             DRB1_1501  728      VTTEILPVSMTKTSV  ILPVSMTKT  4        0.3023
1899.2    60.00  0.60     Sequence
             DRB1_1501  729      TTEILPVSMTKTSVD  ILPVSMTKT  3        0.2945
2066.8    60.00  0.60     Sequence
             DRB1_1501  730      TEILPVSMTKTSVDC  ILPVSMTKT  2        0.2642
2867.8    65.00  0.67     Sequence
             DRB1_1501  731      EILPVSMTKTSVDCT  ILPVSMTKT  1        0.2067
5344.3    80.00  0.61     Sequence
             DRB1_1501  732      ILPVSMTKTSVDCTM  ILPVSMTKT  0        0.1264
12741.0    95.00  0.31     Sequence
             DRB1_1501  733      LPVSMTKTSVDCTMY  VSMTKTSVD  2        0.0918
18520.4   100.00  0.31     Sequence
```

```
            DRB1_1501  734      PVSMTKTSVDCTMYI  TSVDCTMYI  6        0.1178
13972.9    95.00  0.37     Sequence
            DRB1_1501  735      VSMTKTSVDCTMYIC  TSVDCTMYI  5        0.1197
13688.3    95.00  0.45     Sequence
            DRB1_1501  736      SMTKTSVDCTMYICG  TSVDCTMYI  4        0.1298
12278.3    95.00  0.47     Sequence
            DRB1_1501  737      MTKTSVDCTMYICGD  TSVDCTMYI  3        0.1304
12190.0    95.00  0.46     Sequence
            DRB1_1501  738      TKTSVDCTMYICGDS  TSVDCTMYI  2        0.1344
11679.4    95.00  0.44     Sequence
            DRB1_1501  739      KTSVDCTMYICGDST  TMYICGDST  6        0.1582
9029.1    90.00  0.24     Sequence
            DRB1_1501  740      TSVDCTMYICGDSTE  TMYICGDST  5        0.1699
7958.0    85.00  0.36     Sequence
            DRB1_1501  741      SVDCTMYICGDSTEC  TMYICGDST  4        0.1777
7313.9    85.00  0.37     Sequence
            DRB1_1501  742      VDCTMYICGDSTECS  TMYICGDST  3        0.1911
6322.6    80.00  0.35     Sequence
            DRB1_1501  743      DCTMYICGDSTECSN  TMYICGDST  2        0.1894
6439.6    85.00  0.31     Sequence
            DRB1_1501  744      CTMYICGDSTECSNL  MYICGDSTE  2        0.1871
6605.3    85.00  0.28     Sequence
            DRB1_1501  745      TMYICGDSTECSNLL  ICGDSTECS  3        0.1687
8056.7    85.00  0.23     Sequence
            DRB1_1501  746      MYICGDSTECSNLLL  DSTECSNLL  5        0.1821
6974.3    85.00  0.31     Sequence
            DRB1_1501  747      YICGDSTECSNLLLQ  STECSNLLL  5        0.2128
5002.1    80.00  0.39     Sequence
            DRB1_1501  748      ICGDSTECSNLLLQY  STECSNLLL  4        0.2433
3594.8    70.00  0.44     Sequence
            DRB1_1501  749      CGDSTECSNLLLQYG  STECSNLLL  3        0.2457
3502.4    70.00  0.39     Sequence
            DRB1_1501  750      GDSTECSNLLLQYGS  SNLLLQYGS  6        0.2806
2401.9    65.00  0.28     Sequence
            DRB1_1501  751      DSTECSNLLLQYGSF  SNLLLQYGS  5        0.3421
1234.3    47.00  0.41     Sequence
            DRB1_1501  752      STECSNLLLQYGSFC  SNLLLQYGS  4        0.4625
335.4    24.00  0.34     Sequence
            DRB1_1501  753      TECSNLLLQYGSFCT  LLQYGSFCT  6        0.6942
27.4     2.50  0.75     Sequence         WB
            DRB1_1501  754      ECSNLLLQYGSFCTQ  LLQYGSFCT  5        0.7489
15.1     1.00  0.83     Sequence         SB
            DRB1_1501  755      CSNLLLQYGSFCTQL  LLQYGSFCT  4        0.7745
11.5     0.70  0.83     Sequence         SB
            DRB1_1501  756      SNLLLQYGSFCTQLN  LLQYGSFCT  3        0.7824
10.5     0.60  0.82     Sequence         SB
            DRB1_1501  757      NLLLQYGSFCTQLNR  LLQYGSFCT  2        0.7693
12.1     0.70  0.83     Sequence         SB
            DRB1_1501  758      LLLQYGSFCTQLNRA  LLQYGSFCT  1        0.7202
20.6     1.60  0.75     Sequence         SB
            DRB1_1501  759      LLQYGSFCTQLNRAL  LLQYGSFCT  0        0.5802
93.9     9.00  0.53     Sequence         WB
            DRB1_1501  760      LQYGSFCTQLNRALT  FCTQLNRAL  5        0.4598
345.4    24.00  0.65     Sequence
            DRB1_1501  761      QYGSFCTQLNRALTG  FCTQLNRAL  4        0.4608
341.6    24.00  0.69     Sequence
            DRB1_1501  762      YGSFCTQLNRALTGI  FCTQLNRAL  3        0.4757
290.9    22.00  0.69     Sequence
            DRB1_1501  763      GSFCTQLNRALTGIA  FCTQLNRAL  2        0.4844
264.7    21.00  0.65     Sequence
            DRB1_1501  764      SFCTQLNRALTGIAV  FCTQLNRAL  1        0.4631
333.3    24.00  0.51     Sequence
            DRB1_1501  765      FCTQLNRALTGIAVE  FCTQLNRAL  0        0.3877
754.0    38.00  0.31     Sequence
            DRB1_1501  766      CTQLNRALTGIAVEQ  NRALTGIAV  4        0.3016
1913.4    60.00  0.51     Sequence
```

```
              DRB1_1501  767      TQLNRALTGIAVEQD  NRALTGIAV  3        0.2858
2270.3    60.00  0.55     Sequence
              DRB1_1501  768      QLNRALTGIAVEQDK  NRALTGIAV  2        0.2619
2940.8    65.00  0.56     Sequence
              DRB1_1501  769      LNRALTGIAVEQDKN  NRALTGIAV  1        0.2085
5241.0    80.00  0.46     Sequence
              DRB1_1501  770      NRALTGIAVEQDKNT  IAVEQDKNT  6        0.1395
11053.9    90.00  0.26     Sequence
              DRB1_1501  771      RALTGIAVEQDKNTQ  IAVEQDKNT  5        0.1344
11680.2    95.00  0.52     Sequence
              DRB1_1501  772      ALTGIAVEQDKNTQE  IAVEQDKNT  4        0.1330
11859.3    95.00  0.60     Sequence
              DRB1_1501  773      LTGIAVEQDKNTQEV  IAVEQDKNT  3        0.1388
11131.2    90.00  0.60     Sequence
              DRB1_1501  774      TGIAVEQDKNTQEVF  IAVEQDKNT  2        0.1365
11416.2    95.00  0.56     Sequence
              DRB1_1501  775      GIAVEQDKNTQEVFA  IAVEQDKNT  1        0.1219
13372.2    95.00  0.41     Sequence
              DRB1_1501  776      IAVEQDKNTQEVFAQ  VEQDKNTQE  2        0.0891
19063.9   100.00  0.38     Sequence
              DRB1_1501  777      AVEQDKNTQEVFAQV  VEQDKNTQE  1        0.0787
21343.9   100.00  0.27     Sequence
              DRB1_1501  778      VEQDKNTQEVFAQVK  DKNTQEVFA  3        0.0887
19149.3   100.00  0.26     Sequence
              DRB1_1501  779      EQDKNTQEVFAQVKQ  QEVFAQVKQ  6        0.1161
14243.8    95.00  0.31     Sequence
              DRB1_1501  780      QDKNTQEVFAQVKQI  QEVFAQVKQ  5        0.1566
9189.5    90.00  0.35     Sequence
              DRB1_1501  781      DKNTQEVFAQVKQIY  QEVFAQVKQ  4        0.2279
4246.1    75.00  0.30     Sequence
              DRB1_1501  782      KNTQEVFAQVKQIYK  FAQVKQIYK  6        0.2977
1995.6    60.00  0.32     Sequence
              DRB1_1501  783      NTQEVFAQVKQIYKT  FAQVKQIYK  5        0.3238
1505.0    55.00  0.41     Sequence
              DRB1_1501  784      TQEVFAQVKQIYKTP  FAQVKQIYK  4        0.3295
1414.6    50.00  0.42     Sequence
              DRB1_1501  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.3679
933.9    41.00  0.36     Sequence
              DRB1_1501  786      EVFAQVKQIYKTPPI  KQIYKTPPI  6        0.4971
230.8    19.00  0.47     Sequence
              DRB1_1501  787      VFAQVKQIYKTPPIK  KQIYKTPPI  5        0.5477
133.4    12.00  0.58     Sequence
              DRB1_1501  788      FAQVKQIYKTPPIKD  KQIYKTPPI  4        0.5438
139.3    13.00  0.61     Sequence
              DRB1_1501  789      AQVKQIYKTPPIKDF  KQIYKTPPI  3        0.5688
106.2    10.00  0.61     Sequence
              DRB1_1501  790      QVKQIYKTPPIKDFG  KQIYKTPPI  2        0.5501
130.1    12.00  0.60     Sequence
              DRB1_1501  791      VKQIYKTPPIKDFGG  KQIYKTPPI  1        0.4949
236.2    19.00  0.56     Sequence
              DRB1_1501  792      KQIYKTPPIKDFGGF  KQIYKTPPI  0        0.3680
933.2    41.00  0.43     Sequence
              DRB1_1501  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.2336
3992.1    75.00  0.37     Sequence
              DRB1_1501  794      IYKTPPIKDFGGFNF  IKDFGGFNF  6        0.4804
276.3    21.00  0.79     Sequence
              DRB1_1501  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.5300
161.6    14.00  0.80     Sequence
              DRB1_1501  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.5495
130.9    12.00  0.80     Sequence
              DRB1_1501  797      TPPIKDFGGFNFSQI  IKDFGGFNF  3        0.5591
117.9    11.00  0.79     Sequence
              DRB1_1501  798      PPIKDFGGFNFSQIL  IKDFGGFNF  2        0.5568
120.9    12.00  0.75     Sequence
              DRB1_1501  799      PIKDFGGFNFSQILP  IKDFGGFNF  1        0.5274
166.2    15.00  0.66     Sequence
```

```
             DRB1_1501  800      IKDFGGFNFSQILPD  IKDFGGFNF  0        0.4267
494.3    30.00  0.52     Sequence
             DRB1_1501  801      KDFGGFNFSQILPDP  GFNFSQILP  4        0.2081
5259.5    80.00  0.36     Sequence
             DRB1_1501  802      DFGGFNFSQILPDPS  GFNFSQILP  3        0.2060
5384.5    80.00  0.38     Sequence
             DRB1_1501  803      FGGFNFSQILPDPSK  GFNFSQILP  2        0.2166
4797.9    75.00  0.35     Sequence
             DRB1_1501  804      GGFNFSQILPDPSKP  GFNFSQILP  1        0.2149
4887.1    75.00  0.29     Sequence
             DRB1_1501  805      GFNFSQILPDPSKPS  ILPDPSKPS  6        0.2241
4425.5    75.00  0.41     Sequence
             DRB1_1501  806      FNFSQILPDPSKPSK  ILPDPSKPS  5        0.2548
3172.8    70.00  0.57     Sequence
             DRB1_1501  807      NFSQILPDPSKPSKR  ILPDPSKPS  4        0.2824
2355.5    60.00  0.68     Sequence
             DRB1_1501  808      FSQILPDPSKPSKRS  ILPDPSKPS  3        0.2791
2441.8    65.00  0.73     Sequence
             DRB1_1501  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.2675
2768.1    65.00  0.78     Sequence
             DRB1_1501  810      QILPDPSKPSKRSFI  ILPDPSKPS  1        0.2350
3934.3    75.00  0.56     Sequence
             DRB1_1501  811      ILPDPSKPSKRSFIE  ILPDPSKPS  0        0.1671
8202.0    85.00  0.37     Sequence
             DRB1_1501  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.0955
17800.8   100.00  0.31     Sequence
             DRB1_1501  813      PDPSKPSKRSFIEDL  SKPSKRSFI  3        0.1072
15667.9    95.00  0.30     Sequence
             DRB1_1501  814      DPSKPSKRSFIEDLL  KRSFIEDLL  6        0.1400
10993.0    90.00  0.34     Sequence
             DRB1_1501  815      PSKPSKRSFIEDLLF  KRSFIEDLL  5        0.1918
6275.5    80.00  0.35     Sequence
             DRB1_1501  816      SKPSKRSFIEDLLFN  KRSFIEDLL  4        0.2190
4675.4    75.00  0.34     Sequence
             DRB1_1501  817      KPSKRSFIEDLLFNK  KRSFIEDLL  3        0.2512
3299.8    70.00  0.31     Sequence
             DRB1_1501  818      PSKRSFIEDLLFNKV  IEDLLFNKV  6        0.2956
2041.6    60.00  0.23     Sequence
             DRB1_1501  819      SKRSFIEDLLFNKVT  IEDLLFNKV  5        0.3178
1604.9    55.00  0.29     Sequence
             DRB1_1501  820      KRSFIEDLLFNKVTL  IEDLLFNKV  4        0.3709
903.5    41.00  0.25     Sequence
             DRB1_1501  821      RSFIEDLLFNKVTLA  DLLFNKVTL  5        0.3867
761.7    38.00  0.35     Sequence
             DRB1_1501  822      SFIEDLLFNKVTLAD  DLLFNKVTL  4        0.3603
1014.2    43.00  0.39     Sequence
             DRB1_1501  823      FIEDLLFNKVTLADA  DLLFNKVTL  3        0.3526
1102.3    45.00  0.39     Sequence
             DRB1_1501  824      IEDLLFNKVTLADAG  DLLFNKVTL  2        0.3223
1529.3    55.00  0.42     Sequence
             DRB1_1501  825      EDLLFNKVTLADAGF  LLFNKVTLA  2        0.2978
1993.5    60.00  0.34     Sequence
             DRB1_1501  826      DLLFNKVTLADAGFI  VTLADAGFI  6        0.2812
2386.3    65.00  0.24     Sequence
             DRB1_1501  827      LLFNKVTLADAGFIK  VTLADAGFI  5        0.2843
2305.8    60.00  0.39     Sequence
             DRB1_1501  828      LFNKVTLADAGFIKQ  VTLADAGFI  4        0.2989
1968.9    60.00  0.46     Sequence
             DRB1_1501  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.3210
1550.8    55.00  0.47     Sequence
             DRB1_1501  830      NKVTLADAGFIKQYG  VTLADAGFI  2        0.3164
1629.6    55.00  0.45     Sequence
             DRB1_1501  831      KVTLADAGFIKQYGD  VTLADAGFI  1        0.2773
2489.3    65.00  0.40     Sequence
             DRB1_1501  832      VTLADAGFIKQYGDC  VTLADAGFI  0        0.2192
4667.1    75.00  0.31     Sequence
```

```
            DRB1_1501  833      TLADAGFIKQYGDCL  FIKQYGDCL  6        0.3954
693.3    36.00  0.56     Sequence
            DRB1_1501  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.4807
275.6    21.00  0.52     Sequence
            DRB1_1501  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4        0.4996
224.7    18.00  0.50     Sequence
            DRB1_1501  836      DAGFIKQYGDCLGDI  FIKQYGDCL  3        0.5319
158.4    14.00  0.50     Sequence
            DRB1_1501  837      AGFIKQYGDCLGDIA  FIKQYGDCL  2        0.5343
154.3    14.00  0.49     Sequence
            DRB1_1501  838      GFIKQYGDCLGDIAA  FIKQYGDCL  1        0.5050
211.8    18.00  0.47     Sequence
            DRB1_1501  839      FIKQYGDCLGDIAAR  FIKQYGDCL  0        0.4202
530.4    31.00  0.40     Sequence
            DRB1_1501  840      IKQYGDCLGDIAARD  IKQYGDCLG  0        0.1654
8351.4    90.00  0.41     Sequence
            DRB1_1501  841      KQYGDCLGDIAARDL  LGDIAARDL  6        0.1088
15400.6    95.00  0.25     Sequence
            DRB1_1501  842      QYGDCLGDIAARDLI  LGDIAARDL  5        0.1476
10122.6    90.00  0.38     Sequence
            DRB1_1501  843      YGDCLGDIAARDLIC  DIAARDLIC  6        0.2064
5357.6    80.00  0.31     Sequence
            DRB1_1501  844      GDCLGDIAARDLICA  IAARDLICA  6        0.2580
3065.0    70.00  0.30     Sequence
            DRB1_1501  845      DCLGDIAARDLICAQ  IAARDLICA  5        0.2728
2611.5    65.00  0.38     Sequence
            DRB1_1501  846      CLGDIAARDLICAQK  IAARDLICA  4        0.2927
2107.6    60.00  0.41     Sequence
            DRB1_1501  847      LGDIAARDLICAQKF  IAARDLICA  3        0.3044
1856.8    55.00  0.41     Sequence
            DRB1_1501  848      GDIAARDLICAQKFN  IAARDLICA  2        0.2927
2106.3    60.00  0.41     Sequence
            DRB1_1501  849      DIAARDLICAQKFNG  IAARDLICA  1        0.2421
3641.6    70.00  0.25     Sequence
            DRB1_1501  850      IAARDLICAQKFNGL  ICAQKFNGL  6        0.3128
1694.9    55.00  0.37     Sequence
            DRB1_1501  851      AARDLICAQKFNGLT  ICAQKFNGL  5        0.3619
996.3    43.00  0.49     Sequence
            DRB1_1501  852      ARDLICAQKFNGLTV  ICAQKFNGL  4        0.4354
450.0    28.00  0.44     Sequence
            DRB1_1501  853      RDLICAQKFNGLTVL  ICAQKFNGL  3        0.4640
330.0    24.00  0.44     Sequence
            DRB1_1501  854      DLICAQKFNGLTVLP  ICAQKFNGL  2        0.4251
503.0    30.00  0.43     Sequence
            DRB1_1501  855      LICAQKFNGLTVLPP  AQKFNGLTV  3        0.4085
602.1    33.00  0.37     Sequence
            DRB1_1501  856      ICAQKFNGLTVLPPL  AQKFNGLTV  2        0.3649
964.3    42.00  0.40     Sequence
            DRB1_1501  857      CAQKFNGLTVLPPLL  AQKFNGLTV  1        0.3680
933.0    41.00  0.27     Sequence
            DRB1_1501  858      AQKFNGLTVLPPLLT  LTVLPPLLT  6        0.4226
516.4    31.00  0.46     Sequence
            DRB1_1501  859      QKFNGLTVLPPLLTD  LTVLPPLLT  5        0.4218
521.1    31.00  0.61     Sequence
            DRB1_1501  860      KFNGLTVLPPLLTDE  LTVLPPLLT  4        0.4244
506.8    30.00  0.69     Sequence
            DRB1_1501  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.4054
622.3    34.00  0.75     Sequence
            DRB1_1501  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.3895
739.2    37.00  0.79     Sequence
            DRB1_1501  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.3215
1542.4    55.00  0.65     Sequence
            DRB1_1501  864      LTVLPPLLTDEMIAQ  LTVLPPLLT  0        0.2332
4008.8    75.00  0.41     Sequence
            DRB1_1501  865      TVLPPLLTDEMIAQY  PLLTDEMIA  4        0.1973
5912.8    80.00  0.31     Sequence
```

```
             DRB1_1501  866      VLPPLLTDEMIAQYT  LLTDEMIAQ  4        0.2272
4277.8    75.00  0.27     Sequence
             DRB1_1501  867      LPPLLTDEMIAQYTS  LLTDEMIAQ  3        0.2432
3599.4    70.00  0.23     Sequence
             DRB1_1501  868      PPLLTDEMIAQYTSA  DEMIAQYTS  5        0.2745
2564.7    65.00  0.23     Sequence
             DRB1_1501  869      PLLTDEMIAQYTSAL  MIAQYTSAL  6        0.4254
501.1    30.00  0.37     Sequence
             DRB1_1501  870      LLTDEMIAQYTSALL  IAQYTSALL  6        0.6924
27.9     2.50  0.69     Sequence         WB
             DRB1_1501  871      LTDEMIAQYTSALLA  IAQYTSALL  5        0.7667
12.5     0.80  0.72     Sequence         SB
             DRB1_1501  872      TDEMIAQYTSALLAG  IAQYTSALL  4        0.7713
11.9     0.70  0.75     Sequence         SB
             DRB1_1501  873      DEMIAQYTSALLAGT  IAQYTSALL  3        0.7781
11.0     0.60  0.78     Sequence         SB
             DRB1_1501  874      EMIAQYTSALLAGTI  IAQYTSALL  2        0.7754
11.4     0.70  0.80     Sequence         SB
             DRB1_1501  875      MIAQYTSALLAGTIT  IAQYTSALL  1        0.7131
22.3     1.80  0.73     Sequence         SB
             DRB1_1501  876      IAQYTSALLAGTITS  IAQYTSALL  0        0.6137
65.4     6.50  0.62     Sequence         WB
             DRB1_1501  877      AQYTSALLAGTITSG  SALLAGTIT  4        0.2714
2653.7    65.00  0.45     Sequence
             DRB1_1501  878      QYTSALLAGTITSGW  SALLAGTIT  3        0.2868
2246.5    60.00  0.46     Sequence
             DRB1_1501  879      YTSALLAGTITSGWT  SALLAGTIT  2        0.2730
2608.2    65.00  0.43     Sequence
             DRB1_1501  880      TSALLAGTITSGWTF  SALLAGTIT  1        0.2666
2793.3    65.00  0.38     Sequence
             DRB1_1501  881      SALLAGTITSGWTFG  LAGTITSGW  3        0.2329
4024.5    75.00  0.22     Sequence
             DRB1_1501  882      ALLAGTITSGWTFGA  ITSGWTFGA  6        0.3136
1679.6    55.00  0.52     Sequence
             DRB1_1501  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.3515
1115.1    45.00  0.64     Sequence
             DRB1_1501  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.3870
759.6    38.00  0.69     Sequence
             DRB1_1501  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.4128
574.7    33.00  0.67     Sequence
             DRB1_1501  886      GTITSGWTFGAGAAL  ITSGWTFGA  2        0.4399
428.5    28.00  0.56     Sequence
             DRB1_1501  887      TITSGWTFGAGAALQ  ITSGWTFGA  1        0.4281
486.8    30.00  0.38     Sequence
             DRB1_1501  888      ITSGWTFGAGAALQI  WTFGAGAAL  4        0.4333
460.0    29.00  0.30     Sequence
             DRB1_1501  889      TSGWTFGAGAALQIP  WTFGAGAAL  3        0.4300
477.0    29.00  0.34     Sequence
             DRB1_1501  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.4289
482.6    30.00  0.36     Sequence
             DRB1_1501  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.4180
542.9    32.00  0.40     Sequence
             DRB1_1501  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.3793
825.6    39.00  0.41     Sequence
             DRB1_1501  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.3456
1188.0    46.00  0.37     Sequence
             DRB1_1501  894      FGAGAALQIPFAMQM  AALQIPFAM  4        0.3487
1149.3    45.00  0.25     Sequence
             DRB1_1501  895      GAGAALQIPFAMQMA  QIPFAMQMA  6        0.3476
1163.3    46.00  0.21     Sequence
             DRB1_1501  896      AGAALQIPFAMQMAY  QIPFAMQMA  5        0.3730
883.9    40.00  0.26     Sequence
             DRB1_1501  897      GAALQIPFAMQMAYR  QIPFAMQMA  4        0.4223
518.5    31.00  0.25     Sequence
             DRB1_1501  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.5271
166.8    15.00  0.45     Sequence
```

```
             DRB1_1501  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.5614
115.0    11.00  0.54     Sequence
             DRB1_1501  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.5468
134.7    13.00  0.60     Sequence
             DRB1_1501  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.5557
122.5    12.00  0.58     Sequence
             DRB1_1501  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.5362
151.1    14.00  0.54     Sequence
             DRB1_1501  903      PFAMQMAYRFNGIGV  FAMQMAYRF  1        0.5748
99.6     9.50  0.38     Sequence         WB
             DRB1_1501  904      FAMQMAYRFNGIGVT  AYRFNGIGV  5        0.5264
168.0    15.00  0.35     Sequence
             DRB1_1501  905      AMQMAYRFNGIGVTQ  AYRFNGIGV  4        0.4963
232.8    19.00  0.54     Sequence
             DRB1_1501  906      MQMAYRFNGIGVTQN  AYRFNGIGV  3        0.4852
262.5    20.00  0.56     Sequence
             DRB1_1501  907      QMAYRFNGIGVTQNV  AYRFNGIGV  2        0.4668
320.2    23.00  0.61     Sequence
             DRB1_1501  908      MAYRFNGIGVTQNVL  AYRFNGIGV  1        0.4128
574.4    33.00  0.51     Sequence
             DRB1_1501  909      AYRFNGIGVTQNVLY  IGVTQNVLY  6        0.3680
932.8    41.00  0.28     Sequence
             DRB1_1501  910      YRFNGIGVTQNVLYE  IGVTQNVLY  5        0.3134
1683.7    55.00  0.50     Sequence
             DRB1_1501  911      RFNGIGVTQNVLYEN  IGVTQNVLY  4        0.3292
1419.8    50.00  0.58     Sequence
             DRB1_1501  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.3184
1596.0    55.00  0.59     Sequence
             DRB1_1501  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.3252
1482.6    55.00  0.57     Sequence
             DRB1_1501  914      GIGVTQNVLYENQKL  NVLYENQKL  6        0.4822
271.1    21.00  0.52     Sequence
             DRB1_1501  915      IGVTQNVLYENQKLI  NVLYENQKL  5        0.5485
132.3    12.00  0.59     Sequence
             DRB1_1501  916      GVTQNVLYENQKLIA  NVLYENQKL  4        0.5798
94.3     9.00  0.61     Sequence         WB
             DRB1_1501  917      VTQNVLYENQKLIAN  NVLYENQKL  3        0.5877
86.6     8.50  0.60     Sequence         WB
             DRB1_1501  918      TQNVLYENQKLIANQ  NVLYENQKL  2        0.5814
92.7     9.00  0.55     Sequence         WB
             DRB1_1501  919      QNVLYENQKLIANQF  NVLYENQKL  1        0.5459
136.1    13.00  0.49     Sequence
             DRB1_1501  920      NVLYENQKLIANQFN  NVLYENQKL  0        0.4568
356.8    25.00  0.34     Sequence
             DRB1_1501  921      VLYENQKLIANQFNS  NQKLIANQF  4        0.2917
2128.4    60.00  0.26     Sequence
             DRB1_1501  922      LYENQKLIANQFNSA  NQKLIANQF  3        0.2862
2259.5    60.00  0.31     Sequence
             DRB1_1501  923      YENQKLIANQFNSAI  IANQFNSAI  6        0.3693
920.0    41.00  0.30     Sequence
             DRB1_1501  924      ENQKLIANQFNSAIG  IANQFNSAI  5        0.4030
638.6    35.00  0.34     Sequence
             DRB1_1501  925      NQKLIANQFNSAIGK  IANQFNSAI  4        0.4349
452.2    29.00  0.38     Sequence
             DRB1_1501  926      QKLIANQFNSAIGKI  IANQFNSAI  3        0.4362
446.0    28.00  0.40     Sequence
             DRB1_1501  927      KLIANQFNSAIGKIQ  IANQFNSAI  2        0.4317
468.3    29.00  0.38     Sequence
             DRB1_1501  928      LIANQFNSAIGKIQD  ANQFNSAIG  2        0.3877
753.4    38.00  0.38     Sequence
             DRB1_1501  929      IANQFNSAIGKIQDS  ANQFNSAIG  1        0.3153
1649.9    55.00  0.31     Sequence
             DRB1_1501  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.2376
3824.5    70.00  0.44     Sequence
             DRB1_1501  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.2187
4690.1    75.00  0.48     Sequence
```

```
              DRB1_1501  932      QFNSAIGKIQDSLSS  FNSAIGKIQ  1        0.2207
4592.4    75.00  0.33     Sequence
              DRB1_1501  933      FNSAIGKIQDSLSST  IGKIQDSLS  4        0.2074
5301.8    80.00  0.35     Sequence
              DRB1_1501  934      NSAIGKIQDSLSSTA  IGKIQDSLS  3        0.2164
4810.9    75.00  0.35     Sequence
              DRB1_1501  935      SAIGKIQDSLSSTAS  IQDSLSSTA  5        0.2251
4377.0    75.00  0.34     Sequence
              DRB1_1501  936      AIGKIQDSLSSTASA  IQDSLSSTA  4        0.2226
4496.7    75.00  0.41     Sequence
              DRB1_1501  937      IGKIQDSLSSTASAL  IQDSLSSTA  3        0.2077
5282.7    80.00  0.51     Sequence
              DRB1_1501  938      GKIQDSLSSTASALG  IQDSLSSTA  2        0.2084
5244.0    80.00  0.43     Sequence
              DRB1_1501  939      KIQDSLSSTASALGK  LSSTASALG  5        0.2377
3819.9    70.00  0.52     Sequence
              DRB1_1501  940      IQDSLSSTASALGKL  LSSTASALG  4        0.2609
2970.2    65.00  0.68     Sequence
              DRB1_1501  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.2747
2559.2    65.00  0.74     Sequence
              DRB1_1501  942      DSLSSTASALGKLQD  LSSTASALG  2        0.2584
3053.0    70.00  0.73     Sequence
              DRB1_1501  943      SLSSTASALGKLQDV  LSSTASALG  1        0.2291
4192.2    75.00  0.67     Sequence
              DRB1_1501  944      LSSTASALGKLQDVV  LSSTASALG  0        0.1543
9415.8    90.00  0.40     Sequence
              DRB1_1501  945      SSTASALGKLQDVVN  LGKLQDVVN  6        0.1245
13001.8    95.00  0.22     Sequence
              DRB1_1501  946      STASALGKLQDVVNQ  LGKLQDVVN  5        0.1363
11437.0    95.00  0.29     Sequence
              DRB1_1501  947      TASALGKLQDVVNQN  LGKLQDVVN  4        0.1425
10694.1    90.00  0.31     Sequence
              DRB1_1501  948      ASALGKLQDVVNQNA  LGKLQDVVN  3        0.1622
8643.0    90.00  0.26     Sequence
              DRB1_1501  949      SALGKLQDVVNQNAQ  LQDVVNQNA  5        0.1657
8324.8    90.00  0.38     Sequence
              DRB1_1501  950      ALGKLQDVVNQNAQA  LQDVVNQNA  4        0.1824
6950.4    85.00  0.37     Sequence
              DRB1_1501  951      LGKLQDVVNQNAQAL  VVNQNAQAL  6        0.2209
4579.6    75.00  0.31     Sequence
              DRB1_1501  952      GKLQDVVNQNAQALN  VVNQNAQAL  5        0.2582
3060.7    70.00  0.43     Sequence
              DRB1_1501  953      KLQDVVNQNAQALNT  VVNQNAQAL  4        0.2712
2658.2    65.00  0.51     Sequence
              DRB1_1501  954      LQDVVNQNAQALNTL  VVNQNAQAL  3        0.2765
2510.7    65.00  0.56     Sequence
              DRB1_1501  955      QDVVNQNAQALNTLV  VVNQNAQAL  2        0.2864
2254.4    60.00  0.54     Sequence
              DRB1_1501  956      DVVNQNAQALNTLVK  VVNQNAQAL  1        0.2709
2666.6    65.00  0.38     Sequence
              DRB1_1501  957      VVNQNAQALNTLVKQ  NAQALNTLV  4        0.2349
3936.8    75.00  0.22     Sequence
              DRB1_1501  958      VNQNAQALNTLVKQL  AQALNTLVK  4        0.2326
4035.0    75.00  0.34     Sequence
              DRB1_1501  959      NQNAQALNTLVKQLS  AQALNTLVK  3        0.2633
2895.6    65.00  0.28     Sequence
              DRB1_1501  960      QNAQALNTLVKQLSS  LNTLVKQLS  5        0.2750
2550.6    65.00  0.32     Sequence
              DRB1_1501  961      NAQALNTLVKQLSSN  LNTLVKQLS  4        0.2852
2284.2    60.00  0.37     Sequence
              DRB1_1501  962      AQALNTLVKQLSSNF  LVKQLSSNF  6        0.4565
357.9    25.00  0.48     Sequence
              DRB1_1501  963      QALNTLVKQLSSNFG  VKQLSSNFG  6        0.5823
91.8     9.00  0.44     Sequence         WB
              DRB1_1501  964      ALNTLVKQLSSNFGA  VKQLSSNFG  5        0.6536
42.5     4.00  0.50     Sequence         WB
```

```
             DRB1_1501  965      LNTLVKQLSSNFGAI  VKQLSSNFG  4        0.6977
26.3     2.50  0.52     Sequence         WB
             DRB1_1501  966      NTLVKQLSSNFGAIS  VKQLSSNFG  3        0.7003
25.6     2.50  0.52     Sequence         WB
             DRB1_1501  967      TLVKQLSSNFGAISS  VKQLSSNFG  2        0.6614
39.0     4.00  0.53     Sequence         WB
             DRB1_1501  968      LVKQLSSNFGAISSV  VKQLSSNFG  1        0.5421
141.8    13.00  0.47     Sequence
             DRB1_1501  969      VKQLSSNFGAISSVL  LSSNFGAIS  3        0.3947
698.8    36.00  0.25     Sequence
             DRB1_1501  970      KQLSSNFGAISSVLN  LSSNFGAIS  2        0.3476
1163.4    46.00  0.31     Sequence
             DRB1_1501  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.3357
1323.0    48.00  0.35     Sequence
             DRB1_1501  972      LSSNFGAISSVLNDI  FGAISSVLN  4        0.3271
1451.9    50.00  0.44     Sequence
             DRB1_1501  973      SSNFGAISSVLNDIL  FGAISSVLN  3        0.3414
1243.5    47.00  0.45     Sequence
             DRB1_1501  974      SNFGAISSVLNDILS  ISSVLNDIL  5        0.3529
1097.8    45.00  0.38     Sequence
             DRB1_1501  975      NFGAISSVLNDILSR  ISSVLNDIL  4        0.3551
1071.9    44.00  0.47     Sequence
             DRB1_1501  976      FGAISSVLNDILSRL  ISSVLNDIL  3        0.3582
1037.6    44.00  0.50     Sequence
             DRB1_1501  977      GAISSVLNDILSRLD  ISSVLNDIL  2        0.3652
961.9    42.00  0.47     Sequence
             DRB1_1501  978      AISSVLNDILSRLDK  ISSVLNDIL  1        0.3537
1088.5    44.00  0.37     Sequence
             DRB1_1501  979      ISSVLNDILSRLDKV  LNDILSRLD  4        0.3350
1333.2    48.00  0.35     Sequence
             DRB1_1501  980      SSVLNDILSRLDKVE  LNDILSRLD  3        0.2898
2172.7    60.00  0.44     Sequence
             DRB1_1501  981      SVLNDILSRLDKVEA  LNDILSRLD  2        0.2862
2260.4    60.00  0.39     Sequence
             DRB1_1501  982      VLNDILSRLDKVEAE  LNDILSRLD  1        0.2595
3016.7    65.00  0.29     Sequence
             DRB1_1501  983      LNDILSRLDKVEAEV  ILSRLDKVE  3        0.2281
4239.1    75.00  0.34     Sequence
             DRB1_1501  984      NDILSRLDKVEAEVQ  ILSRLDKVE  2        0.2116
5067.7    80.00  0.39     Sequence
             DRB1_1501  985      DILSRLDKVEAEVQI  LSRLDKVEA  2        0.1951
6055.0    80.00  0.33     Sequence
             DRB1_1501  986      ILSRLDKVEAEVQID  LSRLDKVEA  1        0.1598
8876.0    90.00  0.30     Sequence
             DRB1_1501  987      LSRLDKVEAEVQIDR  DKVEAEVQI  4        0.1471
10175.0    90.00  0.32     Sequence
             DRB1_1501  988      SRLDKVEAEVQIDRL  DKVEAEVQI  3        0.1506
9806.2    90.00  0.35     Sequence
             DRB1_1501  989      RLDKVEAEVQIDRLI  VEAEVQIDR  4        0.1610
8760.1    90.00  0.29     Sequence
             DRB1_1501  990      LDKVEAEVQIDRLIT  VEAEVQIDR  3        0.1695
7991.2    85.00  0.29     Sequence
             DRB1_1501  991      DKVEAEVQIDRLITG  VEAEVQIDR  2        0.1673
8178.2    85.00  0.26     Sequence
             DRB1_1501  992      KVEAEVQIDRLITGR  VQIDRLITG  5        0.1857
6707.2    85.00  0.26     Sequence
             DRB1_1501  993      VEAEVQIDRLITGRL  IDRLITGRL  6        0.4454
403.9    27.00  0.59     Sequence
             DRB1_1501  994      EAEVQIDRLITGRLQ  IDRLITGRL  5        0.5185
183.1    16.00  0.60     Sequence
             DRB1_1501  995      AEVQIDRLITGRLQS  IDRLITGRL  4        0.5517
127.9    12.00  0.58     Sequence
             DRB1_1501  996      EVQIDRLITGRLQSL  IDRLITGRL  3        0.5797
94.4     9.00  0.57     Sequence         WB
             DRB1_1501  997      VQIDRLITGRLQSLQ  IDRLITGRL  2        0.5850
89.2     8.50  0.50     Sequence         WB
```

```
             DRB1_1501  998      QIDRLITGRLQSLQT  IDRLITGRL  1        0.5816
92.5     9.00 0.45      Sequence         WB
             DRB1_1501  999      IDRLITGRLQSLQTY  IDRLITGRL  0        0.5363
150.9    14.00  0.41     Sequence
             DRB1_1501 1000      DRLITGRLQSLQTYV  ITGRLQSLQ  3        0.4454
403.5    27.00  0.17     Sequence
             DRB1_1501 1001      RLITGRLQSLQTYVT  LQSLQTYVT  6        0.5887
85.6     8.50 0.68      Sequence         WB
             DRB1_1501 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.6492
44.5     4.50 0.80      Sequence         WB
             DRB1_1501 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.6802
31.8     3.00 0.76      Sequence         WB
             DRB1_1501 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.7393
16.8     1.20 0.66      Sequence         SB
             DRB1_1501 1005      GRLQSLQTYVTQQLI  LQSLQTYVT  2        0.7454
15.7     1.10 0.57      Sequence         SB
             DRB1_1501 1006      RLQSLQTYVTQQLIR  LQTYVTQQL  4        0.7140
22.1     1.80 0.53      Sequence         SB
             DRB1_1501 1007      LQSLQTYVTQQLIRA  LQTYVTQQL  3        0.6660
37.1     3.50 0.69      Sequence         WB
             DRB1_1501 1008      QSLQTYVTQQLIRAA  LQTYVTQQL  2        0.6271
56.5     5.50 0.83      Sequence         WB
             DRB1_1501 1009      SLQTYVTQQLIRAAE  LQTYVTQQL  1        0.5671
108.2    11.00  0.71     Sequence
             DRB1_1501 1010      LQTYVTQQLIRAAEI  LQTYVTQQL  0        0.4615
339.0    24.00  0.40     Sequence
             DRB1_1501 1011      QTYVTQQLIRAAEIR  QQLIRAAEI  5        0.4052
623.3    34.00  0.32     Sequence
             DRB1_1501 1012      TYVTQQLIRAAEIRA  QQLIRAAEI  4        0.3916
722.5    37.00  0.34     Sequence
             DRB1_1501 1013      YVTQQLIRAAEIRAS  QQLIRAAEI  3        0.3915
723.6    37.00  0.39     Sequence
             DRB1_1501 1014      VTQQLIRAAEIRASA  QQLIRAAEI  2        0.4042
630.6    34.00  0.31     Sequence
             DRB1_1501 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.3905
731.4    37.00  0.36     Sequence
             DRB1_1501 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.3697
915.5    41.00  0.45     Sequence
             DRB1_1501 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.3586
1032.3    43.00  0.44     Sequence
             DRB1_1501 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.4294
479.9    30.00  0.64     Sequence
             DRB1_1501 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.5298
161.9    14.00  0.76     Sequence
             DRB1_1501 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.5693
105.6    10.00  0.83     Sequence
             DRB1_1501 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.5751
99.2     9.50 0.83      Sequence         WB
             DRB1_1501 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.5450
137.5    13.00  0.81     Sequence
             DRB1_1501 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.4741
295.9    22.00  0.68     Sequence
             DRB1_1501 1024      IRASANLAAIKMSEC  IRASANLAA  0        0.3761
854.3    40.00  0.49     Sequence
             DRB1_1501 1025      RASANLAAIKMSECV  LAAIKMSEC  5        0.2804
2407.5    65.00  0.40     Sequence
             DRB1_1501 1026      ASANLAAIKMSECVL  LAAIKMSEC  4        0.3201
1565.9    55.00  0.46     Sequence
             DRB1_1501 1027      SANLAAIKMSECVLG  LAAIKMSEC  3        0.3519
1110.0    45.00  0.32     Sequence
             DRB1_1501 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.3733
880.3    40.00  0.34     Sequence
             DRB1_1501 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.3610
1006.6    43.00  0.46     Sequence
             DRB1_1501 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.3513
1117.0    45.00  0.56     Sequence
```

```
             DRB1_1501 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.3295
1415.2    50.00  0.62     Sequence
             DRB1_1501 1032      AIKMSECVLGQSKRV  IKMSECVLG  1        0.2965
2021.0    60.00  0.51     Sequence
             DRB1_1501 1033      IKMSECVLGQSKRVD  IKMSECVLG  0        0.2208
4584.4    75.00  0.29     Sequence
             DRB1_1501 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.1708
7879.9    85.00  0.28     Sequence
             DRB1_1501 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.1713
7833.2    85.00  0.25     Sequence
             DRB1_1501 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.1744
7578.0    85.00  0.26     Sequence
             DRB1_1501 1037      ECVLGQSKRVDFCGK  LGQSKRVDF  3        0.1624
8627.0    90.00  0.27     Sequence
             DRB1_1501 1038      CVLGQSKRVDFCGKG  LGQSKRVDF  2        0.1427
10671.3    90.00  0.29     Sequence
             DRB1_1501 1039      VLGQSKRVDFCGKGY  RVDFCGKGY  6        0.1463
10273.3    90.00  0.21     Sequence
             DRB1_1501 1040      LGQSKRVDFCGKGYH  VDFCGKGYH  6        0.2035
5529.8    80.00  0.33     Sequence
             DRB1_1501 1041      GQSKRVDFCGKGYHL  VDFCGKGYH  5        0.2826
2349.1    60.00  0.31     Sequence
             DRB1_1501 1042      QSKRVDFCGKGYHLM  DFCGKGYHL  5        0.3272
1450.6    50.00  0.29     Sequence
             DRB1_1501 1043      SKRVDFCGKGYHLMS  DFCGKGYHL  4        0.3400
1263.1    47.00  0.32     Sequence
             DRB1_1501 1044      KRVDFCGKGYHLMSF  DFCGKGYHL  3        0.3476
1163.6    46.00  0.29     Sequence
             DRB1_1501 1045      RVDFCGKGYHLMSFP  DFCGKGYHL  2        0.3318
1379.6    49.00  0.29     Sequence
             DRB1_1501 1046      VDFCGKGYHLMSFPQ  GYHLMSFPQ  6        0.3580
1039.1    44.00  0.44     Sequence
             DRB1_1501 1047      DFCGKGYHLMSFPQS  GYHLMSFPQ  5        0.3933
709.5    36.00  0.60     Sequence
             DRB1_1501 1048      FCGKGYHLMSFPQSA  GYHLMSFPQ  4        0.4960
233.6    19.00  0.53     Sequence
             DRB1_1501 1049      CGKGYHLMSFPQSAP  LMSFPQSAP  6        0.5493
131.1    12.00  0.41     Sequence
             DRB1_1501 1050      GKGYHLMSFPQSAPH  LMSFPQSAP  5        0.5813
92.7     9.00  0.51     Sequence         WB
             DRB1_1501 1051      KGYHLMSFPQSAPHG  LMSFPQSAP  4        0.5515
128.0    12.00  0.60     Sequence
             DRB1_1501 1052      GYHLMSFPQSAPHGV  LMSFPQSAP  3        0.5232
174.0    15.00  0.72     Sequence
             DRB1_1501 1053      YHLMSFPQSAPHGVV  LMSFPQSAP  2        0.4699
309.8    23.00  0.79     Sequence
             DRB1_1501 1054      HLMSFPQSAPHGVVF  LMSFPQSAP  1        0.3995
663.6    35.00  0.66     Sequence
             DRB1_1501 1055      LMSFPQSAPHGVVFL  LMSFPQSAP  0        0.2431
3604.8    70.00  0.33     Sequence
             DRB1_1501 1056      MSFPQSAPHGVVFLH  SAPHGVVFL  5        0.1782
7272.0    85.00  0.26     Sequence
             DRB1_1501 1057      SFPQSAPHGVVFLHV  SAPHGVVFL  4        0.2131
4986.7    80.00  0.22     Sequence
             DRB1_1501 1058      FPQSAPHGVVFLHVT  PHGVVFLHV  5        0.2234
4459.4    75.00  0.32     Sequence
             DRB1_1501 1059      PQSAPHGVVFLHVTY  PHGVVFLHV  4        0.2457
3502.6    70.00  0.28     Sequence
             DRB1_1501 1060      QSAPHGVVFLHVTYV  VVFLHVTYV  6        0.3202
1564.8    55.00  0.34     Sequence
             DRB1_1501 1061      SAPHGVVFLHVTYVP  VVFLHVTYV  5        0.3346
1339.1    49.00  0.41     Sequence
             DRB1_1501 1062      APHGVVFLHVTYVPA  VVFLHVTYV  4        0.3526
1102.3    45.00  0.44     Sequence
             DRB1_1501 1063      PHGVVFLHVTYVPAQ  VVFLHVTYV  3        0.3592
1025.6    43.00  0.44     Sequence
```

```
            DRB1_1501 1064      HGVVFLHVTYVPAQE  VVFLHVTYV  2        0.3783
834.1    39.00  0.37     Sequence
            DRB1_1501 1065      GVVFLHVTYVPAQEK  VFLHVTYVP  2        0.3958
690.4    36.00  0.21     Sequence
            DRB1_1501 1066      VVFLHVTYVPAQEKN  VTYVPAQEK  5        0.3819
802.8    39.00  0.34     Sequence
            DRB1_1501 1067      VFLHVTYVPAQEKNF  VTYVPAQEK  4        0.3796
822.5    39.00  0.50     Sequence
            DRB1_1501 1068      FLHVTYVPAQEKNFT  VTYVPAQEK  3        0.3684
928.5    41.00  0.51     Sequence
            DRB1_1501 1069      LHVTYVPAQEKNFTT  VTYVPAQEK  2        0.3503
1130.2    45.00  0.49     Sequence
            DRB1_1501 1070      HVTYVPAQEKNFTTA  VTYVPAQEK  1        0.2806
2401.6    65.00  0.40     Sequence
            DRB1_1501 1071      VTYVPAQEKNFTTAP  PAQEKNFTT  4        0.1843
6803.7    85.00  0.42     Sequence
            DRB1_1501 1072      TYVPAQEKNFTTAPA  PAQEKNFTT  3        0.1922
6246.4    80.00  0.41     Sequence
            DRB1_1501 1073      YVPAQEKNFTTAPAI  EKNFTTAPA  5        0.2136
4958.4    80.00  0.35     Sequence
            DRB1_1501 1074      VPAQEKNFTTAPAIC  EKNFTTAPA  4        0.2179
4732.9    75.00  0.34     Sequence
            DRB1_1501 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.2804
2406.6    65.00  0.56     Sequence
            DRB1_1501 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.3036
1872.7    55.00  0.62     Sequence
            DRB1_1501 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.2985
1977.8    60.00  0.68     Sequence
            DRB1_1501 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.2965
2021.7    60.00  0.77     Sequence
            DRB1_1501 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.2804
2405.9    65.00  0.78     Sequence
            DRB1_1501 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.2154
4862.8    75.00  0.62     Sequence
            DRB1_1501 1081      FTTAPAICHDGKAHF  ICHDGKAHF  6        0.2158
4840.9    75.00  0.43     Sequence
            DRB1_1501 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.2501
3340.3    70.00  0.63     Sequence
            DRB1_1501 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.2968
2015.0    60.00  0.63     Sequence
            DRB1_1501 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.3005
1935.4    60.00  0.65     Sequence
            DRB1_1501 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.2815
2377.4    60.00  0.65     Sequence
            DRB1_1501 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.2601
2997.9    65.00  0.55     Sequence
            DRB1_1501 1087      ICHDGKAHFPREGVF  ICHDGKAHF  0        0.1969
5940.3    80.00  0.36     Sequence
            DRB1_1501 1088      CHDGKAHFPREGVFV  HFPREGVFV  6        0.2252
4375.2    75.00  0.44     Sequence
            DRB1_1501 1089      HDGKAHFPREGVFVS  HFPREGVFV  5        0.2606
2981.1    65.00  0.45     Sequence
            DRB1_1501 1090      DGKAHFPREGVFVSN  HFPREGVFV  4        0.2709
2667.0    65.00  0.50     Sequence
            DRB1_1501 1091      GKAHFPREGVFVSNG  HFPREGVFV  3        0.2629
2907.1    65.00  0.47     Sequence
            DRB1_1501 1092      KAHFPREGVFVSNGT  HFPREGVFV  2        0.2408
3695.0    70.00  0.44     Sequence
            DRB1_1501 1093      AHFPREGVFVSNGTH  HFPREGVFV  1        0.2204
4606.4    75.00  0.34     Sequence
            DRB1_1501 1094      HFPREGVFVSNGTHW  VFVSNGTHW  6        0.2543
3192.8    70.00  0.20     Sequence
            DRB1_1501 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6        0.3106
1736.2    55.00  0.28     Sequence
            DRB1_1501 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.3728
885.7    40.00  0.38     Sequence
```

```
             DRB1_1501 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.3950
696.8    36.00  0.38     Sequence
             DRB1_1501 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.3736
878.1    40.00  0.41     Sequence
             DRB1_1501 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.3563
1058.9    44.00  0.41     Sequence
             DRB1_1501 1100      VFVSNGTHWFVTQRN  VSNGTHWFV  2        0.3236
1508.4    55.00  0.30     Sequence
             DRB1_1501 1101      FVSNGTHWFVTQRNF  THWFVTQRN  5        0.2932
2094.2    60.00  0.27     Sequence
             DRB1_1501 1102      VSNGTHWFVTQRNFY  THWFVTQRN  4        0.3082
1781.3    55.00  0.38     Sequence
             DRB1_1501 1103      SNGTHWFVTQRNFYE  FVTQRNFYE  6        0.4077
606.9    34.00  0.44     Sequence
             DRB1_1501 1104      NGTHWFVTQRNFYEP  FVTQRNFYE  5        0.4425
416.4    27.00  0.53     Sequence
             DRB1_1501 1105      GTHWFVTQRNFYEPQ  FVTQRNFYE  4        0.4512
379.0    26.00  0.58     Sequence
             DRB1_1501 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3        0.4485
390.5    26.00  0.58     Sequence
             DRB1_1501 1107      HWFVTQRNFYEPQII  FVTQRNFYE  2        0.4353
450.2    28.00  0.57     Sequence
             DRB1_1501 1108      WFVTQRNFYEPQIIT  FVTQRNFYE  1        0.4237
510.5    31.00  0.47     Sequence
             DRB1_1501 1109      FVTQRNFYEPQIITT  NFYEPQIIT  5        0.3539
1086.9    44.00  0.27     Sequence
             DRB1_1501 1110      VTQRNFYEPQIITTD  NFYEPQIIT  4        0.2770
2496.6    65.00  0.46     Sequence
             DRB1_1501 1111      TQRNFYEPQIITTDN  NFYEPQIIT  3        0.2743
2569.9    65.00  0.47     Sequence
             DRB1_1501 1112      QRNFYEPQIITTDNT  NFYEPQIIT  2        0.2421
3641.9    70.00  0.50     Sequence
             DRB1_1501 1113      RNFYEPQIITTDNTF  NFYEPQIIT  1        0.1991
5802.5    80.00  0.45     Sequence
             DRB1_1501 1114      NFYEPQIITTDNTFV  IITTDNTFV  6        0.2806
2402.6    65.00  0.52     Sequence
             DRB1_1501 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.3408
1252.3    47.00  0.61     Sequence
             DRB1_1501 1116      YEPQIITTDNTFVSG  IITTDNTFV  4        0.3508
1123.8    45.00  0.61     Sequence
             DRB1_1501 1117      EPQIITTDNTFVSGN  IITTDNTFV  3        0.3639
975.5    42.00  0.62     Sequence
             DRB1_1501 1118      PQIITTDNTFVSGNC  IITTDNTFV  2        0.3600
1016.9    43.00  0.57     Sequence
             DRB1_1501 1119      QIITTDNTFVSGNCD  IITTDNTFV  1        0.3372
1301.0    48.00  0.49     Sequence
             DRB1_1501 1120      IITTDNTFVSGNCDV  IITTDNTFV  0        0.2567
3109.3    70.00  0.32     Sequence
             DRB1_1501 1121      ITTDNTFVSGNCDVV  DNTFVSGNC  3        0.1583
9019.2    90.00  0.44     Sequence
             DRB1_1501 1122      TTDNTFVSGNCDVVI  DNTFVSGNC  2        0.1859
6691.0    85.00  0.31     Sequence
             DRB1_1501 1123      TDNTFVSGNCDVVIG  VSGNCDVVI  5        0.1821
6967.5    85.00  0.30     Sequence
             DRB1_1501 1124      DNTFVSGNCDVVIGI  VSGNCDVVI  4        0.1843
6807.7    85.00  0.34     Sequence
             DRB1_1501 1125      NTFVSGNCDVVIGIV  VSGNCDVVI  3        0.1821
6972.4    85.00  0.41     Sequence
             DRB1_1501 1126      TFVSGNCDVVIGIVN  VSGNCDVVI  2        0.1820
6981.1    85.00  0.37     Sequence
             DRB1_1501 1127      FVSGNCDVVIGIVNN  VSGNCDVVI  1        0.1726
7727.9    85.00  0.22     Sequence
             DRB1_1501 1128      VSGNCDVVIGIVNNT  CDVVIGIVN  4        0.1826
6936.2    85.00  0.23     Sequence
             DRB1_1501 1129      SGNCDVVIGIVNNTV  VIGIVNNTV  6        0.3661
952.3    42.00  0.52     Sequence
```

```
             DRB1_1501 1130      GNCDVVIGIVNNTVY  VIGIVNNTV  5        0.5005
222.3    18.00  0.49     Sequence
             DRB1_1501 1131      NCDVVIGIVNNTVYD  VIGIVNNTV  4        0.5278
165.5    15.00  0.47     Sequence
             DRB1_1501 1132      CDVVIGIVNNTVYDP  VIGIVNNTV  3        0.5325
157.4    14.00  0.46     Sequence
             DRB1_1501 1133      DVVIGIVNNTVYDPL  VIGIVNNTV  2        0.5401
144.8    13.00  0.46     Sequence
             DRB1_1501 1134      VVIGIVNNTVYDPLQ  IGIVNNTVY  2        0.5154
189.3    16.00  0.44     Sequence
             DRB1_1501 1135      VIGIVNNTVYDPLQP  IGIVNNTVY  1        0.4278
488.6    30.00  0.40     Sequence
             DRB1_1501 1136      IGIVNNTVYDPLQPE  IGIVNNTVY  0        0.2610
2968.5    65.00  0.28     Sequence
             DRB1_1501 1137      GIVNNTVYDPLQPEL  NTVYDPLQP  4        0.1935
6160.0    80.00  0.33     Sequence
             DRB1_1501 1138      IVNNTVYDPLQPELD  NTVYDPLQP  3        0.1671
8198.2    85.00  0.37     Sequence
             DRB1_1501 1139      VNNTVYDPLQPELDS  NTVYDPLQP  2        0.1513
9730.4    90.00  0.37     Sequence
             DRB1_1501 1140      NNTVYDPLQPELDSF  NTVYDPLQP  1        0.1247
12975.8    95.00  0.34     Sequence
             DRB1_1501 1141      NTVYDPLQPELDSFK  LQPELDSFK  6        0.1131
14704.7    95.00  0.25     Sequence
             DRB1_1501 1142      TVYDPLQPELDSFKE  LQPELDSFK  5        0.1018
16612.4   100.00  0.41     Sequence
             DRB1_1501 1143      VYDPLQPELDSFKEE  LQPELDSFK  4        0.0968
17537.2   100.00  0.44     Sequence
             DRB1_1501 1144      YDPLQPELDSFKEEL  LQPELDSFK  3        0.1185
13873.4    95.00  0.47     Sequence
             DRB1_1501 1145      DPLQPELDSFKEELD  LQPELDSFK  2        0.1285
12444.8    95.00  0.40     Sequence
             DRB1_1501 1146      PLQPELDSFKEELDK  LDSFKEELD  5        0.1424
10712.1    90.00  0.43     Sequence
             DRB1_1501 1147      LQPELDSFKEELDKY  LDSFKEELD  4        0.1447
10448.0    90.00  0.48     Sequence
             DRB1_1501 1148      QPELDSFKEELDKYF  LDSFKEELD  3        0.1762
7430.5    85.00  0.39     Sequence
             DRB1_1501 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.2013
5666.0    80.00  0.44     Sequence
             DRB1_1501 1150      ELDSFKEELDKYFKN  FKEELDKYF  4        0.1975
5902.6    80.00  0.47     Sequence
             DRB1_1501 1151      LDSFKEELDKYFKNH  FKEELDKYF  3        0.2119
5049.5    80.00  0.49     Sequence
             DRB1_1501 1152      DSFKEELDKYFKNHT  LDKYFKNHT  6        0.3303
1403.2    50.00  0.29     Sequence
             DRB1_1501 1153      SFKEELDKYFKNHTS  DKYFKNHTS  6        0.3860
767.8    38.00  0.37     Sequence
             DRB1_1501 1154      FKEELDKYFKNHTSP  DKYFKNHTS  5        0.3874
756.1    38.00  0.47     Sequence
             DRB1_1501 1155      KEELDKYFKNHTSPD  DKYFKNHTS  4        0.3806
813.9    39.00  0.50     Sequence
             DRB1_1501 1156      EELDKYFKNHTSPDV  DKYFKNHTS  3        0.3991
666.4    35.00  0.45     Sequence
             DRB1_1501 1157      ELDKYFKNHTSPDVD  DKYFKNHTS  2        0.4013
650.6    35.00  0.40     Sequence
             DRB1_1501 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.3673
939.4    42.00  0.49     Sequence
             DRB1_1501 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.2714
2652.2    65.00  0.72     Sequence
             DRB1_1501 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.2526
3249.9    70.00  0.86     Sequence
             DRB1_1501 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.1913
6311.8    80.00  0.75     Sequence
             DRB1_1501 1162      FKNHTSPDVDLGDIS  FKNHTSPDV  0        0.1143
14520.3    95.00  0.47     Sequence
```

```
             DRB1_1501 1163      KNHTSPDVDLGDISG  DVDLGDISG  6        0.0567
27077.5   100.00  0.19     Sequence
             DRB1_1501 1164      NHTSPDVDLGDISGI  VDLGDISGI  6        0.0754
22122.2   100.00  0.28     Sequence
             DRB1_1501 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.0889
19118.6   100.00  0.34     Sequence
             DRB1_1501 1166      TSPDVDLGDISGINA  VDLGDISGI  4        0.1131
14705.9    95.00  0.26     Sequence
             DRB1_1501 1167      SPDVDLGDISGINAS  VDLGDISGI  3        0.1338
11750.1    95.00  0.20     Sequence
             DRB1_1501 1168      PDVDLGDISGINASF  LGDISGINA  4        0.1656
8329.0    90.00  0.24     Sequence
             DRB1_1501 1169      DVDLGDISGINASFV  ISGINASFV  6        0.2693
2713.7    65.00  0.61     Sequence
             DRB1_1501 1170      VDLGDISGINASFVN  ISGINASFV  5        0.3153
1650.3    55.00  0.67     Sequence
             DRB1_1501 1171      DLGDISGINASFVNI  ISGINASFV  4        0.3489
1146.2    45.00  0.70     Sequence
             DRB1_1501 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.3723
889.9    41.00  0.66     Sequence
             DRB1_1501 1173      GDISGINASFVNIQK  ISGINASFV  2        0.4126
575.9    33.00  0.50     Sequence
             DRB1_1501 1174      DISGINASFVNIQKE  NASFVNIQK  5        0.3897
737.3    37.00  0.40     Sequence
             DRB1_1501 1175      ISGINASFVNIQKEI  NASFVNIQK  4        0.3987
669.3    35.00  0.46     Sequence
             DRB1_1501 1176      SGINASFVNIQKEID  NASFVNIQK  3        0.3590
1028.1    43.00  0.59     Sequence
             DRB1_1501 1177      GINASFVNIQKEIDR  NASFVNIQK  2        0.3510
1120.5    45.00  0.53     Sequence
             DRB1_1501 1178      INASFVNIQKEIDRL  NASFVNIQK  1        0.3351
1330.9    48.00  0.41     Sequence
             DRB1_1501 1179      NASFVNIQKEIDRLN  VNIQKEIDR  4        0.2948
2060.2    60.00  0.31     Sequence
             DRB1_1501 1180      ASFVNIQKEIDRLNE  VNIQKEIDR  3        0.2676
2762.8    65.00  0.38     Sequence
             DRB1_1501 1181      SFVNIQKEIDRLNEV  VNIQKEIDR  2        0.2672
2777.0    65.00  0.34     Sequence
             DRB1_1501 1182      FVNIQKEIDRLNEVA  IQKEIDRLN  3        0.2283
4226.7    75.00  0.37     Sequence
             DRB1_1501 1183      VNIQKEIDRLNEVAK  IQKEIDRLN  2        0.2293
4183.9    75.00  0.34     Sequence
             DRB1_1501 1184      NIQKEIDRLNEVAKN  IDRLNEVAK  5        0.2230
4478.9    75.00  0.34     Sequence
             DRB1_1501 1185      IQKEIDRLNEVAKNL  IDRLNEVAK  4        0.2209
4582.1    75.00  0.51     Sequence
             DRB1_1501 1186      QKEIDRLNEVAKNLN  IDRLNEVAK  3        0.2261
4330.5    75.00  0.55     Sequence
             DRB1_1501 1187      KEIDRLNEVAKNLNE  IDRLNEVAK  2        0.2144
4915.9    75.00  0.47     Sequence
             DRB1_1501 1188      EIDRLNEVAKNLNES  IDRLNEVAK  1        0.1779
7296.9    85.00  0.40     Sequence
             DRB1_1501 1189      IDRLNEVAKNLNESL  VAKNLNESL  6        0.1729
7697.7    85.00  0.27     Sequence
             DRB1_1501 1190      DRLNEVAKNLNESLI  VAKNLNESL  5        0.1893
6445.7    85.00  0.50     Sequence
             DRB1_1501 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.1927
6213.0    80.00  0.54     Sequence
             DRB1_1501 1192      LNEVAKNLNESLIDL  VAKNLNESL  3        0.1970
5935.9    80.00  0.57     Sequence
             DRB1_1501 1193      NEVAKNLNESLIDLQ  VAKNLNESL  2        0.1908
6343.3    80.00  0.54     Sequence
             DRB1_1501 1194      EVAKNLNESLIDLQE  VAKNLNESL  1        0.1666
8243.2    85.00  0.44     Sequence
             DRB1_1501 1195      VAKNLNESLIDLQEL  VAKNLNESL  0        0.1333
11822.6    95.00  0.29     Sequence
```

```
             DRB1_1501 1196      AKNLNESLIDLQELG  NLNESLIDL  2        0.0917
18543.9   100.00  0.23     Sequence
             DRB1_1501 1197      KNLNESLIDLQELGK  NESLIDLQE  3        0.0952
17854.2   100.00  0.23     Sequence
             DRB1_1501 1198      NLNESLIDLQELGKY  LIDLQELGK  5        0.1230
13218.6    95.00  0.28     Sequence
             DRB1_1501 1199      LNESLIDLQELGKYE  IDLQELGKY  5        0.1390
11110.2    90.00  0.31     Sequence
             DRB1_1501 1200      NESLIDLQELGKYEQ  IDLQELGKY  4        0.1544
9409.3    90.00  0.33     Sequence
             DRB1_1501 1201      ESLIDLQELGKYEQY  IDLQELGKY  3        0.1649
8394.8    90.00  0.30     Sequence
             DRB1_1501 1202      SLIDLQELGKYEQYI  IDLQELGKY  2        0.2083
5247.6    80.00  0.22     Sequence
             DRB1_1501 1203      LIDLQELGKYEQYIK  LGKYEQYIK  6        0.3084
1777.9    55.00  0.54     Sequence
             DRB1_1501 1204      IDLQELGKYEQYIKW  LGKYEQYIK  5        0.3768
848.4    40.00  0.67     Sequence
             DRB1_1501 1205      DLQELGKYEQYIKWP  LGKYEQYIK  4        0.4022
644.2    35.00  0.65     Sequence
             DRB1_1501 1206      LQELGKYEQYIKWPW  LGKYEQYIK  3        0.4774
285.7    22.00  0.52     Sequence
             DRB1_1501 1207      QELGKYEQYIKWPWY  LGKYEQYIK  2        0.4962
233.1    19.00  0.44     Sequence
             DRB1_1501 1208      ELGKYEQYIKWPWYI  YEQYIKWPW  4        0.5620
114.3    11.00  0.32     Sequence
             DRB1_1501 1209      LGKYEQYIKWPWYIW  YEQYIKWPW  3        0.5885
85.8     8.50  0.28     Sequence         WB
             DRB1_1501 1210      GKYEQYIKWPWYIWL  YEQYIKWPW  2        0.5896
84.8     8.50  0.25     Sequence         WB
             DRB1_1501 1211      KYEQYIKWPWYIWLG  YIKWPWYIW  4        0.5809
93.2     9.00  0.28     Sequence         WB
             DRB1_1501 1212      YEQYIKWPWYIWLGF  YIKWPWYIW  3        0.5513
128.4    12.00  0.34     Sequence
             DRB1_1501 1213      EQYIKWPWYIWLGFI  YIKWPWYIW  2        0.5393
146.1    13.00  0.31     Sequence
             DRB1_1501 1214      QYIKWPWYIWLGFIA  YIKWPWYIW  1        0.5248
170.9    15.00  0.22     Sequence
             DRB1_1501 1215      YIKWPWYIWLGFIAG  WYIWLGFIA  5        0.4307
473.1    29.00  0.27     Sequence
             DRB1_1501 1216      IKWPWYIWLGFIAGL  WYIWLGFIA  4        0.4235
511.5    31.00  0.25     Sequence
             DRB1_1501 1217      KWPWYIWLGFIAGLI  WYIWLGFIA  3        0.4246
505.6    30.00  0.28     Sequence
             DRB1_1501 1218      WPWYIWLGFIAGLIA  WLGFIAGLI  5        0.4387
433.9    28.00  0.28     Sequence
             DRB1_1501 1219      PWYIWLGFIAGLIAI  WLGFIAGLI  4        0.4520
376.0    26.00  0.30     Sequence
             DRB1_1501 1220      WYIWLGFIAGLIAIV  LGFIAGLIA  4        0.4458
402.1    27.00  0.35     Sequence
             DRB1_1501 1221      YIWLGFIAGLIAIVM  LGFIAGLIA  3        0.4382
436.2    28.00  0.39     Sequence
             DRB1_1501 1222      IWLGFIAGLIAIVMV  LGFIAGLIA  2        0.4253
501.9    30.00  0.40     Sequence
             DRB1_1501 1223      WLGFIAGLIAIVMVT  LGFIAGLIA  1        0.3558
1063.9    44.00  0.40     Sequence
             DRB1_1501 1224      LGFIAGLIAIVMVTI  LGFIAGLIA  0        0.2780
2468.6    65.00  0.31     Sequence
             DRB1_1501 1225      GFIAGLIAIVMVTIM  IAGLIAIVM  2        0.2262
4325.8    75.00  0.38     Sequence
             DRB1_1501 1226      FIAGLIAIVMVTIML  AIVMVTIML  6        0.2489
3385.4    70.00  0.28     Sequence
             DRB1_1501 1227      IAGLIAIVMVTIMLC  AIVMVTIML  5        0.2238
4438.4    75.00  0.37     Sequence
             DRB1_1501 1228      AGLIAIVMVTIMLCC  AIVMVTIML  4        0.2172
4770.3    75.00  0.42     Sequence
```

```
             DRB1_1501 1229      GLIAIVMVTIMLCCM  AIVMVTIML  3        0.2159
4835.9    75.00  0.44     Sequence
             DRB1_1501 1230      LIAIVMVTIMLCCMT  AIVMVTIML  2        0.2054
5417.5    80.00  0.39     Sequence
             DRB1_1501 1231      IAIVMVTIMLCCMTS  AIVMVTIML  1        0.2161
4827.7    75.00  0.34     Sequence
             DRB1_1501 1232      AIVMVTIMLCCMTSC  VTIMLCCMT  4        0.1960
5999.7    80.00  0.21     Sequence
             DRB1_1501 1233      IVMVTIMLCCMTSCC  VTIMLCCMT  3        0.1629
8584.3    90.00  0.30     Sequence
             DRB1_1501 1234      VMVTIMLCCMTSCCS  VTIMLCCMT  2        0.1882
6526.8    85.00  0.24     Sequence
             DRB1_1501 1235      MVTIMLCCMTSCCSC  LCCMTSCCS  5        0.1898
6415.1    85.00  0.27     Sequence
             DRB1_1501 1236      VTIMLCCMTSCCSCL  LCCMTSCCS  4        0.1829
6913.6    85.00  0.33     Sequence
             DRB1_1501 1237      TIMLCCMTSCCSCLK  LCCMTSCCS  3        0.1678
8138.0    85.00  0.41     Sequence
             DRB1_1501 1238      IMLCCMTSCCSCLKG  LCCMTSCCS  2        0.1454
10372.0    90.00  0.46     Sequence
             DRB1_1501 1239      MLCCMTSCCSCLKGC  LCCMTSCCS  1        0.1157
14301.0    95.00  0.41     Sequence
             DRB1_1501 1240      LCCMTSCCSCLKGCC  MTSCCSCLK  3        0.0835
20268.7   100.00  0.31     Sequence
             DRB1_1501 1241      CCMTSCCSCLKGCCS  MTSCCSCLK  2        0.0754
22123.6   100.00  0.38     Sequence
             DRB1_1501 1242      CMTSCCSCLKGCCSC  MTSCCSCLK  1        0.0708
23250.3   100.00  0.29     Sequence
             DRB1_1501 1243      MTSCCSCLKGCCSCG  CCSCLKGCC  3        0.0747
22287.2   100.00  0.22     Sequence
             DRB1_1501 1244      TSCCSCLKGCCSCGS  LKGCCSCGS  6        0.0994
17059.4   100.00  0.47     Sequence
             DRB1_1501 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5        0.1127
14768.8    95.00  0.56     Sequence
             DRB1_1501 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.1116
14948.5    95.00  0.59     Sequence
             DRB1_1501 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.1248
12952.0    95.00  0.59     Sequence
             DRB1_1501 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2        0.1275
12578.4    95.00  0.57     Sequence
             DRB1_1501 1249      CLKGCCSCGSCCKFD  LKGCCSCGS  1        0.1139
14577.5    95.00  0.50     Sequence
             DRB1_1501 1250      LKGCCSCGSCCKFDE  LKGCCSCGS  0        0.0868
19545.3   100.00  0.28     Sequence
             DRB1_1501 1251      KGCCSCGSCCKFDED  CCSCGSCCK  2        0.0568
27042.1   100.00  0.43     Sequence
             DRB1_1501 1252      GCCSCGSCCKFDEDD  CCSCGSCCK  1        0.0444
30923.8   100.00  0.32     Sequence
             DRB1_1501 1253      CCSCGSCCKFDEDDS  CCSCGSCCK  0        0.0347
34334.3   100.00  0.19     Sequence
             DRB1_1501 1254      CSCGSCCKFDEDDSE  CCKFDEDDS  5        0.0336
34776.6   100.00  0.39     Sequence
             DRB1_1501 1255      SCGSCCKFDEDDSEP  CCKFDEDDS  4        0.0346
34372.9   100.00  0.38     Sequence
             DRB1_1501 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.0601
26106.3   100.00  0.41     Sequence
             DRB1_1501 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.0864
19623.5   100.00  0.48     Sequence
             DRB1_1501 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.1030
16407.3   100.00  0.47     Sequence
             DRB1_1501 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.1007
16815.6   100.00  0.43     Sequence
             DRB1_1501 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.1029
16430.0   100.00  0.41     Sequence
             DRB1_1501 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.1021
16565.3   100.00  0.35     Sequence
```

```
             DRB1_1501 1262      FDEDDSEPVLKGVKL  EPVLKGVKL  6        0.1420
10758.7    90.00  0.34     Sequence
             DRB1_1501 1263      DEDDSEPVLKGVKLH  EPVLKGVKL  5        0.1853
6732.2    85.00  0.47     Sequence
             DRB1_1501 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.3450
1196.6    46.00  0.42     Sequence
             DRB1_1501 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.4312
470.8    29.00  0.44     Sequence
             DRB3_0101    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.2113
5080.1    65.00  0.55     Sequence
             DRB3_0101    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.2238
4437.3    60.00  0.38     Sequence
             DRB3_0101    3      PIKEMFVFLVLLPLV  VFLVLLPLV  6        0.2418
3653.5    55.00  0.32     Sequence
             DRB3_0101    4      IKEMFVFLVLLPLVS  VFLVLLPLV  5        0.2041
5493.0    70.00  0.38     Sequence
             DRB3_0101    5      KEMFVFLVLLPLVSS  VFLVLLPLV  4        0.1945
6095.5    70.00  0.37     Sequence
             DRB3_0101    6      EMFVFLVLLPLVSSQ  VFLVLLPLV  3        0.1817
7001.3    75.00  0.32     Sequence
             DRB3_0101    7      MFVFLVLLPLVSSQC  VFLVLLPLV  2        0.1611
8753.2    80.00  0.31     Sequence
             DRB3_0101    8      FVFLVLLPLVSSQCV  VFLVLLPLV  1        0.1490
9973.5    85.00  0.21     Sequence
             DRB3_0101    9      VFLVLLPLVSSQCVN  LLPLVSSQC  4        0.1340
11732.8    90.00  0.23     Sequence
             DRB3_0101   10      FLVLLPLVSSQCVNF  LVSSQCVNF  6        0.2094
5189.0    65.00  0.55     Sequence
             DRB3_0101   11      LVLLPLVSSQCVNFT  LVSSQCVNF  5        0.2188
4688.7    65.00  0.58     Sequence
             DRB3_0101   12      VLLPLVSSQCVNFTN  LVSSQCVNF  4        0.2130
4989.3    65.00  0.58     Sequence
             DRB3_0101   13      LLPLVSSQCVNFTNR  LVSSQCVNF  3        0.2026
5585.1    70.00  0.56     Sequence
             DRB3_0101   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.1928
6211.2    70.00  0.47     Sequence
             DRB3_0101   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.1727
7718.9    80.00  0.31     Sequence
             DRB3_0101   16      LVSSQCVNFTNRTQL  QCVNFTNRT  4        0.1477
10117.4    85.00  0.28     Sequence
             DRB3_0101   17      VSSQCVNFTNRTQLP  QCVNFTNRT  3        0.1371
11337.8    90.00  0.27     Sequence
             DRB3_0101   18      SSQCVNFTNRTQLPS  NFTNRTQLP  5        0.1349
11614.2    90.00  0.29     Sequence
             DRB3_0101   19      SQCVNFTNRTQLPSA  NFTNRTQLP  4        0.1314
12070.8    90.00  0.29     Sequence
             DRB3_0101   20      QCVNFTNRTQLPSAY  NRTQLPSAY  6        0.1423
10727.5    90.00  0.25     Sequence
             DRB3_0101   21      CVNFTNRTQLPSAYT  NRTQLPSAY  5        0.1345
11670.4    90.00  0.34     Sequence
             DRB3_0101   22      VNFTNRTQLPSAYTN  NRTQLPSAY  4        0.1310
12117.9    90.00  0.32     Sequence
             DRB3_0101   23      NFTNRTQLPSAYTNS  NRTQLPSAY  3        0.1103
15160.9    95.00  0.34     Sequence
             DRB3_0101   24      FTNRTQLPSAYTNSF  LPSAYTNSF  6        0.1325
11923.1    90.00  0.32     Sequence
             DRB3_0101   25      TNRTQLPSAYTNSFT  LPSAYTNSF  5        0.1330
11857.1    90.00  0.38     Sequence
             DRB3_0101   26      NRTQLPSAYTNSFTR  LPSAYTNSF  4        0.1302
12228.4    90.00  0.38     Sequence
             DRB3_0101   27      RTQLPSAYTNSFTRG  LPSAYTNSF  3        0.1447
10442.5    85.00  0.34     Sequence
             DRB3_0101   28      TQLPSAYTNSFTRGV  YTNSFTRGV  6        0.3253
1480.5    32.00  0.82     Sequence
             DRB3_0101   29      QLPSAYTNSFTRGVY  YTNSFTRGV  5        0.3552
1071.1    26.00  0.81     Sequence
```

```
             DRB3_0101   30      LPSAYTNSFTRGVYY  YTNSFTRGV  4        0.3814
806.7    21.00  0.77     Sequence
             DRB3_0101   31      PSAYTNSFTRGVYYP  YTNSFTRGV  3        0.3627
987.9    24.00  0.74     Sequence
             DRB3_0101   32      SAYTNSFTRGVYYPD  YTNSFTRGV  2        0.3732
881.4    23.00  0.52     Sequence
             DRB3_0101   33      AYTNSFTRGVYYPDK  YTNSFTRGV  1        0.3274
1446.8    31.00  0.41     Sequence
             DRB3_0101   34      YTNSFTRGVYYPDKV  FTRGVYYPD  4        0.2931
2098.0    39.00  0.35     Sequence
             DRB3_0101   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.3156
1643.7    34.00  0.38     Sequence
             DRB3_0101   36      NSFTRGVYYPDKVFR  YYPDKVFRX  7        0.4513
378.7    13.00  0.30     Sequence
             DRB3_0101   37      SFTRGVYYPDKVFRS  YYPDKVFRS  6        0.7818
10.6     0.50  0.91     Sequence         SB
             DRB3_0101   38      FTRGVYYPDKVFRSS  YYPDKVFRS  5        0.8039
8.3     0.40  0.94     Sequence         SB
             DRB3_0101   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.8183
7.1     0.25  0.94     Sequence         SB
             DRB3_0101   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.8214
6.9     0.25  0.94     Sequence         SB
             DRB3_0101   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.7843
10.3     0.50  0.93     Sequence         SB
             DRB3_0101   42      VYYPDKVFRSSVLHS  YYPDKVFRS  1        0.7306
18.5     1.00  0.90     Sequence         SB
             DRB3_0101   43      YYPDKVFRSSVLHST  YYPDKVFRS  0        0.5554
122.7     6.00  0.54     Sequence         WB
             DRB3_0101   44      YPDKVFRSSVLHSTQ  FRSSVLHST  5        0.3542
1082.5    26.00  0.56     Sequence
             DRB3_0101   45      PDKVFRSSVLHSTQD  FRSSVLHST  4        0.3657
955.8    24.00  0.61     Sequence
             DRB3_0101   46      DKVFRSSVLHSTQDL  FRSSVLHST  3        0.3550
1073.4    26.00  0.61     Sequence
             DRB3_0101   47      KVFRSSVLHSTQDLF  FRSSVLHST  2        0.4110
585.7    17.00  0.41     Sequence
             DRB3_0101   48      VFRSSVLHSTQDLFL  VLHSTQDLF  5        0.4132
571.7    17.00  0.63     Sequence
             DRB3_0101   49      FRSSVLHSTQDLFLP  VLHSTQDLF  4        0.3706
907.1    23.00  0.67     Sequence
             DRB3_0101   50      RSSVLHSTQDLFLPF  VLHSTQDLF  3        0.3995
663.5    19.00  0.62     Sequence
             DRB3_0101   51      SSVLHSTQDLFLPFF  VLHSTQDLF  2        0.3843
782.0    21.00  0.50     Sequence
             DRB3_0101   52      SVLHSTQDLFLPFFS  VLHSTQDLF  1        0.3464
1177.9    27.00  0.40     Sequence
             DRB3_0101   53      VLHSTQDLFLPFFSN  STQDLFLPF  3        0.2978
1994.2    38.00  0.34     Sequence
             DRB3_0101   54      LHSTQDLFLPFFSNV  STQDLFLPF  2        0.2576
3079.4    49.00  0.39     Sequence
             DRB3_0101   55      HSTQDLFLPFFSNVT  FLPFFSNVT  6        0.2658
2817.3    46.00  0.35     Sequence
             DRB3_0101   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.2567
3108.3    49.00  0.38     Sequence
             DRB3_0101   57      TQDLFLPFFSNVTWF  FLPFFSNVT  4        0.3290
1421.7    31.00  0.31     Sequence
             DRB3_0101   58      QDLFLPFFSNVTWFH  FFSNVTWFH  6        0.5152
189.8     8.00  0.63     Sequence         WB
             DRB3_0101   59      DLFLPFFSNVTWFHA  FFSNVTWFH  5        0.5486
132.2     6.00  0.61     Sequence         WB
             DRB3_0101   60      LFLPFFSNVTWFHAI  FFSNVTWFH  4        0.5739
100.5     5.00  0.65     Sequence         WB
             DRB3_0101   61      FLPFFSNVTWFHAIH  FFSNVTWFH  3        0.5551
123.2     6.00  0.66     Sequence         WB
             DRB3_0101   62      LPFFSNVTWFHAIHV  FFSNVTWFH  2        0.5333
155.9     7.00  0.63     Sequence         WB
```

```
             DRB3_0101   63      PFFSNVTWFHAIHVS  FFSNVTWFH  1        0.4816
272.9    11.00  0.62     Sequence
             DRB3_0101   64      FFSNVTWFHAIHVSG  FFSNVTWFH  0        0.3524
1104.3    26.00  0.47     Sequence
             DRB3_0101   65      FSNVTWFHAIHVSGT  FHAIHVSGT  6        0.1814
7021.0    75.00  0.33     Sequence
             DRB3_0101   66      SNVTWFHAIHVSGTN  FHAIHVSGT  5        0.1730
7690.3    80.00  0.41     Sequence
             DRB3_0101   67      NVTWFHAIHVSGTNG  WFHAIHVSG  3        0.1612
8740.9    80.00  0.34     Sequence
             DRB3_0101   68      VTWFHAIHVSGTNGT  IHVSGTNGT  6        0.1698
7960.2    80.00  0.35     Sequence
             DRB3_0101   69      TWFHAIHVSGTNGTK  IHVSGTNGT  5        0.1500
9868.1    85.00  0.42     Sequence
             DRB3_0101   70      WFHAIHVSGTNGTKR  IHVSGTNGT  4        0.1269
12660.5    90.00  0.47     Sequence
             DRB3_0101   71      FHAIHVSGTNGTKRF  SGTNGTKRF  6        0.1718
7796.1    80.00  0.41     Sequence
             DRB3_0101   72      HAIHVSGTNGTKRFD  SGTNGTKRF  5        0.1858
6694.9    75.00  0.50     Sequence
             DRB3_0101   73      AIHVSGTNGTKRFDN  SGTNGTKRF  4        0.1737
7630.9    80.00  0.51     Sequence
             DRB3_0101   74      IHVSGTNGTKRFDNP  SGTNGTKRF  3        0.1546
9383.2    85.00  0.58     Sequence
             DRB3_0101   75      HVSGTNGTKRFDNPV  SGTNGTKRF  2        0.1310
12113.7    90.00  0.56     Sequence
             DRB3_0101   76      VSGTNGTKRFDNPVL  SGTNGTKRF  1        0.1713
7837.6    80.00  0.37     Sequence
             DRB3_0101   77      SGTNGTKRFDNPVLP  KRFDNPVLP  6        0.2014
5655.7    70.00  0.56     Sequence
             DRB3_0101   78      GTNGTKRFDNPVLPF  RFDNPVLPF  6        0.3947
698.5    20.00  0.44     Sequence
             DRB3_0101   79      TNGTKRFDNPVLPFN  RFDNPVLPF  5        0.4252
502.4    16.00  0.47     Sequence
             DRB3_0101   80      NGTKRFDNPVLPFND  RFDNPVLPF  4        0.4586
349.8    12.00  0.47     Sequence
             DRB3_0101   81      GTKRFDNPVLPFNDG  RFDNPVLPF  3        0.4301
476.6    15.00  0.49     Sequence
             DRB3_0101   82      TKRFDNPVLPFNDGV  RFDNPVLPF  2        0.3840
784.2    21.00  0.47     Sequence
             DRB3_0101   83      KRFDNPVLPFNDGVY  RFDNPVLPF  1        0.3377
1293.9    29.00  0.48     Sequence
             DRB3_0101   84      RFDNPVLPFNDGVYF  RFDNPVLPF  0        0.3137
1678.9    34.00  0.35     Sequence
             DRB3_0101   85      FDNPVLPFNDGVYFA  PFNDGVYFA  6        0.3219
1536.4    32.00  0.50     Sequence
             DRB3_0101   86      DNPVLPFNDGVYFAS  PFNDGVYFA  5        0.3507
1125.0    27.00  0.52     Sequence
             DRB3_0101   87      NPVLPFNDGVYFAST  PFNDGVYFA  4        0.3537
1089.4    26.00  0.54     Sequence
             DRB3_0101   88      PVLPFNDGVYFASTE  PFNDGVYFA  3        0.3451
1195.4    28.00  0.56     Sequence
             DRB3_0101   89      VLPFNDGVYFASTEK  PFNDGVYFA  2        0.3098
1750.6    35.00  0.56     Sequence
             DRB3_0101   90      LPFNDGVYFASTEKS  PFNDGVYFA  1        0.2913
2138.7    39.00  0.35     Sequence
             DRB3_0101   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.2602
2994.1    48.00  0.36     Sequence
             DRB3_0101   92      FNDGVYFASTEKSNI  VYFASTEKS  4        0.2729
2611.2    44.00  0.34     Sequence
             DRB3_0101   93      NDGVYFASTEKSNII  FASTEKSNI  5        0.3142
1668.7    34.00  0.32     Sequence
             DRB3_0101   94      DGVYFASTEKSNIIR  FASTEKSNI  4        0.3060
1824.5    36.00  0.34     Sequence
             DRB3_0101   95      GVYFASTEKSNIIRG  FASTEKSNI  3        0.2859
2266.6    41.00  0.36     Sequence
```

```
             DRB3_0101   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.2617
2945.5    47.00  0.28     Sequence
             DRB3_0101   97      YFASTEKSNIIRGWI  EKSNIIRGW  5        0.2271
4285.1    60.00  0.41     Sequence
             DRB3_0101   98      FASTEKSNIIRGWIF  EKSNIIRGW  4        0.2272
4276.9    60.00  0.50     Sequence
             DRB3_0101   99      ASTEKSNIIRGWIFG  EKSNIIRGW  3        0.2180
4728.3    65.00  0.50     Sequence
             DRB3_0101  100      STEKSNIIRGWIFGT  EKSNIIRGW  2        0.2330
4019.0    60.00  0.40     Sequence
             DRB3_0101  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5        0.2089
5214.1    65.00  0.39     Sequence
             DRB3_0101  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.1909
6336.7    70.00  0.49     Sequence
             DRB3_0101  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3        0.2128
4999.3    65.00  0.50     Sequence
             DRB3_0101  104      SNIIRGWIFGTTLDS  WIFGTTLDS  6        0.2604
2989.4    48.00  0.43     Sequence
             DRB3_0101  105      NIIRGWIFGTTLDSK  WIFGTTLDS  5        0.2485
3398.6    55.00  0.43     Sequence
             DRB3_0101  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.2400
3727.6    55.00  0.47     Sequence
             DRB3_0101  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3        0.2198
4635.2    65.00  0.48     Sequence
             DRB3_0101  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2        0.2088
5219.5    65.00  0.40     Sequence
             DRB3_0101  109      GWIFGTTLDSKTQSL  TTLDSKTQS  5        0.1959
6005.4    70.00  0.25     Sequence
             DRB3_0101  110      WIFGTTLDSKTQSLL  TTLDSKTQS  4        0.1743
7584.6    80.00  0.36     Sequence
             DRB3_0101  111      IFGTTLDSKTQSLLI  DSKTQSLLI  6        0.2448
3535.6    55.00  0.40     Sequence
             DRB3_0101  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5        0.2660
2811.6    46.00  0.45     Sequence
             DRB3_0101  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4        0.2592
3025.4    48.00  0.51     Sequence
             DRB3_0101  114      TTLDSKTQSLLIVNN  DSKTQSLLI  3        0.2394
3748.0    55.00  0.55     Sequence
             DRB3_0101  115      TLDSKTQSLLIVNNA  DSKTQSLLI  2        0.2113
5084.2    65.00  0.57     Sequence
             DRB3_0101  116      LDSKTQSLLIVNNAT  DSKTQSLLI  1        0.1925
6232.1    70.00  0.47     Sequence
             DRB3_0101  117      DSKTQSLLIVNNATN  DSKTQSLLI  0        0.1719
7782.5    80.00  0.22     Sequence
             DRB3_0101  118      SKTQSLLIVNNATNV  LIVNNATNV  6        0.4119
580.3    17.00  0.79     Sequence
             DRB3_0101  119      KTQSLLIVNNATNVV  LIVNNATNV  5        0.4948
236.5     9.50  0.65     Sequence         WB
             DRB3_0101  120      TQSLLIVNNATNVVI  LIVNNATNV  4        0.5442
138.6     6.50  0.65     Sequence         WB
             DRB3_0101  121      QSLLIVNNATNVVIK  LIVNNATNV  3        0.5276
166.0     7.50  0.65     Sequence         WB
             DRB3_0101  122      SLLIVNNATNVVIKV  LIVNNATNV  2        0.5116
197.2     8.00  0.55     Sequence         WB
             DRB3_0101  123      LLIVNNATNVVIKVC  LIVNNATNV  1        0.4516
377.5    13.00  0.46     Sequence
             DRB3_0101  124      LIVNNATNVVIKVCE  IVNNATNVV  1        0.3362
1316.4    29.00  0.43     Sequence
             DRB3_0101  125      IVNNATNVVIKVCEF  NATNVVIKV  3        0.2399
3731.3    55.00  0.40     Sequence
             DRB3_0101  126      VNNATNVVIKVCEFQ  NATNVVIKV  2        0.1919
6266.2    70.00  0.50     Sequence
             DRB3_0101  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.2630
2904.0    47.00  0.29     Sequence
             DRB3_0101  128      NATNVVIKVCEFQFC  IKVCEFQFC  6        0.3136
1681.0    34.00  0.47     Sequence
```

```
             DRB3_0101  129      ATNVVIKVCEFQFCN  IKVCEFQFC  5        0.3134
1684.6    34.00  0.53     Sequence
             DRB3_0101  130      TNVVIKVCEFQFCNY  IKVCEFQFC  4        0.3239
1502.3    32.00  0.52     Sequence
             DRB3_0101  131      NVVIKVCEFQFCNYP  IKVCEFQFC  3        0.3080
1784.6    35.00  0.54     Sequence
             DRB3_0101  132      VVIKVCEFQFCNYPF  IKVCEFQFC  2        0.3417
1240.4    28.00  0.37     Sequence
             DRB3_0101  133      VIKVCEFQFCNYPFL  FQFCNYPFL  6        0.4694
311.5    12.00  0.58     Sequence
             DRB3_0101  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.4367
443.7    15.00  0.63     Sequence
             DRB3_0101  135      KVCEFQFCNYPFLGV  FQFCNYPFL  4        0.4541
367.3    13.00  0.64     Sequence
             DRB3_0101  136      VCEFQFCNYPFLGVY  FQFCNYPFL  3        0.4449
406.0    14.00  0.65     Sequence
             DRB3_0101  137      CEFQFCNYPFLGVYY  FQFCNYPFL  2        0.4119
580.1    17.00  0.61     Sequence
             DRB3_0101  138      EFQFCNYPFLGVYYH  FQFCNYPFL  1        0.3763
852.7    22.00  0.56     Sequence
             DRB3_0101  139      FQFCNYPFLGVYYHK  FQFCNYPFL  0        0.2740
2579.0    44.00  0.35     Sequence
             DRB3_0101  140      QFCNYPFLGVYYHKN  FLGVYYHKN  6        0.2433
3594.8    55.00  0.50     Sequence
             DRB3_0101  141      FCNYPFLGVYYHKNN  FLGVYYHKN  5        0.2413
3674.5    55.00  0.57     Sequence
             DRB3_0101  142      CNYPFLGVYYHKNNK  FLGVYYHKN  4        0.2222
4517.0    60.00  0.60     Sequence
             DRB3_0101  143      NYPFLGVYYHKNNKS  FLGVYYHKN  3        0.2379
3809.3    55.00  0.54     Sequence
             DRB3_0101  144      YPFLGVYYHKNNKSW  YYHKNNKSW  6        0.3234
1510.8    32.00  0.40     Sequence
             DRB3_0101  145      PFLGVYYHKNNKSWM  YHKNNKSWM  6        0.3799
819.6    22.00  0.37     Sequence
             DRB3_0101  146      FLGVYYHKNNKSWME  YHKNNKSWM  5        0.4055
621.6    18.00  0.41     Sequence
             DRB3_0101  147      LGVYYHKNNKSWMES  YHKNNKSWM  4        0.4007
654.7    19.00  0.42     Sequence
             DRB3_0101  148      GVYYHKNNKSWMESE  YHKNNKSWM  3        0.3816
805.0    21.00  0.44     Sequence
             DRB3_0101  149      VYYHKNNKSWMESEF  YHKNNKSWM  2        0.3377
1295.2    29.00  0.43     Sequence
             DRB3_0101  150      YYHKNNKSWMESEFR  YHKNNKSWM  1        0.2597
3009.9    48.00  0.46     Sequence
             DRB3_0101  151      YHKNNKSWMESEFRV  SWMESEFRV  6        0.2188
4687.2    65.00  0.45     Sequence
             DRB3_0101  152      HKNNKSWMESEFRVY  WMESEFRVY  6        0.2673
2774.2    46.00  0.38     Sequence
             DRB3_0101  153      KNNKSWMESEFRVYS  WMESEFRVY  5        0.2746
2561.2    44.00  0.41     Sequence
             DRB3_0101  154      NNKSWMESEFRVYSS  WMESEFRVY  4        0.2706
2674.3    45.00  0.42     Sequence
             DRB3_0101  155      NKSWMESEFRVYSSA  WMESEFRVY  3        0.2615
2953.7    48.00  0.42     Sequence
             DRB3_0101  156      KSWMESEFRVYSSAN  WMESEFRVY  2        0.2578
3073.2    49.00  0.38     Sequence
             DRB3_0101  157      SWMESEFRVYSSANN  FRVYSSANN  6        0.2579
3071.0    49.00  0.43     Sequence
             DRB3_0101  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.2366
3866.8    55.00  0.50     Sequence
             DRB3_0101  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.2243
4414.5    60.00  0.49     Sequence
             DRB3_0101  160      ESEFRVYSSANNCTF  YSSANNCTF  6        0.4225
517.2    16.00  0.61     Sequence
             DRB3_0101  161      SEFRVYSSANNCTFE  YSSANNCTF  5        0.4524
374.3    13.00  0.62     Sequence
```

```
             DRB3_0101  162      EFRVYSSANNCTFEY  YSSANNCTF  4        0.4659
323.3    12.00  0.63     Sequence
             DRB3_0101  163      FRVYSSANNCTFEYV  YSSANNCTF  3        0.4882
254.1    10.00  0.65     Sequence
             DRB3_0101  164      RVYSSANNCTFEYVS  YSSANNCTF  2        0.4530
371.8    13.00  0.63     Sequence
             DRB3_0101  165      VYSSANNCTFEYVSQ  YSSANNCTF  1        0.3921
718.7    20.00  0.53     Sequence
             DRB3_0101  166      YSSANNCTFEYVSQP  SANNCTFEY  2        0.2970
2011.1    38.00  0.30     Sequence
             DRB3_0101  167      SSANNCTFEYVSQPF  CTFEYVSQP  5        0.2638
2880.1    47.00  0.26     Sequence
             DRB3_0101  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.3237
1506.4    32.00  0.49     Sequence
             DRB3_0101  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.3493
1141.6    27.00  0.50     Sequence
             DRB3_0101  170      NNCTFEYVSQPFLMD  FEYVSQPFL  4        0.4244
506.9    16.00  0.37     Sequence
             DRB3_0101  171      NCTFEYVSQPFLMDL  FEYVSQPFL  3        0.4378
438.4    14.00  0.34     Sequence
             DRB3_0101  172      CTFEYVSQPFLMDLE  YVSQPFLMD  4        0.4189
537.8    16.00  0.41     Sequence
             DRB3_0101  173      TFEYVSQPFLMDLEG  YVSQPFLMD  3        0.3941
703.0    20.00  0.43     Sequence
             DRB3_0101  174      FEYVSQPFLMDLEGK  YVSQPFLMD  2        0.4244
506.5    16.00  0.37     Sequence
             DRB3_0101  175      EYVSQPFLMDLEGKQ  FLMDLEGKQ  6        0.6547
41.9     2.50  0.90     Sequence         WB
             DRB3_0101  176      YVSQPFLMDLEGKQG  FLMDLEGKQ  5        0.6573
40.7     2.50  0.95     Sequence         WB
             DRB3_0101  177      VSQPFLMDLEGKQGN  FLMDLEGKQ  4        0.6548
41.9     2.50  0.97     Sequence         WB
             DRB3_0101  178      SQPFLMDLEGKQGNF  FLMDLEGKQ  3        0.6624
38.6     2.50  0.96     Sequence         WB
             DRB3_0101  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2        0.6263
57.0     3.50  0.95     Sequence         WB
             DRB3_0101  180      PFLMDLEGKQGNFKN  FLMDLEGKQ  1        0.5518
127.7     6.00  0.93     Sequence         WB
             DRB3_0101  181      FLMDLEGKQGNFKNL  FLMDLEGKQ  0        0.2986
1977.3    38.00  0.62     Sequence
             DRB3_0101  182      LMDLEGKQGNFKNLS  LEGKQGNFK  3        0.0643
24945.4   100.00  0.19     Sequence
             DRB3_0101  183      MDLEGKQGNFKNLSE  EGKQGNFKN  3        0.0575
26847.9   100.00  0.17     Sequence
             DRB3_0101  184      DLEGKQGNFKNLSEF  GNFKNLSEF  6        0.0991
17106.9    95.00  0.34     Sequence
             DRB3_0101  185      LEGKQGNFKNLSEFV  NFKNLSEFV  6        0.2106
5120.0    65.00  0.54     Sequence
             DRB3_0101  186      EGKQGNFKNLSEFVF  FKNLSEFVF  6        0.2928
2105.5    39.00  0.38     Sequence
             DRB3_0101  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5        0.2994
1959.5    37.00  0.37     Sequence
             DRB3_0101  188      KQGNFKNLSEFVFKN  FKNLSEFVF  4        0.3062
1820.6    36.00  0.37     Sequence
             DRB3_0101  189      QGNFKNLSEFVFKNI  FKNLSEFVF  3        0.3036
1871.6    36.00  0.38     Sequence
             DRB3_0101  190      GNFKNLSEFVFKNID  FKNLSEFVF  2        0.2779
2473.1    43.00  0.38     Sequence
             DRB3_0101  191      NFKNLSEFVFKNIDG  FKNLSEFVF  1        0.2305
4129.1    60.00  0.34     Sequence
             DRB3_0101  192      FKNLSEFVFKNIDGY  FVFKNIDGY  6        0.3660
953.5    24.00  0.63     Sequence
             DRB3_0101  193      KNLSEFVFKNIDGYF  FVFKNIDGY  5        0.4591
348.1    12.00  0.54     Sequence
             DRB3_0101  194      NLSEFVFKNIDGYFK  FVFKNIDGY  4        0.4789
281.0    11.00  0.47     Sequence
```

```
             DRB3_0101  195      LSEFVFKNIDGYFKI  FVFKNIDGY  3        0.5399
145.2     6.50  0.38     Sequence        WB
             DRB3_0101  196      SEFVFKNIDGYFKIY  KNIDGYFKI  5        0.5373
149.3     7.00  0.29     Sequence        WB
             DRB3_0101  197      EFVFKNIDGYFKIYS  KNIDGYFKI  4        0.5090
202.9     8.50  0.34     Sequence        WB
             DRB3_0101  198      FVFKNIDGYFKIYSK  KNIDGYFKI  3        0.4656
324.4    12.00  0.44     Sequence
             DRB3_0101  199      VFKNIDGYFKIYSKH  KNIDGYFKI  2        0.3629
985.4    24.00  0.56     Sequence
             DRB3_0101  200      FKNIDGYFKIYSKHT  KNIDGYFKI  1        0.3226
1524.3    32.00  0.46     Sequence
             DRB3_0101  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.2514
3293.9    55.00  0.41     Sequence
             DRB3_0101  202      NIDGYFKIYSKHTPI  YFKIYSKHT  4        0.2774
2485.6    43.00  0.40     Sequence
             DRB3_0101  203      IDGYFKIYSKHTPIN  YFKIYSKHT  3        0.2707
2673.3    45.00  0.37     Sequence
             DRB3_0101  204      DGYFKIYSKHTPINL  KIYSKHTPI  4        0.2721
2633.3    45.00  0.37     Sequence
             DRB3_0101  205      GYFKIYSKHTPINLV  KIYSKHTPI  3        0.2896
2179.3    40.00  0.31     Sequence
             DRB3_0101  206      YFKIYSKHTPINLVR  KIYSKHTPI  2        0.2504
3330.1    55.00  0.31     Sequence
             DRB3_0101  207      FKIYSKHTPINLVRD  SKHTPINLV  4        0.2450
3530.1    55.00  0.37     Sequence
             DRB3_0101  208      KIYSKHTPINLVRDL  SKHTPINLV  3        0.2316
4080.8    60.00  0.39     Sequence
             DRB3_0101  209      IYSKHTPINLVRDLP  SKHTPINLV  2        0.2111
5093.8    65.00  0.41     Sequence
             DRB3_0101  210      YSKHTPINLVRDLPQ  INLVRDLPQ  6        0.2168
4786.5    65.00  0.37     Sequence
             DRB3_0101  211      SKHTPINLVRDLPQG  LVRDLPQGX  7        0.2753
2543.2    44.00  0.28     Sequence
             DRB3_0101  212      KHTPINLVRDLPQGF  LVRDLPQGF  6        0.7884
9.9     0.50  0.92     Sequence        SB
             DRB3_0101  213      HTPINLVRDLPQGFS  LVRDLPQGF  5        0.8069
8.1     0.30  0.91     Sequence        SB
             DRB3_0101  214      TPINLVRDLPQGFSA  LVRDLPQGF  4        0.8054
8.2     0.30  0.92     Sequence        SB
             DRB3_0101  215      PINLVRDLPQGFSAL  LVRDLPQGF  3        0.8113
7.7     0.30  0.90     Sequence        SB
             DRB3_0101  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.7864
10.1     0.50  0.89     Sequence        SB
             DRB3_0101  217      NLVRDLPQGFSALEP  LVRDLPQGF  1        0.7115
22.7     1.30  0.87     Sequence        SB
             DRB3_0101  218      LVRDLPQGFSALEPL  LVRDLPQGF  0        0.5199
180.4     7.50  0.63     Sequence        WB
             DRB3_0101  219      VRDLPQGFSALEPLV  GFSALEPLV  6        0.1778
7302.2    75.00  0.34     Sequence
             DRB3_0101  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.2300
4151.2    60.00  0.43     Sequence
             DRB3_0101  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.2600
2999.9    48.00  0.40     Sequence
             DRB3_0101  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.2521
3268.3    50.00  0.39     Sequence
             DRB3_0101  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.2649
2846.1    47.00  0.35     Sequence
             DRB3_0101  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.2390
3767.2    55.00  0.35     Sequence
             DRB3_0101  225      GFSALEPLVDLPIGI  PLVDLPIGI  6        0.2846
2298.7    41.00  0.47     Sequence
             DRB3_0101  226      FSALEPLVDLPIGIN  PLVDLPIGI  5        0.2812
2386.8    42.00  0.56     Sequence
             DRB3_0101  227      SALEPLVDLPIGINI  PLVDLPIGI  4        0.2953
2047.5    38.00  0.63     Sequence
```

```
             DRB3_0101  228      ALEPLVDLPIGINIT  PLVDLPIGI  3        0.2865
2253.5    41.00  0.64     Sequence
             DRB3_0101  229      LEPLVDLPIGINITR  PLVDLPIGI  2        0.2462
3483.5    55.00  0.62     Sequence
             DRB3_0101  230      EPLVDLPIGINITRF  PLVDLPIGI  1        0.2750
2551.0    44.00  0.38     Sequence
             DRB3_0101  231      PLVDLPIGINITRFQ  IGINITRFQ  6        0.3255
1477.1    32.00  0.62     Sequence
             DRB3_0101  232      LVDLPIGINITRFQT  IGINITRFQ  5        0.3337
1351.2    30.00  0.69     Sequence
             DRB3_0101  233      VDLPIGINITRFQTL  IGINITRFQ  4        0.3530
1097.4    26.00  0.69     Sequence
             DRB3_0101  234      DLPIGINITRFQTLL  IGINITRFQ  3        0.3567
1053.5    25.00  0.70     Sequence
             DRB3_0101  235      LPIGINITRFQTLLA  IGINITRFQ  2        0.3576
1044.1    25.00  0.61     Sequence
             DRB3_0101  236      PIGINITRFQTLLAL  IGINITRFQ  1        0.3257
1473.7    31.00  0.44     Sequence
             DRB3_0101  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.2709
2667.3    45.00  0.31     Sequence
             DRB3_0101  238      GINITRFQTLLALHR  FQTLLALHR  6        0.2517
3283.6    50.00  0.29     Sequence
             DRB3_0101  239      INITRFQTLLALHRS  FQTLLALHR  5        0.2305
4130.9    60.00  0.36     Sequence
             DRB3_0101  240      NITRFQTLLALHRSY  TLLALHRSY  6        0.2904
2159.3    40.00  0.34     Sequence
             DRB3_0101  241      ITRFQTLLALHRSYL  TLLALHRSY  5        0.3011
1923.0    37.00  0.40     Sequence
             DRB3_0101  242      TRFQTLLALHRSYLT  TLLALHRSY  4        0.2878
2222.4    40.00  0.39     Sequence
             DRB3_0101  243      RFQTLLALHRSYLTP  TLLALHRSY  3        0.2680
2751.7    46.00  0.41     Sequence
             DRB3_0101  244      FQTLLALHRSYLTPG  TLLALHRSY  2        0.2421
3642.3    55.00  0.37     Sequence
             DRB3_0101  245      QTLLALHRSYLTPGD  TLLALHRSY  1        0.2365
3868.6    55.00  0.28     Sequence
             DRB3_0101  246      TLLALHRSYLTPGDS  LHRSYLTPG  4        0.1963
5979.9    70.00  0.25     Sequence
             DRB3_0101  247      LLALHRSYLTPGDSS  LHRSYLTPG  3        0.1637
8507.0    80.00  0.31     Sequence
             DRB3_0101  248      LALHRSYLTPGDSSS  LHRSYLTPG  2        0.1569
9156.5    85.00  0.26     Sequence
             DRB3_0101  249      ALHRSYLTPGDSSSG  YLTPGDSSS  5        0.1327
11895.1    90.00  0.35     Sequence
             DRB3_0101  250      LHRSYLTPGDSSSGW  YLTPGDSSS  4        0.1250
12931.7    90.00  0.45     Sequence
             DRB3_0101  251      HRSYLTPGDSSSGWT  YLTPGDSSS  3        0.1147
14460.1    95.00  0.49     Sequence
             DRB3_0101  252      RSYLTPGDSSSGWTA  YLTPGDSSS  2        0.1060
15876.1    95.00  0.44     Sequence
             DRB3_0101  253      SYLTPGDSSSGWTAG  YLTPGDSSS  1        0.0861
19702.5   100.00  0.38     Sequence
             DRB3_0101  254      YLTPGDSSSGWTAGA  GDSSSGWTA  4        0.0679
23981.5   100.00  0.25     Sequence
             DRB3_0101  255      LTPGDSSSGWTAGAA  GDSSSGWTA  3        0.0477
29856.6   100.00  0.38     Sequence
             DRB3_0101  256      TPGDSSSGWTAGAAA  GDSSSGWTA  2        0.0416
31895.0   100.00  0.40     Sequence
             DRB3_0101  257      PGDSSSGWTAGAAAY  GWTAGAAAY  6        0.0805
20931.6   100.00  0.63     Sequence
             DRB3_0101  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.2079
5275.8    65.00  0.67     Sequence
             DRB3_0101  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.2608
2975.4    48.00  0.53     Sequence
             DRB3_0101  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.2513
3295.5    55.00  0.47     Sequence
```

```
             DRB3_0101  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.2651
2841.0    47.00  0.44     Sequence
             DRB3_0101  262      SGWTAGAAAYYVGYL  WTAGAAAYY  2        0.2619
2938.7    47.00  0.37     Sequence
             DRB3_0101  263      GWTAGAAAYYVGYLQ  WTAGAAAYY  1        0.2283
4229.4    60.00  0.32     Sequence
             DRB3_0101  264      WTAGAAAYYVGYLQP  GAAAYYVGY  3        0.1724
7739.3    80.00  0.24     Sequence
             DRB3_0101  265      TAGAAAYYVGYLQPR  YYVGYLQPR  6        0.1767
7392.4    75.00  0.22     Sequence
             DRB3_0101  266      AGAAAYYVGYLQPRT  YVGYLQPRT  6        0.1921
6258.4    70.00  0.39     Sequence
             DRB3_0101  267      GAAAYYVGYLQPRTF  YVGYLQPRT  5        0.2228
4487.9    60.00  0.38     Sequence
             DRB3_0101  268      AAAYYVGYLQPRTFL  YVGYLQPRT  4        0.2416
3663.7    55.00  0.38     Sequence
             DRB3_0101  269      AAYYVGYLQPRTFLL  YLQPRTFLL  6        0.3867
762.2    21.00  0.50     Sequence
             DRB3_0101  270      AYYVGYLQPRTFLLK  YLQPRTFLL  5        0.4021
645.2    19.00  0.54     Sequence
             DRB3_0101  271      YYVGYLQPRTFLLKY  YLQPRTFLL  4        0.4078
606.1    18.00  0.58     Sequence
             DRB3_0101  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.3959
689.5    19.00  0.62     Sequence
             DRB3_0101  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.3731
883.0    23.00  0.62     Sequence
             DRB3_0101  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.3382
1287.5    29.00  0.56     Sequence
             DRB3_0101  275      YLQPRTFLLKYNENG  YLQPRTFLL  0        0.2513
3298.3    55.00  0.39     Sequence
             DRB3_0101  276      LQPRTFLLKYNENGT  FLLKYNENG  5        0.1739
7615.1    80.00  0.50     Sequence
             DRB3_0101  277      QPRTFLLKYNENGTI  LKYNENGTI  6        0.3693
919.9    23.00  0.63     Sequence
             DRB3_0101  278      PRTFLLKYNENGTIT  LKYNENGTI  5        0.3968
683.3    19.00  0.65     Sequence
             DRB3_0101  279      RTFLLKYNENGTITD  LKYNENGTI  4        0.4371
441.5    14.00  0.63     Sequence
             DRB3_0101  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.4288
483.0    15.00  0.64     Sequence
             DRB3_0101  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.4099
592.7    18.00  0.60     Sequence
             DRB3_0101  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.3734
879.4    23.00  0.52     Sequence
             DRB3_0101  283      LKYNENGTITDAVDC  YNENGTITD  2        0.2802
2411.7    42.00  0.45     Sequence
             DRB3_0101  284      KYNENGTITDAVDCA  TITDAVDCA  6        0.2768
2501.6    43.00  0.52     Sequence
             DRB3_0101  285      YNENGTITDAVDCAL  TITDAVDCA  5        0.3267
1458.9    31.00  0.62     Sequence
             DRB3_0101  286      NENGTITDAVDCALD  TITDAVDCA  4        0.3848
777.8    21.00  0.58     Sequence
             DRB3_0101  287      ENGTITDAVDCALDP  TITDAVDCA  3        0.3853
773.6    21.00  0.51     Sequence
             DRB3_0101  288      NGTITDAVDCALDPL  TITDAVDCA  2        0.4108
587.2    17.00  0.38     Sequence
             DRB3_0101  289      GTITDAVDCALDPLS  DAVDCALDP  4        0.3861
767.0    21.00  0.31     Sequence
             DRB3_0101  290      TITDAVDCALDPLSE  DAVDCALDP  3        0.3346
1338.1    30.00  0.36     Sequence
             DRB3_0101  291      ITDAVDCALDPLSET  CALDPLSET  6        0.3652
961.7    24.00  0.58     Sequence
             DRB3_0101  292      TDAVDCALDPLSETK  CALDPLSET  5        0.3474
1165.0    27.00  0.69     Sequence
             DRB3_0101  293      DAVDCALDPLSETKC  CALDPLSET  4        0.3167
1625.1    33.00  0.79     Sequence
```

```
             DRB3_0101  294      AVDCALDPLSETKCT  CALDPLSET  3        0.3053
1837.7    36.00  0.87     Sequence
             DRB3_0101  295      VDCALDPLSETKCTL  CALDPLSET  2        0.2519
3276.3    50.00  0.85     Sequence
             DRB3_0101  296      DCALDPLSETKCTLK  CALDPLSET  1        0.1939
6133.2    70.00  0.80     Sequence
             DRB3_0101  297      CALDPLSETKCTLKS  CALDPLSET  0        0.1182
13914.2    95.00  0.55     Sequence
             DRB3_0101  298      ALDPLSETKCTLKSF  ETKCTLKSF  6        0.1449
10426.8    85.00  0.56     Sequence
             DRB3_0101  299      LDPLSETKCTLKSFT  ETKCTLKSF  5        0.1507
9796.1    85.00  0.56     Sequence
             DRB3_0101  300      DPLSETKCTLKSFTV  ETKCTLKSF  4        0.1615
8712.3    80.00  0.48     Sequence
             DRB3_0101  301      PLSETKCTLKSFTVE  ETKCTLKSF  3        0.1610
8754.2    80.00  0.46     Sequence
             DRB3_0101  302      LSETKCTLKSFTVEK  ETKCTLKSF  2        0.1429
10651.4    85.00  0.43     Sequence
             DRB3_0101  303      SETKCTLKSFTVEKG  ETKCTLKSF  1        0.1364
11427.1    90.00  0.34     Sequence
             DRB3_0101  304      ETKCTLKSFTVEKGI  LKSFTVEKG  5        0.1239
13084.8    90.00  0.31     Sequence
             DRB3_0101  305      TKCTLKSFTVEKGIY  FTVEKGIYX  7        0.1824
6951.0    75.00  0.25     Sequence
             DRB3_0101  306      KCTLKSFTVEKGIYQ  FTVEKGIYQ  6        0.4020
645.7    19.00  0.90     Sequence
             DRB3_0101  307      CTLKSFTVEKGIYQT  FTVEKGIYQ  5        0.4371
441.5    14.00  0.92     Sequence
             DRB3_0101  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.4382
436.6    14.00  0.90     Sequence
             DRB3_0101  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.4338
457.9    15.00  0.93     Sequence
             DRB3_0101  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.3971
680.5    19.00  0.88     Sequence
             DRB3_0101  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.3228
1521.2    32.00  0.79     Sequence
             DRB3_0101  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.2689
2726.3    45.00  0.31     Sequence
             DRB3_0101  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.2816
2375.6    42.00  0.47     Sequence
             DRB3_0101  314      VEKGIYQTSNFRVQP  YQTSNFRVQ  5        0.2779
2472.4    43.00  0.40     Sequence
             DRB3_0101  315      EKGIYQTSNFRVQPT  YQTSNFRVQ  4        0.2758
2528.1    44.00  0.41     Sequence
             DRB3_0101  316      KGIYQTSNFRVQPTE  YQTSNFRVQ  3        0.2603
2990.8    48.00  0.44     Sequence
             DRB3_0101  317      GIYQTSNFRVQPTES  YQTSNFRVQ  2        0.2478
3423.2    55.00  0.29     Sequence
             DRB3_0101  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.5938
81.1     4.50  0.92     Sequence         WB
             DRB3_0101  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.6559
41.4     2.50  0.90     Sequence         WB
             DRB3_0101  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.6518
43.3     2.50  0.89     Sequence         WB
             DRB3_0101  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.6628
38.4     2.50  0.85     Sequence         WB
             DRB3_0101  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.6295
55.1     3.00  0.83     Sequence         WB
             DRB3_0101  323      NFRVQPTESIVRFPN  FRVQPTESI  1        0.5515
128.1     6.00  0.81     Sequence         WB
             DRB3_0101  324      FRVQPTESIVRFPNI  FRVQPTESI  0        0.3852
774.4    21.00  0.60     Sequence
             DRB3_0101  325      RVQPTESIVRFPNIT  VQPTESIVR  1        0.1721
7764.2    80.00  0.22     Sequence
             DRB3_0101  326      VQPTESIVRFPNITN  IVRFPNITN  6        0.1706
7898.1    80.00  0.22     Sequence
```

```
             DRB3_0101  327      QPTESIVRFPNITNL  VRFPNITNL  6        0.2195
4648.6    65.00  0.38     Sequence
             DRB3_0101  328      PTESIVRFPNITNLC  VRFPNITNL  5        0.2361
3885.4    55.00  0.37     Sequence
             DRB3_0101  329      TESIVRFPNITNLCP  VRFPNITNL  4        0.2182
4719.4    65.00  0.34     Sequence
             DRB3_0101  330      ESIVRFPNITNLCPF  VRFPNITNL  3        0.2352
3923.6    60.00  0.34     Sequence
             DRB3_0101  331      SIVRFPNITNLCPFG  RFPNITNLC  3        0.2186
4696.6    65.00  0.27     Sequence
             DRB3_0101  332      IVRFPNITNLCPFGE  RFPNITNLC  2        0.1906
6357.3    70.00  0.28     Sequence
             DRB3_0101  333      VRFPNITNLCPFGEV  RFPNITNLC  1        0.1766
7397.8    75.00  0.22     Sequence
             DRB3_0101  334      RFPNITNLCPFGEVF  TNLCPFGEV  5        0.1888
6482.3    75.00  0.25     Sequence
             DRB3_0101  335      FPNITNLCPFGEVFN  TNLCPFGEV  4        0.1814
7020.5    75.00  0.27     Sequence
             DRB3_0101  336      PNITNLCPFGEVFNA  TNLCPFGEV  3        0.1666
8241.2    80.00  0.25     Sequence
             DRB3_0101  337      NITNLCPFGEVFNAT  NLCPFGEVF  3        0.1382
11204.7    90.00  0.23     Sequence
             DRB3_0101  338      ITNLCPFGEVFNATR  NLCPFGEVF  2        0.1146
14465.6    95.00  0.27     Sequence
             DRB3_0101  339      TNLCPFGEVFNATRF  GEVFNATRF  6        0.1602
8832.9    80.00  0.41     Sequence
             DRB3_0101  340      NLCPFGEVFNATRFA  EVFNATRFA  6        0.2325
4039.7    60.00  0.38     Sequence
             DRB3_0101  341      LCPFGEVFNATRFAS  EVFNATRFA  5        0.2496
3358.1    55.00  0.40     Sequence
             DRB3_0101  342      CPFGEVFNATRFASV  EVFNATRFA  4        0.2879
2219.3    40.00  0.32     Sequence
             DRB3_0101  343      PFGEVFNATRFASVY  EVFNATRFA  3        0.3009
1927.3    37.00  0.34     Sequence
             DRB3_0101  344      FGEVFNATRFASVYA  FNATRFASV  4        0.2855
2276.1    41.00  0.27     Sequence
             DRB3_0101  345      GEVFNATRFASVYAW  FNATRFASV  3        0.2839
2317.0    41.00  0.25     Sequence
             DRB3_0101  346      EVFNATRFASVYAWN  TRFASVYAW  5        0.2650
2842.1    47.00  0.30     Sequence
             DRB3_0101  347      VFNATRFASVYAWNR  FASVYAWNR  6        0.2694
2709.3    45.00  0.41     Sequence
             DRB3_0101  348      FNATRFASVYAWNRK  FASVYAWNR  5        0.2538
3209.0    50.00  0.46     Sequence
             DRB3_0101  349      NATRFASVYAWNRKR  FASVYAWNR  4        0.2591
3029.9    48.00  0.42     Sequence
             DRB3_0101  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.2944
2067.5    39.00  0.38     Sequence
             DRB3_0101  351      TRFASVYAWNRKRIS  YAWNRKRIS  6        0.3186
1591.8    33.00  0.40     Sequence
             DRB3_0101  352      RFASVYAWNRKRISN  YAWNRKRIS  5        0.3076
1793.2    35.00  0.49     Sequence
             DRB3_0101  353      FASVYAWNRKRISNC  YAWNRKRIS  4        0.2895
2180.5    40.00  0.54     Sequence
             DRB3_0101  354      ASVYAWNRKRISNCV  YAWNRKRIS  3        0.2902
2164.0    40.00  0.54     Sequence
             DRB3_0101  355      SVYAWNRKRISNCVA  YAWNRKRIS  2        0.2579
3068.8    49.00  0.51     Sequence
             DRB3_0101  356      VYAWNRKRISNCVAD  YAWNRKRIS  1        0.2243
4414.3    60.00  0.44     Sequence
             DRB3_0101  357      YAWNRKRISNCVADY  RISNCVADY  6        0.2683
2742.5    46.00  0.35     Sequence
             DRB3_0101  358      AWNRKRISNCVADYS  ISNCVADYS  6        0.3187
1589.8    33.00  0.54     Sequence
             DRB3_0101  359      WNRKRISNCVADYSV  ISNCVADYS  5        0.3471
1169.7    27.00  0.61     Sequence
```

```
             DRB3_0101  360      NRKRISNCVADYSVL  ISNCVADYS  4        0.3783
834.2    22.00  0.57     Sequence
             DRB3_0101  361      RKRISNCVADYSVLY  CVADYSVLY  6        0.5851
89.1     4.50  0.71     Sequence         WB
             DRB3_0101  362      KRISNCVADYSVLYN  CVADYSVLY  5        0.5992
76.4     4.00  0.74     Sequence         WB
             DRB3_0101  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.5781
96.0     5.00  0.83     Sequence         WB
             DRB3_0101  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.5639
112.0     5.50  0.86     Sequence         WB
             DRB3_0101  365      SNCVADYSVLYNSAS  CVADYSVLY  2        0.5243
172.0     7.50  0.81     Sequence         WB
             DRB3_0101  366      NCVADYSVLYNSASF  CVADYSVLY  1        0.4945
237.3     9.50  0.69     Sequence         WB
             DRB3_0101  367      CVADYSVLYNSASFS  CVADYSVLY  0        0.4189
537.9    16.00  0.49     Sequence
             DRB3_0101  368      VADYSVLYNSASFST  VLYNSASFS  5        0.3322
1374.4    30.00  0.43     Sequence
             DRB3_0101  369      ADYSVLYNSASFSTF  VLYNSASFS  4        0.4162
554.0    17.00  0.26     Sequence
             DRB3_0101  370      DYSVLYNSASFSTFK  VLYNSASFS  3        0.4062
617.2    18.00  0.27     Sequence
             DRB3_0101  371      YSVLYNSASFSTFKC  VLYNSASFS  2        0.3957
690.8    19.00  0.29     Sequence
             DRB3_0101  372      SVLYNSASFSTFKCY  YNSASFSTF  3        0.3715
898.0    23.00  0.33     Sequence
             DRB3_0101  373      VLYNSASFSTFKCYG  YNSASFSTF  2        0.3050
1844.1    36.00  0.36     Sequence
             DRB3_0101  374      LYNSASFSTFKCYGV  YNSASFSTF  1        0.2471
3448.9    55.00  0.34     Sequence
             DRB3_0101  375      YNSASFSTFKCYGVS  FSTFKCYGV  5        0.1816
7012.3    75.00  0.27     Sequence
             DRB3_0101  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.1412
10852.8    90.00  0.32     Sequence
             DRB3_0101  377      SASFSTFKCYGVSPT  FKCYGVSPT  6        0.1579
9061.7    85.00  0.35     Sequence
             DRB3_0101  378      ASFSTFKCYGVSPTK  FKCYGVSPT  5        0.1385
11171.5    90.00  0.38     Sequence
             DRB3_0101  379      SFSTFKCYGVSPTKL  CYGVSPTKL  6        0.2297
4166.5    60.00  0.41     Sequence
             DRB3_0101  380      FSTFKCYGVSPTKLN  YGVSPTKLN  6        0.2828
2344.6    42.00  0.55     Sequence
             DRB3_0101  381      STFKCYGVSPTKLND  YGVSPTKLN  5        0.3064
1816.8    36.00  0.60     Sequence
             DRB3_0101  382      TFKCYGVSPTKLNDL  YGVSPTKLN  4        0.3261
1466.9    31.00  0.68     Sequence
             DRB3_0101  383      FKCYGVSPTKLNDLC  YGVSPTKLN  3        0.3027
1890.6    37.00  0.71     Sequence
             DRB3_0101  384      KCYGVSPTKLNDLCF  YGVSPTKLN  2        0.2725
2621.9    44.00  0.68     Sequence
             DRB3_0101  385      CYGVSPTKLNDLCFT  YGVSPTKLN  1        0.2242
4420.7    60.00  0.49     Sequence
             DRB3_0101  386      YGVSPTKLNDLCFTN  TKLNDLCFT  5        0.1940
6128.3    70.00  0.38     Sequence
             DRB3_0101  387      GVSPTKLNDLCFTNV  TKLNDLCFT  4        0.2157
4844.6    65.00  0.40     Sequence
             DRB3_0101  388      VSPTKLNDLCFTNVY  TKLNDLCFT  3        0.2586
3046.0    48.00  0.33     Sequence
             DRB3_0101  389      SPTKLNDLCFTNVYA  NDLCFTNVY  5        0.2549
3169.7    49.00  0.34     Sequence
             DRB3_0101  390      PTKLNDLCFTNVYAD  NDLCFTNVY  4        0.2654
2829.5    46.00  0.32     Sequence
             DRB3_0101  391      TKLNDLCFTNVYADS  NDLCFTNVY  3        0.2561
3128.7    49.00  0.30     Sequence
             DRB3_0101  392      KLNDLCFTNVYADSF  FTNVYADSF  6        0.4013
650.5    19.00  0.58     Sequence
```

```
             DRB3_0101  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.4267
494.4    16.00  0.65     Sequence
             DRB3_0101  394      NDLCFTNVYADSFVI  FTNVYADSF  4        0.4936
239.7     9.50  0.49     Sequence         WB
             DRB3_0101  395      DLCFTNVYADSFVIR  FTNVYADSF  3        0.5296
162.3     7.00  0.35     Sequence         WB
             DRB3_0101  396      LCFTNVYADSFVIRG  FTNVYADSF  2        0.5060
209.5     8.50  0.38     Sequence         WB
             DRB3_0101  397      CFTNVYADSFVIRGD  VYADSFVIR  4        0.4947
236.8     9.50  0.43     Sequence         WB
             DRB3_0101  398      FTNVYADSFVIRGDE  VYADSFVIR  3        0.4656
324.5    12.00  0.51     Sequence
             DRB3_0101  399      TNVYADSFVIRGDEV  VYADSFVIR  2        0.4348
452.7    15.00  0.46     Sequence
             DRB3_0101  400      NVYADSFVIRGDEVR  VYADSFVIR  1        0.3872
757.8    21.00  0.34     Sequence
             DRB3_0101  401      VYADSFVIRGDEVRQ  FVIRGDEVR  5        0.3511
1119.8    26.00  0.23     Sequence
             DRB3_0101  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.7156
21.7     1.20  0.89     Sequence         SB
             DRB3_0101  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.7340
17.8     1.00  0.90     Sequence         SB
             DRB3_0101  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.7153
21.8     1.20  0.92     Sequence         SB
             DRB3_0101  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.6958
26.9     1.60  0.93     Sequence         SB
             DRB3_0101  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.6455
46.3     3.00  0.92     Sequence         WB
             DRB3_0101  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.5721
102.5     5.00  0.90     Sequence         WB
             DRB3_0101  408      IRGDEVRQIAPGQTG  IRGDEVRQI  0        0.3513
1117.8    26.00  0.62     Sequence
             DRB3_0101  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.0727
22762.2   100.00  0.28     Sequence
             DRB3_0101  410      GDEVRQIAPGQTGTI  IAPGQTGTI  6        0.1239
13089.3    90.00  0.54     Sequence
             DRB3_0101  411      DEVRQIAPGQTGTIA  IAPGQTGTI  5        0.1254
12872.2    90.00  0.56     Sequence
             DRB3_0101  412      EVRQIAPGQTGTIAD  IAPGQTGTI  4        0.1402
10965.3    90.00  0.60     Sequence
             DRB3_0101  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.1407
10914.1    90.00  0.61     Sequence
             DRB3_0101  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.1278
12550.8    90.00  0.54     Sequence
             DRB3_0101  415      QIAPGQTGTIADYNY  TGTIADYNY  6        0.1383
11200.7    90.00  0.28     Sequence
             DRB3_0101  416      IAPGQTGTIADYNYK  TGTIADYNY  5        0.1394
11068.0    90.00  0.35     Sequence
             DRB3_0101  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.3667
945.5    24.00  0.77     Sequence
             DRB3_0101  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.4017
647.4    19.00  0.74     Sequence
             DRB3_0101  419      GQTGTIADYNYKLPD  TIADYNYKL  4        0.4350
451.6    15.00  0.75     Sequence
             DRB3_0101  420      QTGTIADYNYKLPDD  TIADYNYKL  3        0.4537
369.1    13.00  0.74     Sequence
             DRB3_0101  421      TGTIADYNYKLPDDF  TIADYNYKL  2        0.4470
396.7    13.00  0.62     Sequence
             DRB3_0101  422      GTIADYNYKLPDDFT  TIADYNYKL  1        0.4198
532.5    16.00  0.50     Sequence
             DRB3_0101  423      TIADYNYKLPDDFTG  TIADYNYKL  0        0.3458
1186.5    27.00  0.35     Sequence
             DRB3_0101  424      IADYNYKLPDDFTGC  YNYKLPDDF  3        0.2635
2890.3    47.00  0.38     Sequence
             DRB3_0101  425      ADYNYKLPDDFTGCV  YNYKLPDDF  2        0.2710
2663.1    45.00  0.28     Sequence
```

```
             DRB3_0101  426      DYNYKLPDDFTGCVI  KLPDDFTGC  4         0.2736
2589.5    44.00  0.20     Sequence
             DRB3_0101  427      YNYKLPDDFTGCVIA  KLPDDFTGC  3         0.2627
2914.9    47.00  0.25     Sequence
             DRB3_0101  428      NYKLPDDFTGCVIAW  KLPDDFTGC  2         0.2448
3538.6    55.00  0.25     Sequence
             DRB3_0101  429      YKLPDDFTGCVIAWN  LPDDFTGCV  2         0.2180
4727.9    65.00  0.21     Sequence
             DRB3_0101  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5         0.1808
7069.3    75.00  0.26     Sequence
             DRB3_0101  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4         0.1501
9856.0    85.00  0.32     Sequence
             DRB3_0101  432      PDDFTGCVIAWNSNN  CVIAWNSNN  6         0.1546
9381.8    85.00  0.34     Sequence
             DRB3_0101  433      DDFTGCVIAWNSNNL  VIAWNSNNL  6         0.2011
5676.4    70.00  0.33     Sequence
             DRB3_0101  434      DFTGCVIAWNSNNLD  IAWNSNNLD  6         0.2493
3367.6    55.00  0.34     Sequence
             DRB3_0101  435      FTGCVIAWNSNNLDS  IAWNSNNLD  5         0.2497
3353.3    55.00  0.38     Sequence
             DRB3_0101  436      TGCVIAWNSNNLDSK  IAWNSNNLD  4         0.2479
3421.2    55.00  0.35     Sequence
             DRB3_0101  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3         0.2580
3067.3    49.00  0.31     Sequence
             DRB3_0101  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2         0.2235
4451.7    60.00  0.31     Sequence
             DRB3_0101  439      VIAWNSNNLDSKVGG  WNSNNLDSK  3         0.1963
5979.2    70.00  0.34     Sequence
             DRB3_0101  440      IAWNSNNLDSKVGGN  WNSNNLDSK  2         0.1429
10656.4    85.00  0.38     Sequence
             DRB3_0101  441      AWNSNNLDSKVGGNY  WNSNNLDSK  1         0.1163
14199.6    95.00  0.32     Sequence
             DRB3_0101  442      WNSNNLDSKVGGNYN  LDSKVGGNY  5         0.1016
16654.7    95.00  0.27     Sequence
             DRB3_0101  443      NSNNLDSKVGGNYNY  LDSKVGGNY  4         0.1053
16007.5    95.00  0.31     Sequence
             DRB3_0101  444      SNNLDSKVGGNYNYL  LDSKVGGNY  3         0.1272
12630.8    90.00  0.31     Sequence
             DRB3_0101  445      NNLDSKVGGNYNYLY  VGGNYNYLY  6         0.2820
2364.5    42.00  0.75     Sequence
             DRB3_0101  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5         0.3156
1644.3    34.00  0.81     Sequence
             DRB3_0101  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4         0.3712
901.3    23.00  0.69     Sequence
             DRB3_0101  448      DSKVGGNYNYLYRLF  VGGNYNYLY  3         0.4125
576.2    17.00  0.56     Sequence
             DRB3_0101  449      SKVGGNYNYLYRLFR  VGGNYNYLY  2         0.4118
580.9    17.00  0.55     Sequence
             DRB3_0101  450      KVGGNYNYLYRLFRK  VGGNYNYLY  1         0.3820
801.4    21.00  0.49     Sequence
             DRB3_0101  451      VGGNYNYLYRLFRKS  GNYNYLYRL  2         0.3105
1737.7    35.00  0.26     Sequence
             DRB3_0101  452      GGNYNYLYRLFRKSN  GNYNYLYRL  1         0.2349
3937.1    60.00  0.28     Sequence
             DRB3_0101  453      GNYNYLYRLFRKSNL  YRLFRKSNL  6         0.2445
3549.4    55.00  0.28     Sequence
             DRB3_0101  454      NYNYLYRLFRKSNLK  YRLFRKSNL  5         0.2129
4996.7    65.00  0.35     Sequence
             DRB3_0101  455      YNYLYRLFRKSNLKP  YRLFRKSNL  4         0.1895
6437.0    75.00  0.37     Sequence
             DRB3_0101  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6         0.4180
543.1    17.00  0.71     Sequence
             DRB3_0101  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5         0.4477
393.7    13.00  0.76     Sequence
             DRB3_0101  458      LYRLFRKSNLKPFER  FRKSNLKPF  4         0.4473
395.6    13.00  0.77     Sequence
```

```
             DRB3_0101  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.4739
296.6    11.00  0.76     Sequence
             DRB3_0101  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.4344
454.5    15.00  0.72     Sequence
             DRB3_0101  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.3833
790.4    21.00  0.69     Sequence
             DRB3_0101  462      FRKSNLKPFERDIST  FRKSNLKPF  0        0.2948
2060.2    39.00  0.57     Sequence
             DRB3_0101  463      RKSNLKPFERDISTE  FERDISTEX  7        0.2142
4927.0    65.00  0.31     Sequence
             DRB3_0101  464      KSNLKPFERDISTEI  FERDISTEI  6        0.7302
18.5     1.00  0.95     Sequence        SB
             DRB3_0101  465      SNLKPFERDISTEIY  FERDISTEI  5        0.7801
10.8     0.50  0.94     Sequence        SB
             DRB3_0101  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.7779
11.1     0.50  0.95     Sequence        SB
             DRB3_0101  467      LKPFERDISTEIYQA  FERDISTEI  3        0.7759
11.3     0.60  0.95     Sequence        SB
             DRB3_0101  468      KPFERDISTEIYQAG  FERDISTEI  2        0.7482
15.3     0.80  0.92     Sequence        SB
             DRB3_0101  469      PFERDISTEIYQAGS  FERDISTEI  1        0.6695
35.7     2.50  0.88     Sequence        WB
             DRB3_0101  470      FERDISTEIYQAGST  FERDISTEI  0        0.4298
478.0    15.00  0.60     Sequence
             DRB3_0101  471      ERDISTEIYQAGSTP  ISTEIYQAG  3        0.1473
10157.1    85.00  0.34     Sequence
             DRB3_0101  472      RDISTEIYQAGSTPC  IYQAGSTPC  6        0.1529
9562.4    85.00  0.39     Sequence
             DRB3_0101  473      DISTEIYQAGSTPCN  YQAGSTPCN  6        0.1827
6926.2    75.00  0.48     Sequence
             DRB3_0101  474      ISTEIYQAGSTPCNG  YQAGSTPCN  5        0.1646
8419.6    80.00  0.58     Sequence
             DRB3_0101  475      STEIYQAGSTPCNGV  YQAGSTPCN  4        0.1789
7219.7    75.00  0.59     Sequence
             DRB3_0101  476      TEIYQAGSTPCNGVK  YQAGSTPCN  3        0.1645
8434.6    80.00  0.63     Sequence
             DRB3_0101  477      EIYQAGSTPCNGVKG  YQAGSTPCN  2        0.1421
10750.6    90.00  0.62     Sequence
             DRB3_0101  478      IYQAGSTPCNGVKGF  YQAGSTPCN  1        0.1155
14332.6    95.00  0.54     Sequence
             DRB3_0101  479      YQAGSTPCNGVKGFN  TPCNGVKGF  5        0.0801
21011.7   100.00  0.21     Sequence
             DRB3_0101  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.0779
21526.4   100.00  0.35     Sequence
             DRB3_0101  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.0878
19332.5   100.00  0.38     Sequence
             DRB3_0101  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.1103
15156.2    95.00  0.34     Sequence
             DRB3_0101  483      STPCNGVKGFNCYFP  CNGVKGFNC  3        0.1142
14526.5    95.00  0.26     Sequence
             DRB3_0101  484      TPCNGVKGFNCYFPL  KGFNCYFPL  6        0.1882
6523.8    75.00  0.51     Sequence
             DRB3_0101  485      PCNGVKGFNCYFPLQ  KGFNCYFPL  5        0.2069
5329.7    65.00  0.50     Sequence
             DRB3_0101  486      CNGVKGFNCYFPLQS  KGFNCYFPL  4        0.2055
5411.7    65.00  0.49     Sequence
             DRB3_0101  487      NGVKGFNCYFPLQSY  KGFNCYFPL  3        0.2286
4215.2    60.00  0.42     Sequence
             DRB3_0101  488      GVKGFNCYFPLQSYG  KGFNCYFPL  2        0.2295
4175.4    60.00  0.38     Sequence
             DRB3_0101  489      VKGFNCYFPLQSYGF  YFPLQSYGF  6        0.4377
438.7    14.00  0.71     Sequence
             DRB3_0101  490      KGFNCYFPLQSYGFQ  YFPLQSYGF  5        0.4406
425.3    14.00  0.74     Sequence
             DRB3_0101  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.4161
554.4    17.00  0.77     Sequence
```

```
             DRB3_0101  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.4064
615.6    18.00  0.75     Sequence
             DRB3_0101  493      NCYFPLQSYGFQPTY  YFPLQSYGF  2        0.3865
763.1    21.00  0.68     Sequence
             DRB3_0101  494      CYFPLQSYGFQPTYG  YFPLQSYGF  1        0.3401
1261.4    28.00  0.65     Sequence
             DRB3_0101  495      YFPLQSYGFQPTYGV  YGFQPTYGV  6        0.3504
1128.9    27.00  0.53     Sequence
             DRB3_0101  496      FPLQSYGFQPTYGVG  YGFQPTYGV  5        0.2957
2040.1    38.00  0.76     Sequence
             DRB3_0101  497      PLQSYGFQPTYGVGY  FQPTYGVGY  6        0.3853
773.1    21.00  0.44     Sequence
             DRB3_0101  498      LQSYGFQPTYGVGYQ  FQPTYGVGY  5        0.3796
822.4    22.00  0.52     Sequence
             DRB3_0101  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4        0.3512
1118.1    26.00  0.59     Sequence
             DRB3_0101  500      SYGFQPTYGVGYQPY  FQPTYGVGY  3        0.3497
1137.1    27.00  0.58     Sequence
             DRB3_0101  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.3050
1844.4    36.00  0.58     Sequence
             DRB3_0101  502      GFQPTYGVGYQPYRV  FQPTYGVGY  1        0.2888
2197.2    40.00  0.44     Sequence
             DRB3_0101  503      FQPTYGVGYQPYRVV  YGVGYQPYR  4        0.2677
2762.3    46.00  0.29     Sequence
             DRB3_0101  504      QPTYGVGYQPYRVVV  YGVGYQPYR  3        0.2592
3028.3    48.00  0.23     Sequence
             DRB3_0101  505      PTYGVGYQPYRVVVL  YQPYRVVVL  6        0.3270
1454.0    31.00  0.46     Sequence
             DRB3_0101  506      TYGVGYQPYRVVVLS  YQPYRVVVL  5        0.3003
1939.8    37.00  0.47     Sequence
             DRB3_0101  507      YGVGYQPYRVVVLSF  YQPYRVVVL  4        0.3539
1086.0    26.00  0.37     Sequence
             DRB3_0101  508      GVGYQPYRVVVLSFE  YRVVVLSFE  6        0.3773
843.4    22.00  0.43     Sequence
             DRB3_0101  509      VGYQPYRVVVLSFEL  YRVVVLSFE  5        0.3673
940.0    24.00  0.48     Sequence
             DRB3_0101  510      GYQPYRVVVLSFELL  YRVVVLSFE  4        0.3589
1028.8    25.00  0.50     Sequence
             DRB3_0101  511      YQPYRVVVLSFELLH  YRVVVLSFE  3        0.3251
1483.4    32.00  0.50     Sequence
             DRB3_0101  512      QPYRVVVLSFELLHA  YRVVVLSFE  2        0.2963
2026.6    38.00  0.38     Sequence
             DRB3_0101  513      PYRVVVLSFELLHAP  YRVVVLSFE  1        0.2577
3075.7    49.00  0.29     Sequence
             DRB3_0101  514      YRVVVLSFELLHAPA  LSFELLHAP  5        0.2216
4548.2    60.00  0.32     Sequence
             DRB3_0101  515      RVVVLSFELLHAPAT  LSFELLHAP  4        0.2182
4715.5    65.00  0.31     Sequence
             DRB3_0101  516      VVVLSFELLHAPATV  FELLHAPAT  5        0.2158
4840.5    65.00  0.30     Sequence
             DRB3_0101  517      VVLSFELLHAPATVC  LLHAPATVC  6        0.2755
2536.8    44.00  0.49     Sequence
             DRB3_0101  518      VLSFELLHAPATVCG  LLHAPATVC  5        0.2513
3295.4    55.00  0.59     Sequence
             DRB3_0101  519      LSFELLHAPATVCGP  LLHAPATVC  4        0.2250
4382.9    60.00  0.62     Sequence
             DRB3_0101  520      SFELLHAPATVCGPK  LLHAPATVC  3        0.1980
5871.0    70.00  0.65     Sequence
             DRB3_0101  521      FELLHAPATVCGPKK  LLHAPATVC  2        0.1636
8515.8    80.00  0.69     Sequence
             DRB3_0101  522      ELLHAPATVCGPKKS  LLHAPATVC  1        0.1345
11669.9    90.00  0.59     Sequence
             DRB3_0101  523      LLHAPATVCGPKKST  LLHAPATVC  0        0.0853
19869.9   100.00  0.34     Sequence
             DRB3_0101  524      LHAPATVCGPKKSTN  ATVCGPKKS  4        0.0501
29070.5   100.00  0.39     Sequence
```

```
             DRB3_0101  525      HAPATVCGPKKSTNL  ATVCGPKKS  3        0.0536
27996.6   100.00  0.38     Sequence
             DRB3_0101  526      APATVCGPKKSTNLV  ATVCGPKKS  2        0.0527
28284.0   100.00  0.31     Sequence
             DRB3_0101  527      PATVCGPKKSTNLVK  CGPKKSTNL  4        0.0469
30115.5   100.00  0.29     Sequence
             DRB3_0101  528      ATVCGPKKSTNLVKN  KKSTNLVKN  6        0.0492
29347.7   100.00  0.24     Sequence
             DRB3_0101  529      TVCGPKKSTNLVKNK  KKSTNLVKN  5        0.0461
30361.2   100.00  0.28     Sequence
             DRB3_0101  530      VCGPKKSTNLVKNKC  KKSTNLVKN  4        0.0453
30626.8   100.00  0.25     Sequence
             DRB3_0101  531      CGPKKSTNLVKNKCV  TNLVKNKCV  6        0.0694
23592.9   100.00  0.40     Sequence
             DRB3_0101  532      GPKKSTNLVKNKCVN  TNLVKNKCV  5        0.0864
19640.7   100.00  0.43     Sequence
             DRB3_0101  533      PKKSTNLVKNKCVNF  LVKNKCVNF  6        0.2040
5499.7    70.00  0.77     Sequence
             DRB3_0101  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.2133
4971.2    65.00  0.69     Sequence
             DRB3_0101  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.2569
3104.3    49.00  0.62     Sequence
             DRB3_0101  536      STNLVKNKCVNFNFN  LVKNKCVNF  3        0.2568
3106.4    49.00  0.58     Sequence
             DRB3_0101  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2        0.2360
3890.8    55.00  0.54     Sequence
             DRB3_0101  538      NLVKNKCVNFNFNGL  LVKNKCVNF  1        0.2299
4156.2    60.00  0.31     Sequence
             DRB3_0101  539      LVKNKCVNFNFNGLT  VNFNFNGLT  6        0.2250
4381.7    60.00  0.38     Sequence
             DRB3_0101  540      VKNKCVNFNFNGLTG  VNFNFNGLT  5        0.2192
4664.2    65.00  0.46     Sequence
             DRB3_0101  541      KNKCVNFNFNGLTGT  FNFNGLTGT  6        0.2381
3804.9    55.00  0.40     Sequence
             DRB3_0101  542      NKCVNFNFNGLTGTG  FNFNGLTGT  5        0.2077
5281.9    65.00  0.41     Sequence
             DRB3_0101  543      KCVNFNFNGLTGTGV  FNFNGLTGT  4        0.2194
4657.5    65.00  0.41     Sequence
             DRB3_0101  544      CVNFNFNGLTGTGVL  FNFNGLTGT  3        0.2079
5272.1    65.00  0.44     Sequence
             DRB3_0101  545      VNFNFNGLTGTGVLT  FNFNGLTGT  2        0.1909
6339.6    70.00  0.43     Sequence
             DRB3_0101  546      NFNFNGLTGTGVLTE  FNFNGLTGT  1        0.1425
10704.9    85.00  0.32     Sequence
             DRB3_0101  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.1094
15315.2    95.00  0.37     Sequence
             DRB3_0101  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.0861
19701.2   100.00  0.34     Sequence
             DRB3_0101  549      FNGLTGTGVLTESNK  LTGTGVLTE  3        0.0660
24475.1   100.00  0.26     Sequence
             DRB3_0101  550      NGLTGTGVLTESNKK  GVLTESNKK  6        0.0659
24517.0   100.00  0.37     Sequence
             DRB3_0101  551      GLTGTGVLTESNKKF  VLTESNKKF  6        0.3226
1524.6    32.00  0.75     Sequence
             DRB3_0101  552      LTGTGVLTESNKKFL  VLTESNKKF  5        0.3732
881.9    23.00  0.73     Sequence
             DRB3_0101  553      TGTGVLTESNKKFLP  VLTESNKKF  4        0.3548
1075.4    26.00  0.73     Sequence
             DRB3_0101  554      GTGVLTESNKKFLPF  VLTESNKKF  3        0.3851
775.4    21.00  0.66     Sequence
             DRB3_0101  555      TGVLTESNKKFLPFQ  VLTESNKKF  2        0.3446
1201.5    28.00  0.61     Sequence
             DRB3_0101  556      GVLTESNKKFLPFQQ  VLTESNKKF  1        0.3027
1891.5    37.00  0.57     Sequence
             DRB3_0101  557      VLTESNKKFLPFQQF  VLTESNKKF  0        0.2295
4173.0    60.00  0.34     Sequence
```

```
             DRB3_0101  558      LTESNKKFLPFQQFG  KKFLPFQQF  5        0.1739
7621.1    80.00  0.25     Sequence
             DRB3_0101  559      TESNKKFLPFQQFGR  FLPFQQFGR  6        0.2125
5016.4    65.00  0.50     Sequence
             DRB3_0101  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5        0.2397
3739.1    55.00  0.54     Sequence
             DRB3_0101  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4        0.2612
2962.0    48.00  0.51     Sequence
             DRB3_0101  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.2809
2394.4    42.00  0.43     Sequence
             DRB3_0101  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.2779
2471.6    43.00  0.37     Sequence
             DRB3_0101  564      KFLPFQQFGRDIADT  FGRDIADTX  7        0.3136
1680.8    34.00  0.28     Sequence
             DRB3_0101  565      FLPFQQFGRDIADTT  FGRDIADTT  6        0.5908
83.7     4.50  0.91     Sequence         WB
             DRB3_0101  566      LPFQQFGRDIADTTD  FGRDIADTT  5        0.6419
48.2     3.00  0.94     Sequence         WB
             DRB3_0101  567      PFQQFGRDIADTTDA  FGRDIADTT  4        0.6406
48.9     3.00  0.95     Sequence         WB
             DRB3_0101  568      FQQFGRDIADTTDAV  FGRDIADTT  3        0.6502
44.0     2.50  0.88     Sequence         WB
             DRB3_0101  569      QQFGRDIADTTDAVR  FGRDIADTT  2        0.6183
62.2     3.50  0.87     Sequence         WB
             DRB3_0101  570      QFGRDIADTTDAVRD  FGRDIADTT  1        0.5543
124.3     6.00  0.71     Sequence         WB
             DRB3_0101  571      FGRDIADTTDAVRDP  DIADTTDAV  3        0.3864
764.5    21.00  0.54     Sequence
             DRB3_0101  572      GRDIADTTDAVRDPQ  DIADTTDAV  2        0.2953
2049.1    39.00  0.75     Sequence
             DRB3_0101  573      RDIADTTDAVRDPQT  DIADTTDAV  1        0.2375
3828.6    55.00  0.61     Sequence
             DRB3_0101  574      DIADTTDAVRDPQTL  DIADTTDAV  0        0.1822
6961.2    75.00  0.37     Sequence
             DRB3_0101  575      IADTTDAVRDPQTLE  AVRDPQTLE  6        0.2042
5485.8    70.00  0.62     Sequence
             DRB3_0101  576      ADTTDAVRDPQTLEI  AVRDPQTLE  5        0.2605
2983.4    48.00  0.69     Sequence
             DRB3_0101  577      DTTDAVRDPQTLEIL  AVRDPQTLE  4        0.3038
1867.3    36.00  0.67     Sequence
             DRB3_0101  578      TTDAVRDPQTLEILD  AVRDPQTLE  3        0.3346
1338.6    30.00  0.66     Sequence
             DRB3_0101  579      TDAVRDPQTLEILDI  AVRDPQTLE  2        0.3224
1527.4    32.00  0.57     Sequence
             DRB3_0101  580      DAVRDPQTLEILDIT  AVRDPQTLE  1        0.3002
1942.0    37.00  0.41     Sequence
             DRB3_0101  581      AVRDPQTLEILDITP  QTLEILDIT  5        0.2535
3221.0    50.00  0.26     Sequence
             DRB3_0101  582      VRDPQTLEILDITPC  QTLEILDIT  4        0.2440
3566.0    55.00  0.34     Sequence
             DRB3_0101  583      RDPQTLEILDITPCS  EILDITPCS  6        0.3178
1604.9    33.00  0.62     Sequence
             DRB3_0101  584      DPQTLEILDITPCSF  EILDITPCS  5        0.3861
766.5    21.00  0.52     Sequence
             DRB3_0101  585      PQTLEILDITPCSFG  EILDITPCS  4        0.3635
979.5    24.00  0.51     Sequence
             DRB3_0101  586      QTLEILDITPCSFGG  EILDITPCS  3        0.3388
1279.1    29.00  0.50     Sequence
             DRB3_0101  587      TLEILDITPCSFGGV  EILDITPCS  2        0.3372
1301.1    29.00  0.43     Sequence
             DRB3_0101  588      LEILDITPCSFGGVS  EILDITPCS  1        0.2903
2162.4    40.00  0.38     Sequence
             DRB3_0101  589      EILDITPCSFGGVSV  ITPCSFGGV  4        0.2250
4384.2    60.00  0.22     Sequence
             DRB3_0101  590      ILDITPCSFGGVSVI  CSFGGVSVI  6        0.2097
5170.0    65.00  0.41     Sequence
```

```
             DRB3_0101  591      LDITPCSFGGVSVIT  CSFGGVSVI  5        0.1945
6095.9    70.00  0.47     Sequence
             DRB3_0101  592      DITPCSFGGVSVITP  CSFGGVSVI  4        0.1905
6367.3    75.00  0.40     Sequence
             DRB3_0101  593      ITPCSFGGVSVITPG  CSFGGVSVI  3        0.1745
7567.5    80.00  0.41     Sequence
             DRB3_0101  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.1521
9640.2    85.00  0.38     Sequence
             DRB3_0101  595      PCSFGGVSVITPGTN  FGGVSVITP  3        0.1344
11674.1    90.00  0.40     Sequence
             DRB3_0101  596      CSFGGVSVITPGTNT  FGGVSVITP  2        0.1255
12861.6    90.00  0.32     Sequence
             DRB3_0101  597      SFGGVSVITPGTNTS  SVITPGTNT  5        0.1156
14319.8    95.00  0.30     Sequence
             DRB3_0101  598      FGGVSVITPGTNTSN  SVITPGTNT  4        0.1010
16760.1    95.00  0.34     Sequence
             DRB3_0101  599      GGVSVITPGTNTSNQ  SVITPGTNT  3        0.0931
18267.5   100.00  0.32     Sequence
             DRB3_0101  600      GVSVITPGTNTSNQV  ITPGTNTSN  4        0.0904
18805.4   100.00  0.30     Sequence
             DRB3_0101  601      VSVITPGTNTSNQVA  ITPGTNTSN  3        0.0793
21205.1   100.00  0.31     Sequence
             DRB3_0101  602      SVITPGTNTSNQVAV  ITPGTNTSN  2        0.0710
23190.3   100.00  0.23     Sequence
             DRB3_0101  603      VITPGTNTSNQVAVL  NTSNQVAVL  6        0.0944
18011.0   100.00  0.34     Sequence
             DRB3_0101  604      ITPGTNTSNQVAVLY  TSNQVAVLY  6        0.1256
12848.6    90.00  0.43     Sequence
             DRB3_0101  605      TPGTNTSNQVAVLYQ  TSNQVAVLY  5        0.1365
11422.4    90.00  0.41     Sequence
             DRB3_0101  606      PGTNTSNQVAVLYQG  TSNQVAVLY  4        0.1313
12079.8    90.00  0.37     Sequence
             DRB3_0101  607      GTNTSNQVAVLYQGV  QVAVLYQGV  6        0.1614
8721.3    80.00  0.28     Sequence
             DRB3_0101  608      TNTSNQVAVLYQGVN  QVAVLYQGV  5        0.1510
9759.4    85.00  0.30     Sequence
             DRB3_0101  609      NTSNQVAVLYQGVNC  QVAVLYQGV  4        0.1442
10506.6    85.00  0.30     Sequence
             DRB3_0101  610      TSNQVAVLYQGVNCT  VLYQGVNCT  6        0.1518
9672.2    85.00  0.29     Sequence
             DRB3_0101  611      SNQVAVLYQGVNCTE  VLYQGVNCT  5        0.1470
10185.6    85.00  0.38     Sequence
             DRB3_0101  612      NQVAVLYQGVNCTEV  YQGVNCTEV  6        0.2072
5312.5    65.00  0.47     Sequence
             DRB3_0101  613      QVAVLYQGVNCTEVP  YQGVNCTEV  5        0.1990
5805.3    70.00  0.50     Sequence
             DRB3_0101  614      VAVLYQGVNCTEVPV  YQGVNCTEV  4        0.2136
4956.1    65.00  0.47     Sequence
             DRB3_0101  615      AVLYQGVNCTEVPVA  YQGVNCTEV  3        0.2019
5624.3    70.00  0.50     Sequence
             DRB3_0101  616      VLYQGVNCTEVPVAI  YQGVNCTEV  2        0.1993
5789.9    70.00  0.39     Sequence
             DRB3_0101  617      LYQGVNCTEVPVAIH  YQGVNCTEV  1        0.1793
7183.4    75.00  0.26     Sequence
             DRB3_0101  618      YQGVNCTEVPVAIHA  NCTEVPVAI  4        0.1413
10835.5    90.00  0.29     Sequence
             DRB3_0101  619      QGVNCTEVPVAIHAD  NCTEVPVAI  3        0.1399
11008.7    90.00  0.32     Sequence
             DRB3_0101  620      GVNCTEVPVAIHADQ  NCTEVPVAI  2        0.1252
12898.3    90.00  0.31     Sequence
             DRB3_0101  621      VNCTEVPVAIHADQL  PVAIHADQL  6        0.1410
10878.1    90.00  0.36     Sequence
             DRB3_0101  622      NCTEVPVAIHADQLT  PVAIHADQL  5        0.1552
9325.7    85.00  0.32     Sequence
             DRB3_0101  623      CTEVPVAIHADQLTP  VAIHADQLT  5        0.1892
6452.8    75.00  0.27     Sequence
```

```
             DRB3_0101  624      TEVPVAIHADQLTPT  IHADQLTPT  6        0.4404
426.0    14.00  0.88     Sequence
             DRB3_0101  625      EVPVAIHADQLTPTW  IHADQLTPT  5        0.4871
257.1    10.00  0.91     Sequence
             DRB3_0101  626      VPVAIHADQLTPTWR  IHADQLTPT  4        0.4778
284.3    11.00  0.93     Sequence
             DRB3_0101  627      PVAIHADQLTPTWRV  IHADQLTPT  3        0.5418
142.3     6.50  0.65     Sequence         WB
             DRB3_0101  628      VAIHADQLTPTWRVY  IHADQLTPT  2        0.5260
168.8     7.50  0.50     Sequence         WB
             DRB3_0101  629      AIHADQLTPTWRVYS  DQLTPTWRV  4        0.4787
281.6    11.00  0.44     Sequence
             DRB3_0101  630      IHADQLTPTWRVYST  DQLTPTWRV  3        0.4140
567.2    17.00  0.59     Sequence
             DRB3_0101  631      HADQLTPTWRVYSTG  DQLTPTWRV  2        0.3717
896.5    23.00  0.67     Sequence
             DRB3_0101  632      ADQLTPTWRVYSTGS  DQLTPTWRV  1        0.3542
1082.7    26.00  0.57     Sequence
             DRB3_0101  633      DQLTPTWRVYSTGSN  DQLTPTWRV  0        0.3072
1800.3    36.00  0.39     Sequence
             DRB3_0101  634      QLTPTWRVYSTGSNV  WRVYSTGSN  5        0.2623
2926.3    47.00  0.43     Sequence
             DRB3_0101  635      LTPTWRVYSTGSNVF  WRVYSTGSN  4        0.3287
1426.6    31.00  0.34     Sequence
             DRB3_0101  636      TPTWRVYSTGSNVFQ  WRVYSTGSN  3        0.3292
1418.6    31.00  0.31     Sequence
             DRB3_0101  637      PTWRVYSTGSNVFQT  WRVYSTGSN  2        0.3184
1595.1    33.00  0.25     Sequence
             DRB3_0101  638      TWRVYSTGSNVFQTR  YSTGSNVFQ  4        0.2856
2274.2    41.00  0.20     Sequence
             DRB3_0101  639      WRVYSTGSNVFQTRA  YSTGSNVFQ  3        0.2435
3589.1    55.00  0.31     Sequence
             DRB3_0101  640      RVYSTGSNVFQTRAG  YSTGSNVFQ  2        0.2121
5039.6    65.00  0.34     Sequence
             DRB3_0101  641      VYSTGSNVFQTRAGC  YSTGSNVFQ  1        0.1513
9731.1    85.00  0.35     Sequence
             DRB3_0101  642      YSTGSNVFQTRAGCL  VFQTRAGCL  6        0.1453
10376.8    85.00  0.47     Sequence
             DRB3_0101  643      STGSNVFQTRAGCLI  FQTRAGCLI  6        0.2697
2701.9    45.00  0.56     Sequence
             DRB3_0101  644      TGSNVFQTRAGCLIG  FQTRAGCLI  5        0.2652
2836.3    47.00  0.55     Sequence
             DRB3_0101  645      GSNVFQTRAGCLIGA  FQTRAGCLI  4        0.2676
2765.3    46.00  0.55     Sequence
             DRB3_0101  646      SNVFQTRAGCLIGAE  FQTRAGCLI  3        0.2550
3169.3    49.00  0.56     Sequence
             DRB3_0101  647      NVFQTRAGCLIGAEY  FQTRAGCLI  2        0.2325
4041.0    60.00  0.53     Sequence
             DRB3_0101  648      VFQTRAGCLIGAEYV  FQTRAGCLI  1        0.2107
5117.6    65.00  0.46     Sequence
             DRB3_0101  649      FQTRAGCLIGAEYVN  FQTRAGCLI  0        0.1591
8937.4    85.00  0.28     Sequence
             DRB3_0101  650      QTRAGCLIGAEYVNN  LIGAEYVNN  6        0.1500
9866.2    85.00  0.43     Sequence
             DRB3_0101  651      TRAGCLIGAEYVNNS  IGAEYVNNS  6        0.1855
6722.2    75.00  0.46     Sequence
             DRB3_0101  652      RAGCLIGAEYVNNSY  IGAEYVNNS  5        0.2124
5024.3    65.00  0.47     Sequence
             DRB3_0101  653      AGCLIGAEYVNNSYE  IGAEYVNNS  4        0.2131
4985.4    65.00  0.47     Sequence
             DRB3_0101  654      GCLIGAEYVNNSYEC  EYVNNSYEC  6        0.3071
1802.0    36.00  0.32     Sequence
             DRB3_0101  655      CLIGAEYVNNSYECD  YVNNSYECD  6        0.4478
393.1    13.00  0.63     Sequence
             DRB3_0101  656      LIGAEYVNNSYECDI  YVNNSYECD  5        0.5030
216.4     9.00  0.67     Sequence         WB
```

```
             DRB3_0101  657      IGAEYVNNSYECDIP  YVNNSYECD  4        0.4823
270.7    11.00  0.70     Sequence
             DRB3_0101  658      GAEYVNNSYECDIPI  YVNNSYECD  3        0.5024
217.8     9.00  0.67     Sequence         WB
             DRB3_0101  659      AEYVNNSYECDIPIG  YVNNSYECD  2        0.4911
246.3     9.50  0.52     Sequence         WB
             DRB3_0101  660      EYVNNSYECDIPIGA  YECDIPIGA  6        0.5344
154.1     7.00  0.55     Sequence         WB
             DRB3_0101  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.4736
297.6    11.00  0.71     Sequence
             DRB3_0101  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.4732
298.8    11.00  0.81     Sequence
             DRB3_0101  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.4498
384.9    13.00  0.83     Sequence
             DRB3_0101  664      NSYECDIPIGAGICA  YECDIPIGA  2        0.4013
650.7    19.00  0.85     Sequence
             DRB3_0101  665      SYECDIPIGAGICAS  YECDIPIGA  1        0.3114
1720.0    35.00  0.85     Sequence
             DRB3_0101  666      YECDIPIGAGICASY  YECDIPIGA  0        0.1750
7529.3    80.00  0.45     Sequence
             DRB3_0101  667      ECDIPIGAGICASYQ  IGAGICASY  5        0.1009
16782.7    95.00  0.34     Sequence
             DRB3_0101  668      CDIPIGAGICASYQT  AGICASYQT  6        0.1272
12620.8    90.00  0.41     Sequence
             DRB3_0101  669      DIPIGAGICASYQTQ  AGICASYQT  5        0.1298
12279.2    90.00  0.44     Sequence
             DRB3_0101  670      IPIGAGICASYQTQT  AGICASYQT  4        0.1449
10426.9    85.00  0.35     Sequence
             DRB3_0101  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.1530
9554.9    85.00  0.35     Sequence
             DRB3_0101  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.1387
11146.9    90.00  0.39     Sequence
             DRB3_0101  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.1235
13148.1    90.00  0.38     Sequence
             DRB3_0101  674      AGICASYQTQTNSPR  YQTQTNSPR  6        0.1238
13093.7    90.00  0.38     Sequence
             DRB3_0101  675      GICASYQTQTNSPRR  YQTQTNSPR  5        0.1216
13417.1    95.00  0.47     Sequence
             DRB3_0101  676      ICASYQTQTNSPRRA  YQTQTNSPR  4        0.1249
12938.7    90.00  0.46     Sequence
             DRB3_0101  677      CASYQTQTNSPRRAR  YQTQTNSPR  3        0.1175
14022.1    95.00  0.44     Sequence
             DRB3_0101  678      ASYQTQTNSPRRARS  YQTQTNSPR  2        0.1190
13790.5    95.00  0.46     Sequence
             DRB3_0101  679      SYQTQTNSPRRARSV  TQTNSPRRA  3        0.1206
13567.3    95.00  0.29     Sequence
             DRB3_0101  680      YQTQTNSPRRARSVA  NSPRRARSV  5        0.1031
16395.1    95.00  0.26     Sequence
             DRB3_0101  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.1191
13788.3    95.00  0.47     Sequence
             DRB3_0101  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.1226
13274.5    90.00  0.46     Sequence
             DRB3_0101  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.1292
12360.0    90.00  0.40     Sequence
             DRB3_0101  684      TNSPRRARSVASQSI  ARSVASQSI  6        0.2573
3088.7    49.00  0.53     Sequence
             DRB3_0101  685      NSPRRARSVASQSII  ARSVASQSI  5        0.2845
2303.0    41.00  0.52     Sequence
             DRB3_0101  686      SPRRARSVASQSIIA  ARSVASQSI  4        0.2782
2464.6    43.00  0.52     Sequence
             DRB3_0101  687      PRRARSVASQSIIAY  ARSVASQSI  3        0.3007
1931.8    37.00  0.43     Sequence
             DRB3_0101  688      RRARSVASQSIIAYT  ARSVASQSI  2        0.2811
2387.8    42.00  0.37     Sequence
             DRB3_0101  689      RARSVASQSIIAYTM  VASQSIIAY  4        0.2511
3303.1    55.00  0.41     Sequence
```

```
             DRB3_0101  690      ARSVASQSIIAYTMS  VASQSIIAY  3        0.2106
5123.4    65.00  0.48     Sequence
             DRB3_0101  691      RSVASQSIIAYTMSL  VASQSIIAY  2        0.2259
4341.5    60.00  0.28     Sequence
             DRB3_0101  692      SVASQSIIAYTMSLG  SIIAYTMSL  5        0.2021
5615.0    70.00  0.31     Sequence
             DRB3_0101  693      VASQSIIAYTMSLGA  SIIAYTMSL  4        0.2004
5717.8    70.00  0.28     Sequence
             DRB3_0101  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.1929
6204.6    70.00  0.31     Sequence
             DRB3_0101  695      SQSIIAYTMSLGAEN  YTMSLGAEN  6        0.2158
4839.4    65.00  0.47     Sequence
             DRB3_0101  696      QSIIAYTMSLGAENS  YTMSLGAEN  5        0.2130
4988.1    65.00  0.56     Sequence
             DRB3_0101  697      SIIAYTMSLGAENSV  YTMSLGAEN  4        0.2317
4076.2    60.00  0.64     Sequence
             DRB3_0101  698      IIAYTMSLGAENSVA  YTMSLGAEN  3        0.2260
4332.9    60.00  0.62     Sequence
             DRB3_0101  699      IAYTMSLGAENSVAY  LGAENSVAY  6        0.3565
1056.7    25.00  0.70     Sequence
             DRB3_0101  700      AYTMSLGAENSVAYS  LGAENSVAY  5        0.3609
1007.2    25.00  0.79     Sequence
             DRB3_0101  701      YTMSLGAENSVAYSN  LGAENSVAY  4        0.3511
1119.8    26.00  0.89     Sequence
             DRB3_0101  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.3443
1205.4    28.00  0.86     Sequence
             DRB3_0101  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.3097
1752.9    35.00  0.81     Sequence
             DRB3_0101  704      SLGAENSVAYSNNSI  LGAENSVAY  1        0.2736
2589.7    44.00  0.62     Sequence
             DRB3_0101  705      LGAENSVAYSNNSIA  LGAENSVAY  0        0.2203
4611.5    65.00  0.30     Sequence
             DRB3_0101  706      GAENSVAYSNNSIAI  AYSNNSIAI  6        0.3376
1295.4    29.00  0.52     Sequence
             DRB3_0101  707      AENSVAYSNNSIAIP  AYSNNSIAI  5        0.3619
996.3    25.00  0.46     Sequence
             DRB3_0101  708      ENSVAYSNNSIAIPT  AYSNNSIAI  4        0.3687
926.0    23.00  0.49     Sequence
             DRB3_0101  709      NSVAYSNNSIAIPTN  AYSNNSIAI  3        0.3631
984.0    24.00  0.52     Sequence
             DRB3_0101  710      SVAYSNNSIAIPTNF  YSNNSIAIP  3        0.3625
989.9    24.00  0.39     Sequence
             DRB3_0101  711      VAYSNNSIAIPTNFT  YSNNSIAIP  2        0.3201
1566.0    33.00  0.36     Sequence
             DRB3_0101  712      AYSNNSIAIPTNFTI  YSNNSIAIP  1        0.2666
2795.5    46.00  0.30     Sequence
             DRB3_0101  713      YSNNSIAIPTNFTIS  IAIPTNFTI  5        0.2220
4528.8    60.00  0.37     Sequence
             DRB3_0101  714      SNNSIAIPTNFTISV  IAIPTNFTI  4        0.2559
3135.7    49.00  0.31     Sequence
             DRB3_0101  715      NNSIAIPTNFTISVT  IAIPTNFTI  3        0.2539
3204.9    50.00  0.30     Sequence
             DRB3_0101  716      NSIAIPTNFTISVTT  IPTNFTISV  4        0.2326
4037.4    60.00  0.34     Sequence
             DRB3_0101  717      SIAIPTNFTISVTTE  IPTNFTISV  3        0.2479
3420.2    55.00  0.35     Sequence
             DRB3_0101  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.5601
116.7     5.50  0.89     Sequence          WB
             DRB3_0101  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.6146
64.7     3.50  0.84     Sequence          WB
             DRB3_0101  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.5968
78.5     4.00  0.82     Sequence          WB
             DRB3_0101  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.5986
76.9     4.00  0.80     Sequence          WB
             DRB3_0101  722      TNFTISVTTEILPVS  FTISVTTEI  2        0.5559
122.1     6.00  0.78     Sequence          WB
```

```
             DRB3_0101  723      NFTISVTTEILPVSM  FTISVTTEI  1        0.4823
270.9    11.00  0.70     Sequence
             DRB3_0101  724      FTISVTTEILPVSMT  FTISVTTEI  0        0.3279
1439.8    31.00  0.55     Sequence
             DRB3_0101  725      TISVTTEILPVSMTK  VTTEILPVS  3        0.1630
8567.9    80.00  0.25     Sequence
             DRB3_0101  726      ISVTTEILPVSMTKT  ILPVSMTKT  6        0.1493
9943.2    85.00  0.40     Sequence
             DRB3_0101  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.1300
12247.1    90.00  0.55     Sequence
             DRB3_0101  728      VTTEILPVSMTKTSV  ILPVSMTKT  4        0.1481
10070.9    85.00  0.57     Sequence
             DRB3_0101  729      TTEILPVSMTKTSVD  VSMTKTSVD  6        0.1983
5851.4    70.00  0.44     Sequence
             DRB3_0101  730      TEILPVSMTKTSVDC  VSMTKTSVD  5        0.1933
6172.5    70.00  0.50     Sequence
             DRB3_0101  731      EILPVSMTKTSVDCT  VSMTKTSVD  4        0.1914
6304.1    70.00  0.50     Sequence
             DRB3_0101  732      ILPVSMTKTSVDCTM  VSMTKTSVD  3        0.1956
6024.7    70.00  0.54     Sequence
             DRB3_0101  733      LPVSMTKTSVDCTMY  VSMTKTSVD  2        0.2182
4719.1    65.00  0.35     Sequence
             DRB3_0101  734      PVSMTKTSVDCTMYI  TSVDCTMYI  6        0.4119
580.2    17.00  0.75     Sequence
             DRB3_0101  735      VSMTKTSVDCTMYIC  TSVDCTMYI  5        0.4276
489.4    15.00  0.79     Sequence
             DRB3_0101  736      SMTKTSVDCTMYICG  TSVDCTMYI  4        0.4029
639.1    18.00  0.81     Sequence
             DRB3_0101  737      MTKTSVDCTMYICGD  TSVDCTMYI  3        0.4192
535.7    16.00  0.81     Sequence
             DRB3_0101  738      TKTSVDCTMYICGDS  TSVDCTMYI  2        0.3759
856.3    22.00  0.80     Sequence
             DRB3_0101  739      KTSVDCTMYICGDST  TSVDCTMYI  1        0.3294
1416.7    31.00  0.69     Sequence
             DRB3_0101  740      TSVDCTMYICGDSTE  TSVDCTMYI  0        0.2393
3753.2    55.00  0.41     Sequence
             DRB3_0101  741      SVDCTMYICGDSTEC  YICGDSTEC  6        0.2501
3341.4    55.00  0.43     Sequence
             DRB3_0101  742      VDCTMYICGDSTECS  ICGDSTECS  6        0.3110
1729.1    35.00  0.44     Sequence
             DRB3_0101  743      DCTMYICGDSTECSN  ICGDSTECS  5        0.3194
1578.5    33.00  0.49     Sequence
             DRB3_0101  744      CTMYICGDSTECSNL  ICGDSTECS  4        0.3368
1306.7    29.00  0.53     Sequence
             DRB3_0101  745      TMYICGDSTECSNLL  ICGDSTECS  3        0.3479
1158.7    27.00  0.57     Sequence
             DRB3_0101  746      MYICGDSTECSNLLL  ICGDSTECS  2        0.3142
1668.7    34.00  0.55     Sequence
             DRB3_0101  747      YICGDSTECSNLLLQ  ICGDSTECS  1        0.2451
3525.1    55.00  0.51     Sequence
             DRB3_0101  748      ICGDSTECSNLLLQY  ICGDSTECS  0        0.1709
7871.2    80.00  0.23     Sequence
             DRB3_0101  749      CGDSTECSNLLLQYG  DSTECSNLL  2        0.1275
12584.0    90.00  0.29     Sequence
             DRB3_0101  750      GDSTECSNLLLQYGS  DSTECSNLL  1        0.1231
13203.9    90.00  0.27     Sequence
             DRB3_0101  751      DSTECSNLLLQYGSF  NLLLQYGSF  6        0.1664
8259.0    80.00  0.27     Sequence
             DRB3_0101  752      STECSNLLLQYGSFC  LLLQYGSFC  6        0.1958
6007.9    70.00  0.50     Sequence
             DRB3_0101  753      TECSNLLLQYGSFCT  LLLQYGSFC  5        0.2042
5488.5    70.00  0.54     Sequence
             DRB3_0101  754      ECSNLLLQYGSFCTQ  LLLQYGSFC  4        0.2065
5350.7    65.00  0.53     Sequence
             DRB3_0101  755      CSNLLLQYGSFCTQL  LLLQYGSFC  3        0.2155
4857.6    65.00  0.44     Sequence
```

```
             DRB3_0101  756      SNLLLQYGSFCTQLN  LLLQYGSFC  2        0.2548
3174.3    50.00  0.36     Sequence
             DRB3_0101  757      NLLLQYGSFCTQLNR  YGSFCTQLN  5        0.2257
4347.7    60.00  0.31     Sequence
             DRB3_0101  758      LLLQYGSFCTQLNRA  YGSFCTQLN  4        0.1978
5882.0    70.00  0.38     Sequence
             DRB3_0101  759      LLQYGSFCTQLNRAL  FCTQLNRAL  6        0.2289
4200.9    60.00  0.43     Sequence
             DRB3_0101  760      LQYGSFCTQLNRALT  FCTQLNRAL  5        0.2249
4384.8    60.00  0.47     Sequence
             DRB3_0101  761      QYGSFCTQLNRALTG  FCTQLNRAL  4        0.1944
6105.3    70.00  0.51     Sequence
             DRB3_0101  762      YGSFCTQLNRALTGI  FCTQLNRAL  3        0.1868
6623.2    75.00  0.51     Sequence
             DRB3_0101  763      GSFCTQLNRALTGIA  FCTQLNRAL  2        0.1761
7439.7    75.00  0.47     Sequence
             DRB3_0101  764      SFCTQLNRALTGIAV  LNRALTGIA  5        0.1866
6636.2    75.00  0.29     Sequence
             DRB3_0101  765      FCTQLNRALTGIAVE  LNRALTGIA  4        0.1687
8055.1    80.00  0.30     Sequence
             DRB3_0101  766      CTQLNRALTGIAVEQ  LNRALTGIA  3        0.1518
9675.9    85.00  0.34     Sequence
             DRB3_0101  767      TQLNRALTGIAVEQD  NRALTGIAV  3        0.1643
8452.1    80.00  0.42     Sequence
             DRB3_0101  768      QLNRALTGIAVEQDK  NRALTGIAV  2        0.1316
12032.9    90.00  0.44     Sequence
             DRB3_0101  769      LNRALTGIAVEQDKN  NRALTGIAV  1        0.1135
14639.0    95.00  0.35     Sequence
             DRB3_0101  770      NRALTGIAVEQDKNT  IAVEQDKNT  6        0.1691
8026.8    80.00  0.58     Sequence
             DRB3_0101  771      RALTGIAVEQDKNTQ  IAVEQDKNT  5        0.1854
6724.8    75.00  0.60     Sequence
             DRB3_0101  772      ALTGIAVEQDKNTQE  VEQDKNTQE  6        0.2396
3743.6    55.00  0.51     Sequence
             DRB3_0101  773      LTGIAVEQDKNTQEV  VEQDKNTQE  5        0.2798
2423.3    42.00  0.62     Sequence
             DRB3_0101  774      TGIAVEQDKNTQEVF  VEQDKNTQE  4        0.3062
1820.7    36.00  0.68     Sequence
             DRB3_0101  775      GIAVEQDKNTQEVFA  VEQDKNTQE  3        0.3010
1926.4    37.00  0.72     Sequence
             DRB3_0101  776      IAVEQDKNTQEVFAQ  VEQDKNTQE  2        0.2554
3154.0    49.00  0.74     Sequence
             DRB3_0101  777      AVEQDKNTQEVFAQV  VEQDKNTQE  1        0.2029
5568.5    70.00  0.70     Sequence
             DRB3_0101  778      VEQDKNTQEVFAQVK  VEQDKNTQE  0        0.1198
13678.3    95.00  0.36     Sequence
             DRB3_0101  779      EQDKNTQEVFAQVKQ  NTQEVFAQV  4        0.0753
22126.9   100.00  0.30     Sequence
             DRB3_0101  780      QDKNTQEVFAQVKQI  EVFAQVKQI  6        0.2063
5362.2    65.00  0.61     Sequence
             DRB3_0101  781      DKNTQEVFAQVKQIY  EVFAQVKQI  5        0.2656
2825.5    46.00  0.45     Sequence
             DRB3_0101  782      KNTQEVFAQVKQIYK  EVFAQVKQI  4        0.2668
2787.5    46.00  0.39     Sequence
             DRB3_0101  783      NTQEVFAQVKQIYKT  EVFAQVKQI  3        0.2675
2766.1    46.00  0.36     Sequence
             DRB3_0101  784      TQEVFAQVKQIYKTP  EVFAQVKQI  2        0.2497
3354.6    55.00  0.34     Sequence
             DRB3_0101  785      QEVFAQVKQIYKTPP  VFAQVKQIY  2        0.2225
4502.5    60.00  0.36     Sequence
             DRB3_0101  786      EVFAQVKQIYKTPPI  FAQVKQIYK  2        0.1878
6556.1    75.00  0.25     Sequence
             DRB3_0101  787      VFAQVKQIYKTPPIK  KQIYKTPPI  5        0.1429
10648.0    85.00  0.28     Sequence
             DRB3_0101  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6        0.1926
6219.6    70.00  0.49     Sequence
```

```
             DRB3_0101  789      AQVKQIYKTPPIKDF  YKTPPIKDF  6        0.3740
874.1    23.00  0.56     Sequence
             DRB3_0101  790      QVKQIYKTPPIKDFG  YKTPPIKDF  5        0.3651
962.8    24.00  0.57     Sequence
             DRB3_0101  791      VKQIYKTPPIKDFGG  YKTPPIKDF  4        0.3437
1212.8    28.00  0.57     Sequence
             DRB3_0101  792      KQIYKTPPIKDFGGF  YKTPPIKDF  3        0.3462
1180.9    27.00  0.62     Sequence
             DRB3_0101  793      QIYKTPPIKDFGGFN  YKTPPIKDF  2        0.3153
1649.2    34.00  0.54     Sequence
             DRB3_0101  794      IYKTPPIKDFGGFNF  YKTPPIKDF  1        0.3201
1566.9    33.00  0.38     Sequence
             DRB3_0101  795      YKTPPIKDFGGFNFS  PIKDFGGFN  4        0.2741
2577.4    44.00  0.36     Sequence
             DRB3_0101  796      KTPPIKDFGGFNFSQ  PIKDFGGFN  3        0.2416
3662.4    55.00  0.46     Sequence
             DRB3_0101  797      TPPIKDFGGFNFSQI  PIKDFGGFN  2        0.2641
2870.0    47.00  0.32     Sequence
             DRB3_0101  798      PPIKDFGGFNFSQIL  FGGFNFSQI  5        0.2795
2428.8    43.00  0.28     Sequence
             DRB3_0101  799      PIKDFGGFNFSQILP  FGGFNFSQI  4        0.2597
3011.7    48.00  0.29     Sequence
             DRB3_0101  800      IKDFGGFNFSQILPD  FNFSQILPD  6        0.3465
1177.1    27.00  0.50     Sequence
             DRB3_0101  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.3269
1455.4    31.00  0.50     Sequence
             DRB3_0101  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.3265
1460.8    31.00  0.44     Sequence
             DRB3_0101  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.3068
1808.5    36.00  0.48     Sequence
             DRB3_0101  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.3020
1904.5    37.00  0.46     Sequence
             DRB3_0101  805      GFNFSQILPDPSKPS  ILPDPSKPS  6        0.4193
535.4    16.00  0.75     Sequence
             DRB3_0101  806      FNFSQILPDPSKPSK  ILPDPSKPS  5        0.4103
590.0    17.00  0.85     Sequence
             DRB3_0101  807      NFSQILPDPSKPSKR  ILPDPSKPS  4        0.3936
707.2    20.00  0.94     Sequence
             DRB3_0101  808      FSQILPDPSKPSKRS  ILPDPSKPS  3        0.3829
793.9    21.00  0.95     Sequence
             DRB3_0101  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.3354
1327.4    29.00  0.92     Sequence
             DRB3_0101  810      QILPDPSKPSKRSFI  ILPDPSKPS  1        0.2729
2610.3    44.00  0.87     Sequence
             DRB3_0101  811      ILPDPSKPSKRSFIE  ILPDPSKPS  0        0.1538
9471.9    85.00  0.56     Sequence
             DRB3_0101  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.0763
21910.9   100.00  0.41     Sequence
             DRB3_0101  813      PDPSKPSKRSFIEDL  SKRSFIEDL  6        0.1211
13492.8    95.00  0.43     Sequence
             DRB3_0101  814      DPSKPSKRSFIEDLL  KRSFIEDLL  6        0.2050
5438.4    70.00  0.37     Sequence
             DRB3_0101  815      PSKPSKRSFIEDLLF  RSFIEDLLF  6        0.2949
2057.0    39.00  0.38     Sequence
             DRB3_0101  816      SKPSKRSFIEDLLFN  RSFIEDLLF  5        0.3578
1042.0    25.00  0.30     Sequence
             DRB3_0101  817      KPSKRSFIEDLLFNK  FIEDLLFNK  6        0.4447
406.7    14.00  0.63     Sequence
             DRB3_0101  818      PSKRSFIEDLLFNKV  FIEDLLFNK  5        0.4720
302.8    11.00  0.71     Sequence
             DRB3_0101  819      SKRSFIEDLLFNKVT  FIEDLLFNK  4        0.4632
333.0    12.00  0.75     Sequence
             DRB3_0101  820      KRSFIEDLLFNKVTL  FIEDLLFNK  3        0.4593
347.2    12.00  0.80     Sequence
             DRB3_0101  821      RSFIEDLLFNKVTLA  FIEDLLFNK  2        0.4680
316.1    12.00  0.52     Sequence
```

```
             DRB3_0101  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5        0.4445
407.9    14.00  0.52     Sequence
             DRB3_0101  823      FIEDLLFNKVTLADA  LLFNKVTLA  4        0.3788
829.9    22.00  0.66     Sequence
             DRB3_0101  824      IEDLLFNKVTLADAG  LLFNKVTLA  3        0.3447
1199.8    28.00  0.73     Sequence
             DRB3_0101  825      EDLLFNKVTLADAGF  LLFNKVTLA  2        0.3634
980.3    24.00  0.54     Sequence
             DRB3_0101  826      DLLFNKVTLADAGFI  VTLADAGFI  6        0.4125
576.5    17.00  0.37     Sequence
             DRB3_0101  827      LLFNKVTLADAGFIK  VTLADAGFI  5        0.4199
532.1    16.00  0.36     Sequence
             DRB3_0101  828      LFNKVTLADAGFIKQ  TLADAGFIK  5        0.4116
581.8    17.00  0.37     Sequence
             DRB3_0101  829      FNKVTLADAGFIKQY  TLADAGFIK  4        0.4095
595.5    18.00  0.44     Sequence
             DRB3_0101  830      NKVTLADAGFIKQYG  TLADAGFIK  3        0.3800
819.2    22.00  0.45     Sequence
             DRB3_0101  831      KVTLADAGFIKQYGD  TLADAGFIK  2        0.3277
1442.4    31.00  0.49     Sequence
             DRB3_0101  832      VTLADAGFIKQYGDC  TLADAGFIK  1        0.2491
3377.1    55.00  0.52     Sequence
             DRB3_0101  833      TLADAGFIKQYGDCL  FIKQYGDCL  6        0.2571
3098.0    49.00  0.63     Sequence
             DRB3_0101  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.2468
3461.0    55.00  0.74     Sequence
             DRB3_0101  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4        0.2731
2603.0    44.00  0.75     Sequence
             DRB3_0101  836      DAGFIKQYGDCLGDI  FIKQYGDCL  3        0.3588
1030.0    25.00  0.50     Sequence
             DRB3_0101  837      AGFIKQYGDCLGDIA  FIKQYGDCL  2        0.3712
900.6    23.00  0.44     Sequence
             DRB3_0101  838      GFIKQYGDCLGDIAA  QYGDCLGDI  4        0.3418
1237.8    28.00  0.33     Sequence
             DRB3_0101  839      FIKQYGDCLGDIAAR  QYGDCLGDI  3        0.3196
1574.6    33.00  0.38     Sequence
             DRB3_0101  840      IKQYGDCLGDIAARD  CLGDIAARD  6        0.3857
770.0    21.00  0.56     Sequence
             DRB3_0101  841      KQYGDCLGDIAARDL  CLGDIAARD  5        0.4058
619.4    18.00  0.66     Sequence
             DRB3_0101  842      QYGDCLGDIAARDLI  CLGDIAARD  4        0.4082
603.5    18.00  0.76     Sequence
             DRB3_0101  843      YGDCLGDIAARDLIC  CLGDIAARD  3        0.3977
676.1    19.00  0.79     Sequence
             DRB3_0101  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.3711
902.4    23.00  0.72     Sequence
             DRB3_0101  845      DCLGDIAARDLICAQ  CLGDIAARD  1        0.3087
1771.6    35.00  0.56     Sequence
             DRB3_0101  846      CLGDIAARDLICAQK  AARDLICAQ  5        0.2111
5096.0    65.00  0.34     Sequence
             DRB3_0101  847      LGDIAARDLICAQKF  AARDLICAQ  4        0.2239
4436.0    60.00  0.38     Sequence
             DRB3_0101  848      GDIAARDLICAQKFN  AARDLICAQ  3        0.2272
4280.1    60.00  0.37     Sequence
             DRB3_0101  849      DIAARDLICAQKFNG  AARDLICAQ  2        0.1963
5975.9    70.00  0.35     Sequence
             DRB3_0101  850      IAARDLICAQKFNGL  AARDLICAQ  1        0.1866
6639.3    75.00  0.28     Sequence
             DRB3_0101  851      AARDLICAQKFNGLT  LICAQKFNG  4        0.1551
9340.4    85.00  0.23     Sequence
             DRB3_0101  852      ARDLICAQKFNGLTV  LICAQKFNG  3        0.1510
9761.7    85.00  0.22     Sequence
             DRB3_0101  853      RDLICAQKFNGLTVL  QKFNGLTVL  6        0.2019
5629.0    70.00  0.51     Sequence
             DRB3_0101  854      DLICAQKFNGLTVLP  QKFNGLTVL  5        0.2105
5124.3    65.00  0.56     Sequence
```

```
             DRB3_0101  855      LICAQKFNGLTVLPP  QKFNGLTVL  4        0.2219
4530.6    60.00  0.43     Sequence
             DRB3_0101  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.2450
3531.4    55.00  0.37     Sequence
             DRB3_0101  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.2510
3309.1    55.00  0.38     Sequence
             DRB3_0101  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.2463
3479.2    55.00  0.38     Sequence
             DRB3_0101  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.2394
3750.7    55.00  0.29     Sequence
             DRB3_0101  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1        0.2072
5314.9    65.00  0.23     Sequence
             DRB3_0101  861      FNGLTVLPPLLTDEM  TVLPPLLTD  4        0.1806
7084.9    75.00  0.17     Sequence
             DRB3_0101  862      NGLTVLPPLLTDEMI  TVLPPLLTD  3        0.1801
7124.2    75.00  0.20     Sequence
             DRB3_0101  863      GLTVLPPLLTDEMIA  LLTDEMIAX  7        0.2619
2939.4    47.00  0.29     Sequence
             DRB3_0101  864      LTVLPPLLTDEMIAQ  LLTDEMIAQ  6        0.5177
184.6     8.00  0.92    Sequence         WB
             DRB3_0101  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.5766
97.6     5.00  0.88    Sequence         WB
             DRB3_0101  866      VLPPLLTDEMIAQYT  LLTDEMIAQ  4        0.5828
91.3     4.50  0.87    Sequence         WB
             DRB3_0101  867      LPPLLTDEMIAQYTS  LLTDEMIAQ  3        0.5718
102.8     5.00  0.85    Sequence         WB
             DRB3_0101  868      PPLLTDEMIAQYTSA  LLTDEMIAQ  2        0.5257
169.3     7.50  0.79    Sequence         WB
             DRB3_0101  869      PLLTDEMIAQYTSAL  LLTDEMIAQ  1        0.4575
354.2    13.00  0.65    Sequence
             DRB3_0101  870      LLTDEMIAQYTSALL  MIAQYTSAL  5        0.3168
1622.8    33.00  0.39     Sequence
             DRB3_0101  871      LTDEMIAQYTSALLA  MIAQYTSAL  4        0.2436
3584.9    55.00  0.64     Sequence
             DRB3_0101  872      TDEMIAQYTSALLAG  MIAQYTSAL  3        0.2227
4491.4    60.00  0.62     Sequence
             DRB3_0101  873      DEMIAQYTSALLAGT  MIAQYTSAL  2        0.2314
4090.1    60.00  0.42     Sequence
             DRB3_0101  874      EMIAQYTSALLAGTI  YTSALLAGT  5        0.2284
4224.7    60.00  0.47     Sequence
             DRB3_0101  875      MIAQYTSALLAGTIT  YTSALLAGT  4        0.2095
5180.5    65.00  0.55     Sequence
             DRB3_0101  876      IAQYTSALLAGTITS  YTSALLAGT  3        0.1952
6048.9    70.00  0.61     Sequence
             DRB3_0101  877      AQYTSALLAGTITSG  YTSALLAGT  2        0.1690
8034.7    80.00  0.54     Sequence
             DRB3_0101  878      QYTSALLAGTITSGW  LAGTITSGW  6        0.1545
9395.9    85.00  0.32     Sequence
             DRB3_0101  879      YTSALLAGTITSGWT  LAGTITSGW  5        0.1251
12921.9    90.00  0.45     Sequence
             DRB3_0101  880      TSALLAGTITSGWTF  GTITSGWTF  6        0.1979
5872.5    70.00  0.45     Sequence
             DRB3_0101  881      SALLAGTITSGWTFG  GTITSGWTF  5        0.2125
5016.3    65.00  0.50     Sequence
             DRB3_0101  882      ALLAGTITSGWTFGA  GTITSGWTF  4        0.2299
4154.8    60.00  0.46     Sequence
             DRB3_0101  883      LLAGTITSGWTFGAG  GTITSGWTF  3        0.2107
5113.8    65.00  0.42     Sequence
             DRB3_0101  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.1914
6303.1    70.00  0.50     Sequence
             DRB3_0101  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.1742
7589.6    80.00  0.51     Sequence
             DRB3_0101  886      GTITSGWTFGAGAAL  WTFGAGAAL  6        0.1792
7193.3    75.00  0.40     Sequence
             DRB3_0101  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.1622
8642.6    80.00  0.50     Sequence
```

```
             DRB3_0101  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.2597
3009.5    48.00  0.67     Sequence
             DRB3_0101  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.2481
3412.2    55.00  0.71     Sequence
             DRB3_0101  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.2805
2404.1    42.00  0.67     Sequence
             DRB3_0101  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.2717
2645.1    45.00  0.61     Sequence
             DRB3_0101  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.2360
3892.5    55.00  0.54     Sequence
             DRB3_0101  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.2094
5188.5    65.00  0.43     Sequence
             DRB3_0101  894      FGAGAALQIPFAMQM  LQIPFAMQM  6        0.2155
4857.3    65.00  0.46     Sequence
             DRB3_0101  895      GAGAALQIPFAMQMA  LQIPFAMQM  5        0.2138
4946.7    65.00  0.54     Sequence
             DRB3_0101  896      AGAALQIPFAMQMAY  LQIPFAMQM  4        0.2216
4544.6    60.00  0.56     Sequence
             DRB3_0101  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.2503
3332.0    55.00  0.44     Sequence
             DRB3_0101  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.5658
109.8     5.50  0.89    Sequence         WB
             DRB3_0101  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.6120
66.6     3.50  0.90    Sequence         WB
             DRB3_0101  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.5858
88.4     4.50  0.91    Sequence         WB
             DRB3_0101  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.5955
79.5     4.50  0.88    Sequence         WB
             DRB3_0101  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.5620
114.3     5.50  0.87    Sequence         WB
             DRB3_0101  903      PFAMQMAYRFNGIGV  FAMQMAYRF  1        0.5308
160.3     7.00  0.70    Sequence         WB
             DRB3_0101  904      FAMQMAYRFNGIGVT  YRFNGIGVT  6        0.5350
153.1     7.00  0.62    Sequence         WB
             DRB3_0101  905      AMQMAYRFNGIGVTQ  YRFNGIGVT  5        0.4724
301.3    11.00  0.88    Sequence
             DRB3_0101  906      MQMAYRFNGIGVTQN  YRFNGIGVT  4        0.4597
345.8    12.00  0.88    Sequence
             DRB3_0101  907      QMAYRFNGIGVTQNV  YRFNGIGVT  3        0.4560
360.1    13.00  0.85    Sequence
             DRB3_0101  908      MAYRFNGIGVTQNVL  YRFNGIGVT  2        0.4026
641.6    19.00  0.80    Sequence
             DRB3_0101  909      AYRFNGIGVTQNVLY  YRFNGIGVT  1        0.3491
1144.5    27.00  0.62     Sequence
             DRB3_0101  910      YRFNGIGVTQNVLYE  IGVTQNVLY  5        0.2433
3593.4    55.00  0.36     Sequence
             DRB3_0101  911      RFNGIGVTQNVLYEN  IGVTQNVLY  4        0.1958
6009.9    70.00  0.46     Sequence
             DRB3_0101  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.1838
6840.6    75.00  0.44     Sequence
             DRB3_0101  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.1676
8152.6    80.00  0.43     Sequence
             DRB3_0101  914      GIGVTQNVLYENQKL  NVLYENQKL  6        0.2110
5099.4    65.00  0.28     Sequence
             DRB3_0101  915      IGVTQNVLYENQKLI  VLYENQKLI  6        0.4310
471.6    15.00  0.75    Sequence
             DRB3_0101  916      GVTQNVLYENQKLIA  VLYENQKLI  5        0.4648
327.3    12.00  0.74    Sequence
             DRB3_0101  917      VTQNVLYENQKLIAN  VLYENQKLI  4        0.4775
285.3    11.00  0.69    Sequence
             DRB3_0101  918      TQNVLYENQKLIANQ  VLYENQKLI  3        0.4666
321.1    12.00  0.70    Sequence
             DRB3_0101  919      QNVLYENQKLIANQF  VLYENQKLI  2        0.4499
384.3    13.00  0.64    Sequence
             DRB3_0101  920      NVLYENQKLIANQFN  VLYENQKLI  1        0.4028
640.3    18.00  0.57    Sequence
```

```
             DRB3_0101  921      VLYENQKLIANQFNS  VLYENQKLI  0        0.3067
1811.4    36.00  0.40     Sequence
             DRB3_0101  922      LYENQKLIANQFNSA  LIANQFNSA  6        0.2191
4671.6    65.00  0.40     Sequence
             DRB3_0101  923      YENQKLIANQFNSAI  LIANQFNSA  5        0.2526
3252.0    50.00  0.46     Sequence
             DRB3_0101  924      ENQKLIANQFNSAIG  IANQFNSAI  5        0.2446
3545.8    55.00  0.40     Sequence
             DRB3_0101  925      NQKLIANQFNSAIGK  IANQFNSAI  4        0.2449
3532.9    55.00  0.39     Sequence
             DRB3_0101  926      QKLIANQFNSAIGKI  IANQFNSAI  3        0.2858
2269.7    41.00  0.34     Sequence
             DRB3_0101  927      KLIANQFNSAIGKIQ  FNSAIGKIQ  6        0.2757
2530.8    44.00  0.29     Sequence
             DRB3_0101  928      LIANQFNSAIGKIQD  FNSAIGKIQ  5        0.2744
2568.9    44.00  0.35     Sequence
             DRB3_0101  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4        0.2457
3501.3    55.00  0.42     Sequence
             DRB3_0101  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.2215
4549.3    60.00  0.49     Sequence
             DRB3_0101  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.1882
6528.7    75.00  0.49     Sequence
             DRB3_0101  932      QFNSAIGKIQDSLSS  FNSAIGKIQ  1        0.1377
11274.0    90.00  0.41     Sequence
             DRB3_0101  933      FNSAIGKIQDSLSST  KIQDSLSST  6        0.1130
14715.7    95.00  0.41     Sequence
             DRB3_0101  934      NSAIGKIQDSLSSTA  KIQDSLSST  5        0.1209
13522.7    95.00  0.42     Sequence
             DRB3_0101  935      SAIGKIQDSLSSTAS  KIQDSLSST  4        0.1245
13003.2    90.00  0.40     Sequence
             DRB3_0101  936      AIGKIQDSLSSTASA  KIQDSLSST  3        0.1405
10931.6    90.00  0.30     Sequence
             DRB3_0101  937      IGKIQDSLSSTASAL  DSLSSTASA  5        0.1446
10463.3    85.00  0.34     Sequence
             DRB3_0101  938      GKIQDSLSSTASALG  DSLSSTASA  4        0.1260
12787.8    90.00  0.32     Sequence
             DRB3_0101  939      KIQDSLSSTASALGK  DSLSSTASA  3        0.1037
16272.6    95.00  0.37     Sequence
             DRB3_0101  940      IQDSLSSTASALGKL  LSSTASALG  4        0.0954
17809.6   100.00  0.25     Sequence
             DRB3_0101  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.0855
19820.5   100.00  0.25     Sequence
             DRB3_0101  942      DSLSSTASALGKLQD  TASALGKLQ  5        0.0784
21398.0   100.00  0.31     Sequence
             DRB3_0101  943      SLSSTASALGKLQDV  TASALGKLQ  4        0.0855
19825.4   100.00  0.34     Sequence
             DRB3_0101  944      LSSTASALGKLQDVV  TASALGKLQ  3        0.0899
18894.3   100.00  0.30     Sequence
             DRB3_0101  945      SSTASALGKLQDVVN  LGKLQDVVN  6        0.0884
19214.2   100.00  0.19     Sequence
             DRB3_0101  946      STASALGKLQDVVNQ  LGKLQDVVN  5        0.0853
19858.0   100.00  0.22     Sequence
             DRB3_0101  947      TASALGKLQDVVNQN  KLQDVVNQN  6        0.1235
13140.3    90.00  0.44     Sequence
             DRB3_0101  948      ASALGKLQDVVNQNA  KLQDVVNQN  5        0.1294
12326.9    90.00  0.44     Sequence
             DRB3_0101  949      SALGKLQDVVNQNAQ  KLQDVVNQN  4        0.1232
13191.0    90.00  0.45     Sequence
             DRB3_0101  950      ALGKLQDVVNQNAQA  KLQDVVNQN  3        0.1290
12379.0    90.00  0.38     Sequence
             DRB3_0101  951      LGKLQDVVNQNAQAL  VVNQNAQAL  6        0.1809
7058.7    75.00  0.49     Sequence
             DRB3_0101  952      GKLQDVVNQNAQALN  VVNQNAQAL  5        0.1905
6367.1    75.00  0.54     Sequence
             DRB3_0101  953      KLQDVVNQNAQALNT  VVNQNAQAL  4        0.1865
6649.9    75.00  0.52     Sequence
```

```
             DRB3_0101  954       LQDVVNQNAQALNTL  VVNQNAQAL  3        0.1950
6064.5    70.00  0.54     Sequence
             DRB3_0101  955       QDVVNQNAQALNTLV  NAQALNTLV  6        0.2231
4472.1    60.00  0.35     Sequence
             DRB3_0101  956       DVVNQNAQALNTLVK  NAQALNTLV  5        0.2190
4674.6    65.00  0.44     Sequence
             DRB3_0101  957       VVNQNAQALNTLVKQ  NAQALNTLV  4        0.2108
5112.1    65.00  0.45     Sequence
             DRB3_0101  958       VNQNAQALNTLVKQL  NAQALNTLV  3        0.2192
4665.9    65.00  0.44     Sequence
             DRB3_0101  959       NQNAQALNTLVKQLS  NAQALNTLV  2        0.1976
5893.7    70.00  0.42     Sequence
             DRB3_0101  960       QNAQALNTLVKQLSS  NAQALNTLV  1        0.1752
7514.1    80.00  0.34     Sequence
             DRB3_0101  961       NAQALNTLVKQLSSN  QALNTLVKQ  2        0.1372
11327.9    90.00  0.28     Sequence
             DRB3_0101  962       AQALNTLVKQLSSNF  LVKQLSSNF  6        0.2202
4614.6    65.00  0.75     Sequence
             DRB3_0101  963       QALNTLVKQLSSNFG  LVKQLSSNF  5        0.2106
5123.5    65.00  0.75     Sequence
             DRB3_0101  964       ALNTLVKQLSSNFGA  LVKQLSSNF  4        0.2106
5123.7    65.00  0.73     Sequence
             DRB3_0101  965       LNTLVKQLSSNFGAI  LVKQLSSNF  3        0.2435
3586.6    55.00  0.59     Sequence
             DRB3_0101  966       NTLVKQLSSNFGAIS  LSSNFGAIS  6        0.2572
3094.0    49.00  0.42     Sequence
             DRB3_0101  967       TLVKQLSSNFGAISS  LSSNFGAIS  5        0.2500
3344.4    55.00  0.54     Sequence
             DRB3_0101  968       LVKQLSSNFGAISSV  LSSNFGAIS  4        0.2542
3195.5    50.00  0.68     Sequence
             DRB3_0101  969       VKQLSSNFGAISSVL  LSSNFGAIS  3        0.2634
2893.8    47.00  0.62     Sequence
             DRB3_0101  970       KQLSSNFGAISSVLN  LSSNFGAIS  2        0.2542
3196.8    50.00  0.49     Sequence
             DRB3_0101  971       QLSSNFGAISSVLND  FGAISSVLN  5        0.2600
2999.5    48.00  0.32     Sequence
             DRB3_0101  972       LSSNFGAISSVLNDI  FGAISSVLN  4        0.2795
2428.9    43.00  0.35     Sequence
             DRB3_0101  973       SSNFGAISSVLNDIL  ISSVLNDIL  6        0.3226
1524.6    32.00  0.33     Sequence
             DRB3_0101  974       SNFGAISSVLNDILS  ISSVLNDIL  5        0.3113
1723.1    35.00  0.39     Sequence
             DRB3_0101  975       NFGAISSVLNDILSR  ISSVLNDIL  4        0.3094
1757.8    35.00  0.39     Sequence
             DRB3_0101  976       FGAISSVLNDILSRL  VLNDILSRL  6        0.4963
232.7     9.00  0.79     Sequence         WB
             DRB3_0101  977       GAISSVLNDILSRLD  VLNDILSRL  5        0.5379
148.4     6.50  0.82     Sequence         WB
             DRB3_0101  978       AISSVLNDILSRLDK  VLNDILSRL  4        0.5186
182.9     8.00  0.85     Sequence         WB
             DRB3_0101  979       ISSVLNDILSRLDKV  VLNDILSRL  3        0.5220
176.3     7.50  0.83     Sequence         WB
             DRB3_0101  980       SSVLNDILSRLDKVE  VLNDILSRL  2        0.4726
300.9    11.00  0.76     Sequence
             DRB3_0101  981       SVLNDILSRLDKVEA  VLNDILSRL  1        0.4184
540.5    17.00  0.64     Sequence
             DRB3_0101  982       VLNDILSRLDKVEAE  SRLDKVEAE  6        0.3722
891.5    23.00  0.40     Sequence
             DRB3_0101  983       LNDILSRLDKVEAEV  SRLDKVEAE  5        0.3544
1080.8    26.00  0.64     Sequence
             DRB3_0101  984       NDILSRLDKVEAEVQ  SRLDKVEAE  4        0.3345
1339.8    30.00  0.67     Sequence
             DRB3_0101  985       DILSRLDKVEAEVQI  SRLDKVEAE  3        0.3385
1284.0    29.00  0.62     Sequence
             DRB3_0101  986       ILSRLDKVEAEVQID  SRLDKVEAE  2        0.3334
1356.9    30.00  0.55     Sequence
```

```
             DRB3_0101  987      LSRLDKVEAEVQIDR  SRLDKVEAE  1        0.2778
2475.3    43.00  0.48     Sequence
             DRB3_0101  988      SRLDKVEAEVQIDRL  VEAEVQIDR  5        0.2800
2416.3    42.00  0.28     Sequence
             DRB3_0101  989      RLDKVEAEVQIDRLI  VEAEVQIDR  4        0.3073
1799.5    36.00  0.32     Sequence
             DRB3_0101  990      LDKVEAEVQIDRLIT  VQIDRLITX  7        0.3562
1059.4    26.00  0.23     Sequence
             DRB3_0101  991      DKVEAEVQIDRLITG  VQIDRLITG  6        0.4769
287.0    11.00  0.77     Sequence
             DRB3_0101  992      KVEAEVQIDRLITGR  VQIDRLITG  5        0.4749
293.3    11.00  0.81     Sequence
             DRB3_0101  993      VEAEVQIDRLITGRL  VQIDRLITG  4        0.4828
269.5    10.00  0.86     Sequence
             DRB3_0101  994      EAEVQIDRLITGRLQ  VQIDRLITG  3        0.4617
338.5    12.00  0.84     Sequence
             DRB3_0101  995      AEVQIDRLITGRLQS  VQIDRLITG  2        0.4200
531.4    16.00  0.82     Sequence
             DRB3_0101  996      EVQIDRLITGRLQSL  VQIDRLITG  1        0.3496
1138.3    27.00  0.72     Sequence
             DRB3_0101  997      VQIDRLITGRLQSLQ  VQIDRLITG  0        0.2263
4321.7    60.00  0.31     Sequence
             DRB3_0101  998      QIDRLITGRLQSLQT  LITGRLQSL  4        0.1616
8698.1    80.00  0.35     Sequence
             DRB3_0101  999      IDRLITGRLQSLQTY  GRLQSLQTY  6        0.1878
6557.1    75.00  0.35     Sequence
             DRB3_0101 1000      DRLITGRLQSLQTYV  GRLQSLQTY  5        0.2141
4931.8    65.00  0.38     Sequence
             DRB3_0101 1001      RLITGRLQSLQTYVT  GRLQSLQTY  4        0.2242
4421.2    60.00  0.35     Sequence
             DRB3_0101 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.2120
5046.6    65.00  0.40     Sequence
             DRB3_0101 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.1943
6112.0    70.00  0.42     Sequence
             DRB3_0101 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.2052
5429.3    70.00  0.39     Sequence
             DRB3_0101 1005      GRLQSLQTYVTQQLI  LQTYVTQQL  5        0.2052
5427.3    70.00  0.37     Sequence
             DRB3_0101 1006      RLQSLQTYVTQQLIR  LQTYVTQQL  4        0.2073
5306.2    65.00  0.37     Sequence
             DRB3_0101 1007      LQSLQTYVTQQLIRA  YVTQQLIRA  6        0.2888
2196.8    40.00  0.68     Sequence
             DRB3_0101 1008      QSLQTYVTQQLIRAA  YVTQQLIRA  5        0.2951
2053.4    39.00  0.76     Sequence
             DRB3_0101 1009      SLQTYVTQQLIRAAE  YVTQQLIRA  4        0.2874
2230.2    40.00  0.85     Sequence
             DRB3_0101 1010      LQTYVTQQLIRAAEI  YVTQQLIRA  3        0.2990
1967.7    38.00  0.80     Sequence
             DRB3_0101 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.2639
2877.1    47.00  0.73     Sequence
             DRB3_0101 1012      TYVTQQLIRAAEIRA  YVTQQLIRA  1        0.2504
3329.8    55.00  0.44     Sequence
             DRB3_0101 1013      YVTQQLIRAAEIRAS  IRAAEIRAS  6        0.3103
1741.8    35.00  0.62     Sequence
             DRB3_0101 1014      VTQQLIRAAEIRASA  IRAAEIRAS  5        0.3050
1843.8    36.00  0.66     Sequence
             DRB3_0101 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.2966
2019.6    38.00  0.69     Sequence
             DRB3_0101 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.2970
2011.7    38.00  0.70     Sequence
             DRB3_0101 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.3021
1902.0    37.00  0.56     Sequence
             DRB3_0101 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.3151
1654.1    34.00  0.51     Sequence
             DRB3_0101 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.3403
1258.2    28.00  0.64     Sequence
```

```
             DRB3_0101 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.3276
1443.5    31.00  0.68     Sequence
             DRB3_0101 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.3296
1413.2    31.00  0.62     Sequence
             DRB3_0101 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.3010
1924.9    37.00  0.55     Sequence
             DRB3_0101 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.2351
3929.1    60.00  0.50     Sequence
             DRB3_0101 1024      IRASANLAAIKMSEC  LAAIKMSEC  6        0.1606
8796.6    80.00  0.25     Sequence
             DRB3_0101 1025      RASANLAAIKMSECV  LAAIKMSEC  5        0.1483
10047.0    85.00  0.31     Sequence
             DRB3_0101 1026      ASANLAAIKMSECVL  LAAIKMSEC  4        0.1798
7145.1    75.00  0.30     Sequence
             DRB3_0101 1027      SANLAAIKMSECVLG  IKMSECVLG  6        0.1860
6683.9    75.00  0.41     Sequence
             DRB3_0101 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.1897
6420.1    75.00  0.38     Sequence
             DRB3_0101 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.1820
6979.6    75.00  0.33     Sequence
             DRB3_0101 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.1642
8462.2    80.00  0.36     Sequence
             DRB3_0101 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.1436
10575.5    85.00  0.32     Sequence
             DRB3_0101 1032      AIKMSECVLGQSKRV  CVLGQSKRV  6        0.2185
4700.3    65.00  0.59     Sequence
             DRB3_0101 1033      IKMSECVLGQSKRVD  CVLGQSKRV  5        0.2291
4192.9    60.00  0.70     Sequence
             DRB3_0101 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.2455
3511.9    55.00  0.69     Sequence
             DRB3_0101 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.2462
3483.0    55.00  0.67     Sequence
             DRB3_0101 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.2209
4579.5    60.00  0.64     Sequence
             DRB3_0101 1037      ECVLGQSKRVDFCGK  CVLGQSKRV  1        0.1900
6401.4    75.00  0.58     Sequence
             DRB3_0101 1038      CVLGQSKRVDFCGKG  KRVDFCGKG  6        0.1498
9886.7    85.00  0.31     Sequence
             DRB3_0101 1039      VLGQSKRVDFCGKGY  KRVDFCGKG  5        0.1540
9449.1    85.00  0.40     Sequence
             DRB3_0101 1040      LGQSKRVDFCGKGYH  KRVDFCGKG  4        0.1555
9297.6    85.00  0.38     Sequence
             DRB3_0101 1041      GQSKRVDFCGKGYHL  DFCGKGYHL  6        0.1935
6163.0    70.00  0.34     Sequence
             DRB3_0101 1042      QSKRVDFCGKGYHLM  DFCGKGYHL  5        0.2343
3962.5    60.00  0.28     Sequence
             DRB3_0101 1043      SKRVDFCGKGYHLMS  FCGKGYHLM  5        0.2428
3615.2    55.00  0.23     Sequence
             DRB3_0101 1044      KRVDFCGKGYHLMSF  FCGKGYHLM  4        0.2651
2840.7    47.00  0.26     Sequence
             DRB3_0101 1045      RVDFCGKGYHLMSFP  FCGKGYHLM  3        0.2412
3676.4    55.00  0.26     Sequence
             DRB3_0101 1046      VDFCGKGYHLMSFPQ  CGKGYHLMS  3        0.2167
4792.4    65.00  0.28     Sequence
             DRB3_0101 1047      DFCGKGYHLMSFPQS  CGKGYHLMS  2        0.2136
4957.3    65.00  0.23     Sequence
             DRB3_0101 1048      FCGKGYHLMSFPQSA  YHLMSFPQS  5        0.2023
5603.8    70.00  0.23     Sequence
             DRB3_0101 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.1716
7809.9    80.00  0.28     Sequence
             DRB3_0101 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.1746
7560.4    80.00  0.26     Sequence
             DRB3_0101 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.1536
9483.9    85.00  0.27     Sequence
             DRB3_0101 1052      GYHLMSFPQSAPHGV  MSFPQSAPH  4        0.1610
8760.2    80.00  0.22     Sequence
```

```
             DRB3_0101 1053      YHLMSFPQSAPHGVV  MSFPQSAPH  3        0.1572
9122.1    85.00  0.19     Sequence
             DRB3_0101 1054      HLMSFPQSAPHGVVF  PQSAPHGVV  5        0.1782
7272.6    75.00  0.25     Sequence
             DRB3_0101 1055      LMSFPQSAPHGVVFL  QSAPHGVVF  5        0.1924
6238.6    70.00  0.25     Sequence
             DRB3_0101 1056      MSFPQSAPHGVVFLH  QSAPHGVVF  4        0.1805
7091.3    75.00  0.28     Sequence
             DRB3_0101 1057      SFPQSAPHGVVFLHV  QSAPHGVVF  3        0.1725
7737.4    80.00  0.29     Sequence
             DRB3_0101 1058      FPQSAPHGVVFLHVT  QSAPHGVVF  2        0.1456
10341.3    85.00  0.26     Sequence
             DRB3_0101 1059      PQSAPHGVVFLHVTY  HGVVFLHVT  5        0.1341
11717.1    90.00  0.16     Sequence
             DRB3_0101 1060      QSAPHGVVFLHVTYV  VVFLHVTYV  6        0.1684
8086.5    80.00  0.50     Sequence
             DRB3_0101 1061      SAPHGVVFLHVTYVP  VVFLHVTYV  5        0.1646
8423.5    80.00  0.47     Sequence
             DRB3_0101 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.2552
3160.3    49.00  0.52     Sequence
             DRB3_0101 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.2614
2956.9    48.00  0.56     Sequence
             DRB3_0101 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.2624
2925.3    47.00  0.60     Sequence
             DRB3_0101 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.2478
3423.6    55.00  0.56     Sequence
             DRB3_0101 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.2152
4871.0    65.00  0.51     Sequence
             DRB3_0101 1067      VFLHVTYVPAQEKNF  YVPAQEKNF  6        0.3871
758.7    21.00  0.76     Sequence
             DRB3_0101 1068      FLHVTYVPAQEKNFT  YVPAQEKNF  5        0.4024
642.6    19.00  0.87     Sequence
             DRB3_0101 1069      LHVTYVPAQEKNFTT  YVPAQEKNF  4        0.3990
666.6    19.00  0.90     Sequence
             DRB3_0101 1070      HVTYVPAQEKNFTTA  YVPAQEKNF  3        0.3930
711.8    20.00  0.90     Sequence
             DRB3_0101 1071      VTYVPAQEKNFTTAP  YVPAQEKNF  2        0.3518
1111.2    26.00  0.86     Sequence
             DRB3_0101 1072      TYVPAQEKNFTTAPA  YVPAQEKNF  1        0.2924
2113.2    39.00  0.76     Sequence
             DRB3_0101 1073      YVPAQEKNFTTAPAI  YVPAQEKNF  0        0.2096
5175.0    65.00  0.47     Sequence
             DRB3_0101 1074      VPAQEKNFTTAPAIC  KNFTTAPAI  5        0.1535
9503.0    85.00  0.27     Sequence
             DRB3_0101 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.2757
2531.2    44.00  0.75     Sequence
             DRB3_0101 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.3206
1557.4    33.00  0.77     Sequence
             DRB3_0101 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.2885
2205.3    40.00  0.78     Sequence
             DRB3_0101 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.2715
2649.9    45.00  0.80     Sequence
             DRB3_0101 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.2464
3476.1    55.00  0.79     Sequence
             DRB3_0101 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.2060
5381.5    65.00  0.61     Sequence
             DRB3_0101 1081      FTTAPAICHDGKAHF  ICHDGKAHF  6        0.3700
913.1    23.00  0.80     Sequence
             DRB3_0101 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.3968
683.0    19.00  0.84     Sequence
             DRB3_0101 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.3998
661.5    19.00  0.82     Sequence
             DRB3_0101 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.4033
636.5    18.00  0.81     Sequence
             DRB3_0101 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.3635
979.0    24.00  0.80     Sequence
```

```
             DRB3_0101 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.3040
1863.6    36.00  0.74     Sequence
             DRB3_0101 1087      ICHDGKAHFPREGVF  ICHDGKAHF  0        0.2038
5512.2    70.00  0.53     Sequence
             DRB3_0101 1088      CHDGKAHFPREGVFV  HFPREGVFV  6        0.1581
9039.3    85.00  0.38     Sequence
             DRB3_0101 1089      HDGKAHFPREGVFVS  FPREGVFVS  6        0.2217
4540.5    60.00  0.59     Sequence
             DRB3_0101 1090      DGKAHFPREGVFVSN  FPREGVFVS  5        0.2353
3921.6    60.00  0.62     Sequence
             DRB3_0101 1091      GKAHFPREGVFVSNG  FPREGVFVS  4        0.2186
4699.0    65.00  0.62     Sequence
             DRB3_0101 1092      KAHFPREGVFVSNGT  FPREGVFVS  3        0.2104
5132.6    65.00  0.59     Sequence
             DRB3_0101 1093      AHFPREGVFVSNGTH  FPREGVFVS  2        0.1917
6286.4    70.00  0.51     Sequence
             DRB3_0101 1094      HFPREGVFVSNGTHW  VFVSNGTHW  6        0.3217
1539.0    32.00  0.52     Sequence
             DRB3_0101 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6        0.6659
37.2     2.50  0.81     Sequence         WB
             DRB3_0101 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.7265
19.3     1.10  0.83     Sequence         SB
             DRB3_0101 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.7344
17.7     1.00  0.82     Sequence         SB
             DRB3_0101 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.7279
19.0     1.10  0.81     Sequence         SB
             DRB3_0101 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.6990
26.0     1.50  0.81     Sequence         SB
             DRB3_0101 1100      VFVSNGTHWFVTQRN  FVSNGTHWF  1        0.6258
57.3     3.50  0.77     Sequence         WB
             DRB3_0101 1101      FVSNGTHWFVTQRNF  FVSNGTHWF  0        0.4700
309.5    12.00  0.56     Sequence
             DRB3_0101 1102      VSNGTHWFVTQRNFY  WFVTQRNFY  6        0.3349
1334.4    30.00  0.50     Sequence
             DRB3_0101 1103      SNGTHWFVTQRNFYE  WFVTQRNFY  5        0.3651
962.1    24.00  0.52     Sequence
             DRB3_0101 1104      NGTHWFVTQRNFYEP  WFVTQRNFY  4        0.3594
1024.2    25.00  0.53     Sequence
             DRB3_0101 1105      GTHWFVTQRNFYEPQ  WFVTQRNFY  3        0.3440
1208.7    28.00  0.52     Sequence
             DRB3_0101 1106      THWFVTQRNFYEPQI  WFVTQRNFY  2        0.3120
1709.5    34.00  0.46     Sequence
             DRB3_0101 1107      HWFVTQRNFYEPQII  WFVTQRNFY  1        0.2795
2430.5    43.00  0.44     Sequence
             DRB3_0101 1108      WFVTQRNFYEPQIIT  WFVTQRNFY  0        0.2301
4148.5    60.00  0.28     Sequence
             DRB3_0101 1109      FVTQRNFYEPQIITT  FYEPQIITT  6        0.2009
5690.4    70.00  0.28     Sequence
             DRB3_0101 1110      VTQRNFYEPQIITTD  YEPQIITTD  6        0.2475
3434.0    55.00  0.34     Sequence
             DRB3_0101 1111      TQRNFYEPQIITTDN  YEPQIITTD  5        0.2472
3448.1    55.00  0.34     Sequence
             DRB3_0101 1112      QRNFYEPQIITTDNT  YEPQIITTD  4        0.2419
3649.5    55.00  0.33     Sequence
             DRB3_0101 1113      RNFYEPQIITTDNTF  YEPQIITTD  3        0.2669
2784.9    46.00  0.28     Sequence
             DRB3_0101 1114      NFYEPQIITTDNTFV  IITTDNTFV  6        0.3927
714.0    20.00  0.40     Sequence
             DRB3_0101 1115      FYEPQIITTDNTFVS  ITTDNTFVS  6        0.5993
76.4     4.00  0.77     Sequence         WB
             DRB3_0101 1116      YEPQIITTDNTFVSG  ITTDNTFVS  5        0.6114
67.0     4.00  0.81     Sequence         WB
             DRB3_0101 1117      EPQIITTDNTFVSGN  ITTDNTFVS  4        0.6134
65.6     3.50  0.82     Sequence         WB
             DRB3_0101 1118      PQIITTDNTFVSGNC  ITTDNTFVS  3        0.6046
72.1     4.00  0.86     Sequence         WB
```

```
             DRB3_0101 1119      QIITTDNTFVSGNCD  ITTDNTFVS  2        0.5536
125.3     6.00  0.88     Sequence         WB
             DRB3_0101 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.4719
302.9    11.00  0.88     Sequence
             DRB3_0101 1121      ITTDNTFVSGNCDVV  ITTDNTFVS  0        0.3047
1851.1    36.00  0.47     Sequence
             DRB3_0101 1122      TTDNTFVSGNCDVVI  FVSGNCDVV  5        0.2528
3243.6    50.00  0.47     Sequence
             DRB3_0101 1123      TDNTFVSGNCDVVIG  FVSGNCDVV  4        0.2449
3534.5    55.00  0.40     Sequence
             DRB3_0101 1124      DNTFVSGNCDVVIGI  GNCDVVIGI  6        0.3159
1638.8    34.00  0.40     Sequence
             DRB3_0101 1125      NTFVSGNCDVVIGIV  GNCDVVIGI  5        0.3353
1329.2    30.00  0.44     Sequence
             DRB3_0101 1126      TFVSGNCDVVIGIVN  GNCDVVIGI  4        0.3133
1684.9    34.00  0.46     Sequence
             DRB3_0101 1127      FVSGNCDVVIGIVNN  GNCDVVIGI  3        0.2839
2316.1    41.00  0.51     Sequence
             DRB3_0101 1128      VSGNCDVVIGIVNNT  GNCDVVIGI  2        0.2419
3650.1    55.00  0.51     Sequence
             DRB3_0101 1129      SGNCDVVIGIVNNTV  GNCDVVIGI  1        0.2101
5150.3    65.00  0.41     Sequence
             DRB3_0101 1130      GNCDVVIGIVNNTVY  IGIVNNTVY  6        0.2120
5041.9    65.00  0.40     Sequence
             DRB3_0101 1131      NCDVVIGIVNNTVYD  IGIVNNTVY  5        0.2324
4046.5    60.00  0.44     Sequence
             DRB3_0101 1132      CDVVIGIVNNTVYDP  IVNNTVYDP  6        0.2584
3054.2    48.00  0.30     Sequence
             DRB3_0101 1133      DVVIGIVNNTVYDPL  IVNNTVYDP  5        0.3016
1912.2    37.00  0.39     Sequence
             DRB3_0101 1134      VVIGIVNNTVYDPLQ  IVNNTVYDP  4        0.2913
2138.4    39.00  0.41     Sequence
             DRB3_0101 1135      VIGIVNNTVYDPLQP  IVNNTVYDP  3        0.2655
2827.4    46.00  0.43     Sequence
             DRB3_0101 1136      IGIVNNTVYDPLQPE  TVYDPLQPE  6        0.2818
2370.9    42.00  0.44     Sequence
             DRB3_0101 1137      GIVNNTVYDPLQPEL  TVYDPLQPE  5        0.2817
2373.8    42.00  0.62     Sequence
             DRB3_0101 1138      IVNNTVYDPLQPELD  TVYDPLQPE  4        0.2907
2152.2    40.00  0.75     Sequence
             DRB3_0101 1139      VNNTVYDPLQPELDS  TVYDPLQPE  3        0.2771
2494.2    43.00  0.77     Sequence
             DRB3_0101 1140      NNTVYDPLQPELDSF  TVYDPLQPE  2        0.2757
2531.0    44.00  0.64     Sequence
             DRB3_0101 1141      NTVYDPLQPELDSFK  TVYDPLQPE  1        0.2537
3211.0    50.00  0.48     Sequence
             DRB3_0101 1142      TVYDPLQPELDSFKE  LQPELDSFK  5        0.2114
5075.9    65.00  0.29     Sequence
             DRB3_0101 1143      VYDPLQPELDSFKEE  LQPELDSFK  4        0.1705
7905.5    80.00  0.45     Sequence
             DRB3_0101 1144      YDPLQPELDSFKEEL  LQPELDSFK  3        0.1633
8546.9    80.00  0.49     Sequence
             DRB3_0101 1145      DPLQPELDSFKEELD  LQPELDSFK  2        0.1607
8784.2    80.00  0.41     Sequence
             DRB3_0101 1146      PLQPELDSFKEELDK  LQPELDSFK  1        0.1449
10425.4    85.00  0.35     Sequence
             DRB3_0101 1147      LQPELDSFKEELDKY  SFKEELDKY  6        0.1554
9306.9    85.00  0.34     Sequence
             DRB3_0101 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.3441
1208.6    28.00  0.70     Sequence
             DRB3_0101 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.3681
931.3    24.00  0.78     Sequence
             DRB3_0101 1150      ELDSFKEELDKYFKN  FKEELDKYF  4        0.3891
742.1    20.00  0.70     Sequence
             DRB3_0101 1151      LDSFKEELDKYFKNH  FKEELDKYF  3        0.3909
727.8    20.00  0.70     Sequence
```

```
             DRB3_0101 1152      DSFKEELDKYFKNHT  FKEELDKYF  2        0.3648
965.2    24.00  0.64     Sequence
             DRB3_0101 1153      SFKEELDKYFKNHTS  FKEELDKYF  1        0.3404
1257.6    28.00  0.59     Sequence
             DRB3_0101 1154      FKEELDKYFKNHTSP  FKEELDKYF  0        0.2556
3146.5    49.00  0.39     Sequence
             DRB3_0101 1155      KEELDKYFKNHTSPD  YFKNHTSPD  6        0.2182
4717.8    65.00  0.44     Sequence
             DRB3_0101 1156      EELDKYFKNHTSPDV  YFKNHTSPD  5        0.2457
3502.8    55.00  0.49     Sequence
             DRB3_0101 1157      ELDKYFKNHTSPDVD  YFKNHTSPD  4        0.2634
2892.3    47.00  0.53     Sequence
             DRB3_0101 1158      LDKYFKNHTSPDVDL  YFKNHTSPD  3        0.2759
2526.1    44.00  0.51     Sequence
             DRB3_0101 1159      DKYFKNHTSPDVDLG  YFKNHTSPD  2        0.2475
3436.8    55.00  0.49     Sequence
             DRB3_0101 1160      KYFKNHTSPDVDLGD  YFKNHTSPD  1        0.2392
3757.3    55.00  0.38     Sequence
             DRB3_0101 1161      YFKNHTSPDVDLGDI  TSPDVDLGD  5        0.2087
5226.6    65.00  0.35     Sequence
             DRB3_0101 1162      FKNHTSPDVDLGDIS  TSPDVDLGD  4        0.1938
6138.9    70.00  0.41     Sequence
             DRB3_0101 1163      KNHTSPDVDLGDISG  TSPDVDLGD  3        0.1885
6504.3    75.00  0.35     Sequence
             DRB3_0101 1164      NHTSPDVDLGDISGI  PDVDLGDIS  4        0.1972
5919.6    70.00  0.43     Sequence
             DRB3_0101 1165      HTSPDVDLGDISGIN  PDVDLGDIS  3        0.2057
5400.7    65.00  0.34     Sequence
             DRB3_0101 1166      TSPDVDLGDISGINA  PDVDLGDIS  2        0.1844
6796.2    75.00  0.31     Sequence
             DRB3_0101 1167      SPDVDLGDISGINAS  DLGDISGIN  4        0.1649
8399.4    80.00  0.38     Sequence
             DRB3_0101 1168      PDVDLGDISGINASF  DLGDISGIN  3        0.1777
7307.0    75.00  0.30     Sequence
             DRB3_0101 1169      DVDLGDISGINASFV  ISGINASFV  6        0.1952
6048.8    70.00  0.34     Sequence
             DRB3_0101 1170      VDLGDISGINASFVN  ISGINASFV  5        0.1966
5957.2    70.00  0.37     Sequence
             DRB3_0101 1171      DLGDISGINASFVNI  ISGINASFV  4        0.2238
4440.8    60.00  0.34     Sequence
             DRB3_0101 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.2230
4478.3    60.00  0.32     Sequence
             DRB3_0101 1173      GDISGINASFVNIQK  ISGINASFV  2        0.2084
5242.3    65.00  0.28     Sequence
             DRB3_0101 1174      DISGINASFVNIQKE  INASFVNIQ  4        0.1810
7055.1    75.00  0.32     Sequence
             DRB3_0101 1175      ISGINASFVNIQKEI  SFVNIQKEI  6        0.2079
5270.4    65.00  0.31     Sequence
             DRB3_0101 1176      SGINASFVNIQKEID  SFVNIQKEI  5        0.2178
4736.3    65.00  0.35     Sequence
             DRB3_0101 1177      GINASFVNIQKEIDR  FVNIQKEID  5        0.2046
5466.6    70.00  0.38     Sequence
             DRB3_0101 1178      INASFVNIQKEIDRL  FVNIQKEID  4        0.2212
4565.7    60.00  0.40     Sequence
             DRB3_0101 1179      NASFVNIQKEIDRLN  IQKEIDRLN  6        0.2461
3486.3    55.00  0.37     Sequence
             DRB3_0101 1180      ASFVNIQKEIDRLNE  IQKEIDRLN  5        0.2446
3544.1    55.00  0.47     Sequence
             DRB3_0101 1181      SFVNIQKEIDRLNEV  IQKEIDRLN  4        0.2574
3086.4    49.00  0.47     Sequence
             DRB3_0101 1182      FVNIQKEIDRLNEVA  IQKEIDRLN  3        0.2514
3295.0    55.00  0.51     Sequence
             DRB3_0101 1183      VNIQKEIDRLNEVAK  IQKEIDRLN  2        0.2382
3797.5    55.00  0.47     Sequence
             DRB3_0101 1184      NIQKEIDRLNEVAKN  DRLNEVAKN  6        0.2612
2963.6    48.00  0.44     Sequence
```

```
              DRB3_0101 1185      IQKEIDRLNEVAKNL  DRLNEVAKN  5        0.2639
2877.0    47.00  0.45     Sequence
              DRB3_0101 1186      QKEIDRLNEVAKNLN  DRLNEVAKN  4        0.2440
3568.5    55.00  0.50     Sequence
              DRB3_0101 1187      KEIDRLNEVAKNLNE  DRLNEVAKN  3        0.2309
4110.7    60.00  0.52     Sequence
              DRB3_0101 1188      EIDRLNEVAKNLNES  DRLNEVAKN  2        0.1902
6382.7    75.00  0.51     Sequence
              DRB3_0101 1189      IDRLNEVAKNLNESL  VAKNLNESL  6        0.2005
5709.7    70.00  0.48     Sequence
              DRB3_0101 1190      DRLNEVAKNLNESLI  VAKNLNESL  5        0.2296
4170.7    60.00  0.64     Sequence
              DRB3_0101 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.2652
2837.3    47.00  0.68     Sequence
              DRB3_0101 1192      LNEVAKNLNESLIDL  VAKNLNESL  3        0.2883
2209.6    40.00  0.62     Sequence
              DRB3_0101 1193      NEVAKNLNESLIDLQ  VAKNLNESL  2        0.2663
2803.0    46.00  0.57     Sequence
              DRB3_0101 1194      EVAKNLNESLIDLQE  VAKNLNESL  1        0.2347
3945.1    60.00  0.44     Sequence
              DRB3_0101 1195      VAKNLNESLIDLQEL  KNLNESLID  2        0.2005
5712.6    70.00  0.28     Sequence
              DRB3_0101 1196      AKNLNESLIDLQELG  SLIDLQELG  6        0.1619
8670.2    80.00  0.26     Sequence
              DRB3_0101 1197      KNLNESLIDLQELGK  SLIDLQELG  5        0.1372
11333.9    90.00  0.39     Sequence
              DRB3_0101 1198      NLNESLIDLQELGKY  SLIDLQELG  4        0.1766
7396.4    75.00  0.32     Sequence
              DRB3_0101 1199      LNESLIDLQELGKYE  IDLQELGKY  5        0.1896
6427.1    75.00  0.32     Sequence
              DRB3_0101 1200      NESLIDLQELGKYEQ  IDLQELGKY  4        0.1739
7618.0    80.00  0.32     Sequence
              DRB3_0101 1201      ESLIDLQELGKYEQY  IDLQELGKY  3        0.1677
8147.5    80.00  0.36     Sequence
              DRB3_0101 1202      SLIDLQELGKYEQYI  DLQELGKYE  3        0.1589
8957.7    85.00  0.28     Sequence
              DRB3_0101 1203      LIDLQELGKYEQYIK  DLQELGKYE  2        0.1441
10519.0    85.00  0.26     Sequence
              DRB3_0101 1204      IDLQELGKYEQYIKW  GKYEQYIKW  6        0.1860
6685.3    75.00  0.44     Sequence
              DRB3_0101 1205      DLQELGKYEQYIKWP  GKYEQYIKW  5        0.1695
7985.8    80.00  0.56     Sequence
              DRB3_0101 1206      LQELGKYEQYIKWPW  GKYEQYIKW  4        0.2111
5095.7    65.00  0.46     Sequence
              DRB3_0101 1207      QELGKYEQYIKWPWY  GKYEQYIKW  3        0.2337
3986.9    60.00  0.40     Sequence
              DRB3_0101 1208      ELGKYEQYIKWPWYI  QYIKWPWYI  6        0.2924
2113.1    39.00  0.25     Sequence
              DRB3_0101 1209      LGKYEQYIKWPWYIW  QYIKWPWYI  5        0.3216
1540.7    32.00  0.28     Sequence
              DRB3_0101 1210      GKYEQYIKWPWYIWL  QYIKWPWYI  4        0.3382
1287.5    29.00  0.29     Sequence
              DRB3_0101 1211      KYEQYIKWPWYIWLG  QYIKWPWYI  3        0.3081
1782.9    35.00  0.31     Sequence
              DRB3_0101 1212      YEQYIKWPWYIWLGF  QYIKWPWYI  2        0.2908
2150.5    40.00  0.31     Sequence
              DRB3_0101 1213      EQYIKWPWYIWLGFI  PWYIWLGFI  6        0.2944
2067.9    39.00  0.23     Sequence
              DRB3_0101 1214      QYIKWPWYIWLGFIA  PWYIWLGFI  5        0.2750
2551.0    44.00  0.31     Sequence
              DRB3_0101 1215      YIKWPWYIWLGFIAG  PWYIWLGFI  4        0.2220
4527.3    60.00  0.35     Sequence
              DRB3_0101 1216      IKWPWYIWLGFIAGL  PWYIWLGFI  3        0.2175
4753.5    65.00  0.32     Sequence
              DRB3_0101 1217      KWPWYIWLGFIAGLI  WLGFIAGLI  6        0.2779
2471.7    43.00  0.34     Sequence
```

```
            DRB3_0101 1218      WPWYIWLGFIAGLIA  WLGFIAGLI  5        0.2656
2824.0    46.00  0.36     Sequence
            DRB3_0101 1219      PWYIWLGFIAGLIAI  WLGFIAGLI  4        0.2820
2364.4    42.00  0.36     Sequence
            DRB3_0101 1220      WYIWLGFIAGLIAIV  FIAGLIAIV  6        0.3846
779.4    21.00  0.41     Sequence
            DRB3_0101 1221      YIWLGFIAGLIAIVM  FIAGLIAIV  5        0.3931
710.9    20.00  0.40     Sequence
            DRB3_0101 1222      IWLGFIAGLIAIVMV  FIAGLIAIV  4        0.3932
710.1    20.00  0.47     Sequence
            DRB3_0101 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3        0.3614
1001.8    25.00  0.51     Sequence
            DRB3_0101 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.3498
1136.3    27.00  0.44     Sequence
            DRB3_0101 1225      GFIAGLIAIVMVTIM  IAIVMVTIM  6        0.3247
1489.7    32.00  0.27     Sequence
            DRB3_0101 1226      FIAGLIAIVMVTIML  IAIVMVTIM  5        0.2770
2495.4    43.00  0.40     Sequence
            DRB3_0101 1227      IAGLIAIVMVTIMLC  IAIVMVTIM  4        0.2520
3270.9    50.00  0.47     Sequence
            DRB3_0101 1228      AGLIAIVMVTIMLCC  IAIVMVTIM  3        0.2359
3894.6    55.00  0.47     Sequence
            DRB3_0101 1229      GLIAIVMVTIMLCCM  IAIVMVTIM  2        0.2288
4206.8    60.00  0.40     Sequence
            DRB3_0101 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3        0.1912
6315.5    70.00  0.26     Sequence
            DRB3_0101 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2        0.1696
7978.8    80.00  0.28     Sequence
            DRB3_0101 1232      AIVMVTIMLCCMTSC  IMLCCMTSC  6        0.2410
3683.7    55.00  0.62     Sequence
            DRB3_0101 1233      IVMVTIMLCCMTSCC  IMLCCMTSC  5        0.2816
2375.6    42.00  0.53     Sequence
            DRB3_0101 1234      VMVTIMLCCMTSCCS  IMLCCMTSC  4        0.2762
2519.2    43.00  0.52     Sequence
            DRB3_0101 1235      MVTIMLCCMTSCCSC  IMLCCMTSC  3        0.2653
2833.6    46.00  0.51     Sequence
            DRB3_0101 1236      VTIMLCCMTSCCSCL  MLCCMTSCC  3        0.2508
3313.9    55.00  0.46     Sequence
            DRB3_0101 1237      TIMLCCMTSCCSCLK  MLCCMTSCC  2        0.2106
5119.6    65.00  0.44     Sequence
            DRB3_0101 1238      IMLCCMTSCCSCLKG  MLCCMTSCC  1        0.1562
9229.5    85.00  0.47     Sequence
            DRB3_0101 1239      MLCCMTSCCSCLKGC  MTSCCSCLK  4        0.0931
18259.4   100.00  0.32     Sequence
            DRB3_0101 1240      LCCMTSCCSCLKGCC  MTSCCSCLK  3        0.0702
23401.2   100.00  0.40     Sequence
            DRB3_0101 1241      CCMTSCCSCLKGCCS  MTSCCSCLK  2        0.0577
26785.3   100.00  0.37     Sequence
            DRB3_0101 1242      CMTSCCSCLKGCCSC  MTSCCSCLK  1        0.0497
29211.5   100.00  0.32     Sequence
            DRB3_0101 1243      MTSCCSCLKGCCSCG  CCSCLKGCC  3        0.0434
31249.1   100.00  0.25     Sequence
            DRB3_0101 1244      TSCCSCLKGCCSCGS  LKGCCSCGS  6        0.0528
28250.4   100.00  0.47     Sequence
            DRB3_0101 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5        0.0519
28529.9   100.00  0.52     Sequence
            DRB3_0101 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.0538
27930.0   100.00  0.51     Sequence
            DRB3_0101 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.0571
26958.2   100.00  0.44     Sequence
            DRB3_0101 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2        0.0688
23745.5   100.00  0.31     Sequence
            DRB3_0101 1249      CLKGCCSCGSCCKFD  CSCGSCCKF  5        0.0843
20088.4   100.00  0.23     Sequence
            DRB3_0101 1250      LKGCCSCGSCCKFDE  CGSCCKFDE  6        0.0917
18528.9   100.00  0.31     Sequence
```

```
             DRB3_0101 1251      KGCCSCGSCCKFDED  CGSCCKFDE  5        0.1046
16130.4    95.00  0.32     Sequence
             DRB3_0101 1252      GCCSCGSCCKFDEDD  CGSCCKFDE  4        0.1082
15503.0    95.00  0.37     Sequence
             DRB3_0101 1253      CCSCGSCCKFDEDDS  CGSCCKFDE  3        0.1221
13340.6    95.00  0.28     Sequence
             DRB3_0101 1254      CSCGSCCKFDEDDSE  CKFDEDDSE  6        0.1854
6730.0    75.00  0.58     Sequence
             DRB3_0101 1255      SCGSCCKFDEDDSEP  CKFDEDDSE  5        0.1907
6354.5    70.00  0.60     Sequence
             DRB3_0101 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.3489
1146.4    27.00  0.66     Sequence
             DRB3_0101 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.4162
553.8    17.00  0.71     Sequence
             DRB3_0101 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.4056
621.0    18.00  0.75     Sequence
             DRB3_0101 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.3825
797.2    21.00  0.78     Sequence
             DRB3_0101 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.3731
882.3    23.00  0.84     Sequence
             DRB3_0101 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.3493
1142.0    27.00  0.85     Sequence
             DRB3_0101 1262      FDEDDSEPVLKGVKL  FDEDDSEPV  0        0.2197
4640.6    65.00  0.60     Sequence
             DRB3_0101 1263      DEDDSEPVLKGVKLH  DDSEPVLKG  2        0.0753
22130.3   100.00  0.29     Sequence
             DRB3_0101 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.1010
16770.0    95.00  0.32     Sequence
             DRB3_0101 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.1502
9843.4    85.00  0.58     Sequence
             DRB3_0202    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.0645
24878.0    95.00  0.38     Sequence
             DRB3_0202    2      SPIKEMFVFLVLLPL  FVFLVLLPL  6        0.0840
20159.8    95.00  0.26     Sequence
             DRB3_0202    3      PIKEMFVFLVLLPLV  FVFLVLLPL  5        0.1095
15290.2    85.00  0.32     Sequence
             DRB3_0202    4      IKEMFVFLVLLPLVS  VFLVLLPLV  5        0.1439
10535.0    75.00  0.32     Sequence
             DRB3_0202    5      KEMFVFLVLLPLVSS  VFLVLLPLV  4        0.1718
7794.2    65.00  0.33     Sequence
             DRB3_0202    6      EMFVFLVLLPLVSSQ  VFLVLLPLV  3        0.1791
7197.1    65.00  0.37     Sequence
             DRB3_0202    7      MFVFLVLLPLVSSQC  FLVLLPLVS  3        0.1818
6992.1    65.00  0.31     Sequence
             DRB3_0202    8      FVFLVLLPLVSSQCV  FLVLLPLVS  2        0.1715
7822.2    65.00  0.22     Sequence
             DRB3_0202    9      VFLVLLPLVSSQCVN  LPLVSSQCV  5        0.1577
9077.4    70.00  0.23     Sequence
             DRB3_0202   10      FLVLLPLVSSQCVNF  LPLVSSQCV  4        0.1795
7173.4    65.00  0.25     Sequence
             DRB3_0202   11      LVLLPLVSSQCVNFT  LVSSQCVNF  5        0.2168
4787.9    55.00  0.29     Sequence
             DRB3_0202   12      VLLPLVSSQCVNFTN  LVSSQCVNF  4        0.2483
3406.1    44.00  0.34     Sequence
             DRB3_0202   13      LLPLVSSQCVNFTNR  LVSSQCVNF  3        0.3064
1816.5    32.00  0.39     Sequence
             DRB3_0202   14      LPLVSSQCVNFTNRT  QCVNFTNRT  6        0.3494
1140.2    25.00  0.38     Sequence
             DRB3_0202   15      PLVSSQCVNFTNRTQ  QCVNFTNRT  5        0.3560
1061.5    24.00  0.49     Sequence
             DRB3_0202   16      LVSSQCVNFTNRTQL  QCVNFTNRT  4        0.4196
533.7    17.00  0.45     Sequence
             DRB3_0202   17      VSSQCVNFTNRTQLP  QCVNFTNRT  3        0.4433
413.1    14.00  0.41     Sequence
             DRB3_0202   18      SSQCVNFTNRTQLPS  NFTNRTQLP  5        0.4651
326.1    13.00  0.46     Sequence
```

```
             DRB3_0202   19      SQCVNFTNRTQLPSA  NFTNRTQLP  4        0.4823
270.9    11.00  0.53     Sequence
             DRB3_0202   20      QCVNFTNRTQLPSAY  NFTNRTQLP  3        0.4878
255.1    11.00  0.58     Sequence
             DRB3_0202   21      CVNFTNRTQLPSAYT  NFTNRTQLP  2        0.4614
339.5    13.00  0.56     Sequence
             DRB3_0202   22      VNFTNRTQLPSAYTN  NFTNRTQLP  1        0.3839
785.5    20.00  0.40     Sequence
             DRB3_0202   23      NFTNRTQLPSAYTNS  NRTQLPSAY  3        0.2849
2292.3    36.00  0.35     Sequence
             DRB3_0202   24      FTNRTQLPSAYTNSF  NRTQLPSAY  2        0.1920
6263.3    60.00  0.30     Sequence
             DRB3_0202   25      TNRTQLPSAYTNSFT  QLPSAYTNS  4        0.1689
8039.8    70.00  0.32     Sequence
             DRB3_0202   26      NRTQLPSAYTNSFTR  QLPSAYTNS  3        0.2084
5246.8    55.00  0.34     Sequence
             DRB3_0202   27      RTQLPSAYTNSFTRG  AYTNSFTRG  6        0.2449
3534.1    45.00  0.40     Sequence
             DRB3_0202   28      TQLPSAYTNSFTRGV  AYTNSFTRG  5        0.3246
1491.9    29.00  0.50     Sequence
             DRB3_0202   29      QLPSAYTNSFTRGVY  AYTNSFTRG  4        0.3771
845.5    21.00  0.47     Sequence
             DRB3_0202   30      LPSAYTNSFTRGVYY  AYTNSFTRG  3        0.4222
519.0    16.00  0.43     Sequence
             DRB3_0202   31      PSAYTNSFTRGVYYP  YTNSFTRGV  3        0.4383
436.0    15.00  0.36     Sequence
             DRB3_0202   32      SAYTNSFTRGVYYPD  AYTNSFTRG  1        0.4034
635.6    18.00  0.27     Sequence
             DRB3_0202   33      AYTNSFTRGVYYPDK  FTRGVYYPD  5        0.3731
882.5    22.00  0.31     Sequence
             DRB3_0202   34      YTNSFTRGVYYPDKV  FTRGVYYPD  4        0.3684
928.3    22.00  0.40     Sequence
             DRB3_0202   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.3543
1081.7    24.00  0.49     Sequence
             DRB3_0202   36      NSFTRGVYYPDKVFR  YYPDKVFRX  7        0.4233
512.9    16.00  0.38     Sequence
             DRB3_0202   37      SFTRGVYYPDKVFRS  YYPDKVFRS  6        0.5675
107.7     6.00  0.79     Sequence         WB
             DRB3_0202   38      FTRGVYYPDKVFRSS  YYPDKVFRS  5        0.6398
49.3     3.50  0.88     Sequence         WB
             DRB3_0202   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.6689
36.0     3.00  0.91     Sequence         WB
             DRB3_0202   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.6990
26.0     2.50  0.89     Sequence         WB
             DRB3_0202   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.6483
45.0     3.50  0.79     Sequence         WB
             DRB3_0202   42      VYYPDKVFRSSVLHS  YYPDKVFRS  1        0.5551
123.2     7.00  0.62     Sequence         WB
             DRB3_0202   43      YYPDKVFRSSVLHST  FRSSVLHST  6        0.4795
279.2    11.00  0.54     Sequence
             DRB3_0202   44      YPDKVFRSSVLHSTQ  FRSSVLHST  5        0.5246
171.3     8.50  0.70     Sequence         WB
             DRB3_0202   45      PDKVFRSSVLHSTQD  FRSSVLHST  4        0.5426
141.0     7.50  0.69     Sequence         WB
             DRB3_0202   46      DKVFRSSVLHSTQDL  FRSSVLHST  3        0.5558
122.3     7.00  0.75     Sequence         WB
             DRB3_0202   47      KVFRSSVLHSTQDLF  FRSSVLHST  2        0.5284
164.5     8.00  0.71     Sequence         WB
             DRB3_0202   48      VFRSSVLHSTQDLFL  FRSSVLHST  1        0.3880
750.9    20.00  0.54     Sequence
             DRB3_0202   49      FRSSVLHSTQDLFLP  FRSSVLHST  0        0.2730
2605.8    39.00  0.34     Sequence
             DRB3_0202   50      RSSVLHSTQDLFLPF  LHSTQDLFL  4        0.1512
9741.3    75.00  0.36     Sequence
             DRB3_0202   51      SSVLHSTQDLFLPFF  LHSTQDLFL  3        0.1396
11044.2    75.00  0.49     Sequence
```

```
             DRB3_0202   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2        0.1229
13231.3    80.00  0.42     Sequence
             DRB3_0202   53      VLHSTQDLFLPFFSN  LHSTQDLFL  1        0.1208
13530.7    85.00  0.28     Sequence
             DRB3_0202   54      LHSTQDLFLPFFSNV  QDLFLPFFS  4        0.1161
14240.4    85.00  0.20     Sequence
             DRB3_0202   55      HSTQDLFLPFFSNVT  FLPFFSNVT  6        0.1652
8367.6    70.00  0.31     Sequence
             DRB3_0202   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.2294
4177.3    49.00  0.32     Sequence
             DRB3_0202   57      TQDLFLPFFSNVTWF  FFSNVTWFX  7        0.3333
1358.2    27.00  0.38     Sequence
             DRB3_0202   58      QDLFLPFFSNVTWFH  FFSNVTWFH  6        0.5193
181.4     8.50  0.74     Sequence         WB
             DRB3_0202   59      DLFLPFFSNVTWFHA  FFSNVTWFH  5        0.5956
79.5     5.00  0.77     Sequence         WB
             DRB3_0202   60      LFLPFFSNVTWFHAI  FFSNVTWFH  4        0.6303
54.6     4.00  0.79     Sequence         WB
             DRB3_0202   61      FLPFFSNVTWFHAIH  FFSNVTWFH  3        0.6547
41.9     3.00  0.79     Sequence         WB
             DRB3_0202   62      LPFFSNVTWFHAIHV  FFSNVTWFH  2        0.6404
49.0     3.50  0.74     Sequence         WB
             DRB3_0202   63      PFFSNVTWFHAIHVS  FFSNVTWFH  1        0.5554
122.8     7.00  0.62     Sequence         WB
             DRB3_0202   64      FFSNVTWFHAIHVSG  FFSNVTWFH  0        0.3854
773.0    20.00  0.38     Sequence
             DRB3_0202   65      FSNVTWFHAIHVSGT  WFHAIHVSG  5        0.2714
2653.0    39.00  0.40     Sequence
             DRB3_0202   66      SNVTWFHAIHVSGTN  WFHAIHVSG  4        0.3315
1384.5    28.00  0.32     Sequence
             DRB3_0202   67      NVTWFHAIHVSGTNG  WFHAIHVSG  3        0.3611
1005.2    23.00  0.31     Sequence
             DRB3_0202   68      VTWFHAIHVSGTNGT  HAIHVSGTN  4        0.3880
751.4    20.00  0.35     Sequence
             DRB3_0202   69      TWFHAIHVSGTNGTK  HAIHVSGTN  3        0.3816
805.3    21.00  0.38     Sequence
             DRB3_0202   70      WFHAIHVSGTNGTKR  IHVSGTNGT  4        0.3558
1064.8    24.00  0.45     Sequence
             DRB3_0202   71      FHAIHVSGTNGTKRF  IHVSGTNGT  3        0.3406
1254.1    26.00  0.56     Sequence
             DRB3_0202   72      HAIHVSGTNGTKRFD  IHVSGTNGT  2        0.2811
2387.9    37.00  0.52     Sequence
             DRB3_0202   73      AIHVSGTNGTKRFDN  IHVSGTNGT  1        0.2125
5014.7    55.00  0.40     Sequence
             DRB3_0202   74      IHVSGTNGTKRFDNP  SGTNGTKRF  3        0.1740
7606.1    65.00  0.46     Sequence
             DRB3_0202   75      HVSGTNGTKRFDNPV  SGTNGTKRF  2        0.1375
11297.0    80.00  0.41     Sequence
             DRB3_0202   76      VSGTNGTKRFDNPVL  KRFDNPVLX  7        0.1474
10143.0    75.00  0.27     Sequence
             DRB3_0202   77      SGTNGTKRFDNPVLP  KRFDNPVLP  6        0.2167
4794.1    55.00  0.62     Sequence
             DRB3_0202   78      GTNGTKRFDNPVLPF  KRFDNPVLP  5        0.2967
2017.5    34.00  0.62     Sequence
             DRB3_0202   79      TNGTKRFDNPVLPFN  KRFDNPVLP  4        0.3561
1061.3    24.00  0.61     Sequence
             DRB3_0202   80      NGTKRFDNPVLPFND  KRFDNPVLP  3        0.3739
875.3    22.00  0.56     Sequence
             DRB3_0202   81      GTKRFDNPVLPFNDG  KRFDNPVLP  2        0.3640
973.7    23.00  0.54     Sequence
             DRB3_0202   82      TKRFDNPVLPFNDGV  KRFDNPVLP  1        0.3149
1656.5    30.00  0.38     Sequence
             DRB3_0202   83      KRFDNPVLPFNDGVY  DNPVLPFND  3        0.2662
2805.2    40.00  0.20     Sequence
             DRB3_0202   84      RFDNPVLPFNDGVYF  LPFNDGVYF  6        0.2769
2499.5    38.00  0.50     Sequence
```

```
             DRB3_0202   85      FDNPVLPFNDGVYFA  LPFNDGVYF  5        0.3148
1657.8    31.00  0.69     Sequence
             DRB3_0202   86      DNPVLPFNDGVYFAS  LPFNDGVYF  4        0.3461
1181.6    25.00  0.73     Sequence
             DRB3_0202   87      NPVLPFNDGVYFAST  LPFNDGVYF  3        0.3855
771.4    20.00  0.73     Sequence
             DRB3_0202   88      PVLPFNDGVYFASTE  LPFNDGVYF  2        0.3780
837.4    21.00  0.67     Sequence
             DRB3_0202   89      VLPFNDGVYFASTEK  LPFNDGVYF  1        0.3188
1588.0    30.00  0.52     Sequence
             DRB3_0202   90      LPFNDGVYFASTEKS  LPFNDGVYF  0        0.2325
4042.1    48.00  0.25     Sequence
             DRB3_0202   91      PFNDGVYFASTEKSN  YFASTEKSN  6        0.2234
4459.3    50.00  0.36     Sequence
             DRB3_0202   92      FNDGVYFASTEKSNI  YFASTEKSN  5        0.2681
2749.3    40.00  0.44     Sequence
             DRB3_0202   93      NDGVYFASTEKSNII  YFASTEKSN  4        0.2994
1959.9    33.00  0.45     Sequence
             DRB3_0202   94      DGVYFASTEKSNIIR  YFASTEKSN  3        0.3347
1337.8    27.00  0.45     Sequence
             DRB3_0202   95      GVYFASTEKSNIIRG  YFASTEKSN  2        0.3120
1709.9    31.00  0.39     Sequence
             DRB3_0202   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.2531
3233.4    43.00  0.28     Sequence
             DRB3_0202   97      YFASTEKSNIIRGWI  EKSNIIRGW  5        0.2156
4853.3    55.00  0.27     Sequence
             DRB3_0202   98      FASTEKSNIIRGWIF  EKSNIIRGW  4        0.1966
5957.9    60.00  0.38     Sequence
             DRB3_0202   99      ASTEKSNIIRGWIFG  EKSNIIRGW  3        0.1962
5985.9    60.00  0.39     Sequence
             DRB3_0202  100      STEKSNIIRGWIFGT  IIRGWIFGT  6        0.2190
4676.5    55.00  0.30     Sequence
             DRB3_0202  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5        0.2407
3697.1    46.00  0.49     Sequence
             DRB3_0202  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.2796
2427.9    37.00  0.50     Sequence
             DRB3_0202  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3        0.2816
2375.4    37.00  0.52     Sequence
             DRB3_0202  104      SNIIRGWIFGTTLDS  WIFGTTLDS  6        0.2979
1990.3    34.00  0.40     Sequence
             DRB3_0202  105      NIIRGWIFGTTLDSK  WIFGTTLDS  5        0.3180
1601.5    30.00  0.54     Sequence
             DRB3_0202  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.3131
1689.0    31.00  0.67     Sequence
             DRB3_0202  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3        0.3199
1569.7    30.00  0.71     Sequence
             DRB3_0202  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2        0.3049
1845.7    32.00  0.68     Sequence
             DRB3_0202  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1        0.2140
4935.1    55.00  0.46     Sequence
             DRB3_0202  110      WIFGTTLDSKTQSLL  FGTTLDSKT  2        0.1583
9014.2    70.00  0.21     Sequence
             DRB3_0202  111      IFGTTLDSKTQSLLI  TTLDSKTQS  3        0.1309
12136.8    80.00  0.29     Sequence
             DRB3_0202  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5        0.1485
10024.4    75.00  0.28     Sequence
             DRB3_0202  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4        0.1329
11870.6    80.00  0.35     Sequence
             DRB3_0202  114      TTLDSKTQSLLIVNN  DSKTQSLLI  3        0.1460
10303.5    75.00  0.38     Sequence
             DRB3_0202  115      TLDSKTQSLLIVNNA  KTQSLLIVN  4        0.1692
8014.8    70.00  0.32     Sequence
             DRB3_0202  116      LDSKTQSLLIVNNAT  LIVNNATXX  8        0.2688
2727.8    39.00  0.19     Sequence
             DRB3_0202  117      DSKTQSLLIVNNATN  LIVNNATNX  7        0.4604
343.1    13.00  0.41     Sequence
```

```
             DRB3_0202  118      SKTQSLLIVNNATNV  LIVNNATNV  6        0.7759
11.3     0.90  0.75     Sequence         SB
             DRB3_0202  119      KTQSLLIVNNATNVV  LIVNNATNV  5        0.8679
4.2     0.17  0.75     Sequence         SB
             DRB3_0202  120      TQSLLIVNNATNVVI  LIVNNATNV  4        0.8963
3.1     0.08  0.72     Sequence         SB
             DRB3_0202  121      QSLLIVNNATNVVIK  LIVNNATNV  3        0.9162
2.5     0.03  0.69     Sequence         SB
             DRB3_0202  122      SLLIVNNATNVVIKV  LIVNNATNV  2        0.9168
2.5     0.03  0.65     Sequence         SB
             DRB3_0202  123      LLIVNNATNVVIKVC  LIVNNATNV  1        0.8682
4.2     0.17  0.46     Sequence         SB
             DRB3_0202  124      LIVNNATNVVIKVCE  NATNVVIKV  4        0.7834
10.4     0.80  0.28     Sequence         SB
             DRB3_0202  125      IVNNATNVVIKVCEF  NATNVVIKV  3        0.6323
53.4     4.00  0.56     Sequence         WB
             DRB3_0202  126      VNNATNVVIKVCEFQ  NATNVVIKV  2        0.4324
464.6    15.00  0.71     Sequence
             DRB3_0202  127      NNATNVVIKVCEFQF  NATNVVIKV  1        0.3161
1636.3    30.00  0.58     Sequence
             DRB3_0202  128      NATNVVIKVCEFQFC  NATNVVIKV  0        0.1879
6545.5    60.00  0.29     Sequence
             DRB3_0202  129      ATNVVIKVCEFQFCN  IKVCEFQFC  5        0.1635
8524.0    70.00  0.40     Sequence
             DRB3_0202  130      TNVVIKVCEFQFCNY  IKVCEFQFC  4        0.1866
6638.9    65.00  0.45     Sequence
             DRB3_0202  131      NVVIKVCEFQFCNYP  IKVCEFQFC  3        0.1951
6053.9    60.00  0.46     Sequence
             DRB3_0202  132      VVIKVCEFQFCNYPF  IKVCEFQFC  2        0.2203
4608.6    55.00  0.38     Sequence
             DRB3_0202  133      VIKVCEFQFCNYPFL  FQFCNYPFL  6        0.3312
1388.4    28.00  0.46     Sequence
             DRB3_0202  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.3861
766.8    20.00  0.53     Sequence
             DRB3_0202  135      KVCEFQFCNYPFLGV  FQFCNYPFL  4        0.4502
383.1    14.00  0.47     Sequence
             DRB3_0202  136      VCEFQFCNYPFLGVY  FQFCNYPFL  3        0.4806
275.8    11.00  0.46     Sequence
             DRB3_0202  137      CEFQFCNYPFLGVYY  FQFCNYPFL  2        0.4981
228.1    10.00  0.45     Sequence
             DRB3_0202  138      EFQFCNYPFLGVYYH  QFCNYPFLG  2        0.4478
393.5    14.00  0.40     Sequence
             DRB3_0202  139      FQFCNYPFLGVYYHK  QFCNYPFLG  1        0.3489
1146.2    25.00  0.38     Sequence
             DRB3_0202  140      QFCNYPFLGVYYHKN  FLGVYYHKN  6        0.2541
3199.7    43.00  0.40     Sequence
             DRB3_0202  141      FCNYPFLGVYYHKNN  FLGVYYHKN  5        0.2694
2709.9    39.00  0.55     Sequence
             DRB3_0202  142      CNYPFLGVYYHKNNK  FLGVYYHKN  4        0.3158
1641.5    30.00  0.52     Sequence
             DRB3_0202  143      NYPFLGVYYHKNNKS  FLGVYYHKN  3        0.4550
364.0    13.00  0.37     Sequence
             DRB3_0202  144      YPFLGVYYHKNNKSW  YHKNNKSWX  7        0.6053
71.6     4.50  0.39     Sequence         WB
             DRB3_0202  145      PFLGVYYHKNNKSWM  YHKNNKSWM  6        0.7289
18.8     1.50  0.64     Sequence         SB
             DRB3_0202  146      FLGVYYHKNNKSWME  YHKNNKSWM  5        0.7721
11.8     0.90  0.65     Sequence         SB
             DRB3_0202  147      LGVYYHKNNKSWMES  YHKNNKSWM  4        0.7948
9.2     0.70  0.69     Sequence         SB
             DRB3_0202  148      GVYYHKNNKSWMESE  YHKNNKSWM  3        0.8014
8.6     0.60  0.71     Sequence         SB
             DRB3_0202  149      VYYHKNNKSWMESEF  YHKNNKSWM  2        0.7806
10.7     0.80  0.69     Sequence         SB
             DRB3_0202  150      YYHKNNKSWMESEFR  YHKNNKSWM  1        0.6635
38.1     3.00  0.55     Sequence         WB
```

```
            DRB3_0202  151      YHKNNKSWMESEFRV  YHKNNKSWM  0        0.4989
226.4    10.00  0.38     Sequence
            DRB3_0202  152      HKNNKSWMESEFRVY  WMESEFRVY  6        0.2007
5702.7    60.00  0.23     Sequence
            DRB3_0202  153      KNNKSWMESEFRVYS  WMESEFRVY  5        0.1592
8934.2    70.00  0.49     Sequence
            DRB3_0202  154      NNKSWMESEFRVYSS  WMESEFRVY  4        0.1672
8186.6    70.00  0.55     Sequence
            DRB3_0202  155      NKSWMESEFRVYSSA  WMESEFRVY  3        0.1869
6615.0    60.00  0.50     Sequence
            DRB3_0202  156      KSWMESEFRVYSSAN  WMESEFRVY  2        0.2147
4897.7    55.00  0.32     Sequence
            DRB3_0202  157      SWMESEFRVYSSANN  FRVYSSANN  6        0.3870
759.6    20.00  0.55     Sequence
            DRB3_0202  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.4896
250.3    11.00  0.61     Sequence
            DRB3_0202  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.5491
131.4     7.00  0.61     Sequence         WB
            DRB3_0202  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.5893
85.1     5.50  0.57     Sequence         WB
            DRB3_0202  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.6004
75.4     5.00  0.55     Sequence         WB
            DRB3_0202  162      EFRVYSSANNCTFEY  FRVYSSANN  1        0.5465
135.2     7.00  0.43     Sequence         WB
            DRB3_0202  163      FRVYSSANNCTFEYV  VYSSANNCT  2        0.4487
389.6    14.00  0.29     Sequence
            DRB3_0202  164      RVYSSANNCTFEYVS  VYSSANNCT  1        0.3180
1602.9    30.00  0.38     Sequence
            DRB3_0202  165      VYSSANNCTFEYVSQ  SANNCTFEY  3        0.2434
3590.0    45.00  0.36     Sequence
            DRB3_0202  166      YSSANNCTFEYVSQP  SANNCTFEY  2        0.1508
9778.5    75.00  0.37     Sequence
            DRB3_0202  167      SSANNCTFEYVSQPF  CTFEYVSQP  5        0.1230
13216.4    80.00  0.22     Sequence
            DRB3_0202  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.2030
5562.3    60.00  0.41     Sequence
            DRB3_0202  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.3045
1854.0    32.00  0.38     Sequence
            DRB3_0202  170      NNCTFEYVSQPFLMD  EYVSQPFLM  5        0.3547
1077.6    24.00  0.37     Sequence
            DRB3_0202  171      NCTFEYVSQPFLMDL  EYVSQPFLM  4        0.3938
705.2    19.00  0.41     Sequence
            DRB3_0202  172      CTFEYVSQPFLMDLE  EYVSQPFLM  3        0.4240
509.0    16.00  0.38     Sequence
            DRB3_0202  173      TFEYVSQPFLMDLEG  EYVSQPFLM  2        0.3949
697.5    19.00  0.41     Sequence
            DRB3_0202  174      FEYVSQPFLMDLEGK  EYVSQPFLM  1        0.3725
888.8    22.00  0.35     Sequence
            DRB3_0202  175      EYVSQPFLMDLEGKQ  FLMDLEGKQ  6        0.2920
2123.3    35.00  0.56     Sequence
            DRB3_0202  176      YVSQPFLMDLEGKQG  FLMDLEGKQ  5        0.2911
2142.4    35.00  0.81     Sequence
            DRB3_0202  177      VSQPFLMDLEGKQGN  FLMDLEGKQ  4        0.3147
1660.4    31.00  0.88     Sequence
            DRB3_0202  178      SQPFLMDLEGKQGNF  FLMDLEGKQ  3        0.3333
1358.0    27.00  0.87     Sequence
            DRB3_0202  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2        0.2987
1973.4    33.00  0.75     Sequence
            DRB3_0202  180      PFLMDLEGKQGNFKN  FLMDLEGKQ  1        0.2183
4711.2    55.00  0.60     Sequence
            DRB3_0202  181      FLMDLEGKQGNFKNL  FLMDLEGKQ  0        0.1306
12165.5    80.00  0.38     Sequence
            DRB3_0202  182      LMDLEGKQGNFKNLS  KQGNFKNLS  6        0.0746
22311.1    95.00  0.36     Sequence
            DRB3_0202  183      MDLEGKQGNFKNLSE  KQGNFKNLS  5        0.1046
16122.9    90.00  0.41     Sequence
```

```
             DRB3_0202  184      DLEGKQGNFKNLSEF  KQGNFKNLS  4        0.1356
11533.2    80.00  0.41     Sequence
             DRB3_0202  185      LEGKQGNFKNLSEFV  NFKNLSEFV  6        0.2469
3457.5    44.00  0.57     Sequence
             DRB3_0202  186      EGKQGNFKNLSEFVF  NFKNLSEFV  5        0.3483
1154.6    25.00  0.68     Sequence
             DRB3_0202  187      GKQGNFKNLSEFVFK  NFKNLSEFV  4        0.4074
609.1    18.00  0.69     Sequence
             DRB3_0202  188      KQGNFKNLSEFVFKN  NFKNLSEFV  3        0.4460
401.1    14.00  0.64     Sequence
             DRB3_0202  189      QGNFKNLSEFVFKNI  NFKNLSEFV  2        0.4423
417.3    14.00  0.52     Sequence
             DRB3_0202  190      GNFKNLSEFVFKNID  NFKNLSEFV  1        0.4224
517.9    16.00  0.41     Sequence
             DRB3_0202  191      NFKNLSEFVFKNIDG  KNLSEFVFK  2        0.3521
1107.4    25.00  0.32     Sequence
             DRB3_0202  192      FKNLSEFVFKNIDGY  VFKNIDGYX  7        0.2600
2999.4    41.00  0.25     Sequence
             DRB3_0202  193      KNLSEFVFKNIDGYF  VFKNIDGYF  6        0.2696
2705.2    39.00  0.39     Sequence
             DRB3_0202  194      NLSEFVFKNIDGYFK  VFKNIDGYF  5        0.3195
1576.1    30.00  0.44     Sequence
             DRB3_0202  195      LSEFVFKNIDGYFKI  VFKNIDGYF  4        0.3637
977.2    23.00  0.43     Sequence
             DRB3_0202  196      SEFVFKNIDGYFKIY  VFKNIDGYF  3        0.3877
753.8    20.00  0.43     Sequence
             DRB3_0202  197      EFVFKNIDGYFKIYS  VFKNIDGYF  2        0.3599
1018.6    24.00  0.37     Sequence
             DRB3_0202  198      FVFKNIDGYFKIYSK  FKNIDGYFK  2        0.3199
1570.0    30.00  0.32     Sequence
             DRB3_0202  199      VFKNIDGYFKIYSKH  FKNIDGYFK  1        0.2207
4593.5    55.00  0.34     Sequence
             DRB3_0202  200      FKNIDGYFKIYSKHT  YFKIYSKHT  6        0.1956
6020.8    60.00  0.31     Sequence
             DRB3_0202  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.2287
4210.1    49.00  0.41     Sequence
             DRB3_0202  202      NIDGYFKIYSKHTPI  KIYSKHTPI  6        0.3153
1649.8    30.00  0.25     Sequence
             DRB3_0202  203      IDGYFKIYSKHTPIN  KIYSKHTPI  5        0.4243
507.3    16.00  0.26     Sequence
             DRB3_0202  204      DGYFKIYSKHTPINL  YSKHTPINL  6        0.5154
189.2     9.00  0.34     Sequence         WB
             DRB3_0202  205      GYFKIYSKHTPINLV  YSKHTPINL  5        0.5760
98.2     6.00  0.45     Sequence         WB
             DRB3_0202  206      YFKIYSKHTPINLVR  YSKHTPINL  4        0.6041
72.5     4.50  0.55     Sequence         WB
             DRB3_0202  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.5921
82.6     5.00  0.61     Sequence         WB
             DRB3_0202  208      KIYSKHTPINLVRDL  YSKHTPINL  2        0.5124
195.5     9.00  0.56     Sequence         WB
             DRB3_0202  209      IYSKHTPINLVRDLP  YSKHTPINL  1        0.3926
714.5    19.00  0.46     Sequence
             DRB3_0202  210      YSKHTPINLVRDLPQ  TPINLVRDL  4        0.2580
3067.8    42.00  0.28     Sequence
             DRB3_0202  211      SKHTPINLVRDLPQG  LVRDLPQGX  7        0.2415
3666.4    46.00  0.31     Sequence
             DRB3_0202  212      KHTPINLVRDLPQGF  LVRDLPQGF  6        0.2962
2027.8    34.00  0.60     Sequence
             DRB3_0202  213      HTPINLVRDLPQGFS  LVRDLPQGF  5        0.3383
1286.4    27.00  0.77     Sequence
             DRB3_0202  214      TPINLVRDLPQGFSA  LVRDLPQGF  4        0.3738
875.5    22.00  0.80     Sequence
             DRB3_0202  215      PINLVRDLPQGFSAL  LVRDLPQGF  3        0.3997
661.6    19.00  0.85     Sequence
             DRB3_0202  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.3967
683.5    19.00  0.76     Sequence
```

```
             DRB3_0202  217      NLVRDLPQGFSALEP  LVRDLPQGF  1        0.2741
2577.3    38.00  0.60     Sequence
             DRB3_0202  218      LVRDLPQGFSALEPL  LVRDLPQGF  0        0.1347
11638.1    80.00  0.34     Sequence
             DRB3_0202  219      VRDLPQGFSALEPLV  LPQGFSALE  3        0.0732
22640.1    95.00  0.23     Sequence
             DRB3_0202  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.0755
22094.6    95.00  0.28     Sequence
             DRB3_0202  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.0865
19613.6    90.00  0.40     Sequence
             DRB3_0202  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.1006
16838.6    90.00  0.44     Sequence
             DRB3_0202  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.1072
15676.2    85.00  0.50     Sequence
             DRB3_0202  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.1101
15194.7    85.00  0.47     Sequence
             DRB3_0202  225      GFSALEPLVDLPIGI  PLVDLPIGI  6        0.0880
19293.2    90.00  0.32     Sequence
             DRB3_0202  226      FSALEPLVDLPIGIN  PLVDLPIGI  5        0.1055
15964.6    85.00  0.48     Sequence
             DRB3_0202  227      SALEPLVDLPIGINI  PLVDLPIGI  4        0.1213
13454.2    85.00  0.51     Sequence
             DRB3_0202  228      ALEPLVDLPIGINIT  PLVDLPIGI  3        0.1514
9719.9    75.00  0.46     Sequence
             DRB3_0202  229      LEPLVDLPIGINITR  PLVDLPIGI  2        0.1834
6873.1    65.00  0.37     Sequence
             DRB3_0202  230      EPLVDLPIGINITRF  IGINITRFX  7        0.2262
4328.1    50.00  0.33     Sequence
             DRB3_0202  231      PLVDLPIGINITRFQ  IGINITRFQ  6        0.3278
1440.3    28.00  0.67     Sequence
             DRB3_0202  232      LVDLPIGINITRFQT  IGINITRFQ  5        0.3927
714.3    19.00  0.76     Sequence
             DRB3_0202  233      VDLPIGINITRFQTL  IGINITRFQ  4        0.4213
523.8    16.00  0.81     Sequence
             DRB3_0202  234      DLPIGINITRFQTLL  IGINITRFQ  3        0.4462
400.3    14.00  0.81     Sequence
             DRB3_0202  235      LPIGINITRFQTLLA  IGINITRFQ  2        0.4362
446.1    15.00  0.71     Sequence
             DRB3_0202  236      PIGINITRFQTLLAL  IGINITRFQ  1        0.3554
1068.7    24.00  0.55     Sequence
             DRB3_0202  237      IGINITRFQTLLALH  IGINITRFQ  0        0.2779
2473.3    37.00  0.27     Sequence
             DRB3_0202  238      GINITRFQTLLALHR  FQTLLALHR  6        0.2427
3617.3    45.00  0.44     Sequence
             DRB3_0202  239      INITRFQTLLALHRS  FQTLLALHR  5        0.2887
2200.2    35.00  0.51     Sequence
             DRB3_0202  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.3122
1705.3    31.00  0.53     Sequence
             DRB3_0202  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.3441
1208.0    26.00  0.52     Sequence
             DRB3_0202  242      TRFQTLLALHRSYLT  LALHRSYLT  6        0.3894
740.1    20.00  0.41     Sequence
             DRB3_0202  243      RFQTLLALHRSYLTP  LALHRSYLT  5        0.4193
535.4    17.00  0.52     Sequence
             DRB3_0202  244      FQTLLALHRSYLTPG  LALHRSYLT  4        0.4256
500.4    16.00  0.61     Sequence
             DRB3_0202  245      QTLLALHRSYLTPGD  LALHRSYLT  3        0.4268
493.9    16.00  0.65     Sequence
             DRB3_0202  246      TLLALHRSYLTPGDS  LALHRSYLT  2        0.3937
706.5    19.00  0.58     Sequence
             DRB3_0202  247      LLALHRSYLTPGDSS  LALHRSYLT  1        0.3564
1057.7    24.00  0.42     Sequence
             DRB3_0202  248      LALHRSYLTPGDSSS  LHRSYLTPG  2        0.2914
2137.0    35.00  0.37     Sequence
             DRB3_0202  249      ALHRSYLTPGDSSSG  LHRSYLTPG  1        0.2039
5507.8    60.00  0.38     Sequence
```

```
            DRB3_0202  250      LHRSYLTPGDSSSGW  LTPGDSSSG  5        0.1828
6917.4    65.00  0.32     Sequence
            DRB3_0202  251      HRSYLTPGDSSSGWT  LTPGDSSSG  4        0.1821
6967.3    65.00  0.46     Sequence
            DRB3_0202  252      RSYLTPGDSSSGWTA  LTPGDSSSG  3        0.1543
9412.9    70.00  0.61     Sequence
            DRB3_0202  253      SYLTPGDSSSGWTAG  LTPGDSSSG  2        0.1233
13163.2    80.00  0.58     Sequence
            DRB3_0202  254      YLTPGDSSSGWTAGA  LTPGDSSSG  1        0.0683
23887.5    95.00  0.47     Sequence
            DRB3_0202  255      LTPGDSSSGWTAGAA  GDSSSGWTA  3        0.0325
35163.6   100.00  0.33     Sequence
            DRB3_0202  256      TPGDSSSGWTAGAAA  GDSSSGWTA  2        0.0334
34849.6   100.00  0.38     Sequence
            DRB3_0202  257      PGDSSSGWTAGAAAY  WTAGAAAYX  7        0.0664
24366.8    95.00  0.31     Sequence
            DRB3_0202  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.1715
7819.8    65.00  0.69     Sequence
            DRB3_0202  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.2647
2852.1    40.00  0.69     Sequence
            DRB3_0202  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.2899
2172.3    35.00  0.71     Sequence
            DRB3_0202  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.3121
1707.9    31.00  0.74     Sequence
            DRB3_0202  262      SGWTAGAAAYYVGYL  WTAGAAAYY  2        0.3087
1771.7    32.00  0.67     Sequence
            DRB3_0202  263      GWTAGAAAYYVGYLQ  WTAGAAAYY  1        0.2395
3746.2    46.00  0.49     Sequence
            DRB3_0202  264      WTAGAAAYYVGYLQP  WTAGAAAYY  0        0.1559
9255.9    70.00  0.27     Sequence
            DRB3_0202  265      TAGAAAYYVGYLQPR  YYVGYLQPR  6        0.1902
6382.6    60.00  0.64     Sequence
            DRB3_0202  266      AGAAAYYVGYLQPRT  YYVGYLQPR  5        0.2600
3001.0    41.00  0.57     Sequence
            DRB3_0202  267      GAAAYYVGYLQPRTF  YYVGYLQPR  4        0.3165
1628.7    30.00  0.49     Sequence
            DRB3_0202  268      AAAYYVGYLQPRTFL  YYVGYLQPR  3        0.3572
1048.5    24.00  0.41     Sequence
            DRB3_0202  269      AAYYVGYLQPRTFLL  YYVGYLQPR  2        0.4016
648.2    18.00  0.31     Sequence
            DRB3_0202  270      AYYVGYLQPRTFLLK  YLQPRTFLL  5        0.4103
590.1    17.00  0.22     Sequence
            DRB3_0202  271      YYVGYLQPRTFLLKY  YLQPRTFLL  4        0.3990
666.8    19.00  0.31     Sequence
            DRB3_0202  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.3894
740.0    20.00  0.42     Sequence
            DRB3_0202  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.3623
992.3    23.00  0.42     Sequence
            DRB3_0202  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.3185
1593.5    30.00  0.37     Sequence
            DRB3_0202  275      YLQPRTFLLKYNENG  FLLKYNENG  6        0.3021
1903.0    33.00  0.47     Sequence
            DRB3_0202  276      LQPRTFLLKYNENGT  FLLKYNENG  5        0.4156
557.5    17.00  0.56     Sequence
            DRB3_0202  277      QPRTFLLKYNENGTI  LKYNENGTI  6        0.5297
162.2     8.00  0.45     Sequence         WB
            DRB3_0202  278      PRTFLLKYNENGTIT  LKYNENGTI  5        0.6354
51.7     4.00  0.50     Sequence         WB
            DRB3_0202  279      RTFLLKYNENGTITD  LKYNENGTI  4        0.6624
38.6     3.00  0.54     Sequence         WB
            DRB3_0202  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.6859
29.9     2.50  0.54     Sequence         WB
            DRB3_0202  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.6855
30.0     2.50  0.46     Sequence         WB
            DRB3_0202  282      LLKYNENGTITDAVD  YNENGTITD  3        0.6301
54.7     4.00  0.55     Sequence         WB
```

```
             DRB3_0202  283      LKYNENGTITDAVDC  YNENGTITD  2        0.5090
202.8     9.50  0.59     Sequence         WB
             DRB3_0202  284      KYNENGTITDAVDCA  YNENGTITD  1        0.2447
3542.5    45.00  0.63     Sequence
             DRB3_0202  285      YNENGTITDAVDCAL  YNENGTITD  0        0.1024
16506.5    90.00  0.29     Sequence
             DRB3_0202  286      NENGTITDAVDCALD  GTITDAVDC  3        0.0686
23810.6    95.00  0.43     Sequence
             DRB3_0202  287      ENGTITDAVDCALDP  GTITDAVDC  2        0.0696
23555.9    95.00  0.35     Sequence
             DRB3_0202  288      NGTITDAVDCALDPL  DAVDCALDP  5        0.0706
23291.9    95.00  0.32     Sequence
             DRB3_0202  289      GTITDAVDCALDPLS  DAVDCALDP  4        0.0589
26441.2   100.00  0.45     Sequence
             DRB3_0202  290      TITDAVDCALDPLSE  DAVDCALDP  3        0.0610
25846.9   100.00  0.50     Sequence
             DRB3_0202  291      ITDAVDCALDPLSET  CALDPLSET  6        0.0818
20639.7    95.00  0.43     Sequence
             DRB3_0202  292      TDAVDCALDPLSETK  CALDPLSET  5        0.0968
17550.8    90.00  0.69     Sequence
             DRB3_0202  293      DAVDCALDPLSETKC  CALDPLSET  4        0.1040
16220.2    90.00  0.75     Sequence
             DRB3_0202  294      AVDCALDPLSETKCT  CALDPLSET  3        0.1154
14352.6    85.00  0.78     Sequence
             DRB3_0202  295      VDCALDPLSETKCTL  CALDPLSET  2        0.1122
14842.9    85.00  0.66     Sequence
             DRB3_0202  296      DCALDPLSETKCTLK  CALDPLSET  1        0.0857
19786.6    95.00  0.46     Sequence
             DRB3_0202  297      CALDPLSETKCTLKS  DPLSETKCT  3        0.0709
23222.9    95.00  0.44     Sequence
             DRB3_0202  298      ALDPLSETKCTLKSF  DPLSETKCT  2        0.0512
28727.5   100.00  0.44     Sequence
             DRB3_0202  299      LDPLSETKCTLKSFT  LSETKCTLK  3        0.0515
28647.1   100.00  0.31     Sequence
             DRB3_0202  300      DPLSETKCTLKSFTV  TLKSFTVXX  8        0.0599
26140.2   100.00  0.16     Sequence
             DRB3_0202  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.0664
24378.4    95.00  0.22     Sequence
             DRB3_0202  302      LSETKCTLKSFTVEK  TLKSFTVEK  6        0.0936
18155.0    90.00  0.35     Sequence
             DRB3_0202  303      SETKCTLKSFTVEKG  TLKSFTVEK  5        0.1100
15215.8    85.00  0.41     Sequence
             DRB3_0202  304      ETKCTLKSFTVEKGI  TLKSFTVEK  4        0.1309
12125.0    80.00  0.41     Sequence
             DRB3_0202  305      TKCTLKSFTVEKGIY  TLKSFTVEK  3        0.1538
9467.4    70.00  0.41     Sequence
             DRB3_0202  306      KCTLKSFTVEKGIYQ  FTVEKGIYQ  6        0.1860
6683.2    65.00  0.55     Sequence
             DRB3_0202  307      CTLKSFTVEKGIYQT  FTVEKGIYQ  5        0.2471
3450.1    44.00  0.75     Sequence
             DRB3_0202  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.2852
2285.9    36.00  0.80     Sequence
             DRB3_0202  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.3186
1591.9    30.00  0.82     Sequence
             DRB3_0202  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.3213
1545.2    29.00  0.69     Sequence
             DRB3_0202  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.2904
2158.9    35.00  0.47     Sequence
             DRB3_0202  312      FTVEKGIYQTSNFRV  YQTSNFRVX  7        0.3318
1379.9    28.00  0.31     Sequence
             DRB3_0202  313      TVEKGIYQTSNFRVQ  YQTSNFRVQ  6        0.4368
442.8    15.00  0.42     Sequence
             DRB3_0202  314      VEKGIYQTSNFRVQP  YQTSNFRVQ  5        0.4897
249.9    11.00  0.43     Sequence
             DRB3_0202  315      EKGIYQTSNFRVQPT  YQTSNFRVQ  4        0.5272
166.6     8.50  0.44     Sequence         WB
```

```
             DRB3_0202  316      KGIYQTSNFRVQPTE  YQTSNFRVQ  3        0.5532
125.7     7.00  0.43     Sequence         WB
             DRB3_0202  317      GIYQTSNFRVQPTES  YQTSNFRVQ  2        0.5236
173.3     8.50  0.37     Sequence         WB
             DRB3_0202  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.4463
399.7    14.00  0.38     Sequence
             DRB3_0202  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.4699
309.6    12.00  0.73     Sequence
             DRB3_0202  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.5461
135.8     7.50  0.73     Sequence         WB
             DRB3_0202  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.6022
74.0     5.00  0.63     Sequence         WB
             DRB3_0202  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.5861
88.0     5.50  0.52     Sequence         WB
             DRB3_0202  323      NFRVQPTESIVRFPN  VQPTESIVR  3        0.5003
223.0    10.00  0.55     Sequence
             DRB3_0202  324      FRVQPTESIVRFPNI  VQPTESIVR  2        0.4174
546.8    17.00  0.69     Sequence
             DRB3_0202  325      RVQPTESIVRFPNIT  VQPTESIVR  1        0.2732
2601.3    38.00  0.55     Sequence
             DRB3_0202  326      VQPTESIVRFPNITN  VQPTESIVR  0        0.2027
5578.9    60.00  0.27     Sequence
             DRB3_0202  327      QPTESIVRFPNITNL  RFPNITNLX  7        0.2301
4146.6    49.00  0.34     Sequence
             DRB3_0202  328      PTESIVRFPNITNLC  RFPNITNLC  6        0.2759
2527.0    38.00  0.50     Sequence
             DRB3_0202  329      TESIVRFPNITNLCP  RFPNITNLC  5        0.3010
1925.3    33.00  0.54     Sequence
             DRB3_0202  330      ESIVRFPNITNLCPF  RFPNITNLC  4        0.3305
1398.8    28.00  0.52     Sequence
             DRB3_0202  331      SIVRFPNITNLCPFG  RFPNITNLC  3        0.3667
946.0    23.00  0.47     Sequence
             DRB3_0202  332      IVRFPNITNLCPFGE  NITNLCPFG  5        0.3650
963.3    23.00  0.41     Sequence
             DRB3_0202  333      VRFPNITNLCPFGEV  NITNLCPFG  4        0.3163
1632.1    30.00  0.54     Sequence
             DRB3_0202  334      RFPNITNLCPFGEVF  NITNLCPFG  3        0.2949
2056.7    34.00  0.69     Sequence
             DRB3_0202  335      FPNITNLCPFGEVFN  NITNLCPFG  2        0.2579
3068.4    42.00  0.65     Sequence
             DRB3_0202  336      PNITNLCPFGEVFNA  NITNLCPFG  1        0.2072
5314.4    55.00  0.52     Sequence
             DRB3_0202  337      NITNLCPFGEVFNAT  NITNLCPFG  0        0.1585
8996.3    70.00  0.30     Sequence
             DRB3_0202  338      ITNLCPFGEVFNATR  FGEVFNATR  6        0.1009
16790.2    90.00  0.25     Sequence
             DRB3_0202  339      TNLCPFGEVFNATRF  FGEVFNATR  5        0.1231
13203.3    80.00  0.34     Sequence
             DRB3_0202  340      NLCPFGEVFNATRFA  EVFNATRFA  6        0.2356
3908.2    47.00  0.56     Sequence
             DRB3_0202  341      LCPFGEVFNATRFAS  EVFNATRFA  5        0.3425
1228.8    26.00  0.55     Sequence
             DRB3_0202  342      CPFGEVFNATRFASV  EVFNATRFA  4        0.3978
675.6    19.00  0.50     Sequence
             DRB3_0202  343      PFGEVFNATRFASVY  EVFNATRFA  3        0.4484
390.7    14.00  0.42     Sequence
             DRB3_0202  344      FGEVFNATRFASVYA  FNATRFASV  4        0.4744
294.9    12.00  0.48     Sequence
             DRB3_0202  345      GEVFNATRFASVYAW  FNATRFASV  3        0.4600
344.6    13.00  0.56     Sequence
             DRB3_0202  346      EVFNATRFASVYAWN  FNATRFASV  2        0.4113
583.7    17.00  0.49     Sequence
             DRB3_0202  347      VFNATRFASVYAWNR  FASVYAWNR  6        0.3687
925.8    22.00  0.40     Sequence
             DRB3_0202  348      FNATRFASVYAWNRK  FASVYAWNR  5        0.4223
518.3    16.00  0.54     Sequence
```

```
             DRB3_0202  349      NATRFASVYAWNRKR  FASVYAWNR  4        0.4779
284.1    12.00  0.54     Sequence
             DRB3_0202  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.5398
145.4     7.50  0.47     Sequence         WB
             DRB3_0202  351      TRFASVYAWNRKRIS  YAWNRKRIS  6        0.5742
100.2     6.00  0.43     Sequence         WB
             DRB3_0202  352      RFASVYAWNRKRISN  YAWNRKRIS  5        0.5965
78.7     5.00  0.54     Sequence         WB
             DRB3_0202  353      FASVYAWNRKRISNC  YAWNRKRIS  4        0.5796
94.5     5.50  0.67     Sequence         WB
             DRB3_0202  354      ASVYAWNRKRISNCV  YAWNRKRIS  3        0.5620
114.4     6.50  0.75     Sequence         WB
             DRB3_0202  355      SVYAWNRKRISNCVA  YAWNRKRIS  2        0.5455
136.6     7.50  0.68     Sequence         WB
             DRB3_0202  356      VYAWNRKRISNCVAD  YAWNRKRIS  1        0.4664
321.5    12.00  0.50     Sequence
             DRB3_0202  357      YAWNRKRISNCVADY  YAWNRKRIS  0        0.3773
843.7    21.00  0.24     Sequence
             DRB3_0202  358      AWNRKRISNCVADYS  KRISNCVAD  4        0.3020
1906.0    33.00  0.35     Sequence
             DRB3_0202  359      WNRKRISNCVADYSV  KRISNCVAD  3        0.3129
1693.6    31.00  0.35     Sequence
             DRB3_0202  360      NRKRISNCVADYSVL  RISNCVADY  3        0.3336
1354.0    27.00  0.22     Sequence
             DRB3_0202  361      RKRISNCVADYSVLY  CVADYSVLY  6        0.3790
828.0    21.00  0.46     Sequence
             DRB3_0202  362      KRISNCVADYSVLYN  CVADYSVLY  5        0.3827
795.5    21.00  0.69     Sequence
             DRB3_0202  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.3960
689.3    19.00  0.76     Sequence
             DRB3_0202  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.4092
597.1    18.00  0.79     Sequence
             DRB3_0202  365      SNCVADYSVLYNSAS  CVADYSVLY  2        0.4134
570.7    17.00  0.70     Sequence
             DRB3_0202  366      NCVADYSVLYNSASF  CVADYSVLY  1        0.4167
550.7    17.00  0.41     Sequence
             DRB3_0202  367      CVADYSVLYNSASFS  VLYNSASFS  6        0.5659
109.5     6.50  0.78     Sequence         WB
             DRB3_0202  368      VADYSVLYNSASFST  VLYNSASFS  5        0.6773
32.8     2.50  0.81     Sequence         WB
             DRB3_0202  369      ADYSVLYNSASFSTF  VLYNSASFS  4        0.7220
20.2     1.60  0.78     Sequence         SB
             DRB3_0202  370      DYSVLYNSASFSTFK  VLYNSASFS  3        0.7544
14.3     1.10  0.77     Sequence         SB
             DRB3_0202  371      YSVLYNSASFSTFKC  VLYNSASFS  2        0.7594
13.5     1.10  0.70     Sequence         SB
             DRB3_0202  372      SVLYNSASFSTFKCY  VLYNSASFS  1        0.6263
57.0     4.00  0.57     Sequence         WB
             DRB3_0202  373      VLYNSASFSTFKCYG  VLYNSASFS  0        0.5201
180.0     8.50  0.40     Sequence         WB
             DRB3_0202  374      LYNSASFSTFKCYGV  NSASFSTFK  2        0.2072
5313.4    55.00  0.31     Sequence
             DRB3_0202  375      YNSASFSTFKCYGVS  NSASFSTFK  1        0.1046
16119.2    90.00  0.31     Sequence
             DRB3_0202  376      NSASFSTFKCYGVSP  KCYGVSPXX  8        0.1083
15487.4    85.00  0.15     Sequence
             DRB3_0202  377      SASFSTFKCYGVSPT  KCYGVSPTX  7        0.1747
7550.0    65.00  0.23     Sequence
             DRB3_0202  378      ASFSTFKCYGVSPTK  KCYGVSPTK  6        0.2237
4445.2    50.00  0.25     Sequence
             DRB3_0202  379      SFSTFKCYGVSPTKL  KCYGVSPTK  5        0.2776
2480.2    38.00  0.22     Sequence
             DRB3_0202  380      FSTFKCYGVSPTKLN  YGVSPTKLN  6        0.3599
1017.9    23.00  0.33     Sequence
             DRB3_0202  381      STFKCYGVSPTKLND  YGVSPTKLN  5        0.3725
888.7    22.00  0.47     Sequence
```

```
            DRB3_0202  382      TFKCYGVSPTKLNDL  YGVSPTKLN  4        0.3861
766.7    20.00  0.59     Sequence
            DRB3_0202  383      FKCYGVSPTKLNDLC  YGVSPTKLN  3        0.3602
1014.3    23.00  0.75     Sequence
            DRB3_0202  384      KCYGVSPTKLNDLCF  YGVSPTKLN  2        0.2849
2293.1    36.00  0.69     Sequence
            DRB3_0202  385      CYGVSPTKLNDLCFT  YGVSPTKLN  1        0.1834
6876.0    65.00  0.51     Sequence
            DRB3_0202  386      YGVSPTKLNDLCFTN  YGVSPTKLN  0        0.1141
14555.6    85.00  0.27     Sequence
            DRB3_0202  387      GVSPTKLNDLCFTNV  TKLNDLCFT  4        0.1133
14678.6    85.00  0.39     Sequence
            DRB3_0202  388      VSPTKLNDLCFTNVY  TKLNDLCFT  3        0.1624
8629.6    70.00  0.31     Sequence
            DRB3_0202  389      SPTKLNDLCFTNVYA  KLNDLCFTN  3        0.2039
5508.6    60.00  0.24     Sequence
            DRB3_0202  390      PTKLNDLCFTNVYAD  CFTNVYADX  7        0.2151
4876.5    55.00  0.21     Sequence
            DRB3_0202  391      TKLNDLCFTNVYADS  CFTNVYADS  6        0.3555
1067.9    24.00  0.61     Sequence
            DRB3_0202  392      KLNDLCFTNVYADSF  CFTNVYADS  5        0.4364
445.0    15.00  0.71     Sequence
            DRB3_0202  393      LNDLCFTNVYADSFV  CFTNVYADS  4        0.4740
296.3    12.00  0.71     Sequence
            DRB3_0202  394      NDLCFTNVYADSFVI  CFTNVYADS  3        0.4981
228.3    10.00  0.69     Sequence
            DRB3_0202  395      DLCFTNVYADSFVIR  CFTNVYADS  2        0.4914
245.5    11.00  0.52     Sequence
            DRB3_0202  396      LCFTNVYADSFVIRG  CFTNVYADS  1        0.4660
322.9    12.00  0.41     Sequence
            DRB3_0202  397      CFTNVYADSFVIRGD  NVYADSFVI  3        0.4070
611.5    18.00  0.28     Sequence
            DRB3_0202  398      FTNVYADSFVIRGDE  YADSFVIRG  4        0.3308
1394.7    28.00  0.31     Sequence
            DRB3_0202  399      TNVYADSFVIRGDEV  YADSFVIRG  3        0.2986
1975.9    33.00  0.44     Sequence
            DRB3_0202  400      NVYADSFVIRGDEVR  YADSFVIRG  2        0.2123
5029.5    55.00  0.38     Sequence
            DRB3_0202  401      VYADSFVIRGDEVRQ  FVIRGDEVR  5        0.1705
7901.3    65.00  0.25     Sequence
            DRB3_0202  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.1781
7282.7    65.00  0.31     Sequence
            DRB3_0202  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.2099
5158.3    55.00  0.44     Sequence
            DRB3_0202  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.2152
4871.9    55.00  0.49     Sequence
            DRB3_0202  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.2160
4828.4    55.00  0.59     Sequence
            DRB3_0202  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.1988
5820.6    60.00  0.51     Sequence
            DRB3_0202  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.1301
12235.3    80.00  0.32     Sequence
            DRB3_0202  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.1146
14471.7    85.00  0.30     Sequence
            DRB3_0202  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.1385
11167.4    75.00  0.34     Sequence
            DRB3_0202  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.1552
9323.6    70.00  0.34     Sequence
            DRB3_0202  411      DEVRQIAPGQTGTIA  RQIAPGQTG  3        0.1485
10029.5    75.00  0.39     Sequence
            DRB3_0202  412      EVRQIAPGQTGTIAD  RQIAPGQTG  2        0.1375
11295.2    80.00  0.39     Sequence
            DRB3_0202  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.0962
17666.5    90.00  0.41     Sequence
            DRB3_0202  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.0729
22713.5    95.00  0.46     Sequence
```

```
             DRB3_0202  415      QIAPGQTGTIADYNY  IAPGQTGTI  1        0.0543
27778.7   100.00  0.28     Sequence
             DRB3_0202  416      IAPGQTGTIADYNYK  QTGTIADYN  4        0.0684
23863.0    95.00  0.28     Sequence
             DRB3_0202  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.1307
12157.3    80.00  0.54     Sequence
             DRB3_0202  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.1984
5844.7    60.00  0.62     Sequence
             DRB3_0202  419      GQTGTIADYNYKLPD  TIADYNYKL  4        0.2188
4684.6    55.00  0.65     Sequence
             DRB3_0202  420      QTGTIADYNYKLPDD  TIADYNYKL  3        0.2282
4234.0    49.00  0.64     Sequence
             DRB3_0202  421      TGTIADYNYKLPDDF  TIADYNYKL  2        0.2356
3908.5    47.00  0.62     Sequence
             DRB3_0202  422      GTIADYNYKLPDDFT  TIADYNYKL  1        0.2092
5198.4    55.00  0.50     Sequence
             DRB3_0202  423      TIADYNYKLPDDFTG  TIADYNYKL  0        0.1609
8772.5    70.00  0.29     Sequence
             DRB3_0202  424      IADYNYKLPDDFTGC  YKLPDDFTG  5        0.1093
15318.5    85.00  0.35     Sequence
             DRB3_0202  425      ADYNYKLPDDFTGCV  YKLPDDFTG  4        0.1078
15580.6    85.00  0.44     Sequence
             DRB3_0202  426      DYNYKLPDDFTGCVI  YKLPDDFTG  3        0.1121
14867.1    85.00  0.48     Sequence
             DRB3_0202  427      YNYKLPDDFTGCVIA  YKLPDDFTG  2        0.1212
13473.0    85.00  0.44     Sequence
             DRB3_0202  428      NYKLPDDFTGCVIAW  YKLPDDFTG  1        0.0944
18010.0    90.00  0.28     Sequence
             DRB3_0202  429      YKLPDDFTGCVIAWN  FTGCVIAWN  6        0.1018
16627.1    90.00  0.35     Sequence
             DRB3_0202  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.1433
10611.0    75.00  0.47     Sequence
             DRB3_0202  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.2328
4027.8    48.00  0.43     Sequence
             DRB3_0202  432      PDDFTGCVIAWNSNN  CVIAWNSNN  6        0.4767
287.8    12.00  0.55     Sequence
             DRB3_0202  433      DDFTGCVIAWNSNNL  CVIAWNSNN  5        0.6378
50.4     3.50  0.51     Sequence         WB
             DRB3_0202  434      DFTGCVIAWNSNNLD  CVIAWNSNN  4        0.6784
32.5     2.50  0.47     Sequence         WB
             DRB3_0202  435      FTGCVIAWNSNNLDS  IAWNSNNLD  5        0.7269
19.2     1.60  0.47     Sequence         SB
             DRB3_0202  436      TGCVIAWNSNNLDSK  IAWNSNNLD  4        0.7496
15.0     1.20  0.49     Sequence         SB
             DRB3_0202  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3        0.7552
14.1     1.10  0.51     Sequence         SB
             DRB3_0202  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2        0.7047
24.4     2.00  0.47     Sequence         WB
             DRB3_0202  439      VIAWNSNNLDSKVGG  WNSNNLDSK  3        0.6082
69.3     4.50  0.37     Sequence         WB
             DRB3_0202  440      IAWNSNNLDSKVGGN  WNSNNLDSK  2        0.4884
253.5    11.00  0.49     Sequence
             DRB3_0202  441      AWNSNNLDSKVGGNY  WNSNNLDSK  1        0.2420
3644.2    46.00  0.48     Sequence
             DRB3_0202  442      WNSNNLDSKVGGNYN  NNLDSKVGG  3        0.1460
10298.7    75.00  0.28     Sequence
             DRB3_0202  443      NSNNLDSKVGGNYNY  NNLDSKVGG  2        0.1208
13535.4    85.00  0.21     Sequence
             DRB3_0202  444      SNNLDSKVGGNYNYL  VGGNYNYLX  7        0.1500
9866.8    75.00  0.29     Sequence
             DRB3_0202  445      NNLDSKVGGNYNYLY  VGGNYNYLY  6        0.2109
5104.8    55.00  0.53     Sequence
             DRB3_0202  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.2828
2345.7    36.00  0.67     Sequence
             DRB3_0202  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4        0.3132
1687.6    31.00  0.67     Sequence
```

```
             DRB3_0202  448      DSKVGGNYNYLYRLF  VGGNYNYLY  3        0.3385
1283.0    27.00  0.68     Sequence
             DRB3_0202  449      SKVGGNYNYLYRLFR  VGGNYNYLY  2        0.3585
1033.9    24.00  0.58     Sequence
             DRB3_0202  450      KVGGNYNYLYRLFRK  VGGNYNYLY  1        0.3361
1317.2    27.00  0.36     Sequence
             DRB3_0202  451      VGGNYNYLYRLFRKS  YNYLYRLFR  4        0.2974
2002.3    34.00  0.31     Sequence
             DRB3_0202  452      GGNYNYLYRLFRKSN  YNYLYRLFR  3        0.2930
2099.3    34.00  0.35     Sequence
             DRB3_0202  453      GNYNYLYRLFRKSNL  YNYLYRLFR  2        0.3310
1392.6    28.00  0.25     Sequence
             DRB3_0202  454      NYNYLYRLFRKSNLK  YRLFRKSNL  5        0.3805
814.8    21.00  0.25     Sequence
             DRB3_0202  455      YNYLYRLFRKSNLKP  YRLFRKSNL  4        0.4050
624.8    18.00  0.28     Sequence
             DRB3_0202  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6        0.4531
371.4    14.00  0.25     Sequence
             DRB3_0202  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.4921
243.5    11.00  0.34     Sequence
             DRB3_0202  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.5274
166.3     8.50  0.40     Sequence         WB
             DRB3_0202  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.5221
176.0     8.50  0.44     Sequence         WB
             DRB3_0202  460      RLFRKSNLKPFERDI  RKSNLKPFE  3        0.4975
229.7    10.00  0.50     Sequence
             DRB3_0202  461      LFRKSNLKPFERDIS  RKSNLKPFE  2        0.3933
709.5    19.00  0.47     Sequence
             DRB3_0202  462      FRKSNLKPFERDIST  RKSNLKPFE  1        0.2645
2858.3    40.00  0.38     Sequence
             DRB3_0202  463      RKSNLKPFERDISTE  FERDISTEX  7        0.1746
7560.7    65.00  0.33     Sequence
             DRB3_0202  464      KSNLKPFERDISTEI  FERDISTEI  6        0.2430
3606.2    45.00  0.72     Sequence
             DRB3_0202  465      SNLKPFERDISTEIY  FERDISTEI  5        0.3150
1655.3    30.00  0.84     Sequence
             DRB3_0202  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.3549
1074.8    24.00  0.88     Sequence
             DRB3_0202  467      LKPFERDISTEIYQA  FERDISTEI  3        0.3794
824.1    21.00  0.88     Sequence
             DRB3_0202  468      KPFERDISTEIYQAG  FERDISTEI  2        0.3479
1158.8    25.00  0.79     Sequence
             DRB3_0202  469      PFERDISTEIYQAGS  FERDISTEI  1        0.2199
4632.0    55.00  0.56     Sequence
             DRB3_0202  470      FERDISTEIYQAGST  DISTEIYQA  3        0.1455
10355.1    75.00  0.39     Sequence
             DRB3_0202  471      ERDISTEIYQAGSTP  DISTEIYQA  2        0.1065
15798.8    85.00  0.32     Sequence
             DRB3_0202  472      RDISTEIYQAGSTPC  YQAGSTPCX  7        0.1800
7134.6    65.00  0.33     Sequence
             DRB3_0202  473      DISTEIYQAGSTPCN  YQAGSTPCN  6        0.3821
800.5    21.00  0.68     Sequence
             DRB3_0202  474      ISTEIYQAGSTPCNG  YQAGSTPCN  5        0.4529
372.3    14.00  0.73     Sequence
             DRB3_0202  475      STEIYQAGSTPCNGV  YQAGSTPCN  4        0.5001
223.3    10.00  0.73     Sequence
             DRB3_0202  476      TEIYQAGSTPCNGVK  YQAGSTPCN  3        0.5361
151.3     8.00  0.78     Sequence         WB
             DRB3_0202  477      EIYQAGSTPCNGVKG  YQAGSTPCN  2        0.5197
180.6     8.50  0.74     Sequence         WB
             DRB3_0202  478      IYQAGSTPCNGVKGF  YQAGSTPCN  1        0.3716
897.5    22.00  0.61     Sequence
             DRB3_0202  479      YQAGSTPCNGVKGFN  YQAGSTPCN  0        0.1865
6650.0    65.00  0.38     Sequence
             DRB3_0202  480      QAGSTPCNGVKGFNC  STPCNGVKG  3        0.0581
26658.6   100.00  0.44     Sequence
```

```
             DRB3_0202  481      AGSTPCNGVKGFNCY  STPCNGVKG  2        0.0728
22749.6    95.00  0.34     Sequence
             DRB3_0202  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.0828
20403.6    95.00  0.25     Sequence
             DRB3_0202  483      STPCNGVKGFNCYFP  KGFNCYFPX  7        0.0886
19161.1    90.00  0.23     Sequence
             DRB3_0202  484      TPCNGVKGFNCYFPL  KGFNCYFPL  6        0.1209
13519.0    85.00  0.47     Sequence
             DRB3_0202  485      PCNGVKGFNCYFPLQ  KGFNCYFPL  5        0.1634
8535.1    70.00  0.52     Sequence
             DRB3_0202  486      CNGVKGFNCYFPLQS  KGFNCYFPL  4        0.1871
6600.3    60.00  0.47     Sequence
             DRB3_0202  487      NGVKGFNCYFPLQSY  KGFNCYFPL  3        0.2248
4391.5    50.00  0.44     Sequence
             DRB3_0202  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.2175
4753.3    55.00  0.34     Sequence
             DRB3_0202  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3        0.2146
4906.9    55.00  0.29     Sequence
             DRB3_0202  490      KGFNCYFPLQSYGFQ  FNCYFPLQS  2        0.2227
4491.6    55.00  0.27     Sequence
             DRB3_0202  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.2062
5373.2    55.00  0.31     Sequence
             DRB3_0202  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.2419
3651.4    46.00  0.31     Sequence
             DRB3_0202  493      NCYFPLQSYGFQPTY  PLQSYGFQP  4        0.2426
3622.8    45.00  0.19     Sequence
             DRB3_0202  494      CYFPLQSYGFQPTYG  PLQSYGFQP  3        0.2139
4939.5    55.00  0.27     Sequence
             DRB3_0202  495      YFPLQSYGFQPTYGV  PLQSYGFQP  2        0.2054
5416.8    55.00  0.23     Sequence
             DRB3_0202  496      FPLQSYGFQPTYGVG  YGFQPTYGV  5        0.2087
5224.9    55.00  0.25     Sequence
             DRB3_0202  497      PLQSYGFQPTYGVGY  FQPTYGVGY  6        0.3124
1702.8    31.00  0.60     Sequence
             DRB3_0202  498      LQSYGFQPTYGVGYQ  FQPTYGVGY  5        0.3932
710.3    19.00  0.70     Sequence
             DRB3_0202  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4        0.3800
819.2    21.00  0.78     Sequence
             DRB3_0202  500      SYGFQPTYGVGYQPY  FQPTYGVGY  3        0.4247
505.0    16.00  0.72     Sequence
             DRB3_0202  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.4609
341.2    13.00  0.50     Sequence
             DRB3_0202  502      GFQPTYGVGYQPYRV  YGVGYQPYR  5        0.4453
404.1    14.00  0.50     Sequence
             DRB3_0202  503      FQPTYGVGYQPYRVV  YGVGYQPYR  4        0.4364
445.0    15.00  0.64     Sequence
             DRB3_0202  504      QPTYGVGYQPYRVVV  YGVGYQPYR  3        0.4130
573.3    17.00  0.71     Sequence
             DRB3_0202  505      PTYGVGYQPYRVVVL  YGVGYQPYR  2        0.4324
464.8    15.00  0.62     Sequence
             DRB3_0202  506      TYGVGYQPYRVVVLS  YGVGYQPYR  1        0.3942
702.7    19.00  0.40     Sequence
             DRB3_0202  507      YGVGYQPYRVVVLSF  YQPYRVVVL  4        0.3402
1260.0    26.00  0.41     Sequence
             DRB3_0202  508      GVGYQPYRVVVLSFE  YQPYRVVVL  3        0.3373
1300.3    27.00  0.46     Sequence
             DRB3_0202  509      VGYQPYRVVVLSFEL  YRVVVLSFE  5        0.3546
1078.2    24.00  0.38     Sequence
             DRB3_0202  510      GYQPYRVVVLSFELL  YRVVVLSFE  4        0.3489
1147.1    25.00  0.47     Sequence
             DRB3_0202  511      YQPYRVVVLSFELLH  YRVVVLSFE  3        0.3230
1518.2    29.00  0.51     Sequence
             DRB3_0202  512      QPYRVVVLSFELLHA  YRVVVLSFE  2        0.2901
2167.5    35.00  0.45     Sequence
             DRB3_0202  513      PYRVVVLSFELLHAP  VVLSFELLH  4        0.2398
3734.8    46.00  0.29     Sequence
```

```
             DRB3_0202  514      YRVVVLSFELLHAPA  VVLSFELLH  3        0.2094
5187.8    55.00  0.36     Sequence
             DRB3_0202  515      RVVVLSFELLHAPAT  FELLHAPAT  6        0.2571
3096.7    42.00  0.42     Sequence
             DRB3_0202  516      VVVLSFELLHAPATV  FELLHAPAT  5        0.3449
1197.8    26.00  0.54     Sequence
             DRB3_0202  517      VVLSFELLHAPATVC  FELLHAPAT  4        0.3814
807.1    21.00  0.52     Sequence
             DRB3_0202  518      VLSFELLHAPATVCG  FELLHAPAT  3        0.3937
706.5    19.00  0.52     Sequence
             DRB3_0202  519      LSFELLHAPATVCGP  FELLHAPAT  2        0.3994
663.7    19.00  0.48     Sequence
             DRB3_0202  520      SFELLHAPATVCGPK  LLHAPATVC  3        0.3612
1003.5    23.00  0.38     Sequence
             DRB3_0202  521      FELLHAPATVCGPKK  LLHAPATVC  2        0.2708
2668.6    39.00  0.40     Sequence
             DRB3_0202  522      ELLHAPATVCGPKKS  LLHAPATVC  1        0.1236
13128.2    80.00  0.43     Sequence
             DRB3_0202  523      LLHAPATVCGPKKST  LHAPATVCG  1        0.0767
21816.5    95.00  0.21     Sequence
             DRB3_0202  524      LHAPATVCGPKKSTN  ATVCGPKKS  4        0.0532
28130.5   100.00  0.29     Sequence
             DRB3_0202  525      HAPATVCGPKKSTNL  CGPKKSTNL  6        0.0602
26073.3   100.00  0.35     Sequence
             DRB3_0202  526      APATVCGPKKSTNLV  CGPKKSTNL  5        0.0721
22913.9    95.00  0.46     Sequence
             DRB3_0202  527      PATVCGPKKSTNLVK  CGPKKSTNL  4        0.0975
17414.8    90.00  0.41     Sequence
             DRB3_0202  528      ATVCGPKKSTNLVKN  CGPKKSTNL  3        0.1387
11150.0    75.00  0.34     Sequence
             DRB3_0202  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.1615
8712.8    70.00  0.29     Sequence
             DRB3_0202  530      VCGPKKSTNLVKNKC  KSTNLVKNK  5        0.1689
8040.2    70.00  0.36     Sequence
             DRB3_0202  531      CGPKKSTNLVKNKCV  KSTNLVKNK  4        0.2110
5099.1    55.00  0.32     Sequence
             DRB3_0202  532      GPKKSTNLVKNKCVN  LVKNKCVNX  7        0.2696
2706.0    39.00  0.35     Sequence
             DRB3_0202  533      PKKSTNLVKNKCVNF  LVKNKCVNF  6        0.4045
628.1    18.00  0.74     Sequence
             DRB3_0202  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.5279
165.3     8.00  0.81     Sequence         WB
             DRB3_0202  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.5791
95.1     5.50  0.77     Sequence         WB
             DRB3_0202  536      STNLVKNKCVNFNFN  LVKNKCVNF  3        0.6243
58.3     4.00  0.73     Sequence         WB
             DRB3_0202  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2        0.6173
62.9     4.50  0.62     Sequence         WB
             DRB3_0202  538      NLVKNKCVNFNFNGL  LVKNKCVNF  1        0.5765
97.7     6.00  0.43     Sequence         WB
             DRB3_0202  539      LVKNKCVNFNFNGLT  KCVNFNFNG  4        0.5326
157.2     8.00  0.33     Sequence         WB
             DRB3_0202  540      VKNKCVNFNFNGLTG  KCVNFNFNG  3        0.4739
296.5    12.00  0.41     Sequence
             DRB3_0202  541      KNKCVNFNFNGLTGT  VNFNFNGLT  4        0.5055
210.8     9.50  0.34     Sequence         WB
             DRB3_0202  542      NKCVNFNFNGLTGTG  FNFNGLTGT  5        0.5017
219.6    10.00  0.40     Sequence
             DRB3_0202  543      KCVNFNFNGLTGTGV  FNFNGLTGT  4        0.4739
296.6    12.00  0.55     Sequence
             DRB3_0202  544      CVNFNFNGLTGTGVL  FNFNGLTGT  3        0.4448
406.2    14.00  0.69     Sequence
             DRB3_0202  545      VNFNFNGLTGTGVLT  FNFNGLTGT  2        0.3960
689.2    19.00  0.57     Sequence
             DRB3_0202  546      NFNFNGLTGTGVLTE  FNFNGLTGT  1        0.2728
2613.4    39.00  0.40     Sequence
```

```
             DRB3_0202  547      FNFNGLTGTGVLTES  GLTGTGVLT  4        0.2017
5639.9    60.00  0.35     Sequence
             DRB3_0202  548      NFNGLTGTGVLTESN  GLTGTGVLT  3        0.1689
8045.3    70.00  0.49     Sequence
             DRB3_0202  549      FNGLTGTGVLTESNK  GLTGTGVLT  2        0.1622
8642.1    70.00  0.46     Sequence
             DRB3_0202  550      NGLTGTGVLTESNKK  GVLTESNKK  6        0.1412
10853.5    75.00  0.46     Sequence
             DRB3_0202  551      GLTGTGVLTESNKKF  GVLTESNKK  5        0.1759
7455.9    65.00  0.67     Sequence
             DRB3_0202  552      LTGTGVLTESNKKFL  GVLTESNKK  4        0.2043
5482.6    60.00  0.70     Sequence
             DRB3_0202  553      TGTGVLTESNKKFLP  GVLTESNKK  3        0.2259
4338.7    50.00  0.59     Sequence
             DRB3_0202  554      GTGVLTESNKKFLPF  GVLTESNKK  2        0.2476
3432.1    44.00  0.51     Sequence
             DRB3_0202  555      TGVLTESNKKFLPFQ  LTESNKKFL  3        0.2247
4398.0    50.00  0.39     Sequence
             DRB3_0202  556      GVLTESNKKFLPFQQ  LTESNKKFL  2        0.2154
4862.4    55.00  0.34     Sequence
             DRB3_0202  557      VLTESNKKFLPFQQF  TESNKKFLP  2        0.1707
7884.4    65.00  0.28     Sequence
             DRB3_0202  558      LTESNKKFLPFQQFG  SNKKFLPFQ  3        0.1315
12049.4    80.00  0.19     Sequence
             DRB3_0202  559      TESNKKFLPFQQFGR  KFLPFQQFG  5        0.1407
10913.1    75.00  0.24     Sequence
             DRB3_0202  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5        0.1412
10846.2    75.00  0.25     Sequence
             DRB3_0202  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4        0.1463
10268.3    75.00  0.31     Sequence
             DRB3_0202  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.1768
7379.8    65.00  0.29     Sequence
             DRB3_0202  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.2031
5555.5    60.00  0.24     Sequence
             DRB3_0202  564      KFLPFQQFGRDIADT  FGRDIADTX  7        0.2263
4322.5    50.00  0.32     Sequence
             DRB3_0202  565      FLPFQQFGRDIADTT  FGRDIADTT  6        0.2884
2207.0    35.00  0.68     Sequence
             DRB3_0202  566      LPFQQFGRDIADTTD  FGRDIADTT  5        0.3257
1473.9    29.00  0.78     Sequence
             DRB3_0202  567      PFQQFGRDIADTTDA  FGRDIADTT  4        0.3624
990.5    23.00  0.84     Sequence
             DRB3_0202  568      FQQFGRDIADTTDAV  FGRDIADTT  3        0.3883
748.8    20.00  0.87     Sequence
             DRB3_0202  569      QQFGRDIADTTDAVR  FGRDIADTT  2        0.3294
1415.9    28.00  0.71     Sequence
             DRB3_0202  570      QFGRDIADTTDAVRD  FGRDIADTT  1        0.2185
4700.4    55.00  0.53     Sequence
             DRB3_0202  571      FGRDIADTTDAVRDP  DIADTTDAV  3        0.1359
11485.5    80.00  0.46     Sequence
             DRB3_0202  572      GRDIADTTDAVRDPQ  DIADTTDAV  2        0.0734
22595.1    95.00  0.53     Sequence
             DRB3_0202  573      RDIADTTDAVRDPQT  DIADTTDAV  1        0.0580
26706.3   100.00  0.38     Sequence
             DRB3_0202  574      DIADTTDAVRDPQTL  DIADTTDAV  0        0.0457
30483.3   100.00  0.26     Sequence
             DRB3_0202  575      IADTTDAVRDPQTLE  AVRDPQTLE  6        0.0402
32348.9   100.00  0.35     Sequence
             DRB3_0202  576      ADTTDAVRDPQTLEI  AVRDPQTLE  5        0.0498
29172.6   100.00  0.54     Sequence
             DRB3_0202  577      DTTDAVRDPQTLEIL  AVRDPQTLE  4        0.0617
25642.4   100.00  0.57     Sequence
             DRB3_0202  578      TTDAVRDPQTLEILD  AVRDPQTLE  3        0.0693
23629.7    95.00  0.59     Sequence
             DRB3_0202  579      TDAVRDPQTLEILDI  AVRDPQTLE  2        0.0665
24341.0    95.00  0.51     Sequence
```

```
             DRB3_0202  580      DAVRDPQTLEILDIT  AVRDPQTLE  1        0.0511
28775.4   100.00  0.34     Sequence
             DRB3_0202  581      AVRDPQTLEILDITP  QTLEILDIT  5        0.0433
31294.8   100.00  0.22     Sequence
             DRB3_0202  582      VRDPQTLEILDITPC  EILDITPCX  7        0.0593
26332.1   100.00  0.32     Sequence
             DRB3_0202  583      RDPQTLEILDITPCS  EILDITPCS  6        0.1471
10175.9    75.00  0.74     Sequence
             DRB3_0202  584      DPQTLEILDITPCSF  EILDITPCS  5        0.2037
5516.1    60.00  0.76     Sequence
             DRB3_0202  585      PQTLEILDITPCSFG  EILDITPCS  4        0.2184
4708.7    55.00  0.74     Sequence
             DRB3_0202  586      QTLEILDITPCSFGG  EILDITPCS  3        0.2274
4268.0    49.00  0.74     Sequence
             DRB3_0202  587      TLEILDITPCSFGGV  EILDITPCS  2        0.2279
4247.7    49.00  0.69     Sequence
             DRB3_0202  588      LEILDITPCSFGGVS  EILDITPCS  1        0.1952
6049.3    60.00  0.51     Sequence
             DRB3_0202  589      EILDITPCSFGGVSV  EILDITPCS  0        0.1290
12381.1    80.00  0.31     Sequence
             DRB3_0202  590      ILDITPCSFGGVSVI  LDITPCSFG  1        0.0889
19108.3    90.00  0.18     Sequence
             DRB3_0202  591      LDITPCSFGGVSVIT  TPCSFGGVS  3        0.0813
20748.2    95.00  0.14     Sequence
             DRB3_0202  592      DITPCSFGGVSVITP  GGVSVITPX  7        0.0783
21431.4    95.00  0.22     Sequence
             DRB3_0202  593      ITPCSFGGVSVITPG  GGVSVITPG  6        0.0787
21341.1    95.00  0.25     Sequence
             DRB3_0202  594      TPCSFGGVSVITPGT  GGVSVITPG  5        0.0938
18121.4    90.00  0.28     Sequence
             DRB3_0202  595      PCSFGGVSVITPGTN  GGVSVITPG  4        0.1150
14404.5    85.00  0.25     Sequence
             DRB3_0202  596      CSFGGVSVITPGTNT  SVITPGTNT  6        0.1378
11257.2    75.00  0.31     Sequence
             DRB3_0202  597      SFGGVSVITPGTNTS  SVITPGTNT  5        0.1788
7226.6    65.00  0.47     Sequence
             DRB3_0202  598      FGGVSVITPGTNTSN  SVITPGTNT  4        0.2275
4267.1    49.00  0.44     Sequence
             DRB3_0202  599      GGVSVITPGTNTSNQ  ITPGTNTSN  5        0.2927
2105.8    34.00  0.47     Sequence
             DRB3_0202  600      GVSVITPGTNTSNQV  ITPGTNTSN  4        0.3303
1403.2    28.00  0.54     Sequence
             DRB3_0202  601      VSVITPGTNTSNQVA  ITPGTNTSN  3        0.3590
1027.6    24.00  0.61     Sequence
             DRB3_0202  602      SVITPGTNTSNQVAV  ITPGTNTSN  2        0.3634
979.8    23.00  0.49     Sequence
             DRB3_0202  603      VITPGTNTSNQVAVL  NTSNQVAVL  6        0.3759
856.5    21.00  0.32     Sequence
             DRB3_0202  604      ITPGTNTSNQVAVLY  NTSNQVAVL  5        0.3555
1067.4    24.00  0.48     Sequence
             DRB3_0202  605      TPGTNTSNQVAVLYQ  NTSNQVAVL  4        0.3470
1170.2    25.00  0.58     Sequence
             DRB3_0202  606      PGTNTSNQVAVLYQG  NTSNQVAVL  3        0.3495
1139.6    25.00  0.63     Sequence
             DRB3_0202  607      GTNTSNQVAVLYQGV  NTSNQVAVL  2        0.3121
1708.3    31.00  0.56     Sequence
             DRB3_0202  608      TNTSNQVAVLYQGVN  NTSNQVAVL  1        0.2119
5048.1    55.00  0.41     Sequence
             DRB3_0202  609      NTSNQVAVLYQGVNC  NQVAVLYQG  3        0.1563
9215.5    70.00  0.28     Sequence
             DRB3_0202  610      TSNQVAVLYQGVNCT  QVAVLYQGV  3        0.1393
11081.1    75.00  0.26     Sequence
             DRB3_0202  611      SNQVAVLYQGVNCTE  QVAVLYQGV  2        0.1354
11552.4    80.00  0.23     Sequence
             DRB3_0202  612      NQVAVLYQGVNCTEV  QGVNCTEVX  7        0.1657
8328.2    70.00  0.23     Sequence
```

```
            DRB3_0202  613      QVAVLYQGVNCTEVP  QGVNCTEVP  6        0.1904
6372.3    60.00  0.34     Sequence
            DRB3_0202  614      VAVLYQGVNCTEVPV  QGVNCTEVP  5        0.2184
4705.1    55.00  0.44     Sequence
            DRB3_0202  615      AVLYQGVNCTEVPVA  QGVNCTEVP  4        0.2367
3862.8    47.00  0.50     Sequence
            DRB3_0202  616      VLYQGVNCTEVPVAI  QGVNCTEVP  3        0.2560
3133.8    42.00  0.54     Sequence
            DRB3_0202  617      LYQGVNCTEVPVAIH  QGVNCTEVP  2        0.2186
4698.2    55.00  0.43     Sequence
            DRB3_0202  618      YQGVNCTEVPVAIHA  QGVNCTEVP  1        0.1653
8357.9    70.00  0.23     Sequence
            DRB3_0202  619      QGVNCTEVPVAIHAD  VNCTEVPVA  2        0.1244
13012.8    80.00  0.28     Sequence
            DRB3_0202  620      GVNCTEVPVAIHADQ  CTEVPVAIH  3        0.0962
17664.9    90.00  0.34     Sequence
            DRB3_0202  621      VNCTEVPVAIHADQL  CTEVPVAIH  2        0.0821
20565.6    95.00  0.31     Sequence
            DRB3_0202  622      NCTEVPVAIHADQLT  PVAIHADQL  5        0.0727
22764.1    95.00  0.17     Sequence
            DRB3_0202  623      CTEVPVAIHADQLTP  VAIHADQLT  5        0.0930
18272.8    90.00  0.38     Sequence
            DRB3_0202  624      TEVPVAIHADQLTPT  VAIHADQLT  4        0.1128
14762.2    85.00  0.38     Sequence
            DRB3_0202  625      EVPVAIHADQLTPTW  IHADQLTPT  5        0.1397
11033.7    75.00  0.38     Sequence
            DRB3_0202  626      VPVAIHADQLTPTWR  IHADQLTPT  4        0.1772
7350.9    65.00  0.38     Sequence
            DRB3_0202  627      PVAIHADQLTPTWRV  IHADQLTPT  3        0.2179
4734.0    55.00  0.34     Sequence
            DRB3_0202  628      VAIHADQLTPTWRVY  DQLTPTWRV  5        0.2556
3147.9    42.00  0.46     Sequence
            DRB3_0202  629      AIHADQLTPTWRVYS  DQLTPTWRV  4        0.3107
1733.9    31.00  0.44     Sequence
            DRB3_0202  630      IHADQLTPTWRVYST  LTPTWRVYS  5        0.3705
908.2    22.00  0.51     Sequence
            DRB3_0202  631      HADQLTPTWRVYSTG  LTPTWRVYS  4        0.3751
863.9    22.00  0.54     Sequence
            DRB3_0202  632      ADQLTPTWRVYSTGS  LTPTWRVYS  3        0.3730
883.7    22.00  0.60     Sequence
            DRB3_0202  633      DQLTPTWRVYSTGSN  LTPTWRVYS  2        0.3773
843.3    21.00  0.51     Sequence
            DRB3_0202  634      QLTPTWRVYSTGSNV  WRVYSTGSN  5        0.3876
754.4    20.00  0.31     Sequence
            DRB3_0202  635      LTPTWRVYSTGSNVF  WRVYSTGSN  4        0.4118
580.9    17.00  0.43     Sequence
            DRB3_0202  636      TPTWRVYSTGSNVFQ  WRVYSTGSN  3        0.4495
386.0    14.00  0.40     Sequence
            DRB3_0202  637      PTWRVYSTGSNVFQT  YSTGSNVFQ  5        0.4974
230.1    10.00  0.39     Sequence
            DRB3_0202  638      TWRVYSTGSNVFQTR  YSTGSNVFQ  4        0.5267
167.5     8.50  0.47     Sequence         WB
            DRB3_0202  639      WRVYSTGSNVFQTRA  YSTGSNVFQ  3        0.5136
192.9     9.00  0.61     Sequence         WB
            DRB3_0202  640      RVYSTGSNVFQTRAG  YSTGSNVFQ  2        0.4903
248.3    11.00  0.62     Sequence
            DRB3_0202  641      VYSTGSNVFQTRAGC  YSTGSNVFQ  1        0.3900
735.3    20.00  0.51     Sequence
            DRB3_0202  642      YSTGSNVFQTRAGCL  TGSNVFQTR  2        0.2568
3106.6    42.00  0.25     Sequence
            DRB3_0202  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.1678
8133.4    70.00  0.44     Sequence
            DRB3_0202  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.1744
7577.4    65.00  0.49     Sequence
            DRB3_0202  645      GSNVFQTRAGCLIGA  VFQTRAGCL  3        0.2007
5699.0    60.00  0.52     Sequence
```

```
             DRB3_0202  646      SNVFQTRAGCLIGAE  VFQTRAGCL  2        0.2051
5437.4    55.00  0.49     Sequence
             DRB3_0202  647      NVFQTRAGCLIGAEY  QTRAGCLIG  3        0.1508
9780.1    75.00  0.33     Sequence
             DRB3_0202  648      VFQTRAGCLIGAEYV  QTRAGCLIG  2        0.1107
15090.7    85.00  0.29     Sequence
             DRB3_0202  649      FQTRAGCLIGAEYVN  CLIGAEYVN  6        0.1093
15328.0    85.00  0.29     Sequence
             DRB3_0202  650      QTRAGCLIGAEYVNN  CLIGAEYVN  5        0.1362
11449.6    80.00  0.34     Sequence
             DRB3_0202  651      TRAGCLIGAEYVNNS  CLIGAEYVN  4        0.1736
7646.0    65.00  0.32     Sequence
             DRB3_0202  652      RAGCLIGAEYVNNSY  CLIGAEYVN  3        0.2471
3448.9    44.00  0.28     Sequence
             DRB3_0202  653      AGCLIGAEYVNNSYE  LIGAEYVNN  3        0.2870
2240.2    36.00  0.20     Sequence
             DRB3_0202  654      GCLIGAEYVNNSYEC  YVNNSYECX  7        0.3552
1070.8    24.00  0.26     Sequence
             DRB3_0202  655      CLIGAEYVNNSYECD  YVNNSYECD  6        0.4011
651.7    18.00  0.43    Sequence
             DRB3_0202  656      LIGAEYVNNSYECDI  YVNNSYECD  5        0.4467
398.1    14.00  0.50    Sequence
             DRB3_0202  657      IGAEYVNNSYECDIP  YVNNSYECD  4        0.4605
342.8    13.00  0.51    Sequence
             DRB3_0202  658      GAEYVNNSYECDIPI  YVNNSYECD  3        0.4742
295.7    12.00  0.56    Sequence
             DRB3_0202  659      AEYVNNSYECDIPIG  YVNNSYECD  2        0.4136
569.2    17.00  0.52    Sequence
             DRB3_0202  660      EYVNNSYECDIPIGA  YVNNSYECD  1        0.2689
2723.9    39.00  0.38     Sequence
             DRB3_0202  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.1843
6805.3    65.00  0.58     Sequence
             DRB3_0202  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.1695
7989.6    70.00  0.80     Sequence
             DRB3_0202  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.1817
7000.7    65.00  0.75     Sequence
             DRB3_0202  664      NSYECDIPIGAGICA  YECDIPIGA  2        0.1602
8834.8    70.00  0.61     Sequence
             DRB3_0202  665      SYECDIPIGAGICAS  YECDIPIGA  1        0.1268
12674.5    80.00  0.41     Sequence
             DRB3_0202  666      YECDIPIGAGICASY  IPIGAGICA  4        0.0971
17486.0    90.00  0.28     Sequence
             DRB3_0202  667      ECDIPIGAGICASYQ  IPIGAGICA  3        0.0752
22150.9    95.00  0.42     Sequence
             DRB3_0202  668      CDIPIGAGICASYQT  IPIGAGICA  2        0.0921
18457.6    90.00  0.37     Sequence
             DRB3_0202  669      DIPIGAGICASYQTQ  IPIGAGICA  1        0.0906
18750.9    90.00  0.22     Sequence
             DRB3_0202  670      IPIGAGICASYQTQT  ICASYQTQT  6        0.1110
15050.3    85.00  0.42     Sequence
             DRB3_0202  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.1415
10819.0    75.00  0.55     Sequence
             DRB3_0202  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.1743
7581.7    65.00  0.52     Sequence
             DRB3_0202  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.2029
5565.7    60.00  0.50     Sequence
             DRB3_0202  674      AGICASYQTQTNSPR  YQTQTNSPR  6        0.3043
1858.8    32.00  0.49     Sequence
             DRB3_0202  675      GICASYQTQTNSPRR  YQTQTNSPR  5        0.4097
594.2    18.00  0.60    Sequence
             DRB3_0202  676      ICASYQTQTNSPRRA  YQTQTNSPR  4        0.5046
212.7     9.50  0.54    Sequence         WB
             DRB3_0202  677      CASYQTQTNSPRRAR  YQTQTNSPR  3        0.5715
103.2     6.00  0.50    Sequence         WB
             DRB3_0202  678      ASYQTQTNSPRRARS  TQTNSPRRA  4        0.5806
93.5     5.50  0.35     Sequence         WB
```

```
             DRB3_0202  679      SYQTQTNSPRRARSV  TQTNSPRRA  3        0.5546
123.9     7.00  0.44     Sequence         WB
             DRB3_0202  680      YQTQTNSPRRARSVA  TQTNSPRRA  2        0.4807
275.5    11.00  0.56     Sequence
             DRB3_0202  681      QTQTNSPRRARSVAS  TQTNSPRRA  1        0.3008
1929.4    33.00  0.45     Sequence
             DRB3_0202  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.2547
3176.6    43.00  0.38     Sequence
             DRB3_0202  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.2404
3709.1    46.00  0.51     Sequence
             DRB3_0202  684      TNSPRRARSVASQSI  PRRARSVAS  3        0.2652
2835.9    40.00  0.46     Sequence
             DRB3_0202  685      NSPRRARSVASQSII  PRRARSVAS  2        0.2896
2179.2    35.00  0.37     Sequence
             DRB3_0202  686      SPRRARSVASQSIIA  RARSVASQS  3        0.3134
1683.3    31.00  0.25     Sequence
             DRB3_0202  687      PRRARSVASQSIIAY  SVASQSIIA  5        0.3349
1335.1    27.00  0.46     Sequence
             DRB3_0202  688      RRARSVASQSIIAYT  SVASQSIIA  4        0.3282
1435.5    28.00  0.58     Sequence
             DRB3_0202  689      RARSVASQSIIAYTM  SVASQSIIA  3        0.3249
1486.2    29.00  0.70     Sequence
             DRB3_0202  690      ARSVASQSIIAYTMS  SVASQSIIA  2        0.2853
2283.3    36.00  0.63     Sequence
             DRB3_0202  691      RSVASQSIIAYTMSL  SVASQSIIA  1        0.2711
2662.5    39.00  0.39     Sequence
             DRB3_0202  692      SVASQSIIAYTMSLG  SIIAYTMSL  5        0.2282
4231.8    49.00  0.32     Sequence
             DRB3_0202  693      VASQSIIAYTMSLGA  SIIAYTMSL  4        0.2431
3601.3    45.00  0.40     Sequence
             DRB3_0202  694      ASQSIIAYTMSLGAE  YTMSLGAEX  7        0.2958
2037.8    34.00  0.27     Sequence
             DRB3_0202  695      SQSIIAYTMSLGAEN  YTMSLGAEN  6        0.5044
213.3     9.50  0.73     Sequence         WB
             DRB3_0202  696      QSIIAYTMSLGAENS  YTMSLGAEN  5        0.6030
73.4     5.00  0.83     Sequence         WB
             DRB3_0202  697      SIIAYTMSLGAENSV  YTMSLGAEN  4        0.6383
50.1     3.50  0.88     Sequence         WB
             DRB3_0202  698      IIAYTMSLGAENSVA  YTMSLGAEN  3        0.6680
36.3     3.00  0.91     Sequence         WB
             DRB3_0202  699      IAYTMSLGAENSVAY  YTMSLGAEN  2        0.6311
54.1     4.00  0.77     Sequence         WB
             DRB3_0202  700      AYTMSLGAENSVAYS  YTMSLGAEN  1        0.5468
134.8     7.00  0.62     Sequence         WB
             DRB3_0202  701      YTMSLGAENSVAYSN  YTMSLGAEN  0        0.4021
644.8    18.00  0.39     Sequence
             DRB3_0202  702      TMSLGAENSVAYSNN  GAENSVAYS  4        0.2465
3471.2    45.00  0.48     Sequence
             DRB3_0202  703      MSLGAENSVAYSNNS  GAENSVAYS  3        0.2769
2499.4    38.00  0.49     Sequence
             DRB3_0202  704      SLGAENSVAYSNNSI  GAENSVAYS  2        0.2924
2112.7    35.00  0.36     Sequence
             DRB3_0202  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.3832
791.3    21.00  0.22     Sequence
             DRB3_0202  706      GAENSVAYSNNSIAI  AYSNNSIAI  6        0.5612
115.4     6.50  0.42     Sequence         WB
             DRB3_0202  707      AENSVAYSNNSIAIP  AYSNNSIAI  5        0.6608
39.3     3.00  0.48     Sequence         WB
             DRB3_0202  708      ENSVAYSNNSIAIPT  AYSNNSIAI  4        0.7192
20.9     1.70  0.51     Sequence         SB
             DRB3_0202  709      NSVAYSNNSIAIPTN  AYSNNSIAI  3        0.7539
14.3     1.20  0.49     Sequence         SB
             DRB3_0202  710      SVAYSNNSIAIPTNF  AYSNNSIAI  2        0.7554
14.1     1.10  0.46     Sequence         SB
             DRB3_0202  711      VAYSNNSIAIPTNFT  AYSNNSIAI  1        0.7050
24.3     2.00  0.44     Sequence         WB
```

```
             DRB3_0202  712      AYSNNSIAIPTNFTI  YSNNSIAIP  1        0.4961
233.2    10.00  0.24     Sequence
             DRB3_0202  713      YSNNSIAIPTNFTIS  NSIAIPTNF  3        0.3158
1641.5    30.00  0.27     Sequence
             DRB3_0202  714      SNNSIAIPTNFTISV  IPTNFTISV  6        0.3204
1561.7    30.00  0.43     Sequence
             DRB3_0202  715      NNSIAIPTNFTISVT  IPTNFTISV  5        0.3687
925.3    22.00  0.53     Sequence
             DRB3_0202  716      NSIAIPTNFTISVTT  IPTNFTISV  4        0.4078
606.6    18.00  0.60     Sequence
             DRB3_0202  717      SIAIPTNFTISVTTE  IPTNFTISV  3        0.4411
422.9    15.00  0.56     Sequence
             DRB3_0202  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.4938
239.0    11.00  0.57     Sequence
             DRB3_0202  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.5554
122.7     7.00  0.77     Sequence         WB
             DRB3_0202  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.5680
107.1     6.00  0.87     Sequence         WB
             DRB3_0202  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.5881
86.2     5.50  0.92     Sequence         WB
             DRB3_0202  722      TNFTISVTTEILPVS  FTISVTTEI  2        0.5456
136.5     7.50  0.80     Sequence         WB
             DRB3_0202  723      NFTISVTTEILPVSM  FTISVTTEI  1        0.4285
484.5    16.00  0.61     Sequence
             DRB3_0202  724      FTISVTTEILPVSMT  FTISVTTEI  0        0.2818
2369.1    37.00  0.35     Sequence
             DRB3_0202  725      TISVTTEILPVSMTK  SVTTEILPV  2        0.1409
10885.8    75.00  0.38     Sequence
             DRB3_0202  726      ISVTTEILPVSMTKT  ILPVSMTKT  6        0.1642
8463.3    70.00  0.28     Sequence
             DRB3_0202  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.1800
7128.8    65.00  0.42     Sequence
             DRB3_0202  728      VTTEILPVSMTKTSV  ILPVSMTKT  4        0.2046
5464.7    55.00  0.47     Sequence
             DRB3_0202  729      TTEILPVSMTKTSVD  ILPVSMTKT  3        0.2145
4910.6    55.00  0.46     Sequence
             DRB3_0202  730      TEILPVSMTKTSVDC  ILPVSMTKT  2        0.2255
4357.7    50.00  0.43     Sequence
             DRB3_0202  731      EILPVSMTKTSVDCT  ILPVSMTKT  1        0.1678
8139.1    70.00  0.31     Sequence
             DRB3_0202  732      ILPVSMTKTSVDCTM  VSMTKTSVD  3        0.1234
13162.1    80.00  0.53     Sequence
             DRB3_0202  733      LPVSMTKTSVDCTMY  VSMTKTSVD  2        0.1045
16149.3    90.00  0.50     Sequence
             DRB3_0202  734      PVSMTKTSVDCTMYI  MTKTSVDCT  3        0.0891
19062.9    90.00  0.32     Sequence
             DRB3_0202  735      VSMTKTSVDCTMYIC  MTKTSVDCT  2        0.0757
22042.4    95.00  0.31     Sequence
             DRB3_0202  736      SMTKTSVDCTMYICG  TSVDCTMYI  4        0.0622
25522.3   100.00  0.40     Sequence
             DRB3_0202  737      MTKTSVDCTMYICGD  TSVDCTMYI  3        0.0576
26803.8   100.00  0.56     Sequence
             DRB3_0202  738      TKTSVDCTMYICGDS  TSVDCTMYI  2        0.0530
28192.7   100.00  0.44     Sequence
             DRB3_0202  739      KTSVDCTMYICGDST  TSVDCTMYI  1        0.0565
27125.0   100.00  0.28     Sequence
             DRB3_0202  740      TSVDCTMYICGDSTE  CTMYICGDS  4        0.0588
26454.0   100.00  0.21     Sequence
             DRB3_0202  741      SVDCTMYICGDSTEC  YICGDSTEC  6        0.0726
22793.7    95.00  0.23     Sequence
             DRB3_0202  742      VDCTMYICGDSTECS  YICGDSTEC  5        0.0900
18881.8    90.00  0.28     Sequence
             DRB3_0202  743      DCTMYICGDSTECSN  ICGDSTECS  5        0.1032
16376.3    90.00  0.32     Sequence
             DRB3_0202  744      CTMYICGDSTECSNL  ICGDSTECS  4        0.1180
13952.9    85.00  0.32     Sequence
```

```
             DRB3_0202  745      TMYICGDSTECSNLL  ICGDSTECS  3        0.1235
13138.7    80.00  0.41     Sequence
             DRB3_0202  746      MYICGDSTECSNLLL  ICGDSTECS  2        0.1076
15616.3    85.00  0.40     Sequence
             DRB3_0202  747      YICGDSTECSNLLLQ  ICGDSTECS  1        0.0614
25737.5   100.00  0.22     Sequence
             DRB3_0202  748      ICGDSTECSNLLLQY  ECSNLLLQY  6        0.0617
25652.7   100.00  0.41     Sequence
             DRB3_0202  749      CGDSTECSNLLLQYG  ECSNLLLQY  5        0.0710
23204.1    95.00  0.46     Sequence
             DRB3_0202  750      GDSTECSNLLLQYGS  ECSNLLLQY  4        0.0921
18467.8    90.00  0.42     Sequence
             DRB3_0202  751      DSTECSNLLLQYGSF  LLLQYGSFX  7        0.1222
13333.8    80.00  0.28     Sequence
             DRB3_0202  752      STECSNLLLQYGSFC  LLLQYGSFC  6        0.1776
7318.8    65.00  0.57     Sequence
             DRB3_0202  753      TECSNLLLQYGSFCT  LLLQYGSFC  5        0.2237
4443.1    50.00  0.70     Sequence
             DRB3_0202  754      ECSNLLLQYGSFCTQ  LLLQYGSFC  4        0.2505
3326.5    44.00  0.72     Sequence
             DRB3_0202  755      CSNLLLQYGSFCTQL  LLLQYGSFC  3        0.2811
2389.2    37.00  0.70     Sequence
             DRB3_0202  756      SNLLLQYGSFCTQLN  LLLQYGSFC  2        0.3254
1478.2    29.00  0.55     Sequence
             DRB3_0202  757      NLLLQYGSFCTQLNR  LLLQYGSFC  1        0.3018
1908.4    33.00  0.32     Sequence
             DRB3_0202  758      LLLQYGSFCTQLNRA  YGSFCTQLN  4        0.2937
2085.0    34.00  0.17     Sequence
             DRB3_0202  759      LLQYGSFCTQLNRAL  FCTQLNRAL  6        0.3275
1446.0    28.00  0.34     Sequence
             DRB3_0202  760      LQYGSFCTQLNRALT  FCTQLNRAL  5        0.3674
939.2    22.00  0.39     Sequence
             DRB3_0202  761      QYGSFCTQLNRALTG  TQLNRALTG  6        0.4192
535.9    17.00  0.44     Sequence
             DRB3_0202  762      YGSFCTQLNRALTGI  TQLNRALTG  5        0.4927
241.9    11.00  0.57     Sequence
             DRB3_0202  763      GSFCTQLNRALTGIA  TQLNRALTG  4        0.5064
208.7     9.50  0.68     Sequence         WB
             DRB3_0202  764      SFCTQLNRALTGIAV  TQLNRALTG  3        0.5110
198.6     9.00  0.74     Sequence         WB
             DRB3_0202  765      FCTQLNRALTGIAVE  TQLNRALTG  2        0.4762
289.3    12.00  0.64     Sequence
             DRB3_0202  766      CTQLNRALTGIAVEQ  TQLNRALTG  1        0.3693
920.0    22.00  0.49     Sequence
             DRB3_0202  767      TQLNRALTGIAVEQD  LNRALTGIA  2        0.2898
2173.2    35.00  0.37     Sequence
             DRB3_0202  768      QLNRALTGIAVEQDK  ALTGIAVEQ  4        0.1549
9358.3    70.00  0.34     Sequence
             DRB3_0202  769      LNRALTGIAVEQDKN  ALTGIAVEQ  3        0.1241
13058.2    80.00  0.49     Sequence
             DRB3_0202  770      NRALTGIAVEQDKNT  ALTGIAVEQ  2        0.0828
20404.5    95.00  0.46     Sequence
             DRB3_0202  771      RALTGIAVEQDKNTQ  ALTGIAVEQ  1        0.0607
25938.2   100.00  0.32     Sequence
             DRB3_0202  772      ALTGIAVEQDKNTQE  GIAVEQDKN  3        0.0524
28350.5   100.00  0.23     Sequence
             DRB3_0202  773      LTGIAVEQDKNTQEV  VEQDKNTQE  5        0.0630
25277.1   100.00  0.32     Sequence
             DRB3_0202  774      TGIAVEQDKNTQEVF  VEQDKNTQE  4        0.0735
22578.0    95.00  0.37     Sequence
             DRB3_0202  775      GIAVEQDKNTQEVFA  VEQDKNTQE  3        0.0861
19692.7    95.00  0.41     Sequence
             DRB3_0202  776      IAVEQDKNTQEVFAQ  VEQDKNTQE  2        0.0950
17890.4    90.00  0.34     Sequence
             DRB3_0202  777      AVEQDKNTQEVFAQV  QDKNTQEVF  3        0.0845
20037.6    95.00  0.44     Sequence
```

```
             DRB3_0202  778      VEQDKNTQEVFAQVK  QDKNTQEVF  2        0.0845
20036.7    95.00  0.34     Sequence
             DRB3_0202  779      EQDKNTQEVFAQVKQ  QDKNTQEVF  1        0.0854
19843.9    95.00  0.22     Sequence
             DRB3_0202  780      QDKNTQEVFAQVKQI  TQEVFAQVK  4        0.0911
18658.8    90.00  0.19     Sequence
             DRB3_0202  781      DKNTQEVFAQVKQIY  FAQVKQIYX  7        0.1013
16713.7    90.00  0.23     Sequence
             DRB3_0202  782      KNTQEVFAQVKQIYK  FAQVKQIYK  6        0.1485
10022.6    75.00  0.56     Sequence
             DRB3_0202  783      NTQEVFAQVKQIYKT  FAQVKQIYK  5        0.1846
6785.0    65.00  0.66     Sequence
             DRB3_0202  784      TQEVFAQVKQIYKTP  FAQVKQIYK  4        0.2002
5730.8    60.00  0.66     Sequence
             DRB3_0202  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.2115
5069.2    55.00  0.71     Sequence
             DRB3_0202  786      EVFAQVKQIYKTPPI  FAQVKQIYK  2        0.2444
3551.8    45.00  0.49     Sequence
             DRB3_0202  787      VFAQVKQIYKTPPIK  IYKTPPIKX  7        0.2838
2319.7    36.00  0.26     Sequence
             DRB3_0202  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6        0.2873
2233.3    36.00  0.40     Sequence
             DRB3_0202  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.3330
1361.9    27.00  0.50     Sequence
             DRB3_0202  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.3478
1160.8    25.00  0.51     Sequence
             DRB3_0202  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.3509
1122.0    25.00  0.61     Sequence
             DRB3_0202  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.3281
1435.7    28.00  0.61     Sequence
             DRB3_0202  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.2007
5699.0    60.00  0.47     Sequence
             DRB3_0202  794      IYKTPPIKDFGGFNF  PIKDFGGFN  5        0.0997
16997.3    90.00  0.33     Sequence
             DRB3_0202  795      YKTPPIKDFGGFNFS  PIKDFGGFN  4        0.0830
20358.4    95.00  0.52     Sequence
             DRB3_0202  796      KTPPIKDFGGFNFSQ  PIKDFGGFN  3        0.1128
14758.4    85.00  0.38     Sequence
             DRB3_0202  797      TPPIKDFGGFNFSQI  GGFNFSQIX  7        0.1758
7460.0    65.00  0.33     Sequence
             DRB3_0202  798      PPIKDFGGFNFSQIL  GGFNFSQIL  6        0.2118
5054.3    55.00  0.41     Sequence
             DRB3_0202  799      PIKDFGGFNFSQILP  GGFNFSQIL  5        0.2402
3718.5    46.00  0.42     Sequence
             DRB3_0202  800      IKDFGGFNFSQILPD  GGFNFSQIL  4        0.2678
2757.0    40.00  0.36     Sequence
             DRB3_0202  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.3023
1898.0    33.00  0.38     Sequence
             DRB3_0202  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.3169
1620.9    30.00  0.45     Sequence
             DRB3_0202  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.3386
1282.6    27.00  0.49     Sequence
             DRB3_0202  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.3199
1569.1    30.00  0.41     Sequence
             DRB3_0202  805      GFNFSQILPDPSKPS  ILPDPSKPS  6        0.3188
1588.1    30.00  0.35     Sequence
             DRB3_0202  806      FNFSQILPDPSKPSK  ILPDPSKPS  5        0.3334
1356.3    27.00  0.60     Sequence
             DRB3_0202  807      NFSQILPDPSKPSKR  ILPDPSKPS  4        0.3564
1057.7    24.00  0.73     Sequence
             DRB3_0202  808      FSQILPDPSKPSKRS  ILPDPSKPS  3        0.3575
1045.0    24.00  0.81     Sequence
             DRB3_0202  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.3057
1830.7    32.00  0.71     Sequence
             DRB3_0202  810      QILPDPSKPSKRSFI  ILPDPSKPS  1        0.2130
4992.1    55.00  0.54     Sequence
```

```
             DRB3_0202  811      ILPDPSKPSKRSFIE  SKPSKRSFI  5        0.1371
11347.9    80.00  0.34     Sequence
             DRB3_0202  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.0937
18137.9    90.00  0.68     Sequence
             DRB3_0202  813      PDPSKPSKRSFIEDL  SKPSKRSFI  3        0.1020
16589.4    90.00  0.67     Sequence
             DRB3_0202  814      DPSKPSKRSFIEDLL  SKPSKRSFI  2        0.1154
14337.7    85.00  0.60     Sequence
             DRB3_0202  815      PSKPSKRSFIEDLLF  SKPSKRSFI  1        0.1126
14783.5    85.00  0.41     Sequence
             DRB3_0202  816      SKPSKRSFIEDLLFN  SKRSFIEDL  3        0.1080
15548.0    85.00  0.29     Sequence
             DRB3_0202  817      KPSKRSFIEDLLFNK  FIEDLLFNK  6        0.1834
6870.2    65.00  0.62     Sequence
             DRB3_0202  818      PSKRSFIEDLLFNKV  FIEDLLFNK  5        0.2600
2999.6    41.00  0.67     Sequence
             DRB3_0202  819      SKRSFIEDLLFNKVT  FIEDLLFNK  4        0.3272
1450.2    28.00  0.62     Sequence
             DRB3_0202  820      KRSFIEDLLFNKVTL  FIEDLLFNK  3        0.4075
608.4    18.00  0.47     Sequence
             DRB3_0202  821      RSFIEDLLFNKVTLA  LLFNKVTLA  6        0.5384
147.6     7.50  0.72     Sequence         WB
             DRB3_0202  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5        0.5729
101.6     6.00  0.83     Sequence         WB
             DRB3_0202  823      FIEDLLFNKVTLADA  LLFNKVTLA  4        0.6067
70.5     4.50  0.87     Sequence         WB
             DRB3_0202  824      IEDLLFNKVTLADAG  LLFNKVTLA  3        0.6019
74.2     5.00  0.86     Sequence         WB
             DRB3_0202  825      EDLLFNKVTLADAGF  LLFNKVTLA  2        0.5513
128.4     7.00  0.75     Sequence         WB
             DRB3_0202  826      DLLFNKVTLADAGFI  LLFNKVTLA  1        0.4816
272.7    11.00  0.59     Sequence
             DRB3_0202  827      LLFNKVTLADAGFIK  LLFNKVTLA  0        0.3862
766.2    20.00  0.34     Sequence
             DRB3_0202  828      LFNKVTLADAGFIKQ  VTLADAGFI  4        0.2844
2305.5    36.00  0.50     Sequence
             DRB3_0202  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.2905
2156.5    35.00  0.57     Sequence
             DRB3_0202  830      NKVTLADAGFIKQYG  VTLADAGFI  2        0.2688
2728.2    39.00  0.47     Sequence
             DRB3_0202  831      KVTLADAGFIKQYGD  TLADAGFIK  2        0.2333
4007.3    48.00  0.38     Sequence
             DRB3_0202  832      VTLADAGFIKQYGDC  TLADAGFIK  1        0.1727
7716.3    65.00  0.39     Sequence
             DRB3_0202  833      TLADAGFIKQYGDCL  FIKQYGDCL  6        0.2042
5487.4    60.00  0.63     Sequence
             DRB3_0202  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.2392
3760.0    46.00  0.74     Sequence
             DRB3_0202  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4        0.2557
3143.9    42.00  0.77     Sequence
             DRB3_0202  836      DAGFIKQYGDCLGDI  FIKQYGDCL  3        0.2801
2413.9    37.00  0.76     Sequence
             DRB3_0202  837      AGFIKQYGDCLGDIA  FIKQYGDCL  2        0.2843
2307.1    36.00  0.68     Sequence
             DRB3_0202  838      GFIKQYGDCLGDIAA  FIKQYGDCL  1        0.2360
3890.0    47.00  0.51     Sequence
             DRB3_0202  839      FIKQYGDCLGDIAAR  FIKQYGDCL  0        0.1965
5964.1    60.00  0.34     Sequence
             DRB3_0202  840      IKQYGDCLGDIAARD  CLGDIAARD  6        0.1468
10217.4    75.00  0.58     Sequence
             DRB3_0202  841      KQYGDCLGDIAARDL  CLGDIAARD  5        0.1883
6517.7    60.00  0.70     Sequence
             DRB3_0202  842      QYGDCLGDIAARDLI  CLGDIAARD  4        0.2125
5019.6    55.00  0.77     Sequence
             DRB3_0202  843      YGDCLGDIAARDLIC  CLGDIAARD  3        0.2167
4794.5    55.00  0.78     Sequence
```

```
             DRB3_0202  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.2053
5424.9    55.00  0.69     Sequence
             DRB3_0202  845      DCLGDIAARDLICAQ  CLGDIAARD  1        0.1543
9413.2    70.00  0.48     Sequence
             DRB3_0202  846      CLGDIAARDLICAQK  DIAARDLIC  3        0.1236
13129.6    80.00  0.31     Sequence
             DRB3_0202  847      LGDIAARDLICAQKF  AARDLICAQ  4        0.0992
17100.4    90.00  0.24     Sequence
             DRB3_0202  848      GDIAARDLICAQKFN  AARDLICAQ  3        0.1095
15288.4    85.00  0.26     Sequence
             DRB3_0202  849      DIAARDLICAQKFNG  DLICAQKFN  5        0.1103
15152.5    85.00  0.32     Sequence
             DRB3_0202  850      IAARDLICAQKFNGL  DLICAQKFN  4        0.1371
11337.6    80.00  0.34     Sequence
             DRB3_0202  851      AARDLICAQKFNGLT  LICAQKFNG  4        0.1581
9038.5    70.00  0.26     Sequence
             DRB3_0202  852      ARDLICAQKFNGLTV  LICAQKFNG  3        0.1815
7014.7    65.00  0.24     Sequence
             DRB3_0202  853      RDLICAQKFNGLTVL  QKFNGLTVL  6        0.2170
4776.3    55.00  0.34     Sequence
             DRB3_0202  854      DLICAQKFNGLTVLP  QKFNGLTVL  5        0.2365
3869.9    47.00  0.46     Sequence
             DRB3_0202  855      LICAQKFNGLTVLPP  QKFNGLTVL  4        0.2414
3670.1    46.00  0.52     Sequence
             DRB3_0202  856      ICAQKFNGLTVLPPL  QKFNGLTVL  3        0.2639
2876.9    41.00  0.47     Sequence
             DRB3_0202  857      CAQKFNGLTVLPPLL  QKFNGLTVL  2        0.2592
3026.1    42.00  0.35     Sequence
             DRB3_0202  858      AQKFNGLTVLPPLLT  NGLTVLPPL  4        0.2570
3098.3    42.00  0.28     Sequence
             DRB3_0202  859      QKFNGLTVLPPLLTD  NGLTVLPPL  3        0.2420
3646.5    46.00  0.32     Sequence
             DRB3_0202  860      KFNGLTVLPPLLTDE  NGLTVLPPL  2        0.1975
5904.1    60.00  0.26     Sequence
             DRB3_0202  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.1595
8898.6    70.00  0.35     Sequence
             DRB3_0202  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.1225
13286.4    80.00  0.38     Sequence
             DRB3_0202  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.0986
17205.1    90.00  0.30     Sequence
             DRB3_0202  864      LTVLPPLLTDEMIAQ  LLTDEMIAQ  6        0.1204
13583.2    85.00  0.56     Sequence
             DRB3_0202  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.1555
9291.5    70.00  0.73     Sequence
             DRB3_0202  866      VLPPLLTDEMIAQYT  LLTDEMIAQ  4        0.1861
6678.0    65.00  0.75     Sequence
             DRB3_0202  867      LPPLLTDEMIAQYTS  LLTDEMIAQ  3        0.2107
5113.0    55.00  0.68     Sequence
             DRB3_0202  868      PPLLTDEMIAQYTSA  LLTDEMIAQ  2        0.2156
4850.3    55.00  0.54     Sequence
             DRB3_0202  869      PLLTDEMIAQYTSAL  MIAQYTSAL  6        0.2166
4798.9    55.00  0.47     Sequence
             DRB3_0202  870      LLTDEMIAQYTSALL  MIAQYTSAL  5        0.2538
3209.6    43.00  0.69     Sequence
             DRB3_0202  871      LTDEMIAQYTSALLA  MIAQYTSAL  4        0.3129
1692.2    31.00  0.69     Sequence
             DRB3_0202  872      TDEMIAQYTSALLAG  MIAQYTSAL  3        0.3256
1475.5    29.00  0.65     Sequence
             DRB3_0202  873      DEMIAQYTSALLAGT  MIAQYTSAL  2        0.3295
1415.2    28.00  0.56     Sequence
             DRB3_0202  874      EMIAQYTSALLAGTI  MIAQYTSAL  1        0.2841
2311.7    36.00  0.35     Sequence
             DRB3_0202  875      MIAQYTSALLAGTIT  AQYTSALLA  2        0.2475
3434.4    44.00  0.32     Sequence
             DRB3_0202  876      IAQYTSALLAGTITS  YTSALLAGT  3        0.1889
6476.8    60.00  0.41     Sequence
```

```
             DRB3_0202  877      AQYTSALLAGTITSG  YTSALLAGT  2        0.1558
9268.1    70.00  0.41     Sequence
             DRB3_0202  878      QYTSALLAGTITSGW  ALLAGTITS  4        0.1050
16049.5    85.00  0.28     Sequence
             DRB3_0202  879      YTSALLAGTITSGWT  ALLAGTITS  3        0.1025
16499.5    90.00  0.38     Sequence
             DRB3_0202  880      TSALLAGTITSGWTF  LLAGTITSG  3        0.1017
16640.4    90.00  0.28     Sequence
             DRB3_0202  881      SALLAGTITSGWTFG  LLAGTITSG  2        0.1014
16688.6    90.00  0.25     Sequence
             DRB3_0202  882      ALLAGTITSGWTFGA  GTITSGWTF  4        0.1028
16432.3    90.00  0.31     Sequence
             DRB3_0202  883      LLAGTITSGWTFGAG  GTITSGWTF  3        0.0992
17099.8    90.00  0.36     Sequence
             DRB3_0202  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.1060
15879.3    85.00  0.49     Sequence
             DRB3_0202  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.1123
14827.7    85.00  0.47     Sequence
             DRB3_0202  886      GTITSGWTFGAGAAL  WTFGAGAAL  6        0.1592
8930.8    70.00  0.44     Sequence
             DRB3_0202  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.2207
4592.5    55.00  0.60     Sequence
             DRB3_0202  888      ITSGWTFGAGAALQI  WTFGAGAAL  4        0.2685
2736.1    40.00  0.56     Sequence
             DRB3_0202  889      TSGWTFGAGAALQIP  WTFGAGAAL  3        0.2941
2075.9    34.00  0.51     Sequence
             DRB3_0202  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.3140
1673.4    31.00  0.43     Sequence
             DRB3_0202  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.2880
2216.8    35.00  0.56     Sequence
             DRB3_0202  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.2120
5046.3    55.00  0.47     Sequence
             DRB3_0202  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.1636
8514.0    70.00  0.32     Sequence
             DRB3_0202  894      FGAGAALQIPFAMQM  AALQIPFAM  4        0.1598
8874.8    70.00  0.38     Sequence
             DRB3_0202  895      GAGAALQIPFAMQMA  LQIPFAMQM  5        0.1899
6406.1    60.00  0.34     Sequence
             DRB3_0202  896      AGAALQIPFAMQMAY  LQIPFAMQM  4        0.2066
5348.7    55.00  0.41     Sequence
             DRB3_0202  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.2576
3080.3    42.00  0.38     Sequence
             DRB3_0202  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.3043
1858.6    32.00  0.53     Sequence
             DRB3_0202  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.3631
983.1    23.00  0.68     Sequence
             DRB3_0202  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.3883
748.6    20.00  0.75     Sequence
             DRB3_0202  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.4177
544.8    17.00  0.75     Sequence
             DRB3_0202  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.4349
452.1    15.00  0.62     Sequence
             DRB3_0202  903      PFAMQMAYRFNGIGV  FAMQMAYRF  1        0.4167
550.7    17.00  0.44     Sequence
             DRB3_0202  904      FAMQMAYRFNGIGVT  YRFNGIGVT  6        0.5660
109.5     6.50  0.80     Sequence         WB
             DRB3_0202  905      AMQMAYRFNGIGVTQ  YRFNGIGVT  5        0.6326
53.3     4.00  0.88     Sequence         WB
             DRB3_0202  906      MQMAYRFNGIGVTQN  YRFNGIGVT  4        0.6707
35.3     3.00  0.88     Sequence         WB
             DRB3_0202  907      QMAYRFNGIGVTQNV  YRFNGIGVT  3        0.6890
28.9     2.50  0.87     Sequence         WB
             DRB3_0202  908      MAYRFNGIGVTQNVL  YRFNGIGVT  2        0.6437
47.2     3.50  0.75     Sequence         WB
             DRB3_0202  909      AYRFNGIGVTQNVLY  YRFNGIGVT  1        0.5522
127.1     7.00  0.57     Sequence         WB
```

```
             DRB3_0202  910      YRFNGIGVTQNVLYE  YRFNGIGVT  0        0.4024
642.7    18.00  0.32     Sequence
             DRB3_0202  911      RFNGIGVTQNVLYEN  IGVTQNVLY  4        0.3108
1732.4    31.00  0.33     Sequence
             DRB3_0202  912      FNGIGVTQNVLYENQ  VTQNVLYEN  5        0.3642
972.2    23.00  0.44     Sequence
             DRB3_0202  913      NGIGVTQNVLYENQK  VTQNVLYEN  4        0.3888
744.8    20.00  0.50     Sequence
             DRB3_0202  914      GIGVTQNVLYENQKL  VTQNVLYEN  3        0.3827
795.3    21.00  0.56     Sequence
             DRB3_0202  915      IGVTQNVLYENQKLI  VTQNVLYEN  2        0.3837
786.9    20.00  0.49     Sequence
             DRB3_0202  916      GVTQNVLYENQKLIA  LYENQKLIA  6        0.4316
468.8    15.00  0.50     Sequence
             DRB3_0202  917      VTQNVLYENQKLIAN  LYENQKLIA  5        0.4784
282.5    12.00  0.64     Sequence
             DRB3_0202  918      TQNVLYENQKLIANQ  LYENQKLIA  4        0.4902
248.6    11.00  0.74     Sequence
             DRB3_0202  919      QNVLYENQKLIANQF  LYENQKLIA  3        0.5317
158.7     8.00  0.74     Sequence         WB
             DRB3_0202  920      NVLYENQKLIANQFN  LYENQKLIA  2        0.5451
137.2     7.50  0.56     Sequence         WB
             DRB3_0202  921      VLYENQKLIANQFNS  LYENQKLIA  1        0.5365
150.7     8.00  0.38     Sequence         WB
             DRB3_0202  922      LYENQKLIANQFNSA  LIANQFNSA  6        0.5794
94.7     5.50  0.55     Sequence         WB
             DRB3_0202  923      YENQKLIANQFNSAI  LIANQFNSA  5        0.6539
42.3     3.50  0.66     Sequence         WB
             DRB3_0202  924      ENQKLIANQFNSAIG  LIANQFNSA  4        0.6615
39.0     3.00  0.68     Sequence         WB
             DRB3_0202  925      NQKLIANQFNSAIGK  LIANQFNSA  3        0.7097
23.1     1.90  0.64     Sequence         SB
             DRB3_0202  926      QKLIANQFNSAIGKI  LIANQFNSA  2        0.7045
24.5     2.00  0.57     Sequence         WB
             DRB3_0202  927      KLIANQFNSAIGKIQ  NQFNSAIGK  4        0.6494
44.4     3.50  0.40     Sequence         WB
             DRB3_0202  928      LIANQFNSAIGKIQD  NQFNSAIGK  3        0.5585
118.7     6.50  0.52     Sequence         WB
             DRB3_0202  929      IANQFNSAIGKIQDS  NQFNSAIGK  2        0.4469
397.3    14.00  0.62     Sequence
             DRB3_0202  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.3618
997.0    23.00  0.43     Sequence
             DRB3_0202  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.2540
3201.0    43.00  0.42     Sequence
             DRB3_0202  932      QFNSAIGKIQDSLSS  SAIGKIQDS  3        0.1280
12511.1    80.00  0.22     Sequence
             DRB3_0202  933      FNSAIGKIQDSLSST  GKIQDSLSS  5        0.1341
11721.8    80.00  0.31     Sequence
             DRB3_0202  934      NSAIGKIQDSLSSTA  GKIQDSLSS  4        0.1517
9681.9    75.00  0.33     Sequence
             DRB3_0202  935      SAIGKIQDSLSSTAS  IQDSLSSTA  5        0.1755
7489.8    65.00  0.44     Sequence
             DRB3_0202  936      AIGKIQDSLSSTASA  IQDSLSSTA  4        0.1977
5890.4    60.00  0.50     Sequence
             DRB3_0202  937      IGKIQDSLSSTASAL  IQDSLSSTA  3        0.2196
4646.3    55.00  0.49     Sequence
             DRB3_0202  938      GKIQDSLSSTASALG  IQDSLSSTA  2        0.2109
5104.6    55.00  0.43     Sequence
             DRB3_0202  939      KIQDSLSSTASALGK  DSLSSTASA  3        0.1802
7115.1    65.00  0.41     Sequence
             DRB3_0202  940      IQDSLSSTASALGKL  SLSSTASAL  3        0.1774
7335.2    65.00  0.31     Sequence
             DRB3_0202  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.1363
11443.7    80.00  0.37     Sequence
             DRB3_0202  942      DSLSSTASALGKLQD  LSSTASALG  2        0.0936
18163.8    90.00  0.41     Sequence
```

```
             DRB3_0202  943      SLSSTASALGKLQDV  LSSTASALG  1        0.0631
25269.8   100.00  0.33     Sequence
             DRB3_0202  944      LSSTASALGKLQDVV  SALGKLQDV  5        0.0457
30479.7   100.00  0.23     Sequence
             DRB3_0202  945      SSTASALGKLQDVVN  SALGKLQDV  4        0.0477
29826.6   100.00  0.28     Sequence
             DRB3_0202  946      STASALGKLQDVVNQ  SALGKLQDV  3        0.0571
26950.1   100.00  0.26     Sequence
             DRB3_0202  947      TASALGKLQDVVNQN  KLQDVVNQN  6        0.0936
18157.9    90.00  0.22     Sequence
             DRB3_0202  948      ASALGKLQDVVNQNA  KLQDVVNQN  5        0.1749
7533.4    65.00  0.25     Sequence
             DRB3_0202  949      SALGKLQDVVNQNAQ  DVVNQNAQX  7        0.2244
4409.5    50.00  0.28     Sequence
             DRB3_0202  950      ALGKLQDVVNQNAQA  DVVNQNAQA  6        0.4013
650.9    18.00  0.62     Sequence
             DRB3_0202  951      LGKLQDVVNQNAQAL  DVVNQNAQA  5        0.5609
115.7     6.50  0.65     Sequence          WB
             DRB3_0202  952      GKLQDVVNQNAQALN  DVVNQNAQA  4        0.6291
55.3     4.00  0.60     Sequence          WB
             DRB3_0202  953      KLQDVVNQNAQALNT  DVVNQNAQA  3        0.6728
34.5     3.00  0.51     Sequence          WB
             DRB3_0202  954      LQDVVNQNAQALNTL  VNQNAQALN  4        0.6849
30.2     2.50  0.37     Sequence          WB
             DRB3_0202  955      QDVVNQNAQALNTLV  VNQNAQALN  3        0.6400
49.2     3.50  0.53     Sequence          WB
             DRB3_0202  956      DVVNQNAQALNTLVK  VNQNAQALN  2        0.6019
74.3     5.00  0.55     Sequence          WB
             DRB3_0202  957      VVNQNAQALNTLVKQ  VNQNAQALN  1        0.4665
321.3    12.00  0.51     Sequence
             DRB3_0202  958      VNQNAQALNTLVKQL  QALNTLVKQ  5        0.3810
810.4    21.00  0.55     Sequence
             DRB3_0202  959      NQNAQALNTLVKQLS  QALNTLVKQ  4        0.3620
995.7    23.00  0.74     Sequence
             DRB3_0202  960      QNAQALNTLVKQLSS  QALNTLVKQ  3        0.3554
1069.0    24.00  0.75     Sequence
             DRB3_0202  961      NAQALNTLVKQLSSN  QALNTLVKQ  2        0.3494
1141.1    25.00  0.63     Sequence
             DRB3_0202  962      AQALNTLVKQLSSNF  LVKQLSSNF  6        0.3074
1796.7    32.00  0.34     Sequence
             DRB3_0202  963      QALNTLVKQLSSNFG  LVKQLSSNF  5        0.2704
2682.1    39.00  0.51     Sequence
             DRB3_0202  964      ALNTLVKQLSSNFGA  LVKQLSSNF  4        0.3200
1567.2    30.00  0.57     Sequence
             DRB3_0202  965      LNTLVKQLSSNFGAI  LVKQLSSNF  3        0.3988
668.7    19.00  0.50     Sequence
             DRB3_0202  966      NTLVKQLSSNFGAIS  LSSNFGAIS  6        0.4234
512.0    16.00  0.41     Sequence
             DRB3_0202  967      TLVKQLSSNFGAISS  LSSNFGAIS  5        0.4651
326.0    13.00  0.64     Sequence
             DRB3_0202  968      LVKQLSSNFGAISSV  LSSNFGAIS  4        0.4978
228.9    10.00  0.75     Sequence
             DRB3_0202  969      VKQLSSNFGAISSVL  LSSNFGAIS  3        0.5106
199.5     9.00  0.75     Sequence          WB
             DRB3_0202  970      KQLSSNFGAISSVLN  LSSNFGAIS  2        0.5087
203.6     9.50  0.56     Sequence          WB
             DRB3_0202  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.4569
356.3    13.00  0.51     Sequence
             DRB3_0202  972      LSSNFGAISSVLNDI  FGAISSVLN  4        0.4668
320.2    12.00  0.65     Sequence
             DRB3_0202  973      SSNFGAISSVLNDIL  FGAISSVLN  3        0.4727
300.4    12.00  0.73     Sequence
             DRB3_0202  974      SNFGAISSVLNDILS  FGAISSVLN  2        0.4547
365.0    13.00  0.69     Sequence
             DRB3_0202  975      NFGAISSVLNDILSR  FGAISSVLN  1        0.3599
1018.3    24.00  0.47     Sequence
```

```
              DRB3_0202  976      FGAISSVLNDILSRL  SVLNDILSR  5        0.2703
2684.5    39.00  0.39     Sequence
              DRB3_0202  977      GAISSVLNDILSRLD  SVLNDILSR  4        0.2109
5107.2    55.00  0.58     Sequence
              DRB3_0202  978      AISSVLNDILSRLDK  SVLNDILSR  3        0.2348
3940.3    47.00  0.56     Sequence
              DRB3_0202  979      ISSVLNDILSRLDKV  SVLNDILSR  2        0.2528
3244.8    43.00  0.44     Sequence
              DRB3_0202  980      SSVLNDILSRLDKVE  DILSRLDKV  5        0.2237
4443.3    50.00  0.32     Sequence
              DRB3_0202  981      SVLNDILSRLDKVEA  DILSRLDKV  4        0.2028
5571.7    60.00  0.49     Sequence
              DRB3_0202  982      VLNDILSRLDKVEAE  DILSRLDKV  3        0.1952
6049.3    60.00  0.55     Sequence
              DRB3_0202  983      LNDILSRLDKVEAEV  DILSRLDKV  2        0.1886
6497.3    60.00  0.45     Sequence
              DRB3_0202  984      NDILSRLDKVEAEVQ  SRLDKVEAE  4        0.1811
7043.2    65.00  0.43     Sequence
              DRB3_0202  985      DILSRLDKVEAEVQI  SRLDKVEAE  3        0.1791
7198.9    65.00  0.56     Sequence
              DRB3_0202  986      ILSRLDKVEAEVQID  SRLDKVEAE  2        0.1680
8118.3    70.00  0.49     Sequence
              DRB3_0202  987      LSRLDKVEAEVQIDR  SRLDKVEAE  1        0.1163
14210.6    85.00  0.32     Sequence
              DRB3_0202  988      SRLDKVEAEVQIDRL  LDKVEAEVQ  2        0.0716
23039.7    95.00  0.26     Sequence
              DRB3_0202  989      RLDKVEAEVQIDRLI  KVEAEVQID  3        0.0643
24946.2    95.00  0.28     Sequence
              DRB3_0202  990      LDKVEAEVQIDRLIT  KVEAEVQID  2        0.0674
24101.7    95.00  0.20     Sequence
              DRB3_0202  991      DKVEAEVQIDRLITG  VQIDRLITG  6        0.0691
23682.9    95.00  0.36     Sequence
              DRB3_0202  992      KVEAEVQIDRLITGR  VQIDRLITG  5        0.1104
15139.3    85.00  0.51     Sequence
              DRB3_0202  993      VEAEVQIDRLITGRL  VQIDRLITG  4        0.1547
9373.0    70.00  0.46     Sequence
              DRB3_0202  994      EAEVQIDRLITGRLQ  DRLITGRLQ  6        0.2151
4877.0    55.00  0.34     Sequence
              DRB3_0202  995      AEVQIDRLITGRLQS  DRLITGRLQ  5        0.2523
3262.1    43.00  0.43     Sequence
              DRB3_0202  996      EVQIDRLITGRLQSL  DRLITGRLQ  4        0.2681
2750.4    40.00  0.49     Sequence
              DRB3_0202  997      VQIDRLITGRLQSLQ  DRLITGRLQ  3        0.2924
2113.6    35.00  0.49     Sequence
              DRB3_0202  998      QIDRLITGRLQSLQT  DRLITGRLQ  2        0.2923
2116.8    35.00  0.44     Sequence
              DRB3_0202  999      IDRLITGRLQSLQTY  LITGRLQSL  3        0.2747
2560.4    38.00  0.47     Sequence
              DRB3_0202 1000      DRLITGRLQSLQTYV  LITGRLQSL  2        0.2110
5098.1    55.00  0.49     Sequence
              DRB3_0202 1001      RLITGRLQSLQTYVT  LITGRLQSL  1        0.1513
9726.4    75.00  0.29     Sequence
              DRB3_0202 1002      LITGRLQSLQTYVTQ  RLQSLQTYV  4        0.1437
10562.5    75.00  0.31     Sequence
              DRB3_0202 1003      ITGRLQSLQTYVTQQ  RLQSLQTYV  3        0.1524
9614.6    75.00  0.32     Sequence
              DRB3_0202 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.1616
8702.1    70.00  0.31     Sequence
              DRB3_0202 1005      GRLQSLQTYVTQQLI  LQTYVTQQL  5        0.1845
6789.9    65.00  0.22     Sequence
              DRB3_0202 1006      RLQSLQTYVTQQLIR  LQTYVTQQL  4        0.2249
4387.0    50.00  0.29     Sequence
              DRB3_0202 1007      LQSLQTYVTQQLIRA  YVTQQLIRA  6        0.2924
2113.7    35.00  0.47     Sequence
              DRB3_0202 1008      QSLQTYVTQQLIRAA  YVTQQLIRA  5        0.3646
967.8    23.00  0.65     Sequence
```

```
            DRB3_0202 1009      SLQTYVTQQLIRAAE  YVTQQLIRA  4        0.3907
729.9    20.00  0.69     Sequence
            DRB3_0202 1010      LQTYVTQQLIRAAEI  YVTQQLIRA  3        0.4220
520.0    16.00  0.72     Sequence
            DRB3_0202 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.3933
709.1    19.00  0.50     Sequence
            DRB3_0202 1012      TYVTQQLIRAAEIRA  QQLIRAAEI  4        0.3618
997.2    23.00  0.33     Sequence
            DRB3_0202 1013      YVTQQLIRAAEIRAS  QQLIRAAEI  3        0.3463
1179.8    25.00  0.41     Sequence
            DRB3_0202 1014      VTQQLIRAAEIRASA  IRAAEIRAS  5        0.3584
1034.6    24.00  0.46     Sequence
            DRB3_0202 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.3678
935.2    22.00  0.52     Sequence
            DRB3_0202 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.3724
889.4    22.00  0.65     Sequence
            DRB3_0202 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.3516
1113.7    25.00  0.57     Sequence
            DRB3_0202 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.3623
991.5    23.00  0.49     Sequence
            DRB3_0202 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.4705
307.6    12.00  0.75     Sequence
            DRB3_0202 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.5594
117.5     6.50  0.74     Sequence         WB
            DRB3_0202 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.5963
78.9     5.00  0.69     Sequence         WB
            DRB3_0202 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.5935
81.3     5.00  0.62     Sequence         WB
            DRB3_0202 1023      EIRASANLAAIKMSE  ASANLAAIK  3        0.5439
139.0     7.50  0.43     Sequence         WB
            DRB3_0202 1024      IRASANLAAIKMSEC  ASANLAAIK  2        0.4086
601.0    18.00  0.55     Sequence
            DRB3_0202 1025      RASANLAAIKMSECV  ASANLAAIK  1        0.2844
2303.3    36.00  0.47     Sequence
            DRB3_0202 1026      ASANLAAIKMSECVL  LAAIKMSEC  4        0.2321
4058.7    48.00  0.34     Sequence
            DRB3_0202 1027      SANLAAIKMSECVLG  IKMSECVLG  6        0.2444
3553.8    45.00  0.38     Sequence
            DRB3_0202 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.3102
1742.7    31.00  0.52     Sequence
            DRB3_0202 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.3029
1886.3    33.00  0.71     Sequence
            DRB3_0202 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.3262
1466.0    29.00  0.80     Sequence
            DRB3_0202 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.3110
1728.6    31.00  0.64     Sequence
            DRB3_0202 1032      AIKMSECVLGQSKRV  IKMSECVLG  1        0.2822
2359.3    37.00  0.47     Sequence
            DRB3_0202 1033      IKMSECVLGQSKRVD  CVLGQSKRV  5        0.2369
3854.2    47.00  0.53     Sequence
            DRB3_0202 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.2080
5265.4    55.00  0.75     Sequence
            DRB3_0202 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.2132
4981.2    55.00  0.77     Sequence
            DRB3_0202 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.2092
5199.4    55.00  0.68     Sequence
            DRB3_0202 1037      ECVLGQSKRVDFCGK  CVLGQSKRV  1        0.1645
8429.2    70.00  0.58     Sequence
            DRB3_0202 1038      CVLGQSKRVDFCGKG  LGQSKRVDF  2        0.1203
13597.6    85.00  0.28     Sequence
            DRB3_0202 1039      VLGQSKRVDFCGKGY  KRVDFCGKG  5        0.0853
19866.0    95.00  0.42     Sequence
            DRB3_0202 1040      LGQSKRVDFCGKGYH  KRVDFCGKG  4        0.1009
16784.9    90.00  0.45     Sequence
            DRB3_0202 1041      GQSKRVDFCGKGYHL  KRVDFCGKG  3        0.1421
10743.2    75.00  0.36     Sequence
```

```
            DRB3_0202 1042      QSKRVDFCGKGYHLM  DFCGKGYHL  5        0.1773
7340.8    65.00  0.30     Sequence
            DRB3_0202 1043      SKRVDFCGKGYHLMS  CGKGYHLMS  6        0.2074
5303.0    55.00  0.31     Sequence
            DRB3_0202 1044      KRVDFCGKGYHLMSF  CGKGYHLMS  5        0.2256
4356.2    50.00  0.43     Sequence
            DRB3_0202 1045      RVDFCGKGYHLMSFP  CGKGYHLMS  4        0.2479
3420.9    44.00  0.43     Sequence
            DRB3_0202 1046      VDFCGKGYHLMSFPQ  CGKGYHLMS  3        0.2700
2693.2    39.00  0.41     Sequence
            DRB3_0202 1047      DFCGKGYHLMSFPQS  YHLMSFPQS  6        0.3627
988.1    23.00  0.41     Sequence
            DRB3_0202 1048      FCGKGYHLMSFPQSA  HLMSFPQSA  6        0.4780
283.6    12.00  0.48     Sequence
            DRB3_0202 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.5118
196.8     9.00  0.48     Sequence        WB
            DRB3_0202 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.5415
142.8     7.50  0.47     Sequence        WB
            DRB3_0202 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.5403
144.6     7.50  0.50     Sequence        WB
            DRB3_0202 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.4708
306.6    12.00  0.47     Sequence
            DRB3_0202 1053      YHLMSFPQSAPHGVV  HLMSFPQSA  1        0.3837
787.0    20.00  0.38     Sequence
            DRB3_0202 1054      HLMSFPQSAPHGVVF  FPQSAPHGV  4        0.3072
1801.5    32.00  0.44     Sequence
            DRB3_0202 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.2705
2678.6    39.00  0.57     Sequence
            DRB3_0202 1056      MSFPQSAPHGVVFLH  FPQSAPHGV  2        0.2219
4531.4    55.00  0.47     Sequence
            DRB3_0202 1057      SFPQSAPHGVVFLHV  FPQSAPHGV  1        0.1392
11091.2    75.00  0.29     Sequence
            DRB3_0202 1058      FPQSAPHGVVFLHVT  SAPHGVVFL  3        0.1160
14245.4    85.00  0.28     Sequence
            DRB3_0202 1059      PQSAPHGVVFLHVTY  SAPHGVVFL  2        0.0739
22475.9    95.00  0.28     Sequence
            DRB3_0202 1060      QSAPHGVVFLHVTYV  HGVVFLHVT  4        0.0935
18188.8    90.00  0.19     Sequence
            DRB3_0202 1061      SAPHGVVFLHVTYVP  VFLHVTYVP  6        0.1178
13978.0    85.00  0.20     Sequence
            DRB3_0202 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.2820
2366.2    37.00  0.40     Sequence
            DRB3_0202 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.4004
656.6    19.00  0.41     Sequence
            DRB3_0202 1064      HGVVFLHVTYVPAQE  LHVTYVPAQ  5        0.4514
378.2    14.00  0.43     Sequence
            DRB3_0202 1065      GVVFLHVTYVPAQEK  LHVTYVPAQ  4        0.4928
241.7    11.00  0.44     Sequence
            DRB3_0202 1066      VVFLHVTYVPAQEKN  LHVTYVPAQ  3        0.4883
253.9    11.00  0.49     Sequence
            DRB3_0202 1067      VFLHVTYVPAQEKNF  LHVTYVPAQ  2        0.4624
335.9    13.00  0.46     Sequence
            DRB3_0202 1068      FLHVTYVPAQEKNFT  LHVTYVPAQ  1        0.3579
1040.8    24.00  0.41     Sequence
            DRB3_0202 1069      LHVTYVPAQEKNFTT  YVPAQEKNF  4        0.2158
4841.3    55.00  0.44     Sequence
            DRB3_0202 1070      HVTYVPAQEKNFTTA  YVPAQEKNF  3        0.1947
6080.0    60.00  0.50     Sequence
            DRB3_0202 1071      VTYVPAQEKNFTTAP  YVPAQEKNF  2        0.1767
7392.4    65.00  0.39     Sequence
            DRB3_0202 1072      TYVPAQEKNFTTAPA  QEKNFTTAP  5        0.1725
7731.5    65.00  0.38     Sequence
            DRB3_0202 1073      YVPAQEKNFTTAPAI  FTTAPAIXX  8        0.2499
3346.7    44.00  0.20     Sequence
            DRB3_0202 1074      VPAQEKNFTTAPAIC  FTTAPAICX  7        0.3490
1145.6    25.00  0.40     Sequence
```

```
             DRB3_0202 1075      PAQEKNFTTAPAICH  FTTAPAICH  6         0.4856
261.2    11.00  0.71     Sequence
             DRB3_0202 1076      AQEKNFTTAPAICHD  FTTAPAICH  5         0.5461
135.8     7.50  0.80     Sequence         WB
             DRB3_0202 1077      QEKNFTTAPAICHDG  FTTAPAICH  4         0.5690
106.0     6.00  0.84     Sequence         WB
             DRB3_0202 1078      EKNFTTAPAICHDGK  FTTAPAICH  3         0.5964
78.8     5.00  0.91     Sequence         WB
             DRB3_0202 1079      KNFTTAPAICHDGKA  FTTAPAICH  2         0.5310
160.0     8.00  0.77     Sequence         WB
             DRB3_0202 1080      NFTTAPAICHDGKAH  FTTAPAICH  1         0.3185
1594.0    30.00  0.64     Sequence
             DRB3_0202 1081      FTTAPAICHDGKAHF  FTTAPAICH  0         0.1635
8521.8    70.00  0.38     Sequence
             DRB3_0202 1082      TTAPAICHDGKAHFP  CHDGKAHFP  6         0.0725
22813.2    95.00  0.38     Sequence
             DRB3_0202 1083      TAPAICHDGKAHFPR  CHDGKAHFP  5         0.1032
16366.0    90.00  0.41     Sequence
             DRB3_0202 1084      APAICHDGKAHFPRE  CHDGKAHFP  4         0.1167
14139.7    85.00  0.43     Sequence
             DRB3_0202 1085      PAICHDGKAHFPREG  CHDGKAHFP  3         0.1274
12603.7    80.00  0.44     Sequence
             DRB3_0202 1086      AICHDGKAHFPREGV  CHDGKAHFP  2         0.1120
14889.6    85.00  0.40     Sequence
             DRB3_0202 1087      ICHDGKAHFPREGVF  CHDGKAHFP  1         0.0934
18191.8    90.00  0.30     Sequence
             DRB3_0202 1088      CHDGKAHFPREGVFV  GKAHFPREG  3         0.0763
21904.7    95.00  0.30     Sequence
             DRB3_0202 1089      HDGKAHFPREGVFVS  HFPREGVFV  5         0.0928
18317.6    90.00  0.34     Sequence
             DRB3_0202 1090      DGKAHFPREGVFVSN  HFPREGVFV  4         0.1043
16177.8    90.00  0.40     Sequence
             DRB3_0202 1091      GKAHFPREGVFVSNG  HFPREGVFV  3         0.1185
13866.1    85.00  0.35     Sequence
             DRB3_0202 1092      KAHFPREGVFVSNGT  FVSNGTXXX  9         0.1835
6869.6    65.00  0.11     Sequence
             DRB3_0202 1093      AHFPREGVFVSNGTH  FVSNGTHXX  8         0.2829
2343.3    36.00  0.26     Sequence
             DRB3_0202 1094      HFPREGVFVSNGTHW  FVSNGTHWX  7         0.4303
475.2    16.00  0.48     Sequence
             DRB3_0202 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6         0.6158
63.9     4.50  0.79     Sequence         WB
             DRB3_0202 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5         0.6966
26.6     2.50  0.83     Sequence         WB
             DRB3_0202 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4         0.7315
18.3     1.50  0.83     Sequence         SB
             DRB3_0202 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3         0.7382
17.0     1.40  0.86     Sequence         SB
             DRB3_0202 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2         0.7120
22.6     1.80  0.75     Sequence         SB
             DRB3_0202 1100      VFVSNGTHWFVTQRN  FVSNGTHWF  1         0.4957
234.2    10.00  0.61     Sequence
             DRB3_0202 1101      FVSNGTHWFVTQRNF  FVSNGTHWF  0         0.3191
1582.4    30.00  0.34     Sequence
             DRB3_0202 1102      VSNGTHWFVTQRNFY  WFVTQRNFY  6         0.2338
3985.5    48.00  0.40     Sequence
             DRB3_0202 1103      SNGTHWFVTQRNFYE  FVTQRNFYE  6         0.3091
1764.9    32.00  0.43     Sequence
             DRB3_0202 1104      NGTHWFVTQRNFYEP  FVTQRNFYE  5         0.3620
994.9    23.00  0.47     Sequence
             DRB3_0202 1105      GTHWFVTQRNFYEPQ  FVTQRNFYE  4         0.4034
636.0    18.00  0.45     Sequence
             DRB3_0202 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3         0.4194
535.1    17.00  0.47     Sequence
             DRB3_0202 1107      HWFVTQRNFYEPQII  FVTQRNFYE  2         0.3990
666.8    19.00  0.38     Sequence
```

```
             DRB3_0202 1108      WFVTQRNFYEPQIIT  TQRNFYEPQ  3        0.3617
998.0    23.00  0.34     Sequence
             DRB3_0202 1109      FVTQRNFYEPQIITT  TQRNFYEPQ  2        0.2964
2024.6    34.00  0.36     Sequence
             DRB3_0202 1110      VTQRNFYEPQIITTD  YEPQIITTD  6        0.2062
5370.3    55.00  0.41     Sequence
             DRB3_0202 1111      TQRNFYEPQIITTDN  YEPQIITTD  5        0.2032
5547.3    60.00  0.53     Sequence
             DRB3_0202 1112      QRNFYEPQIITTDNT  YEPQIITTD  4        0.2136
4958.4    55.00  0.60     Sequence
             DRB3_0202 1113      RNFYEPQIITTDNTF  YEPQIITTD  3        0.2335
3996.7    48.00  0.62     Sequence
             DRB3_0202 1114      NFYEPQIITTDNTFV  YEPQIITTD  2        0.2258
4344.9    50.00  0.33     Sequence
             DRB3_0202 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.2928
2105.2    34.00  0.47     Sequence
             DRB3_0202 1116      YEPQIITTDNTFVSG  IITTDNTFV  4        0.3360
1318.6    27.00  0.43     Sequence
             DRB3_0202 1117      EPQIITTDNTFVSGN  ITTDNTFVS  4        0.3814
807.2    21.00  0.45     Sequence
             DRB3_0202 1118      PQIITTDNTFVSGNC  ITTDNTFVS  3        0.4073
609.5    18.00  0.46     Sequence
             DRB3_0202 1119      QIITTDNTFVSGNCD  ITTDNTFVS  2        0.3725
888.8    22.00  0.46     Sequence
             DRB3_0202 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.2775
2483.1    38.00  0.41     Sequence
             DRB3_0202 1121      ITTDNTFVSGNCDVV  TFVSGNCDV  5        0.1652
8372.2    70.00  0.18     Sequence
             DRB3_0202 1122      TTDNTFVSGNCDVVI  VSGNCDVVI  6        0.1868
6622.2    60.00  0.32     Sequence
             DRB3_0202 1123      TDNTFVSGNCDVVIG  VSGNCDVVI  5        0.2099
5162.2    55.00  0.37     Sequence
             DRB3_0202 1124      DNTFVSGNCDVVIGI  VSGNCDVVI  4        0.2279
4248.8    49.00  0.44     Sequence
             DRB3_0202 1125      NTFVSGNCDVVIGIV  VSGNCDVVI  3        0.2457
3502.3    45.00  0.50     Sequence
             DRB3_0202 1126      TFVSGNCDVVIGIVN  VSGNCDVVI  2        0.1967
5950.7    60.00  0.46     Sequence
             DRB3_0202 1127      FVSGNCDVVIGIVNN  VSGNCDVVI  1        0.1737
7630.2    65.00  0.33     Sequence
             DRB3_0202 1128      VSGNCDVVIGIVNNT  CDVVIGIVN  4        0.1423
10717.4    75.00  0.34     Sequence
             DRB3_0202 1129      SGNCDVVIGIVNNTV  VVIGIVNNT  5        0.2097
5171.8    55.00  0.28     Sequence
             DRB3_0202 1130      GNCDVVIGIVNNTVY  GIVNNTVYX  7        0.2923
2116.4    35.00  0.25     Sequence
             DRB3_0202 1131      NCDVVIGIVNNTVYD  GIVNNTVYD  6        0.3490
1145.9    25.00  0.43     Sequence
             DRB3_0202 1132      CDVVIGIVNNTVYDP  GIVNNTVYD  5        0.4045
628.6    18.00  0.50     Sequence
             DRB3_0202 1133      DVVIGIVNNTVYDPL  GIVNNTVYD  4        0.4465
398.9    14.00  0.47     Sequence
             DRB3_0202 1134      VVIGIVNNTVYDPLQ  GIVNNTVYD  3        0.4878
255.2    11.00  0.48     Sequence
             DRB3_0202 1135      VIGIVNNTVYDPLQP  GIVNNTVYD  2        0.4948
236.6    10.00  0.47     Sequence
             DRB3_0202 1136      IGIVNNTVYDPLQPE  GIVNNTVYD  1        0.4140
566.8    17.00  0.39     Sequence
             DRB3_0202 1137      GIVNNTVYDPLQPEL  IVNNTVYDP  1        0.2851
2286.2    36.00  0.34     Sequence
             DRB3_0202 1138      IVNNTVYDPLQPELD  TVYDPLQPE  4        0.1607
8783.6    70.00  0.20     Sequence
             DRB3_0202 1139      VNNTVYDPLQPELDS  TVYDPLQPE  3        0.1225
13282.2    80.00  0.35     Sequence
             DRB3_0202 1140      NNTVYDPLQPELDSF  TVYDPLQPE  2        0.1104
15136.5    85.00  0.29     Sequence
```

```
             DRB3_0202 1141      NTVYDPLQPELDSFK  YDPLQPELD  3        0.0891
19075.7    90.00  0.34     Sequence
             DRB3_0202 1142      TVYDPLQPELDSFKE  LQPELDSFK  5        0.0872
19459.9    90.00  0.34     Sequence
             DRB3_0202 1143      VYDPLQPELDSFKEE  LQPELDSFK  4        0.0765
21843.9    95.00  0.47     Sequence
             DRB3_0202 1144      YDPLQPELDSFKEEL  LQPELDSFK  3        0.0596
26226.3   100.00  0.68     Sequence
             DRB3_0202 1145      DPLQPELDSFKEELD  LQPELDSFK  2        0.0506
28934.7   100.00  0.63     Sequence
             DRB3_0202 1146      PLQPELDSFKEELDK  LQPELDSFK  1        0.0411
32040.7   100.00  0.50     Sequence
             DRB3_0202 1147      LQPELDSFKEELDKY  ELDSFKEEL  3        0.0319
35417.2   100.00  0.25     Sequence
             DRB3_0202 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.0186
40890.3   100.00  0.28     Sequence
             DRB3_0202 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.0237
38696.4   100.00  0.32     Sequence
             DRB3_0202 1150      ELDSFKEELDKYFKN  EELDKYFKN  6        0.0483
29633.6   100.00  0.44     Sequence
             DRB3_0202 1151      LDSFKEELDKYFKNH  EELDKYFKN  5        0.0664
24368.7    95.00  0.55     Sequence
             DRB3_0202 1152      DSFKEELDKYFKNHT  EELDKYFKN  4        0.1025
16501.7    90.00  0.57     Sequence
             DRB3_0202 1153      SFKEELDKYFKNHTS  YFKNHTSXX  8        0.1994
5783.3    60.00  0.22     Sequence
             DRB3_0202 1154      FKEELDKYFKNHTSP  YFKNHTSPX  7        0.3223
1529.4    29.00  0.44     Sequence
             DRB3_0202 1155      KEELDKYFKNHTSPD  YFKNHTSPD  6        0.4914
245.4    11.00  0.75     Sequence
             DRB3_0202 1156      EELDKYFKNHTSPDV  YFKNHTSPD  5        0.6139
65.2     4.50  0.62     Sequence         WB
             DRB3_0202 1157      ELDKYFKNHTSPDVD  YFKNHTSPD  4        0.6622
38.7     3.00  0.56     Sequence         WB
             DRB3_0202 1158      LDKYFKNHTSPDVDL  YFKNHTSPD  3        0.6995
25.8     2.50  0.56     Sequence         WB
             DRB3_0202 1159      DKYFKNHTSPDVDLG  YFKNHTSPD  2        0.6848
30.3     2.50  0.50     Sequence         WB
             DRB3_0202 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.6120
66.5     4.50  0.45     Sequence         WB
             DRB3_0202 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.4039
632.5    18.00  0.47     Sequence
             DRB3_0202 1162      FKNHTSPDVDLGDIS  FKNHTSPDV  0        0.1684
8082.3    70.00  0.41     Sequence
             DRB3_0202 1163      KNHTSPDVDLGDISG  NHTSPDVDL  1        0.0270
37341.9   100.00  0.34     Sequence
             DRB3_0202 1164      NHTSPDVDLGDISGI  TSPDVDLGD  2        0.0220
39397.2   100.00  0.21     Sequence
             DRB3_0202 1165      HTSPDVDLGDISGIN  DLGDISGIN  6        0.0259
37782.5   100.00  0.56     Sequence
             DRB3_0202 1166      TSPDVDLGDISGINA  DLGDISGIN  5        0.0405
32246.9   100.00  0.63     Sequence
             DRB3_0202 1167      SPDVDLGDISGINAS  DLGDISGIN  4        0.0531
28136.0   100.00  0.55     Sequence
             DRB3_0202 1168      PDVDLGDISGINASF  DLGDISGIN  3        0.0698
23504.5    95.00  0.49     Sequence
             DRB3_0202 1169      DVDLGDISGINASFV  SGINASFVX  7        0.1231
13193.4    80.00  0.30     Sequence
             DRB3_0202 1170      VDLGDISGINASFVN  SGINASFVN  6        0.2391
3760.4    46.00  0.56     Sequence
             DRB3_0202 1171      DLGDISGINASFVNI  SGINASFVN  5        0.3326
1367.9    28.00  0.65     Sequence
             DRB3_0202 1172      LGDISGINASFVNIQ  SGINASFVN  4        0.3865
763.2    20.00  0.62     Sequence
             DRB3_0202 1173      GDISGINASFVNIQK  SGINASFVN  3        0.4242
508.0    16.00  0.61     Sequence
```

```
             DRB3_0202 1174      DISGINASFVNIQKE  SGINASFVN  2        0.3963
686.8    19.00  0.54     Sequence
             DRB3_0202 1175      ISGINASFVNIQKEI  SGINASFVN  1        0.3762
853.4    21.00  0.44     Sequence
             DRB3_0202 1176      SGINASFVNIQKEID  INASFVNIQ  2        0.2864
2255.5    36.00  0.35     Sequence
             DRB3_0202 1177      GINASFVNIQKEIDR  SFVNIQKEI  4        0.2260
4335.9    50.00  0.43     Sequence
             DRB3_0202 1178      INASFVNIQKEIDRL  SFVNIQKEI  3        0.2141
4929.1    55.00  0.47     Sequence
             DRB3_0202 1179      NASFVNIQKEIDRLN  SFVNIQKEI  2        0.2070
5323.7    55.00  0.44     Sequence
             DRB3_0202 1180      ASFVNIQKEIDRLNE  VNIQKEIDR  3        0.1816
7012.0    65.00  0.25     Sequence
             DRB3_0202 1181      SFVNIQKEIDRLNEV  IQKEIDRLN  4        0.1738
7628.0    65.00  0.28     Sequence
             DRB3_0202 1182      FVNIQKEIDRLNEVA  DRLNEVAXX  8        0.1890
6468.7    60.00  0.22     Sequence
             DRB3_0202 1183      VNIQKEIDRLNEVAK  DRLNEVAKX  7        0.2904
2159.8    35.00  0.45     Sequence
             DRB3_0202 1184      NIQKEIDRLNEVAKN  DRLNEVAKN  6        0.4709
306.4    12.00  0.88     Sequence
             DRB3_0202 1185      IQKEIDRLNEVAKNL  DRLNEVAKN  5        0.5775
96.7     6.00  0.92     Sequence         WB
             DRB3_0202 1186      QKEIDRLNEVAKNLN  DRLNEVAKN  4        0.6227
59.3     4.00  0.88     Sequence         WB
             DRB3_0202 1187      KEIDRLNEVAKNLNE  DRLNEVAKN  3        0.6393
49.5     3.50  0.86     Sequence         WB
             DRB3_0202 1188      EIDRLNEVAKNLNES  DRLNEVAKN  2        0.6103
67.8     4.50  0.75     Sequence         WB
             DRB3_0202 1189      IDRLNEVAKNLNESL  DRLNEVAKN  1        0.5520
127.4     7.00  0.55     Sequence         WB
             DRB3_0202 1190      DRLNEVAKNLNESLI  VAKNLNESL  5        0.5334
155.8     8.00  0.60     Sequence         WB
             DRB3_0202 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.5430
140.4     7.50  0.73     Sequence         WB
             DRB3_0202 1192      LNEVAKNLNESLIDL  VAKNLNESL  3        0.5776
96.6     6.00  0.67     Sequence         WB
             DRB3_0202 1193      NEVAKNLNESLIDLQ  VAKNLNESL  2        0.5368
150.1     8.00  0.50     Sequence         WB
             DRB3_0202 1194      EVAKNLNESLIDLQE  KNLNESLID  3        0.4998
224.1    10.00  0.54     Sequence
             DRB3_0202 1195      VAKNLNESLIDLQEL  KNLNESLID  2        0.4557
361.0    13.00  0.55     Sequence
             DRB3_0202 1196      AKNLNESLIDLQELG  KNLNESLID  1        0.3047
1850.9    32.00  0.52     Sequence
             DRB3_0202 1197      KNLNESLIDLQELGK  LNESLIDLQ  2        0.2175
4750.8    55.00  0.41     Sequence
             DRB3_0202 1198      NLNESLIDLQELGKY  LNESLIDLQ  1        0.1142
14536.0    85.00  0.35     Sequence
             DRB3_0202 1199      LNESLIDLQELGKYE  SLIDLQELG  3        0.0716
23038.0    95.00  0.65     Sequence
             DRB3_0202 1200      NESLIDLQELGKYEQ  SLIDLQELG  2        0.0614
25744.2   100.00  0.57     Sequence
             DRB3_0202 1201      ESLIDLQELGKYEQY  SLIDLQELG  1        0.0476
29888.3   100.00  0.29     Sequence
             DRB3_0202 1202      SLIDLQELGKYEQYI  QELGKYEQY  5        0.0524
28367.1   100.00  0.28     Sequence
             DRB3_0202 1203      LIDLQELGKYEQYIK  QELGKYEQY  4        0.0683
23867.4    95.00  0.29     Sequence
             DRB3_0202 1204      IDLQELGKYEQYIKW  LGKYEQYIK  5        0.0809
20847.0    95.00  0.28     Sequence
             DRB3_0202 1205      DLQELGKYEQYIKWP  LGKYEQYIK  4        0.0913
18614.1    90.00  0.26     Sequence
             DRB3_0202 1206      LQELGKYEQYIKWPW  YEQYIKWPW  6        0.1101
15192.3    85.00  0.28     Sequence
```

```
             DRB3_0202 1207      QELGKYEQYIKWPWY  YEQYIKWPW  5        0.1263
12748.9    80.00  0.31     Sequence
             DRB3_0202 1208      ELGKYEQYIKWPWYI  QYIKWPWYI  6        0.1664
8264.5    70.00  0.32     Sequence
             DRB3_0202 1209      LGKYEQYIKWPWYIW  QYIKWPWYI  5        0.2161
4823.9    55.00  0.38     Sequence
             DRB3_0202 1210      GKYEQYIKWPWYIWL  QYIKWPWYI  4        0.2317
4076.8    48.00  0.41     Sequence
             DRB3_0202 1211      KYEQYIKWPWYIWLG  QYIKWPWYI  3        0.2319
4066.9    48.00  0.44     Sequence
             DRB3_0202 1212      YEQYIKWPWYIWLGF  QYIKWPWYI  2        0.2205
4599.8    55.00  0.44     Sequence
             DRB3_0202 1213      EQYIKWPWYIWLGFI  QYIKWPWYI  1        0.2140
4934.3    55.00  0.39     Sequence
             DRB3_0202 1214      QYIKWPWYIWLGFIA  QYIKWPWYI  0        0.1819
6984.5    65.00  0.19     Sequence
             DRB3_0202 1215      YIKWPWYIWLGFIAG  WYIWLGFIA  5        0.1555
9296.4    70.00  0.26     Sequence
             DRB3_0202 1216      IKWPWYIWLGFIAGL  WYIWLGFIA  4        0.1456
10344.8    75.00  0.32     Sequence
             DRB3_0202 1217      KWPWYIWLGFIAGLI  WYIWLGFIA  3        0.1585
9002.1    70.00  0.27     Sequence
             DRB3_0202 1218      WPWYIWLGFIAGLIA  IWLGFIAGL  4        0.1696
7979.7    70.00  0.22     Sequence
             DRB3_0202 1219      PWYIWLGFIAGLIAI  IWLGFIAGL  3        0.1990
5808.0    60.00  0.19     Sequence
             DRB3_0202 1220      WYIWLGFIAGLIAIV  FIAGLIAIV  6        0.2172
4766.5    55.00  0.35     Sequence
             DRB3_0202 1221      YIWLGFIAGLIAIVM  FIAGLIAIV  5        0.2503
3333.2    44.00  0.49     Sequence
             DRB3_0202 1222      IWLGFIAGLIAIVMV  FIAGLIAIV  4        0.2718
2642.3    39.00  0.54     Sequence
             DRB3_0202 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3        0.2793
2435.1    37.00  0.57     Sequence
             DRB3_0202 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.2848
2294.7    36.00  0.53     Sequence
             DRB3_0202 1225      GFIAGLIAIVMVTIM  FIAGLIAIV  1        0.2359
3894.0    47.00  0.34     Sequence
             DRB3_0202 1226      FIAGLIAIVMVTIML  LIAIVMVTI  4        0.1980
5869.7    60.00  0.29     Sequence
             DRB3_0202 1227      IAGLIAIVMVTIMLC  LIAIVMVTI  3        0.1929
6201.4    60.00  0.37     Sequence
             DRB3_0202 1228      AGLIAIVMVTIMLCC  IAIVMVTIM  3        0.1970
5931.6    60.00  0.36     Sequence
             DRB3_0202 1229      GLIAIVMVTIMLCCM  IAIVMVTIM  2        0.1624
8628.7    70.00  0.27     Sequence
             DRB3_0202 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3        0.1236
13132.8    80.00  0.38     Sequence
             DRB3_0202 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2        0.1048
16086.8    85.00  0.37     Sequence
             DRB3_0202 1232      AIVMVTIMLCCMTSC  IVMVTIMLC  1        0.1021
16569.6    90.00  0.27     Sequence
             DRB3_0202 1233      IVMVTIMLCCMTSCC  IMLCCMTSC  5        0.0844
20069.5    95.00  0.31     Sequence
             DRB3_0202 1234      VMVTIMLCCMTSCCS  MLCCMTSCC  5        0.0913
18628.8    90.00  0.34     Sequence
             DRB3_0202 1235      MVTIMLCCMTSCCSC  MLCCMTSCC  4        0.0971
17480.3    90.00  0.38     Sequence
             DRB3_0202 1236      VTIMLCCMTSCCSCL  MLCCMTSCC  3        0.1101
15193.8    85.00  0.34     Sequence
             DRB3_0202 1237      TIMLCCMTSCCSCLK  MLCCMTSCC  2        0.1230
13219.2    80.00  0.25     Sequence
             DRB3_0202 1238      IMLCCMTSCCSCLKG  CMTSCCSCL  4        0.1129
14738.4    85.00  0.40     Sequence
             DRB3_0202 1239      MLCCMTSCCSCLKGC  CMTSCCSCL  3        0.0903
18821.6    90.00  0.47     Sequence
```

```
             DRB3_0202 1240      LCCMTSCCSCLKGCC  CMTSCCSCL  2        0.0841
20135.2    95.00  0.44     Sequence
             DRB3_0202 1241      CCMTSCCSCLKGCCS  CMTSCCSCL  1        0.0722
22887.4    95.00  0.38     Sequence
             DRB3_0202 1242      CMTSCCSCLKGCCSC  CMTSCCSCL  0        0.0554
27467.9   100.00  0.28     Sequence
             DRB3_0202 1243      MTSCCSCLKGCCSCG  CLKGCCSCG  6        0.0314
35594.3   100.00  0.32     Sequence
             DRB3_0202 1244      TSCCSCLKGCCSCGS  CLKGCCSCG  5        0.0394
32630.9   100.00  0.41     Sequence
             DRB3_0202 1245      SCCSCLKGCCSCGSC  CLKGCCSCG  4        0.0427
31517.0   100.00  0.46     Sequence
             DRB3_0202 1246      CCSCLKGCCSCGSCC  CLKGCCSCG  3        0.0451
30693.8   100.00  0.50     Sequence
             DRB3_0202 1247      CSCLKGCCSCGSCCK  CLKGCCSCG  2        0.0511
28777.6   100.00  0.38     Sequence
             DRB3_0202 1248      SCLKGCCSCGSCCKF  GCCSCGSCC  4        0.0461
30366.5   100.00  0.23     Sequence
             DRB3_0202 1249      CLKGCCSCGSCCKFD  GCCSCGSCC  3        0.0396
32561.4   100.00  0.34     Sequence
             DRB3_0202 1250      LKGCCSCGSCCKFDE  CCSCGSCCK  3        0.0283
36797.6   100.00  0.31     Sequence
             DRB3_0202 1251      KGCCSCGSCCKFDED  CCSCGSCCK  2        0.0226
39157.6   100.00  0.27     Sequence
             DRB3_0202 1252      GCCSCGSCCKFDEDD  CGSCCKFDE  4        0.0165
41824.6   100.00  0.32     Sequence
             DRB3_0202 1253      CCSCGSCCKFDEDDS  CKFDEDDSX  7        0.0167
41714.8   100.00  0.25     Sequence
             DRB3_0202 1254      CSCGSCCKFDEDDSE  CKFDEDDSE  6        0.0218
39478.3   100.00  0.42     Sequence
             DRB3_0202 1255      SCGSCCKFDEDDSEP  CKFDEDDSE  5        0.0276
37086.6   100.00  0.47     Sequence
             DRB3_0202 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.0501
29071.8   100.00  0.49     Sequence
             DRB3_0202 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.0691
23663.7    95.00  0.56     Sequence
             DRB3_0202 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.0823
20520.7    95.00  0.60     Sequence
             DRB3_0202 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.0806
20904.4    95.00  0.67     Sequence
             DRB3_0202 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.0778
21543.2    95.00  0.59     Sequence
             DRB3_0202 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.0572
26926.2   100.00  0.41     Sequence
             DRB3_0202 1262      FDEDDSEPVLKGVKL  VLKGVKLXX  8        0.0488
29481.7   100.00  0.17     Sequence
             DRB3_0202 1263      DEDDSEPVLKGVKLH  VLKGVKLHX  7        0.0461
30349.7   100.00  0.30     Sequence
             DRB3_0202 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.0668
24268.4    95.00  0.50     Sequence
             DRB3_0202 1265      DDSEPVLKGVKLHYT  VLKGVKLHY  5        0.1010
16771.5    90.00  0.48     Sequence
             DRB4_0101    1      PSPIKEMFVFLVLLP  PIKEMFVFL  2        0.5110
198.6    13.00  0.61     Sequence
             DRB4_0101    2      SPIKEMFVFLVLLPL  PIKEMFVFL  1        0.4624
335.8    20.00  0.48     Sequence
             DRB4_0101    3      PIKEMFVFLVLLPLV  PIKEMFVFL  0        0.3913
725.0    34.00  0.29     Sequence
             DRB4_0101    4      IKEMFVFLVLLPLVS  MFVFLVLLP  3        0.3445
1202.1    45.00  0.26     Sequence
             DRB4_0101    5      KEMFVFLVLLPLVSS  FLVLLPLVS  5        0.3618
997.1    41.00  0.28     Sequence
             DRB4_0101    6      EMFVFLVLLPLVSSQ  FLVLLPLVS  4        0.3263
1465.3    50.00  0.35     Sequence
             DRB4_0101    7      MFVFLVLLPLVSSQC  FLVLLPLVS  3        0.3659
954.1    40.00  0.32     Sequence
```

```
             DRB4_0101    8      FVFLVLLPLVSSQCV  LLPLVSSQC  5        0.5126
195.2    13.00  0.34     Sequence
             DRB4_0101    9      VFLVLLPLVSSQCVN  LLPLVSSQC  4        0.5828
91.3     6.00  0.32     Sequence        WB
             DRB4_0101   10      FLVLLPLVSSQCVNF  PLVSSQCVN  5        0.6517
43.3     2.50  0.32     Sequence        WB
             DRB4_0101   11      LVLLPLVSSQCVNFT  PLVSSQCVN  4        0.6861
29.9     1.20  0.35     Sequence        SB
             DRB4_0101   12      VLLPLVSSQCVNFTN  PLVSSQCVN  3        0.6938
27.5     1.00  0.36     Sequence        SB
             DRB4_0101   13      LLPLVSSQCVNFTNR  LVSSQCVNF  3        0.6978
26.3     0.90  0.35     Sequence        SB
             DRB4_0101   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.6425
47.9     2.50  0.44     Sequence        WB
             DRB4_0101   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.4181
542.4    28.00  0.51     Sequence
             DRB4_0101   16      LVSSQCVNFTNRTQL  LVSSQCVNF  0        0.2718
2639.8    65.00  0.37     Sequence
             DRB4_0101   17      VSSQCVNFTNRTQLP  CVNFTNRTQ  4        0.1971
5929.6    85.00  0.31     Sequence
             DRB4_0101   18      SSQCVNFTNRTQLPS  CVNFTNRTQ  3        0.2072
5311.2    80.00  0.34     Sequence
             DRB4_0101   19      SQCVNFTNRTQLPSA  CVNFTNRTQ  2        0.2372
3839.0    75.00  0.28     Sequence
             DRB4_0101   20      QCVNFTNRTQLPSAY  CVNFTNRTQ  1        0.2509
3311.6    70.00  0.17     Sequence
             DRB4_0101   21      CVNFTNRTQLPSAYT  TNRTQLPSA  4        0.2463
3479.9    75.00  0.20     Sequence
             DRB4_0101   22      VNFTNRTQLPSAYTN  TNRTQLPSA  3        0.2366
3863.6    75.00  0.25     Sequence
             DRB4_0101   23      NFTNRTQLPSAYTNS  TNRTQLPSA  2        0.1957
6016.6    85.00  0.28     Sequence
             DRB4_0101   24      FTNRTQLPSAYTNSF  QLPSAYTNS  5        0.2223
4511.7    80.00  0.36     Sequence
             DRB4_0101   25      TNRTQLPSAYTNSFT  QLPSAYTNS  4        0.2197
4638.7    80.00  0.47     Sequence
             DRB4_0101   26      NRTQLPSAYTNSFTR  QLPSAYTNS  3        0.2194
4653.5    80.00  0.51     Sequence
             DRB4_0101   27      RTQLPSAYTNSFTRG  QLPSAYTNS  2        0.2118
5056.5    80.00  0.58     Sequence
             DRB4_0101   28      TQLPSAYTNSFTRGV  QLPSAYTNS  1        0.1925
6226.8    85.00  0.49     Sequence
             DRB4_0101   29      QLPSAYTNSFTRGVY  QLPSAYTNS  0        0.1633
8539.3    90.00  0.32     Sequence
             DRB4_0101   30      LPSAYTNSFTRGVYY  SAYTNSFTR  2        0.1153
14357.1   100.00  0.22     Sequence
             DRB4_0101   31      PSAYTNSFTRGVYYP  TNSFTRGVY  4        0.0840
20153.7   100.00  0.30     Sequence
             DRB4_0101   32      SAYTNSFTRGVYYPD  TNSFTRGVY  3        0.0813
20754.5   100.00  0.26     Sequence
             DRB4_0101   33      AYTNSFTRGVYYPDK  TNSFTRGVY  2        0.0828
20403.8   100.00  0.23     Sequence
             DRB4_0101   34      YTNSFTRGVYYPDKV  TRGVYYPDK  5        0.0965
17592.5   100.00  0.22     Sequence
             DRB4_0101   35      TNSFTRGVYYPDKVF  TRGVYYPDK  4        0.1063
15838.0   100.00  0.19     Sequence
             DRB4_0101   36      NSFTRGVYYPDKVFR  VYYPDKVFR  6        0.1299
12266.2    95.00  0.23     Sequence
             DRB4_0101   37      SFTRGVYYPDKVFRS  VYYPDKVFR  5        0.1498
9884.3    95.00  0.34     Sequence
             DRB4_0101   38      FTRGVYYPDKVFRSS  VYYPDKVFR  4        0.1718
7794.4    90.00  0.35     Sequence
             DRB4_0101   39      TRGVYYPDKVFRSSV  VYYPDKVFR  3        0.2097
5172.8    80.00  0.34     Sequence
             DRB4_0101   40      RGVYYPDKVFRSSVL  PDKVFRSSV  5        0.2484
3403.0    70.00  0.28     Sequence
```

```
             DRB4_0101   41      GVYYPDKVFRSSVLH  KVFRSSVLH  6        0.3066
1812.7    55.00  0.31     Sequence
             DRB4_0101   42      VYYPDKVFRSSVLHS  KVFRSSVLH  5        0.4212
524.6    28.00  0.36     Sequence
             DRB4_0101   43      YYPDKVFRSSVLHST  VFRSSVLHS  5        0.4868
258.0    16.00  0.47     Sequence
             DRB4_0101   44      YPDKVFRSSVLHSTQ  VFRSSVLHS  4        0.5152
189.6    12.00  0.49     Sequence
             DRB4_0101   45      PDKVFRSSVLHSTQD  VFRSSVLHS  3        0.5105
199.7    13.00  0.50     Sequence
             DRB4_0101   46      DKVFRSSVLHSTQDL  VFRSSVLHS  2        0.5056
210.4    14.00  0.50     Sequence
             DRB4_0101   47      KVFRSSVLHSTQDLF  VFRSSVLHS  1        0.5062
209.0    14.00  0.40     Sequence
             DRB4_0101   48      VFRSSVLHSTQDLFL  VLHSTQDLF  5        0.4700
309.5    19.00  0.31     Sequence
             DRB4_0101   49      FRSSVLHSTQDLFLP  VLHSTQDLF  4        0.4650
326.7    20.00  0.37     Sequence
             DRB4_0101   50      RSSVLHSTQDLFLPF  VLHSTQDLF  3        0.4920
243.9    16.00  0.38     Sequence
             DRB4_0101   51      SSVLHSTQDLFLPFF  VLHSTQDLF  2        0.4876
255.8    16.00  0.41     Sequence
             DRB4_0101   52      SVLHSTQDLFLPFFS  VLHSTQDLF  1        0.4614
339.6    20.00  0.47     Sequence
             DRB4_0101   53      VLHSTQDLFLPFFSN  VLHSTQDLF  0        0.3683
929.4    40.00  0.27     Sequence
             DRB4_0101   54      LHSTQDLFLPFFSNV  QDLFLPFFS  4        0.2517
3283.3    70.00  0.23     Sequence
             DRB4_0101   55      HSTQDLFLPFFSNVT  QDLFLPFFS  3        0.2339
3978.4    75.00  0.26     Sequence
             DRB4_0101   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.2533
3226.6    70.00  0.23     Sequence
             DRB4_0101   57      TQDLFLPFFSNVTWF  FLPFFSNVT  4        0.2928
2105.2    60.00  0.27     Sequence
             DRB4_0101   58      QDLFLPFFSNVTWFH  PFFSNVTWF  5        0.3053
1838.4    55.00  0.28     Sequence
             DRB4_0101   59      DLFLPFFSNVTWFHA  PFFSNVTWF  4        0.3337
1352.1    48.00  0.33     Sequence
             DRB4_0101   60      LFLPFFSNVTWFHAI  PFFSNVTWF  3        0.3596
1021.5    42.00  0.31     Sequence
             DRB4_0101   61      FLPFFSNVTWFHAIH  PFFSNVTWF  2        0.3568
1052.6    42.00  0.31     Sequence
             DRB4_0101   62      LPFFSNVTWFHAIHV  NVTWFHAIH  5        0.3510
1120.9    44.00  0.31     Sequence
             DRB4_0101   63      PFFSNVTWFHAIHVS  NVTWFHAIH  4        0.3189
1586.7    55.00  0.43     Sequence
             DRB4_0101   64      FFSNVTWFHAIHVSG  NVTWFHAIH  3        0.3049
1845.4    60.00  0.54     Sequence
             DRB4_0101   65      FSNVTWFHAIHVSGT  NVTWFHAIH  2        0.3295
1414.4    49.00  0.54     Sequence
             DRB4_0101   66      SNVTWFHAIHVSGTN  NVTWFHAIH  1        0.3431
1220.9    46.00  0.47     Sequence
             DRB4_0101   67      NVTWFHAIHVSGTNG  WFHAIHVSG  3        0.3223
1529.5    55.00  0.23     Sequence
             DRB4_0101   68      VTWFHAIHVSGTNGT  AIHVSGTNG  5        0.3147
1661.1    55.00  0.44     Sequence
             DRB4_0101   69      TWFHAIHVSGTNGTK  AIHVSGTNG  4        0.3295
1415.3    49.00  0.49     Sequence
             DRB4_0101   70      WFHAIHVSGTNGTKR  AIHVSGTNG  3        0.3380
1290.9    47.00  0.56     Sequence
             DRB4_0101   71      FHAIHVSGTNGTKRF  AIHVSGTNG  2        0.3396
1268.5    47.00  0.61     Sequence
             DRB4_0101   72      HAIHVSGTNGTKRFD  AIHVSGTNG  1        0.3168
1623.6    55.00  0.61     Sequence
             DRB4_0101   73      AIHVSGTNGTKRFDN  AIHVSGTNG  0        0.2361
3888.4    75.00  0.44     Sequence
```

```
             DRB4_0101   74      IHVSGTNGTKRFDNP  HVSGTNGTK  1        0.1313
12078.4    95.00  0.50     Sequence
             DRB4_0101   75      HVSGTNGTKRFDNPV  HVSGTNGTK  0        0.0702
23382.0   100.00  0.20     Sequence
             DRB4_0101   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.0815
20691.3   100.00  0.37     Sequence
             DRB4_0101   77      SGTNGTKRFDNPVLP  TKRFDNPVL  5        0.0997
17005.0   100.00  0.39     Sequence
             DRB4_0101   78      GTNGTKRFDNPVLPF  TKRFDNPVL  4        0.1431
10630.6    95.00  0.37     Sequence
             DRB4_0101   79      TNGTKRFDNPVLPFN  TKRFDNPVL  3        0.1605
8804.5    90.00  0.34    Sequence
             DRB4_0101   80      NGTKRFDNPVLPFND  TKRFDNPVL  2        0.1748
7541.8    90.00  0.33    Sequence
             DRB4_0101   81      GTKRFDNPVLPFNDG  TKRFDNPVL  1        0.1840
6831.3    85.00  0.26    Sequence
             DRB4_0101   82      TKRFDNPVLPFNDGV  FDNPVLPFN  3        0.1942
6117.1    85.00  0.17    Sequence
             DRB4_0101   83      KRFDNPVLPFNDGVY  PVLPFNDGV  5        0.2042
5491.1    85.00  0.20    Sequence
             DRB4_0101   84      RFDNPVLPFNDGVYF  PVLPFNDGV  4        0.2221
4520.4    80.00  0.28    Sequence
             DRB4_0101   85      FDNPVLPFNDGVYFA  PVLPFNDGV  3        0.2220
4528.7    80.00  0.31    Sequence
             DRB4_0101   86      DNPVLPFNDGVYFAS  PVLPFNDGV  2        0.2361
3886.4    75.00  0.31    Sequence
             DRB4_0101   87      NPVLPFNDGVYFAST  VLPFNDGVY  2        0.2395
3746.8    75.00  0.34    Sequence
             DRB4_0101   88      PVLPFNDGVYFASTE  VLPFNDGVY  1        0.1988
5816.5    85.00  0.37    Sequence
             DRB4_0101   89      VLPFNDGVYFASTEK  VLPFNDGVY  0        0.1608
8773.2    90.00  0.26    Sequence
             DRB4_0101   90      LPFNDGVYFASTEKS  GVYFASTEK  5        0.1783
7267.2    90.00  0.41    Sequence
             DRB4_0101   91      PFNDGVYFASTEKSN  GVYFASTEK  4        0.1999
5746.8    85.00  0.47    Sequence
             DRB4_0101   92      FNDGVYFASTEKSNI  GVYFASTEK  3        0.2323
4048.5    75.00  0.46    Sequence
             DRB4_0101   93      NDGVYFASTEKSNII  GVYFASTEK  2        0.2511
3305.9    70.00  0.41    Sequence
             DRB4_0101   94      DGVYFASTEKSNIIR  GVYFASTEK  1        0.2533
3226.1    70.00  0.36    Sequence
             DRB4_0101   95      GVYFASTEKSNIIRG  YFASTEKSN  2        0.2502
3336.5    70.00  0.40    Sequence
             DRB4_0101   96      VYFASTEKSNIIRGW  YFASTEKSN  1        0.2411
3680.7    75.00  0.28    Sequence
             DRB4_0101   97      YFASTEKSNIIRGWI  KSNIIRGWI  6        0.3293
1417.6    49.00  0.46    Sequence
             DRB4_0101   98      FASTEKSNIIRGWIF  KSNIIRGWI  5        0.4060
618.5    31.00  0.50    Sequence
             DRB4_0101   99      ASTEKSNIIRGWIFG  KSNIIRGWI  4        0.4223
518.3    28.00  0.49    Sequence
             DRB4_0101  100      STEKSNIIRGWIFGT  KSNIIRGWI  3        0.4688
313.5    19.00  0.38    Sequence
             DRB4_0101  101      TEKSNIIRGWIFGTT  KSNIIRGWI  2        0.4955
234.9    15.00  0.35    Sequence
             DRB4_0101  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.5123
195.7    13.00  0.31    Sequence
             DRB4_0101  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3        0.4971
230.7    15.00  0.35    Sequence
             DRB4_0101  104      SNIIRGWIFGTTLDS  IIRGWIFGT  2        0.4453
404.1    23.00  0.41    Sequence
             DRB4_0101  105      NIIRGWIFGTTLDSK  IIRGWIFGT  1        0.3921
718.3    34.00  0.32    Sequence
             DRB4_0101  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.3539
1086.7    43.00  0.43    Sequence
```

```
             DRB4_0101  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3        0.3426
1227.8    46.00  0.51     Sequence
             DRB4_0101  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2        0.3353
1328.1    48.00  0.54     Sequence
             DRB4_0101  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1        0.2748
2558.1    65.00  0.51     Sequence
             DRB4_0101  110      WIFGTTLDSKTQSLL  WIFGTTLDS  0        0.2556
3148.3    70.00  0.34     Sequence
             DRB4_0101  111      IFGTTLDSKTQSLLI  DSKTQSLLI  6        0.2541
3197.5    70.00  0.32     Sequence
             DRB4_0101  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5        0.3022
1901.2    60.00  0.41     Sequence
             DRB4_0101  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4        0.3484
1153.2    44.00  0.34     Sequence
             DRB4_0101  114      TTLDSKTQSLLIVNN  KTQSLLIVN  5        0.3652
961.5    40.00  0.39     Sequence
             DRB4_0101  115      TLDSKTQSLLIVNNA  KTQSLLIVN  4        0.3873
756.6    35.00  0.43     Sequence
             DRB4_0101  116      LDSKTQSLLIVNNAT  KTQSLLIVN  3        0.3950
696.1    33.00  0.41     Sequence
             DRB4_0101  117      DSKTQSLLIVNNATN  KTQSLLIVN  2        0.4119
580.0    30.00  0.34     Sequence
             DRB4_0101  118      SKTQSLLIVNNATNV  SLLIVNNAT  4        0.4351
451.4    25.00  0.28     Sequence
             DRB4_0101  119      KTQSLLIVNNATNVV  SLLIVNNAT  3        0.4401
427.5    24.00  0.34     Sequence
             DRB4_0101  120      TQSLLIVNNATNVVI  SLLIVNNAT  2        0.4620
337.3    20.00  0.35     Sequence
             DRB4_0101  121      QSLLIVNNATNVVIK  SLLIVNNAT  1        0.4868
258.0    16.00  0.34     Sequence
             DRB4_0101  122      SLLIVNNATNVVIKV  IVNNATNVV  3        0.4627
334.9    20.00  0.25     Sequence
             DRB4_0101  123      LLIVNNATNVVIKVC  IVNNATNVV  2        0.4013
650.4    32.00  0.38     Sequence
             DRB4_0101  124      LIVNNATNVVIKVCE  IVNNATNVV  1        0.2953
2048.7    60.00  0.41     Sequence
             DRB4_0101  125      IVNNATNVVIKVCEF  IVNNATNVV  0        0.2123
5028.7    80.00  0.25     Sequence
             DRB4_0101  126      VNNATNVVIKVCEFQ  TNVVIKVCE  4        0.1890
6468.9    85.00  0.17     Sequence
             DRB4_0101  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.3411
1247.8    46.00  0.54     Sequence
             DRB4_0101  128      NATNVVIKVCEFQFC  VIKVCEFQF  5        0.3991
666.2    32.00  0.62     Sequence
             DRB4_0101  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.4432
413.4    24.00  0.61     Sequence
             DRB4_0101  130      TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.4662
322.4    19.00  0.61     Sequence
             DRB4_0101  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.4757
290.9    18.00  0.58     Sequence
             DRB4_0101  132      VVIKVCEFQFCNYPF  VIKVCEFQF  1        0.4760
289.8    18.00  0.53     Sequence
             DRB4_0101  133      VIKVCEFQFCNYPFL  VIKVCEFQF  0        0.4160
554.7    29.00  0.37     Sequence
             DRB4_0101  134      IKVCEFQFCNYPFLG  EFQFCNYPF  4        0.3289
1423.5    49.00  0.25     Sequence
             DRB4_0101  135      KVCEFQFCNYPFLGV  EFQFCNYPF  3        0.2740
2577.7    65.00  0.39     Sequence
             DRB4_0101  136      VCEFQFCNYPFLGVY  EFQFCNYPF  2        0.2334
3999.8    75.00  0.45     Sequence
             DRB4_0101  137      CEFQFCNYPFLGVYY  EFQFCNYPF  1        0.2398
3733.0    75.00  0.38     Sequence
             DRB4_0101  138      EFQFCNYPFLGVYYH  NYPFLGVYY  5        0.2333
4006.5    75.00  0.29     Sequence
             DRB4_0101  139      FQFCNYPFLGVYYHK  NYPFLGVYY  4        0.2434
3589.4    75.00  0.32     Sequence
```

```
            DRB4_0101  140      QFCNYPFLGVYYHKN  PFLGVYYHK  5        0.2475
3437.2    75.00  0.37     Sequence
            DRB4_0101  141      FCNYPFLGVYYHKNN  PFLGVYYHK  4        0.2516
3285.7    70.00  0.40     Sequence
            DRB4_0101  142      CNYPFLGVYYHKNNK  PFLGVYYHK  3        0.2559
3138.4    70.00  0.41     Sequence
            DRB4_0101  143      NYPFLGVYYHKNNKS  PFLGVYYHK  2        0.2500
3342.8    70.00  0.44     Sequence
            DRB4_0101  144      YPFLGVYYHKNNKSW  PFLGVYYHK  1        0.2204
4606.7    80.00  0.43     Sequence
            DRB4_0101  145      PFLGVYYHKNNKSWM  GVYYHKNNK  3        0.1728
7708.1    90.00  0.28     Sequence
            DRB4_0101  146      FLGVYYHKNNKSWME  GVYYHKNNK  2        0.1511
9744.0    95.00  0.36     Sequence
            DRB4_0101  147      LGVYYHKNNKSWMES  GVYYHKNNK  1        0.1581
9042.5    90.00  0.29     Sequence
            DRB4_0101  148      GVYYHKNNKSWMESE  YHKNNKSWM  3        0.1486
10019.8    95.00  0.27     Sequence
            DRB4_0101  149      VYYHKNNKSWMESEF  YHKNNKSWM  2        0.1453
10379.7    95.00  0.25     Sequence
            DRB4_0101  150      YYHKNNKSWMESEFR  NKSWMESEF  5        0.1631
8559.5    90.00  0.25     Sequence
            DRB4_0101  151      YHKNNKSWMESEFRV  NKSWMESEF  4        0.1619
8669.7    90.00  0.26     Sequence
            DRB4_0101  152      HKNNKSWMESEFRVY  NKSWMESEF  3        0.1608
8780.4    90.00  0.30     Sequence
            DRB4_0101  153      KNNKSWMESEFRVYS  NKSWMESEF  2        0.1696
7983.2    90.00  0.26     Sequence
            DRB4_0101  154      NNKSWMESEFRVYSS  NKSWMESEF  1        0.1679
8124.3    90.00  0.20     Sequence
            DRB4_0101  155      NKSWMESEFRVYSSA  MESEFRVYS  4        0.1894
6439.5    85.00  0.22     Sequence
            DRB4_0101  156      KSWMESEFRVYSSAN  EFRVYSSAN  6        0.2167
4792.2    80.00  0.47     Sequence
            DRB4_0101  157      SWMESEFRVYSSANN  EFRVYSSAN  5        0.2444
3554.1    75.00  0.58     Sequence
            DRB4_0101  158      WMESEFRVYSSANNC  EFRVYSSAN  4        0.2476
3432.0    75.00  0.58     Sequence
            DRB4_0101  159      MESEFRVYSSANNCT  EFRVYSSAN  3        0.2608
2975.9    70.00  0.60     Sequence
            DRB4_0101  160      ESEFRVYSSANNCTF  EFRVYSSAN  2        0.2718
2642.4    65.00  0.58     Sequence
            DRB4_0101  161      SEFRVYSSANNCTFE  EFRVYSSAN  1        0.2689
2725.7    65.00  0.55     Sequence
            DRB4_0101  162      EFRVYSSANNCTFEY  RVYSSANNC  2        0.2054
5415.7    80.00  0.36     Sequence
            DRB4_0101  163      FRVYSSANNCTFEYV  RVYSSANNC  1        0.1633
8547.2    90.00  0.41     Sequence
            DRB4_0101  164      RVYSSANNCTFEYVS  RVYSSANNC  0        0.1019
16594.2   100.00  0.25     Sequence
            DRB4_0101  165      VYSSANNCTFEYVSQ  SANNCTFEY  3        0.0984
17240.5   100.00  0.28     Sequence
            DRB4_0101  166      YSSANNCTFEYVSQP  NCTFEYVSQ  5        0.1195
13729.2    95.00  0.32     Sequence
            DRB4_0101  167      SSANNCTFEYVSQPF  TFEYVSQPF  6        0.1867
6630.3    85.00  0.28     Sequence
            DRB4_0101  168      SANNCTFEYVSQPFL  TFEYVSQPF  5        0.2947
2062.0    60.00  0.28     Sequence
            DRB4_0101  169      ANNCTFEYVSQPFLM  EYVSQPFLM  6        0.3706
906.4    39.00  0.44     Sequence
            DRB4_0101  170      NNCTFEYVSQPFLMD  EYVSQPFLM  5        0.3943
702.0    34.00  0.47     Sequence
            DRB4_0101  171      NCTFEYVSQPFLMDL  EYVSQPFLM  4        0.4159
555.3    29.00  0.49     Sequence
            DRB4_0101  172      CTFEYVSQPFLMDLE  EYVSQPFLM  3        0.4353
450.1    25.00  0.44     Sequence
```

```
             DRB4_0101  173      TFEYVSQPFLMDLEG  EYVSQPFLM  2        0.4359
447.3    25.00  0.41     Sequence
             DRB4_0101  174      FEYVSQPFLMDLEGK  EYVSQPFLM  1        0.4076
607.8    31.00  0.35     Sequence
             DRB4_0101  175      EYVSQPFLMDLEGKQ  QPFLMDLEG  4        0.3294
1416.0    49.00  0.28     Sequence
             DRB4_0101  176      YVSQPFLMDLEGKQG  QPFLMDLEG  3        0.3090
1766.1    55.00  0.32     Sequence
             DRB4_0101  177      VSQPFLMDLEGKQGN  QPFLMDLEG  2        0.3119
1712.0    55.00  0.34     Sequence
             DRB4_0101  178      SQPFLMDLEGKQGNF  PFLMDLEGK  2        0.3092
1761.5    55.00  0.29     Sequence
             DRB4_0101  179      QPFLMDLEGKQGNFK  LMDLEGKQG  3        0.2614
2955.2    70.00  0.27     Sequence
             DRB4_0101  180      PFLMDLEGKQGNFKN  LMDLEGKQG  2        0.2205
4602.3    80.00  0.38     Sequence
             DRB4_0101  181      FLMDLEGKQGNFKNL  LMDLEGKQG  1        0.1744
7580.1    90.00  0.43     Sequence
             DRB4_0101  182      LMDLEGKQGNFKNLS  LMDLEGKQG  0        0.1404
10947.6    95.00  0.26     Sequence
             DRB4_0101  183      MDLEGKQGNFKNLSE  DLEGKQGNF  1        0.1096
15274.7   100.00  0.21     Sequence
             DRB4_0101  184      DLEGKQGNFKNLSEF  KQGNFKNLS  4        0.1190
13789.9    95.00  0.16     Sequence
             DRB4_0101  185      LEGKQGNFKNLSEFV  NFKNLSEFV  6        0.1593
8925.6    90.00  0.38     Sequence
             DRB4_0101  186      EGKQGNFKNLSEFVF  NFKNLSEFV  5        0.2031
5553.0    85.00  0.47     Sequence
             DRB4_0101  187      GKQGNFKNLSEFVFK  NFKNLSEFV  4        0.2238
4437.3    80.00  0.44     Sequence
             DRB4_0101  188      KQGNFKNLSEFVFKN  NFKNLSEFV  3        0.2403
3712.6    75.00  0.46     Sequence
             DRB4_0101  189      QGNFKNLSEFVFKNI  NFKNLSEFV  2        0.2630
2904.2    70.00  0.41     Sequence
             DRB4_0101  190      GNFKNLSEFVFKNID  NFKNLSEFV  1        0.3147
1660.7    55.00  0.23     Sequence
             DRB4_0101  191      NFKNLSEFVFKNIDG  EFVFKNIDG  6        0.3567
1053.5    42.00  0.48     Sequence
             DRB4_0101  192      FKNLSEFVFKNIDGY  EFVFKNIDG  5        0.3908
729.2    34.00  0.57     Sequence
             DRB4_0101  193      KNLSEFVFKNIDGYF  EFVFKNIDG  4        0.4360
446.8    25.00  0.63     Sequence
             DRB4_0101  194      NLSEFVFKNIDGYFK  EFVFKNIDG  3        0.4503
382.7    22.00  0.67     Sequence
             DRB4_0101  195      LSEFVFKNIDGYFKI  EFVFKNIDG  2        0.4623
336.1    20.00  0.63     Sequence
             DRB4_0101  196      SEFVFKNIDGYFKIY  EFVFKNIDG  1        0.4391
432.1    24.00  0.57     Sequence
             DRB4_0101  197      EFVFKNIDGYFKIYS  VFKNIDGYF  2        0.3202
1565.0    55.00  0.36     Sequence
             DRB4_0101  198      FVFKNIDGYFKIYSK  VFKNIDGYF  1        0.2653
2833.1    70.00  0.43     Sequence
             DRB4_0101  199      VFKNIDGYFKIYSKH  IDGYFKIYS  4        0.2207
4590.0    80.00  0.23     Sequence
             DRB4_0101  200      FKNIDGYFKIYSKHT  YFKIYSKHT  6        0.2465
3471.9    75.00  0.25     Sequence
             DRB4_0101  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.2686
2733.8    65.00  0.31     Sequence
             DRB4_0101  202      NIDGYFKIYSKHTPI  YFKIYSKHT  4        0.3184
1595.7    55.00  0.31     Sequence
             DRB4_0101  203      IDGYFKIYSKHTPIN  YFKIYSKHT  3        0.3524
1104.1    43.00  0.33     Sequence
             DRB4_0101  204      DGYFKIYSKHTPINL  YFKIYSKHT  2        0.3741
873.1    38.00  0.31     Sequence
             DRB4_0101  205      GYFKIYSKHTPINLV  YFKIYSKHT  1        0.4011
652.1    32.00  0.26     Sequence
```

```
             DRB4_0101  206      YFKIYSKHTPINLVR  KIYSKHTPI  2        0.4173
546.9    29.00  0.18     Sequence
             DRB4_0101  207      FKIYSKHTPINLVRD  KHTPINLVR  5        0.4106
588.1    30.00  0.28     Sequence
             DRB4_0101  208      KIYSKHTPINLVRDL  KHTPINLVR  4        0.4239
509.3    27.00  0.29     Sequence
             DRB4_0101  209      IYSKHTPINLVRDLP  PINLVRDLP  6        0.4444
408.3    23.00  0.45     Sequence
             DRB4_0101  210      YSKHTPINLVRDLPQ  PINLVRDLP  5        0.5233
173.7    11.00  0.57     Sequence
             DRB4_0101  211      SKHTPINLVRDLPQG  PINLVRDLP  4        0.5638
112.1     7.50  0.54     Sequence         WB
             DRB4_0101  212      KHTPINLVRDLPQGF  PINLVRDLP  3        0.5921
82.6     5.00  0.54     Sequence         WB
             DRB4_0101  213      HTPINLVRDLPQGFS  PINLVRDLP  2        0.6057
71.2     4.50  0.50     Sequence         WB
             DRB4_0101  214      TPINLVRDLPQGFSA  PINLVRDLP  1        0.6057
71.3     4.50  0.43     Sequence         WB
             DRB4_0101  215      PINLVRDLPQGFSAL  NLVRDLPQG  2        0.5824
91.7     6.00  0.42     Sequence         WB
             DRB4_0101  216      INLVRDLPQGFSALE  NLVRDLPQG  1        0.5198
180.5    12.00  0.47     Sequence
             DRB4_0101  217      NLVRDLPQGFSALEP  LVRDLPQGF  1        0.4051
624.5    31.00  0.31     Sequence
             DRB4_0101  218      LVRDLPQGFSALEPL  LVRDLPQGF  0        0.3561
1060.5    43.00  0.21     Sequence
             DRB4_0101  219      VRDLPQGFSALEPLV  GFSALEPLV  6        0.3749
865.4    38.00  0.44     Sequence
             DRB4_0101  220      RDLPQGFSALEPLVD  GFSALEPLV  5        0.3928
713.0    34.00  0.52     Sequence
             DRB4_0101  221      DLPQGFSALEPLVDL  GFSALEPLV  4        0.4172
547.7    29.00  0.55     Sequence
             DRB4_0101  222      LPQGFSALEPLVDLP  GFSALEPLV  3        0.4332
460.8    25.00  0.55     Sequence
             DRB4_0101  223      PQGFSALEPLVDLPI  GFSALEPLV  2        0.4855
261.5    16.00  0.47     Sequence
             DRB4_0101  224      QGFSALEPLVDLPIG  GFSALEPLV  1        0.4803
276.7    17.00  0.41     Sequence
             DRB4_0101  225      GFSALEPLVDLPIGI  ALEPLVDLP  3        0.4247
505.2    27.00  0.34     Sequence
             DRB4_0101  226      FSALEPLVDLPIGIN  ALEPLVDLP  2        0.4028
639.8    32.00  0.38     Sequence
             DRB4_0101  227      SALEPLVDLPIGINI  ALEPLVDLP  1        0.4148
562.3    29.00  0.34     Sequence
             DRB4_0101  228      ALEPLVDLPIGINIT  PLVDLPIGI  3        0.4007
654.6    32.00  0.28     Sequence
             DRB4_0101  229      LEPLVDLPIGINITR  PLVDLPIGI  2        0.3974
678.2    33.00  0.31     Sequence
             DRB4_0101  230      EPLVDLPIGINITRF  LPIGINITR  5        0.4128
574.5    29.00  0.25     Sequence
             DRB4_0101  231      PLVDLPIGINITRFQ  LPIGINITR  4        0.4049
626.0    31.00  0.29     Sequence
             DRB4_0101  232      LVDLPIGINITRFQT  LPIGINITR  3        0.4478
393.3    23.00  0.26     Sequence
             DRB4_0101  233      VDLPIGINITRFQTL  GINITRFQT  5        0.5063
208.9    14.00  0.34     Sequence
             DRB4_0101  234      DLPIGINITRFQTLL  GINITRFQT  4        0.5599
117.0     7.50  0.33     Sequence         WB
             DRB4_0101  235      LPIGINITRFQTLLA  GINITRFQT  3        0.6251
57.7     3.50  0.29     Sequence         WB
             DRB4_0101  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.6680
36.3     1.60  0.41     Sequence         SB
             DRB4_0101  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.6847
30.3     1.20  0.44     Sequence         SB
             DRB4_0101  238      GINITRFQTLLALHR  ITRFQTLLA  3        0.6939
27.4     1.00  0.44     Sequence         SB
```

```
             DRB4_0101  239      INITRFQTLLALHRS  ITRFQTLLA  2        0.6795
32.1     1.40  0.44     Sequence         SB
             DRB4_0101  240      NITRFQTLLALHRSY  ITRFQTLLA  1        0.6254
57.6     3.50  0.37     Sequence         WB
             DRB4_0101  241      ITRFQTLLALHRSYL  RFQTLLALH  2        0.5416
142.6     9.50  0.44     Sequence         WB
             DRB4_0101  242      TRFQTLLALHRSYLT  RFQTLLALH  1        0.4838
266.6    17.00  0.46     Sequence
             DRB4_0101  243      RFQTLLALHRSYLTP  TLLALHRSY  3        0.4103
589.9    30.00  0.28     Sequence
             DRB4_0101  244      FQTLLALHRSYLTPG  TLLALHRSY  2        0.3721
892.5    39.00  0.33     Sequence
             DRB4_0101  245      QTLLALHRSYLTPGD  ALHRSYLTP  4        0.3573
1047.7    42.00  0.30     Sequence
             DRB4_0101  246      TLLALHRSYLTPGDS  ALHRSYLTP  3        0.3203
1562.6    55.00  0.37     Sequence
             DRB4_0101  247      LLALHRSYLTPGDSS  ALHRSYLTP  2        0.2883
2210.0    60.00  0.47     Sequence
             DRB4_0101  248      LALHRSYLTPGDSSS  ALHRSYLTP  1        0.2577
3076.3    70.00  0.48     Sequence
             DRB4_0101  249      ALHRSYLTPGDSSSG  ALHRSYLTP  0        0.2141
4932.8    80.00  0.27     Sequence
             DRB4_0101  250      LHRSYLTPGDSSSGW  HRSYLTPGD  1        0.1828
6915.4    85.00  0.31     Sequence
             DRB4_0101  251      HRSYLTPGDSSSGWT  YLTPGDSSS  3        0.1252
12904.6    95.00  0.33     Sequence
             DRB4_0101  252      RSYLTPGDSSSGWTA  YLTPGDSSS  2        0.1113
14994.3   100.00  0.46     Sequence
             DRB4_0101  253      SYLTPGDSSSGWTAG  YLTPGDSSS  1        0.0973
17448.8   100.00  0.43     Sequence
             DRB4_0101  254      YLTPGDSSSGWTAGA  PGDSSSGWT  3        0.0870
19501.0   100.00  0.34     Sequence
             DRB4_0101  255      LTPGDSSSGWTAGAA  PGDSSSGWT  2        0.0784
21403.3   100.00  0.41     Sequence
             DRB4_0101  256      TPGDSSSGWTAGAAA  PGDSSSGWT  1        0.0677
24046.2   100.00  0.35     Sequence
             DRB4_0101  257      PGDSSSGWTAGAAAY  DSSSGWTAG  2        0.0585
26548.4   100.00  0.23     Sequence
             DRB4_0101  258      GDSSSGWTAGAAAYY  SGWTAGAAA  4        0.0575
26836.0   100.00  0.22     Sequence
             DRB4_0101  259      DSSSGWTAGAAAYYV  SGWTAGAAA  3        0.0636
25112.8   100.00  0.23     Sequence
             DRB4_0101  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.0675
24082.2   100.00  0.22     Sequence
             DRB4_0101  261      SSGWTAGAAAYYVGY  AGAAAYYVG  5        0.0680
23951.5   100.00  0.22     Sequence
             DRB4_0101  262      SGWTAGAAAYYVGYL  AGAAAYYVG  4        0.0716
23054.2   100.00  0.24     Sequence
             DRB4_0101  263      GWTAGAAAYYVGYLQ  AGAAAYYVG  3        0.0806
20911.4   100.00  0.22     Sequence
             DRB4_0101  264      WTAGAAAYYVGYLQP  AAYYVGYLQ  5        0.1176
14003.6    95.00  0.24     Sequence
             DRB4_0101  265      TAGAAAYYVGYLQPR  YVGYLQPRX  7        0.1860
6684.2    85.00  0.26     Sequence
             DRB4_0101  266      AGAAAYYVGYLQPRT  YVGYLQPRT  6        0.2597
3010.3    70.00  0.50     Sequence
             DRB4_0101  267      GAAAYYVGYLQPRTF  YVGYLQPRT  5        0.3387
1281.3    47.00  0.60     Sequence
             DRB4_0101  268      AAAYYVGYLQPRTFL  YVGYLQPRT  4        0.3686
926.6    40.00  0.63     Sequence
             DRB4_0101  269      AAYYVGYLQPRTFLL  YVGYLQPRT  3        0.3950
696.4    33.00  0.64     Sequence
             DRB4_0101  270      AYYVGYLQPRTFLLK  YVGYLQPRT  2        0.4099
592.5    30.00  0.64     Sequence
             DRB4_0101  271      YYVGYLQPRTFLLKY  YVGYLQPRT  1        0.3999
660.4    32.00  0.57     Sequence
```

```
             DRB4_0101  272      YVGYLQPRTFLLKYN  YVGYLQPRT  0        0.3422
1233.4    46.00  0.32     Sequence
             DRB4_0101  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.2890
2192.7    60.00  0.37     Sequence
             DRB4_0101  274      GYLQPRTFLLKYNEN  RTFLLKYNE  5        0.2952
2050.0    60.00  0.31     Sequence
             DRB4_0101  275      YLQPRTFLLKYNENG  RTFLLKYNE  4        0.3031
1881.9    60.00  0.31     Sequence
             DRB4_0101  276      LQPRTFLLKYNENGT  RTFLLKYNE  3        0.3357
1323.4    48.00  0.31     Sequence
             DRB4_0101  277      QPRTFLLKYNENGTI  RTFLLKYNE  2        0.3603
1014.2    42.00  0.29     Sequence
             DRB4_0101  278      PRTFLLKYNENGTIT  FLLKYNENG  3        0.3699
914.2    39.00  0.30     Sequence
             DRB4_0101  279      RTFLLKYNENGTITD  FLLKYNENG  2        0.3584
1034.6    42.00  0.38     Sequence
             DRB4_0101  280      TFLLKYNENGTITDA  FLLKYNENG  1        0.3175
1610.7    55.00  0.37     Sequence
             DRB4_0101  281      FLLKYNENGTITDAV  LLKYNENGT  1        0.2585
3051.1    70.00  0.46     Sequence
             DRB4_0101  282      LLKYNENGTITDAVD  LLKYNENGT  0        0.1538
9470.7    90.00  0.37     Sequence
             DRB4_0101  283      LKYNENGTITDAVDC  NGTITDAVD  5        0.1235
13147.1    95.00  0.26     Sequence
             DRB4_0101  284      KYNENGTITDAVDCA  GTITDAVDC  5        0.1744
7580.3    90.00  0.39     Sequence
             DRB4_0101  285      YNENGTITDAVDCAL  GTITDAVDC  4        0.2504
3328.0    70.00  0.35     Sequence
             DRB4_0101  286      NENGTITDAVDCALD  GTITDAVDC  3        0.2798
2422.1    65.00  0.32     Sequence
             DRB4_0101  287      ENGTITDAVDCALDP  GTITDAVDC  2        0.2901
2166.7    60.00  0.31     Sequence
             DRB4_0101  288      NGTITDAVDCALDPL  GTITDAVDC  1        0.3054
1835.9    55.00  0.27     Sequence
             DRB4_0101  289      GTITDAVDCALDPLS  ITDAVDCAL  2        0.3229
1519.2    55.00  0.17     Sequence
             DRB4_0101  290      TITDAVDCALDPLSE  VDCALDPLS  5        0.2948
2058.5    60.00  0.21     Sequence
             DRB4_0101  291      ITDAVDCALDPLSET  VDCALDPLS  4        0.2645
2857.8    70.00  0.25     Sequence
             DRB4_0101  292      TDAVDCALDPLSETK  VDCALDPLS  3        0.2390
3765.0    75.00  0.27     Sequence
             DRB4_0101  293      DAVDCALDPLSETKC  VDCALDPLS  2        0.2287
4210.1    75.00  0.30     Sequence
             DRB4_0101  294      AVDCALDPLSETKCT  VDCALDPLS  1        0.2220
4528.5    80.00  0.31     Sequence
             DRB4_0101  295      VDCALDPLSETKCTL  ALDPLSETK  3        0.1702
7927.6    90.00  0.35     Sequence
             DRB4_0101  296      DCALDPLSETKCTLK  ALDPLSETK  2        0.1478
10106.0    95.00  0.43     Sequence
             DRB4_0101  297      CALDPLSETKCTLKS  ALDPLSETK  1        0.1511
9745.5    95.00  0.38     Sequence
             DRB4_0101  298      ALDPLSETKCTLKSF  PLSETKCTL  3        0.1428
10666.2    95.00  0.41     Sequence
             DRB4_0101  299      LDPLSETKCTLKSFT  PLSETKCTL  2        0.1323
11949.1    95.00  0.44     Sequence
             DRB4_0101  300      DPLSETKCTLKSFTV  PLSETKCTL  1        0.1614
8722.3    90.00  0.34     Sequence
             DRB4_0101  301      PLSETKCTLKSFTVE  TLKSFTVEX  7        0.1727
7715.2    90.00  0.25     Sequence
             DRB4_0101  302      LSETKCTLKSFTVEK  TLKSFTVEK  6        0.2366
3866.6    75.00  0.64     Sequence
             DRB4_0101  303      SETKCTLKSFTVEKG  TLKSFTVEK  5        0.3164
1630.3    55.00  0.72     Sequence
             DRB4_0101  304      ETKCTLKSFTVEKGI  TLKSFTVEK  4        0.3591
1027.2    42.00  0.73     Sequence
```

```
             DRB4_0101  305      TKCTLKSFTVEKGIY  TLKSFTVEK  3        0.3853
773.7    36.00  0.70     Sequence
             DRB4_0101  306      KCTLKSFTVEKGIYQ  TLKSFTVEK  2        0.4054
622.0    31.00  0.62     Sequence
             DRB4_0101  307      CTLKSFTVEKGIYQT  TLKSFTVEK  1        0.3870
759.1    35.00  0.50     Sequence
             DRB4_0101  308      TLKSFTVEKGIYQTS  SFTVEKGIY  3        0.3527
1100.8    43.00  0.52     Sequence
             DRB4_0101  309      LKSFTVEKGIYQTSN  SFTVEKGIY  2        0.3316
1383.3    49.00  0.65     Sequence
             DRB4_0101  310      KSFTVEKGIYQTSNF  SFTVEKGIY  1        0.3111
1727.1    55.00  0.50     Sequence
             DRB4_0101  311      SFTVEKGIYQTSNFR  SFTVEKGIY  0        0.2679
2754.1    65.00  0.30     Sequence
             DRB4_0101  312      FTVEKGIYQTSNFRV  GIYQTSNFR  5        0.2560
3134.6    70.00  0.26     Sequence
             DRB4_0101  313      TVEKGIYQTSNFRVQ  GIYQTSNFR  4        0.2717
2644.4    65.00  0.34     Sequence
             DRB4_0101  314      VEKGIYQTSNFRVQP  GIYQTSNFR  3        0.3122
1706.8    55.00  0.34     Sequence
             DRB4_0101  315      EKGIYQTSNFRVQPT  GIYQTSNFR  2        0.3575
1044.5    42.00  0.28     Sequence
             DRB4_0101  316      KGIYQTSNFRVQPTE  QTSNFRVQP  4        0.3725
888.5    39.00  0.25     Sequence
             DRB4_0101  317      GIYQTSNFRVQPTES  NFRVQPTES  6        0.4359
447.4    25.00  0.48     Sequence
             DRB4_0101  318      IYQTSNFRVQPTESI  NFRVQPTES  5        0.5052
211.3    14.00  0.61     Sequence
             DRB4_0101  319      YQTSNFRVQPTESIV  NFRVQPTES  4        0.5390
146.7     9.50  0.69     Sequence         WB
             DRB4_0101  320      QTSNFRVQPTESIVR  NFRVQPTES  3        0.5730
101.5     6.50  0.64     Sequence         WB
             DRB4_0101  321      TSNFRVQPTESIVRF  NFRVQPTES  2        0.5852
89.0     5.50  0.60     Sequence         WB
             DRB4_0101  322      SNFRVQPTESIVRFP  NFRVQPTES  1        0.5584
118.9     7.50  0.51     Sequence         WB
             DRB4_0101  323      NFRVQPTESIVRFPN  RVQPTESIV  2        0.4930
241.3    15.00  0.37     Sequence
             DRB4_0101  324      FRVQPTESIVRFPNI  RVQPTESIV  1        0.4095
595.4    30.00  0.41     Sequence
             DRB4_0101  325      RVQPTESIVRFPNIT  SIVRFPNIT  6        0.3555
1068.0    43.00  0.29     Sequence
             DRB4_0101  326      VQPTESIVRFPNITN  SIVRFPNIT  5        0.3607
1009.4    41.00  0.41     Sequence
             DRB4_0101  327      QPTESIVRFPNITNL  SIVRFPNIT  4        0.3537
1089.0    43.00  0.50     Sequence
             DRB4_0101  328      PTESIVRFPNITNLC  SIVRFPNIT  3        0.3495
1139.4    44.00  0.52     Sequence
             DRB4_0101  329      TESIVRFPNITNLCP  SIVRFPNIT  2        0.3566
1055.3    42.00  0.51     Sequence
             DRB4_0101  330      ESIVRFPNITNLCPF  SIVRFPNIT  1        0.3797
821.6    37.00  0.44     Sequence
             DRB4_0101  331      SIVRFPNITNLCPFG  NITNLCPFG  6        0.3416
1241.2    46.00  0.25     Sequence
             DRB4_0101  332      IVRFPNITNLCPFGE  NITNLCPFG  5        0.3039
1865.4    60.00  0.43     Sequence
             DRB4_0101  333      VRFPNITNLCPFGEV  NITNLCPFG  4        0.3043
1858.7    60.00  0.55     Sequence
             DRB4_0101  334      RFPNITNLCPFGEVF  NITNLCPFG  3        0.2990
1967.1    60.00  0.60     Sequence
             DRB4_0101  335      FPNITNLCPFGEVFN  NITNLCPFG  2        0.2956
2040.6    60.00  0.58     Sequence
             DRB4_0101  336      PNITNLCPFGEVFNA  NITNLCPFG  1        0.2934
2090.9    60.00  0.49     Sequence
             DRB4_0101  337      NITNLCPFGEVFNAT  NLCPFGEVF  3        0.2124
5022.2    80.00  0.30     Sequence
```

```
              DRB4_0101  338      ITNLCPFGEVFNATR  NLCPFGEVF  2        0.1954
6038.2    85.00  0.35     Sequence
              DRB4_0101  339      TNLCPFGEVFNATRF  NLCPFGEVF  1        0.2092
5196.6    80.00  0.31     Sequence
              DRB4_0101  340      NLCPFGEVFNATRFA  FGEVFNATR  4        0.2105
5128.5    80.00  0.19     Sequence
              DRB4_0101  341      LCPFGEVFNATRFAS  VFNATRFAS  6        0.2272
4281.1    75.00  0.27     Sequence
              DRB4_0101  342      CPFGEVFNATRFASV  VFNATRFAS  5        0.2802
2410.6    65.00  0.35     Sequence
              DRB4_0101  343      PFGEVFNATRFASVY  VFNATRFAS  4        0.3022
1900.6    60.00  0.38     Sequence
              DRB4_0101  344      FGEVFNATRFASVYA  VFNATRFAS  3        0.3232
1514.7    55.00  0.32     Sequence
              DRB4_0101  345      GEVFNATRFASVYAW  VFNATRFAS  2        0.3377
1294.7    47.00  0.31     Sequence
              DRB4_0101  346      EVFNATRFASVYAWN  ATRFASVYA  4        0.3300
1407.1    49.00  0.40     Sequence
              DRB4_0101  347      VFNATRFASVYAWNR  ATRFASVYA  3        0.3249
1486.4    50.00  0.42     Sequence
              DRB4_0101  348      FNATRFASVYAWNRK  ATRFASVYA  2        0.3117
1715.8    55.00  0.44     Sequence
              DRB4_0101  349      NATRFASVYAWNRKR  RFASVYAWN  3        0.2853
2282.5    65.00  0.40     Sequence
              DRB4_0101  350      ATRFASVYAWNRKRI  RFASVYAWN  2        0.2676
2764.0    65.00  0.44     Sequence
              DRB4_0101  351      TRFASVYAWNRKRIS  RFASVYAWN  1        0.2630
2906.3    70.00  0.38     Sequence
              DRB4_0101  352      RFASVYAWNRKRISN  SVYAWNRKR  3        0.2375
3827.4    75.00  0.28     Sequence
              DRB4_0101  353      FASVYAWNRKRISNC  SVYAWNRKR  2        0.2005
5714.4    85.00  0.34     Sequence
              DRB4_0101  354      ASVYAWNRKRISNCV  SVYAWNRKR  1        0.2045
5469.2    85.00  0.28     Sequence
              DRB4_0101  355      SVYAWNRKRISNCVA  RKRISNCVA  6        0.2038
5511.5    85.00  0.19     Sequence
              DRB4_0101  356      VYAWNRKRISNCVAD  RKRISNCVA  5        0.1909
6340.7    85.00  0.25     Sequence
              DRB4_0101  357      YAWNRKRISNCVADY  RISNCVADY  6        0.2488
3386.1    70.00  0.43     Sequence
              DRB4_0101  358      AWNRKRISNCVADYS  RISNCVADY  5        0.3667
945.9    40.00  0.59     Sequence
              DRB4_0101  359      WNRKRISNCVADYSV  RISNCVADY  4        0.4079
605.6    31.00  0.62     Sequence
              DRB4_0101  360      NRKRISNCVADYSVL  RISNCVADY  3        0.4296
478.8    26.00  0.63     Sequence
              DRB4_0101  361      RKRISNCVADYSVLY  RISNCVADY  2        0.4338
457.8    25.00  0.64     Sequence
              DRB4_0101  362      KRISNCVADYSVLYN  RISNCVADY  1        0.4046
627.8    31.00  0.62     Sequence
              DRB4_0101  363      RISNCVADYSVLYNS  RISNCVADY  0        0.3088
1770.2    55.00  0.38     Sequence
              DRB4_0101  364      ISNCVADYSVLYNSA  NCVADYSVL  2        0.2285
4220.5    75.00  0.22     Sequence
              DRB4_0101  365      SNCVADYSVLYNSAS  CVADYSVLY  2        0.1743
7586.3    90.00  0.28     Sequence
              DRB4_0101  366      NCVADYSVLYNSASF  SVLYNSASF  6        0.1863
6662.6    85.00  0.22     Sequence
              DRB4_0101  367      CVADYSVLYNSASFS  SVLYNSASF  5        0.1963
5979.9    85.00  0.33     Sequence
              DRB4_0101  368      VADYSVLYNSASFST  SVLYNSASF  4        0.2190
4675.1    80.00  0.37     Sequence
              DRB4_0101  369      ADYSVLYNSASFSTF  SVLYNSASF  3        0.2483
3406.4    70.00  0.36     Sequence
              DRB4_0101  370      DYSVLYNSASFSTFK  SVLYNSASF  2        0.2613
2958.2    70.00  0.38     Sequence
```

```
             DRB4_0101  371      YSVLYNSASFSTFKC  SVLYNSASF  1        0.2593
3024.1    70.00  0.35     Sequence
             DRB4_0101  372      SVLYNSASFSTFKCY  VLYNSASFS  1        0.2192
4666.1    80.00  0.34     Sequence
             DRB4_0101  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.1637
8506.6    90.00  0.20     Sequence
             DRB4_0101  374      LYNSASFSTFKCYGV  SFSTFKCYG  5        0.1323
11948.2    95.00  0.31     Sequence
             DRB4_0101  375      YNSASFSTFKCYGVS  SFSTFKCYG  4        0.1332
11834.6    95.00  0.38     Sequence
             DRB4_0101  376      NSASFSTFKCYGVSP  SFSTFKCYG  3        0.1256
12847.5    95.00  0.41     Sequence
             DRB4_0101  377      SASFSTFKCYGVSPT  SFSTFKCYG  2        0.1296
12306.3    95.00  0.38     Sequence
             DRB4_0101  378      ASFSTFKCYGVSPTK  SFSTFKCYG  1        0.1353
11561.3    95.00  0.31     Sequence
             DRB4_0101  379      SFSTFKCYGVSPTKL  TFKCYGVSP  3        0.1470
10189.8    95.00  0.26     Sequence
             DRB4_0101  380      FSTFKCYGVSPTKLN  TFKCYGVSP  2        0.1497
9894.2    95.00  0.26     Sequence
             DRB4_0101  381      STFKCYGVSPTKLND  GVSPTKLND  6        0.1544
9403.8    90.00  0.31     Sequence
             DRB4_0101  382      TFKCYGVSPTKLNDL  GVSPTKLND  5        0.1918
6277.9    85.00  0.41     Sequence
             DRB4_0101  383      FKCYGVSPTKLNDLC  GVSPTKLND  4        0.2019
5628.4    85.00  0.43     Sequence
             DRB4_0101  384      KCYGVSPTKLNDLCF  GVSPTKLND  3        0.2317
4076.6    75.00  0.41     Sequence
             DRB4_0101  385      CYGVSPTKLNDLCFT  GVSPTKLND  2        0.2269
4294.0    80.00  0.44     Sequence
             DRB4_0101  386      YGVSPTKLNDLCFTN  GVSPTKLND  1        0.2269
4293.4    80.00  0.34     Sequence
             DRB4_0101  387      GVSPTKLNDLCFTNV  PTKLNDLCF  3        0.2240
4432.3    80.00  0.29     Sequence
             DRB4_0101  388      VSPTKLNDLCFTNVY  KLNDLCFTN  4        0.2192
4667.5    80.00  0.30     Sequence
             DRB4_0101  389      SPTKLNDLCFTNVYA  KLNDLCFTN  3        0.2110
5099.2    80.00  0.35     Sequence
             DRB4_0101  390      PTKLNDLCFTNVYAD  KLNDLCFTN  2        0.1990
5803.3    85.00  0.41     Sequence
             DRB4_0101  391      TKLNDLCFTNVYADS  DLCFTNVYA  4        0.1911
6325.3    85.00  0.33     Sequence
             DRB4_0101  392      KLNDLCFTNVYADSF  DLCFTNVYA  3        0.2174
4759.2    80.00  0.32     Sequence
             DRB4_0101  393      LNDLCFTNVYADSFV  DLCFTNVYA  2        0.2107
5114.8    80.00  0.31     Sequence
             DRB4_0101  394      NDLCFTNVYADSFVI  CFTNVYADS  3        0.2165
4805.4    80.00  0.31     Sequence
             DRB4_0101  395      DLCFTNVYADSFVIR  CFTNVYADS  2        0.2057
5397.5    80.00  0.34     Sequence
             DRB4_0101  396      LCFTNVYADSFVIRG  NVYADSFVI  4        0.2087
5227.8    80.00  0.35     Sequence
             DRB4_0101  397      CFTNVYADSFVIRGD  NVYADSFVI  3        0.1852
6743.6    85.00  0.39     Sequence
             DRB4_0101  398      FTNVYADSFVIRGDE  NVYADSFVI  2        0.1813
7030.9    85.00  0.40     Sequence
             DRB4_0101  399      TNVYADSFVIRGDEV  NVYADSFVI  1        0.2224
4505.5    80.00  0.28     Sequence
             DRB4_0101  400      NVYADSFVIRGDEVR  DSFVIRGDE  4        0.2320
4060.8    75.00  0.25     Sequence
             DRB4_0101  401      VYADSFVIRGDEVRQ  VIRGDEVRQ  6        0.2688
2729.0    65.00  0.34     Sequence
             DRB4_0101  402      YADSFVIRGDEVRQI  VIRGDEVRQ  5        0.3160
1637.8    55.00  0.41     Sequence
             DRB4_0101  403      ADSFVIRGDEVRQIA  VIRGDEVRQ  4        0.3510
1121.2    44.00  0.47     Sequence
```

```
             DRB4_0101  404      DSFVIRGDEVRQIAP  VIRGDEVRQ  3        0.3627
987.6    41.00  0.47     Sequence
             DRB4_0101  405      SFVIRGDEVRQIAPG  VIRGDEVRQ  2        0.3794
824.1    37.00  0.49     Sequence
             DRB4_0101  406      FVIRGDEVRQIAPGQ  EVRQIAPGQ  6        0.3765
851.1    38.00  0.32     Sequence
             DRB4_0101  407      VIRGDEVRQIAPGQT  EVRQIAPGQ  5        0.3989
667.6    33.00  0.52     Sequence
             DRB4_0101  408      IRGDEVRQIAPGQTG  EVRQIAPGQ  4        0.4110
585.7    30.00  0.60     Sequence
             DRB4_0101  409      RGDEVRQIAPGQTGT  EVRQIAPGQ  3        0.4296
479.1    26.00  0.63     Sequence
             DRB4_0101  410      GDEVRQIAPGQTGTI  EVRQIAPGQ  2        0.4326
463.4    25.00  0.58     Sequence
             DRB4_0101  411      DEVRQIAPGQTGTIA  EVRQIAPGQ  1        0.4138
568.2    29.00  0.51     Sequence
             DRB4_0101  412      EVRQIAPGQTGTIAD  EVRQIAPGQ  0        0.3427
1226.9    46.00  0.35     Sequence
             DRB4_0101  413      VRQIAPGQTGTIADY  QIAPGQTGT  2        0.2700
2693.2    65.00  0.46     Sequence
             DRB4_0101  414      RQIAPGQTGTIADYN  QIAPGQTGT  1        0.2114
5077.6    80.00  0.43     Sequence
             DRB4_0101  415      QIAPGQTGTIADYNY  PGQTGTIAD  3        0.1410
10877.2    95.00  0.28     Sequence
             DRB4_0101  416      IAPGQTGTIADYNYK  PGQTGTIAD  2        0.1199
13660.7    95.00  0.31     Sequence
             DRB4_0101  417      APGQTGTIADYNYKL  GTIADYNYK  5        0.1164
14192.4   100.00  0.25     Sequence
             DRB4_0101  418      PGQTGTIADYNYKLP  GTIADYNYK  4        0.1189
13814.7    95.00  0.26     Sequence
             DRB4_0101  419      GQTGTIADYNYKLPD  GTIADYNYK  3        0.1206
13567.2    95.00  0.32     Sequence
             DRB4_0101  420      QTGTIADYNYKLPDD  GTIADYNYK  2        0.1207
13545.6    95.00  0.30     Sequence
             DRB4_0101  421      TGTIADYNYKLPDDF  GTIADYNYK  1        0.1325
11924.1    95.00  0.22     Sequence
             DRB4_0101  422      GTIADYNYKLPDDFT  DYNYKLPDD  4        0.1347
11640.3    95.00  0.23     Sequence
             DRB4_0101  423      TIADYNYKLPDDFTG  DYNYKLPDD  3        0.1208
13537.4    95.00  0.31     Sequence
             DRB4_0101  424      IADYNYKLPDDFTGC  DYNYKLPDD  2        0.1111
15034.0   100.00  0.37     Sequence
             DRB4_0101  425      ADYNYKLPDDFTGCV  DYNYKLPDD  1        0.1158
14285.8   100.00  0.31     Sequence
             DRB4_0101  426      DYNYKLPDDFTGCVI  PDDFTGCVI  6        0.1243
13032.8    95.00  0.14     Sequence
             DRB4_0101  427      YNYKLPDDFTGCVIA  PDDFTGCVI  5        0.1292
12350.6    95.00  0.15     Sequence
             DRB4_0101  428      NYKLPDDFTGCVIAW  DFTGCVIAW  6        0.1487
10009.7    95.00  0.32     Sequence
             DRB4_0101  429      YKLPDDFTGCVIAWN  DFTGCVIAW  5        0.1700
7948.4    90.00  0.38     Sequence
             DRB4_0101  430      KLPDDFTGCVIAWNS  DFTGCVIAW  4        0.1832
6886.9    85.00  0.40     Sequence
             DRB4_0101  431      LPDDFTGCVIAWNSN  DFTGCVIAW  3        0.2019
5624.6    85.00  0.38     Sequence
             DRB4_0101  432      PDDFTGCVIAWNSNN  DFTGCVIAW  2        0.2298
4162.0    75.00  0.34     Sequence
             DRB4_0101  433      DDFTGCVIAWNSNNL  CVIAWNSNN  5        0.3051
1842.4    60.00  0.31     Sequence
             DRB4_0101  434      DFTGCVIAWNSNNLD  VIAWNSNNL  5        0.3397
1266.7    47.00  0.38     Sequence
             DRB4_0101  435      FTGCVIAWNSNNLDS  VIAWNSNNL  4        0.3721
892.1    39.00  0.39     Sequence
             DRB4_0101  436      TGCVIAWNSNNLDSK  VIAWNSNNL  3        0.3935
708.1    34.00  0.41     Sequence
```

```
             DRB4_0101  437      GCVIAWNSNNLDSKV  VIAWNSNNL  2        0.4058
619.8    31.00  0.42     Sequence
             DRB4_0101  438      CVIAWNSNNLDSKVG  VIAWNSNNL  1        0.3573
1047.3    42.00  0.41     Sequence
             DRB4_0101  439      VIAWNSNNLDSKVGG  VIAWNSNNL  0        0.2547
3178.1    70.00  0.31     Sequence
             DRB4_0101  440      IAWNSNNLDSKVGGN  AWNSNNLDS  1        0.1358
11499.4    95.00  0.41     Sequence
             DRB4_0101  441      AWNSNNLDSKVGGNY  AWNSNNLDS  0        0.0893
19029.9   100.00  0.22     Sequence
             DRB4_0101  442      WNSNNLDSKVGGNYN  SNNLDSKVG  2        0.0759
21994.5   100.00  0.27     Sequence
             DRB4_0101  443      NSNNLDSKVGGNYNY  LDSKVGGNY  4        0.0751
22178.9   100.00  0.22     Sequence
             DRB4_0101  444      SNNLDSKVGGNYNYL  LDSKVGGNY  3        0.0833
20305.2   100.00  0.21     Sequence
             DRB4_0101  445      NNLDSKVGGNYNYLY  KVGGNYNYL  5        0.0825
20476.8   100.00  0.24     Sequence
             DRB4_0101  446      NLDSKVGGNYNYLYR  KVGGNYNYL  4        0.0814
20726.2   100.00  0.26     Sequence
             DRB4_0101  447      LDSKVGGNYNYLYRL  GGNYNYLYR  5        0.1099
15231.4   100.00  0.28     Sequence
             DRB4_0101  448      DSKVGGNYNYLYRLF  GGNYNYLYR  4        0.1275
12586.2    95.00  0.28     Sequence
             DRB4_0101  449      SKVGGNYNYLYRLFR  NYNYLYRLF  5        0.1769
7377.2    90.00  0.28     Sequence
             DRB4_0101  450      KVGGNYNYLYRLFRK  NYNYLYRLF  4        0.1914
6301.0    85.00  0.25     Sequence
             DRB4_0101  451      VGGNYNYLYRLFRKS  YLYRLFRKS  6        0.2215
4553.2    80.00  0.25     Sequence
             DRB4_0101  452      GGNYNYLYRLFRKSN  YLYRLFRKS  5        0.2582
3061.1    70.00  0.29     Sequence
             DRB4_0101  453      GNYNYLYRLFRKSNL  LYRLFRKSN  5        0.3231
1516.4    55.00  0.25     Sequence
             DRB4_0101  454      NYNYLYRLFRKSNLK  LYRLFRKSN  4        0.3441
1207.5    45.00  0.26     Sequence
             DRB4_0101  455      YNYLYRLFRKSNLKP  LYRLFRKSN  3        0.3705
908.0    39.00  0.22     Sequence
             DRB4_0101  456      NYLYRLFRKSNLKPF  LFRKSNLKP  5        0.4064
615.5    31.00  0.33     Sequence
             DRB4_0101  457      YLYRLFRKSNLKPFE  LFRKSNLKP  4        0.4086
601.0    30.00  0.38     Sequence
             DRB4_0101  458      LYRLFRKSNLKPFER  LFRKSNLKP  3        0.4136
569.8    29.00  0.40     Sequence
             DRB4_0101  459      YRLFRKSNLKPFERD  LFRKSNLKP  2        0.3919
720.0    34.00  0.38     Sequence
             DRB4_0101  460      RLFRKSNLKPFERDI  NLKPFERDI  6        0.3667
946.3    40.00  0.35     Sequence
             DRB4_0101  461      LFRKSNLKPFERDIS  NLKPFERDI  5        0.3972
680.2    33.00  0.58     Sequence
             DRB4_0101  462      FRKSNLKPFERDIST  NLKPFERDI  4        0.4046
627.5    31.00  0.67     Sequence
             DRB4_0101  463      RKSNLKPFERDISTE  NLKPFERDI  3        0.4099
592.9    30.00  0.73     Sequence
             DRB4_0101  464      KSNLKPFERDISTEI  NLKPFERDI  2        0.4197
533.3    28.00  0.67     Sequence
             DRB4_0101  465      SNLKPFERDISTEIY  NLKPFERDI  1        0.4006
655.7    32.00  0.61     Sequence
             DRB4_0101  466      NLKPFERDISTEIYQ  NLKPFERDI  0        0.3414
1244.2    46.00  0.38     Sequence
             DRB4_0101  467      LKPFERDISTEIYQA  PFERDISTE  2        0.2910
2145.0    60.00  0.23     Sequence
             DRB4_0101  468      KPFERDISTEIYQAG  DISTEIYQA  5        0.2713
2656.2    65.00  0.31     Sequence
             DRB4_0101  469      PFERDISTEIYQAGS  DISTEIYQA  4        0.2747
2559.8    65.00  0.41     Sequence
```

```
            DRB4_0101  470      FERDISTEIYQAGST  DISTEIYQA  3        0.2820
2365.8    65.00  0.43     Sequence
            DRB4_0101  471      ERDISTEIYQAGSTP  DISTEIYQA  2        0.2693
2713.3    65.00  0.49     Sequence
            DRB4_0101  472      RDISTEIYQAGSTPC  DISTEIYQA  1        0.2484
3401.1    70.00  0.44     Sequence
            DRB4_0101  473      DISTEIYQAGSTPCN  EIYQAGSTP  4        0.1875
6573.8    85.00  0.40     Sequence
            DRB4_0101  474      ISTEIYQAGSTPCNG  EIYQAGSTP  3        0.1788
7223.0    90.00  0.53     Sequence
            DRB4_0101  475      STEIYQAGSTPCNGV  EIYQAGSTP  2        0.1709
7867.3    90.00  0.63     Sequence
            DRB4_0101  476      TEIYQAGSTPCNGVK  EIYQAGSTP  1        0.1602
8836.7    90.00  0.60     Sequence
            DRB4_0101  477      EIYQAGSTPCNGVKG  EIYQAGSTP  0        0.1155
14322.2   100.00  0.37     Sequence
            DRB4_0101  478      IYQAGSTPCNGVKGF  QAGSTPCNG  2        0.0807
20885.9   100.00  0.19     Sequence
            DRB4_0101  479      YQAGSTPCNGVKGFN  PCNGVKGFN  6        0.0771
21717.3   100.00  0.30     Sequence
            DRB4_0101  480      QAGSTPCNGVKGFNC  PCNGVKGFN  5        0.0934
18203.8   100.00  0.41     Sequence
            DRB4_0101  481      AGSTPCNGVKGFNCY  PCNGVKGFN  4        0.1013
16712.6   100.00  0.40     Sequence
            DRB4_0101  482      GSTPCNGVKGFNCYF  GVKGFNCYF  6        0.1288
12412.8    95.00  0.31     Sequence
            DRB4_0101  483      STPCNGVKGFNCYFP  GVKGFNCYF  5        0.1494
9930.0    95.00  0.38     Sequence
            DRB4_0101  484      TPCNGVKGFNCYFPL  GVKGFNCYF  4        0.1782
7270.2    90.00  0.34     Sequence
            DRB4_0101  485      PCNGVKGFNCYFPLQ  GVKGFNCYF  3        0.2029
5564.7    85.00  0.32     Sequence
            DRB4_0101  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.2704
2681.5    65.00  0.25     Sequence
            DRB4_0101  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.3342
1343.9    48.00  0.33     Sequence
            DRB4_0101  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.3418
1238.2    46.00  0.35     Sequence
            DRB4_0101  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3        0.3821
800.7    36.00  0.32     Sequence
            DRB4_0101  490      KGFNCYFPLQSYGFQ  FNCYFPLQS  2        0.4148
562.2    29.00  0.26     Sequence
            DRB4_0101  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.4177
545.0    29.00  0.25     Sequence
            DRB4_0101  492      FNCYFPLQSYGFQPT  PLQSYGFQP  5        0.4335
459.2    25.00  0.34     Sequence
            DRB4_0101  493      NCYFPLQSYGFQPTY  PLQSYGFQP  4        0.4315
469.2    26.00  0.39     Sequence
            DRB4_0101  494      CYFPLQSYGFQPTYG  PLQSYGFQP  3        0.4128
574.2    29.00  0.44     Sequence
            DRB4_0101  495      YFPLQSYGFQPTYGV  PLQSYGFQP  2        0.3956
692.2    33.00  0.49     Sequence
            DRB4_0101  496      FPLQSYGFQPTYGVG  PLQSYGFQP  1        0.3529
1098.3    43.00  0.45     Sequence
            DRB4_0101  497      PLQSYGFQPTYGVGY  SYGFQPTYG  3        0.2788
2449.2    65.00  0.37     Sequence
            DRB4_0101  498      LQSYGFQPTYGVGYQ  SYGFQPTYG  2        0.2528
3245.2    70.00  0.41     Sequence
            DRB4_0101  499      QSYGFQPTYGVGYQP  GFQPTYGVG  3        0.2112
5089.6    80.00  0.38     Sequence
            DRB4_0101  500      SYGFQPTYGVGYQPY  GFQPTYGVG  2        0.1948
6078.8    85.00  0.41     Sequence
            DRB4_0101  501      YGFQPTYGVGYQPYR  GFQPTYGVG  1        0.2018
5634.0    85.00  0.31     Sequence
            DRB4_0101  502      GFQPTYGVGYQPYRV  YGVGYQPYR  5        0.2150
4880.8    80.00  0.34     Sequence
```

```
             DRB4_0101  503      FQPTYGVGYQPYRVV  YGVGYQPYR  4        0.2350
3931.4    75.00  0.37     Sequence
             DRB4_0101  504      QPTYGVGYQPYRVVV  YGVGYQPYR  3        0.2576
3078.9    70.00  0.35     Sequence
             DRB4_0101  505      PTYGVGYQPYRVVVL  GVGYQPYRV  3        0.3035
1873.3    60.00  0.32     Sequence
             DRB4_0101  506      TYGVGYQPYRVVVLS  GVGYQPYRV  2        0.3284
1431.2    49.00  0.26     Sequence
             DRB4_0101  507      YGVGYQPYRVVVLSF  PYRVVVLSF  6        0.4124
576.7    30.00  0.40     Sequence
             DRB4_0101  508      GVGYQPYRVVVLSFE  PYRVVVLSF  5        0.4476
394.1    23.00  0.44     Sequence
             DRB4_0101  509      VGYQPYRVVVLSFEL  RVVVLSFEL  6        0.5350
153.1    10.00  0.41     Sequence
             DRB4_0101  510      GYQPYRVVVLSFELL  RVVVLSFEL  5        0.5769
97.3     6.00  0.47     Sequence         WB
             DRB4_0101  511      YQPYRVVVLSFELLH  RVVVLSFEL  4        0.6017
74.4     4.50  0.49     Sequence         WB
             DRB4_0101  512      QPYRVVVLSFELLHA  RVVVLSFEL  3        0.6290
55.4     3.00  0.48     Sequence         WB
             DRB4_0101  513      PYRVVVLSFELLHAP  RVVVLSFEL  2        0.6187
61.9     3.50  0.52     Sequence         WB
             DRB4_0101  514      YRVVVLSFELLHAPA  RVVVLSFEL  1        0.6129
65.9     4.00  0.46     Sequence         WB
             DRB4_0101  515      RVVVLSFELLHAPAT  VVLSFELLH  2        0.5613
115.2     7.50  0.31     Sequence         WB
             DRB4_0101  516      VVVLSFELLHAPATV  VVLSFELLH  1        0.4873
256.4    16.00  0.38     Sequence
             DRB4_0101  517      VVLSFELLHAPATVC  VVLSFELLH  0        0.4500
384.2    22.00  0.28     Sequence
             DRB4_0101  518      VLSFELLHAPATVCG  ELLHAPATV  4        0.3593
1025.2    42.00  0.39     Sequence
             DRB4_0101  519      LSFELLHAPATVCGP  ELLHAPATV  3        0.3199
1569.0    55.00  0.49     Sequence
             DRB4_0101  520      SFELLHAPATVCGPK  ELLHAPATV  2        0.2968
2014.4    60.00  0.59     Sequence
             DRB4_0101  521      FELLHAPATVCGPKK  ELLHAPATV  1        0.2621
2934.4    70.00  0.60     Sequence
             DRB4_0101  522      ELLHAPATVCGPKKS  ELLHAPATV  0        0.1667
8234.4    90.00  0.38     Sequence
             DRB4_0101  523      LLHAPATVCGPKKST  PATVCGPKK  4        0.0902
18834.9   100.00  0.26     Sequence
             DRB4_0101  524      LHAPATVCGPKKSTN  PATVCGPKK  3        0.0661
24445.2   100.00  0.34     Sequence
             DRB4_0101  525      HAPATVCGPKKSTNL  PATVCGPKK  2        0.0724
22855.0   100.00  0.31     Sequence
             DRB4_0101  526      APATVCGPKKSTNLV  PKKSTNLVX  7        0.0888
19123.4   100.00  0.20     Sequence
             DRB4_0101  527      PATVCGPKKSTNLVK  PKKSTNLVK  6        0.1402
10968.7    95.00  0.50     Sequence
             DRB4_0101  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5        0.1632
8555.7    90.00  0.50     Sequence
             DRB4_0101  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.1750
7528.7    90.00  0.50     Sequence
             DRB4_0101  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3        0.1744
7575.3    90.00  0.44     Sequence
             DRB4_0101  531      CGPKKSTNLVKNKCV  PKKSTNLVK  2        0.1898
6413.8    85.00  0.38     Sequence
             DRB4_0101  532      GPKKSTNLVKNKCVN  PKKSTNLVK  1        0.1883
6518.2    85.00  0.31     Sequence
             DRB4_0101  533      PKKSTNLVKNKCVNF  NLVKNKCVN  5        0.2243
4417.5    80.00  0.29     Sequence
             DRB4_0101  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.2532
3228.9    70.00  0.35     Sequence
             DRB4_0101  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.2921
2119.3    60.00  0.35     Sequence
```

```
             DRB4_0101  536      STNLVKNKCVNFNFN  LVKNKCVNF  3        0.3067
1810.7    55.00  0.38     Sequence
             DRB4_0101  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2        0.3117
1714.9    55.00  0.37     Sequence
             DRB4_0101  538      NLVKNKCVNFNFNGL  LVKNKCVNF  1        0.2926
2108.6    60.00  0.31     Sequence
             DRB4_0101  539      LVKNKCVNFNFNGLT  KCVNFNFNG  4        0.2770
2496.0    65.00  0.20     Sequence
             DRB4_0101  540      VKNKCVNFNFNGLTG  KCVNFNFNG  3        0.2456
3508.5    75.00  0.25     Sequence
             DRB4_0101  541      KNKCVNFNFNGLTGT  KCVNFNFNG  2        0.2488
3385.9    70.00  0.25     Sequence
             DRB4_0101  542      NKCVNFNFNGLTGTG  NFNFNGLTG  4        0.2280
4242.4    75.00  0.32     Sequence
             DRB4_0101  543      KCVNFNFNGLTGTGV  NFNFNGLTG  3        0.2252
4372.6    80.00  0.31     Sequence
             DRB4_0101  544      CVNFNFNGLTGTGVL  NFNFNGLTG  2        0.2116
5068.6    80.00  0.32     Sequence
             DRB4_0101  545      VNFNFNGLTGTGVLT  NFNGLTGTG  3        0.2007
5703.2    85.00  0.34     Sequence
             DRB4_0101  546      NFNFNGLTGTGVLTE  NFNGLTGTG  2        0.1746
7556.5    90.00  0.40     Sequence
             DRB4_0101  547      FNFNGLTGTGVLTES  GLTGTGVLT  4        0.1655
8341.9    90.00  0.37     Sequence
             DRB4_0101  548      NFNGLTGTGVLTESN  GLTGTGVLT  3        0.1486
10011.5    95.00  0.46     Sequence
             DRB4_0101  549      FNGLTGTGVLTESNK  GLTGTGVLT  2        0.1431
10633.0    95.00  0.45     Sequence
             DRB4_0101  550      NGLTGTGVLTESNKK  GLTGTGVLT  1        0.1328
11887.4    95.00  0.46     Sequence
             DRB4_0101  551      GLTGTGVLTESNKKF  GVLTESNKK  5        0.1215
13428.2    95.00  0.27     Sequence
             DRB4_0101  552      LTGTGVLTESNKKFL  GVLTESNKK  4        0.1360
11481.1    95.00  0.34     Sequence
             DRB4_0101  553      TGTGVLTESNKKFLP  GVLTESNKK  3        0.1479
10090.4    95.00  0.32     Sequence
             DRB4_0101  554      GTGVLTESNKKFLPF  GVLTESNKK  2        0.1756
7476.2    90.00  0.29     Sequence
             DRB4_0101  555      TGVLTESNKKFLPFQ  GVLTESNKK  1        0.2067
5344.3    80.00  0.23     Sequence
             DRB4_0101  556      GVLTESNKKFLPFQQ  NKKFLPFQQ  6        0.2762
2518.7    65.00  0.41     Sequence
             DRB4_0101  557      VLTESNKKFLPFQQF  NKKFLPFQQ  5        0.3671
941.6    40.00  0.50    Sequence
             DRB4_0101  558      LTESNKKFLPFQQFG  NKKFLPFQQ  4        0.4431
414.0    24.00  0.42    Sequence
             DRB4_0101  559      TESNKKFLPFQQFGR  NKKFLPFQQ  3        0.4962
232.9    15.00  0.35    Sequence
             DRB4_0101  560      ESNKKFLPFQQFGRD  NKKFLPFQQ  2        0.5197
180.6    12.00  0.31    Sequence
             DRB4_0101  561      SNKKFLPFQQFGRDI  KFLPFQQFG  3        0.5398
145.4     9.50  0.29    Sequence         WB
             DRB4_0101  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.5531
125.9     8.00  0.29    Sequence         WB
             DRB4_0101  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.5414
142.9     9.50  0.35    Sequence         WB
             DRB4_0101  564      KFLPFQQFGRDIADT  PFQQFGRDI  3        0.4767
287.6    18.00  0.34    Sequence
             DRB4_0101  565      FLPFQQFGRDIADTT  PFQQFGRDI  2        0.3774
842.7    37.00  0.46    Sequence
             DRB4_0101  566      LPFQQFGRDIADTTD  PFQQFGRDI  1        0.3335
1355.1    48.00  0.51     Sequence
             DRB4_0101  567      PFQQFGRDIADTTDA  QFGRDIADT  3        0.2741
2577.1    65.00  0.33     Sequence
             DRB4_0101  568      FQQFGRDIADTTDAV  QFGRDIADT  2        0.2194
4655.7    80.00  0.43     Sequence
```

```
             DRB4_0101  569      QQFGRDIADTTDAVR  QFGRDIADT  1        0.2091
5202.9    80.00  0.28     Sequence
             DRB4_0101  570      QFGRDIADTTDAVRD  RDIADTTDA  3        0.1929
6200.6    85.00  0.23     Sequence
             DRB4_0101  571      FGRDIADTTDAVRDP  RDIADTTDA  2        0.1766
7401.0    90.00  0.31     Sequence
             DRB4_0101  572      GRDIADTTDAVRDPQ  RDIADTTDA  1        0.1715
7818.6    90.00  0.28     Sequence
             DRB4_0101  573      RDIADTTDAVRDPQT  IADTTDAVR  2        0.1634
8534.3    90.00  0.28     Sequence
             DRB4_0101  574      DIADTTDAVRDPQTL  IADTTDAVR  1        0.1292
12359.6    95.00  0.26     Sequence
             DRB4_0101  575      IADTTDAVRDPQTLE  AVRDPQTLE  6        0.1102
15172.7   100.00  0.21     Sequence
             DRB4_0101  576      ADTTDAVRDPQTLEI  VRDPQTLEI  6        0.1179
13963.2    95.00  0.26     Sequence
             DRB4_0101  577      DTTDAVRDPQTLEIL  DPQTLEILX  7        0.2224
4506.8    80.00  0.22     Sequence
             DRB4_0101  578      TTDAVRDPQTLEILD  DPQTLEILD  6        0.2965
2022.5    60.00  0.47     Sequence
             DRB4_0101  579      TDAVRDPQTLEILDI  DPQTLEILD  5        0.4009
653.2    32.00  0.56     Sequence
             DRB4_0101  580      DAVRDPQTLEILDIT  DPQTLEILD  4        0.4311
471.2    26.00  0.49     Sequence
             DRB4_0101  581      AVRDPQTLEILDITP  DPQTLEILD  3        0.4483
391.3    23.00  0.47     Sequence
             DRB4_0101  582      VRDPQTLEILDITPC  DPQTLEILD  2        0.4462
400.1    23.00  0.43     Sequence
             DRB4_0101  583      RDPQTLEILDITPCS  TLEILDITP  4        0.4372
440.9    25.00  0.38     Sequence
             DRB4_0101  584      DPQTLEILDITPCSF  TLEILDITP  3        0.4152
559.6    29.00  0.48     Sequence
             DRB4_0101  585      PQTLEILDITPCSFG  TLEILDITP  2        0.4286
484.2    26.00  0.52     Sequence
             DRB4_0101  586      QTLEILDITPCSFGG  TLEILDITP  1        0.3897
737.6    35.00  0.46     Sequence
             DRB4_0101  587      TLEILDITPCSFGGV  EILDITPCS  2        0.3358
1321.9    48.00  0.27     Sequence
             DRB4_0101  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.2960
2031.9    60.00  0.33     Sequence
             DRB4_0101  589      EILDITPCSFGGVSV  ILDITPCSF  1        0.2181
4719.9    80.00  0.34     Sequence
             DRB4_0101  590      ILDITPCSFGGVSVI  DITPCSFGG  2        0.1807
7073.8    90.00  0.38     Sequence
             DRB4_0101  591      LDITPCSFGGVSVIT  DITPCSFGG  1        0.1465
10249.4    95.00  0.31     Sequence
             DRB4_0101  592      DITPCSFGGVSVITP  SFGGVSVIT  5        0.1292
12360.3    95.00  0.44     Sequence
             DRB4_0101  593      ITPCSFGGVSVITPG  SFGGVSVIT  4        0.1621
8657.9    90.00  0.38     Sequence
             DRB4_0101  594      TPCSFGGVSVITPGT  GVSVITPGT  6        0.1997
5759.8    85.00  0.34     Sequence
             DRB4_0101  595      PCSFGGVSVITPGTN  GVSVITPGT  5        0.2278
4253.5    75.00  0.41     Sequence
             DRB4_0101  596      CSFGGVSVITPGTNT  GVSVITPGT  4        0.2433
3593.5    75.00  0.46     Sequence
             DRB4_0101  597      SFGGVSVITPGTNTS  GVSVITPGT  3        0.2482
3408.6    70.00  0.54     Sequence
             DRB4_0101  598      FGGVSVITPGTNTSN  GVSVITPGT  2        0.2407
3699.3    75.00  0.56     Sequence
             DRB4_0101  599      GGVSVITPGTNTSNQ  GVSVITPGT  1        0.2312
4096.8    75.00  0.56     Sequence
             DRB4_0101  600      GVSVITPGTNTSNQV  VITPGTNTS  3        0.1571
9133.8    90.00  0.26     Sequence
             DRB4_0101  601      VSVITPGTNTSNQVA  VITPGTNTS  2        0.1203
13603.5    95.00  0.38     Sequence
```

```
             DRB4_0101  602      SVITPGTNTSNQVAV  VITPGTNTS  1        0.1147
14457.1   100.00  0.29     Sequence
             DRB4_0101  603      VITPGTNTSNQVAVL  NTSNQVAVL  6        0.1393
11080.5    95.00  0.23     Sequence
             DRB4_0101  604      ITPGTNTSNQVAVLY  NTSNQVAVL  5        0.1709
7872.2    90.00  0.28     Sequence
             DRB4_0101  605      TPGTNTSNQVAVLYQ  TSNQVAVLY  5        0.2374
3830.8    75.00  0.34     Sequence
             DRB4_0101  606      PGTNTSNQVAVLYQG  TSNQVAVLY  4        0.2654
2829.0    70.00  0.31     Sequence
             DRB4_0101  607      GTNTSNQVAVLYQGV  TSNQVAVLY  3        0.3309
1393.0    49.00  0.22     Sequence
             DRB4_0101  608      TNTSNQVAVLYQGVN  AVLYQGVNX  7        0.4083
603.0    30.00  0.26     Sequence
             DRB4_0101  609      NTSNQVAVLYQGVNC  AVLYQGVNC  6        0.4684
314.8    19.00  0.49     Sequence
             DRB4_0101  610      TSNQVAVLYQGVNCT  AVLYQGVNC  5        0.5179
184.1    12.00  0.63     Sequence
             DRB4_0101  611      SNQVAVLYQGVNCTE  AVLYQGVNC  4        0.5409
143.7     9.50  0.69     Sequence         WB
             DRB4_0101  612      NQVAVLYQGVNCTEV  AVLYQGVNC  3        0.5527
126.5     8.00  0.74     Sequence         WB
             DRB4_0101  613      QVAVLYQGVNCTEVP  AVLYQGVNC  2        0.5498
130.4     8.50  0.79     Sequence         WB
             DRB4_0101  614      VAVLYQGVNCTEVPV  AVLYQGVNC  1        0.4998
224.0    14.00  0.76     Sequence
             DRB4_0101  615      AVLYQGVNCTEVPVA  AVLYQGVNC  0        0.3502
1130.8    44.00  0.47     Sequence
             DRB4_0101  616      VLYQGVNCTEVPVAI  QGVNCTEVP  3        0.2185
4700.5    80.00  0.19     Sequence
             DRB4_0101  617      LYQGVNCTEVPVAIH  GVNCTEVPV  3        0.1723
7754.7    90.00  0.25     Sequence
             DRB4_0101  618      YQGVNCTEVPVAIHA  GVNCTEVPV  2        0.1842
6814.0    85.00  0.24     Sequence
             DRB4_0101  619      QGVNCTEVPVAIHAD  VNCTEVPVA  2        0.1835
6865.1    85.00  0.19     Sequence
             DRB4_0101  620      GVNCTEVPVAIHADQ  EVPVAIHAD  5        0.2361
3887.3    75.00  0.24     Sequence
             DRB4_0101  621      VNCTEVPVAIHADQL  VPVAIHADQ  5        0.3084
1777.2    55.00  0.28     Sequence
             DRB4_0101  622      NCTEVPVAIHADQLT  VPVAIHADQ  4        0.3481
1157.3    44.00  0.28     Sequence
             DRB4_0101  623      CTEVPVAIHADQLTP  VPVAIHADQ  3        0.3841
783.2    36.00  0.24     Sequence
             DRB4_0101  624      TEVPVAIHADQLTPT  AIHADQLTP  5        0.4330
461.8    25.00  0.34     Sequence
             DRB4_0101  625      EVPVAIHADQLTPTW  AIHADQLTP  4        0.4477
393.6    23.00  0.41     Sequence
             DRB4_0101  626      VPVAIHADQLTPTWR  AIHADQLTP  3        0.4513
378.7    22.00  0.46     Sequence
             DRB4_0101  627      PVAIHADQLTPTWRV  AIHADQLTP  2        0.4115
582.3    30.00  0.55     Sequence
             DRB4_0101  628      VAIHADQLTPTWRVY  AIHADQLTP  1        0.3774
842.2    37.00  0.55     Sequence
             DRB4_0101  629      AIHADQLTPTWRVYS  AIHADQLTP  0        0.3142
1669.2    55.00  0.31     Sequence
             DRB4_0101  630      IHADQLTPTWRVYST  HADQLTPTW  1        0.2748
2558.0    65.00  0.25     Sequence
             DRB4_0101  631      HADQLTPTWRVYSTG  LTPTWRVYS  4        0.2454
3514.6    75.00  0.30     Sequence
             DRB4_0101  632      ADQLTPTWRVYSTGS  LTPTWRVYS  3        0.2429
3611.7    75.00  0.31     Sequence
             DRB4_0101  633      DQLTPTWRVYSTGSN  LTPTWRVYS  2        0.2421
3643.4    75.00  0.30     Sequence
             DRB4_0101  634      QLTPTWRVYSTGSNV  LTPTWRVYS  1        0.2265
4312.2    80.00  0.24     Sequence
```

```
             DRB4_0101  635      LTPTWRVYSTGSNVF  RVYSTGSNV  5        0.2183
4712.7    80.00  0.26     Sequence
             DRB4_0101  636      TPTWRVYSTGSNVFQ  RVYSTGSNV  4        0.2112
5090.3    80.00  0.28     Sequence
             DRB4_0101  637      PTWRVYSTGSNVFQT  RVYSTGSNV  3        0.2119
5047.0    80.00  0.34     Sequence
             DRB4_0101  638      TWRVYSTGSNVFQTR  RVYSTGSNV  2        0.1913
6309.2    85.00  0.39     Sequence
             DRB4_0101  639      WRVYSTGSNVFQTRA  RVYSTGSNV  1        0.1916
6289.2    85.00  0.36     Sequence
             DRB4_0101  640      RVYSTGSNVFQTRAG  YSTGSNVFQ  2        0.1650
8387.4    90.00  0.19     Sequence
             DRB4_0101  641      VYSTGSNVFQTRAGC  NVFQTRAGC  6        0.1290
12386.4    95.00  0.15     Sequence
             DRB4_0101  642      YSTGSNVFQTRAGCL  NVFQTRAGC  5        0.1405
10931.0    95.00  0.27     Sequence
             DRB4_0101  643      STGSNVFQTRAGCLI  NVFQTRAGC  4        0.1721
7770.5    90.00  0.32     Sequence
             DRB4_0101  644      TGSNVFQTRAGCLIG  NVFQTRAGC  3        0.1885
6503.0    85.00  0.31     Sequence
             DRB4_0101  645      GSNVFQTRAGCLIGA  NVFQTRAGC  2        0.2058
5394.2    80.00  0.29     Sequence
             DRB4_0101  646      SNVFQTRAGCLIGAE  QTRAGCLIG  4        0.1921
6254.6    85.00  0.25     Sequence
             DRB4_0101  647      NVFQTRAGCLIGAEY  QTRAGCLIG  3        0.1796
7163.4    90.00  0.32     Sequence
             DRB4_0101  648      VFQTRAGCLIGAEYV  QTRAGCLIG  2        0.1723
7747.8    90.00  0.35     Sequence
             DRB4_0101  649      FQTRAGCLIGAEYVN  QTRAGCLIG  1        0.1651
8375.2    90.00  0.24     Sequence
             DRB4_0101  650      QTRAGCLIGAEYVNN  CLIGAEYVN  5        0.1872
6598.2    85.00  0.31     Sequence
             DRB4_0101  651      TRAGCLIGAEYVNNS  LIGAEYVNN  5        0.2266
4307.6    80.00  0.38     Sequence
             DRB4_0101  652      RAGCLIGAEYVNNSY  LIGAEYVNN  4        0.2493
3370.2    70.00  0.39     Sequence
             DRB4_0101  653      AGCLIGAEYVNNSYE  LIGAEYVNN  3        0.2494
3364.4    70.00  0.44     Sequence
             DRB4_0101  654      GCLIGAEYVNNSYEC  LIGAEYVNN  2        0.2438
3574.3    75.00  0.45     Sequence
             DRB4_0101  655      CLIGAEYVNNSYECD  LIGAEYVNN  1        0.1977
5885.5    85.00  0.42     Sequence
             DRB4_0101  656      LIGAEYVNNSYECDI  LIGAEYVNN  0        0.1476
10130.1    95.00  0.33     Sequence
             DRB4_0101  657      IGAEYVNNSYECDIP  GAEYVNNSY  1        0.0997
16996.5    100.00  0.29     Sequence
             DRB4_0101  658      GAEYVNNSYECDIPI  YVNNSYECD  3        0.0828
20413.6    100.00  0.20     Sequence
             DRB4_0101  659      AEYVNNSYECDIPIG  NNSYECDIP  4        0.0839
20172.1    100.00  0.24     Sequence
             DRB4_0101  660      EYVNNSYECDIPIGA  NNSYECDIP  3        0.0925
18382.3    100.00  0.26     Sequence
             DRB4_0101  661      YVNNSYECDIPIGAG  NNSYECDIP  2        0.0940
18076.0    100.00  0.23     Sequence
             DRB4_0101  662      VNNSYECDIPIGAGI  SYECDIPIG  3        0.1068
15738.6    100.00  0.19     Sequence
             DRB4_0101  663      NNSYECDIPIGAGIC  DIPIGAGIC  6        0.1134
14665.1    100.00  0.32     Sequence
             DRB4_0101  664      NSYECDIPIGAGICA  DIPIGAGIC  5        0.1511
9751.0    95.00  0.45     Sequence
             DRB4_0101  665      SYECDIPIGAGICAS  DIPIGAGIC  4        0.1779
7294.6    90.00  0.50     Sequence
             DRB4_0101  666      YECDIPIGAGICASY  DIPIGAGIC  3        0.2038
5513.4    85.00  0.46     Sequence
             DRB4_0101  667      ECDIPIGAGICASYQ  DIPIGAGIC  2        0.2247
4396.9    80.00  0.40     Sequence
```

```
             DRB4_0101  668      CDIPIGAGICASYQT  DIPIGAGIC  1        0.2334
4003.6    75.00  0.37     Sequence
             DRB4_0101  669      DIPIGAGICASYQTQ  DIPIGAGIC  0        0.2265
4313.3    80.00  0.22     Sequence
             DRB4_0101  670      IPIGAGICASYQTQT  IGAGICASY  2        0.2309
4111.5    75.00  0.17     Sequence
             DRB4_0101  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.2431
3603.2    75.00  0.18     Sequence
             DRB4_0101  672      IGAGICASYQTQTNS  CASYQTQTN  5        0.2696
2704.5    65.00  0.23     Sequence
             DRB4_0101  673      GAGICASYQTQTNSP  CASYQTQTN  4        0.2808
2397.1    65.00  0.28     Sequence
             DRB4_0101  674      AGICASYQTQTNSPR  CASYQTQTN  3        0.2821
2361.4    65.00  0.31     Sequence
             DRB4_0101  675      GICASYQTQTNSPRR  CASYQTQTN  2        0.2739
2581.8    65.00  0.31     Sequence
             DRB4_0101  676      ICASYQTQTNSPRRA  CASYQTQTN  1        0.2426
3620.7    75.00  0.25     Sequence
             DRB4_0101  677      CASYQTQTNSPRRAR  SYQTQTNSP  2        0.2017
5641.4    85.00  0.38     Sequence
             DRB4_0101  678      ASYQTQTNSPRRARS  SYQTQTNSP  1        0.1831
6894.3    85.00  0.34     Sequence
             DRB4_0101  679      SYQTQTNSPRRARSV  QTQTNSPRR  2        0.1585
8994.7    90.00  0.37     Sequence
             DRB4_0101  680      YQTQTNSPRRARSVA  SPRRARSVA  6        0.1672
8193.1    90.00  0.28     Sequence
             DRB4_0101  681      QTQTNSPRRARSVAS  SPRRARSVA  5        0.2140
4934.1    80.00  0.40     Sequence
             DRB4_0101  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.2614
2956.7    70.00  0.34     Sequence
             DRB4_0101  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.3141
1672.0    55.00  0.27     Sequence
             DRB4_0101  684      TNSPRRARSVASQSI  RARSVASQS  5        0.4260
497.8    27.00  0.36     Sequence
             DRB4_0101  685      NSPRRARSVASQSII  RARSVASQS  4        0.5198
180.5    12.00  0.31     Sequence
             DRB4_0101  686      SPRRARSVASQSIIA  SVASQSIIA  6        0.6135
65.5     4.00  0.58     Sequence         WB
             DRB4_0101  687      PRRARSVASQSIIAY  SVASQSIIA  5        0.6627
38.5     1.80  0.70     Sequence         SB
             DRB4_0101  688      RRARSVASQSIIAYT  SVASQSIIA  4        0.6851
30.2     1.20  0.76     Sequence         SB
             DRB4_0101  689      RARSVASQSIIAYTM  SVASQSIIA  3        0.6906
28.4     1.10  0.77     Sequence         SB
             DRB4_0101  690      ARSVASQSIIAYTMS  SVASQSIIA  2        0.6649
37.5     1.70  0.79     Sequence         SB
             DRB4_0101  691      RSVASQSIIAYTMSL  SVASQSIIA  1        0.6067
70.5     4.50  0.68     Sequence         WB
             DRB4_0101  692      SVASQSIIAYTMSLG  SIIAYTMSL  5        0.4491
387.7    22.00  0.26     Sequence
             DRB4_0101  693      VASQSIIAYTMSLGA  SIIAYTMSL  4        0.4384
435.5    24.00  0.41     Sequence
             DRB4_0101  694      ASQSIIAYTMSLGAE  SIIAYTMSL  3        0.4683
315.1    19.00  0.42     Sequence
             DRB4_0101  695      SQSIIAYTMSLGAEN  SIIAYTMSL  2        0.4951
235.9    15.00  0.40     Sequence
             DRB4_0101  696      QSIIAYTMSLGAENS  IIAYTMSLG  2        0.5036
215.0    14.00  0.40     Sequence
             DRB4_0101  697      SIIAYTMSLGAENSV  IIAYTMSLG  1        0.4659
323.3    20.00  0.41     Sequence
             DRB4_0101  698      IIAYTMSLGAENSVA  YTMSLGAEN  3        0.3613
1002.7    41.00  0.23     Sequence
             DRB4_0101  699      IAYTMSLGAENSVAY  YTMSLGAEN  2        0.2973
2003.4    60.00  0.31     Sequence
             DRB4_0101  700      AYTMSLGAENSVAYS  SLGAENSVA  4        0.2542
3194.8    70.00  0.36     Sequence
```

```
             DRB4_0101  701      YTMSLGAENSVAYSN  SLGAENSVA  3        0.2498
3351.8    70.00  0.44     Sequence
             DRB4_0101  702      TMSLGAENSVAYSNN  SLGAENSVA  2        0.2233
4465.8    80.00  0.56     Sequence
             DRB4_0101  703      MSLGAENSVAYSNNS  SLGAENSVA  1        0.2130
4989.7    80.00  0.50     Sequence
             DRB4_0101  704      SLGAENSVAYSNNSI  SLGAENSVA  0        0.1529
9562.0    95.00  0.24     Sequence
             DRB4_0101  705      LGAENSVAYSNNSIA  SVAYSNNSI  5        0.1670
8212.3    90.00  0.43     Sequence
             DRB4_0101  706      GAENSVAYSNNSIAI  SVAYSNNSI  4        0.2025
5587.6    85.00  0.48     Sequence
             DRB4_0101  707      AENSVAYSNNSIAIP  SVAYSNNSI  3        0.2183
4710.6    80.00  0.54     Sequence
             DRB4_0101  708      ENSVAYSNNSIAIPT  SVAYSNNSI  2        0.2350
3933.1    75.00  0.53     Sequence
             DRB4_0101  709      NSVAYSNNSIAIPTN  SVAYSNNSI  1        0.2368
3856.2    75.00  0.50     Sequence
             DRB4_0101  710      SVAYSNNSIAIPTNF  SVAYSNNSI  0        0.2095
5180.3    80.00  0.30     Sequence
             DRB4_0101  711      VAYSNNSIAIPTNFT  NSIAIPTNF  5        0.1737
7637.6    90.00  0.14     Sequence
             DRB4_0101  712      AYSNNSIAIPTNFTI  NSIAIPTNF  4        0.1627
8600.4    90.00  0.19     Sequence
             DRB4_0101  713      YSNNSIAIPTNFTIS  SIAIPTNFT  4        0.1846
6786.0    85.00  0.22     Sequence
             DRB4_0101  714      SNNSIAIPTNFTISV  AIPTNFTIS  5        0.2245
4408.4    80.00  0.17     Sequence
             DRB4_0101  715      NNSIAIPTNFTISVT  AIPTNFTIS  4        0.2368
3856.0    75.00  0.23     Sequence
             DRB4_0101  716      NSIAIPTNFTISVTT  AIPTNFTIS  3        0.2403
3712.1    75.00  0.25     Sequence
             DRB4_0101  717      SIAIPTNFTISVTTE  AIPTNFTIS  2        0.2305
4130.6    75.00  0.31     Sequence
             DRB4_0101  718      IAIPTNFTISVTTEI  AIPTNFTIS  1        0.2544
3189.4    70.00  0.21     Sequence
             DRB4_0101  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.2676
2764.4    65.00  0.20     Sequence
             DRB4_0101  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.2784
2458.5    65.00  0.23     Sequence
             DRB4_0101  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.3030
1885.3    60.00  0.20     Sequence
             DRB4_0101  722      TNFTISVTTEILPVS  TISVTTEIL  3        0.3266
1460.0    50.00  0.25     Sequence
             DRB4_0101  723      NFTISVTTEILPVSM  TISVTTEIL  2        0.3583
1036.1    42.00  0.22     Sequence
             DRB4_0101  724      FTISVTTEILPVSMT  ISVTTEILP  2        0.3823
798.6    36.00  0.20     Sequence
             DRB4_0101  725      TISVTTEILPVSMTK  EILPVSMTK  6        0.3834
789.6    36.00  0.28     Sequence
             DRB4_0101  726      ISVTTEILPVSMTKT  EILPVSMTK  5        0.4068
613.0    31.00  0.44     Sequence
             DRB4_0101  727      SVTTEILPVSMTKTS  EILPVSMTK  4        0.4226
516.6    27.00  0.51     Sequence
             DRB4_0101  728      VTTEILPVSMTKTSV  EILPVSMTK  3        0.4529
372.3    22.00  0.51     Sequence
             DRB4_0101  729      TTEILPVSMTKTSVD  EILPVSMTK  2        0.4608
341.7    20.00  0.49     Sequence
             DRB4_0101  730      TEILPVSMTKTSVDC  EILPVSMTK  1        0.4491
387.9    22.00  0.44     Sequence
             DRB4_0101  731      EILPVSMTKTSVDCT  PVSMTKTSV  3        0.4039
632.4    31.00  0.41     Sequence
             DRB4_0101  732      ILPVSMTKTSVDCTM  PVSMTKTSV  2        0.3920
719.4    34.00  0.50     Sequence
             DRB4_0101  733      LPVSMTKTSVDCTMY  PVSMTKTSV  1        0.3712
901.1    39.00  0.41     Sequence
```

```
             DRB4_0101  734      PVSMTKTSVDCTMYI  SMTKTSVDC  2        0.3122
1705.6    55.00  0.55     Sequence
             DRB4_0101  735      VSMTKTSVDCTMYIC  SMTKTSVDC  1        0.2543
3193.4    70.00  0.67     Sequence
             DRB4_0101  736      SMTKTSVDCTMYICG  SMTKTSVDC  0        0.1715
7816.7    90.00  0.42     Sequence
             DRB4_0101  737      MTKTSVDCTMYICGD  KTSVDCTMY  2        0.1324
11938.0    95.00  0.34     Sequence
             DRB4_0101  738      TKTSVDCTMYICGDS  CTMYICGDS  6        0.1225
13280.5    95.00  0.26     Sequence
             DRB4_0101  739      KTSVDCTMYICGDST  CTMYICGDS  5        0.1501
9855.9    95.00  0.41     Sequence
             DRB4_0101  740      TSVDCTMYICGDSTE  CTMYICGDS  4        0.1550
9346.7    90.00  0.46     Sequence
             DRB4_0101  741      SVDCTMYICGDSTEC  CTMYICGDS  3        0.1582
9025.4    90.00  0.42     Sequence
             DRB4_0101  742      VDCTMYICGDSTECS  CTMYICGDS  2        0.1796
7165.4    90.00  0.34     Sequence
             DRB4_0101  743      DCTMYICGDSTECSN  YICGDSTEC  4        0.1875
6575.3    85.00  0.41     Sequence
             DRB4_0101  744      CTMYICGDSTECSNL  YICGDSTEC  3        0.1864
6656.0    85.00  0.45     Sequence
             DRB4_0101  745      TMYICGDSTECSNLL  YICGDSTEC  2        0.1760
7444.8    90.00  0.51     Sequence
             DRB4_0101  746      MYICGDSTECSNLLL  YICGDSTEC  1        0.1714
7823.5    90.00  0.43     Sequence
             DRB4_0101  747      YICGDSTECSNLLLQ  YICGDSTEC  0        0.1649
8400.2    90.00  0.25     Sequence
             DRB4_0101  748      ICGDSTECSNLLLQY  ECSNLLLQY  6        0.1852
6739.0    85.00  0.38     Sequence
             DRB4_0101  749      CGDSTECSNLLLQYG  ECSNLLLQY  5        0.2689
2725.9    65.00  0.43     Sequence
             DRB4_0101  750      GDSTECSNLLLQYGS  ECSNLLLQY  4        0.3022
1901.2    60.00  0.36     Sequence
             DRB4_0101  751      DSTECSNLLLQYGSF  NLLLQYGSF  6        0.3522
1106.3    43.00  0.41     Sequence
             DRB4_0101  752      STECSNLLLQYGSFC  NLLLQYGSF  5        0.3578
1041.7    42.00  0.45     Sequence
             DRB4_0101  753      TECSNLLLQYGSFCT  NLLLQYGSF  4        0.3677
935.5    40.00  0.50     Sequence
             DRB4_0101  754      ECSNLLLQYGSFCTQ  NLLLQYGSF  3        0.3710
903.1    39.00  0.54     Sequence
             DRB4_0101  755      CSNLLLQYGSFCTQL  NLLLQYGSF  2        0.3822
799.5    36.00  0.58     Sequence
             DRB4_0101  756      SNLLLQYGSFCTQLN  NLLLQYGSF  1        0.3803
816.7    37.00  0.50     Sequence
             DRB4_0101  757      NLLLQYGSFCTQLNR  NLLLQYGSF  0        0.3248
1489.0    50.00  0.27     Sequence
             DRB4_0101  758      LLLQYGSFCTQLNRA  YGSFCTQLN  4        0.2773
2488.5    65.00  0.25     Sequence
             DRB4_0101  759      LLQYGSFCTQLNRAL  YGSFCTQLN  3        0.2839
2316.8    65.00  0.27     Sequence
             DRB4_0101  760      LQYGSFCTQLNRALT  SFCTQLNRA  4        0.3117
1714.3    55.00  0.22     Sequence
             DRB4_0101  761      QYGSFCTQLNRALTG  SFCTQLNRA  3        0.3168
1622.7    55.00  0.22     Sequence
             DRB4_0101  762      YGSFCTQLNRALTGI  SFCTQLNRA  2        0.3295
1415.2    49.00  0.20     Sequence
             DRB4_0101  763      GSFCTQLNRALTGIA  CTQLNRALT  3        0.3424
1230.3    46.00  0.19     Sequence
             DRB4_0101  764      SFCTQLNRALTGIAV  LNRALTGIA  5        0.3304
1400.7    49.00  0.31     Sequence
             DRB4_0101  765      FCTQLNRALTGIAVE  LNRALTGIA  4        0.3464
1177.7    45.00  0.33     Sequence
             DRB4_0101  766      CTQLNRALTGIAVEQ  ALTGIAVEQ  6        0.3810
810.5    37.00  0.34     Sequence
```

```
             DRB4_0101  767      TQLNRALTGIAVEQD  ALTGIAVEQ  5        0.4174
546.4    29.00  0.44     Sequence
             DRB4_0101  768      QLNRALTGIAVEQDK  ALTGIAVEQ  4        0.4329
462.1    25.00  0.50     Sequence
             DRB4_0101  769      LNRALTGIAVEQDKN  ALTGIAVEQ  3        0.4292
480.9    26.00  0.56     Sequence
             DRB4_0101  770      NRALTGIAVEQDKNT  ALTGIAVEQ  2        0.4213
524.1    28.00  0.60     Sequence
             DRB4_0101  771      RALTGIAVEQDKNTQ  ALTGIAVEQ  1        0.4183
541.5    28.00  0.51     Sequence
             DRB4_0101  772      ALTGIAVEQDKNTQE  GIAVEQDKN  3        0.3134
1684.3    55.00  0.29     Sequence
             DRB4_0101  773      LTGIAVEQDKNTQEV  GIAVEQDKN  2        0.3063
1817.9    55.00  0.38     Sequence
             DRB4_0101  774      TGIAVEQDKNTQEVF  GIAVEQDKN  1        0.2852
2284.1    65.00  0.35     Sequence
             DRB4_0101  775      GIAVEQDKNTQEVFA  AVEQDKNTQ  2        0.2516
3285.4    70.00  0.39     Sequence
             DRB4_0101  776      IAVEQDKNTQEVFAQ  AVEQDKNTQ  1        0.2068
5335.2    80.00  0.35     Sequence
             DRB4_0101  777      AVEQDKNTQEVFAQV  DKNTQEVFA  4        0.1958
6011.9    85.00  0.39     Sequence
             DRB4_0101  778      VEQDKNTQEVFAQVK  DKNTQEVFA  3        0.2214
4554.5    80.00  0.38     Sequence
             DRB4_0101  779      EQDKNTQEVFAQVKQ  DKNTQEVFA  2        0.2828
2344.2    65.00  0.28     Sequence
             DRB4_0101  780      QDKNTQEVFAQVKQI  EVFAQVKQI  6        0.3330
1362.3    48.00  0.37     Sequence
             DRB4_0101  781      DKNTQEVFAQVKQIY  EVFAQVKQI  5        0.3908
728.5    34.00  0.39     Sequence
             DRB4_0101  782      KNTQEVFAQVKQIYK  EVFAQVKQI  4        0.4267
494.0    27.00  0.40     Sequence
             DRB4_0101  783      NTQEVFAQVKQIYKT  EVFAQVKQI  3        0.4374
440.0    25.00  0.41     Sequence
             DRB4_0101  784      TQEVFAQVKQIYKTP  EVFAQVKQI  2        0.4531
371.2    22.00  0.41     Sequence
             DRB4_0101  785      QEVFAQVKQIYKTPP  VFAQVKQIY  2        0.4676
317.7    19.00  0.31     Sequence
             DRB4_0101  786      EVFAQVKQIYKTPPI  QVKQIYKTP  4        0.4266
494.8    27.00  0.28     Sequence
             DRB4_0101  787      VFAQVKQIYKTPPIK  QVKQIYKTP  3        0.4166
551.4    29.00  0.35     Sequence
             DRB4_0101  788      FAQVKQIYKTPPIKD  QIYKTPPIK  5        0.3837
786.7    36.00  0.37     Sequence
             DRB4_0101  789      AQVKQIYKTPPIKDF  QIYKTPPIK  4        0.3946
699.6    33.00  0.46     Sequence
             DRB4_0101  790      QVKQIYKTPPIKDFG  QIYKTPPIK  3        0.3725
888.1    39.00  0.61     Sequence
             DRB4_0101  791      VKQIYKTPPIKDFGG  QIYKTPPIK  2        0.3481
1157.4    44.00  0.70     Sequence
             DRB4_0101  792      KQIYKTPPIKDFGGF  QIYKTPPIK  1        0.3109
1729.3    55.00  0.58     Sequence
             DRB4_0101  793      QIYKTPPIKDFGGFN  PIKDFGGFN  6        0.2055
5411.5    80.00  0.28     Sequence
             DRB4_0101  794      IYKTPPIKDFGGFNF  PIKDFGGFN  5        0.2158
4838.7    80.00  0.50     Sequence
             DRB4_0101  795      YKTPPIKDFGGFNFS  PIKDFGGFN  4        0.2271
4285.3    75.00  0.58     Sequence
             DRB4_0101  796      KTPPIKDFGGFNFSQ  PIKDFGGFN  3        0.2448
3536.5    75.00  0.57     Sequence
             DRB4_0101  797      TPPIKDFGGFNFSQI  PIKDFGGFN  2        0.2497
3353.8    70.00  0.51     Sequence
             DRB4_0101  798      PPIKDFGGFNFSQIL  PIKDFGGFN  1        0.2741
2576.9    65.00  0.40     Sequence
             DRB4_0101  799      PIKDFGGFNFSQILP  GFNFSQILP  6        0.2688
2727.3    65.00  0.34     Sequence
```

```
             DRB4_0101  800      IKDFGGFNFSQILPD  GFNFSQILP  5        0.3261
1468.0    50.00  0.43     Sequence
             DRB4_0101  801      KDFGGFNFSQILPDP  NFSQILPDP  6        0.4240
508.8    27.00  0.40     Sequence
             DRB4_0101  802      DFGGFNFSQILPDPS  NFSQILPDP  5        0.5115
197.4    13.00  0.54     Sequence
             DRB4_0101  803      FGGFNFSQILPDPSK  NFSQILPDP  4        0.5344
154.2    10.00  0.57     Sequence
             DRB4_0101  804      GGFNFSQILPDPSKP  NFSQILPDP  3        0.5438
139.2     9.00  0.58     Sequence         WB
             DRB4_0101  805      GFNFSQILPDPSKPS  NFSQILPDP  2        0.5132
193.8    13.00  0.67     Sequence
             DRB4_0101  806      FNFSQILPDPSKPSK  NFSQILPDP  1        0.4669
319.8    19.00  0.69     Sequence
             DRB4_0101  807      NFSQILPDPSKPSKR  NFSQILPDP  0        0.3531
1096.0    43.00  0.50     Sequence
             DRB4_0101  808      FSQILPDPSKPSKRS  QILPDPSKP  2        0.2091
5204.9    80.00  0.49     Sequence
             DRB4_0101  809      SQILPDPSKPSKRSF  QILPDPSKP  1        0.1115
14964.0   100.00  0.49     Sequence
             DRB4_0101  810      QILPDPSKPSKRSFI  LPDPSKPSK  2        0.0992
17099.1   100.00  0.24     Sequence
             DRB4_0101  811      ILPDPSKPSKRSFIE  PSKRSFIEX  7        0.0961
17685.6   100.00  0.19     Sequence
             DRB4_0101  812      LPDPSKPSKRSFIED  PSKRSFIED  6        0.1107
15094.6   100.00  0.37     Sequence
             DRB4_0101  813      PDPSKPSKRSFIEDL  PSKRSFIED  5        0.1738
7626.9    90.00  0.40     Sequence
             DRB4_0101  814      DPSKPSKRSFIEDLL  KRSFIEDLL  6        0.3438
1212.4    46.00  0.28     Sequence
             DRB4_0101  815      PSKPSKRSFIEDLLF  KRSFIEDLL  5        0.4121
578.5    30.00  0.30     Sequence
             DRB4_0101  816      SKPSKRSFIEDLLFN  RSFIEDLLF  5        0.4266
494.6    27.00  0.30     Sequence
             DRB4_0101  817      KPSKRSFIEDLLFNK  RSFIEDLLF  4        0.4369
442.5    25.00  0.29     Sequence
             DRB4_0101  818      PSKRSFIEDLLFNKV  RSFIEDLLF  3        0.4428
415.4    24.00  0.29     Sequence
             DRB4_0101  819      SKRSFIEDLLFNKVT  RSFIEDLLF  2        0.4407
424.6    24.00  0.28     Sequence
             DRB4_0101  820      KRSFIEDLLFNKVTL  RSFIEDLLF  1        0.4357
448.4    25.00  0.25     Sequence
             DRB4_0101  821      RSFIEDLLFNKVTLA  DLLFNKVTL  5        0.3545
1079.6    43.00  0.24     Sequence
             DRB4_0101  822      SFIEDLLFNKVTLAD  DLLFNKVTL  4        0.3302
1404.5    49.00  0.31     Sequence
             DRB4_0101  823      FIEDLLFNKVTLADA  DLLFNKVTL  3        0.4023
643.4    32.00  0.28     Sequence
             DRB4_0101  824      IEDLLFNKVTLADAG  DLLFNKVTL  2        0.4167
551.0    29.00  0.29     Sequence
             DRB4_0101  825      EDLLFNKVTLADAGF  LFNKVTLAD  3        0.4216
522.2    28.00  0.32     Sequence
             DRB4_0101  826      DLLFNKVTLADAGFI  LFNKVTLAD  2        0.3857
770.3    36.00  0.35     Sequence
             DRB4_0101  827      LLFNKVTLADAGFIK  LFNKVTLAD  1        0.3754
861.0    38.00  0.37     Sequence
             DRB4_0101  828      LFNKVTLADAGFIKQ  KVTLADAGF  3        0.3318
1380.5    49.00  0.29     Sequence
             DRB4_0101  829      FNKVTLADAGFIKQY  KVTLADAGF  2        0.2953
2049.1    60.00  0.33     Sequence
             DRB4_0101  830      NKVTLADAGFIKQYG  TLADAGFIK  3        0.2616
2950.5    70.00  0.22     Sequence
             DRB4_0101  831      KVTLADAGFIKQYGD  TLADAGFIK  2        0.2422
3640.0    75.00  0.27     Sequence
             DRB4_0101  832      VTLADAGFIKQYGDC  GFIKQYGDC  6        0.2313
4093.3    75.00  0.37     Sequence
```

```
             DRB4_0101  833      TLADAGFIKQYGDCL  GFIKQYGDC  5        0.3141
1670.3    55.00  0.58     Sequence
             DRB4_0101  834      LADAGFIKQYGDCLG  GFIKQYGDC  4        0.3473
1167.5    45.00  0.61     Sequence
             DRB4_0101  835      ADAGFIKQYGDCLGD  GFIKQYGDC  3        0.3525
1102.5    43.00  0.62     Sequence
             DRB4_0101  836      DAGFIKQYGDCLGDI  GFIKQYGDC  2        0.3640
974.0    41.00  0.60     Sequence
             DRB4_0101  837      AGFIKQYGDCLGDIA  GFIKQYGDC  1        0.3629
985.2    41.00  0.50     Sequence
             DRB4_0101  838      GFIKQYGDCLGDIAA  GFIKQYGDC  0        0.3099
1749.4    55.00  0.33     Sequence
             DRB4_0101  839      FIKQYGDCLGDIAAR  FIKQYGDCL  0        0.2174
4757.6    80.00  0.18     Sequence
             DRB4_0101  840      IKQYGDCLGDIAARD  QYGDCLGDI  2        0.1440
10524.9    95.00  0.27     Sequence
             DRB4_0101  841      KQYGDCLGDIAARDL  QYGDCLGDI  1        0.1905
6361.9    85.00  0.19     Sequence
             DRB4_0101  842      QYGDCLGDIAARDLI  GDIAARDLI  6        0.2186
4695.6    80.00  0.22     Sequence
             DRB4_0101  843      YGDCLGDIAARDLIC  DIAARDLIC  6        0.2199
4628.8    80.00  0.25     Sequence
             DRB4_0101  844      GDCLGDIAARDLICA  DIAARDLIC  5        0.2460
3492.5    75.00  0.38     Sequence
             DRB4_0101  845      DCLGDIAARDLICAQ  DIAARDLIC  4        0.2645
2857.7    70.00  0.47     Sequence
             DRB4_0101  846      CLGDIAARDLICAQK  DIAARDLIC  3        0.2947
2061.1    60.00  0.46     Sequence
             DRB4_0101  847      LGDIAARDLICAQKF  DIAARDLIC  2        0.3587
1031.3    42.00  0.38     Sequence
             DRB4_0101  848      GDIAARDLICAQKFN  DIAARDLIC  1        0.3592
1026.1    42.00  0.27     Sequence
             DRB4_0101  849      DIAARDLICAQKFNG  LICAQKFNG  6        0.4136
569.5    29.00  0.44     Sequence
             DRB4_0101  850      IAARDLICAQKFNGL  LICAQKFNG  5        0.4831
268.3    17.00  0.56     Sequence
             DRB4_0101  851      AARDLICAQKFNGLT  LICAQKFNG  4        0.5125
195.2    13.00  0.61     Sequence
             DRB4_0101  852      ARDLICAQKFNGLTV  LICAQKFNG  3        0.5357
152.0    10.00  0.62     Sequence
             DRB4_0101  853      RDLICAQKFNGLTVL  LICAQKFNG  2        0.5472
134.2     8.50  0.62     Sequence         WB
             DRB4_0101  854      DLICAQKFNGLTVLP  LICAQKFNG  1        0.4928
241.9    15.00  0.54     Sequence
             DRB4_0101  855      LICAQKFNGLTVLPP  KFNGLTVLP  5        0.4500
383.9    22.00  0.39     Sequence
             DRB4_0101  856      ICAQKFNGLTVLPPL  KFNGLTVLP  4        0.4067
613.7    31.00  0.46     Sequence
             DRB4_0101  857      CAQKFNGLTVLPPLL  GLTVLPPLL  6        0.4802
276.9    17.00  0.47     Sequence
             DRB4_0101  858      AQKFNGLTVLPPLLT  GLTVLPPLL  5        0.5171
185.8    12.00  0.56     Sequence
             DRB4_0101  859      QKFNGLTVLPPLLTD  GLTVLPPLL  4        0.5155
189.1    12.00  0.58     Sequence
             DRB4_0101  860      KFNGLTVLPPLLTDE  GLTVLPPLL  3        0.4974
230.1    15.00  0.72     Sequence
             DRB4_0101  861      FNGLTVLPPLLTDEM  GLTVLPPLL  2        0.5236
173.2    11.00  0.65     Sequence
             DRB4_0101  862      NGLTVLPPLLTDEMI  GLTVLPPLL  1        0.5458
136.2     9.00  0.56     Sequence         WB
             DRB4_0101  863      GLTVLPPLLTDEMIA  PLLTDEMIA  6        0.5451
137.3     9.00  0.34     Sequence         WB
             DRB4_0101  864      LTVLPPLLTDEMIAQ  PLLTDEMIA  5        0.5344
154.1    10.00  0.64     Sequence
             DRB4_0101  865      TVLPPLLTDEMIAQY  PLLTDEMIA  4        0.5551
123.2     8.00  0.69     Sequence         WB
```

```
             DRB4_0101  866      VLPPLLTDEMIAQYT  PLLTDEMIA  3        0.5843
89.9     5.50  0.68     Sequence         WB
             DRB4_0101  867      LPPLLTDEMIAQYTS  PLLTDEMIA  2        0.5850
89.1     5.50  0.67     Sequence         WB
             DRB4_0101  868      PPLLTDEMIAQYTSA  PLLTDEMIA  1        0.5602
116.6     7.50  0.60     Sequence         WB
             DRB4_0101  869      PLLTDEMIAQYTSAL  EMIAQYTSA  5        0.4550
363.9    21.00  0.41     Sequence
             DRB4_0101  870      LLTDEMIAQYTSALL  EMIAQYTSA  4        0.4246
505.6    27.00  0.60     Sequence
             DRB4_0101  871      LTDEMIAQYTSALLA  EMIAQYTSA  3        0.4571
355.5    21.00  0.58     Sequence
             DRB4_0101  872      TDEMIAQYTSALLAG  EMIAQYTSA  2        0.4644
328.7    20.00  0.58     Sequence
             DRB4_0101  873      DEMIAQYTSALLAGT  EMIAQYTSA  1        0.4527
373.0    22.00  0.46     Sequence
             DRB4_0101  874      EMIAQYTSALLAGTI  MIAQYTSAL  1        0.4024
643.0    32.00  0.34     Sequence
             DRB4_0101  875      MIAQYTSALLAGTIT  IAQYTSALL  1        0.2973
2003.4    60.00  0.38     Sequence
             DRB4_0101  876      IAQYTSALLAGTITS  IAQYTSALL  0        0.2068
5333.8    80.00  0.22     Sequence
             DRB4_0101  877      AQYTSALLAGTITSG  ALLAGTITS  5        0.1941
6122.0    85.00  0.39     Sequence
             DRB4_0101  878      QYTSALLAGTITSGW  ALLAGTITS  4        0.1975
5903.7    85.00  0.44     Sequence
             DRB4_0101  879      YTSALLAGTITSGWT  ALLAGTITS  3        0.2147
4901.0    80.00  0.43     Sequence
             DRB4_0101  880      TSALLAGTITSGWTF  ALLAGTITS  2        0.2364
3873.8    75.00  0.41     Sequence
             DRB4_0101  881      SALLAGTITSGWTFG  ALLAGTITS  1        0.2380
3806.8    75.00  0.36     Sequence
             DRB4_0101  882      ALLAGTITSGWTFGA  AGTITSGWT  3        0.2125
5017.1    80.00  0.22     Sequence
             DRB4_0101  883      LLAGTITSGWTFGAG  AGTITSGWT  2        0.1936
6155.4    85.00  0.32     Sequence
             DRB4_0101  884      LAGTITSGWTFGAGA  TITSGWTFG  3        0.1823
6952.7    85.00  0.31     Sequence
             DRB4_0101  885      AGTITSGWTFGAGAA  TITSGWTFG  2        0.1631
8563.5    90.00  0.44     Sequence
             DRB4_0101  886      GTITSGWTFGAGAAL  TITSGWTFG  1        0.1605
8809.1    90.00  0.43     Sequence
             DRB4_0101  887      TITSGWTFGAGAALQ  TFGAGAALQ  6        0.1288
12403.9    95.00  0.23     Sequence
             DRB4_0101  888      ITSGWTFGAGAALQI  TFGAGAALQ  5        0.1876
6565.5    85.00  0.36     Sequence
             DRB4_0101  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.2310
4105.0    75.00  0.35     Sequence
             DRB4_0101  890      SGWTFGAGAALQIPF  AGAALQIPF  6        0.3291
1420.6    49.00  0.28     Sequence
             DRB4_0101  891      GWTFGAGAALQIPFA  AGAALQIPF  5        0.4284
485.3    26.00  0.27     Sequence
             DRB4_0101  892      WTFGAGAALQIPFAM  AGAALQIPF  4        0.4692
312.1    19.00  0.28     Sequence
             DRB4_0101  893      TFGAGAALQIPFAMQ  AGAALQIPF  3        0.4923
243.1    15.00  0.26     Sequence
             DRB4_0101  894      FGAGAALQIPFAMQM  AGAALQIPF  2        0.5232
174.1    11.00  0.24     Sequence
             DRB4_0101  895      GAGAALQIPFAMQMA  AALQIPFAM  3        0.5716
103.1     6.50  0.22     Sequence         WB
             DRB4_0101  896      AGAALQIPFAMQMAY  AALQIPFAM  2        0.6243
58.2     3.50  0.19     Sequence         WB
             DRB4_0101  897      GAALQIPFAMQMAYR  PFAMQMAYR  6        0.6657
37.2     1.70  0.44     Sequence         SB
             DRB4_0101  898      AALQIPFAMQMAYRF  PFAMQMAYR  5        0.6981
26.2     0.90  0.56     Sequence         SB
```

```
             DRB4_0101  899      ALQIPFAMQMAYRFN  PFAMQMAYR  4         0.7058
24.1     0.80  0.59     Sequence         SB
             DRB4_0101  900      LQIPFAMQMAYRFNG  PFAMQMAYR  3         0.7134
22.2     0.70  0.62     Sequence         SB
             DRB4_0101  901      QIPFAMQMAYRFNGI  PFAMQMAYR  2         0.7042
24.5     0.80  0.62     Sequence         SB
             DRB4_0101  902      IPFAMQMAYRFNGIG  PFAMQMAYR  1         0.6461
46.0     2.50  0.57     Sequence         WB
             DRB4_0101  903      PFAMQMAYRFNGIGV  PFAMQMAYR  0         0.4965
232.2    15.00  0.35     Sequence
             DRB4_0101  904      FAMQMAYRFNGIGVT  MAYRFNGIG  4         0.3910
727.4    34.00  0.20     Sequence
             DRB4_0101  905      AMQMAYRFNGIGVTQ  MAYRFNGIG  3         0.3694
918.7    39.00  0.20     Sequence
             DRB4_0101  906      MQMAYRFNGIGVTQN  RFNGIGVTQ  5         0.3724
889.8    39.00  0.26     Sequence
             DRB4_0101  907      QMAYRFNGIGVTQNV  RFNGIGVTQ  4         0.3556
1066.8    43.00  0.29     Sequence
             DRB4_0101  908      MAYRFNGIGVTQNVL  RFNGIGVTQ  3         0.3542
1082.7    43.00  0.32     Sequence
             DRB4_0101  909      AYRFNGIGVTQNVLY  IGVTQNVLY  6         0.3721
892.7    39.00  0.28     Sequence
             DRB4_0101  910      YRFNGIGVTQNVLYE  IGVTQNVLY  5         0.3886
746.2    35.00  0.37     Sequence
             DRB4_0101  911      RFNGIGVTQNVLYEN  IGVTQNVLY  4         0.3880
751.3    35.00  0.43     Sequence
             DRB4_0101  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3         0.3903
732.7    34.00  0.47     Sequence
             DRB4_0101  913      NGIGVTQNVLYENQK  IGVTQNVLY  2         0.4058
619.8    31.00  0.49     Sequence
             DRB4_0101  914      GIGVTQNVLYENQKL  IGVTQNVLY  1         0.3780
837.0    37.00  0.44     Sequence
             DRB4_0101  915      IGVTQNVLYENQKLI  NVLYENQKL  5         0.2811
2388.2    65.00  0.22     Sequence
             DRB4_0101  916      GVTQNVLYENQKLIA  NVLYENQKL  4         0.2996
1954.5    60.00  0.28     Sequence
             DRB4_0101  917      VTQNVLYENQKLIAN  LYENQKLIA  5         0.3342
1345.1    48.00  0.34     Sequence
             DRB4_0101  918      TQNVLYENQKLIANQ  LYENQKLIA  4         0.3613
1003.2    41.00  0.32     Sequence
             DRB4_0101  919      QNVLYENQKLIANQF  LYENQKLIA  3         0.4018
647.3    32.00  0.34     Sequence
             DRB4_0101  920      NVLYENQKLIANQFN  LYENQKLIA  2         0.4317
468.4    26.00  0.31     Sequence
             DRB4_0101  921      VLYENQKLIANQFNS  KLIANQFNS  6         0.4784
282.4    18.00  0.28     Sequence
             DRB4_0101  922      LYENQKLIANQFNSA  KLIANQFNS  5         0.5482
132.8    8.50  0.41     Sequence         WB
             DRB4_0101  923      YENQKLIANQFNSAI  KLIANQFNS  4         0.5988
76.8     4.50  0.44     Sequence         WB
             DRB4_0101  924      ENQKLIANQFNSAIG  KLIANQFNS  3         0.6230
59.1     3.50  0.44     Sequence         WB
             DRB4_0101  925      NQKLIANQFNSAIGK  KLIANQFNS  2         0.6376
50.5     3.00  0.44     Sequence         WB
             DRB4_0101  926      QKLIANQFNSAIGKI  KLIANQFNS  1         0.6243
58.3     3.50  0.43     Sequence         WB
             DRB4_0101  927      KLIANQFNSAIGKIQ  LIANQFNSA  1         0.5248
171.1    11.00  0.38     Sequence
             DRB4_0101  928      LIANQFNSAIGKIQD  LIANQFNSA  0         0.3432
1219.3    46.00  0.27     Sequence
             DRB4_0101  929      IANQFNSAIGKIQDS  NSAIGKIQD  5         0.2394
3750.6    75.00  0.22     Sequence
             DRB4_0101  930      ANQFNSAIGKIQDSL  NSAIGKIQD  4         0.2810
2389.8    65.00  0.26     Sequence
             DRB4_0101  931      NQFNSAIGKIQDSLS  IGKIQDSLS  6         0.3600
1017.3    42.00  0.31     Sequence
```

```
             DRB4_0101  932      QFNSAIGKIQDSLSS  IGKIQDSLS  5        0.4036
634.7    32.00  0.37     Sequence
             DRB4_0101  933      FNSAIGKIQDSLSST  IGKIQDSLS  4        0.4169
549.3    29.00  0.41     Sequence
             DRB4_0101  934      NSAIGKIQDSLSSTA  IGKIQDSLS  3        0.4311
471.2    26.00  0.43     Sequence
             DRB4_0101  935      SAIGKIQDSLSSTAS  IGKIQDSLS  2        0.4323
465.4    26.00  0.45     Sequence
             DRB4_0101  936      AIGKIQDSLSSTASA  IGKIQDSLS  1        0.3905
731.2    34.00  0.41     Sequence
             DRB4_0101  937      IGKIQDSLSSTASAL  KIQDSLSST  2        0.3164
1630.4    55.00  0.26     Sequence
             DRB4_0101  938      GKIQDSLSSTASALG  KIQDSLSST  1        0.2447
3539.6    75.00  0.22     Sequence
             DRB4_0101  939      KIQDSLSSTASALGK  SLSSTASAL  4        0.2075
5295.7    80.00  0.34     Sequence
             DRB4_0101  940      IQDSLSSTASALGKL  SLSSTASAL  3        0.2154
4861.5    80.00  0.44     Sequence
             DRB4_0101  941      QDSLSSTASALGKLQ  SLSSTASAL  2        0.2231
4473.7    80.00  0.46     Sequence
             DRB4_0101  942      DSLSSTASALGKLQD  SLSSTASAL  1        0.2293
4182.7    75.00  0.38     Sequence
             DRB4_0101  943      SLSSTASALGKLQDV  TASALGKLQ  4        0.2514
3292.2    70.00  0.16     Sequence
             DRB4_0101  944      LSSTASALGKLQDVV  ALGKLQDVV  6        0.2658
2818.5    70.00  0.21     Sequence
             DRB4_0101  945      SSTASALGKLQDVVN  ALGKLQDVV  5        0.2820
2365.3    65.00  0.28     Sequence
             DRB4_0101  946      STASALGKLQDVVNQ  LGKLQDVVN  5        0.3234
1511.1    55.00  0.37     Sequence
             DRB4_0101  947      TASALGKLQDVVNQN  LGKLQDVVN  4        0.3598
1019.5    42.00  0.34     Sequence
             DRB4_0101  948      ASALGKLQDVVNQNA  LGKLQDVVN  3        0.4035
635.2    32.00  0.28     Sequence
             DRB4_0101  949      SALGKLQDVVNQNAQ  KLQDVVNQN  4        0.4136
569.7    29.00  0.33     Sequence
             DRB4_0101  950      ALGKLQDVVNQNAQA  KLQDVVNQN  3        0.4005
656.1    32.00  0.41     Sequence
             DRB4_0101  951      LGKLQDVVNQNAQAL  KLQDVVNQN  2        0.3947
699.0    33.00  0.43     Sequence
             DRB4_0101  952      GKLQDVVNQNAQALN  KLQDVVNQN  1        0.3811
809.6    37.00  0.35     Sequence
             DRB4_0101  953      KLQDVVNQNAQALNT  DVVNQNAQA  3        0.3415
1242.8    46.00  0.31     Sequence
             DRB4_0101  954      LQDVVNQNAQALNTL  DVVNQNAQA  2        0.3238
1504.8    55.00  0.31     Sequence
             DRB4_0101  955      QDVVNQNAQALNTLV  DVVNQNAQA  1        0.3051
1842.3    60.00  0.22     Sequence
             DRB4_0101  956      DVVNQNAQALNTLVK  NAQALNTLV  5        0.2885
2205.2    60.00  0.25     Sequence
             DRB4_0101  957      VVNQNAQALNTLVKQ  NAQALNTLV  4        0.3006
1935.0    60.00  0.28     Sequence
             DRB4_0101  958      VNQNAQALNTLVKQL  ALNTLVKQL  6        0.3305
1400.1    49.00  0.31     Sequence
             DRB4_0101  959      NQNAQALNTLVKQLS  ALNTLVKQL  5        0.4306
473.7    26.00  0.32     Sequence
             DRB4_0101  960      QNAQALNTLVKQLSS  ALNTLVKQL  4        0.4539
368.3    22.00  0.34     Sequence
             DRB4_0101  961      NAQALNTLVKQLSSN  ALNTLVKQL  3        0.4593
347.2    21.00  0.35     Sequence
             DRB4_0101  962      AQALNTLVKQLSSNF  ALNTLVKQL  2        0.5035
215.2    14.00  0.30     Sequence
             DRB4_0101  963      QALNTLVKQLSSNFG  LVKQLSSNF  5        0.5353
152.7    10.00  0.31     Sequence
             DRB4_0101  964      ALNTLVKQLSSNFGA  LVKQLSSNF  4        0.5551
123.2     8.00  0.41     Sequence          WB
```

```
             DRB4_0101  965      LNTLVKQLSSNFGAI  LVKQLSSNF  3        0.5650
110.7     7.00  0.50     Sequence         WB
             DRB4_0101  966      NTLVKQLSSNFGAIS  LVKQLSSNF  2        0.5336
155.5    10.00  0.59     Sequence
             DRB4_0101  967      TLVKQLSSNFGAISS  LVKQLSSNF  1        0.4776
284.9    18.00  0.58     Sequence
             DRB4_0101  968      LVKQLSSNFGAISSV  LVKQLSSNF  0        0.3863
764.9    35.00  0.42     Sequence
             DRB4_0101  969      VKQLSSNFGAISSVL  QLSSNFGAI  2        0.3027
1891.3    60.00  0.26     Sequence
             DRB4_0101  970      KQLSSNFGAISSVLN  NFGAISSVL  5        0.3032
1880.1    60.00  0.28     Sequence
             DRB4_0101  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.3177
1606.8    55.00  0.26     Sequence
             DRB4_0101  972      LSSNFGAISSVLNDI  AISSVLNDI  6        0.3744
869.9    38.00  0.33     Sequence
             DRB4_0101  973      SSNFGAISSVLNDIL  AISSVLNDI  5        0.4893
251.1    16.00  0.41     Sequence
             DRB4_0101  974      SNFGAISSVLNDILS  AISSVLNDI  4        0.5208
178.6    12.00  0.44     Sequence
             DRB4_0101  975      NFGAISSVLNDILSR  AISSVLNDI  3        0.5306
160.5    11.00  0.48     Sequence
             DRB4_0101  976      FGAISSVLNDILSRL  AISSVLNDI  2        0.5359
151.7    10.00  0.47     Sequence
             DRB4_0101  977      GAISSVLNDILSRLD  AISSVLNDI  1        0.5368
150.2     9.50  0.47     Sequence         WB
             DRB4_0101  978      AISSVLNDILSRLDK  AISSVLNDI  0        0.4721
302.5    19.00  0.28     Sequence
             DRB4_0101  979      ISSVLNDILSRLDKV  NDILSRLDK  5        0.4409
424.0    24.00  0.25     Sequence
             DRB4_0101  980      SSVLNDILSRLDKVE  NDILSRLDK  4        0.4063
616.2    31.00  0.31     Sequence
             DRB4_0101  981      SVLNDILSRLDKVEA  NDILSRLDK  3        0.4554
362.3    21.00  0.31     Sequence
             DRB4_0101  982      VLNDILSRLDKVEAE  ILSRLDKVE  4        0.4696
310.7    19.00  0.39     Sequence
             DRB4_0101  983      LNDILSRLDKVEAEV  ILSRLDKVE  3        0.4833
267.9    17.00  0.40     Sequence
             DRB4_0101  984      NDILSRLDKVEAEVQ  ILSRLDKVE  2        0.4759
290.2    18.00  0.39     Sequence
             DRB4_0101  985      DILSRLDKVEAEVQI  ILSRLDKVE  1        0.4605
342.9    20.00  0.36     Sequence
             DRB4_0101  986      ILSRLDKVEAEVQID  RLDKVEAEV  3        0.4235
511.6    27.00  0.32     Sequence
             DRB4_0101  987      LSRLDKVEAEVQIDR  RLDKVEAEV  2        0.4220
520.0    28.00  0.31     Sequence
             DRB4_0101  988      SRLDKVEAEVQIDRL  VEAEVQIDR  5        0.4557
361.1    21.00  0.26     Sequence
             DRB4_0101  989      RLDKVEAEVQIDRLI  VEAEVQIDR  4        0.4832
268.1    17.00  0.31     Sequence
             DRB4_0101  990      LDKVEAEVQIDRLIT  VEAEVQIDR  3        0.5032
216.1    14.00  0.31     Sequence
             DRB4_0101  991      DKVEAEVQIDRLITG  EVQIDRLIT  5        0.5162
187.6    12.00  0.34     Sequence
             DRB4_0101  992      KVEAEVQIDRLITGR  EVQIDRLIT  4        0.5274
166.2    11.00  0.40     Sequence
             DRB4_0101  993      VEAEVQIDRLITGRL  EVQIDRLIT  3        0.5003
222.8    14.00  0.46     Sequence
             DRB4_0101  994      EAEVQIDRLITGRLQ  EVQIDRLIT  2        0.4820
271.6    17.00  0.50     Sequence
             DRB4_0101  995      AEVQIDRLITGRLQS  EVQIDRLIT  1        0.4816
272.8    17.00  0.37     Sequence
             DRB4_0101  996      EVQIDRLITGRLQSL  RLITGRLQS  5        0.4873
256.4    16.00  0.32     Sequence
             DRB4_0101  997      VQIDRLITGRLQSLQ  RLITGRLQS  4        0.5093
202.1    13.00  0.39     Sequence
```

```
             DRB4_0101  998      QIDRLITGRLQSLQT  RLITGRLQS  3        0.5579
119.5     8.00  0.37     Sequence         WB
             DRB4_0101  999      IDRLITGRLQSLQTY  RLITGRLQS  2        0.5755
98.8     6.50  0.32     Sequence         WB
             DRB4_0101 1000      DRLITGRLQSLQTYV  TGRLQSLQT  4        0.5900
84.5     5.50  0.35     Sequence         WB
             DRB4_0101 1001      RLITGRLQSLQTYVT  TGRLQSLQT  3        0.5883
86.0     5.50  0.37     Sequence         WB
             DRB4_0101 1002      LITGRLQSLQTYVTQ  TGRLQSLQT  2        0.5558
122.2     8.00  0.37     Sequence         WB
             DRB4_0101 1003      ITGRLQSLQTYVTQQ  RLQSLQTYV  3        0.5276
165.8    11.00  0.32     Sequence
             DRB4_0101 1004      TGRLQSLQTYVTQQL  RLQSLQTYV  2        0.5469
134.6     9.00  0.34     Sequence         WB
             DRB4_0101 1005      GRLQSLQTYVTQQLI  RLQSLQTYV  1        0.5574
120.1     8.00  0.29     Sequence         WB
             DRB4_0101 1006      RLQSLQTYVTQQLIR  TYVTQQLIR  6        0.5580
119.4     7.50  0.28     Sequence         WB
             DRB4_0101 1007      LQSLQTYVTQQLIRA  TYVTQQLIR  5        0.5868
87.4     5.50  0.37     Sequence         WB
             DRB4_0101 1008      QSLQTYVTQQLIRAA  TYVTQQLIR  4        0.6243
58.3     3.50  0.41     Sequence         WB
             DRB4_0101 1009      SLQTYVTQQLIRAAE  TYVTQQLIR  3        0.6278
56.1     3.00  0.44     Sequence         WB
             DRB4_0101 1010      LQTYVTQQLIRAAEI  TYVTQQLIR  2        0.6399
49.2     2.50  0.42     Sequence         WB
             DRB4_0101 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.6212
60.3     3.50  0.32     Sequence         WB
             DRB4_0101 1012      TYVTQQLIRAAEIRA  YVTQQLIRA  1        0.5618
114.6     7.50  0.30     Sequence         WB
             DRB4_0101 1013      YVTQQLIRAAEIRAS  LIRAAEIRA  5        0.5519
127.6     8.50  0.36     Sequence         WB
             DRB4_0101 1014      VTQQLIRAAEIRASA  LIRAAEIRA  4        0.5616
114.8     7.50  0.47     Sequence         WB
             DRB4_0101 1015      TQQLIRAAEIRASAN  LIRAAEIRA  3        0.5762
98.0     6.00  0.52     Sequence         WB
             DRB4_0101 1016      QQLIRAAEIRASANL  LIRAAEIRA  2        0.5931
81.7     5.00  0.56     Sequence         WB
             DRB4_0101 1017      QLIRAAEIRASANLA  LIRAAEIRA  1        0.5300
161.6    11.00  0.37     Sequence
             DRB4_0101 1018      LIRAAEIRASANLAA  EIRASANLA  5        0.5263
168.2    11.00  0.56     Sequence
             DRB4_0101 1019      IRAAEIRASANLAAI  EIRASANLA  4        0.5507
129.2     8.50  0.65     Sequence         WB
             DRB4_0101 1020      RAAEIRASANLAAIK  EIRASANLA  3        0.5653
110.3     7.00  0.69     Sequence         WB
             DRB4_0101 1021      AAEIRASANLAAIKM  EIRASANLA  2        0.5783
95.9     6.00  0.69     Sequence         WB
             DRB4_0101 1022      AEIRASANLAAIKMS  EIRASANLA  1        0.5762
98.0     6.00  0.61     Sequence         WB
             DRB4_0101 1023      EIRASANLAAIKMSE  EIRASANLA  0        0.5092
202.4    13.00  0.30     Sequence
             DRB4_0101 1024      IRASANLAAIKMSEC  NLAAIKMSE  5        0.4605
343.0    20.00  0.54     Sequence
             DRB4_0101 1025      RASANLAAIKMSECV  NLAAIKMSE  4        0.4586
349.9    21.00  0.64     Sequence
             DRB4_0101 1026      ASANLAAIKMSECVL  NLAAIKMSE  3        0.4824
270.4    17.00  0.62     Sequence
             DRB4_0101 1027      SANLAAIKMSECVLG  NLAAIKMSE  2        0.5023
218.2    14.00  0.56     Sequence
             DRB4_0101 1028      ANLAAIKMSECVLGQ  NLAAIKMSE  1        0.4999
223.9    14.00  0.47     Sequence
             DRB4_0101 1029      NLAAIKMSECVLGQS  AIKMSECVL  3        0.4540
368.0    22.00  0.48     Sequence
             DRB4_0101 1030      LAAIKMSECVLGQSK  AIKMSECVL  2        0.4161
554.5    29.00  0.59     Sequence
```

```
             DRB4_0101 1031      AAIKMSECVLGQSKR  AIKMSECVL  1        0.3707
906.0    39.00  0.54     Sequence
             DRB4_0101 1032      AIKMSECVLGQSKRV  AIKMSECVL  0        0.2883
2210.1    60.00  0.31     Sequence
             DRB4_0101 1033      IKMSECVLGQSKRVD  KMSECVLGQ  1        0.2151
4876.5    80.00  0.22     Sequence
             DRB4_0101 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.2095
5184.3    80.00  0.30     Sequence
             DRB4_0101 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.2273
4276.6    75.00  0.26     Sequence
             DRB4_0101 1036      SECVLGQSKRVDFCG  LGQSKRVDF  4        0.2430
3607.4    75.00  0.25     Sequence
             DRB4_0101 1037      ECVLGQSKRVDFCGK  LGQSKRVDF  3        0.2489
3384.1    70.00  0.28     Sequence
             DRB4_0101 1038      CVLGQSKRVDFCGKG  LGQSKRVDF  2        0.2231
4471.1    80.00  0.32     Sequence
             DRB4_0101 1039      VLGQSKRVDFCGKGY  LGQSKRVDF  1        0.1984
5845.8    85.00  0.33     Sequence
             DRB4_0101 1040      LGQSKRVDFCGKGYH  QSKRVDFCG  2        0.1687
8061.0    90.00  0.25     Sequence
             DRB4_0101 1041      GQSKRVDFCGKGYHL  RVDFCGKGY  4        0.1190
13799.3    95.00  0.22     Sequence
             DRB4_0101 1042      QSKRVDFCGKGYHLM  RVDFCGKGY  3        0.1164
14190.1   100.00  0.24     Sequence
             DRB4_0101 1043      SKRVDFCGKGYHLMS  RVDFCGKGY  2        0.1347
11646.8    95.00  0.22     Sequence
             DRB4_0101 1044      KRVDFCGKGYHLMSF  CGKGYHLMS  5        0.1712
7842.0    90.00  0.29     Sequence
             DRB4_0101 1045      RVDFCGKGYHLMSFP  CGKGYHLMS  4        0.1986
5830.8    85.00  0.28     Sequence
             DRB4_0101 1046      VDFCGKGYHLMSFPQ  GYHLMSFPQ  6        0.2518
3279.2    70.00  0.31     Sequence
             DRB4_0101 1047      DFCGKGYHLMSFPQS  GYHLMSFPQ  5        0.3469
1171.8    45.00  0.34     Sequence
             DRB4_0101 1048      FCGKGYHLMSFPQSA  HLMSFPQSA  6        0.4742
295.5    18.00  0.32     Sequence
             DRB4_0101 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.5361
151.3    10.00  0.40     Sequence
             DRB4_0101 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.5672
108.0     7.00  0.41     Sequence         WB
             DRB4_0101 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.5742
100.2     6.50  0.45     Sequence         WB
             DRB4_0101 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.5475
133.8     8.50  0.50     Sequence         WB
             DRB4_0101 1053      YHLMSFPQSAPHGVV  HLMSFPQSA  1        0.5167
186.7    12.00  0.50     Sequence
             DRB4_0101 1054      HLMSFPQSAPHGVVF  SFPQSAPHG  3        0.4037
634.0    31.00  0.31     Sequence
             DRB4_0101 1055      LMSFPQSAPHGVVFL  SFPQSAPHG  2        0.2972
2007.3    60.00  0.56     Sequence
             DRB4_0101 1056      MSFPQSAPHGVVFLH  SFPQSAPHG  1        0.2614
2956.1    70.00  0.44     Sequence
             DRB4_0101 1057      SFPQSAPHGVVFLHV  SFPQSAPHG  0        0.2802
2412.3    65.00  0.23     Sequence
             DRB4_0101 1058      FPQSAPHGVVFLHVT  GVVFLHVTX  7        0.2759
2526.6    65.00  0.17     Sequence
             DRB4_0101 1059      PQSAPHGVVFLHVTY  GVVFLHVTY  6        0.2809
2392.8    65.00  0.31     Sequence
             DRB4_0101 1060      QSAPHGVVFLHVTYV  GVVFLHVTY  5        0.2945
2066.0    60.00  0.38     Sequence
             DRB4_0101 1061      SAPHGVVFLHVTYVP  GVVFLHVTY  4        0.2993
1961.0    60.00  0.40     Sequence
             DRB4_0101 1062      APHGVVFLHVTYVPA  GVVFLHVTY  3        0.3172
1616.5    55.00  0.38     Sequence
             DRB4_0101 1063      PHGVVFLHVTYVPAQ  GVVFLHVTY  2        0.3470
1171.2    45.00  0.32     Sequence
```

```
             DRB4_0101 1064      HGVVFLHVTYVPAQE  HVTYVPAQE  6        0.3686
926.8    40.00  0.28     Sequence
             DRB4_0101 1065      GVVFLHVTYVPAQEK  HVTYVPAQE  5        0.3681
931.9    40.00  0.42     Sequence
             DRB4_0101 1066      VVFLHVTYVPAQEKN  HVTYVPAQE  4        0.3808
812.3    37.00  0.47     Sequence
             DRB4_0101 1067      VFLHVTYVPAQEKNF  HVTYVPAQE  3        0.3923
716.8    34.00  0.54     Sequence
             DRB4_0101 1068      FLHVTYVPAQEKNFT  HVTYVPAQE  2        0.3915
723.1    34.00  0.56     Sequence
             DRB4_0101 1069      LHVTYVPAQEKNFTT  HVTYVPAQE  1        0.3749
865.4    38.00  0.58     Sequence
             DRB4_0101 1070      HVTYVPAQEKNFTTA  YVPAQEKNF  3        0.2908
2150.1    60.00  0.38     Sequence
             DRB4_0101 1071      VTYVPAQEKNFTTAP  YVPAQEKNF  2        0.2185
4700.7    80.00  0.51     Sequence
             DRB4_0101 1072      TYVPAQEKNFTTAPA  YVPAQEKNF  1        0.1968
5946.3    85.00  0.47     Sequence
             DRB4_0101 1073      YVPAQEKNFTTAPAI  YVPAQEKNF  0        0.1927
6214.5    85.00  0.27     Sequence
             DRB4_0101 1074      VPAQEKNFTTAPAIC  NFTTAPAIC  6        0.1758
7460.0    90.00  0.36     Sequence
             DRB4_0101 1075      PAQEKNFTTAPAICH  NFTTAPAIC  5        0.1981
5863.9    85.00  0.56     Sequence
             DRB4_0101 1076      AQEKNFTTAPAICHD  NFTTAPAIC  4        0.2082
5253.4    80.00  0.58     Sequence
             DRB4_0101 1077      QEKNFTTAPAICHDG  NFTTAPAIC  3        0.2173
4761.9    80.00  0.59     Sequence
             DRB4_0101 1078      EKNFTTAPAICHDGK  NFTTAPAIC  2        0.2232
4470.8    80.00  0.61     Sequence
             DRB4_0101 1079      KNFTTAPAICHDGKA  NFTTAPAIC  1        0.2172
4766.3    80.00  0.59     Sequence
             DRB4_0101 1080      NFTTAPAICHDGKAH  NFTTAPAIC  0        0.1483
10049.3    95.00  0.31     Sequence
             DRB4_0101 1081      FTTAPAICHDGKAHF  AICHDGKAH  5        0.1357
11515.9    95.00  0.25     Sequence
             DRB4_0101 1082      TTAPAICHDGKAHFP  AICHDGKAH  4        0.1482
10064.2    95.00  0.31     Sequence
             DRB4_0101 1083      TAPAICHDGKAHFPR  AICHDGKAH  3        0.1615
8708.4    90.00  0.37     Sequence
             DRB4_0101 1084      APAICHDGKAHFPRE  AICHDGKAH  2        0.1585
8995.1    90.00  0.42     Sequence
             DRB4_0101 1085      PAICHDGKAHFPREG  AICHDGKAH  1        0.1563
9219.0    90.00  0.35     Sequence
             DRB4_0101 1086      AICHDGKAHFPREGV  AICHDGKAH  0        0.1478
10101.1    95.00  0.23     Sequence
             DRB4_0101 1087      ICHDGKAHFPREGVF  HDGKAHFPR  2        0.1306
12169.6    95.00  0.20     Sequence
             DRB4_0101 1088      CHDGKAHFPREGVFV  HFPREGVFV  6        0.1565
9194.3    90.00  0.40     Sequence
             DRB4_0101 1089      HDGKAHFPREGVFVS  HFPREGVFV  5        0.2113
5083.2    80.00  0.52     Sequence
             DRB4_0101 1090      DGKAHFPREGVFVSN  HFPREGVFV  4        0.2273
4275.8    75.00  0.55     Sequence
             DRB4_0101 1091      GKAHFPREGVFVSNG  HFPREGVFV  3        0.2479
3420.2    70.00  0.52     Sequence
             DRB4_0101 1092      KAHFPREGVFVSNGT  HFPREGVFV  2        0.2570
3100.2    70.00  0.50     Sequence
             DRB4_0101 1093      AHFPREGVFVSNGTH  HFPREGVFV  1        0.2672
2777.2    70.00  0.33     Sequence
             DRB4_0101 1094      HFPREGVFVSNGTHW  GVFVSNGTH  5        0.2666
2793.3    70.00  0.29     Sequence
             DRB4_0101 1095      FPREGVFVSNGTHWF  GVFVSNGTH  4        0.2778
2475.8    65.00  0.37     Sequence
             DRB4_0101 1096      PREGVFVSNGTHWFV  GVFVSNGTH  3        0.3006
1933.5    60.00  0.38     Sequence
```

```
             DRB4_0101 1097      REGVFVSNGTHWFVT  GVFVSNGTH  2        0.3125
1701.1    55.00  0.41     Sequence
             DRB4_0101 1098      EGVFVSNGTHWFVTQ  GVFVSNGTH  1        0.2996
1956.0    60.00  0.38     Sequence
             DRB4_0101 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.2711
2662.1    65.00  0.27     Sequence
             DRB4_0101 1100      VFVSNGTHWFVTQRN  GTHWFVTQR  5        0.2956
2042.1    60.00  0.34     Sequence
             DRB4_0101 1101      FVSNGTHWFVTQRNF  GTHWFVTQR  4        0.3145
1663.2    55.00  0.38     Sequence
             DRB4_0101 1102      VSNGTHWFVTQRNFY  WFVTQRNFY  6        0.3423
1231.7    46.00  0.32     Sequence
             DRB4_0101 1103      SNGTHWFVTQRNFYE  WFVTQRNFY  5        0.3660
952.6    40.00  0.41     Sequence
             DRB4_0101 1104      NGTHWFVTQRNFYEP  WFVTQRNFY  4        0.3732
881.9    38.00  0.45     Sequence
             DRB4_0101 1105      GTHWFVTQRNFYEPQ  WFVTQRNFY  3        0.3699
914.0    39.00  0.49     Sequence
             DRB4_0101 1106      THWFVTQRNFYEPQI  WFVTQRNFY  2        0.3491
1143.8    44.00  0.55     Sequence
             DRB4_0101 1107      HWFVTQRNFYEPQII  WFVTQRNFY  1        0.3099
1748.4    55.00  0.46     Sequence
             DRB4_0101 1108      WFVTQRNFYEPQIIT  QRNFYEPQI  4        0.2533
3227.7    70.00  0.21     Sequence
             DRB4_0101 1109      FVTQRNFYEPQIITT  QRNFYEPQI  3        0.2371
3842.7    75.00  0.30     Sequence
             DRB4_0101 1110      VTQRNFYEPQIITTD  FYEPQIITT  5        0.2536
3216.9    70.00  0.28     Sequence
             DRB4_0101 1111      TQRNFYEPQIITTDN  FYEPQIITT  4        0.2841
2310.9    65.00  0.24     Sequence
             DRB4_0101 1112      QRNFYEPQIITTDNT  EPQIITTDN  5        0.3180
1601.9    55.00  0.33     Sequence
             DRB4_0101 1113      RNFYEPQIITTDNTF  EPQIITTDN  4        0.3323
1372.8    49.00  0.40     Sequence
             DRB4_0101 1114      NFYEPQIITTDNTFV  EPQIITTDN  3        0.3026
1891.7    60.00  0.43     Sequence
             DRB4_0101 1115      FYEPQIITTDNTFVS  EPQIITTDN  2        0.3202
1564.4    55.00  0.40     Sequence
             DRB4_0101 1116      YEPQIITTDNTFVSG  QIITTDNTF  3        0.3308
1395.1    49.00  0.28     Sequence
             DRB4_0101 1117      EPQIITTDNTFVSGN  QIITTDNTF  2        0.3186
1591.6    55.00  0.40     Sequence
             DRB4_0101 1118      PQIITTDNTFVSGNC  QIITTDNTF  1        0.2969
2013.1    60.00  0.47     Sequence
             DRB4_0101 1119      QIITTDNTFVSGNCD  IITTDNTFV  1        0.2035
5529.1    85.00  0.39     Sequence
             DRB4_0101 1120      IITTDNTFVSGNCDV  IITTDNTFV  0        0.0897
18940.7   100.00  0.29     Sequence
             DRB4_0101 1121      ITTDNTFVSGNCDVV  TFVSGNCDV  5        0.1002
16912.7   100.00  0.38     Sequence
             DRB4_0101 1122      TTDNTFVSGNCDVVI  TFVSGNCDV  4        0.1293
12340.3    95.00  0.37     Sequence
             DRB4_0101 1123      TDNTFVSGNCDVVIG  TFVSGNCDV  3        0.1512
9737.9    95.00  0.34     Sequence
             DRB4_0101 1124      DNTFVSGNCDVVIGI  TFVSGNCDV  2        0.1761
7440.3    90.00  0.29     Sequence
             DRB4_0101 1125      NTFVSGNCDVVIGIV  TFVSGNCDV  1        0.2044
5474.8    85.00  0.22     Sequence
             DRB4_0101 1126      TFVSGNCDVVIGIVN  SGNCDVVIG  3        0.2085
5238.4    80.00  0.17     Sequence
             DRB4_0101 1127      FVSGNCDVVIGIVNN  CDVVIGIVN  5        0.2012
5666.9    85.00  0.21     Sequence
             DRB4_0101 1128      VSGNCDVVIGIVNNT  CDVVIGIVN  4        0.1876
6566.4    85.00  0.23     Sequence
             DRB4_0101 1129      SGNCDVVIGIVNNTV  VIGIVNNTV  6        0.2535
3220.8    70.00  0.20     Sequence
```

```
             DRB4_0101 1130      GNCDVVIGIVNNTVY  VIGIVNNTV  5        0.2858
2271.0    65.00  0.26     Sequence
             DRB4_0101 1131      NCDVVIGIVNNTVYD  VIGIVNNTV  4        0.2916
2130.9    60.00  0.30     Sequence
             DRB4_0101 1132      CDVVIGIVNNTVYDP  VIGIVNNTV  3        0.2987
1974.4    60.00  0.35     Sequence
             DRB4_0101 1133      DVVIGIVNNTVYDPL  VIGIVNNTV  2        0.3279
1439.9    50.00  0.31     Sequence
             DRB4_0101 1134      VVIGIVNNTVYDPLQ  VIGIVNNTV  1        0.3537
1088.5    43.00  0.30     Sequence
             DRB4_0101 1135      VIGIVNNTVYDPLQP  IVNNTVYDP  3        0.3355
1326.1    48.00  0.22     Sequence
             DRB4_0101 1136      IGIVNNTVYDPLQPE  IVNNTVYDP  2        0.2724
2624.1    65.00  0.31     Sequence
             DRB4_0101 1137      GIVNNTVYDPLQPEL  NTVYDPLQP  4        0.2789
2446.2    65.00  0.28     Sequence
             DRB4_0101 1138      IVNNTVYDPLQPELD  VYDPLQPEL  5        0.2731
2603.8    65.00  0.28     Sequence
             DRB4_0101 1139      VNNTVYDPLQPELDS  VYDPLQPEL  4        0.2724
2625.0    65.00  0.38     Sequence
             DRB4_0101 1140      NNTVYDPLQPELDSF  VYDPLQPEL  3        0.2578
3071.8    70.00  0.41     Sequence
             DRB4_0101 1141      NTVYDPLQPELDSFK  VYDPLQPEL  2        0.2550
3166.8    70.00  0.41     Sequence
             DRB4_0101 1142      TVYDPLQPELDSFKE  VYDPLQPEL  1        0.2490
3379.5    70.00  0.41     Sequence
             DRB4_0101 1143      VYDPLQPELDSFKEE  PLQPELDSF  3        0.2256
4356.2    80.00  0.29     Sequence
             DRB4_0101 1144      YDPLQPELDSFKEEL  ELDSFKEEL  6        0.2041
5493.0    85.00  0.38     Sequence
             DRB4_0101 1145      DPLQPELDSFKEELD  ELDSFKEEL  5        0.2177
4744.9    80.00  0.49     Sequence
             DRB4_0101 1146      PLQPELDSFKEELDK  ELDSFKEEL  4        0.2217
4540.2    80.00  0.60     Sequence
             DRB4_0101 1147      LQPELDSFKEELDKY  ELDSFKEEL  3        0.2258
4345.1    80.00  0.61     Sequence
             DRB4_0101 1148      QPELDSFKEELDKYF  ELDSFKEEL  2        0.2262
4323.4    80.00  0.57     Sequence
             DRB4_0101 1149      PELDSFKEELDKYFK  ELDSFKEEL  1        0.2234
4458.8    80.00  0.46     Sequence
             DRB4_0101 1150      ELDSFKEELDKYFKN  ELDSFKEEL  0        0.1682
8098.3    90.00  0.25     Sequence
             DRB4_0101 1151      LDSFKEELDKYFKNH  DSFKEELDK  1        0.1383
11198.0    95.00  0.22     Sequence
             DRB4_0101 1152      DSFKEELDKYFKNHT  ELDKYFKNH  5        0.1491
9960.5    95.00  0.28     Sequence
             DRB4_0101 1153      SFKEELDKYFKNHTS  ELDKYFKNH  4        0.1596
8887.7    90.00  0.29     Sequence
             DRB4_0101 1154      FKEELDKYFKNHTSP  ELDKYFKNH  3        0.1609
8771.5    90.00  0.31     Sequence
             DRB4_0101 1155      KEELDKYFKNHTSPD  ELDKYFKNH  2        0.1580
9045.2    90.00  0.30     Sequence
             DRB4_0101 1156      EELDKYFKNHTSPDV  YFKNHTSPD  5        0.1689
8043.2    90.00  0.24     Sequence
             DRB4_0101 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.1712
7843.4    90.00  0.22     Sequence
             DRB4_0101 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.1725
7734.2    90.00  0.28     Sequence
             DRB4_0101 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.1613
8734.2    90.00  0.33     Sequence
             DRB4_0101 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.1528
9568.8    95.00  0.35     Sequence
             DRB4_0101 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.1554
9309.8    90.00  0.31     Sequence
             DRB4_0101 1162      FKNHTSPDVDLGDIS  DVDLGDISX  7        0.1488
9994.1    95.00  0.17     Sequence
```

```
             DRB4_0101 1163      KNHTSPDVDLGDISG  DVDLGDISG  6        0.1468
10208.2    95.00  0.25     Sequence
             DRB4_0101 1164      NHTSPDVDLGDISGI  DVDLGDISG  5        0.1618
8678.7    90.00  0.31     Sequence
             DRB4_0101 1165      HTSPDVDLGDISGIN  DVDLGDISG  4        0.1761
7437.5    90.00  0.34     Sequence
             DRB4_0101 1166      TSPDVDLGDISGINA  DVDLGDISG  3        0.2041
5494.2    85.00  0.30     Sequence
             DRB4_0101 1167      SPDVDLGDISGINAS  DVDLGDISG  2        0.2167
4794.4    80.00  0.26     Sequence
             DRB4_0101 1168      PDVDLGDISGINASF  DISGINASF  6        0.2253
4368.7    80.00  0.25     Sequence
             DRB4_0101 1169      DVDLGDISGINASFV  DISGINASF  5        0.2406
3699.8    75.00  0.38     Sequence
             DRB4_0101 1170      VDLGDISGINASFVN  DISGINASF  4        0.2564
3120.2    70.00  0.41     Sequence
             DRB4_0101 1171      DLGDISGINASFVNI  DISGINASF  3        0.2592
3025.8    70.00  0.40     Sequence
             DRB4_0101 1172      LGDISGINASFVNIQ  DISGINASF  2        0.3196
1575.4    55.00  0.31     Sequence
             DRB4_0101 1173      GDISGINASFVNIQK  NASFVNIQK  6        0.3718
895.4    39.00  0.36     Sequence
             DRB4_0101 1174      DISGINASFVNIQKE  NASFVNIQK  5        0.4149
561.6    29.00  0.43     Sequence
             DRB4_0101 1175      ISGINASFVNIQKEI  NASFVNIQK  4        0.4820
271.7    17.00  0.37     Sequence
             DRB4_0101 1176      SGINASFVNIQKEID  FVNIQKEID  6        0.5217
176.9    12.00  0.38     Sequence
             DRB4_0101 1177      GINASFVNIQKEIDR  FVNIQKEID  5        0.5710
103.7     6.50  0.47     Sequence         WB
             DRB4_0101 1178      INASFVNIQKEIDRL  FVNIQKEID  4        0.5927
82.0     5.00  0.55     Sequence         WB
             DRB4_0101 1179      NASFVNIQKEIDRLN  FVNIQKEID  3        0.5910
83.5     5.00  0.62     Sequence         WB
             DRB4_0101 1180      ASFVNIQKEIDRLNE  FVNIQKEID  2        0.5948
80.2     5.00  0.62     Sequence         WB
             DRB4_0101 1181      SFVNIQKEIDRLNEV  FVNIQKEID  1        0.5824
91.7     6.00  0.54     Sequence         WB
             DRB4_0101 1182      FVNIQKEIDRLNEVA  FVNIQKEID  0        0.4981
228.2    15.00  0.30     Sequence
             DRB4_0101 1183      VNIQKEIDRLNEVAK  EIDRLNEVA  5        0.4459
401.5    23.00  0.33     Sequence
             DRB4_0101 1184      NIQKEIDRLNEVAKN  EIDRLNEVA  4        0.3770
846.5    38.00  0.47     Sequence
             DRB4_0101 1185      IQKEIDRLNEVAKNL  EIDRLNEVA  3        0.3598
1019.3    42.00  0.55     Sequence
             DRB4_0101 1186      QKEIDRLNEVAKNLN  EIDRLNEVA  2        0.3611
1005.3    41.00  0.54     Sequence
             DRB4_0101 1187      KEIDRLNEVAKNLNE  EIDRLNEVA  1        0.3410
1248.9    46.00  0.47     Sequence
             DRB4_0101 1188      EIDRLNEVAKNLNES  RLNEVAKNL  3        0.2702
2687.8    65.00  0.28     Sequence
             DRB4_0101 1189      IDRLNEVAKNLNESL  RLNEVAKNL  2        0.2636
2885.5    70.00  0.31     Sequence
             DRB4_0101 1190      DRLNEVAKNLNESLI  EVAKNLNES  4        0.2681
2747.6    65.00  0.28     Sequence
             DRB4_0101 1191      RLNEVAKNLNESLID  EVAKNLNES  3        0.2715
2649.7    65.00  0.31     Sequence
             DRB4_0101 1192      LNEVAKNLNESLIDL  EVAKNLNES  2        0.2704
2682.0    65.00  0.28     Sequence
             DRB4_0101 1193      NEVAKNLNESLIDLQ  NLNESLIDL  5        0.3265
1462.0    50.00  0.44     Sequence
             DRB4_0101 1194      EVAKNLNESLIDLQE  NLNESLIDL  4        0.3564
1057.2    42.00  0.44     Sequence
             DRB4_0101 1195      VAKNLNESLIDLQEL  NLNESLIDL  3        0.4182
541.7    28.00  0.44     Sequence
```

```
             DRB4_0101 1196      AKNLNESLIDLQELG  NLNESLIDL  2        0.4361
446.5    25.00  0.41     Sequence
             DRB4_0101 1197      KNLNESLIDLQELGK  NLNESLIDL  1        0.4594
347.1    21.00  0.28     Sequence
             DRB4_0101 1198      NLNESLIDLQELGKY  LIDLQELGK  5        0.4645
328.2    20.00  0.41     Sequence
             DRB4_0101 1199      LNESLIDLQELGKYE  LIDLQELGK  4        0.4649
326.9    20.00  0.45     Sequence
             DRB4_0101 1200      NESLIDLQELGKYEQ  LIDLQELGK  3        0.4657
324.0    20.00  0.54     Sequence
             DRB4_0101 1201      ESLIDLQELGKYEQY  LIDLQELGK  2        0.4670
319.7    19.00  0.54     Sequence
             DRB4_0101 1202      SLIDLQELGKYEQYI  LIDLQELGK  1        0.3945
700.1    34.00  0.53     Sequence
             DRB4_0101 1203      LIDLQELGKYEQYIK  LIDLQELGK  0        0.2825
2353.4    65.00  0.34     Sequence
             DRB4_0101 1204      IDLQELGKYEQYIKW  DLQELGKYE  1        0.2141
4930.1    80.00  0.29     Sequence
             DRB4_0101 1205      DLQELGKYEQYIKWP  LGKYEQYIK  4        0.1729
7700.2    90.00  0.34     Sequence
             DRB4_0101 1206      LQELGKYEQYIKWPW  LGKYEQYIK  3        0.2143
4919.4    80.00  0.32     Sequence
             DRB4_0101 1207      QELGKYEQYIKWPWY  LGKYEQYIK  2        0.2525
3256.1    70.00  0.24     Sequence
             DRB4_0101 1208      ELGKYEQYIKWPWYI  EQYIKWPWY  5        0.3014
1918.0    60.00  0.22     Sequence
             DRB4_0101 1209      LGKYEQYIKWPWYIW  YIKWPWYIW  6        0.3143
1667.4    55.00  0.25     Sequence
             DRB4_0101 1210      GKYEQYIKWPWYIWL  YIKWPWYIW  5        0.3252
1482.6    50.00  0.26     Sequence
             DRB4_0101 1211      KYEQYIKWPWYIWLG  YIKWPWYIW  4        0.3275
1445.9    50.00  0.29     Sequence
             DRB4_0101 1212      YEQYIKWPWYIWLGF  YIKWPWYIW  3        0.3249
1487.3    50.00  0.30     Sequence
             DRB4_0101 1213      EQYIKWPWYIWLGFI  YIKWPWYIW  2        0.3198
1572.1    55.00  0.36     Sequence
             DRB4_0101 1214      QYIKWPWYIWLGFIA  YIKWPWYIW  1        0.2972
2005.9    60.00  0.28     Sequence
             DRB4_0101 1215      YIKWPWYIWLGFIAG  PWYIWLGFI  4        0.2382
3800.4    75.00  0.26     Sequence
             DRB4_0101 1216      IKWPWYIWLGFIAGL  PWYIWLGFI  3        0.2694
2712.0    65.00  0.22     Sequence
             DRB4_0101 1217      KWPWYIWLGFIAGLI  PWYIWLGFI  2        0.2904
2158.7    60.00  0.20     Sequence
             DRB4_0101 1218      WPWYIWLGFIAGLIA  WLGFIAGLI  5        0.3585
1033.5    42.00  0.31     Sequence
             DRB4_0101 1219      PWYIWLGFIAGLIAI  WLGFIAGLI  4        0.3926
714.7    34.00  0.30     Sequence
             DRB4_0101 1220      WYIWLGFIAGLIAIV  WLGFIAGLI  3        0.4029
639.5    32.00  0.31     Sequence
             DRB4_0101 1221      YIWLGFIAGLIAIVM  FIAGLIAIV  5        0.4212
524.4    28.00  0.32     Sequence
             DRB4_0101 1222      IWLGFIAGLIAIVMV  FIAGLIAIV  4        0.4246
505.5    27.00  0.35     Sequence
             DRB4_0101 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3        0.4092
597.0    30.00  0.41     Sequence
             DRB4_0101 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.3976
677.1    33.00  0.46     Sequence
             DRB4_0101 1225      GFIAGLIAIVMVTIM  FIAGLIAIV  1        0.3343
1343.4    48.00  0.32     Sequence
             DRB4_0101 1226      FIAGLIAIVMVTIML  AIVMVTIML  6        0.3113
1721.9    55.00  0.31     Sequence
             DRB4_0101 1227      IAGLIAIVMVTIMLC  AIVMVTIML  5        0.3017
1910.8    60.00  0.39     Sequence
             DRB4_0101 1228      AGLIAIVMVTIMLCC  AIVMVTIML  4        0.2957
2039.6    60.00  0.42     Sequence
```

```
             DRB4_0101 1229      GLIAIVMVTIMLCCM  AIVMVTIML  3        0.2665
2796.0    70.00  0.53     Sequence
             DRB4_0101 1230      LIAIVMVTIMLCCMT  AIVMVTIML  2        0.2465
3471.0    75.00  0.57     Sequence
             DRB4_0101 1231      IAIVMVTIMLCCMTS  AIVMVTIML  1        0.2427
3620.5    75.00  0.53     Sequence
             DRB4_0101 1232      AIVMVTIMLCCMTSC  AIVMVTIML  0        0.1792
7197.0    90.00  0.31     Sequence
             DRB4_0101 1233      IVMVTIMLCCMTSCC  TIMLCCMTS  4        0.1330
11854.7    95.00  0.30     Sequence
             DRB4_0101 1234      VMVTIMLCCMTSCCS  TIMLCCMTS  3        0.1372
11334.9    95.00  0.35     Sequence
             DRB4_0101 1235      MVTIMLCCMTSCCSC  TIMLCCMTS  2        0.1338
11751.6    95.00  0.41     Sequence
             DRB4_0101 1236      VTIMLCCMTSCCSCL  TIMLCCMTS  1        0.1269
12669.1    95.00  0.38     Sequence
             DRB4_0101 1237      TIMLCCMTSCCSCLK  MLCCMTSCC  2        0.1144
14497.2   100.00  0.29     Sequence
             DRB4_0101 1238      IMLCCMTSCCSCLKG  MLCCMTSCC  1        0.0929
18293.4   100.00  0.31     Sequence
             DRB4_0101 1239      MLCCMTSCCSCLKGC  MTSCCSCLK  4        0.0749
22239.7   100.00  0.20     Sequence
             DRB4_0101 1240      LCCMTSCCSCLKGCC  MTSCCSCLK  3        0.0652
24686.8   100.00  0.26     Sequence
             DRB4_0101 1241      CCMTSCCSCLKGCCS  MTSCCSCLK  2        0.0529
28223.8   100.00  0.28     Sequence
             DRB4_0101 1242      CMTSCCSCLKGCCSC  MTSCCSCLK  1        0.0489
29448.5   100.00  0.26     Sequence
             DRB4_0101 1243      MTSCCSCLKGCCSCG  CLKGCCSCG  6        0.0440
31057.6   100.00  0.23     Sequence
             DRB4_0101 1244      TSCCSCLKGCCSCGS  CLKGCCSCG  5        0.0524
28373.5   100.00  0.35     Sequence
             DRB4_0101 1245      SCCSCLKGCCSCGSC  CLKGCCSCG  4        0.0532
28105.5   100.00  0.35     Sequence
             DRB4_0101 1246      CCSCLKGCCSCGSCC  CLKGCCSCG  3        0.0528
28249.1   100.00  0.37     Sequence
             DRB4_0101 1247      CSCLKGCCSCGSCCK  CLKGCCSCG  2        0.0526
28314.6   100.00  0.41     Sequence
             DRB4_0101 1248      SCLKGCCSCGSCCKF  CLKGCCSCG  1        0.0528
28233.6   100.00  0.38     Sequence
             DRB4_0101 1249      CLKGCCSCGSCCKFD  CLKGCCSCG  0        0.0457
30484.0   100.00  0.29     Sequence
             DRB4_0101 1250      LKGCCSCGSCCKFDE  CGSCCKFDE  6        0.0439
31080.8   100.00  0.25     Sequence
             DRB4_0101 1251      KGCCSCGSCCKFDED  CGSCCKFDE  5        0.0434
31250.1   100.00  0.38     Sequence
             DRB4_0101 1252      GCCSCGSCCKFDEDD  CGSCCKFDE  4        0.0510
28805.9   100.00  0.37     Sequence
             DRB4_0101 1253      CCSCGSCCKFDEDDS  CCKFDEDDS  6        0.0796
21124.0   100.00  0.22     Sequence
             DRB4_0101 1254      CSCGSCCKFDEDDSE  CCKFDEDDS  5        0.0908
18723.5   100.00  0.28     Sequence
             DRB4_0101 1255      SCGSCCKFDEDDSEP  CCKFDEDDS  4        0.0978
17352.6   100.00  0.32     Sequence
             DRB4_0101 1256      CGSCCKFDEDDSEPV  CCKFDEDDS  3        0.1014
16700.3   100.00  0.35     Sequence
             DRB4_0101 1257      GSCCKFDEDDSEPVL  CCKFDEDDS  2        0.1052
16025.7   100.00  0.38     Sequence
             DRB4_0101 1258      SCCKFDEDDSEPVLK  CCKFDEDDS  1        0.1010
16762.8   100.00  0.32     Sequence
             DRB4_0101 1259      CCKFDEDDSEPVLKG  CCKFDEDDS  0        0.0875
19405.4   100.00  0.19     Sequence
             DRB4_0101 1260      CKFDEDDSEPVLKGV  EDDSEPVLK  4        0.0655
24604.5   100.00  0.32     Sequence
             DRB4_0101 1261      KFDEDDSEPVLKGVK  EDDSEPVLK  3        0.0720
22954.8   100.00  0.31     Sequence
```

```
            DRB4_0101 1262      FDEDDSEPVLKGVKL  SEPVLKGVK  5        0.1274
12595.8    95.00  0.32     Sequence
            DRB4_0101 1263      DEDDSEPVLKGVKLH  PVLKGVKLH  6        0.2367
3863.1    75.00  0.32     Sequence
            DRB4_0101 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.4070
611.6    31.00  0.60     Sequence
            DRB4_0101 1265      DDSEPVLKGVKLHYT  VLKGVKLHY  5        0.5335
155.6    10.00  0.64     Sequence
            DRB5_0101    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.2180
4727.4    75.00  0.64     Sequence
            DRB5_0101    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.2164
4811.1    75.00  0.54     Sequence
            DRB5_0101    3      PIKEMFVFLVLLPLV  IKEMFVFLV  1        0.1937
6145.6    80.00  0.44     Sequence
            DRB5_0101    4      IKEMFVFLVLLPLVS  FLVLLPLVS  6        0.2387
3778.9    70.00  0.50     Sequence
            DRB5_0101    5      KEMFVFLVLLPLVSS  FLVLLPLVS  5        0.2539
3206.1    65.00  0.55     Sequence
            DRB5_0101    6      EMFVFLVLLPLVSSQ  FLVLLPLVS  4        0.2898
2174.7    60.00  0.53     Sequence
            DRB5_0101    7      MFVFLVLLPLVSSQC  FLVLLPLVS  3        0.3411
1247.5    46.00  0.37     Sequence
            DRB5_0101    8      FVFLVLLPLVSSQCV  LLPLVSSQC  5        0.3682
931.1    41.00  0.38     Sequence
            DRB5_0101    9      VFLVLLPLVSSQCVN  LLPLVSSQC  4        0.3695
917.5    41.00  0.40     Sequence
            DRB5_0101   10      FLVLLPLVSSQCVNF  LLPLVSSQC  3        0.3529
1098.7    44.00  0.44     Sequence
            DRB5_0101   11      LVLLPLVSSQCVNFT  LLPLVSSQC  2        0.3221
1533.3    50.00  0.43     Sequence
            DRB5_0101   12      VLLPLVSSQCVNFTN  LLPLVSSQC  1        0.2912
2140.7    60.00  0.34     Sequence
            DRB5_0101   13      LLPLVSSQCVNFTNR  VSSQCVNFT  4        0.2550
3167.2    65.00  0.40     Sequence
            DRB5_0101   14      LPLVSSQCVNFTNRT  VSSQCVNFT  3        0.2192
4664.9    75.00  0.53     Sequence
            DRB5_0101   15      PLVSSQCVNFTNRTQ  VSSQCVNFT  2        0.2157
4847.4    75.00  0.43     Sequence
            DRB5_0101   16      LVSSQCVNFTNRTQL  CVNFTNRTQ  5        0.2269
4291.3    75.00  0.41     Sequence
            DRB5_0101   17      VSSQCVNFTNRTQLP  CVNFTNRTQ  4        0.1945
6098.9    80.00  0.49     Sequence
            DRB5_0101   18      SSQCVNFTNRTQLPS  CVNFTNRTQ  3        0.1899
6404.8    80.00  0.55     Sequence
            DRB5_0101   19      SQCVNFTNRTQLPSA  CVNFTNRTQ  2        0.1878
6550.8    80.00  0.47     Sequence
            DRB5_0101   20      QCVNFTNRTQLPSAY  CVNFTNRTQ  1        0.1978
5884.3    80.00  0.34     Sequence
            DRB5_0101   21      CVNFTNRTQLPSAYT  NRTQLPSAY  5        0.2259
4342.1    75.00  0.33     Sequence
            DRB5_0101   22      VNFTNRTQLPSAYTN  RTQLPSAYT  5        0.2415
3664.6    70.00  0.34     Sequence
            DRB5_0101   23      NFTNRTQLPSAYTNS  RTQLPSAYT  4        0.2589
3037.9    65.00  0.40     Sequence
            DRB5_0101   24      FTNRTQLPSAYTNSF  RTQLPSAYT  3        0.2554
3154.0    65.00  0.44     Sequence
            DRB5_0101   25      TNRTQLPSAYTNSFT  RTQLPSAYT  2        0.2273
4275.7    75.00  0.43     Sequence
            DRB5_0101   26      NRTQLPSAYTNSFTR  SAYTNSFTR  6        0.2527
3248.1    65.00  0.41     Sequence
            DRB5_0101   27      RTQLPSAYTNSFTRG  SAYTNSFTR  5        0.2607
2979.3    65.00  0.54     Sequence
            DRB5_0101   28      TQLPSAYTNSFTRGV  YTNSFTRGV  6        0.3590
1028.6    43.00  0.46     Sequence
            DRB5_0101   29      QLPSAYTNSFTRGVY  YTNSFTRGV  5        0.4089
599.3    34.00  0.57     Sequence
```

```
             DRB5_0101   30      LPSAYTNSFTRGVYY  YTNSFTRGV  4        0.4308
472.6    31.00  0.63     Sequence
             DRB5_0101   31      PSAYTNSFTRGVYYP  YTNSFTRGV  3        0.4188
538.4    32.00  0.64     Sequence
             DRB5_0101   32      SAYTNSFTRGVYYPD  YTNSFTRGV  2        0.4117
581.2    34.00  0.59     Sequence
             DRB5_0101   33      AYTNSFTRGVYYPDK  YTNSFTRGV  1        0.4078
606.4    34.00  0.46     Sequence
             DRB5_0101   34      YTNSFTRGVYYPDKV  YTNSFTRGV  0        0.3615
1000.5    43.00  0.28     Sequence
             DRB5_0101   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.3035
1874.5    55.00  0.41     Sequence
             DRB5_0101   36      NSFTRGVYYPDKVFR  VYYPDKVFR  6        0.3574
1046.5    43.00  0.32     Sequence
             DRB5_0101   37      SFTRGVYYPDKVFRS  VYYPDKVFR  5        0.4153
559.1    33.00  0.38     Sequence
             DRB5_0101   38      FTRGVYYPDKVFRSS  VYYPDKVFR  4        0.4364
445.0    30.00  0.43     Sequence
             DRB5_0101   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.4461
400.5    28.00  0.44     Sequence
             DRB5_0101   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.4396
429.9    29.00  0.47     Sequence
             DRB5_0101   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.4015
649.2    35.00  0.44     Sequence
             DRB5_0101   42      VYYPDKVFRSSVLHS  YYPDKVFRS  1        0.4059
619.2    35.00  0.29     Sequence
             DRB5_0101   43      YYPDKVFRSSVLHST  KVFRSSVLH  4        0.3846
779.2    38.00  0.33     Sequence
             DRB5_0101   44      YPDKVFRSSVLHSTQ  KVFRSSVLH  3        0.3969
682.4    36.00  0.34     Sequence
             DRB5_0101   45      PDKVFRSSVLHSTQD  VFRSSVLHS  3        0.3879
752.3    38.00  0.31     Sequence
             DRB5_0101   46      DKVFRSSVLHSTQDL  FRSSVLHST  3        0.3847
778.2    38.00  0.40     Sequence
             DRB5_0101   47      KVFRSSVLHSTQDLF  FRSSVLHST  2        0.3623
991.8    42.00  0.44     Sequence
             DRB5_0101   48      VFRSSVLHSTQDLFL  FRSSVLHST  1        0.2883
2209.0    60.00  0.47     Sequence
             DRB5_0101   49      FRSSVLHSTQDLFLP  FRSSVLHST  0        0.2017
5637.2    80.00  0.37     Sequence
             DRB5_0101   50      RSSVLHSTQDLFLPF  LHSTQDLFL  4        0.1636
8515.2    85.00  0.46     Sequence
             DRB5_0101   51      SSVLHSTQDLFLPFF  LHSTQDLFL  3        0.1489
9984.7    90.00  0.51     Sequence
             DRB5_0101   52      SVLHSTQDLFLPFFS  QDLFLPFFS  6        0.1876
6569.4    80.00  0.40     Sequence
             DRB5_0101   53      VLHSTQDLFLPFFSN  QDLFLPFFS  5        0.2158
4842.1    75.00  0.46     Sequence
             DRB5_0101   54      LHSTQDLFLPFFSNV  QDLFLPFFS  4        0.2372
3839.4    70.00  0.57     Sequence
             DRB5_0101   55      HSTQDLFLPFFSNVT  FLPFFSNVT  6        0.5305
160.7    17.00  0.74     Sequence
             DRB5_0101   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.5939
80.9    11.00  0.79     Sequence
             DRB5_0101   57      TQDLFLPFFSNVTWF  FLPFFSNVT  4        0.6164
63.4     9.50  0.81     Sequence         WB
             DRB5_0101   58      QDLFLPFFSNVTWFH  FLPFFSNVT  3        0.6633
38.2     6.00  0.66     Sequence         WB
             DRB5_0101   59      DLFLPFFSNVTWFHA  FLPFFSNVT  2        0.6737
34.2     5.50  0.58     Sequence         WB
             DRB5_0101   60      LFLPFFSNVTWFHAI  FLPFFSNVT  1        0.6715
35.0     6.00  0.55     Sequence         WB
             DRB5_0101   61      FLPFFSNVTWFHAIH  FFSNVTWFH  3        0.6217
60.0     9.00  0.44     Sequence         WB
             DRB5_0101   62      LPFFSNVTWFHAIHV  FFSNVTWFH  2        0.5250
170.6    18.00  0.58     Sequence
```

```
             DRB5_0101   63      PFFSNVTWFHAIHVS  FFSNVTWFH  1        0.4990
226.0    21.00  0.53     Sequence
             DRB5_0101   64      FFSNVTWFHAIHVSG  FFSNVTWFH  0        0.4521
375.6    27.00  0.39     Sequence
             DRB5_0101   65      FSNVTWFHAIHVSGT  FHAIHVSGT  6        0.4146
563.5    33.00  0.37     Sequence
             DRB5_0101   66      SNVTWFHAIHVSGTN  FHAIHVSGT  5        0.4415
421.0    29.00  0.51     Sequence
             DRB5_0101   67      NVTWFHAIHVSGTNG  FHAIHVSGT  4        0.4469
397.4    28.00  0.59     Sequence
             DRB5_0101   68      VTWFHAIHVSGTNGT  FHAIHVSGT  3        0.4514
378.4    27.00  0.66     Sequence
             DRB5_0101   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.4420
418.7    29.00  0.60     Sequence
             DRB5_0101   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1        0.4876
255.6    22.00  0.35     Sequence
             DRB5_0101   71      FHAIHVSGTNGTKRF  VSGTNGTKR  5        0.4966
231.9    21.00  0.38     Sequence
             DRB5_0101   72      HAIHVSGTNGTKRFD  VSGTNGTKR  4        0.4661
322.8    25.00  0.51     Sequence
             DRB5_0101   73      AIHVSGTNGTKRFDN  VSGTNGTKR  3        0.4552
363.3    27.00  0.55     Sequence
             DRB5_0101   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.4060
618.5    34.00  0.59     Sequence
             DRB5_0101   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.3105
1738.4    55.00  0.66     Sequence
             DRB5_0101   76      VSGTNGTKRFDNPVL  VSGTNGTKR  0        0.1729
7698.4    85.00  0.63     Sequence
             DRB5_0101   77      SGTNGTKRFDNPVLP  TKRFDNPVL  5        0.1213
13458.4    95.00  0.44     Sequence
             DRB5_0101   78      GTNGTKRFDNPVLPF  KRFDNPVLP  5        0.1759
7451.1    85.00  0.36     Sequence
             DRB5_0101   79      TNGTKRFDNPVLPFN  KRFDNPVLP  4        0.1957
6019.3    80.00  0.37     Sequence
             DRB5_0101   80      NGTKRFDNPVLPFND  KRFDNPVLP  3        0.1986
5832.6    80.00  0.32     Sequence
             DRB5_0101   81      GTKRFDNPVLPFNDG  KRFDNPVLP  2        0.1831
6897.8    85.00  0.29     Sequence
             DRB5_0101   82      TKRFDNPVLPFNDGV  KRFDNPVLP  1        0.1554
9303.9    90.00  0.25     Sequence
             DRB5_0101   83      KRFDNPVLPFNDGVY  FDNPVLPFN  2        0.1388
11139.7    90.00  0.19     Sequence
             DRB5_0101   84      RFDNPVLPFNDGVYF  VLPFNDGVY  5        0.1298
12272.4    95.00  0.38     Sequence
             DRB5_0101   85      FDNPVLPFNDGVYFA  VLPFNDGVY  4        0.1398
11014.5    90.00  0.44     Sequence
             DRB5_0101   86      DNPVLPFNDGVYFAS  VLPFNDGVY  3        0.1805
7091.5    85.00  0.36     Sequence
             DRB5_0101   87      NPVLPFNDGVYFAST  FNDGVYFAS  5        0.2022
5609.4    80.00  0.40     Sequence
             DRB5_0101   88      PVLPFNDGVYFASTE  FNDGVYFAS  4        0.1940
6131.8    80.00  0.41     Sequence
             DRB5_0101   89      VLPFNDGVYFASTEK  GVYFASTEK  6        0.2520
3272.5    70.00  0.37     Sequence
             DRB5_0101   90      LPFNDGVYFASTEKS  GVYFASTEK  5        0.3253
1480.8    50.00  0.46     Sequence
             DRB5_0101   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.3746
868.3    40.00  0.38     Sequence
             DRB5_0101   92      FNDGVYFASTEKSNI  VYFASTEKS  4        0.4212
524.5    32.00  0.38     Sequence
             DRB5_0101   93      NDGVYFASTEKSNII  VYFASTEKS  3        0.4327
463.2    30.00  0.38     Sequence
             DRB5_0101   94      DGVYFASTEKSNIIR  VYFASTEKS  2        0.4486
390.1    28.00  0.28     Sequence
             DRB5_0101   95      GVYFASTEKSNIIRG  VYFASTEKS  1        0.4401
427.4    29.00  0.23     Sequence
```

```
             DRB5_0101   96      VYFASTEKSNIIRGW  STEKSNIIR  4        0.3815
805.8    39.00  0.28     Sequence
             DRB5_0101   97      YFASTEKSNIIRGWI  STEKSNIIR  3        0.3363
1314.8    47.00  0.41     Sequence
             DRB5_0101   98      FASTEKSNIIRGWIF  SNIIRGWIF  6        0.3269
1454.9    49.00  0.34     Sequence
             DRB5_0101   99      ASTEKSNIIRGWIFG  SNIIRGWIF  5        0.3350
1332.7    48.00  0.47     Sequence
             DRB5_0101  100      STEKSNIIRGWIFGT  SNIIRGWIF  4        0.3623
992.4    42.00  0.47     Sequence
             DRB5_0101  101      TEKSNIIRGWIFGTT  SNIIRGWIF  3        0.3665
948.3    42.00  0.50     Sequence
             DRB5_0101  102      EKSNIIRGWIFGTTL  SNIIRGWIF  2        0.3663
949.7    42.00  0.43     Sequence
             DRB5_0101  103      KSNIIRGWIFGTTLD  SNIIRGWIF  1        0.3468
1173.2    45.00  0.40     Sequence
             DRB5_0101  104      SNIIRGWIFGTTLDS  IIRGWIFGT  2        0.3182
1599.3    55.00  0.30     Sequence
             DRB5_0101  105      NIIRGWIFGTTLDSK  WIFGTTLDS  5        0.3189
1587.3    55.00  0.34     Sequence
             DRB5_0101  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.3174
1613.1    55.00  0.40     Sequence
             DRB5_0101  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3        0.3163
1632.0    55.00  0.44     Sequence
             DRB5_0101  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2        0.3091
1764.7    55.00  0.41     Sequence
             DRB5_0101  109      GWIFGTTLDSKTQSL  FGTTLDSKT  3        0.2819
2367.7    60.00  0.49     Sequence
             DRB5_0101  110      WIFGTTLDSKTQSLL  FGTTLDSKT  2        0.2405
3705.7    70.00  0.51     Sequence
             DRB5_0101  111      IFGTTLDSKTQSLLI  FGTTLDSKT  1        0.1882
6526.3    80.00  0.55     Sequence
             DRB5_0101  112      FGTTLDSKTQSLLIV  FGTTLDSKT  0        0.1183
13903.6    95.00  0.31     Sequence
             DRB5_0101  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4        0.0902
18838.8   100.00  0.31     Sequence
             DRB5_0101  114      TTLDSKTQSLLIVNN  DSKTQSLLI  3        0.0918
18512.8   100.00  0.30     Sequence
             DRB5_0101  115      TLDSKTQSLLIVNNA  DSKTQSLLI  2        0.0988
17174.8   100.00  0.25     Sequence
             DRB5_0101  116      LDSKTQSLLIVNNAT  SLLIVNNAT  6        0.1310
12119.2    95.00  0.29     Sequence
             DRB5_0101  117      DSKTQSLLIVNNATN  LLIVNNATN  6        0.2445
3550.4    70.00  0.60     Sequence
             DRB5_0101  118      SKTQSLLIVNNATNV  LLIVNNATN  5        0.3148
1659.3    55.00  0.64     Sequence
             DRB5_0101  119      KTQSLLIVNNATNVV  LLIVNNATN  4        0.3602
1015.2    43.00  0.65     Sequence
             DRB5_0101  120      TQSLLIVNNATNVVI  LLIVNNATN  3        0.3814
806.5    39.00  0.64     Sequence
             DRB5_0101  121      QSLLIVNNATNVVIK  LLIVNNATN  2        0.3825
797.0    39.00  0.51     Sequence
             DRB5_0101  122      SLLIVNNATNVVIKV  LLIVNNATN  1        0.3598
1018.9    43.00  0.38     Sequence
             DRB5_0101  123      LLIVNNATNVVIKVC  VNNATNVVI  3        0.3022
1900.7    55.00  0.25     Sequence
             DRB5_0101  124      LIVNNATNVVIKVCE  VNNATNVVI  2        0.2374
3831.1    70.00  0.31     Sequence
             DRB5_0101  125      IVNNATNVVIKVCEF  NNATNVVIK  2        0.1897
6420.0    80.00  0.32     Sequence
             DRB5_0101  126      VNNATNVVIKVCEFQ  NNATNVVIK  1        0.1510
9759.5    90.00  0.33     Sequence
             DRB5_0101  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.2225
4501.2    75.00  0.58     Sequence
             DRB5_0101  128      NATNVVIKVCEFQFC  VIKVCEFQF  5        0.2585
3051.2    65.00  0.62     Sequence
```

```
             DRB5_0101  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.2731
2605.5    65.00  0.61     Sequence
             DRB5_0101  130      TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.2773
2489.7    60.00  0.60     Sequence
             DRB5_0101  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.2564
3121.6    65.00  0.60     Sequence
             DRB5_0101  132      VVIKVCEFQFCNYPF  VIKVCEFQF  1        0.2712
2657.7    65.00  0.42     Sequence
             DRB5_0101  133      VIKVCEFQFCNYPFL  FQFCNYPFL  6        0.3764
851.6    40.00  0.50     Sequence
             DRB5_0101  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.3981
673.2    36.00  0.58     Sequence
             DRB5_0101  135      KVCEFQFCNYPFLGV  FQFCNYPFL  4        0.4265
495.5    31.00  0.62     Sequence
             DRB5_0101  136      VCEFQFCNYPFLGVY  FQFCNYPFL  3        0.4238
509.9    32.00  0.64     Sequence
             DRB5_0101  137      CEFQFCNYPFLGVYY  FQFCNYPFL  2        0.4260
498.0    31.00  0.56     Sequence
             DRB5_0101  138      EFQFCNYPFLGVYYH  FQFCNYPFL  1        0.4588
349.0    26.00  0.42     Sequence
             DRB5_0101  139      FQFCNYPFLGVYYHK  YPFLGVYYH  5        0.4683
315.2    25.00  0.27     Sequence
             DRB5_0101  140      QFCNYPFLGVYYHKN  YPFLGVYYH  4        0.4755
291.5    24.00  0.31     Sequence
             DRB5_0101  141      FCNYPFLGVYYHKNN  FLGVYYHKN  5        0.4884
253.5    22.00  0.40     Sequence
             DRB5_0101  142      CNYPFLGVYYHKNNK  FLGVYYHKN  4        0.5038
214.6    20.00  0.44     Sequence
             DRB5_0101  143      NYPFLGVYYHKNNKS  FLGVYYHKN  3        0.5280
165.1    18.00  0.46     Sequence
             DRB5_0101  144      YPFLGVYYHKNNKSW  YYHKNNKSW  6        0.5941
80.7    11.00  0.31     Sequence
             DRB5_0101  145      PFLGVYYHKNNKSWM  YYHKNNKSW  5        0.6257
57.4     8.50  0.47     Sequence         WB
             DRB5_0101  146      FLGVYYHKNNKSWME  YYHKNNKSW  4        0.6283
55.8     8.50  0.56     Sequence         WB
             DRB5_0101  147      LGVYYHKNNKSWMES  YYHKNNKSW  3        0.6195
61.4     9.00  0.61     Sequence         WB
             DRB5_0101  148      GVYYHKNNKSWMESE  YYHKNNKSW  2        0.5841
90.0    12.00  0.57     Sequence
             DRB5_0101  149      VYYHKNNKSWMESEF  YYHKNNKSW  1        0.5132
193.8    19.00  0.60     Sequence
             DRB5_0101  150      YYHKNNKSWMESEFR  YYHKNNKSW  0        0.4761
289.6    24.00  0.37     Sequence
             DRB5_0101  151      YHKNNKSWMESEFRV  KSWMESEFR  5        0.4045
628.4    35.00  0.58     Sequence
             DRB5_0101  152      HKNNKSWMESEFRVY  KSWMESEFR  4        0.4091
597.9    34.00  0.69     Sequence
             DRB5_0101  153      KNNKSWMESEFRVYS  KSWMESEFR  3        0.4292
481.0    31.00  0.65     Sequence
             DRB5_0101  154      NNKSWMESEFRVYSS  KSWMESEFR  2        0.3996
662.8    36.00  0.57     Sequence
             DRB5_0101  155      NKSWMESEFRVYSSA  KSWMESEFR  1        0.3735
879.1    40.00  0.52     Sequence
             DRB5_0101  156      KSWMESEFRVYSSAN  KSWMESEFR  0        0.3209
1552.1    55.00  0.38     Sequence
             DRB5_0101  157      SWMESEFRVYSSANN  FRVYSSANN  6        0.2852
2284.1    60.00  0.43     Sequence
             DRB5_0101  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.3006
1933.6    55.00  0.56     Sequence
             DRB5_0101  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.3235
1510.2    50.00  0.66     Sequence
             DRB5_0101  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.3527
1100.1    44.00  0.60     Sequence
             DRB5_0101  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.3566
1055.1    43.00  0.54     Sequence
```

```
             DRB5_0101  162      EFRVYSSANNCTFEY  FRVYSSANN  1        0.3386
1281.4    47.00  0.47     Sequence
             DRB5_0101  163      FRVYSSANNCTFEYV  YSSANNCTF  3        0.3011
1922.8    55.00  0.40     Sequence
             DRB5_0101  164      RVYSSANNCTFEYVS  YSSANNCTF  2        0.2059
5386.4    80.00  0.54     Sequence
             DRB5_0101  165      VYSSANNCTFEYVSQ  YSSANNCTF  1        0.1414
10831.2    90.00  0.54     Sequence
             DRB5_0101  166      YSSANNCTFEYVSQP  YSSANNCTF  0        0.0918
18516.6   100.00  0.37     Sequence
             DRB5_0101  167      SSANNCTFEYVSQPF  TFEYVSQPF  6        0.1119
14904.1    95.00  0.44     Sequence
             DRB5_0101  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.2255
4357.5    75.00  0.61     Sequence
             DRB5_0101  169      ANNCTFEYVSQPFLM  EYVSQPFLM  6        0.3911
726.1    37.00  0.41     Sequence
             DRB5_0101  170      NNCTFEYVSQPFLMD  EYVSQPFLM  5        0.4434
412.5    29.00  0.48     Sequence
             DRB5_0101  171      NCTFEYVSQPFLMDL  EYVSQPFLM  4        0.4756
291.3    24.00  0.50     Sequence
             DRB5_0101  172      CTFEYVSQPFLMDLE  EYVSQPFLM  3        0.4643
329.0    26.00  0.53     Sequence
             DRB5_0101  173      TFEYVSQPFLMDLEG  EYVSQPFLM  2        0.4402
426.9    29.00  0.56     Sequence
             DRB5_0101  174      FEYVSQPFLMDLEGK  EYVSQPFLM  1        0.3955
692.3    36.00  0.54     Sequence
             DRB5_0101  175      EYVSQPFLMDLEGKQ  FLMDLEGKQ  6        0.4056
621.2    35.00  0.59     Sequence
             DRB5_0101  176      YVSQPFLMDLEGKQG  FLMDLEGKQ  5        0.4068
613.1    34.00  0.75     Sequence
             DRB5_0101  177      VSQPFLMDLEGKQGN  FLMDLEGKQ  4        0.4206
527.7    32.00  0.76     Sequence
             DRB5_0101  178      SQPFLMDLEGKQGNF  FLMDLEGKQ  3        0.4311
471.3    30.00  0.75     Sequence
             DRB5_0101  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2        0.4681
315.9    25.00  0.56     Sequence
             DRB5_0101  180      PFLMDLEGKQGNFKN  FLMDLEGKQ  1        0.4829
269.0    23.00  0.41     Sequence
             DRB5_0101  181      FLMDLEGKQGNFKNL  LEGKQGNFK  4        0.4673
318.6    25.00  0.61     Sequence
             DRB5_0101  182      LMDLEGKQGNFKNLS  LEGKQGNFK  3        0.4254
501.5    31.00  0.83     Sequence
             DRB5_0101  183      MDLEGKQGNFKNLSE  LEGKQGNFK  2        0.3954
693.5    36.00  0.81     Sequence
             DRB5_0101  184      DLEGKQGNFKNLSEF  LEGKQGNFK  1        0.3533
1093.3    44.00  0.76     Sequence
             DRB5_0101  185      LEGKQGNFKNLSEFV  LEGKQGNFK  0        0.3029
1887.2    55.00  0.65     Sequence
             DRB5_0101  186      EGKQGNFKNLSEFVF  FKNLSEFVF  6        0.2607
2979.0    65.00  0.60     Sequence
             DRB5_0101  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5        0.3920
719.7    37.00  0.54     Sequence
             DRB5_0101  188      KQGNFKNLSEFVFKN  FKNLSEFVF  4        0.4245
506.0    32.00  0.47     Sequence
             DRB5_0101  189      QGNFKNLSEFVFKNI  FKNLSEFVF  3        0.4406
425.1    29.00  0.49     Sequence
             DRB5_0101  190      GNFKNLSEFVFKNID  FKNLSEFVF  2        0.4172
547.8    33.00  0.47     Sequence
             DRB5_0101  191      NFKNLSEFVFKNIDG  FKNLSEFVF  1        0.3657
956.7    42.00  0.41     Sequence
             DRB5_0101  192      FKNLSEFVFKNIDGY  KNLSEFVFK  1        0.3186
1591.6    55.00  0.34     Sequence
             DRB5_0101  193      KNLSEFVFKNIDGYF  FVFKNIDGY  5        0.2903
2162.2    60.00  0.32     Sequence
             DRB5_0101  194      NLSEFVFKNIDGYFK  FKNIDGYFK  6        0.6926
27.8     4.50  0.86     Sequence          WB
```

```
             DRB5_0101  195      LSEFVFKNIDGYFKI  FKNIDGYFK  5        0.7603
13.4     2.00  0.87     Sequence         WB
             DRB5_0101  196      SEFVFKNIDGYFKIY  FKNIDGYFK  4        0.7750
11.4     1.60  0.87     Sequence         SB
             DRB5_0101  197      EFVFKNIDGYFKIYS  FKNIDGYFK  3        0.7842
10.3     1.40  0.88     Sequence         SB
             DRB5_0101  198      FVFKNIDGYFKIYSK  FKNIDGYFK  2        0.7784
11.0     1.60  0.89     Sequence         SB
             DRB5_0101  199      VFKNIDGYFKIYSKH  FKNIDGYFK  1        0.7672
12.4     1.80  0.83     Sequence         SB
             DRB5_0101  200      FKNIDGYFKIYSKHT  FKNIDGYFK  0        0.7531
14.5     2.50  0.58     Sequence         WB
             DRB5_0101  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.6117
66.8     9.50  0.65     Sequence         WB
             DRB5_0101  202      NIDGYFKIYSKHTPI  YFKIYSKHT  4        0.6278
56.1     8.50  0.69     Sequence         WB
             DRB5_0101  203      IDGYFKIYSKHTPIN  YFKIYSKHT  3        0.6287
55.5     8.50  0.70     Sequence         WB
             DRB5_0101  204      DGYFKIYSKHTPINL  YFKIYSKHT  2        0.6170
63.1     9.00  0.63     Sequence         WB
             DRB5_0101  205      GYFKIYSKHTPINLV  YFKIYSKHT  1        0.6100
68.0     9.50  0.63     Sequence         WB
             DRB5_0101  206      YFKIYSKHTPINLVR  YFKIYSKHT  0        0.5391
146.5    16.00  0.43     Sequence
             DRB5_0101  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.4174
546.4    33.00  0.37     Sequence
             DRB5_0101  208      KIYSKHTPINLVRDL  YSKHTPINL  2        0.3830
792.7    38.00  0.39     Sequence
             DRB5_0101  209      IYSKHTPINLVRDLP  YSKHTPINL  1        0.3093
1760.5    55.00  0.36     Sequence
             DRB5_0101  210      YSKHTPINLVRDLPQ  KHTPINLVR  2        0.2618
2943.5    65.00  0.28     Sequence
             DRB5_0101  211      SKHTPINLVRDLPQG  INLVRDLPQ  5        0.2192
4665.8    75.00  0.51     Sequence
             DRB5_0101  212      KHTPINLVRDLPQGF  LVRDLPQGF  6        0.2789
2446.7    60.00  0.47     Sequence
             DRB5_0101  213      HTPINLVRDLPQGFS  LVRDLPQGF  5        0.3353
1328.2    48.00  0.65     Sequence
             DRB5_0101  214      TPINLVRDLPQGFSA  LVRDLPQGF  4        0.3707
906.2    41.00  0.69     Sequence
             DRB5_0101  215      PINLVRDLPQGFSAL  LVRDLPQGF  3        0.3903
733.1    37.00  0.73     Sequence
             DRB5_0101  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.3728
885.2    40.00  0.75     Sequence
             DRB5_0101  217      NLVRDLPQGFSALEP  LVRDLPQGF  1        0.3184
1594.9    55.00  0.74     Sequence
             DRB5_0101  218      LVRDLPQGFSALEPL  LVRDLPQGF  0        0.2417
3656.4    70.00  0.56     Sequence
             DRB5_0101  219      VRDLPQGFSALEPLV  LPQGFSALE  3        0.1452
10392.3    90.00  0.39     Sequence
             DRB5_0101  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.2618
2942.9    65.00  0.71     Sequence
             DRB5_0101  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.3596
1021.9    43.00  0.82     Sequence
             DRB5_0101  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.3686
926.6    41.00  0.85     Sequence
             DRB5_0101  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.3903
732.6    37.00  0.81     Sequence
             DRB5_0101  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.3791
827.5    39.00  0.79     Sequence
             DRB5_0101  225      GFSALEPLVDLPIGI  FSALEPLVD  1        0.3338
1350.3    48.00  0.73     Sequence
             DRB5_0101  226      FSALEPLVDLPIGIN  FSALEPLVD  0        0.2446
3544.3    70.00  0.50     Sequence
             DRB5_0101  227      SALEPLVDLPIGINI  LEPLVDLPI  2        0.1728
7708.3    85.00  0.41     Sequence
```

```
            DRB5_0101  228      ALEPLVDLPIGINIT  PLVDLPIGI  3        0.1721
7769.4    85.00  0.26     Sequence
            DRB5_0101  229      LEPLVDLPIGINITR  LPIGINITR  6        0.2048
5454.1    80.00  0.34     Sequence
            DRB5_0101  230      EPLVDLPIGINITRF  LPIGINITR  5        0.2167
4794.4    75.00  0.41     Sequence
            DRB5_0101  231      PLVDLPIGINITRFQ  LPIGINITR  4        0.2437
3580.6    70.00  0.33     Sequence
            DRB5_0101  232      LVDLPIGINITRFQT  LPIGINITR  3        0.2527
3247.4    65.00  0.31     Sequence
            DRB5_0101  233      VDLPIGINITRFQTL  IGINITRFQ  4        0.2573
3090.0    65.00  0.28     Sequence
            DRB5_0101  234      DLPIGINITRFQTLL  IGINITRFQ  3        0.2604
2989.3    65.00  0.29     Sequence
            DRB5_0101  235      LPIGINITRFQTLLA  ITRFQTLLA  6        0.3101
1745.7    55.00  0.31     Sequence
            DRB5_0101  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.3628
986.4    42.00  0.46     Sequence
            DRB5_0101  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.4003
657.7    35.00  0.45     Sequence
            DRB5_0101  238      GINITRFQTLLALHR  FQTLLALHR  6        0.8232
6.8     0.80  0.89     Sequence        SB
            DRB5_0101  239      INITRFQTLLALHRS  FQTLLALHR  5        0.8423
5.5     0.50  0.90     Sequence        SB
            DRB5_0101  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.8434
5.4     0.50  0.92     Sequence        SB
            DRB5_0101  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.8498
5.1     0.40  0.93     Sequence        SB
            DRB5_0101  242      TRFQTLLALHRSYLT  FQTLLALHR  2        0.8387
5.7     0.60  0.90     Sequence        SB
            DRB5_0101  243      RFQTLLALHRSYLTP  FQTLLALHR  1        0.8187
7.1     0.80  0.90     Sequence        SB
            DRB5_0101  244      FQTLLALHRSYLTPG  FQTLLALHR  0        0.7411
16.5     3.00  0.89     Sequence        WB
            DRB5_0101  245      QTLLALHRSYLTPGD  LALHRSYLT  3        0.2963
2026.9    60.00  0.41     Sequence
            DRB5_0101  246      TLLALHRSYLTPGDS  LALHRSYLT  2        0.2580
3066.0    65.00  0.43     Sequence
            DRB5_0101  247      LLALHRSYLTPGDSS  LALHRSYLT  1        0.2359
3895.4    70.00  0.38     Sequence
            DRB5_0101  248      LALHRSYLTPGDSSS  RSYLTPGDS  4        0.2054
5416.1    80.00  0.34     Sequence
            DRB5_0101  249      ALHRSYLTPGDSSSG  RSYLTPGDS  3        0.1814
7025.4    85.00  0.43     Sequence
            DRB5_0101  250      LHRSYLTPGDSSSGW  RSYLTPGDS  2        0.1746
7557.3    85.00  0.38     Sequence
            DRB5_0101  251      HRSYLTPGDSSSGWT  YLTPGDSSS  3        0.1595
8905.1    90.00  0.40     Sequence
            DRB5_0101  252      RSYLTPGDSSSGWTA  YLTPGDSSS  2        0.1385
11174.3    90.00  0.45     Sequence
            DRB5_0101  253      SYLTPGDSSSGWTAG  YLTPGDSSS  1        0.0936
18156.4   100.00  0.46     Sequence
            DRB5_0101  254      YLTPGDSSSGWTAGA  YLTPGDSSS  0        0.0748
22264.8   100.00  0.25     Sequence
            DRB5_0101  255      LTPGDSSSGWTAGAA  SSSGWTAGA  5        0.0752
22151.6   100.00  0.29     Sequence
            DRB5_0101  256      TPGDSSSGWTAGAAA  SSGWTAGAA  5        0.0895
18987.5   100.00  0.35     Sequence
            DRB5_0101  257      PGDSSSGWTAGAAAY  SSGWTAGAA  4        0.1115
14959.3    95.00  0.31     Sequence
            DRB5_0101  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.2884
2207.3    60.00  0.69     Sequence
            DRB5_0101  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.3998
661.1    36.00  0.75     Sequence
            DRB5_0101  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.4257
499.6    31.00  0.72     Sequence
```

```
             DRB5_0101  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.4403
426.4    29.00  0.74     Sequence
             DRB5_0101  262      SGWTAGAAAYYVGYL  WTAGAAAYY  2        0.4237
510.5    32.00  0.73     Sequence
             DRB5_0101  263      GWTAGAAAYYVGYLQ  WTAGAAAYY  1        0.3892
741.5    37.00  0.69     Sequence
             DRB5_0101  264      WTAGAAAYYVGYLQP  WTAGAAAYY  0        0.3107
1733.3    55.00  0.54     Sequence
             DRB5_0101  265      TAGAAAYYVGYLQPR  YYVGYLQPR  6        0.4312
470.6    30.00  0.65     Sequence
             DRB5_0101  266      AGAAAYYVGYLQPRT  YYVGYLQPR  5        0.4938
239.0    22.00  0.64     Sequence
             DRB5_0101  267      GAAAYYVGYLQPRTF  YYVGYLQPR  4        0.5654
110.2    14.00  0.56     Sequence
             DRB5_0101  268      AAAYYVGYLQPRTFL  YYVGYLQPR  3        0.6168
63.2     9.00  0.48    Sequence        WB
             DRB5_0101  269      AAYYVGYLQPRTFLL  YYVGYLQPR  2        0.6590
40.0     6.50  0.38    Sequence        WB
             DRB5_0101  270      AYYVGYLQPRTFLLK  VGYLQPRTF  3        0.6811
31.5     5.50  0.34    Sequence        WB
             DRB5_0101  271      YYVGYLQPRTFLLKY  YLQPRTFLL  4        0.6518
43.3     7.00  0.34    Sequence        WB
             DRB5_0101  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.5821
92.0    12.00  0.49    Sequence
             DRB5_0101  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.5129
194.5    19.00  0.56     Sequence
             DRB5_0101  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.4246
505.4    31.00  0.67     Sequence
             DRB5_0101  275      YLQPRTFLLKYNENG  YLQPRTFLL  0        0.3307
1397.1    49.00  0.48     Sequence
             DRB5_0101  276      LQPRTFLLKYNENGT  FLLKYNENG  5        0.2339
3980.7    70.00  0.43     Sequence
             DRB5_0101  277      QPRTFLLKYNENGTI  FLLKYNENG  4        0.2401
3721.8    70.00  0.45     Sequence
             DRB5_0101  278      PRTFLLKYNENGTIT  FLLKYNENG  3        0.2604
2986.9    65.00  0.42     Sequence
             DRB5_0101  279      RTFLLKYNENGTITD  FLLKYNENG  2        0.2567
3111.1    65.00  0.38     Sequence
             DRB5_0101  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.2305
4128.6    70.00  0.45     Sequence
             DRB5_0101  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.2000
5742.4    80.00  0.51     Sequence
             DRB5_0101  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.1463
10267.8    90.00  0.55     Sequence
             DRB5_0101  283      LKYNENGTITDAVDC  LKYNENGTI  0        0.0943
18019.2   100.00  0.44     Sequence
             DRB5_0101  284      KYNENGTITDAVDCA  YNENGTITD  1        0.0594
26301.9   100.00  0.28     Sequence
             DRB5_0101  285      YNENGTITDAVDCAL  ITDAVDCAL  6        0.0514
28659.2   100.00  0.23     Sequence
             DRB5_0101  286      NENGTITDAVDCALD  ITDAVDCAL  5        0.0503
29009.3   100.00  0.31     Sequence
             DRB5_0101  287      ENGTITDAVDCALDP  ITDAVDCAL  4        0.0552
27508.7   100.00  0.31     Sequence
             DRB5_0101  288      NGTITDAVDCALDPL  ITDAVDCAL  3        0.0619
25588.9   100.00  0.31     Sequence
             DRB5_0101  289      GTITDAVDCALDPLS  DAVDCALDP  4        0.0641
25002.4   100.00  0.28     Sequence
             DRB5_0101  290      TITDAVDCALDPLSE  DAVDCALDP  3        0.0665
24361.3   100.00  0.25     Sequence
             DRB5_0101  291      ITDAVDCALDPLSET  DCALDPLSE  5        0.0628
25349.2   100.00  0.25     Sequence
             DRB5_0101  292      TDAVDCALDPLSETK  ALDPLSETK  6        0.0859
19738.7   100.00  0.35     Sequence
             DRB5_0101  293      DAVDCALDPLSETKC  ALDPLSETK  5        0.0934
18201.2   100.00  0.46     Sequence
```

```
             DRB5_0101  294      AVDCALDPLSETKCT  ALDPLSETK  4        0.1000
16941.6   100.00  0.50     Sequence
             DRB5_0101  295      VDCALDPLSETKCTL  ALDPLSETK  3        0.1024
16507.0    95.00  0.51     Sequence
             DRB5_0101  296      DCALDPLSETKCTLK  ALDPLSETK  2        0.1227
13260.8    95.00  0.34     Sequence
             DRB5_0101  297      CALDPLSETKCTLKS  LSETKCTLK  5        0.1532
9533.8    90.00  0.46     Sequence
             DRB5_0101  298      ALDPLSETKCTLKSF  LSETKCTLK  4        0.1598
8869.4    90.00  0.49     Sequence
             DRB5_0101  299      LDPLSETKCTLKSFT  LSETKCTLK  3        0.1668
8227.2    85.00  0.55     Sequence
             DRB5_0101  300      DPLSETKCTLKSFTV  LSETKCTLK  2        0.1791
7201.5    85.00  0.39     Sequence
             DRB5_0101  301      PLSETKCTLKSFTVE  LSETKCTLK  1        0.1846
6783.3    80.00  0.32     Sequence
             DRB5_0101  302      LSETKCTLKSFTVEK  TLKSFTVEK  6        0.2664
2799.2    65.00  0.49     Sequence
             DRB5_0101  303      SETKCTLKSFTVEKG  TLKSFTVEK  5        0.2869
2242.9    60.00  0.58     Sequence
             DRB5_0101  304      ETKCTLKSFTVEKGI  TLKSFTVEK  4        0.3077
1790.3    55.00  0.64     Sequence
             DRB5_0101  305      TKCTLKSFTVEKGIY  TLKSFTVEK  3        0.3146
1661.4    55.00  0.63     Sequence
             DRB5_0101  306      KCTLKSFTVEKGIYQ  FTVEKGIYQ  6        0.4371
441.7    30.00  0.60     Sequence
             DRB5_0101  307      CTLKSFTVEKGIYQT  FTVEKGIYQ  5        0.4719
303.1    24.00  0.78     Sequence
             DRB5_0101  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.4857
261.1    23.00  0.83     Sequence
             DRB5_0101  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.4704
308.0    25.00  0.92     Sequence
             DRB5_0101  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.4389
433.0    29.00  0.90     Sequence
             DRB5_0101  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.4694
311.4    25.00  0.57     Sequence
             DRB5_0101  312      FTVEKGIYQTSNFRV  GIYQTSNFR  5        0.5249
170.7    18.00  0.47     Sequence
             DRB5_0101  313      TVEKGIYQTSNFRVQ  GIYQTSNFR  4        0.5380
148.2    16.00  0.58     Sequence
             DRB5_0101  314      VEKGIYQTSNFRVQP  GIYQTSNFR  3        0.5310
160.0    17.00  0.57     Sequence
             DRB5_0101  315      EKGIYQTSNFRVQPT  GIYQTSNFR  2        0.5188
182.4    19.00  0.51     Sequence
             DRB5_0101  316      KGIYQTSNFRVQPTE  GIYQTSNFR  1        0.4932
240.8    22.00  0.49     Sequence
             DRB5_0101  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.3926
714.9    37.00  0.50     Sequence
             DRB5_0101  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.4177
544.9    33.00  0.73     Sequence
             DRB5_0101  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.4904
248.2    22.00  0.87     Sequence
             DRB5_0101  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.5773
96.9    13.00  0.75     Sequence
             DRB5_0101  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.6124
66.3     9.50  0.70     Sequence          WB
             DRB5_0101  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.5948
80.2    11.00  0.64     Sequence
             DRB5_0101  323      NFRVQPTESIVRFPN  FRVQPTESI  1        0.5639
112.0    14.00  0.57     Sequence
             DRB5_0101  324      FRVQPTESIVRFPNI  VQPTESIVR  2        0.4649
327.0    25.00  0.45     Sequence
             DRB5_0101  325      RVQPTESIVRFPNIT  VQPTESIVR  1        0.3196
1574.8    55.00  0.73     Sequence
             DRB5_0101  326      VQPTESIVRFPNITN  VQPTESIVR  0        0.2492
3373.5    70.00  0.47     Sequence
```

```
             DRB5_0101  327      QPTESIVRFPNITNL  IVRFPNITN  5        0.2029
5568.7    80.00  0.52     Sequence
             DRB5_0101  328      PTESIVRFPNITNLC  IVRFPNITN  4        0.2101
5146.3    75.00  0.54     Sequence
             DRB5_0101  329      TESIVRFPNITNLCP  IVRFPNITN  3        0.2226
4495.2    75.00  0.44     Sequence
             DRB5_0101  330      ESIVRFPNITNLCPF  IVRFPNITN  2        0.2279
4247.1    75.00  0.38     Sequence
             DRB5_0101  331      SIVRFPNITNLCPFG  IVRFPNITN  1        0.2133
4974.7    75.00  0.38     Sequence
             DRB5_0101  332      IVRFPNITNLCPFGE  ITNLCPFGE  6        0.2771
2493.8    60.00  0.49     Sequence
             DRB5_0101  333      VRFPNITNLCPFGEV  ITNLCPFGE  5        0.3078
1788.7    55.00  0.65     Sequence
             DRB5_0101  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.3124
1702.8    55.00  0.70     Sequence
             DRB5_0101  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.2954
2046.6    60.00  0.77     Sequence
             DRB5_0101  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.2669
2784.8    65.00  0.75     Sequence
             DRB5_0101  337      NITNLCPFGEVFNAT  ITNLCPFGE  1        0.2537
3211.7    65.00  0.65     Sequence
             DRB5_0101  338      ITNLCPFGEVFNATR  FGEVFNATR  6        0.4545
365.9    27.00  0.75     Sequence
             DRB5_0101  339      TNLCPFGEVFNATRF  FGEVFNATR  5        0.5296
162.2    17.00  0.87     Sequence
             DRB5_0101  340      NLCPFGEVFNATRFA  FGEVFNATR  4        0.5850
89.1    12.00  0.86     Sequence
             DRB5_0101  341      LCPFGEVFNATRFAS  FGEVFNATR  3        0.6145
64.8     9.50  0.83     Sequence         WB
             DRB5_0101  342      CPFGEVFNATRFASV  FGEVFNATR  2        0.6044
72.2    10.00  0.75     Sequence
             DRB5_0101  343      PFGEVFNATRFASVY  FGEVFNATR  1        0.5894
85.0    12.00  0.71     Sequence
             DRB5_0101  344      FGEVFNATRFASVYA  FGEVFNATR  0        0.5248
170.9    18.00  0.54     Sequence
             DRB5_0101  345      GEVFNATRFASVYAW  FNATRFASV  3        0.4123
577.4    33.00  0.43     Sequence
             DRB5_0101  346      EVFNATRFASVYAWN  FNATRFASV  2        0.4170
549.1    33.00  0.37     Sequence
             DRB5_0101  347      VFNATRFASVYAWNR  FASVYAWNR  6        0.6590
40.0     6.50  0.70     Sequence         WB
             DRB5_0101  348      FNATRFASVYAWNRK  FASVYAWNR  5        0.7395
16.8     3.00  0.74     Sequence         WB
             DRB5_0101  349      NATRFASVYAWNRKR  FASVYAWNR  4        0.8038
8.4     1.10  0.64     Sequence         SB
             DRB5_0101  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.8242
6.7     0.80  0.62     Sequence         SB
             DRB5_0101  351      TRFASVYAWNRKRIS  FASVYAWNR  2        0.8232
6.8     0.80  0.57     Sequence         SB
             DRB5_0101  352      RFASVYAWNRKRISN  FASVYAWNR  1        0.8076
8.0     1.00  0.54     Sequence         SB
             DRB5_0101  353      FASVYAWNRKRISNC  FASVYAWNR  0        0.7236
19.9     3.50  0.44     Sequence         WB
             DRB5_0101  354      ASVYAWNRKRISNCV  SVYAWNRKR  1        0.5544
124.1    15.00  0.51     Sequence
             DRB5_0101  355      SVYAWNRKRISNCVA  SVYAWNRKR  0        0.4765
288.3    24.00  0.37     Sequence
             DRB5_0101  356      VYAWNRKRISNCVAD  YAWNRKRIS  1        0.3322
1374.0    48.00  0.22     Sequence
             DRB5_0101  357      YAWNRKRISNCVADY  WNRKRISNC  2        0.2610
2968.5    65.00  0.31     Sequence
             DRB5_0101  358      AWNRKRISNCVADYS  WNRKRISNC  1        0.2319
4067.1    70.00  0.27     Sequence
             DRB5_0101  359      WNRKRISNCVADYSV  ISNCVADYS  5        0.2367
3862.4    70.00  0.38     Sequence
```

```
             DRB5_0101  360      NRKRISNCVADYSVL  ISNCVADYS  4        0.2280
4243.3    75.00  0.56     Sequence
             DRB5_0101  361      RKRISNCVADYSVLY  ISNCVADYS  3        0.2450
3528.4    70.00  0.53     Sequence
             DRB5_0101  362      KRISNCVADYSVLYN  ISNCVADYS  2        0.2189
4682.9    75.00  0.48     Sequence
             DRB5_0101  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.2040
5498.8    80.00  0.47     Sequence
             DRB5_0101  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.1875
6576.3    80.00  0.56     Sequence
             DRB5_0101  365      SNCVADYSVLYNSAS  YSVLYNSAS  6        0.2444
3550.7    70.00  0.54     Sequence
             DRB5_0101  366      NCVADYSVLYNSASF  YSVLYNSAS  5        0.2990
1968.6    55.00  0.63     Sequence
             DRB5_0101  367      CVADYSVLYNSASFS  YSVLYNSAS  4        0.3432
1219.6    46.00  0.67     Sequence
             DRB5_0101  368      VADYSVLYNSASFST  YSVLYNSAS  3        0.3908
729.0    37.00  0.55     Sequence
             DRB5_0101  369      ADYSVLYNSASFSTF  YSVLYNSAS  2        0.4004
656.5    35.00  0.44     Sequence
             DRB5_0101  370      DYSVLYNSASFSTFK  NSASFSTFK  6        0.5099
200.9    20.00  0.35     Sequence
             DRB5_0101  371      YSVLYNSASFSTFKC  NSASFSTFK  5        0.5511
128.7    15.00  0.51     Sequence
             DRB5_0101  372      SVLYNSASFSTFKCY  NSASFSTFK  4        0.5507
129.2    15.00  0.58     Sequence
             DRB5_0101  373      VLYNSASFSTFKCYG  NSASFSTFK  3        0.5348
153.4    17.00  0.63     Sequence
             DRB5_0101  374      LYNSASFSTFKCYGV  NSASFSTFK  2        0.5042
213.7    20.00  0.59     Sequence
             DRB5_0101  375      YNSASFSTFKCYGVS  NSASFSTFK  1        0.4522
375.2    27.00  0.56     Sequence
             DRB5_0101  376      NSASFSTFKCYGVSP  NSASFSTFK  0        0.3515
1114.7    44.00  0.41     Sequence
             DRB5_0101  377      SASFSTFKCYGVSPT  FSTFKCYGV  3        0.2642
2867.7    65.00  0.52     Sequence
             DRB5_0101  378      ASFSTFKCYGVSPTK  FSTFKCYGV  2        0.2931
2097.7    60.00  0.35     Sequence
             DRB5_0101  379      SFSTFKCYGVSPTKL  CYGVSPTKL  6        0.4454
403.8    28.00  0.47     Sequence
             DRB5_0101  380      FSTFKCYGVSPTKLN  CYGVSPTKL  5        0.5051
211.6    20.00  0.56     Sequence
             DRB5_0101  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.5184
183.2    19.00  0.62     Sequence
             DRB5_0101  382      TFKCYGVSPTKLNDL  CYGVSPTKL  3        0.5379
148.3    16.00  0.64     Sequence
             DRB5_0101  383      FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.5084
204.1    20.00  0.65     Sequence
             DRB5_0101  384      KCYGVSPTKLNDLCF  CYGVSPTKL  1        0.4354
449.6    30.00  0.65     Sequence
             DRB5_0101  385      CYGVSPTKLNDLCFT  CYGVSPTKL  0        0.3037
1869.3    55.00  0.51     Sequence
             DRB5_0101  386      YGVSPTKLNDLCFTN  PTKLNDLCF  4        0.1562
9227.0    90.00  0.36     Sequence
             DRB5_0101  387      GVSPTKLNDLCFTNV  PTKLNDLCF  3        0.1323
11951.6    95.00  0.55     Sequence
             DRB5_0101  388      VSPTKLNDLCFTNVY  PTKLNDLCF  2        0.1383
11198.5    90.00  0.42     Sequence
             DRB5_0101  389      SPTKLNDLCFTNVYA  PTKLNDLCF  1        0.1420
10752.9    90.00  0.31     Sequence
             DRB5_0101  390      PTKLNDLCFTNVYAD  NDLCFTNVY  4        0.1286
12437.8    95.00  0.25     Sequence
             DRB5_0101  391      TKLNDLCFTNVYADS  NDLCFTNVY  3        0.1190
13797.7    95.00  0.34     Sequence
             DRB5_0101  392      KLNDLCFTNVYADSF  FTNVYADSF  6        0.2333
4006.8    70.00  0.71     Sequence
```

```
             DRB5_0101  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.3300
1406.3    49.00  0.81     Sequence
             DRB5_0101  394      NDLCFTNVYADSFVI  FTNVYADSF  4        0.3744
870.3    40.00  0.80     Sequence
             DRB5_0101  395      DLCFTNVYADSFVIR  FTNVYADSF  3        0.4604
343.1    26.00  0.63     Sequence
             DRB5_0101  396      LCFTNVYADSFVIRG  FTNVYADSF  2        0.4742
295.5    24.00  0.58     Sequence
             DRB5_0101  397      CFTNVYADSFVIRGD  FTNVYADSF  1        0.4390
432.8    29.00  0.49     Sequence
             DRB5_0101  398      FTNVYADSFVIRGDE  VYADSFVIR  3        0.3754
861.4    40.00  0.37     Sequence
             DRB5_0101  399      TNVYADSFVIRGDEV  VYADSFVIR  2        0.2980
1988.6    55.00  0.50     Sequence
             DRB5_0101  400      NVYADSFVIRGDEVR  FVIRGDEVR  6        0.3460
1182.9    45.00  0.41     Sequence
             DRB5_0101  401      VYADSFVIRGDEVRQ  FVIRGDEVR  5        0.3640
974.3    42.00  0.55     Sequence
             DRB5_0101  402      YADSFVIRGDEVRQI  FVIRGDEVR  4        0.3613
1002.4    43.00  0.66     Sequence
             DRB5_0101  403      ADSFVIRGDEVRQIA  FVIRGDEVR  3        0.3783
834.6    39.00  0.67     Sequence
             DRB5_0101  404      DSFVIRGDEVRQIAP  FVIRGDEVR  2        0.3563
1058.2    43.00  0.66     Sequence
             DRB5_0101  405      SFVIRGDEVRQIAPG  FVIRGDEVR  1        0.3449
1197.7    46.00  0.62     Sequence
             DRB5_0101  406      FVIRGDEVRQIAPGQ  FVIRGDEVR  0        0.3009
1928.6    55.00  0.47     Sequence
             DRB5_0101  407      VIRGDEVRQIAPGQT  VRQIAPGQT  6        0.2803
2408.5    60.00  0.41     Sequence
             DRB5_0101  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.3273
1449.4    49.00  0.55     Sequence
             DRB5_0101  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.3655
957.9    42.00  0.57     Sequence
             DRB5_0101  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.3799
820.4    39.00  0.63     Sequence
             DRB5_0101  411      DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.3587
1031.8    43.00  0.58     Sequence
             DRB5_0101  412      EVRQIAPGQTGTIAD  VRQIAPGQT  1        0.3334
1355.6    48.00  0.59     Sequence
             DRB5_0101  413      VRQIAPGQTGTIADY  VRQIAPGQT  0        0.2496
3356.6    70.00  0.52     Sequence
             DRB5_0101  414      RQIAPGQTGTIADYN  IAPGQTGTI  2        0.1351
11592.6    90.00  0.55     Sequence
             DRB5_0101  415      QIAPGQTGTIADYNY  IAPGQTGTI  1        0.1009
16783.5    95.00  0.49     Sequence
             DRB5_0101  416      IAPGQTGTIADYNYK  GTIADYNYK  6        0.1370
11353.0    90.00  0.47     Sequence
             DRB5_0101  417      APGQTGTIADYNYKL  GTIADYNYK  5        0.1966
5961.5    80.00  0.43     Sequence
             DRB5_0101  418      PGQTGTIADYNYKLP  GTIADYNYK  4        0.2003
5727.9    80.00  0.40     Sequence
             DRB5_0101  419      GQTGTIADYNYKLPD  GTIADYNYK  3        0.1989
5810.7    80.00  0.42     Sequence
             DRB5_0101  420      QTGTIADYNYKLPDD  TIADYNYKL  3        0.1795
7170.5    85.00  0.44     Sequence
             DRB5_0101  421      TGTIADYNYKLPDDF  YNYKLPDDF  6        0.2008
5696.1    80.00  0.40     Sequence
             DRB5_0101  422      GTIADYNYKLPDDFT  YNYKLPDDF  5        0.2308
4115.2    70.00  0.56     Sequence
             DRB5_0101  423      TIADYNYKLPDDFTG  YNYKLPDDF  4        0.2417
3658.5    70.00  0.63     Sequence
             DRB5_0101  424      IADYNYKLPDDFTGC  YNYKLPDDF  3        0.2451
3526.4    70.00  0.64     Sequence
             DRB5_0101  425      ADYNYKLPDDFTGCV  YNYKLPDDF  2        0.2371
3843.4    70.00  0.57     Sequence
```

```
              DRB5_0101  426      DYNYKLPDDFTGCVI  YNYKLPDDF  1        0.2164
4808.3    75.00  0.54     Sequence
              DRB5_0101  427      YNYKLPDDFTGCVIA  YNYKLPDDF  0        0.1806
7087.2    85.00  0.42     Sequence
              DRB5_0101  428      NYKLPDDFTGCVIAW  YKLPDDFTG  1        0.1055
15963.2    95.00  0.52     Sequence
              DRB5_0101  429      YKLPDDFTGCVIAWN  FTGCVIAWN  6        0.1239
13081.4    95.00  0.44     Sequence
              DRB5_0101  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.1422
10729.1    90.00  0.54     Sequence
              DRB5_0101  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.1549
9352.5    90.00  0.55     Sequence
              DRB5_0101  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.2019
5625.9    80.00  0.39     Sequence
              DRB5_0101  433      DDFTGCVIAWNSNNL  VIAWNSNNL  6        0.2783
2461.4    60.00  0.29     Sequence
              DRB5_0101  434      DFTGCVIAWNSNNLD  VIAWNSNNL  5        0.3037
1870.5    55.00  0.38     Sequence
              DRB5_0101  435      FTGCVIAWNSNNLDS  VIAWNSNNL  4        0.3120
1708.9    55.00  0.44     Sequence
              DRB5_0101  436      TGCVIAWNSNNLDSK  VIAWNSNNL  3        0.3211
1549.5    55.00  0.55     Sequence
              DRB5_0101  437      GCVIAWNSNNLDSKV  VIAWNSNNL  2        0.3074
1797.6    55.00  0.56     Sequence
              DRB5_0101  438      CVIAWNSNNLDSKVG  VIAWNSNNL  1        0.2632
2898.1    65.00  0.53     Sequence
              DRB5_0101  439      VIAWNSNNLDSKVGG  VIAWNSNNL  0        0.2022
5610.9    80.00  0.45     Sequence
              DRB5_0101  440      IAWNSNNLDSKVGGN  WNSNNLDSK  2        0.1237
13115.4    95.00  0.34     Sequence
              DRB5_0101  441      AWNSNNLDSKVGGNY  WNSNNLDSK  1        0.1201
13640.2    95.00  0.23     Sequence
              DRB5_0101  442      WNSNNLDSKVGGNYN  LDSKVGGNY  5        0.1147
14460.7    95.00  0.33     Sequence
              DRB5_0101  443      NSNNLDSKVGGNYNY  LDSKVGGNY  4        0.1131
14707.1    95.00  0.39     Sequence
              DRB5_0101  444      SNNLDSKVGGNYNYL  LDSKVGGNY  3        0.1286
12433.4    95.00  0.34     Sequence
              DRB5_0101  445      NNLDSKVGGNYNYLY  LDSKVGGNY  2        0.1395
11048.4    90.00  0.25     Sequence
              DRB5_0101  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.1740
7613.5    85.00  0.25     Sequence
              DRB5_0101  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4        0.1919
6272.5    80.00  0.31     Sequence
              DRB5_0101  448      DSKVGGNYNYLYRLF  VGGNYNYLY  3        0.2093
5192.8    75.00  0.32     Sequence
              DRB5_0101  449      SKVGGNYNYLYRLFR  YNYLYRLFR  6        0.5706
104.1    13.00  0.82     Sequence
              DRB5_0101  450      KVGGNYNYLYRLFRK  YNYLYRLFR  5        0.6904
28.5     5.00  0.62     Sequence         WB
              DRB5_0101  451      VGGNYNYLYRLFRKS  YNYLYRLFR  4        0.7039
24.6     4.00  0.62     Sequence         WB
              DRB5_0101  452      GGNYNYLYRLFRKSN  YNYLYRLFR  3        0.7114
22.7     4.00  0.61     Sequence         WB
              DRB5_0101  453      GNYNYLYRLFRKSNL  YNYLYRLFR  2        0.7080
23.5     4.00  0.52     Sequence         WB
              DRB5_0101  454      NYNYLYRLFRKSNLK  YNYLYRLFR  1        0.7262
19.3     3.50  0.43     Sequence         WB
              DRB5_0101  455      YNYLYRLFRKSNLKP  YNYLYRLFR  0        0.7051
24.3     4.00  0.35     Sequence         WB
              DRB5_0101  456      NYLYRLFRKSNLKPF  RLFRKSNLK  4        0.6303
54.6     8.50  0.43     Sequence         WB
              DRB5_0101  457      YLYRLFRKSNLKPFE  RLFRKSNLK  3        0.6115
66.9     9.50  0.48     Sequence         WB
              DRB5_0101  458      LYRLFRKSNLKPFER  RLFRKSNLK  2        0.6352
51.8     8.00  0.32     Sequence         WB
```

```
             DRB5_0101  459      YRLFRKSNLKPFERD  KSNLKPFER  5        0.6231
59.0     9.00  0.41     Sequence         WB
             DRB5_0101  460      RLFRKSNLKPFERDI  KSNLKPFER  4        0.5976
77.8    11.00  0.51     Sequence
             DRB5_0101  461      LFRKSNLKPFERDIS  KSNLKPFER  3        0.5393
146.1    16.00  0.68     Sequence
             DRB5_0101  462      FRKSNLKPFERDIST  KSNLKPFER  2        0.4757
290.9    24.00  0.79     Sequence
             DRB5_0101  463      RKSNLKPFERDISTE  KSNLKPFER  1        0.3948
697.8    36.00  0.88     Sequence
             DRB5_0101  464      KSNLKPFERDISTEI  KSNLKPFER  0        0.2930
2099.6    60.00  0.60     Sequence
             DRB5_0101  465      SNLKPFERDISTEIY  FERDISTEI  5        0.2161
4824.8    75.00  0.70     Sequence
             DRB5_0101  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.2495
3362.1    70.00  0.71     Sequence
             DRB5_0101  467      LKPFERDISTEIYQA  FERDISTEI  3        0.2768
2502.5    60.00  0.70     Sequence
             DRB5_0101  468      KPFERDISTEIYQAG  FERDISTEI  2        0.2529
3240.9    65.00  0.69     Sequence
             DRB5_0101  469      PFERDISTEIYQAGS  FERDISTEI  1        0.2031
5557.0    80.00  0.65     Sequence
             DRB5_0101  470      FERDISTEIYQAGST  FERDISTEI  0        0.1478
10101.0    90.00  0.54     Sequence
             DRB5_0101  471      ERDISTEIYQAGSTP  TEIYQAGST  5        0.0880
19300.7   100.00  0.25     Sequence
             DRB5_0101  472      RDISTEIYQAGSTPC  IYQAGSTPC  6        0.1530
9546.8    90.00  0.53     Sequence
             DRB5_0101  473      DISTEIYQAGSTPCN  IYQAGSTPC  5        0.2165
4801.9    75.00  0.60     Sequence
             DRB5_0101  474      ISTEIYQAGSTPCNG  IYQAGSTPC  4        0.2411
3681.8    70.00  0.57     Sequence
             DRB5_0101  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.2652
2835.3    65.00  0.59     Sequence
             DRB5_0101  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.2826
2350.1    60.00  0.45     Sequence
             DRB5_0101  477      EIYQAGSTPCNGVKG  IYQAGSTPC  1        0.2779
2471.7    60.00  0.35     Sequence
             DRB5_0101  478      IYQAGSTPCNGVKGF  GSTPCNGVK  4        0.2497
3355.7    70.00  0.36     Sequence
             DRB5_0101  479      YQAGSTPCNGVKGFN  GSTPCNGVK  3        0.2040
5500.9    80.00  0.50     Sequence
             DRB5_0101  480      QAGSTPCNGVKGFNC  GSTPCNGVK  2        0.2043
5485.1    80.00  0.37     Sequence
             DRB5_0101  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.2120
5044.0    75.00  0.37     Sequence
             DRB5_0101  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.2059
5386.9    80.00  0.47     Sequence
             DRB5_0101  483      STPCNGVKGFNCYFP  CNGVKGFNC  3        0.1879
6544.1    80.00  0.51     Sequence
             DRB5_0101  484      TPCNGVKGFNCYFPL  CNGVKGFNC  2        0.1915
6296.8    80.00  0.46     Sequence
             DRB5_0101  485      PCNGVKGFNCYFPLQ  CNGVKGFNC  1        0.1943
6107.7    80.00  0.36     Sequence
             DRB5_0101  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.2854
2279.1    60.00  0.49     Sequence
             DRB5_0101  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.2910
2145.6    60.00  0.61     Sequence
             DRB5_0101  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.2941
2074.1    60.00  0.68     Sequence
             DRB5_0101  489      VKGFNCYFPLQSYGF  YFPLQSYGF  6        0.5897
84.7    12.00  0.76     Sequence
             DRB5_0101  490      KGFNCYFPLQSYGFQ  YFPLQSYGF  5        0.6419
48.2     7.50  0.82     Sequence         WB
             DRB5_0101  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.6365
51.0     8.00  0.83     Sequence         WB
```

```
             DRB5_0101  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.6405
48.9     7.50  0.88     Sequence         WB
             DRB5_0101  493      NCYFPLQSYGFQPTY  YFPLQSYGF  2        0.6080
69.5    10.00  0.89     Sequence
             DRB5_0101  494      CYFPLQSYGFQPTYG  YFPLQSYGF  1        0.5660
109.5    14.00  0.85     Sequence
             DRB5_0101  495      YFPLQSYGFQPTYGV  YFPLQSYGF  0        0.5171
185.9    19.00  0.60     Sequence
             DRB5_0101  496      FPLQSYGFQPTYGVG  YGFQPTYGV  5        0.3428
1224.9    46.00  0.71     Sequence
             DRB5_0101  497      PLQSYGFQPTYGVGY  YGFQPTYGV  4        0.4611
340.7    26.00  0.46     Sequence
             DRB5_0101  498      LQSYGFQPTYGVGYQ  FQPTYGVGY  5        0.5221
176.0    18.00  0.54     Sequence
             DRB5_0101  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4        0.5109
198.8    19.00  0.58     Sequence
             DRB5_0101  500      SYGFQPTYGVGYQPY  FQPTYGVGY  3        0.5029
216.7    20.00  0.61     Sequence
             DRB5_0101  501      YGFQPTYGVGYQPYR  FQPTYGVGY  2        0.4852
262.5    23.00  0.55     Sequence
             DRB5_0101  502      GFQPTYGVGYQPYRV  FQPTYGVGY  1        0.4704
308.0    25.00  0.46     Sequence
             DRB5_0101  503      FQPTYGVGYQPYRVV  YGVGYQPYR  4        0.4492
387.4    28.00  0.41     Sequence
             DRB5_0101  504      QPTYGVGYQPYRVVV  YGVGYQPYR  3        0.4387
434.1    29.00  0.51     Sequence
             DRB5_0101  505      PTYGVGYQPYRVVVL  YGVGYQPYR  2        0.4410
423.6    29.00  0.44     Sequence
             DRB5_0101  506      TYGVGYQPYRVVVLS  YGVGYQPYR  1        0.4246
505.5    31.00  0.43     Sequence
             DRB5_0101  507      YGVGYQPYRVVVLSF  YGVGYQPYR  0        0.3919
719.8    37.00  0.28     Sequence
             DRB5_0101  508      GVGYQPYRVVVLSFE  PYRVVVLSF  5        0.3407
1253.7    47.00  0.28     Sequence
             DRB5_0101  509      VGYQPYRVVVLSFEL  PYRVVVLSF  4        0.3516
1113.5    44.00  0.28     Sequence
             DRB5_0101  510      GYQPYRVVVLSFELL  YRVVVLSFE  4        0.3735
879.2    40.00  0.31     Sequence
             DRB5_0101  511      YQPYRVVVLSFELLH  YRVVVLSFE  3        0.3972
679.8    36.00  0.28     Sequence
             DRB5_0101  512      QPYRVVVLSFELLHA  VVLSFELLH  5        0.4242
507.9    32.00  0.28     Sequence
             DRB5_0101  513      PYRVVVLSFELLHAP  VVLSFELLH  4        0.4007
654.5    35.00  0.31     Sequence
             DRB5_0101  514      YRVVVLSFELLHAPA  VVLSFELLH  3        0.3905
731.4    37.00  0.35     Sequence
             DRB5_0101  515      RVVVLSFELLHAPAT  FELLHAPAT  6        0.4291
481.6    31.00  0.40     Sequence
             DRB5_0101  516      VVVLSFELLHAPATV  FELLHAPAT  5        0.4706
307.3    25.00  0.62     Sequence
             DRB5_0101  517      VVLSFELLHAPATVC  FELLHAPAT  4        0.4745
294.5    24.00  0.64     Sequence
             DRB5_0101  518      VLSFELLHAPATVCG  FELLHAPAT  3        0.4728
300.1    24.00  0.69     Sequence
             DRB5_0101  519      LSFELLHAPATVCGP  FELLHAPAT  2        0.4453
404.2    28.00  0.70     Sequence
             DRB5_0101  520      SFELLHAPATVCGPK  FELLHAPAT  1        0.4153
558.8    33.00  0.64     Sequence
             DRB5_0101  521      FELLHAPATVCGPKK  FELLHAPAT  0        0.3816
804.8    39.00  0.43     Sequence
             DRB5_0101  522      ELLHAPATVCGPKKS  PATVCGPKK  5        0.3314
1385.3    48.00  0.40     Sequence
             DRB5_0101  523      LLHAPATVCGPKKST  PATVCGPKK  4        0.3355
1326.4    48.00  0.43     Sequence
             DRB5_0101  524      LHAPATVCGPKKSTN  PATVCGPKK  3        0.3231
1515.7    50.00  0.50     Sequence
```

```
             DRB5_0101  525      HAPATVCGPKKSTNL  ATVCGPKKS  3        0.3571
1049.9    43.00  0.41     Sequence
             DRB5_0101  526      APATVCGPKKSTNLV  ATVCGPKKS  2        0.3534
1091.9    44.00  0.39     Sequence
             DRB5_0101  527      PATVCGPKKSTNLVK  PKKSTNLVK  6        0.4451
404.9    28.00  0.49     Sequence
             DRB5_0101  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5        0.4639
330.4    26.00  0.62     Sequence
             DRB5_0101  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.4926
242.3    22.00  0.73     Sequence
             DRB5_0101  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3        0.4818
272.2    23.00  0.73     Sequence
             DRB5_0101  531      CGPKKSTNLVKNKCV  PKKSTNLVK  2        0.4601
344.4    26.00  0.62     Sequence
             DRB5_0101  532      GPKKSTNLVKNKCVN  PKKSTNLVK  1        0.4479
392.9    28.00  0.55     Sequence
             DRB5_0101  533      PKKSTNLVKNKCVNF  TNLVKNKCV  4        0.3835
788.4    38.00  0.41     Sequence
             DRB5_0101  534      KKSTNLVKNKCVNFN  TNLVKNKCV  3        0.3233
1512.5    50.00  0.63     Sequence
             DRB5_0101  535      KSTNLVKNKCVNFNF  TNLVKNKCV  2        0.2878
2222.4    60.00  0.56     Sequence
             DRB5_0101  536      STNLVKNKCVNFNFN  TNLVKNKCV  1        0.2360
3891.1    70.00  0.47     Sequence
             DRB5_0101  537      TNLVKNKCVNFNFNG  TNLVKNKCV  0        0.1806
7087.9    85.00  0.28     Sequence
             DRB5_0101  538      NLVKNKCVNFNFNGL  VKNKCVNFN  2        0.1508
9775.3    90.00  0.39     Sequence
             DRB5_0101  539      LVKNKCVNFNFNGLT  VNFNFNGLT  6        0.1656
8329.3    85.00  0.26     Sequence
             DRB5_0101  540      VKNKCVNFNFNGLTG  VNFNFNGLT  5        0.1736
7638.5    85.00  0.39     Sequence
             DRB5_0101  541      KNKCVNFNFNGLTGT  VNFNFNGLT  4        0.1833
6881.0    85.00  0.47     Sequence
             DRB5_0101  542      NKCVNFNFNGLTGTG  VNFNFNGLT  3        0.1898
6416.5    80.00  0.50     Sequence
             DRB5_0101  543      KCVNFNFNGLTGTGV  FNGLTGTGV  6        0.3502
1131.3    45.00  0.63     Sequence
             DRB5_0101  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5        0.4348
452.5    30.00  0.75     Sequence
             DRB5_0101  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.4624
335.9    26.00  0.80     Sequence
             DRB5_0101  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3        0.4601
344.2    26.00  0.86     Sequence
             DRB5_0101  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.4293
480.6    31.00  0.87     Sequence
             DRB5_0101  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.3630
984.5    42.00  0.86     Sequence
             DRB5_0101  549      FNGLTGTGVLTESNK  FNGLTGTGV  0        0.2526
3251.7    65.00  0.76     Sequence
             DRB5_0101  550      NGLTGTGVLTESNKK  GVLTESNKK  6        0.2564
3118.4    65.00  0.69     Sequence
             DRB5_0101  551      GLTGTGVLTESNKKF  GVLTESNKK  5        0.3791
827.4    39.00  0.47     Sequence
             DRB5_0101  552      LTGTGVLTESNKKFL  GVLTESNKK  4        0.4473
395.6    28.00  0.41     Sequence
             DRB5_0101  553      TGTGVLTESNKKFLP  VLTESNKKF  4        0.4362
446.0    30.00  0.44     Sequence
             DRB5_0101  554      GTGVLTESNKKFLPF  VLTESNKKF  3        0.4318
467.5    30.00  0.50     Sequence
             DRB5_0101  555      TGVLTESNKKFLPFQ  VLTESNKKF  2        0.3917
722.1    37.00  0.49     Sequence
             DRB5_0101  556      GVLTESNKKFLPFQQ  VLTESNKKF  1        0.3557
1065.4    44.00  0.42     Sequence
             DRB5_0101  557      VLTESNKKFLPFQQF  NKKFLPFQQ  5        0.2723
2626.6    65.00  0.33     Sequence
```

```
             DRB5_0101  558      LTESNKKFLPFQQFG  NKKFLPFQQ  4        0.2370
3847.2    70.00  0.46     Sequence
             DRB5_0101  559      TESNKKFLPFQQFGR  FLPFQQFGR  6        0.5640
111.9    14.00  0.77     Sequence
             DRB5_0101  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5        0.5954
79.7    11.00  0.82     Sequence
             DRB5_0101  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4        0.6113
67.1     9.50  0.86     Sequence         WB
             DRB5_0101  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.6237
58.6     8.50  0.88     Sequence         WB
             DRB5_0101  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.5980
77.4    11.00  0.90     Sequence
             DRB5_0101  564      KFLPFQQFGRDIADT  FLPFQQFGR  1        0.5452
137.2    16.00  0.89     Sequence
             DRB5_0101  565      FLPFQQFGRDIADTT  FLPFQQFGR  0        0.4305
474.4    31.00  0.77     Sequence
             DRB5_0101  566      LPFQQFGRDIADTTD  FGRDIADTT  5        0.1635
8525.3    85.00  0.41     Sequence
             DRB5_0101  567      PFQQFGRDIADTTDA  FGRDIADTT  4        0.1588
8965.7    90.00  0.54     Sequence
             DRB5_0101  568      FQQFGRDIADTTDAV  FGRDIADTT  3        0.1551
9333.4    90.00  0.64     Sequence
             DRB5_0101  569      QQFGRDIADTTDAVR  FGRDIADTT  2        0.1545
9398.8    90.00  0.43     Sequence
             DRB5_0101  570      QFGRDIADTTDAVRD  IADTTDAVR  5        0.1650
8384.8    85.00  0.61     Sequence
             DRB5_0101  571      FGRDIADTTDAVRDP  IADTTDAVR  4        0.1435
10585.2    90.00  0.71     Sequence
             DRB5_0101  572      GRDIADTTDAVRDPQ  IADTTDAVR  3        0.1385
11167.3    90.00  0.83     Sequence
             DRB5_0101  573      RDIADTTDAVRDPQT  IADTTDAVR  2        0.1212
13474.0    95.00  0.77     Sequence
             DRB5_0101  574      DIADTTDAVRDPQTL  IADTTDAVR  1        0.0925
18388.1   100.00  0.68     Sequence
             DRB5_0101  575      IADTTDAVRDPQTLE  IADTTDAVR  0        0.0692
23646.6   100.00  0.47     Sequence
             DRB5_0101  576      ADTTDAVRDPQTLEI  TDAVRDPQT  3        0.0590
26403.1   100.00  0.25     Sequence
             DRB5_0101  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5        0.0664
24367.3   100.00  0.33     Sequence
             DRB5_0101  578      TTDAVRDPQTLEILD  VRDPQTLEI  4        0.0668
24273.1   100.00  0.38     Sequence
             DRB5_0101  579      TDAVRDPQTLEILDI  VRDPQTLEI  3        0.0693
23623.8   100.00  0.38     Sequence
             DRB5_0101  580      DAVRDPQTLEILDIT  VRDPQTLEI  2        0.0655
24620.7   100.00  0.34     Sequence
             DRB5_0101  581      AVRDPQTLEILDITP  VRDPQTLEI  1        0.0662
24441.0   100.00  0.29     Sequence
             DRB5_0101  582      VRDPQTLEILDITPC  LEILDITPC  6        0.0836
20241.4   100.00  0.37     Sequence
             DRB5_0101  583      RDPQTLEILDITPCS  LEILDITPC  5        0.1025
16489.0    95.00  0.44     Sequence
             DRB5_0101  584      DPQTLEILDITPCSF  ILDITPCSF  6        0.1437
10558.1    90.00  0.35     Sequence
             DRB5_0101  585      PQTLEILDITPCSFG  ILDITPCSF  5        0.1632
8549.6    85.00  0.46     Sequence
             DRB5_0101  586      QTLEILDITPCSFGG  ILDITPCSF  4        0.1673
8180.1    85.00  0.45     Sequence
             DRB5_0101  587      TLEILDITPCSFGGV  ILDITPCSF  3        0.1731
7686.4    85.00  0.47     Sequence
             DRB5_0101  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.1614
8721.9    85.00  0.44     Sequence
             DRB5_0101  589      EILDITPCSFGGVSV  ILDITPCSF  1        0.1338
11761.3    90.00  0.40     Sequence
             DRB5_0101  590      ILDITPCSFGGVSVI  ILDITPCSF  0        0.1180
13951.6    95.00  0.22     Sequence
```

```
             DRB5_0101  591      LDITPCSFGGVSVIT  CSFGGVSVI  5        0.1048
16089.5    95.00  0.22     Sequence
             DRB5_0101  592      DITPCSFGGVSVITP  CSFGGVSVI  4        0.1092
15337.3    95.00  0.22     Sequence
             DRB5_0101  593      ITPCSFGGVSVITPG  FGGVSVITP  5        0.1126
14789.2    95.00  0.37     Sequence
             DRB5_0101  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.1212
13476.6    95.00  0.40     Sequence
             DRB5_0101  595      PCSFGGVSVITPGTN  VSVITPGTN  6        0.2620
2936.1    65.00  0.72     Sequence
             DRB5_0101  596      CSFGGVSVITPGTNT  VSVITPGTN  5        0.3694
919.0    41.00  0.82     Sequence
             DRB5_0101  597      SFGGVSVITPGTNTS  VSVITPGTN  4        0.4120
579.5    34.00  0.86     Sequence
             DRB5_0101  598      FGGVSVITPGTNTSN  VSVITPGTN  3        0.4218
521.3    32.00  0.86     Sequence
             DRB5_0101  599      GGVSVITPGTNTSNQ  VSVITPGTN  2        0.3843
781.6    38.00  0.82     Sequence
             DRB5_0101  600      GVSVITPGTNTSNQV  VSVITPGTN  1        0.3252
1482.5    50.00  0.74     Sequence
             DRB5_0101  601      VSVITPGTNTSNQVA  VSVITPGTN  0        0.2075
5293.0    75.00  0.58     Sequence
             DRB5_0101  602      SVITPGTNTSNQVAV  ITPGTNTSN  2        0.0869
19521.4   100.00  0.46     Sequence
             DRB5_0101  603      VITPGTNTSNQVAVL  ITPGTNTSN  1        0.0649
24782.4   100.00  0.44     Sequence
             DRB5_0101  604      ITPGTNTSNQVAVLY  TSNQVAVLY  6        0.1328
11890.0    95.00  0.70     Sequence
             DRB5_0101  605      TPGTNTSNQVAVLYQ  TSNQVAVLY  5        0.1917
6285.2    80.00  0.73     Sequence
             DRB5_0101  606      PGTNTSNQVAVLYQG  TSNQVAVLY  4        0.2044
5475.6    80.00  0.70     Sequence
             DRB5_0101  607      GTNTSNQVAVLYQGV  TSNQVAVLY  3        0.2235
4455.3    75.00  0.68     Sequence
             DRB5_0101  608      TNTSNQVAVLYQGVN  TSNQVAVLY  2        0.2004
5716.9    80.00  0.58     Sequence
             DRB5_0101  609      NTSNQVAVLYQGVNC  TSNQVAVLY  1        0.1828
6920.2    85.00  0.48     Sequence
             DRB5_0101  610      TSNQVAVLYQGVNCT  VLYQGVNCT  6        0.1771
7356.3    85.00  0.24     Sequence
             DRB5_0101  611      SNQVAVLYQGVNCTE  VLYQGVNCT  5        0.1792
7196.9    85.00  0.39     Sequence
             DRB5_0101  612      NQVAVLYQGVNCTEV  VLYQGVNCT  4        0.1895
6432.4    80.00  0.46     Sequence
             DRB5_0101  613      QVAVLYQGVNCTEVP  VLYQGVNCT  3        0.1833
6878.2    85.00  0.49     Sequence
             DRB5_0101  614      VAVLYQGVNCTEVPV  VLYQGVNCT  2        0.1686
8071.5    85.00  0.47     Sequence
             DRB5_0101  615      AVLYQGVNCTEVPVA  VLYQGVNCT  1        0.1473
10159.7    90.00  0.44     Sequence
             DRB5_0101  616      VLYQGVNCTEVPVAI  VLYQGVNCT  0        0.1099
15222.1    95.00  0.34     Sequence
             DRB5_0101  617      LYQGVNCTEVPVAIH  CTEVPVAIH  6        0.1268
12677.7    95.00  0.49     Sequence
             DRB5_0101  618      YQGVNCTEVPVAIHA  CTEVPVAIH  5        0.1666
8246.8    85.00  0.62     Sequence
             DRB5_0101  619      QGVNCTEVPVAIHAD  CTEVPVAIH  4        0.1742
7597.0    85.00  0.65     Sequence
             DRB5_0101  620      GVNCTEVPVAIHADQ  CTEVPVAIH  3        0.1801
7123.5    85.00  0.66     Sequence
             DRB5_0101  621      VNCTEVPVAIHADQL  CTEVPVAIH  2        0.1715
7819.1    85.00  0.54     Sequence
             DRB5_0101  622      NCTEVPVAIHADQLT  CTEVPVAIH  1        0.1568
9168.1    90.00  0.48     Sequence
             DRB5_0101  623      CTEVPVAIHADQLTP  CTEVPVAIH  0        0.1250
12933.4    95.00  0.31     Sequence
```

```
             DRB5_0101  624      TEVPVAIHADQLTPT  PVAIHADQL  3        0.0987
17194.5   100.00  0.31     Sequence
             DRB5_0101  625      EVPVAIHADQLTPTW  PVAIHADQL  2        0.0938
18127.5   100.00  0.28     Sequence
             DRB5_0101  626      VPVAIHADQLTPTWR  ADQLTPTWR  6        0.2213
4559.7    75.00  0.62     Sequence
             DRB5_0101  627      PVAIHADQLTPTWRV  ADQLTPTWR  5        0.3329
1363.2    48.00  0.71     Sequence
             DRB5_0101  628      VAIHADQLTPTWRVY  ADQLTPTWR  4        0.3663
950.0    42.00  0.71     Sequence
             DRB5_0101  629      AIHADQLTPTWRVYS  ADQLTPTWR  3        0.4025
641.8    35.00  0.64     Sequence
             DRB5_0101  630      IHADQLTPTWRVYST  ADQLTPTWR  2        0.3924
716.4    37.00  0.58     Sequence
             DRB5_0101  631      HADQLTPTWRVYSTG  ADQLTPTWR  1        0.3527
1100.1    44.00  0.53     Sequence
             DRB5_0101  632      ADQLTPTWRVYSTGS  ADQLTPTWR  0        0.2977
1995.4    55.00  0.34     Sequence
             DRB5_0101  633      DQLTPTWRVYSTGSN  WRVYSTGSN  6        0.3031
1882.5    55.00  0.52     Sequence
             DRB5_0101  634      QLTPTWRVYSTGSNV  WRVYSTGSN  5        0.3556
1066.2    44.00  0.69     Sequence
             DRB5_0101  635      LTPTWRVYSTGSNVF  WRVYSTGSN  4        0.3841
783.7    38.00  0.73     Sequence
             DRB5_0101  636      TPTWRVYSTGSNVFQ  WRVYSTGSN  3        0.4265
495.2    31.00  0.61     Sequence
             DRB5_0101  637      PTWRVYSTGSNVFQT  WRVYSTGSN  2        0.4368
443.0    30.00  0.52     Sequence
             DRB5_0101  638      TWRVYSTGSNVFQTR  WRVYSTGSN  1        0.4450
405.3    28.00  0.41     Sequence
             DRB5_0101  639      WRVYSTGSNVFQTRA  YSTGSNVFQ  3        0.4090
598.3    34.00  0.50     Sequence
             DRB5_0101  640      RVYSTGSNVFQTRAG  YSTGSNVFQ  2        0.3328
1364.5    48.00  0.65     Sequence
             DRB5_0101  641      VYSTGSNVFQTRAGC  YSTGSNVFQ  1        0.2481
3412.7    70.00  0.66     Sequence
             DRB5_0101  642      YSTGSNVFQTRAGCL  VFQTRAGCL  6        0.2722
2629.5    65.00  0.46     Sequence
             DRB5_0101  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.3189
1587.2    55.00  0.67     Sequence
             DRB5_0101  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.3361
1317.6    47.00  0.68     Sequence
             DRB5_0101  645      GSNVFQTRAGCLIGA  VFQTRAGCL  3        0.3651
962.0    42.00  0.67     Sequence
             DRB5_0101  646      SNVFQTRAGCLIGAE  VFQTRAGCL  2        0.3339
1348.3    48.00  0.67     Sequence
             DRB5_0101  647      NVFQTRAGCLIGAEY  VFQTRAGCL  1        0.2995
1957.7    55.00  0.62     Sequence
             DRB5_0101  648      VFQTRAGCLIGAEYV  VFQTRAGCL  0        0.2315
4084.0    70.00  0.43     Sequence
             DRB5_0101  649      FQTRAGCLIGAEYVN  GCLIGAEYV  5        0.1653
8356.6    85.00  0.22     Sequence
             DRB5_0101  650      QTRAGCLIGAEYVNN  CLIGAEYVN  5        0.1584
9010.9    90.00  0.30     Sequence
             DRB5_0101  651      TRAGCLIGAEYVNNS  CLIGAEYVN  4        0.1666
8241.8    85.00  0.31     Sequence
             DRB5_0101  652      RAGCLIGAEYVNNSY  CLIGAEYVN  3        0.1649
8400.2    85.00  0.32     Sequence
             DRB5_0101  653      AGCLIGAEYVNNSYE  CLIGAEYVN  2        0.1463
10265.3    90.00  0.28     Sequence
             DRB5_0101  654      GCLIGAEYVNNSYEC  CLIGAEYVN  1        0.1431
10628.0    90.00  0.22     Sequence
             DRB5_0101  655      CLIGAEYVNNSYECD  EYVNNSYEC  5        0.1192
13765.6    95.00  0.18     Sequence
             DRB5_0101  656      LIGAEYVNNSYECDI  EYVNNSYEC  4        0.1097
15263.0    95.00  0.28     Sequence
```

```
             DRB5_0101  657      IGAEYVNNSYECDIP  EYVNNSYEC  3        0.0898
18923.1   100.00  0.33     Sequence
             DRB5_0101  658      GAEYVNNSYECDIPI  NSYECDIPI  6        0.0963
17631.7   100.00  0.32     Sequence
             DRB5_0101  659      AEYVNNSYECDIPIG  NSYECDIPI  5        0.1007
16809.8    95.00  0.41     Sequence
             DRB5_0101  660      EYVNNSYECDIPIGA  YECDIPIGA  6        0.1479
10093.1    90.00  0.44     Sequence
             DRB5_0101  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.1578
9062.9    90.00  0.54     Sequence
             DRB5_0101  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.1737
7636.2    85.00  0.49     Sequence
             DRB5_0101  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.1772
7347.8    85.00  0.47     Sequence
             DRB5_0101  664      NSYECDIPIGAGICA  YECDIPIGA  2        0.1747
7553.3    85.00  0.44     Sequence
             DRB5_0101  665      SYECDIPIGAGICAS  YECDIPIGA  1        0.1703
7918.1    85.00  0.38     Sequence
             DRB5_0101  666      YECDIPIGAGICASY  YECDIPIGA  0        0.1608
8780.8    85.00  0.23     Sequence
             DRB5_0101  667      ECDIPIGAGICASYQ  IGAGICASY  5        0.1498
9888.0    90.00  0.22     Sequence
             DRB5_0101  668      CDIPIGAGICASYQT  GAGICASYQ  5        0.1763
7418.3    85.00  0.25     Sequence
             DRB5_0101  669      DIPIGAGICASYQTQ  GAGICASYQ  4        0.1831
6897.4    85.00  0.28     Sequence
             DRB5_0101  670      IPIGAGICASYQTQT  GAGICASYQ  3        0.1877
6563.3    80.00  0.30     Sequence
             DRB5_0101  671      PIGAGICASYQTQTN  AGICASYQT  3        0.1833
6880.5    85.00  0.26     Sequence
             DRB5_0101  672      IGAGICASYQTQTNS  AGICASYQT  2        0.1757
7468.8    85.00  0.25     Sequence
             DRB5_0101  673      GAGICASYQTQTNSP  CASYQTQTN  4        0.1484
10036.2    90.00  0.37     Sequence
             DRB5_0101  674      AGICASYQTQTNSPR  YQTQTNSPR  6        0.4065
615.0    34.00  0.80     Sequence
             DRB5_0101  675      GICASYQTQTNSPRR  YQTQTNSPR  5        0.5363
151.1    17.00  0.81     Sequence
             DRB5_0101  676      ICASYQTQTNSPRRA  YQTQTNSPR  4        0.5843
89.8    12.00  0.84     Sequence
             DRB5_0101  677      CASYQTQTNSPRRAR  YQTQTNSPR  3        0.6201
60.9     9.00  0.84     Sequence         WB
             DRB5_0101  678      ASYQTQTNSPRRARS  YQTQTNSPR  2        0.6122
66.4     9.50  0.79     Sequence         WB
             DRB5_0101  679      SYQTQTNSPRRARSV  YQTQTNSPR  1        0.5672
108.1    14.00  0.76     Sequence
             DRB5_0101  680      YQTQTNSPRRARSVA  YQTQTNSPR  0        0.4620
337.3    26.00  0.63     Sequence
             DRB5_0101  681      QTQTNSPRRARSVAS  QTNSPRRAR  2        0.2703
2683.0    65.00  0.28     Sequence
             DRB5_0101  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.2754
2540.0    60.00  0.50     Sequence
             DRB5_0101  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.2882
2212.4    60.00  0.52     Sequence
             DRB5_0101  684      TNSPRRARSVASQSI  PRRARSVAS  3        0.3290
1422.2    49.00  0.48     Sequence
             DRB5_0101  685      NSPRRARSVASQSII  PRRARSVAS  2        0.3543
1081.7    44.00  0.35     Sequence
             DRB5_0101  686      SPRRARSVASQSIIA  ARSVASQSI  4        0.3708
905.3    41.00  0.34     Sequence
             DRB5_0101  687      PRRARSVASQSIIAY  ARSVASQSI  3        0.3667
945.4    41.00  0.36     Sequence
             DRB5_0101  688      RRARSVASQSIIAYT  ARSVASQSI  2        0.3601
1015.7    43.00  0.29     Sequence
             DRB5_0101  689      RARSVASQSIIAYTM  VASQSIIAY  4        0.3665
948.3    42.00  0.29     Sequence
```

```
             DRB5_0101  690      ARSVASQSIIAYTMS  SQSIIAYTM  5        0.3686
926.7    41.00  0.38     Sequence
             DRB5_0101  691      RSVASQSIIAYTMSL  SQSIIAYTM  4        0.3819
802.9    39.00  0.43     Sequence
             DRB5_0101  692      SVASQSIIAYTMSLG  SQSIIAYTM  3        0.3416
1241.4    46.00  0.50     Sequence
             DRB5_0101  693      VASQSIIAYTMSLGA  SQSIIAYTM  2        0.3202
1564.9    55.00  0.44     Sequence
             DRB5_0101  694      ASQSIIAYTMSLGAE  SQSIIAYTM  1        0.2964
2023.8    60.00  0.38     Sequence
             DRB5_0101  695      SQSIIAYTMSLGAEN  YTMSLGAEN  6        0.4921
243.6    22.00  0.69     Sequence
             DRB5_0101  696      QSIIAYTMSLGAENS  YTMSLGAEN  5        0.5753
99.0    13.00  0.83     Sequence
             DRB5_0101  697      SIIAYTMSLGAENSV  YTMSLGAEN  4        0.6119
66.6     9.50  0.88     Sequence        WB
             DRB5_0101  698      IIAYTMSLGAENSVA  YTMSLGAEN  3        0.6366
51.0     8.00  0.90     Sequence        WB
             DRB5_0101  699      IAYTMSLGAENSVAY  YTMSLGAEN  2        0.6046
72.1    10.00  0.88     Sequence
             DRB5_0101  700      AYTMSLGAENSVAYS  YTMSLGAEN  1        0.5513
128.3    15.00  0.87     Sequence
             DRB5_0101  701      YTMSLGAENSVAYSN  YTMSLGAEN  0        0.4172
547.7    33.00  0.72     Sequence
             DRB5_0101  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.1771
7354.4    85.00  0.57     Sequence
             DRB5_0101  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.1698
7966.6    85.00  0.50     Sequence
             DRB5_0101  704      SLGAENSVAYSNNSI  LGAENSVAY  1        0.1595
8901.5    90.00  0.38     Sequence
             DRB5_0101  705      LGAENSVAYSNNSIA  NSVAYSNNS  4        0.1472
10168.4    90.00  0.29     Sequence
             DRB5_0101  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.1653
8364.7    85.00  0.29     Sequence
             DRB5_0101  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.1659
8310.5    85.00  0.31     Sequence
             DRB5_0101  708      ENSVAYSNNSIAIPT  VAYSNNSIA  3        0.1796
7163.6    85.00  0.31     Sequence
             DRB5_0101  709      NSVAYSNNSIAIPTN  AYSNNSIAI  3        0.1794
7176.8    85.00  0.32     Sequence
             DRB5_0101  710      SVAYSNNSIAIPTNF  AYSNNSIAI  2        0.1659
8302.8    85.00  0.31     Sequence
             DRB5_0101  711      VAYSNNSIAIPTNFT  SNNSIAIPT  3        0.1646
8422.9    85.00  0.28     Sequence
             DRB5_0101  712      AYSNNSIAIPTNFTI  SIAIPTNFT  5        0.1661
8292.9    85.00  0.25     Sequence
             DRB5_0101  713      YSNNSIAIPTNFTIS  SIAIPTNFT  4        0.1725
7735.3    85.00  0.34     Sequence
             DRB5_0101  714      SNNSIAIPTNFTISV  SIAIPTNFT  3        0.1737
7634.8    85.00  0.40     Sequence
             DRB5_0101  715      NNSIAIPTNFTISVT  SIAIPTNFT  2        0.1642
8462.7    85.00  0.39     Sequence
             DRB5_0101  716      NSIAIPTNFTISVTT  SIAIPTNFT  1        0.1443
10494.1    90.00  0.35     Sequence
             DRB5_0101  717      SIAIPTNFTISVTTE  IAIPTNFTI  1        0.1203
13608.5    95.00  0.37     Sequence
             DRB5_0101  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.2483
3405.0    70.00  0.80     Sequence
             DRB5_0101  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.3253
1480.2    50.00  0.86     Sequence
             DRB5_0101  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.3252
1481.5    50.00  0.86     Sequence
             DRB5_0101  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.3409
1250.1    47.00  0.86     Sequence
             DRB5_0101  722      TNFTISVTTEILPVS  FTISVTTEI  2        0.3236
1507.7    50.00  0.83     Sequence
```

```
             DRB5_0101  723      NFTISVTTEILPVSM  FTISVTTEI  1        0.2987
1973.2    55.00  0.73     Sequence
             DRB5_0101  724      FTISVTTEILPVSMT  FTISVTTEI  0        0.2441
3564.5    70.00  0.43     Sequence
             DRB5_0101  725      TISVTTEILPVSMTK  EILPVSMTK  6        0.3202
1563.9    55.00  0.52     Sequence
             DRB5_0101  726      ISVTTEILPVSMTKT  EILPVSMTK  5        0.3599
1018.3    43.00  0.56     Sequence
             DRB5_0101  727      SVTTEILPVSMTKTS  EILPVSMTK  4        0.3698
914.5    41.00  0.57     Sequence
             DRB5_0101  728      VTTEILPVSMTKTSV  EILPVSMTK  3        0.3712
901.0    41.00  0.63     Sequence
             DRB5_0101  729      TTEILPVSMTKTSVD  EILPVSMTK  2        0.3319
1377.8    48.00  0.67     Sequence
             DRB5_0101  730      TEILPVSMTKTSVDC  EILPVSMTK  1        0.2823
2358.5    60.00  0.67     Sequence
             DRB5_0101  731      EILPVSMTKTSVDCT  EILPVSMTK  0        0.1984
5842.0    80.00  0.58     Sequence
             DRB5_0101  732      ILPVSMTKTSVDCTM  VSMTKTSVD  3        0.0999
16971.6   100.00  0.42     Sequence
             DRB5_0101  733      LPVSMTKTSVDCTMY  VSMTKTSVD  2        0.0855
19821.8   100.00  0.41     Sequence
             DRB5_0101  734      PVSMTKTSVDCTMYI  TSVDCTMYI  6        0.1182
13921.9    95.00  0.47     Sequence
             DRB5_0101  735      VSMTKTSVDCTMYIC  TSVDCTMYI  5        0.1273
12605.7    95.00  0.61     Sequence
             DRB5_0101  736      SMTKTSVDCTMYICG  TSVDCTMYI  4        0.1238
13093.9    95.00  0.67     Sequence
             DRB5_0101  737      MTKTSVDCTMYICGD  TSVDCTMYI  3        0.1194
13738.6    95.00  0.74     Sequence
             DRB5_0101  738      TKTSVDCTMYICGDS  TSVDCTMYI  2        0.1032
16360.9    95.00  0.68     Sequence
             DRB5_0101  739      KTSVDCTMYICGDST  TSVDCTMYI  1        0.0974
17433.5   100.00  0.47     Sequence
             DRB5_0101  740      TSVDCTMYICGDSTE  TMYICGDST  5        0.0770
21745.1   100.00  0.29     Sequence
             DRB5_0101  741      SVDCTMYICGDSTEC  YICGDSTEC  6        0.0901
18868.5   100.00  0.28     Sequence
             DRB5_0101  742      VDCTMYICGDSTECS  YICGDSTEC  5        0.1045
16134.4    95.00  0.39     Sequence
             DRB5_0101  743      DCTMYICGDSTECSN  YICGDSTEC  4        0.1083
15497.8    95.00  0.46     Sequence
             DRB5_0101  744      CTMYICGDSTECSNL  YICGDSTEC  3        0.1128
14751.2    95.00  0.50     Sequence
             DRB5_0101  745      TMYICGDSTECSNLL  YICGDSTEC  2        0.1128
14749.9    95.00  0.44     Sequence
             DRB5_0101  746      MYICGDSTECSNLLL  YICGDSTEC  1        0.1035
16323.0    95.00  0.38     Sequence
             DRB5_0101  747      YICGDSTECSNLLLQ  DSTECSNLL  4        0.0872
19459.7   100.00  0.44     Sequence
             DRB5_0101  748      ICGDSTECSNLLLQY  DSTECSNLL  3        0.0706
23281.0   100.00  0.52     Sequence
             DRB5_0101  749      CGDSTECSNLLLQYG  DSTECSNLL  2        0.0732
22645.0   100.00  0.40     Sequence
             DRB5_0101  750      GDSTECSNLLLQYGS  CSNLLLQYG  5        0.0816
20669.4   100.00  0.25     Sequence
             DRB5_0101  751      DSTECSNLLLQYGSF  CSNLLLQYG  4        0.0852
19887.1   100.00  0.25     Sequence
             DRB5_0101  752      STECSNLLLQYGSFC  LLLQYGSFC  6        0.1608
8774.8    85.00  0.51     Sequence
             DRB5_0101  753      TECSNLLLQYGSFCT  LLLQYGSFC  5        0.2273
4272.9    75.00  0.54     Sequence
             DRB5_0101  754      ECSNLLLQYGSFCTQ  LLLQYGSFC  4        0.2589
3036.9    65.00  0.52     Sequence
             DRB5_0101  755      CSNLLLQYGSFCTQL  LLLQYGSFC  3        0.2818
2370.3    60.00  0.51     Sequence
```

```
             DRB5_0101  756      SNLLLQYGSFCTQLN  LLLQYGSFC  2        0.3094
1757.9    55.00  0.38     Sequence
             DRB5_0101  757      NLLLQYGSFCTQLNR  YGSFCTQLN  5        0.3327
1366.1    48.00  0.31     Sequence
             DRB5_0101  758      LLLQYGSFCTQLNRA  YGSFCTQLN  4        0.3513
1117.8    44.00  0.38     Sequence
             DRB5_0101  759      LLQYGSFCTQLNRAL  FCTQLNRAL  6        0.4335
459.1    30.00  0.44     Sequence
             DRB5_0101  760      LQYGSFCTQLNRALT  FCTQLNRAL  5        0.4627
335.0    26.00  0.54     Sequence
             DRB5_0101  761      QYGSFCTQLNRALTG  FCTQLNRAL  4        0.4516
377.6    27.00  0.58     Sequence
             DRB5_0101  762      YGSFCTQLNRALTGI  FCTQLNRAL  3        0.4455
403.4    28.00  0.60     Sequence
             DRB5_0101  763      GSFCTQLNRALTGIA  FCTQLNRAL  2        0.4291
481.8    31.00  0.54     Sequence
             DRB5_0101  764      SFCTQLNRALTGIAV  FCTQLNRAL  1        0.4298
477.9    31.00  0.40     Sequence
             DRB5_0101  765      FCTQLNRALTGIAVE  LNRALTGIA  4        0.3959
689.8    36.00  0.53     Sequence
             DRB5_0101  766      CTQLNRALTGIAVEQ  LNRALTGIA  3        0.3709
903.9    41.00  0.68     Sequence
             DRB5_0101  767      TQLNRALTGIAVEQD  LNRALTGIA  2        0.3585
1033.2    43.00  0.70     Sequence
             DRB5_0101  768      QLNRALTGIAVEQDK  LNRALTGIA  1        0.3383
1286.8    47.00  0.53     Sequence
             DRB5_0101  769      LNRALTGIAVEQDKN  LNRALTGIA  0        0.2581
3064.3    65.00  0.33     Sequence
             DRB5_0101  770      NRALTGIAVEQDKNT  TGIAVEQDK  4        0.2025
5593.1    80.00  0.53     Sequence
             DRB5_0101  771      RALTGIAVEQDKNTQ  TGIAVEQDK  3        0.1996
5766.2    80.00  0.55     Sequence
             DRB5_0101  772      ALTGIAVEQDKNTQE  TGIAVEQDK  2        0.1654
8351.0    85.00  0.52     Sequence
             DRB5_0101  773      LTGIAVEQDKNTQEV  TGIAVEQDK  1        0.1504
9822.4    90.00  0.41     Sequence
             DRB5_0101  774      TGIAVEQDKNTQEVF  IAVEQDKNT  2        0.1150
14402.3    95.00  0.38     Sequence
             DRB5_0101  775      GIAVEQDKNTQEVFA  IAVEQDKNT  1        0.0901
18857.5   100.00  0.43     Sequence
             DRB5_0101  776      IAVEQDKNTQEVFAQ  KNTQEVFAQ  6        0.0797
21119.7   100.00  0.25     Sequence
             DRB5_0101  777      AVEQDKNTQEVFAQV  KNTQEVFAQ  5        0.0799
21055.1   100.00  0.40     Sequence
             DRB5_0101  778      VEQDKNTQEVFAQVK  TQEVFAQVK  6        0.3222
1530.6    50.00  0.79     Sequence
             DRB5_0101  779      EQDKNTQEVFAQVKQ  TQEVFAQVK  5        0.4257
499.9    31.00  0.80     Sequence
             DRB5_0101  780      QDKNTQEVFAQVKQI  TQEVFAQVK  4        0.4689
312.9    25.00  0.80     Sequence
             DRB5_0101  781      DKNTQEVFAQVKQIY  TQEVFAQVK  3        0.4863
259.5    23.00  0.77     Sequence
             DRB5_0101  782      KNTQEVFAQVKQIYK  FAQVKQIYK  6        0.6374
50.6     8.00  0.51     Sequence         WB
             DRB5_0101  783      NTQEVFAQVKQIYKT  FAQVKQIYK  5        0.6748
33.7     5.50  0.61     Sequence         WB
             DRB5_0101  784      TQEVFAQVKQIYKTP  FAQVKQIYK  4        0.6529
42.7     7.00  0.68     Sequence         WB
             DRB5_0101  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.6145
64.8     9.50  0.79     Sequence         WB
             DRB5_0101  786      EVFAQVKQIYKTPPI  FAQVKQIYK  2        0.5886
85.8    12.00  0.76     Sequence
             DRB5_0101  787      VFAQVKQIYKTPPIK  FAQVKQIYK  1        0.6281
55.9     8.50  0.56     Sequence         WB
             DRB5_0101  788      FAQVKQIYKTPPIKD  QIYKTPPIK  5        0.6309
54.2     8.00  0.40     Sequence         WB
```

```
             DRB5_0101  789      AQVKQIYKTPPIKDF  QIYKTPPIK  4        0.6000
75.8    11.00  0.51     Sequence
             DRB5_0101  790      QVKQIYKTPPIKDFG  QIYKTPPIK  3        0.5925
82.2    11.00  0.54     Sequence
             DRB5_0101  791      VKQIYKTPPIKDFGG  QIYKTPPIK  2        0.5659
109.6    14.00  0.54     Sequence
             DRB5_0101  792      KQIYKTPPIKDFGGF  QIYKTPPIK  1        0.5137
192.8    19.00  0.52     Sequence
             DRB5_0101  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.3976
677.4    36.00  0.46     Sequence
             DRB5_0101  794      IYKTPPIKDFGGFNF  IYKTPPIKD  0        0.2185
4703.7    75.00  0.47     Sequence
             DRB5_0101  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.1464
10251.9    90.00  0.44     Sequence
             DRB5_0101  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.1678
8138.0    85.00  0.43     Sequence
             DRB5_0101  797      TPPIKDFGGFNFSQI  IKDFGGFNF  3        0.1886
6494.6    80.00  0.41     Sequence
             DRB5_0101  798      PPIKDFGGFNFSQIL  IKDFGGFNF  2        0.1940
6131.8    80.00  0.35     Sequence
             DRB5_0101  799      PIKDFGGFNFSQILP  IKDFGGFNF  1        0.1891
6461.2    80.00  0.33     Sequence
             DRB5_0101  800      IKDFGGFNFSQILPD  FNFSQILPD  6        0.2024
5593.5    80.00  0.27     Sequence
             DRB5_0101  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.1769
7375.7    85.00  0.40     Sequence
             DRB5_0101  802      DFGGFNFSQILPDPS  FSQILPDPS  6        0.2300
4152.2    70.00  0.42     Sequence
             DRB5_0101  803      FGGFNFSQILPDPSK  FSQILPDPS  5        0.3238
1503.9    50.00  0.53     Sequence
             DRB5_0101  804      GGFNFSQILPDPSKP  FSQILPDPS  4        0.3317
1382.1    48.00  0.56     Sequence
             DRB5_0101  805      GFNFSQILPDPSKPS  FSQILPDPS  3        0.3458
1185.9    46.00  0.57     Sequence
             DRB5_0101  806      FNFSQILPDPSKPSK  FSQILPDPS  2        0.3289
1424.2    49.00  0.50     Sequence
             DRB5_0101  807      NFSQILPDPSKPSKR  FSQILPDPS  1        0.3440
1209.2    46.00  0.35     Sequence
             DRB5_0101  808      FSQILPDPSKPSKRS  PDPSKPSKR  5        0.3222
1531.0    50.00  0.34     Sequence
             DRB5_0101  809      SQILPDPSKPSKRSF  PDPSKPSKR  4        0.2871
2237.1    60.00  0.48     Sequence
             DRB5_0101  810      QILPDPSKPSKRSFI  PDPSKPSKR  3        0.2848
2294.9    60.00  0.54     Sequence
             DRB5_0101  811      ILPDPSKPSKRSFIE  PDPSKPSKR  2        0.2550
3168.4    65.00  0.54     Sequence
             DRB5_0101  812      LPDPSKPSKRSFIED  PDPSKPSKR  1        0.2204
4608.2    75.00  0.53     Sequence
             DRB5_0101  813      PDPSKPSKRSFIEDL  PDPSKPSKR  0        0.1681
8114.5    85.00  0.43     Sequence
             DRB5_0101  814      DPSKPSKRSFIEDLL  SKPSKRSFI  2        0.0999
16960.3   100.00  0.28     Sequence
             DRB5_0101  815      PSKPSKRSFIEDLLF  RSFIEDLLF  6        0.1459
10310.1    90.00  0.47     Sequence
             DRB5_0101  816      SKPSKRSFIEDLLFN  RSFIEDLLF  5        0.1767
7393.0    85.00  0.52     Sequence
             DRB5_0101  817      KPSKRSFIEDLLFNK  FIEDLLFNK  6        0.3375
1298.0    47.00  0.58     Sequence
             DRB5_0101  818      PSKRSFIEDLLFNKV  FIEDLLFNK  5        0.3798
820.8    39.00  0.61     Sequence
             DRB5_0101  819      SKRSFIEDLLFNKVT  FIEDLLFNK  4        0.4025
641.9    35.00  0.62     Sequence
             DRB5_0101  820      KRSFIEDLLFNKVTL  FIEDLLFNK  3        0.4150
561.0    33.00  0.62     Sequence
             DRB5_0101  821      RSFIEDLLFNKVTLA  FIEDLLFNK  2        0.3821
800.5    39.00  0.58     Sequence
```

```
             DRB5_0101  822      SFIEDLLFNKVTLAD  FIEDLLFNK  1        0.3247
1489.9    50.00  0.56     Sequence
             DRB5_0101  823      FIEDLLFNKVTLADA  FIEDLLFNK  0        0.2784
2458.8    60.00  0.37     Sequence
             DRB5_0101  824      IEDLLFNKVTLADAG  FNKVTLADA  5        0.2128
4999.5    75.00  0.41     Sequence
             DRB5_0101  825      EDLLFNKVTLADAGF  FNKVTLADA  4        0.2113
5082.4    75.00  0.50     Sequence
             DRB5_0101  826      DLLFNKVTLADAGFI  VTLADAGFI  6        0.3983
671.9    36.00  0.67     Sequence
             DRB5_0101  827      LLFNKVTLADAGFIK  VTLADAGFI  5        0.5729
101.6    13.00  0.62     Sequence
             DRB5_0101  828      LFNKVTLADAGFIKQ  VTLADAGFI  4        0.6256
57.4     8.50  0.58     Sequence        WB
             DRB5_0101  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.6407
48.8     7.50  0.57     Sequence        WB
             DRB5_0101  830      NKVTLADAGFIKQYG  VTLADAGFI  2        0.6185
62.0     9.00  0.56     Sequence        WB
             DRB5_0101  831      KVTLADAGFIKQYGD  VTLADAGFI  1        0.5770
97.2    13.00  0.54     Sequence
             DRB5_0101  832      VTLADAGFIKQYGDC  VTLADAGFI  0        0.4630
333.6    26.00  0.44     Sequence
             DRB5_0101  833      TLADAGFIKQYGDCL  FIKQYGDCL  6        0.3191
1582.9    55.00  0.44     Sequence
             DRB5_0101  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.3065
1813.7    55.00  0.80     Sequence
             DRB5_0101  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4        0.3216
1541.1    50.00  0.81     Sequence
             DRB5_0101  836      DAGFIKQYGDCLGDI  FIKQYGDCL  3        0.3368
1307.2    47.00  0.82     Sequence
             DRB5_0101  837      AGFIKQYGDCLGDIA  FIKQYGDCL  2        0.3386
1281.9    47.00  0.81     Sequence
             DRB5_0101  838      GFIKQYGDCLGDIAA  FIKQYGDCL  1        0.2976
1998.5    60.00  0.81     Sequence
             DRB5_0101  839      FIKQYGDCLGDIAAR  FIKQYGDCL  0        0.2158
4838.4    75.00  0.64     Sequence
             DRB5_0101  840      IKQYGDCLGDIAARD  CLGDIAARD  6        0.1213
13459.2    95.00  0.34     Sequence
             DRB5_0101  841      KQYGDCLGDIAARDL  CLGDIAARD  5        0.1651
8381.6    85.00  0.40     Sequence
             DRB5_0101  842      QYGDCLGDIAARDLI  CLGDIAARD  4        0.1922
6246.1    80.00  0.42     Sequence
             DRB5_0101  843      YGDCLGDIAARDLIC  CLGDIAARD  3        0.1918
6277.9    80.00  0.41     Sequence
             DRB5_0101  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.1932
6184.3    80.00  0.33     Sequence
             DRB5_0101  845      DCLGDIAARDLICAQ  CLGDIAARD  1        0.1766
7398.4    85.00  0.25     Sequence
             DRB5_0101  846      CLGDIAARDLICAQK  ARDLICAQK  6        0.1870
6610.5    80.00  0.22     Sequence
             DRB5_0101  847      LGDIAARDLICAQKF  RDLICAQKF  6        0.2928
2105.1    60.00  0.54     Sequence
             DRB5_0101  848      GDIAARDLICAQKFN  RDLICAQKF  5        0.3192
1581.5    55.00  0.60     Sequence
             DRB5_0101  849      DIAARDLICAQKFNG  RDLICAQKF  4        0.3169
1620.8    55.00  0.62     Sequence
             DRB5_0101  850      IAARDLICAQKFNGL  RDLICAQKF  3        0.3465
1177.5    45.00  0.58     Sequence
             DRB5_0101  851      AARDLICAQKFNGLT  RDLICAQKF  2        0.3388
1278.7    47.00  0.47     Sequence
             DRB5_0101  852      ARDLICAQKFNGLTV  RDLICAQKF  1        0.3224
1527.1    50.00  0.39     Sequence
             DRB5_0101  853      RDLICAQKFNGLTVL  ICAQKFNGL  3        0.3017
1911.1    55.00  0.31     Sequence
             DRB5_0101  854      DLICAQKFNGLTVLP  ICAQKFNGL  2        0.2578
3073.4    65.00  0.30     Sequence
```

```
             DRB5_0101  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.3288
1425.9    49.00  0.44     Sequence
             DRB5_0101  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.3615
1001.2    43.00  0.62     Sequence
             DRB5_0101  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.3710
902.9    41.00  0.74     Sequence
             DRB5_0101  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.4098
593.4    34.00  0.56     Sequence
             DRB5_0101  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.4036
634.2    35.00  0.46     Sequence
             DRB5_0101  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1        0.3676
936.8    41.00  0.37     Sequence
             DRB5_0101  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.3002
1941.4    55.00  0.65     Sequence
             DRB5_0101  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.2430
3607.4    70.00  0.85     Sequence
             DRB5_0101  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.2041
5495.9    80.00  0.81     Sequence
             DRB5_0101  864      LTVLPPLLTDEMIAQ  LTVLPPLLT  0        0.1458
10321.2    90.00  0.62     Sequence
             DRB5_0101  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.0840
20157.0   100.00  0.26     Sequence
             DRB5_0101  866      VLPPLLTDEMIAQYT  TDEMIAQYT  6        0.1290
12378.7    95.00  0.44     Sequence
             DRB5_0101  867      LPPLLTDEMIAQYTS  TDEMIAQYT  5        0.1582
9028.2    90.00  0.54     Sequence
             DRB5_0101  868      PPLLTDEMIAQYTSA  TDEMIAQYT  4        0.1760
7449.5    85.00  0.55     Sequence
             DRB5_0101  869      PLLTDEMIAQYTSAL  TDEMIAQYT  3        0.2170
4779.5    75.00  0.44     Sequence
             DRB5_0101  870      LLTDEMIAQYTSALL  MIAQYTSAL  5        0.2687
2730.8    65.00  0.34     Sequence
             DRB5_0101  871      LTDEMIAQYTSALLA  IAQYTSALL  5        0.3198
1570.8    55.00  0.34     Sequence
             DRB5_0101  872      TDEMIAQYTSALLAG  IAQYTSALL  4        0.3351
1331.9    48.00  0.35     Sequence
             DRB5_0101  873      DEMIAQYTSALLAGT  IAQYTSALL  3        0.3653
960.7    42.00  0.32     Sequence
             DRB5_0101  874      EMIAQYTSALLAGTI  YTSALLAGT  5        0.4002
658.4    35.00  0.31     Sequence
             DRB5_0101  875      MIAQYTSALLAGTIT  YTSALLAGT  4        0.4024
642.8    35.00  0.40     Sequence
             DRB5_0101  876      IAQYTSALLAGTITS  YTSALLAGT  3        0.3957
691.0    36.00  0.50     Sequence
             DRB5_0101  877      AQYTSALLAGTITSG  YTSALLAGT  2        0.3671
941.7    41.00  0.50     Sequence
             DRB5_0101  878      QYTSALLAGTITSGW  YTSALLAGT  1        0.3325
1370.2    48.00  0.44     Sequence
             DRB5_0101  879      YTSALLAGTITSGWT  ALLAGTITS  3        0.2537
3211.0    65.00  0.34     Sequence
             DRB5_0101  880      TSALLAGTITSGWTF  ALLAGTITS  2        0.2077
5285.5    75.00  0.44     Sequence
             DRB5_0101  881      SALLAGTITSGWTFG  ALLAGTITS  1        0.1872
6593.5    80.00  0.38     Sequence
             DRB5_0101  882      ALLAGTITSGWTFGA  ITSGWTFGA  6        0.1969
5942.6    80.00  0.34     Sequence
             DRB5_0101  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.2058
5395.7    80.00  0.51     Sequence
             DRB5_0101  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.2160
4830.6    75.00  0.62     Sequence
             DRB5_0101  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.2295
4171.9    75.00  0.69     Sequence
             DRB5_0101  886      GTITSGWTFGAGAAL  WTFGAGAAL  6        0.2826
2350.6    60.00  0.43     Sequence
             DRB5_0101  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.3375
1297.3    47.00  0.56     Sequence
```

```
             DRB5_0101  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.4704
308.0    25.00  0.47     Sequence
             DRB5_0101  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.4916
245.0    22.00  0.57     Sequence
             DRB5_0101  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.5015
220.0    21.00  0.65     Sequence
             DRB5_0101  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.5095
201.8    20.00  0.70     Sequence
             DRB5_0101  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.5085
203.9    20.00  0.55     Sequence
             DRB5_0101  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.5106
199.3    19.00  0.44     Sequence
             DRB5_0101  894      FGAGAALQIPFAMQM  AALQIPFAM  4        0.5166
186.8    19.00  0.47     Sequence
             DRB5_0101  895      GAGAALQIPFAMQMA  AALQIPFAM  3        0.5265
168.0    18.00  0.54     Sequence
             DRB5_0101  896      AGAALQIPFAMQMAY  AALQIPFAM  2        0.5106
199.4    19.00  0.46     Sequence
             DRB5_0101  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.5504
129.7    15.00  0.45     Sequence
             DRB5_0101  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.7355
17.5     3.00  0.75     Sequence         WB
             DRB5_0101  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.7503
14.9     2.50  0.81     Sequence         WB
             DRB5_0101  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.7441
15.9     2.50  0.81     Sequence         WB
             DRB5_0101  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.7370
17.2     3.00  0.83     Sequence         WB
             DRB5_0101  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.7086
23.4     4.00  0.84     Sequence         WB
             DRB5_0101  903      PFAMQMAYRFNGIGV  FAMQMAYRF  1        0.6691
35.9     6.00  0.85     Sequence         WB
             DRB5_0101  904      FAMQMAYRFNGIGVT  FAMQMAYRF  0        0.5755
98.8    13.00  0.79     Sequence
             DRB5_0101  905      AMQMAYRFNGIGVTQ  YRFNGIGVT  5        0.3195
1575.6    55.00  0.31     Sequence
             DRB5_0101  906      MQMAYRFNGIGVTQN  YRFNGIGVT  4        0.3424
1230.5    46.00  0.34     Sequence
             DRB5_0101  907      QMAYRFNGIGVTQNV  YRFNGIGVT  3        0.3700
913.0    41.00  0.35     Sequence
             DRB5_0101  908      MAYRFNGIGVTQNVL  FNGIGVTQN  4        0.3635
979.8    42.00  0.31     Sequence
             DRB5_0101  909      AYRFNGIGVTQNVLY  FNGIGVTQN  3        0.3428
1225.4    46.00  0.38     Sequence
             DRB5_0101  910      YRFNGIGVTQNVLYE  FNGIGVTQN  2        0.3004
1937.7    55.00  0.41     Sequence
             DRB5_0101  911      RFNGIGVTQNVLYEN  FNGIGVTQN  1        0.2446
3545.8    70.00  0.39     Sequence
             DRB5_0101  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.1856
6711.5    80.00  0.44     Sequence
             DRB5_0101  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.1759
7450.6    85.00  0.41     Sequence
             DRB5_0101  914      GIGVTQNVLYENQKL  QNVLYENQK  5        0.1975
5899.4    80.00  0.28     Sequence
             DRB5_0101  915      IGVTQNVLYENQKLI  VLYENQKLI  6        0.2344
3956.8    70.00  0.31     Sequence
             DRB5_0101  916      GVTQNVLYENQKLIA  VLYENQKLI  5        0.2715
2648.5    65.00  0.49     Sequence
             DRB5_0101  917      VTQNVLYENQKLIAN  VLYENQKLI  4        0.2858
2270.8    60.00  0.45     Sequence
             DRB5_0101  918      TQNVLYENQKLIANQ  VLYENQKLI  3        0.2947
2060.9    60.00  0.45     Sequence
             DRB5_0101  919      QNVLYENQKLIANQF  VLYENQKLI  2        0.3086
1773.1    55.00  0.35     Sequence
             DRB5_0101  920      NVLYENQKLIANQFN  VLYENQKLI  1        0.3206
1558.1    55.00  0.22     Sequence
```

```
             DRB5_0101  921      VLYENQKLIANQFNS  QKLIANQFN  5        0.3088
1770.7    55.00  0.30     Sequence
             DRB5_0101  922      LYENQKLIANQFNSA  QKLIANQFN  4        0.3119
1710.6    55.00  0.41     Sequence
             DRB5_0101  923      YENQKLIANQFNSAI  QKLIANQFN  3        0.3184
1595.3    55.00  0.41     Sequence
             DRB5_0101  924      ENQKLIANQFNSAIG  QKLIANQFN  2        0.3052
1841.1    55.00  0.33     Sequence
             DRB5_0101  925      NQKLIANQFNSAIGK  NQFNSAIGK  6        0.4075
608.6    34.00  0.35     Sequence
             DRB5_0101  926      QKLIANQFNSAIGKI  NQFNSAIGK  5        0.4460
401.2    28.00  0.47     Sequence
             DRB5_0101  927      KLIANQFNSAIGKIQ  NQFNSAIGK  4        0.5130
194.2    19.00  0.38     Sequence
             DRB5_0101  928      LIANQFNSAIGKIQD  FNSAIGKIQ  5        0.5228
174.7    18.00  0.44     Sequence
             DRB5_0101  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4        0.5172
185.7    19.00  0.53     Sequence
             DRB5_0101  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.5084
204.3    20.00  0.63     Sequence
             DRB5_0101  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.4549
364.4    27.00  0.68     Sequence
             DRB5_0101  932      QFNSAIGKIQDSLSS  FNSAIGKIQ  1        0.3779
838.1    39.00  0.77     Sequence
             DRB5_0101  933      FNSAIGKIQDSLSST  FNSAIGKIQ  0        0.2827
2347.1    60.00  0.59     Sequence
             DRB5_0101  934      NSAIGKIQDSLSSTA  IGKIQDSLS  3        0.1857
6701.2    80.00  0.37     Sequence
             DRB5_0101  935      SAIGKIQDSLSSTAS  GKIQDSLSS  3        0.1930
6192.0    80.00  0.41     Sequence
             DRB5_0101  936      AIGKIQDSLSSTASA  GKIQDSLSS  2        0.1859
6692.2    80.00  0.36     Sequence
             DRB5_0101  937      IGKIQDSLSSTASAL  IQDSLSSTA  3        0.1712
7841.1    85.00  0.33     Sequence
             DRB5_0101  938      GKIQDSLSSTASALG  IQDSLSSTA  2        0.1391
11103.0    90.00  0.36     Sequence
             DRB5_0101  939      KIQDSLSSTASALGK  SSTASALGK  6        0.3100
1747.2    55.00  0.69     Sequence
             DRB5_0101  940      IQDSLSSTASALGKL  SSTASALGK  5        0.4092
597.3    34.00  0.75     Sequence
             DRB5_0101  941      QDSLSSTASALGKLQ  SSTASALGK  4        0.4413
422.2    29.00  0.74     Sequence
             DRB5_0101  942      DSLSSTASALGKLQD  SSTASALGK  3        0.4331
461.1    30.00  0.75     Sequence
             DRB5_0101  943      SLSSTASALGKLQDV  SSTASALGK  2        0.4301
476.4    31.00  0.74     Sequence
             DRB5_0101  944      LSSTASALGKLQDVV  SSTASALGK  1        0.3754
861.1    40.00  0.66     Sequence
             DRB5_0101  945      SSTASALGKLQDVVN  SSTASALGK  0        0.2464
3476.2    70.00  0.52     Sequence
             DRB5_0101  946      STASALGKLQDVVNQ  TASALGKLQ  1        0.1368
11379.6    90.00  0.35     Sequence
             DRB5_0101  947      TASALGKLQDVVNQN  LGKLQDVVN  4        0.1150
14414.7    95.00  0.45     Sequence
             DRB5_0101  948      ASALGKLQDVVNQNA  LGKLQDVVN  3        0.1217
13405.7    95.00  0.47     Sequence
             DRB5_0101  949      SALGKLQDVVNQNAQ  LGKLQDVVN  2        0.1248
12961.4    95.00  0.40     Sequence
             DRB5_0101  950      ALGKLQDVVNQNAQA  LQDVVNQNA  4        0.1261
12783.8    95.00  0.34     Sequence
             DRB5_0101  951      LGKLQDVVNQNAQAL  VVNQNAQAL  6        0.2646
2856.3    65.00  0.71     Sequence
             DRB5_0101  952      GKLQDVVNQNAQALN  VVNQNAQAL  5        0.3372
1302.0    47.00  0.81     Sequence
             DRB5_0101  953      KLQDVVNQNAQALNT  VVNQNAQAL  4        0.3728
886.0    40.00  0.81     Sequence
```

```
             DRB5_0101  954      LQDVVNQNAQALNTL  VVNQNAQAL  3        0.4066
614.4    34.00  0.81     Sequence
             DRB5_0101  955      QDVVNQNAQALNTLV  VVNQNAQAL  2        0.3743
871.1    40.00  0.77     Sequence
             DRB5_0101  956      DVVNQNAQALNTLVK  AQALNTLVK  6        0.4701
308.9    25.00  0.52     Sequence
             DRB5_0101  957      VVNQNAQALNTLVKQ  AQALNTLVK  5        0.5071
207.0    20.00  0.73     Sequence
             DRB5_0101  958      VNQNAQALNTLVKQL  AQALNTLVK  4        0.5348
153.4    17.00  0.86     Sequence
             DRB5_0101  959      NQNAQALNTLVKQLS  AQALNTLVK  3        0.5519
127.6    15.00  0.83     Sequence
             DRB5_0101  960      QNAQALNTLVKQLSS  AQALNTLVK  2        0.5246
171.4    18.00  0.77     Sequence
             DRB5_0101  961      NAQALNTLVKQLSSN  AQALNTLVK  1        0.4695
311.0    25.00  0.73     Sequence
             DRB5_0101  962      AQALNTLVKQLSSNF  AQALNTLVK  0        0.3833
790.3    38.00  0.49     Sequence
             DRB5_0101  963      QALNTLVKQLSSNFG  LVKQLSSNF  5        0.3088
1770.4    55.00  0.43     Sequence
             DRB5_0101  964      ALNTLVKQLSSNFGA  LVKQLSSNF  4        0.3544
1080.9    44.00  0.43     Sequence
             DRB5_0101  965      LNTLVKQLSSNFGAI  VKQLSSNFG  4        0.3837
786.9    38.00  0.44     Sequence
             DRB5_0101  966      NTLVKQLSSNFGAIS  VKQLSSNFG  3        0.3845
780.4    38.00  0.54     Sequence
             DRB5_0101  967      TLVKQLSSNFGAISS  VKQLSSNFG  2        0.3592
1025.8    43.00  0.54     Sequence
             DRB5_0101  968      LVKQLSSNFGAISSV  VKQLSSNFG  1        0.3273
1448.0    49.00  0.47     Sequence
             DRB5_0101  969      VKQLSSNFGAISSVL  LSSNFGAIS  3        0.2914
2135.4    60.00  0.41     Sequence
             DRB5_0101  970      KQLSSNFGAISSVLN  FGAISSVLN  6        0.3250
1485.4    50.00  0.47     Sequence
             DRB5_0101  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.3467
1175.0    45.00  0.67     Sequence
             DRB5_0101  972      LSSNFGAISSVLNDI  FGAISSVLN  4        0.3659
954.1    42.00  0.76     Sequence
             DRB5_0101  973      SSNFGAISSVLNDIL  FGAISSVLN  3        0.3777
839.4    39.00  0.83     Sequence
             DRB5_0101  974      SNFGAISSVLNDILS  FGAISSVLN  2        0.3553
1070.0    44.00  0.81     Sequence
             DRB5_0101  975      NFGAISSVLNDILSR  FGAISSVLN  1        0.3433
1218.8    46.00  0.65     Sequence
             DRB5_0101  976      FGAISSVLNDILSRL  FGAISSVLN  0        0.2981
1986.4    55.00  0.41     Sequence
             DRB5_0101  977      GAISSVLNDILSRLD  SVLNDILSR  4        0.2601
2998.8    65.00  0.31     Sequence
             DRB5_0101  978      AISSVLNDILSRLDK  LNDILSRLD  5        0.3119
1711.3    55.00  0.37     Sequence
             DRB5_0101  979      ISSVLNDILSRLDKV  LNDILSRLD  4        0.3212
1548.0    50.00  0.38     Sequence
             DRB5_0101  980      SSVLNDILSRLDKVE  LNDILSRLD  3        0.3050
1843.3    55.00  0.41     Sequence
             DRB5_0101  981      SVLNDILSRLDKVEA  LNDILSRLD  2        0.2756
2535.8    60.00  0.41     Sequence
             DRB5_0101  982      VLNDILSRLDKVEAE  LNDILSRLD  1        0.2157
4847.0    75.00  0.38     Sequence
             DRB5_0101  983      LNDILSRLDKVEAEV  LSRLDKVEA  4        0.1638
8499.2    85.00  0.29     Sequence
             DRB5_0101  984      NDILSRLDKVEAEVQ  LSRLDKVEA  3        0.1287
12427.0    95.00  0.48     Sequence
             DRB5_0101  985      DILSRLDKVEAEVQI  LSRLDKVEA  2        0.1286
12433.5    95.00  0.42     Sequence
             DRB5_0101  986      ILSRLDKVEAEVQID  LSRLDKVEA  1        0.1235
13134.6    95.00  0.38     Sequence
```

```
             DRB5_0101  987      LSRLDKVEAEVQIDR  LDKVEAEVQ  3        0.1365
11419.5    90.00  0.31     Sequence
             DRB5_0101  988      SRLDKVEAEVQIDRL  VEAEVQIDR  5        0.1433
10603.6    90.00  0.38     Sequence
             DRB5_0101  989      RLDKVEAEVQIDRLI  VEAEVQIDR  4        0.1670
8211.8    85.00  0.38     Sequence
             DRB5_0101  990      LDKVEAEVQIDRLIT  VEAEVQIDR  3        0.1792
7191.5    85.00  0.37     Sequence
             DRB5_0101  991      DKVEAEVQIDRLITG  AEVQIDRLI  4        0.1718
7789.3    85.00  0.29     Sequence
             DRB5_0101  992      KVEAEVQIDRLITGR  AEVQIDRLI  3        0.2204
4605.1    75.00  0.27     Sequence
             DRB5_0101  993      VEAEVQIDRLITGRL  IDRLITGRL  6        0.3747
867.3    40.00  0.68     Sequence
             DRB5_0101  994      EAEVQIDRLITGRLQ  IDRLITGRL  5        0.4514
378.5    27.00  0.62     Sequence
             DRB5_0101  995      AEVQIDRLITGRLQS  IDRLITGRL  4        0.4924
242.8    22.00  0.58     Sequence
             DRB5_0101  996      EVQIDRLITGRLQSL  IDRLITGRL  3        0.5137
192.8    19.00  0.59     Sequence
             DRB5_0101  997      VQIDRLITGRLQSLQ  IDRLITGRL  2        0.5033
215.7    20.00  0.55     Sequence
             DRB5_0101  998      QIDRLITGRLQSLQT  IDRLITGRL  1        0.4420
418.8    29.00  0.53     Sequence
             DRB5_0101  999      IDRLITGRLQSLQTY  DRLITGRLQ  1        0.3245
1493.6    50.00  0.40     Sequence
             DRB5_0101 1000      DRLITGRLQSLQTYV  DRLITGRLQ  0        0.2470
3453.3    70.00  0.34     Sequence
             DRB5_0101 1001      RLITGRLQSLQTYVT  LQSLQTYVT  6        0.2544
3187.4    65.00  0.35     Sequence
             DRB5_0101 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.2897
2176.2    60.00  0.56     Sequence
             DRB5_0101 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.3019
1906.4    55.00  0.64     Sequence
             DRB5_0101 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.3158
1640.6    55.00  0.71     Sequence
             DRB5_0101 1005      GRLQSLQTYVTQQLI  LQSLQTYVT  2        0.2984
1981.3    55.00  0.65     Sequence
             DRB5_0101 1006      RLQSLQTYVTQQLIR  LQSLQTYVT  1        0.2952
2050.2    60.00  0.41     Sequence
             DRB5_0101 1007      LQSLQTYVTQQLIRA  YVTQQLIRA  6        0.3602
1015.3    43.00  0.43     Sequence
             DRB5_0101 1008      QSLQTYVTQQLIRAA  YVTQQLIRA  5        0.4009
653.0    35.00  0.52     Sequence
             DRB5_0101 1009      SLQTYVTQQLIRAAE  YVTQQLIRA  4        0.4000
659.5    35.00  0.52     Sequence
             DRB5_0101 1010      LQTYVTQQLIRAAEI  YVTQQLIRA  3        0.4085
602.0    34.00  0.56     Sequence
             DRB5_0101 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.4124
577.0    33.00  0.46     Sequence
             DRB5_0101 1012      TYVTQQLIRAAEIRA  QLIRAAEIR  5        0.4265
495.3    31.00  0.27     Sequence
             DRB5_0101 1013      YVTQQLIRAAEIRAS  QLIRAAEIR  4        0.4518
376.9    27.00  0.31     Sequence
             DRB5_0101 1014      VTQQLIRAAEIRASA  QLIRAAEIR  3        0.4939
238.8    22.00  0.30     Sequence
             DRB5_0101 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.4918
244.3    22.00  0.35     Sequence
             DRB5_0101 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.4910
246.4    22.00  0.44     Sequence
             DRB5_0101 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.4327
463.1    30.00  0.47     Sequence
             DRB5_0101 1018      LIRAAEIRASANLAA  IRAAEIRAS  1        0.3711
902.1    41.00  0.46     Sequence
             DRB5_0101 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.3220
1534.4    50.00  0.31     Sequence
```

```
             DRB5_0101 1020      RAAEIRASANLAAIK  ASANLAAIK  6        0.4628
334.3    26.00  0.55     Sequence
             DRB5_0101 1021      AAEIRASANLAAIKM  ASANLAAIK  5        0.6063
70.8    10.00  0.62     Sequence
             DRB5_0101 1022      AEIRASANLAAIKMS  ASANLAAIK  4        0.6540
42.3     7.00  0.64     Sequence         WB
             DRB5_0101 1023      EIRASANLAAIKMSE  ASANLAAIK  3        0.6596
39.8     6.50  0.64     Sequence         WB
             DRB5_0101 1024      IRASANLAAIKMSEC  ASANLAAIK  2        0.6427
47.7     7.50  0.63     Sequence         WB
             DRB5_0101 1025      RASANLAAIKMSECV  ASANLAAIK  1        0.5913
83.2    11.00  0.62     Sequence
             DRB5_0101 1026      ASANLAAIKMSECVL  ASANLAAIK  0        0.4447
406.9    28.00  0.44     Sequence
             DRB5_0101 1027      SANLAAIKMSECVLG  SANLAAIKM  0        0.3052
1840.4    55.00  0.25     Sequence
             DRB5_0101 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.2577
3076.9    65.00  0.37     Sequence
             DRB5_0101 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.2414
3669.6    70.00  0.41     Sequence
             DRB5_0101 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.2746
2562.6    65.00  0.40     Sequence
             DRB5_0101 1031      AAIKMSECVLGQSKR  KMSECVLGQ  3        0.2961
2031.0    60.00  0.28     Sequence
             DRB5_0101 1032      AIKMSECVLGQSKRV  CVLGQSKRV  6        0.3690
922.6    41.00  0.32     Sequence
             DRB5_0101 1033      IKMSECVLGQSKRVD  CVLGQSKRV  5        0.3795
823.2    39.00  0.43     Sequence
             DRB5_0101 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.3714
898.7    41.00  0.50     Sequence
             DRB5_0101 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.3513
1117.0    44.00  0.58     Sequence
             DRB5_0101 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.3205
1558.5    55.00  0.61     Sequence
             DRB5_0101 1037      ECVLGQSKRVDFCGK  CVLGQSKRV  1        0.3127
1697.2    55.00  0.54     Sequence
             DRB5_0101 1038      CVLGQSKRVDFCGKG  CVLGQSKRV  0        0.2714
2653.4    65.00  0.46     Sequence
             DRB5_0101 1039      VLGQSKRVDFCGKGY  SKRVDFCGK  4        0.2140
4934.6    75.00  0.28     Sequence
             DRB5_0101 1040      LGQSKRVDFCGKGYH  VDFCGKGYH  6        0.2541
3199.0    65.00  0.28     Sequence
             DRB5_0101 1041      GQSKRVDFCGKGYHL  VDFCGKGYH  5        0.3152
1651.4    55.00  0.38     Sequence
             DRB5_0101 1042      QSKRVDFCGKGYHLM  VDFCGKGYH  4        0.3786
831.8    39.00  0.38     Sequence
             DRB5_0101 1043      SKRVDFCGKGYHLMS  VDFCGKGYH  3        0.4073
609.4    34.00  0.33     Sequence
             DRB5_0101 1044      KRVDFCGKGYHLMSF  FCGKGYHLM  4        0.4077
607.2    34.00  0.29     Sequence
             DRB5_0101 1045      RVDFCGKGYHLMSFP  FCGKGYHLM  3        0.3757
858.0    40.00  0.31     Sequence
             DRB5_0101 1046      VDFCGKGYHLMSFPQ  GYHLMSFPQ  6        0.4112
584.8    34.00  0.43     Sequence
             DRB5_0101 1047      DFCGKGYHLMSFPQS  GYHLMSFPQ  5        0.4634
332.4    26.00  0.52     Sequence
             DRB5_0101 1048      FCGKGYHLMSFPQSA  GYHLMSFPQ  4        0.4934
240.0    22.00  0.58     Sequence
             DRB5_0101 1049      CGKGYHLMSFPQSAP  GYHLMSFPQ  3        0.4781
283.4    24.00  0.59     Sequence
             DRB5_0101 1050      GKGYHLMSFPQSAPH  GYHLMSFPQ  2        0.4803
276.8    23.00  0.56     Sequence
             DRB5_0101 1051      KGYHLMSFPQSAPHG  GYHLMSFPQ  1        0.4378
438.4    29.00  0.48     Sequence
             DRB5_0101 1052      GYHLMSFPQSAPHGV  GYHLMSFPQ  0        0.3686
926.6    41.00  0.24     Sequence
```

```
             DRB5_0101 1053      YHLMSFPQSAPHGVV  FPQSAPHGV  5        0.3220
1535.0    50.00  0.37     Sequence
             DRB5_0101 1054      HLMSFPQSAPHGVVF  FPQSAPHGV  4        0.3016
1914.0    55.00  0.55     Sequence
             DRB5_0101 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.3058
1828.9    55.00  0.64     Sequence
             DRB5_0101 1056      MSFPQSAPHGVVFLH  FPQSAPHGV  2        0.2778
2475.8    60.00  0.64     Sequence
             DRB5_0101 1057      SFPQSAPHGVVFLHV  FPQSAPHGV  1        0.2469
3457.6    70.00  0.58     Sequence
             DRB5_0101 1058      FPQSAPHGVVFLHVT  FPQSAPHGV  0        0.1934
6166.0    80.00  0.38     Sequence
             DRB5_0101 1059      PQSAPHGVVFLHVTY  APHGVVFLH  3        0.1460
10296.6    90.00  0.47     Sequence
             DRB5_0101 1060      QSAPHGVVFLHVTYV  APHGVVFLH  2        0.1852
6741.9    80.00  0.32     Sequence
             DRB5_0101 1061      SAPHGVVFLHVTYVP  VVFLHVTYV  5        0.1914
6301.8    80.00  0.38     Sequence
             DRB5_0101 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.2419
3649.2    70.00  0.44     Sequence
             DRB5_0101 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.2644
2860.9    65.00  0.50     Sequence
             DRB5_0101 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.2669
2785.4    65.00  0.54     Sequence
             DRB5_0101 1065      GVVFLHVTYVPAQEK  VTYVPAQEK  6        0.5575
120.0    14.00  0.71     Sequence
             DRB5_0101 1066      VVFLHVTYVPAQEKN  VTYVPAQEK  5        0.6192
61.6     9.00  0.81     Sequence        WB
             DRB5_0101 1067      VFLHVTYVPAQEKNF  VTYVPAQEK  4        0.6389
49.7     7.50  0.83     Sequence        WB
             DRB5_0101 1068      FLHVTYVPAQEKNFT  VTYVPAQEK  3        0.6472
45.5     7.00  0.85     Sequence        WB
             DRB5_0101 1069      LHVTYVPAQEKNFTT  VTYVPAQEK  2        0.6155
64.1     9.50  0.86     Sequence        WB
             DRB5_0101 1070      HVTYVPAQEKNFTTA  VTYVPAQEK  1        0.5687
106.3    13.00  0.82     Sequence
             DRB5_0101 1071      VTYVPAQEKNFTTAP  VTYVPAQEK  0        0.4700
309.4    25.00  0.75     Sequence
             DRB5_0101 1072      TYVPAQEKNFTTAPA  YVPAQEKNF  1        0.1749
7535.6    85.00  0.38     Sequence
             DRB5_0101 1073      YVPAQEKNFTTAPAI  EKNFTTAPA  5        0.1557
9271.2    90.00  0.26     Sequence
             DRB5_0101 1074      VPAQEKNFTTAPAIC  KNFTTAPAI  5        0.1793
7186.9    85.00  0.32     Sequence
             DRB5_0101 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.6320
53.6     8.00  0.83     Sequence        WB
             DRB5_0101 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.6887
29.0     5.00  0.85     Sequence        WB
             DRB5_0101 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.6928
27.8     4.50  0.87     Sequence        WB
             DRB5_0101 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.7149
21.9     3.50  0.89     Sequence        WB
             DRB5_0101 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.6992
25.9     4.50  0.89     Sequence        WB
             DRB5_0101 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.6351
51.8     8.00  0.90     Sequence        WB
             DRB5_0101 1081      FTTAPAICHDGKAHF  FTTAPAICH  0        0.5002
223.1    21.00  0.82     Sequence
             DRB5_0101 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.1985
5837.4    80.00  0.36     Sequence
             DRB5_0101 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.2521
3267.5    70.00  0.34     Sequence
             DRB5_0101 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.2612
2960.7    65.00  0.35     Sequence
             DRB5_0101 1085      PAICHDGKAHFPREG  CHDGKAHFP  3        0.2480
3415.2    70.00  0.31     Sequence
```

```
             DRB5_0101 1086      AICHDGKAHFPREGV  CHDGKAHFP  2        0.2295
4172.1    75.00  0.34     Sequence
             DRB5_0101 1087      ICHDGKAHFPREGVF  CHDGKAHFP  1        0.1800
7130.1    85.00  0.34     Sequence
             DRB5_0101 1088      CHDGKAHFPREGVFV  HFPREGVFV  6        0.1579
9061.5    90.00  0.24     Sequence
             DRB5_0101 1089      HDGKAHFPREGVFVS  HFPREGVFV  5        0.1839
6833.2    85.00  0.38     Sequence
             DRB5_0101 1090      DGKAHFPREGVFVSN  HFPREGVFV  4        0.1959
6005.8    80.00  0.40     Sequence
             DRB5_0101 1091      GKAHFPREGVFVSNG  HFPREGVFV  3        0.1906
6359.9    80.00  0.41     Sequence
             DRB5_0101 1092      KAHFPREGVFVSNGT  FPREGVFVS  3        0.1778
7302.2    85.00  0.38     Sequence
             DRB5_0101 1093      AHFPREGVFVSNGTH  GVFVSNGTH  6        0.1922
6251.8    80.00  0.33     Sequence
             DRB5_0101 1094      HFPREGVFVSNGTHW  VFVSNGTHW  6        0.3079
1787.2    55.00  0.48     Sequence
             DRB5_0101 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6        0.4635
331.9    26.00  0.38     Sequence
             DRB5_0101 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.5365
150.6    17.00  0.43     Sequence
             DRB5_0101 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.5637
112.3    14.00  0.44     Sequence
             DRB5_0101 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.5443
138.5    16.00  0.52     Sequence
             DRB5_0101 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.5318
158.5    17.00  0.52     Sequence
             DRB5_0101 1100      VFVSNGTHWFVTQRN  FVSNGTHWF  1        0.4936
239.7    22.00  0.47     Sequence
             DRB5_0101 1101      FVSNGTHWFVTQRNF  FVSNGTHWF  0        0.4314
469.7    30.00  0.32     Sequence
             DRB5_0101 1102      VSNGTHWFVTQRNFY  THWFVTQRN  4        0.3589
1028.9    43.00  0.43     Sequence
             DRB5_0101 1103      SNGTHWFVTQRNFYE  FVTQRNFYE  6        0.4382
436.5    29.00  0.39     Sequence
             DRB5_0101 1104      NGTHWFVTQRNFYEP  FVTQRNFYE  5        0.4484
390.6    28.00  0.47     Sequence
             DRB5_0101 1105      GTHWFVTQRNFYEPQ  FVTQRNFYE  4        0.4509
380.2    27.00  0.54     Sequence
             DRB5_0101 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3        0.4285
484.9    31.00  0.65     Sequence
             DRB5_0101 1107      HWFVTQRNFYEPQII  FVTQRNFYE  2        0.4010
652.9    35.00  0.65     Sequence
             DRB5_0101 1108      WFVTQRNFYEPQIIT  FVTQRNFYE  1        0.3861
767.2    38.00  0.61     Sequence
             DRB5_0101 1109      FVTQRNFYEPQIITT  FVTQRNFYE  0        0.3405
1255.6    47.00  0.47     Sequence
             DRB5_0101 1110      VTQRNFYEPQIITTD  RNFYEPQII  3        0.2626
2918.9    65.00  0.51     Sequence
             DRB5_0101 1111      TQRNFYEPQIITTDN  RNFYEPQII  2        0.2516
3286.1    70.00  0.45     Sequence
             DRB5_0101 1112      QRNFYEPQIITTDNT  FYEPQIITT  3        0.2380
3807.0    70.00  0.44     Sequence
             DRB5_0101 1113      RNFYEPQIITTDNTF  FYEPQIITT  2        0.1922
6246.3    80.00  0.50     Sequence
             DRB5_0101 1114      NFYEPQIITTDNTFV  FYEPQIITT  1        0.1369
11371.7    90.00  0.50     Sequence
             DRB5_0101 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.1378
11259.3    90.00  0.36     Sequence
             DRB5_0101 1116      YEPQIITTDNTFVSG  IITTDNTFV  4        0.1336
11784.3    90.00  0.50     Sequence
             DRB5_0101 1117      EPQIITTDNTFVSGN  IITTDNTFV  3        0.1394
11066.8    90.00  0.50     Sequence
             DRB5_0101 1118      PQIITTDNTFVSGNC  IITTDNTFV  2        0.1360
11475.7    90.00  0.48     Sequence
```

```
             DRB5_0101 1119      QIITTDNTFVSGNCD  ITTDNTFVS  2        0.1256
12844.4    95.00  0.34     Sequence
             DRB5_0101 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.0973
17449.1   100.00  0.34     Sequence
             DRB5_0101 1121      ITTDNTFVSGNCDVV  NTFVSGNCD  4        0.0756
22066.2   100.00  0.19     Sequence
             DRB5_0101 1122      TTDNTFVSGNCDVVI  FVSGNCDVV  5        0.0861
19696.1   100.00  0.28     Sequence
             DRB5_0101 1123      TDNTFVSGNCDVVIG  FVSGNCDVV  4        0.0900
18874.7   100.00  0.28     Sequence
             DRB5_0101 1124      DNTFVSGNCDVVIGI  VSGNCDVVI  4        0.0970
17506.3   100.00  0.31     Sequence
             DRB5_0101 1125      NTFVSGNCDVVIGIV  VSGNCDVVI  3        0.0987
17188.3   100.00  0.31     Sequence
             DRB5_0101 1126      TFVSGNCDVVIGIVN  CDVVIGIVN  6        0.1400
10996.9    90.00  0.44     Sequence
             DRB5_0101 1127      FVSGNCDVVIGIVNN  CDVVIGIVN  5        0.1469
10207.0    90.00  0.53     Sequence
             DRB5_0101 1128      VSGNCDVVIGIVNNT  CDVVIGIVN  4        0.1518
9674.1    90.00  0.52     Sequence
             DRB5_0101 1129      SGNCDVVIGIVNNTV  CDVVIGIVN  3        0.1791
7204.1    85.00  0.42     Sequence
             DRB5_0101 1130      GNCDVVIGIVNNTVY  VIGIVNNTV  5        0.1968
5943.3    80.00  0.29     Sequence
             DRB5_0101 1131      NCDVVIGIVNNTVYD  VIGIVNNTV  4        0.1990
5808.6    80.00  0.34     Sequence
             DRB5_0101 1132      CDVVIGIVNNTVYDP  VIGIVNNTV  3        0.1821
6971.9    85.00  0.37     Sequence
             DRB5_0101 1133      DVVIGIVNNTVYDPL  VIGIVNNTV  2        0.1739
7618.8    85.00  0.34     Sequence
             DRB5_0101 1134      VVIGIVNNTVYDPLQ  IGIVNNTVY  2        0.1616
8702.5    85.00  0.43     Sequence
             DRB5_0101 1135      VIGIVNNTVYDPLQP  IGIVNNTVY  1        0.1162
14220.1    95.00  0.40     Sequence
             DRB5_0101 1136      IGIVNNTVYDPLQPE  IGIVNNTVY  0        0.0736
22542.8   100.00  0.35     Sequence
             DRB5_0101 1137      GIVNNTVYDPLQPEL  NTVYDPLQP  4        0.0602
26067.3   100.00  0.29     Sequence
             DRB5_0101 1138      IVNNTVYDPLQPELD  YDPLQPELD  6        0.0719
22973.5   100.00  0.34     Sequence
             DRB5_0101 1139      VNNTVYDPLQPELDS  YDPLQPELD  5        0.0859
19735.1   100.00  0.46     Sequence
             DRB5_0101 1140      NNTVYDPLQPELDSF  YDPLQPELD  4        0.0958
17724.5   100.00  0.53     Sequence
             DRB5_0101 1141      NTVYDPLQPELDSFK  LQPELDSFK  6        0.2257
4347.8    75.00  0.62     Sequence
             DRB5_0101 1142      TVYDPLQPELDSFKE  LQPELDSFK  5        0.2745
2565.9    65.00  0.73     Sequence
             DRB5_0101 1143      VYDPLQPELDSFKEE  LQPELDSFK  4        0.2853
2282.1    60.00  0.76     Sequence
             DRB5_0101 1144      YDPLQPELDSFKEEL  LQPELDSFK  3        0.2972
2007.3    60.00  0.82     Sequence
             DRB5_0101 1145      DPLQPELDSFKEELD  LQPELDSFK  2        0.2724
2623.0    65.00  0.85     Sequence
             DRB5_0101 1146      PLQPELDSFKEELDK  LQPELDSFK  1        0.2726
2619.0    65.00  0.76     Sequence
             DRB5_0101 1147      LQPELDSFKEELDKY  LQPELDSFK  0        0.2321
4058.4    70.00  0.63     Sequence
             DRB5_0101 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.2193
4659.8    75.00  0.64     Sequence
             DRB5_0101 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.3482
1155.5    45.00  0.52     Sequence
             DRB5_0101 1150      ELDSFKEELDKYFKN  FKEELDKYF  4        0.3769
847.4    40.00  0.50     Sequence
             DRB5_0101 1151      LDSFKEELDKYFKNH  FKEELDKYF  3        0.3875
755.3    38.00  0.50     Sequence
```

```
             DRB5_0101 1152      DSFKEELDKYFKNHT  FKEELDKYF  2        0.3690
922.3    41.00  0.47     Sequence
             DRB5_0101 1153      SFKEELDKYFKNHTS  FKEELDKYF  1        0.3562
1059.7    44.00  0.45     Sequence
             DRB5_0101 1154      FKEELDKYFKNHTSP  KEELDKYFK  1        0.2918
2127.7    60.00  0.43     Sequence
             DRB5_0101 1155      KEELDKYFKNHTSPD  KEELDKYFK  0        0.1986
5833.9    80.00  0.41     Sequence
             DRB5_0101 1156      EELDKYFKNHTSPDV  FKNHTSPDV  6        0.1911
6323.0    80.00  0.29     Sequence
             DRB5_0101 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.2127
5003.6    75.00  0.41     Sequence
             DRB5_0101 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.2338
3985.8    70.00  0.52     Sequence
             DRB5_0101 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.2178
4736.7    75.00  0.60     Sequence
             DRB5_0101 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.2056
5403.8    80.00  0.65     Sequence
             DRB5_0101 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.1564
9201.6    90.00  0.65     Sequence
             DRB5_0101 1162      FKNHTSPDVDLGDIS  FKNHTSPDV  0        0.0909
18705.7   100.00  0.59     Sequence
             DRB5_0101 1163      KNHTSPDVDLGDISG  NHTSPDVDL  1        0.0377
33259.6   100.00  0.23     Sequence
             DRB5_0101 1164      NHTSPDVDLGDISGI  VDLGDISGI  6        0.0456
30536.8   100.00  0.39     Sequence
             DRB5_0101 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.0588
26458.3   100.00  0.49     Sequence
             DRB5_0101 1166      TSPDVDLGDISGINA  VDLGDISGI  4        0.0813
20735.2   100.00  0.44     Sequence
             DRB5_0101 1167      SPDVDLGDISGINAS  VDLGDISGI  3        0.0965
17599.5   100.00  0.39     Sequence
             DRB5_0101 1168      PDVDLGDISGINASF  VDLGDISGI  2        0.1040
16229.2    95.00  0.28     Sequence
             DRB5_0101 1169      DVDLGDISGINASFV  ISGINASFV  6        0.2170
4776.8    75.00  0.64     Sequence
             DRB5_0101 1170      VDLGDISGINASFVN  ISGINASFV  5        0.2872
2235.0    60.00  0.75     Sequence
             DRB5_0101 1171      DLGDISGINASFVNI  ISGINASFV  4        0.3178
1606.0    55.00  0.80     Sequence
             DRB5_0101 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.3413
1244.8    46.00  0.74     Sequence
             DRB5_0101 1173      GDISGINASFVNIQK  ISGINASFV  2        0.3760
855.6    40.00  0.52     Sequence
             DRB5_0101 1174      DISGINASFVNIQKE  NASFVNIQK  5        0.3744
870.8    40.00  0.37     Sequence
             DRB5_0101 1175      ISGINASFVNIQKEI  NASFVNIQK  4        0.3799
819.6    39.00  0.47     Sequence
             DRB5_0101 1176      SGINASFVNIQKEID  NASFVNIQK  3        0.3559
1062.6    44.00  0.52     Sequence
             DRB5_0101 1177      GINASFVNIQKEIDR  NASFVNIQK  2        0.3915
723.0    37.00  0.37     Sequence
             DRB5_0101 1178      INASFVNIQKEIDRL  VNIQKEIDR  5        0.3850
776.2    38.00  0.38     Sequence
             DRB5_0101 1179      NASFVNIQKEIDRLN  VNIQKEIDR  4        0.3577
1043.1    43.00  0.43     Sequence
             DRB5_0101 1180      ASFVNIQKEIDRLNE  VNIQKEIDR  3        0.3298
1410.1    49.00  0.48     Sequence
             DRB5_0101 1181      SFVNIQKEIDRLNEV  VNIQKEIDR  2        0.3042
1860.2    55.00  0.47     Sequence
             DRB5_0101 1182      FVNIQKEIDRLNEVA  VNIQKEIDR  1        0.2464
3476.0    70.00  0.41     Sequence
             DRB5_0101 1183      VNIQKEIDRLNEVAK  IDRLNEVAK  6        0.2864
2255.6    60.00  0.54     Sequence
             DRB5_0101 1184      NIQKEIDRLNEVAKN  IDRLNEVAK  5        0.3065
1814.8    55.00  0.67     Sequence
```

```
             DRB5_0101 1185      IQKEIDRLNEVAKNL  IDRLNEVAK  4        0.3343
1343.6    48.00  0.73     Sequence
             DRB5_0101 1186      QKEIDRLNEVAKNLN  IDRLNEVAK  3        0.3398
1265.3    47.00  0.73     Sequence
             DRB5_0101 1187      KEIDRLNEVAKNLNE  IDRLNEVAK  2        0.3203
1562.7    55.00  0.69     Sequence
             DRB5_0101 1188      EIDRLNEVAKNLNES  IDRLNEVAK  1        0.2796
2428.6    60.00  0.63     Sequence
             DRB5_0101 1189      IDRLNEVAKNLNESL  IDRLNEVAK  0        0.2281
4235.5    75.00  0.47     Sequence
             DRB5_0101 1190      DRLNEVAKNLNESLI  LNEVAKNLN  2        0.1384
11188.7    90.00  0.34     Sequence
             DRB5_0101 1191      RLNEVAKNLNESLID  LNEVAKNLN  1        0.1217
13393.2    95.00  0.29     Sequence
             DRB5_0101 1192      LNEVAKNLNESLIDL  VAKNLNESL  3        0.0917
18542.1   100.00  0.30     Sequence
             DRB5_0101 1193      NEVAKNLNESLIDLQ  VAKNLNESL  2        0.0947
17938.1   100.00  0.27     Sequence
             DRB5_0101 1194      EVAKNLNESLIDLQE  KNLNESLID  3        0.0921
18466.6   100.00  0.22     Sequence
             DRB5_0101 1195      VAKNLNESLIDLQEL  LNESLIDLQ  4        0.0965
17600.3   100.00  0.22     Sequence
             DRB5_0101 1196      AKNLNESLIDLQELG  LNESLIDLQ  3        0.0905
18778.7   100.00  0.23     Sequence
             DRB5_0101 1197      KNLNESLIDLQELGK  LIDLQELGK  6        0.2432
3599.5    70.00  0.80     Sequence
             DRB5_0101 1198      NLNESLIDLQELGKY  LIDLQELGK  5        0.3177
1606.8    55.00  0.70     Sequence
             DRB5_0101 1199      LNESLIDLQELGKYE  LIDLQELGK  4        0.3401
1261.8    47.00  0.68     Sequence
             DRB5_0101 1200      NESLIDLQELGKYEQ  LIDLQELGK  3        0.3543
1081.7    44.00  0.65     Sequence
             DRB5_0101 1201      ESLIDLQELGKYEQY  LIDLQELGK  2        0.3381
1289.4    47.00  0.63     Sequence
             DRB5_0101 1202      SLIDLQELGKYEQYI  LIDLQELGK  1        0.3174
1613.2    55.00  0.59     Sequence
             DRB5_0101 1203      LIDLQELGKYEQYIK  LIDLQELGK  0        0.2671
2779.7    65.00  0.38     Sequence
             DRB5_0101 1204      IDLQELGKYEQYIKW  LGKYEQYIK  5        0.2500
3344.9    70.00  0.40     Sequence
             DRB5_0101 1205      DLQELGKYEQYIKWP  GKYEQYIKW  5        0.2804
2407.5    60.00  0.28     Sequence
             DRB5_0101 1206      LQELGKYEQYIKWPW  YEQYIKWPW  6        0.3525
1103.2    44.00  0.36     Sequence
             DRB5_0101 1207      QELGKYEQYIKWPWY  YEQYIKWPW  5        0.3752
863.1    40.00  0.41     Sequence
             DRB5_0101 1208      ELGKYEQYIKWPWYI  YEQYIKWPW  4        0.4231
513.8    32.00  0.33     Sequence
             DRB5_0101 1209      LGKYEQYIKWPWYIW  YEQYIKWPW  3        0.4502
383.4    28.00  0.31     Sequence
             DRB5_0101 1210      GKYEQYIKWPWYIWL  QYIKWPWYI  4        0.4399
428.6    29.00  0.39     Sequence
             DRB5_0101 1211      KYEQYIKWPWYIWLG  QYIKWPWYI  3        0.4047
626.7    35.00  0.44     Sequence
             DRB5_0101 1212      YEQYIKWPWYIWLGF  QYIKWPWYI  2        0.3503
1129.7    45.00  0.46     Sequence
             DRB5_0101 1213      EQYIKWPWYIWLGFI  QYIKWPWYI  1        0.3022
1900.1    55.00  0.45     Sequence
             DRB5_0101 1214      QYIKWPWYIWLGFIA  YIKWPWYIW  1        0.2968
2014.4    60.00  0.28     Sequence
             DRB5_0101 1215      YIKWPWYIWLGFIAG  WYIWLGFIA  5        0.2420
3646.1    70.00  0.28     Sequence
             DRB5_0101 1216      IKWPWYIWLGFIAGL  WYIWLGFIA  4        0.2282
4232.7    75.00  0.30     Sequence
             DRB5_0101 1217      KWPWYIWLGFIAGLI  WLGFIAGLI  6        0.2936
2086.3    60.00  0.38     Sequence
```

```
              DRB5_0101 1218      WPWYIWLGFIAGLIA  WLGFIAGLI  5        0.3360
1318.1    47.00  0.43     Sequence
              DRB5_0101 1219      PWYIWLGFIAGLIAI  WLGFIAGLI  4        0.3643
971.1    42.00  0.40     Sequence
              DRB5_0101 1220      WYIWLGFIAGLIAIV  WLGFIAGLI  3        0.3839
785.1    38.00  0.38     Sequence
              DRB5_0101 1221      YIWLGFIAGLIAIVM  WLGFIAGLI  2        0.4097
594.0    34.00  0.28     Sequence
              DRB5_0101 1222      IWLGFIAGLIAIVMV  IAGLIAIVM  5        0.4103
590.2    34.00  0.26     Sequence
              DRB5_0101 1223      WLGFIAGLIAIVMVT  IAGLIAIVM  4        0.3905
731.2    37.00  0.34     Sequence
              DRB5_0101 1224      LGFIAGLIAIVMVTI  IAGLIAIVM  3        0.3520
1108.5    44.00  0.49     Sequence
              DRB5_0101 1225      GFIAGLIAIVMVTIM  IAGLIAIVM  2        0.3102
1743.0    55.00  0.52     Sequence
              DRB5_0101 1226      FIAGLIAIVMVTIML  IAGLIAIVM  1        0.2503
3333.6    70.00  0.45     Sequence
              DRB5_0101 1227      IAGLIAIVMVTIMLC  IAGLIAIVM  0        0.2181
4723.0    75.00  0.24     Sequence
              DRB5_0101 1228      AGLIAIVMVTIMLCC  IVMVTIMLC  5        0.1832
6887.4    85.00  0.31     Sequence
              DRB5_0101 1229      GLIAIVMVTIMLCCM  IVMVTIMLC  4        0.1703
7919.9    85.00  0.40     Sequence
              DRB5_0101 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3        0.1613
8727.6    85.00  0.46     Sequence
              DRB5_0101 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2        0.1704
7908.6    85.00  0.36     Sequence
              DRB5_0101 1232      AIVMVTIMLCCMTSC  TIMLCCMTS  5        0.1677
8143.2    85.00  0.31     Sequence
              DRB5_0101 1233      IVMVTIMLCCMTSCC  TIMLCCMTS  4        0.1549
9357.4    90.00  0.37     Sequence
              DRB5_0101 1234      VMVTIMLCCMTSCCS  TIMLCCMTS  3        0.1587
8982.0    90.00  0.41     Sequence
              DRB5_0101 1235      MVTIMLCCMTSCCSC  TIMLCCMTS  2        0.1495
9920.8    90.00  0.38     Sequence
              DRB5_0101 1236      VTIMLCCMTSCCSCL  TIMLCCMTS  1        0.1437
10562.8    90.00  0.31     Sequence
              DRB5_0101 1237      TIMLCCMTSCCSCLK  MTSCCSCLK  6        0.2188
4686.3    75.00  0.51     Sequence
              DRB5_0101 1238      IMLCCMTSCCSCLKG  MTSCCSCLK  5        0.2503
3332.4    70.00  0.59     Sequence
              DRB5_0101 1239      MLCCMTSCCSCLKGC  MTSCCSCLK  4        0.2466
3468.3    70.00  0.65     Sequence
              DRB5_0101 1240      LCCMTSCCSCLKGCC  MTSCCSCLK  3        0.2354
3914.3    70.00  0.69     Sequence
              DRB5_0101 1241      CCMTSCCSCLKGCCS  MTSCCSCLK  2        0.2069
5328.0    80.00  0.70     Sequence
              DRB5_0101 1242      CMTSCCSCLKGCCSC  MTSCCSCLK  1        0.1901
6396.0    80.00  0.67     Sequence
              DRB5_0101 1243      MTSCCSCLKGCCSCG  MTSCCSCLK  0        0.1424
10715.0    90.00  0.53     Sequence
              DRB5_0101 1244      TSCCSCLKGCCSCGS  CSCLKGCCS  3        0.0835
20255.8   100.00  0.35     Sequence
              DRB5_0101 1245      SCCSCLKGCCSCGSC  CSCLKGCCS  2        0.0856
19795.4   100.00  0.34     Sequence
              DRB5_0101 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.0807
20871.2   100.00  0.32     Sequence
              DRB5_0101 1247      CSCLKGCCSCGSCCK  CCSCGSCCK  6        0.1386
11158.4    90.00  0.39     Sequence
              DRB5_0101 1248      SCLKGCCSCGSCCKF  CCSCGSCCK  5        0.1671
8196.4    85.00  0.52     Sequence
              DRB5_0101 1249      CLKGCCSCGSCCKFD  CCSCGSCCK  4        0.1687
8057.3    85.00  0.58     Sequence
              DRB5_0101 1250      LKGCCSCGSCCKFDE  CCSCGSCCK  3        0.1827
6922.8    85.00  0.56     Sequence
```

```
             DRB5_0101 1251      KGCCSCGSCCKFDED  CCSCGSCCK  2        0.1671
8201.3    85.00  0.56     Sequence
             DRB5_0101 1252      GCCSCGSCCKFDEDD  CCSCGSCCK  1        0.1392
11088.9    90.00  0.57     Sequence
             DRB5_0101 1253      CCSCGSCCKFDEDDS  CCSCGSCCK  0        0.1055
15972.4    95.00  0.38     Sequence
             DRB5_0101 1254      CSCGSCCKFDEDDSE  CGSCCKFDE  2        0.0670
24208.6   100.00  0.38     Sequence
             DRB5_0101 1255      SCGSCCKFDEDDSEP  CGSCCKFDE  1        0.0564
27163.8   100.00  0.37     Sequence
             DRB5_0101 1256      CGSCCKFDEDDSEPV  CGSCCKFDE  0        0.0513
28689.0   100.00  0.19     Sequence
             DRB5_0101 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.0473
29981.6   100.00  0.50     Sequence
             DRB5_0101 1258      SCCKFDEDDSEPVLK  EDDSEPVLK  6        0.1168
14124.7    95.00  0.57     Sequence
             DRB5_0101 1259      CCKFDEDDSEPVLKG  EDDSEPVLK  5        0.1420
10762.0    90.00  0.61     Sequence
             DRB5_0101 1260      CKFDEDDSEPVLKGV  EDDSEPVLK  4        0.1600
8850.6    90.00  0.65     Sequence
             DRB5_0101 1261      KFDEDDSEPVLKGVK  EDDSEPVLK  3        0.1929
6203.1    80.00  0.60     Sequence
             DRB5_0101 1262      FDEDDSEPVLKGVKL  EDDSEPVLK  2        0.2236
4451.6    75.00  0.37     Sequence
             DRB5_0101 1263      DEDDSEPVLKGVKLH  SEPVLKGVK  4        0.2559
3135.9    65.00  0.29     Sequence
             DRB5_0101 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.3386
1281.5    47.00  0.49     Sequence
             DRB5_0101 1265      DDSEPVLKGVKLHYT  VLKGVKLHY  5        0.3844
780.8    38.00  0.57     Sequence
 HLA-DQA10501-DQB10201    1      PSPIKEMFVFLVLLP  EMFVFLVLL  5        0.2337
3989.3    55.00  0.29     Sequence
 HLA-DQA10501-DQB10201    2      SPIKEMFVFLVLLPL  FVFLVLLPL  6        0.2628
2910.0    45.00  0.39     Sequence
 HLA-DQA10501-DQB10201    3      PIKEMFVFLVLLPLV  FVFLVLLPL  5        0.2683
2742.9    43.00  0.25     Sequence
 HLA-DQA10501-DQB10201    4      IKEMFVFLVLLPLVS  FLVLLPLVS  6        0.2870
2240.0    38.00  0.32     Sequence
 HLA-DQA10501-DQB10201    5      KEMFVFLVLLPLVSS  FLVLLPLVS  5        0.2699
2695.1    43.00  0.32     Sequence
 HLA-DQA10501-DQB10201    6      EMFVFLVLLPLVSSQ  FLVLLPLVS  4        0.2686
2733.1    43.00  0.31     Sequence
 HLA-DQA10501-DQB10201    7      MFVFLVLLPLVSSQC  FLVLLPLVS  3        0.2664
2801.3    44.00  0.31     Sequence
 HLA-DQA10501-DQB10201    8      FVFLVLLPLVSSQCV  LPLVSSQCV  6        0.2867
2247.1    38.00  0.25     Sequence
 HLA-DQA10501-DQB10201    9      VFLVLLPLVSSQCVN  LPLVSSQCV  5        0.2652
2838.2    44.00  0.28     Sequence
 HLA-DQA10501-DQB10201   10      FLVLLPLVSSQCVNF  LPLVSSQCV  4        0.2753
2542.2    41.00  0.28     Sequence
 HLA-DQA10501-DQB10201   11      LVLLPLVSSQCVNFT  LPLVSSQCV  3        0.2648
2847.6    44.00  0.31     Sequence
 HLA-DQA10501-DQB10201   12      VLLPLVSSQCVNFTN  LPLVSSQCV  2        0.2489
3385.4    49.00  0.34     Sequence
 HLA-DQA10501-DQB10201   13      LLPLVSSQCVNFTNR  LPLVSSQCV  1        0.2231
4475.2    60.00  0.34     Sequence
 HLA-DQA10501-DQB10201   14      LPLVSSQCVNFTNRT  VSSQCVNFT  3        0.1954
6036.7    65.00  0.28     Sequence
 HLA-DQA10501-DQB10201   15      PLVSSQCVNFTNRTQ  VSSQCVNFT  2        0.1525
9607.1    80.00  0.39     Sequence
 HLA-DQA10501-DQB10201   16      LVSSQCVNFTNRTQL  VSSQCVNFT  1        0.1482
10057.4    80.00  0.34     Sequence
 HLA-DQA10501-DQB10201   17      VSSQCVNFTNRTQLP  VNFTNRTQL  5        0.1320
11984.3    85.00  0.34     Sequence
 HLA-DQA10501-DQB10201   18      SSQCVNFTNRTQLPS  VNFTNRTQL  4        0.1160
14247.8    85.00  0.41     Sequence
```

```
 HLA-DQA10501-DQB10201   19      SQCVNFTNRTQLPSA  VNFTNRTQL  3         0.1305
12184.5    85.00  0.32     Sequence
 HLA-DQA10501-DQB10201   20      QCVNFTNRTQLPSAY  NRTQLPSAY  6         0.1542
9425.2    75.00  0.29     Sequence
 HLA-DQA10501-DQB10201   21      CVNFTNRTQLPSAYT  NRTQLPSAY  5         0.1498
9882.7    80.00  0.31     Sequence
 HLA-DQA10501-DQB10201   22      VNFTNRTQLPSAYTN  NRTQLPSAY  4         0.1396
11035.5    80.00  0.30     Sequence
 HLA-DQA10501-DQB10201   23      NFTNRTQLPSAYTNS  NRTQLPSAY  3         0.1197
13696.4    85.00  0.34     Sequence
 HLA-DQA10501-DQB10201   24      FTNRTQLPSAYTNSF  LPSAYTNSF  6         0.1560
9250.4    75.00  0.41     Sequence
 HLA-DQA10501-DQB10201   25      TNRTQLPSAYTNSFT  PSAYTNSFT  6         0.1729
7698.3    70.00  0.37     Sequence
 HLA-DQA10501-DQB10201   26      NRTQLPSAYTNSFTR  PSAYTNSFT  5         0.1543
9416.5    75.00  0.38     Sequence
 HLA-DQA10501-DQB10201   27      RTQLPSAYTNSFTRG  PSAYTNSFT  4         0.1391
11095.1    80.00  0.37     Sequence
 HLA-DQA10501-DQB10201   28      TQLPSAYTNSFTRGV  PSAYTNSFT  3         0.1349
11614.5    80.00  0.33     Sequence
 HLA-DQA10501-DQB10201   29      QLPSAYTNSFTRGVY  PSAYTNSFT  2         0.1361
11465.6    80.00  0.26     Sequence
 HLA-DQA10501-DQB10201   30      LPSAYTNSFTRGVYY  NSFTRGVYY  6         0.1636
8518.6    75.00  0.43     Sequence
 HLA-DQA10501-DQB10201   31      PSAYTNSFTRGVYYP  NSFTRGVYY  5         0.1776
7320.7    70.00  0.47     Sequence
 HLA-DQA10501-DQB10201   32      SAYTNSFTRGVYYPD  FTRGVYYPD  6         0.2247
4396.2    55.00  0.34     Sequence
 HLA-DQA10501-DQB10201   33      AYTNSFTRGVYYPDK  FTRGVYYPD  5         0.2237
4446.5    60.00  0.28     Sequence
 HLA-DQA10501-DQB10201   34      YTNSFTRGVYYPDKV  RGVYYPDKV  6         0.3004
1939.1    35.00  0.49     Sequence
 HLA-DQA10501-DQB10201   35      TNSFTRGVYYPDKVF  RGVYYPDKV  5         0.3090
1766.2    33.00  0.49     Sequence
 HLA-DQA10501-DQB10201   36      NSFTRGVYYPDKVFR  RGVYYPDKV  4         0.2900
2168.8    38.00  0.46     Sequence
 HLA-DQA10501-DQB10201   37      SFTRGVYYPDKVFRS  RGVYYPDKV  3         0.2691
2719.7    43.00  0.46     Sequence
 HLA-DQA10501-DQB10201   38      FTRGVYYPDKVFRSS  RGVYYPDKV  2         0.2396
3740.1    55.00  0.48     Sequence
 HLA-DQA10501-DQB10201   39      TRGVYYPDKVFRSSV  RGVYYPDKV  1         0.2005
5713.6    65.00  0.52     Sequence
 HLA-DQA10501-DQB10201   40      RGVYYPDKVFRSSVL  RGVYYPDKV  0         0.1917
6285.6    65.00  0.30     Sequence
 HLA-DQA10501-DQB10201   41      GVYYPDKVFRSSVLH  DKVFRSSVL  5         0.1529
9559.9    80.00  0.34     Sequence
 HLA-DQA10501-DQB10201   42      VYYPDKVFRSSVLHS  VFRSSVLHS  6         0.1705
7901.4    75.00  0.40     Sequence
 HLA-DQA10501-DQB10201   43      YYPDKVFRSSVLHST  FRSSVLHST  6         0.1978
5881.1    65.00  0.40     Sequence
 HLA-DQA10501-DQB10201   44      YPDKVFRSSVLHSTQ  FRSSVLHST  5         0.1842
6815.5    70.00  0.41     Sequence
 HLA-DQA10501-DQB10201   45      PDKVFRSSVLHSTQD  FRSSVLHST  4         0.1936
6155.6    65.00  0.46     Sequence
 HLA-DQA10501-DQB10201   46      DKVFRSSVLHSTQDL  SVLHSTQDL  6         0.2536
3216.9    47.00  0.41     Sequence
 HLA-DQA10501-DQB10201   47      KVFRSSVLHSTQDLF  VLHSTQDLF  6         0.3782
835.6    19.00  0.65     Sequence
 HLA-DQA10501-DQB10201   48      VFRSSVLHSTQDLFL  LHSTQDLFL  6         0.4579
352.5     9.00  0.44     Sequence          WB
 HLA-DQA10501-DQB10201   49      FRSSVLHSTQDLFLP  LHSTQDLFL  5         0.4694
311.4     8.00  0.41     Sequence          WB
 HLA-DQA10501-DQB10201   50      RSSVLHSTQDLFLPF  VLHSTQDLF  3         0.4796
278.9     7.00  0.43     Sequence          WB
 HLA-DQA10501-DQB10201   51      SSVLHSTQDLFLPFF  TQDLFLPFF  6         0.5687
106.3     2.50  0.42     Sequence          WB
```

```
 HLA-DQA10501-DQB10201   52      SVLHSTQDLFLPFFS  TQDLFLPFF  5        0.5394
146.0     3.50  0.39     Sequence         WB
 HLA-DQA10501-DQB10201   53      VLHSTQDLFLPFFSN  TQDLFLPFF  4        0.5025
217.6     5.50  0.40     Sequence         WB
 HLA-DQA10501-DQB10201   54      LHSTQDLFLPFFSNV  TQDLFLPFF  3        0.4373
440.6    11.00  0.52     Sequence
 HLA-DQA10501-DQB10201   55      HSTQDLFLPFFSNVT  TQDLFLPFF  2        0.4115
582.4    14.00  0.56     Sequence
 HLA-DQA10501-DQB10201   56      STQDLFLPFFSNVTW  TQDLFLPFF  1        0.4184
540.7    13.00  0.51     Sequence
 HLA-DQA10501-DQB10201   57      TQDLFLPFFSNVTWF  TQDLFLPFF  0        0.4076
607.7    15.00  0.35     Sequence
 HLA-DQA10501-DQB10201   58      QDLFLPFFSNVTWFH  FLPFFSNVT  3        0.3194
1578.5    31.00  0.29     Sequence
 HLA-DQA10501-DQB10201   59      DLFLPFFSNVTWFHA  FLPFFSNVT  2        0.3166
1626.2    31.00  0.30     Sequence
 HLA-DQA10501-DQB10201   60      LFLPFFSNVTWFHAI  PFFSNVTWF  3        0.2977
1994.6    36.00  0.25     Sequence
 HLA-DQA10501-DQB10201   61      FLPFFSNVTWFHAIH  PFFSNVTWF  2        0.2731
2603.8    42.00  0.27     Sequence
 HLA-DQA10501-DQB10201   62      LPFFSNVTWFHAIHV  VTWFHAIHV  6        0.3008
1930.4    35.00  0.43     Sequence
 HLA-DQA10501-DQB10201   63      PFFSNVTWFHAIHVS  VTWFHAIHV  5        0.2824
2354.1    40.00  0.40     Sequence
 HLA-DQA10501-DQB10201   64      FFSNVTWFHAIHVSG  VTWFHAIHV  4        0.2884
2206.4    38.00  0.35     Sequence
 HLA-DQA10501-DQB10201   65      FSNVTWFHAIHVSGT  WFHAIHVSG  5        0.2791
2441.4    40.00  0.32     Sequence
 HLA-DQA10501-DQB10201   66      SNVTWFHAIHVSGTN  WFHAIHVSG  4        0.2622
2929.2    45.00  0.36     Sequence
 HLA-DQA10501-DQB10201   67      NVTWFHAIHVSGTNG  WFHAIHVSG  3        0.2420
3647.6    50.00  0.41     Sequence
 HLA-DQA10501-DQB10201   68      VTWFHAIHVSGTNGT  WFHAIHVSG  2        0.2193
4661.7    60.00  0.41     Sequence
 HLA-DQA10501-DQB10201   69      TWFHAIHVSGTNGTK  WFHAIHVSG  1        0.1869
6617.4    70.00  0.46     Sequence
 HLA-DQA10501-DQB10201   70      WFHAIHVSGTNGTKR  WFHAIHVSG  0        0.1535
9499.7    80.00  0.40     Sequence
 HLA-DQA10501-DQB10201   71      FHAIHVSGTNGTKRF  FHAIHVSGT  0        0.0952
17841.1    90.00  0.33     Sequence
 HLA-DQA10501-DQB10201   72      HAIHVSGTNGTKRFD  AIHVSGTNG  1        0.0700
23450.1    95.00  0.26     Sequence
 HLA-DQA10501-DQB10201   73      AIHVSGTNGTKRFDN  IHVSGTNGT  1        0.0592
26338.1   100.00  0.29     Sequence
 HLA-DQA10501-DQB10201   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.0496
29246.9   100.00  0.25     Sequence
 HLA-DQA10501-DQB10201   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.0472
29993.3   100.00  0.25     Sequence
 HLA-DQA10501-DQB10201   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.0830
20375.4    95.00  0.60     Sequence
 HLA-DQA10501-DQB10201   77      SGTNGTKRFDNPVLP  KRFDNPVLP  6        0.1348
11626.0    80.00  0.56     Sequence
 HLA-DQA10501-DQB10201   78      GTNGTKRFDNPVLPF  RFDNPVLPF  6        0.2834
2329.7    39.00  0.57     Sequence
 HLA-DQA10501-DQB10201   79      TNGTKRFDNPVLPFN  RFDNPVLPF  5        0.2772
2491.3    41.00  0.52     Sequence
 HLA-DQA10501-DQB10201   80      NGTKRFDNPVLPFND  RFDNPVLPF  4        0.2823
2357.6    40.00  0.54     Sequence
 HLA-DQA10501-DQB10201   81      GTKRFDNPVLPFNDG  RFDNPVLPF  3        0.2643
2864.2    44.00  0.52     Sequence
 HLA-DQA10501-DQB10201   82      TKRFDNPVLPFNDGV  RFDNPVLPF  2        0.2730
2607.1    42.00  0.46     Sequence
 HLA-DQA10501-DQB10201   83      KRFDNPVLPFNDGVY  RFDNPVLPF  1        0.2750
2550.5    41.00  0.35     Sequence
 HLA-DQA10501-DQB10201   84      RFDNPVLPFNDGVYF  LPFNDGVYF  6        0.3022
1901.4    35.00  0.30     Sequence
```

```
 HLA-DQA10501-DQB10201   85      FDNPVLPFNDGVYFA  LPFNDGVYF  5         0.2773
2488.6    41.00  0.28     Sequence
 HLA-DQA10501-DQB10201   86      DNPVLPFNDGVYFAS  LPFNDGVYF  4         0.2604
2987.5    45.00  0.26     Sequence
 HLA-DQA10501-DQB10201   87      NPVLPFNDGVYFAST  LPFNDGVYF  3         0.2491
3377.5    48.00  0.26     Sequence
 HLA-DQA10501-DQB10201   88      PVLPFNDGVYFASTE  DGVYFASTE  6         0.2813
2382.1    40.00  0.30     Sequence
 HLA-DQA10501-DQB10201   89      VLPFNDGVYFASTEK  GVYFASTEK  6         0.2778
2474.8    41.00  0.25     Sequence
 HLA-DQA10501-DQB10201   90      LPFNDGVYFASTEKS  VYFASTEKS  6         0.3095
1756.0    33.00  0.37     Sequence
 HLA-DQA10501-DQB10201   91      PFNDGVYFASTEKSN  VYFASTEKS  5         0.2859
2267.8    39.00  0.43     Sequence
 HLA-DQA10501-DQB10201   92      FNDGVYFASTEKSNI  VYFASTEKS  4         0.2814
2381.4    40.00  0.49     Sequence
 HLA-DQA10501-DQB10201   93      NDGVYFASTEKSNII  VYFASTEKS  3         0.2629
2908.1    45.00  0.50     Sequence
 HLA-DQA10501-DQB10201   94      DGVYFASTEKSNIIR  VYFASTEKS  2         0.2450
3530.8    50.00  0.54     Sequence
 HLA-DQA10501-DQB10201   95      GVYFASTEKSNIIRG  VYFASTEKS  1         0.1983
5852.6    65.00  0.57     Sequence
 HLA-DQA10501-DQB10201   96      VYFASTEKSNIIRGW  VYFASTEKS  0         0.1628
8593.9    75.00  0.47     Sequence
 HLA-DQA10501-DQB10201   97      YFASTEKSNIIRGWI  KSNIIRGWI  6         0.1191
13786.2    85.00  0.35     Sequence
 HLA-DQA10501-DQB10201   98      FASTEKSNIIRGWIF  SNIIRGWIF  6         0.1435
10582.3    80.00  0.31     Sequence
 HLA-DQA10501-DQB10201   99      ASTEKSNIIRGWIFG  SNIIRGWIF  5         0.1281
12502.2    85.00  0.32     Sequence
 HLA-DQA10501-DQB10201  100      STEKSNIIRGWIFGT  IIRGWIFGT  6         0.1435
10583.2    80.00  0.24     Sequence
 HLA-DQA10501-DQB10201  101      TEKSNIIRGWIFGTT  IRGWIFGTT  6         0.1528
9573.2    80.00  0.22     Sequence
 HLA-DQA10501-DQB10201  102      EKSNIIRGWIFGTTL  RGWIFGTTL  6         0.2398
3732.1    55.00  0.63     Sequence
 HLA-DQA10501-DQB10201  103      KSNIIRGWIFGTTLD  RGWIFGTTL  5         0.2721
2633.6    42.00  0.52     Sequence
 HLA-DQA10501-DQB10201  104      SNIIRGWIFGTTLDS  WIFGTTLDS  6         0.3382
1287.9    27.00  0.41     Sequence
 HLA-DQA10501-DQB10201  105      NIIRGWIFGTTLDSK  WIFGTTLDS  5         0.3411
1247.2    26.00  0.37     Sequence
 HLA-DQA10501-DQB10201  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4         0.3320
1377.3    28.00  0.37     Sequence
 HLA-DQA10501-DQB10201  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3         0.3097
1752.8    33.00  0.39     Sequence
 HLA-DQA10501-DQB10201  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2         0.2827
2348.1    39.00  0.46     Sequence
 HLA-DQA10501-DQB10201  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1         0.2579
3069.0    46.00  0.47     Sequence
 HLA-DQA10501-DQB10201  110      WIFGTTLDSKTQSLL  WIFGTTLDS  0         0.2157
4844.9    60.00  0.42     Sequence
 HLA-DQA10501-DQB10201  111      IFGTTLDSKTQSLLI  IFGTTLDSK  0         0.1409
10888.4    80.00  0.28     Sequence
 HLA-DQA10501-DQB10201  112      FGTTLDSKTQSLLIV  SKTQSLLIV  6         0.1166
14161.3    85.00  0.34     Sequence
 HLA-DQA10501-DQB10201  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4         0.1087
15424.5    90.00  0.25     Sequence
 HLA-DQA10501-DQB10201  114      TTLDSKTQSLLIVNN  TQSLLIVNN  6         0.1242
13037.5    85.00  0.38     Sequence
 HLA-DQA10501-DQB10201  115      TLDSKTQSLLIVNNA  QSLLIVNNA  6         0.1691
8027.4    75.00  0.52     Sequence
 HLA-DQA10501-DQB10201  116      LDSKTQSLLIVNNAT  QSLLIVNNA  5         0.1589
8959.2    75.00  0.45     Sequence
 HLA-DQA10501-DQB10201  117      DSKTQSLLIVNNATN  QSLLIVNNA  4         0.1510
9763.5    80.00  0.41     Sequence
```

```
 HLA-DQA10501-DQB10201  118      SKTQSLLIVNNATNV  LIVNNATNV  6        0.1776
7321.4    70.00  0.39     Sequence
 HLA-DQA10501-DQB10201  119      KTQSLLIVNNATNVV  IVNNATNVV  6        0.2329
4021.8    55.00  0.49     Sequence
 HLA-DQA10501-DQB10201  120      TQSLLIVNNATNVVI  IVNNATNVV  5        0.2592
3025.5    46.00  0.37     Sequence
 HLA-DQA10501-DQB10201  121      QSLLIVNNATNVVIK  IVNNATNVV  4        0.2238
4441.7    60.00  0.37     Sequence
 HLA-DQA10501-DQB10201  122      SLLIVNNATNVVIKV  IVNNATNVV  3        0.2168
4788.7    60.00  0.34     Sequence
 HLA-DQA10501-DQB10201  123      LLIVNNATNVVIKVC  IVNNATNVV  2        0.2026
5583.1    65.00  0.36     Sequence
 HLA-DQA10501-DQB10201  124      LIVNNATNVVIKVCE  IVNNATNVV  1        0.2047
5460.0    65.00  0.29     Sequence
 HLA-DQA10501-DQB10201  125      IVNNATNVVIKVCEF  NVVIKVCEF  6        0.2639
2877.2    44.00  0.52     Sequence
 HLA-DQA10501-DQB10201  126      VNNATNVVIKVCEFQ  NVVIKVCEF  5        0.2487
3392.3    49.00  0.48     Sequence
 HLA-DQA10501-DQB10201  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.3037
1870.1    34.00  0.33     Sequence
 HLA-DQA10501-DQB10201  128      NATNVVIKVCEFQFC  NVVIKVCEF  3        0.2970
2011.3    36.00  0.34     Sequence
 HLA-DQA10501-DQB10201  129      ATNVVIKVCEFQFCN  NVVIKVCEF  2        0.2825
2351.9    39.00  0.34     Sequence
 HLA-DQA10501-DQB10201  130      TNVVIKVCEFQFCNY  NVVIKVCEF  1        0.2771
2495.1    41.00  0.29     Sequence
 HLA-DQA10501-DQB10201  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.2585
3051.3    46.00  0.33     Sequence
 HLA-DQA10501-DQB10201  132      VVIKVCEFQFCNYPF  EFQFCNYPF  6        0.2541
3197.4    47.00  0.30     Sequence
 HLA-DQA10501-DQB10201  133      VIKVCEFQFCNYPFL  FQFCNYPFL  6        0.3137
1679.2    32.00  0.47     Sequence
 HLA-DQA10501-DQB10201  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.3010
1925.0    35.00  0.41     Sequence
 HLA-DQA10501-DQB10201  135      KVCEFQFCNYPFLGV  FQFCNYPFL  4        0.3057
1830.0    34.00  0.41     Sequence
 HLA-DQA10501-DQB10201  136      VCEFQFCNYPFLGVY  FQFCNYPFL  3        0.3086
1773.7    33.00  0.40     Sequence
 HLA-DQA10501-DQB10201  137      CEFQFCNYPFLGVYY  FQFCNYPFL  2        0.3347
1337.8    27.00  0.30     Sequence
 HLA-DQA10501-DQB10201  138      EFQFCNYPFLGVYYH  FQFCNYPFL  1        0.3142
1669.7    32.00  0.31     Sequence
 HLA-DQA10501-DQB10201  139      FQFCNYPFLGVYYHK  FQFCNYPFL  0        0.2682
2746.9    43.00  0.26     Sequence
 HLA-DQA10501-DQB10201  140      QFCNYPFLGVYYHKN  NYPFLGVYY  3        0.2080
5264.7    60.00  0.34     Sequence
 HLA-DQA10501-DQB10201  141      FCNYPFLGVYYHKNN  NYPFLGVYY  2        0.1873
6586.9    70.00  0.38     Sequence
 HLA-DQA10501-DQB10201  142      CNYPFLGVYYHKNNK  NYPFLGVYY  1        0.1553
9312.2    75.00  0.41     Sequence
 HLA-DQA10501-DQB10201  143      NYPFLGVYYHKNNKS  NYPFLGVYY  0        0.1379
11250.0    80.00  0.38     Sequence
 HLA-DQA10501-DQB10201  144      YPFLGVYYHKNNKSW  FLGVYYHKN  2        0.0946
17962.3    90.00  0.32     Sequence
 HLA-DQA10501-DQB10201  145      PFLGVYYHKNNKSWM  FLGVYYHKN  1        0.0707
23278.0    95.00  0.29     Sequence
 HLA-DQA10501-DQB10201  146      FLGVYYHKNNKSWME  YHKNNKSWM  5        0.0594
26290.5   100.00  0.28     Sequence
 HLA-DQA10501-DQB10201  147      LGVYYHKNNKSWMES  YHKNNKSWM  4        0.0517
28581.2   100.00  0.36     Sequence
 HLA-DQA10501-DQB10201  148      GVYYHKNNKSWMESE  NNKSWMESE  6        0.0830
20369.0    95.00  0.50     Sequence
 HLA-DQA10501-DQB10201  149      VYYHKNNKSWMESEF  NKSWMESEF  6        0.1870
6613.3    70.00  0.54     Sequence
 HLA-DQA10501-DQB10201  150      YYHKNNKSWMESEFR  KSWMESEFR  6        0.2360
3889.3    55.00  0.54     Sequence
```

```
 HLA-DQA10501-DQB10201  151      YHKNNKSWMESEFRV  KSWMESEFR  5        0.2512
3299.1    48.00  0.48     Sequence
 HLA-DQA10501-DQB10201  152      HKNNKSWMESEFRVY  KSWMESEFR  4        0.2778
2474.0    41.00  0.34     Sequence
 HLA-DQA10501-DQB10201  153      KNNKSWMESEFRVYS  KSWMESEFR  3        0.2689
2724.0    43.00  0.34     Sequence
 HLA-DQA10501-DQB10201  154      NNKSWMESEFRVYSS  KSWMESEFR  2        0.2611
2964.4    45.00  0.31     Sequence
 HLA-DQA10501-DQB10201  155      NKSWMESEFRVYSSA  KSWMESEFR  1        0.2389
3772.4    55.00  0.31     Sequence
 HLA-DQA10501-DQB10201  156      KSWMESEFRVYSSAN  WMESEFRVY  2        0.2137
4953.3    60.00  0.26     Sequence
 HLA-DQA10501-DQB10201  157      SWMESEFRVYSSANN  WMESEFRVY  1        0.1948
6072.8    65.00  0.30     Sequence
 HLA-DQA10501-DQB10201  158      WMESEFRVYSSANNC  RVYSSANNC  6        0.1994
5781.3    65.00  0.25     Sequence
 HLA-DQA10501-DQB10201  159      MESEFRVYSSANNCT  RVYSSANNC  5        0.1930
6198.3    65.00  0.26     Sequence
 HLA-DQA10501-DQB10201  160      ESEFRVYSSANNCTF  YSSANNCTF  6        0.2248
4393.6    55.00  0.32     Sequence
 HLA-DQA10501-DQB10201  161      SEFRVYSSANNCTFE  YSSANNCTF  5        0.2175
4753.9    60.00  0.28     Sequence
 HLA-DQA10501-DQB10201  162      EFRVYSSANNCTFEY  YSSANNCTF  4        0.2315
4085.6    55.00  0.25     Sequence
 HLA-DQA10501-DQB10201  163      FRVYSSANNCTFEYV  ANNCTFEYV  6        0.2684
2739.7    43.00  0.34     Sequence
 HLA-DQA10501-DQB10201  164      RVYSSANNCTFEYVS  ANNCTFEYV  5        0.2374
3833.8    55.00  0.36     Sequence
 HLA-DQA10501-DQB10201  165      VYSSANNCTFEYVSQ  ANNCTFEYV  4        0.2070
5323.4    60.00  0.40     Sequence
 HLA-DQA10501-DQB10201  166      YSSANNCTFEYVSQP  ANNCTFEYV  3        0.2159
4836.5    60.00  0.43     Sequence
 HLA-DQA10501-DQB10201  167      SSANNCTFEYVSQPF  TFEYVSQPF  6        0.4642
329.2     8.50  0.81     Sequence         WB
 HLA-DQA10501-DQB10201  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.5974
77.9     1.40  0.57     Sequence         SB
 HLA-DQA10501-DQB10201  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.6083
69.3     1.10  0.49     Sequence         SB
 HLA-DQA10501-DQB10201  170      NNCTFEYVSQPFLMD  FEYVSQPFL  4        0.6279
56.0     0.80  0.47     Sequence         SB
 HLA-DQA10501-DQB10201  171      NCTFEYVSQPFLMDL  FEYVSQPFL  3        0.6248
57.9     0.80  0.47     Sequence         SB
 HLA-DQA10501-DQB10201  172      CTFEYVSQPFLMDLE  FEYVSQPFL  2        0.6139
65.2     1.00  0.46     Sequence         SB
 HLA-DQA10501-DQB10201  173      TFEYVSQPFLMDLEG  FEYVSQPFL  1        0.5939
81.0     1.40  0.50     Sequence         SB
 HLA-DQA10501-DQB10201  174      FEYVSQPFLMDLEGK  FEYVSQPFL  0        0.5039
214.5     5.50  0.46     Sequence         WB
 HLA-DQA10501-DQB10201  175      EYVSQPFLMDLEGKQ  EYVSQPFLM  0        0.3656
957.3    21.00  0.29     Sequence
 HLA-DQA10501-DQB10201  176      YVSQPFLMDLEGKQG  SQPFLMDLE  2        0.3006
1935.0    35.00  0.31     Sequence
 HLA-DQA10501-DQB10201  177      VSQPFLMDLEGKQGN  SQPFLMDLE  1        0.2640
2874.5    44.00  0.28     Sequence
 HLA-DQA10501-DQB10201  178      SQPFLMDLEGKQGNF  PFLMDLEGK  2        0.2441
3562.7    50.00  0.25     Sequence
 HLA-DQA10501-DQB10201  179      QPFLMDLEGKQGNFK  PFLMDLEGK  1        0.2103
5139.5    60.00  0.32     Sequence
 HLA-DQA10501-DQB10201  180      PFLMDLEGKQGNFKN  FLMDLEGKQ  1        0.1771
7357.0    70.00  0.40     Sequence
 HLA-DQA10501-DQB10201  181      FLMDLEGKQGNFKNL  FLMDLEGKQ  0        0.1204
13584.8    85.00  0.40     Sequence
 HLA-DQA10501-DQB10201  182      LMDLEGKQGNFKNLS  LMDLEGKQG  0        0.0612
25793.5   100.00  0.40     Sequence
 HLA-DQA10501-DQB10201  183      MDLEGKQGNFKNLSE  QGNFKNLSE  6        0.0731
22671.7    95.00  0.48     Sequence
```

```
 HLA-DQA10501-DQB10201  184      DLEGKQGNFKNLSEF  GNFKNLSEF  6        0.1001
16920.8    90.00  0.37     Sequence
 HLA-DQA10501-DQB10201  185      LEGKQGNFKNLSEFV  NFKNLSEFV  6        0.2771
2495.1    41.00  0.77     Sequence
 HLA-DQA10501-DQB10201  186      EGKQGNFKNLSEFVF  NFKNLSEFV  5        0.3761
854.1    20.00  0.54     Sequence
 HLA-DQA10501-DQB10201  187      GKQGNFKNLSEFVFK  NFKNLSEFV  4        0.3337
1352.4    28.00  0.51     Sequence
 HLA-DQA10501-DQB10201  188      KQGNFKNLSEFVFKN  NFKNLSEFV  3        0.3169
1620.6    31.00  0.52     Sequence
 HLA-DQA10501-DQB10201  189      QGNFKNLSEFVFKNI  NFKNLSEFV  2        0.3117
1716.0    32.00  0.50     Sequence
 HLA-DQA10501-DQB10201  190      GNFKNLSEFVFKNID  NFKNLSEFV  1        0.2978
1992.7    36.00  0.44     Sequence
 HLA-DQA10501-DQB10201  191      NFKNLSEFVFKNIDG  FKNLSEFVF  1        0.2634
2892.8    45.00  0.38     Sequence
 HLA-DQA10501-DQB10201  192      FKNLSEFVFKNIDGY  FVFKNIDGY  6        0.2754
2539.4    41.00  0.47     Sequence
 HLA-DQA10501-DQB10201  193      KNLSEFVFKNIDGYF  VFKNIDGYF  6        0.3951
695.6    17.00  0.54     Sequence
 HLA-DQA10501-DQB10201  194      NLSEFVFKNIDGYFK  VFKNIDGYF  5        0.3823
798.6    19.00  0.47     Sequence
 HLA-DQA10501-DQB10201  195      LSEFVFKNIDGYFKI  VFKNIDGYF  4        0.3847
778.6    18.00  0.45     Sequence
 HLA-DQA10501-DQB10201  196      SEFVFKNIDGYFKIY  VFKNIDGYF  3        0.3934
708.4    17.00  0.43     Sequence
 HLA-DQA10501-DQB10201  197      EFVFKNIDGYFKIYS  VFKNIDGYF  2        0.3796
822.6    19.00  0.44     Sequence
 HLA-DQA10501-DQB10201  198      FVFKNIDGYFKIYSK  VFKNIDGYF  1        0.3441
1207.6    25.00  0.47     Sequence
 HLA-DQA10501-DQB10201  199      VFKNIDGYFKIYSKH  VFKNIDGYF  0        0.2533
3224.8    47.00  0.50     Sequence
 HLA-DQA10501-DQB10201  200      FKNIDGYFKIYSKHT  FKNIDGYFK  0        0.1439
10542.4    80.00  0.31     Sequence
 HLA-DQA10501-DQB10201  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.1071
15685.2    90.00  0.30     Sequence
 HLA-DQA10501-DQB10201  202      NIDGYFKIYSKHTPI  YFKIYSKHT  4        0.1097
15260.6    90.00  0.25     Sequence
 HLA-DQA10501-DQB10201  203      IDGYFKIYSKHTPIN  YFKIYSKHT  3        0.0915
18570.6    90.00  0.28     Sequence
 HLA-DQA10501-DQB10201  204      DGYFKIYSKHTPINL  YSKHTPINL  6        0.1265
12724.9    85.00  0.47     Sequence
 HLA-DQA10501-DQB10201  205      GYFKIYSKHTPINLV  YSKHTPINL  5        0.1386
11163.4    80.00  0.43     Sequence
 HLA-DQA10501-DQB10201  206      YFKIYSKHTPINLVR  YSKHTPINL  4        0.1278
12541.0    85.00  0.39     Sequence
 HLA-DQA10501-DQB10201  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.1558
9270.0    75.00  0.31     Sequence
 HLA-DQA10501-DQB10201  208      KIYSKHTPINLVRDL  TPINLVRDL  6        0.1665
8248.5    75.00  0.28     Sequence
 HLA-DQA10501-DQB10201  209      IYSKHTPINLVRDLP  PINLVRDLP  6        0.2651
2840.7    44.00  0.57     Sequence
 HLA-DQA10501-DQB10201  210      YSKHTPINLVRDLPQ  PINLVRDLP  5        0.2899
2171.4    38.00  0.44     Sequence
 HLA-DQA10501-DQB10201  211      SKHTPINLVRDLPQG  PINLVRDLP  4        0.2666
2794.0    44.00  0.44     Sequence
 HLA-DQA10501-DQB10201  212      KHTPINLVRDLPQGF  LVRDLPQGF  6        0.3312
1389.4    28.00  0.41     Sequence
 HLA-DQA10501-DQB10201  213      HTPINLVRDLPQGFS  LVRDLPQGF  5        0.3306
1398.0    28.00  0.42     Sequence
 HLA-DQA10501-DQB10201  214      TPINLVRDLPQGFSA  LVRDLPQGF  4        0.3198
1571.1    31.00  0.47     Sequence
 HLA-DQA10501-DQB10201  215      PINLVRDLPQGFSAL  LVRDLPQGF  3        0.2980
1989.2    36.00  0.50     Sequence
 HLA-DQA10501-DQB10201  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.2745
2564.0    42.00  0.58     Sequence
```

```
 HLA-DQA10501-DQB10201  217      NLVRDLPQGFSALEP  PQGFSALEP  6        0.3661
952.5    21.00  0.57     Sequence
 HLA-DQA10501-DQB10201  218      LVRDLPQGFSALEPL  QGFSALEPL  6        0.4778
284.3     7.00  0.51     Sequence         WB
 HLA-DQA10501-DQB10201  219      VRDLPQGFSALEPLV  QGFSALEPL  5        0.5020
218.8     5.50  0.43     Sequence         WB
 HLA-DQA10501-DQB10201  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.5537
125.1     3.00  0.31     Sequence         WB
 HLA-DQA10501-DQB10201  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.5580
119.4     2.50  0.33     Sequence         WB
 HLA-DQA10501-DQB10201  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.5563
121.6     3.00  0.38     Sequence         WB
 HLA-DQA10501-DQB10201  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.5419
142.1     3.50  0.41     Sequence         WB
 HLA-DQA10501-DQB10201  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.5140
192.1     4.50  0.44     Sequence         WB
 HLA-DQA10501-DQB10201  225      GFSALEPLVDLPIGI  FSALEPLVD  1        0.4606
342.7     8.50  0.49     Sequence         WB
 HLA-DQA10501-DQB10201  226      FSALEPLVDLPIGIN  FSALEPLVD  0        0.3687
926.0    21.00  0.47     Sequence
 HLA-DQA10501-DQB10201  227      SALEPLVDLPIGINI  PLVDLPIGI  4        0.2466
3470.0    49.00  0.26     Sequence
 HLA-DQA10501-DQB10201  228      ALEPLVDLPIGINIT  PLVDLPIGI  3        0.2149
4889.9    60.00  0.32     Sequence
 HLA-DQA10501-DQB10201  229      LEPLVDLPIGINITR  PLVDLPIGI  2        0.1834
6870.1    70.00  0.38     Sequence
 HLA-DQA10501-DQB10201  230      EPLVDLPIGINITRF  PIGINITRF  6        0.2540
3203.0    47.00  0.60     Sequence
 HLA-DQA10501-DQB10201  231      PLVDLPIGINITRFQ  PIGINITRF  5        0.2301
4148.5    55.00  0.57     Sequence
 HLA-DQA10501-DQB10201  232      LVDLPIGINITRFQT  PIGINITRF  4        0.2111
5095.8    60.00  0.61     Sequence
 HLA-DQA10501-DQB10201  233      VDLPIGINITRFQTL  PIGINITRF  3        0.2222
4517.0    60.00  0.53     Sequence
 HLA-DQA10501-DQB10201  234      DLPIGINITRFQTLL  PIGINITRF  2        0.2362
3882.9    55.00  0.45     Sequence
 HLA-DQA10501-DQB10201  235      LPIGINITRFQTLLA  ITRFQTLLA  6        0.2976
1997.1    36.00  0.47     Sequence
 HLA-DQA10501-DQB10201  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.3250
1485.3    29.00  0.35     Sequence
 HLA-DQA10501-DQB10201  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.2982
1985.2    36.00  0.34     Sequence
 HLA-DQA10501-DQB10201  238      GINITRFQTLLALHR  ITRFQTLLA  3        0.3028
1887.5    34.00  0.27     Sequence
 HLA-DQA10501-DQB10201  239      INITRFQTLLALHRS  ITRFQTLLA  2        0.2889
2194.4    38.00  0.25     Sequence
 HLA-DQA10501-DQB10201  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.2726
2618.7    42.00  0.25     Sequence
 HLA-DQA10501-DQB10201  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.2605
2984.8    45.00  0.28     Sequence
 HLA-DQA10501-DQB10201  242      TRFQTLLALHRSYLT  FQTLLALHR  2        0.2407
3699.6    55.00  0.32     Sequence
 HLA-DQA10501-DQB10201  243      RFQTLLALHRSYLTP  FQTLLALHR  1        0.2260
4335.2    55.00  0.29     Sequence
 HLA-DQA10501-DQB10201  244      FQTLLALHRSYLTPG  FQTLLALHR  0        0.1996
5767.3    65.00  0.25     Sequence
 HLA-DQA10501-DQB10201  245      QTLLALHRSYLTPGD  LLALHRSYL  2        0.1804
7099.2    70.00  0.22     Sequence
 HLA-DQA10501-DQB10201  246      TLLALHRSYLTPGDS  RSYLTPGDS  6        0.1761
7435.1    70.00  0.17     Sequence
 HLA-DQA10501-DQB10201  247      LLALHRSYLTPGDSS  SYLTPGDSS  6        0.1737
7631.7    70.00  0.17     Sequence
 HLA-DQA10501-DQB10201  248      LALHRSYLTPGDSSS  SYLTPGDSS  5        0.1485
10022.8    80.00  0.25     Sequence
 HLA-DQA10501-DQB10201  249      ALHRSYLTPGDSSSG  SYLTPGDSS  4        0.1260
12790.0    85.00  0.30     Sequence
```

```
 HLA-DQA10501-DQB10201  250      LHRSYLTPGDSSSGW  SYLTPGDSS  3        0.1212
13469.9    85.00  0.32     Sequence
 HLA-DQA10501-DQB10201  251      HRSYLTPGDSSSGWT  SYLTPGDSS  2        0.1159
14267.4    85.00  0.34     Sequence
 HLA-DQA10501-DQB10201  252      RSYLTPGDSSSGWTA  SYLTPGDSS  1        0.0960
17701.5    90.00  0.38     Sequence
 HLA-DQA10501-DQB10201  253      SYLTPGDSSSGWTAG  SYLTPGDSS  0        0.0800
21039.9    95.00  0.37     Sequence
 HLA-DQA10501-DQB10201  254      YLTPGDSSSGWTAGA  PGDSSSGWT  3        0.0617
25658.8   100.00  0.30     Sequence
 HLA-DQA10501-DQB10201  255      LTPGDSSSGWTAGAA  SSGWTAGAA  6        0.0781
21467.6    95.00  0.46     Sequence
 HLA-DQA10501-DQB10201  256      TPGDSSSGWTAGAAA  SGWTAGAAA  6        0.1279
12535.5    85.00  0.67     Sequence
 HLA-DQA10501-DQB10201  257      PGDSSSGWTAGAAAY  SGWTAGAAA  5        0.1622
8643.7    75.00  0.46     Sequence
 HLA-DQA10501-DQB10201  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.3849
776.8    18.00  0.76    Sequence
 HLA-DQA10501-DQB10201  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.4680
316.1     8.00  0.47    Sequence         WB
 HLA-DQA10501-DQB10201  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.4441
409.6    11.00  0.49    Sequence
 HLA-DQA10501-DQB10201  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.4509
380.5     9.50  0.48    Sequence         WB
 HLA-DQA10501-DQB10201  262      SGWTAGAAAYYVGYL  WTAGAAAYY  2        0.4796
278.7     7.00  0.34    Sequence         WB
 HLA-DQA10501-DQB10201  263      GWTAGAAAYYVGYLQ  WTAGAAAYY  1        0.4886
252.9     6.50  0.32    Sequence         WB
 HLA-DQA10501-DQB10201  264      WTAGAAAYYVGYLQP  AAAYYVGYL  4        0.5041
213.8     5.50  0.26    Sequence         WB
 HLA-DQA10501-DQB10201  265      TAGAAAYYVGYLQPR  AAAYYVGYL  3        0.4507
381.1     9.50  0.36    Sequence         WB
 HLA-DQA10501-DQB10201  266      AGAAAYYVGYLQPRT  AAAYYVGYL  2        0.4432
413.2    11.00  0.33    Sequence
 HLA-DQA10501-DQB10201  267      GAAAYYVGYLQPRTF  VGYLQPRTF  6        0.4624
335.7     8.50  0.21    Sequence         WB
 HLA-DQA10501-DQB10201  268      AAAYYVGYLQPRTFL  VGYLQPRTF  5        0.4375
439.7    11.00  0.19    Sequence
 HLA-DQA10501-DQB10201  269      AAYYVGYLQPRTFLL  VGYLQPRTF  4        0.4003
657.8    16.00  0.25    Sequence
 HLA-DQA10501-DQB10201  270      AYYVGYLQPRTFLLK  VGYLQPRTF  3        0.3415
1242.6    26.00  0.28     Sequence
 HLA-DQA10501-DQB10201  271      YYVGYLQPRTFLLKY  VGYLQPRTF  2        0.2827
2347.1    39.00  0.44     Sequence
 HLA-DQA10501-DQB10201  272      YVGYLQPRTFLLKYN  VGYLQPRTF  1        0.2303
4136.0    55.00  0.49     Sequence
 HLA-DQA10501-DQB10201  273      VGYLQPRTFLLKYNE  VGYLQPRTF  0        0.1600
8855.6    75.00  0.41     Sequence
 HLA-DQA10501-DQB10201  274      GYLQPRTFLLKYNEN  TFLLKYNEN  6        0.1376
11280.9    80.00  0.40     Sequence
 HLA-DQA10501-DQB10201  275      YLQPRTFLLKYNENG  TFLLKYNEN  5        0.1345
11665.9    80.00  0.34     Sequence
 HLA-DQA10501-DQB10201  276      LQPRTFLLKYNENGT  TFLLKYNEN  4        0.1257
12826.3    85.00  0.34     Sequence
 HLA-DQA10501-DQB10201  277      QPRTFLLKYNENGTI  TFLLKYNEN  3        0.1333
11815.6    85.00  0.28     Sequence
 HLA-DQA10501-DQB10201  278      PRTFLLKYNENGTIT  TFLLKYNEN  2        0.1288
12403.1    85.00  0.29     Sequence
 HLA-DQA10501-DQB10201  279      RTFLLKYNENGTITD  YNENGTITD  6        0.1465
10240.8    80.00  0.20     Sequence
 HLA-DQA10501-DQB10201  280      TFLLKYNENGTITDA  YNENGTITD  5        0.1403
10952.8    80.00  0.20     Sequence
 HLA-DQA10501-DQB10201  281      FLLKYNENGTITDAV  ENGTITDAV  6        0.2092
5199.5    60.00  0.57     Sequence
 HLA-DQA10501-DQB10201  282      LLKYNENGTITDAVD  NGTITDAVD  6        0.2757
2531.7    41.00  0.41     Sequence
```

```
 HLA-DQA10501-DQB10201  283       LKYNENGTITDAVDC  NGTITDAVD  5         0.2927
2106.6    37.00  0.38     Sequence
 HLA-DQA10501-DQB10201  284       KYNENGTITDAVDCA  TITDAVDCA  6         0.3865
763.8    18.00  0.47     Sequence
 HLA-DQA10501-DQB10201  285       YNENGTITDAVDCAL  ITDAVDCAL  6         0.4462
400.3    10.00  0.36     Sequence
 HLA-DQA10501-DQB10201  286       NENGTITDAVDCALD  TITDAVDCA  4         0.4508
380.8     9.50  0.37     Sequence         WB
 HLA-DQA10501-DQB10201  287       ENGTITDAVDCALDP  TITDAVDCA  3         0.4724
301.3     7.50  0.34     Sequence         WB
 HLA-DQA10501-DQB10201  288       NGTITDAVDCALDPL  AVDCALDPL  6         0.5074
206.3     5.00  0.25     Sequence         WB
 HLA-DQA10501-DQB10201  289       GTITDAVDCALDPLS  AVDCALDPL  5         0.4905
247.8     6.00  0.23     Sequence         WB
 HLA-DQA10501-DQB10201  290       TITDAVDCALDPLSE  AVDCALDPL  4         0.4741
295.8     7.50  0.26     Sequence         WB
 HLA-DQA10501-DQB10201  291       ITDAVDCALDPLSET  AVDCALDPL  3         0.4126
575.9    14.00  0.37     Sequence
 HLA-DQA10501-DQB10201  292       TDAVDCALDPLSETK  AVDCALDPL  2         0.3476
1163.4    25.00  0.51     Sequence
 HLA-DQA10501-DQB10201  293       DAVDCALDPLSETKC  AVDCALDPL  1         0.3135
1682.9    32.00  0.52     Sequence
 HLA-DQA10501-DQB10201  294       AVDCALDPLSETKCT  AVDCALDPL  0         0.2596
3014.8    46.00  0.49     Sequence
 HLA-DQA10501-DQB10201  295       VDCALDPLSETKCTL  VDCALDPLS  0         0.1408
10903.5    80.00  0.26     Sequence
 HLA-DQA10501-DQB10201  296       DCALDPLSETKCTLK  CALDPLSET  1         0.1002
16903.2    90.00  0.29     Sequence
 HLA-DQA10501-DQB10201  297       CALDPLSETKCTLKS  PLSETKCTL  4         0.0662
24417.5    95.00  0.29     Sequence
 HLA-DQA10501-DQB10201  298       ALDPLSETKCTLKSF  PLSETKCTL  3         0.0605
25971.9   100.00  0.37     Sequence
 HLA-DQA10501-DQB10201  299       LDPLSETKCTLKSFT  PLSETKCTL  2         0.0577
26769.3   100.00  0.35     Sequence
 HLA-DQA10501-DQB10201  300       DPLSETKCTLKSFTV  PLSETKCTL  1         0.0572
26932.3   100.00  0.30     Sequence
 HLA-DQA10501-DQB10201  301       PLSETKCTLKSFTVE  CTLKSFTVE  6         0.0648
24809.7    95.00  0.28     Sequence
 HLA-DQA10501-DQB10201  302       LSETKCTLKSFTVEK  TLKSFTVEK  6         0.0954
17818.5    90.00  0.51     Sequence
 HLA-DQA10501-DQB10201  303       SETKCTLKSFTVEKG  LKSFTVEKG  6         0.1389
11126.6    80.00  0.61     Sequence
 HLA-DQA10501-DQB10201  304       ETKCTLKSFTVEKGI  LKSFTVEKG  5         0.1379
11246.7    80.00  0.58     Sequence
 HLA-DQA10501-DQB10201  305       TKCTLKSFTVEKGIY  LKSFTVEKG  4         0.1453
10380.1    80.00  0.52     Sequence
 HLA-DQA10501-DQB10201  306       KCTLKSFTVEKGIYQ  LKSFTVEKG  3         0.1489
9986.6    80.00  0.38     Sequence
 HLA-DQA10501-DQB10201  307       CTLKSFTVEKGIYQT  LKSFTVEKG  2         0.1461
10287.0    80.00  0.36     Sequence
 HLA-DQA10501-DQB10201  308       TLKSFTVEKGIYQTS  LKSFTVEKG  1         0.1399
11003.3    80.00  0.31     Sequence
 HLA-DQA10501-DQB10201  309       LKSFTVEKGIYQTSN  FTVEKGIYQ  3         0.1283
12471.4    85.00  0.28     Sequence
 HLA-DQA10501-DQB10201  310       KSFTVEKGIYQTSNF  KGIYQTSNF  6         0.1587
8980.6    75.00  0.39     Sequence
 HLA-DQA10501-DQB10201  311       SFTVEKGIYQTSNFR  KGIYQTSNF  5         0.1473
10154.2    80.00  0.32     Sequence
 HLA-DQA10501-DQB10201  312       FTVEKGIYQTSNFRV  IYQTSNFRV  6         0.1598
8877.1    75.00  0.34     Sequence
 HLA-DQA10501-DQB10201  313       TVEKGIYQTSNFRVQ  IYQTSNFRV  5         0.1401
10976.5    80.00  0.37     Sequence
 HLA-DQA10501-DQB10201  314       VEKGIYQTSNFRVQP  IYQTSNFRV  4         0.1446
10453.6    80.00  0.37     Sequence
 HLA-DQA10501-DQB10201  315       EKGIYQTSNFRVQPT  TSNFRVQPT  6         0.1742
7596.5    70.00  0.38     Sequence
```

```
 HLA-DQA10501-DQB10201  316      KGIYQTSNFRVQPTE  TSNFRVQPT  5        0.1729
7701.2    70.00  0.38     Sequence
 HLA-DQA10501-DQB10201  317      GIYQTSNFRVQPTES  NFRVQPTES  6        0.2313
4094.3    55.00  0.52     Sequence
 HLA-DQA10501-DQB10201  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.3137
1677.8    32.00  0.44     Sequence
 HLA-DQA10501-DQB10201  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.3186
1592.2    31.00  0.44     Sequence
 HLA-DQA10501-DQB10201  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.2946
2063.6    36.00  0.46     Sequence
 HLA-DQA10501-DQB10201  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.3016
1912.2    35.00  0.46     Sequence
 HLA-DQA10501-DQB10201  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.2997
1954.0    35.00  0.43     Sequence
 HLA-DQA10501-DQB10201  323      NFRVQPTESIVRFPN  FRVQPTESI  1        0.2743
2569.8    42.00  0.46     Sequence
 HLA-DQA10501-DQB10201  324      FRVQPTESIVRFPNI  FRVQPTESI  0        0.2334
4003.4    55.00  0.34     Sequence
 HLA-DQA10501-DQB10201  325      RVQPTESIVRFPNIT  PTESIVRFP  3        0.1824
6951.8    70.00  0.21     Sequence
 HLA-DQA10501-DQB10201  326      VQPTESIVRFPNITN  PTESIVRFP  2        0.1731
7684.2    70.00  0.21     Sequence
 HLA-DQA10501-DQB10201  327      QPTESIVRFPNITNL  VRFPNITNL  6        0.2093
5195.3    60.00  0.26     Sequence
 HLA-DQA10501-DQB10201  328      PTESIVRFPNITNLC  RFPNITNLC  6        0.2329
4023.0    55.00  0.28     Sequence
 HLA-DQA10501-DQB10201  329      TESIVRFPNITNLCP  FPNITNLCP  6        0.2926
2108.9    37.00  0.28     Sequence
 HLA-DQA10501-DQB10201  330      ESIVRFPNITNLCPF  PNITNLCPF  6        0.3487
1149.7    25.00  0.31     Sequence
 HLA-DQA10501-DQB10201  331      SIVRFPNITNLCPFG  PNITNLCPF  5        0.3453
1192.3    25.00  0.25     Sequence
 HLA-DQA10501-DQB10201  332      IVRFPNITNLCPFGE  ITNLCPFGE  6        0.3512
1118.4    24.00  0.17     Sequence
 HLA-DQA10501-DQB10201  333      VRFPNITNLCPFGEV  ITNLCPFGE  5        0.3391
1275.0    26.00  0.21     Sequence
 HLA-DQA10501-DQB10201  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.3445
1202.1    25.00  0.22     Sequence
 HLA-DQA10501-DQB10201  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.3173
1614.1    31.00  0.25     Sequence
 HLA-DQA10501-DQB10201  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.2674
2770.8    43.00  0.29     Sequence
 HLA-DQA10501-DQB10201  337      NITNLCPFGEVFNAT  PFGEVFNAT  6        0.2691
2719.1    43.00  0.26     Sequence
 HLA-DQA10501-DQB10201  338      ITNLCPFGEVFNATR  PFGEVFNAT  5        0.2389
3768.7    55.00  0.26     Sequence
 HLA-DQA10501-DQB10201  339      TNLCPFGEVFNATRF  GEVFNATRF  6        0.2694
2710.3    43.00  0.34     Sequence
 HLA-DQA10501-DQB10201  340      NLCPFGEVFNATRFA  GEVFNATRF  5        0.2694
2710.6    43.00  0.28     Sequence
 HLA-DQA10501-DQB10201  341      LCPFGEVFNATRFAS  GEVFNATRF  4        0.2480
3415.5    49.00  0.26     Sequence
 HLA-DQA10501-DQB10201  342      CPFGEVFNATRFASV  GEVFNATRF  3        0.2494
3366.5    48.00  0.20     Sequence
 HLA-DQA10501-DQB10201  343      PFGEVFNATRFASVY  NATRFASVY  6        0.2611
2964.1    45.00  0.24     Sequence
 HLA-DQA10501-DQB10201  344      FGEVFNATRFASVYA  ATRFASVYA  6        0.2830
2340.2    39.00  0.38     Sequence
 HLA-DQA10501-DQB10201  345      GEVFNATRFASVYAW  TRFASVYAW  6        0.3425
1229.6    26.00  0.37     Sequence
 HLA-DQA10501-DQB10201  346      EVFNATRFASVYAWN  TRFASVYAW  5        0.3445
1202.7    25.00  0.34     Sequence
 HLA-DQA10501-DQB10201  347      VFNATRFASVYAWNR  TRFASVYAW  4        0.3209
1552.1    30.00  0.34     Sequence
 HLA-DQA10501-DQB10201  348      FNATRFASVYAWNRK  TRFASVYAW  3        0.2903
2162.6    38.00  0.32     Sequence
```

```
 HLA-DQA10501-DQB10201  349      NATRFASVYAWNRKR  TRFASVYAW  2        0.2466
3467.9    49.00  0.35     Sequence
 HLA-DQA10501-DQB10201  350      ATRFASVYAWNRKRI  TRFASVYAW  1        0.2166
4800.7    60.00  0.38     Sequence
 HLA-DQA10501-DQB10201  351      TRFASVYAWNRKRIS  TRFASVYAW  0        0.1716
7806.9    75.00  0.38     Sequence
 HLA-DQA10501-DQB10201  352      RFASVYAWNRKRISN  RFASVYAWN  0        0.1050
16048.8    90.00  0.39     Sequence
 HLA-DQA10501-DQB10201  353      FASVYAWNRKRISNC  FASVYAWNR  0        0.0641
25001.9    95.00  0.41     Sequence
 HLA-DQA10501-DQB10201  354      ASVYAWNRKRISNCV  NRKRISNCV  6        0.0486
29538.5   100.00  0.38     Sequence
 HLA-DQA10501-DQB10201  355      SVYAWNRKRISNCVA  RKRISNCVA  6        0.0889
19111.4    95.00  0.62     Sequence
 HLA-DQA10501-DQB10201  356      VYAWNRKRISNCVAD  RKRISNCVA  5        0.1019
16608.1    90.00  0.51     Sequence
 HLA-DQA10501-DQB10201  357      YAWNRKRISNCVADY  RISNCVADY  6        0.2450
3528.9    50.00  0.71     Sequence
 HLA-DQA10501-DQB10201  358      AWNRKRISNCVADYS  ISNCVADYS  6        0.3267
1457.6    29.00  0.53     Sequence
 HLA-DQA10501-DQB10201  359      WNRKRISNCVADYSV  ISNCVADYS  5        0.3357
1323.4    27.00  0.56     Sequence
 HLA-DQA10501-DQB10201  360      NRKRISNCVADYSVL  ISNCVADYS  4        0.3404
1257.6    26.00  0.56     Sequence
 HLA-DQA10501-DQB10201  361      RKRISNCVADYSVLY  ISNCVADYS  3        0.4116
581.9    14.00  0.41     Sequence
 HLA-DQA10501-DQB10201  362      KRISNCVADYSVLYN  ISNCVADYS  2        0.4429
415.0    11.00  0.29     Sequence
 HLA-DQA10501-DQB10201  363      RISNCVADYSVLYNS  ISNCVADYS  1        0.4200
531.2    13.00  0.28     Sequence
 HLA-DQA10501-DQB10201  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.3954
693.7    17.00  0.34     Sequence
 HLA-DQA10501-DQB10201  365      SNCVADYSVLYNSAS  CVADYSVLY  2        0.3499
1134.8    24.00  0.39     Sequence
 HLA-DQA10501-DQB10201  366      NCVADYSVLYNSASF  CVADYSVLY  1        0.3661
951.8    21.00  0.28     Sequence
 HLA-DQA10501-DQB10201  367      CVADYSVLYNSASFS  VLYNSASFS  6        0.3563
1058.4    23.00  0.25     Sequence
 HLA-DQA10501-DQB10201  368      VADYSVLYNSASFST  VLYNSASFS  5        0.3102
1742.6    33.00  0.32     Sequence
 HLA-DQA10501-DQB10201  369      ADYSVLYNSASFSTF  VLYNSASFS  4        0.3081
1782.7    33.00  0.35     Sequence
 HLA-DQA10501-DQB10201  370      DYSVLYNSASFSTFK  VLYNSASFS  3        0.2719
2639.3    42.00  0.38     Sequence
 HLA-DQA10501-DQB10201  371      YSVLYNSASFSTFKC  VLYNSASFS  2        0.2384
3792.8    55.00  0.43     Sequence
 HLA-DQA10501-DQB10201  372      SVLYNSASFSTFKCY  VLYNSASFS  1        0.2122
5033.0    60.00  0.38     Sequence
 HLA-DQA10501-DQB10201  373      VLYNSASFSTFKCYG  VLYNSASFS  0        0.1686
8063.6    75.00  0.34     Sequence
 HLA-DQA10501-DQB10201  374      LYNSASFSTFKCYGV  YNSASFSTF  1        0.1346
11659.3    80.00  0.31     Sequence
 HLA-DQA10501-DQB10201  375      YNSASFSTFKCYGVS  YNSASFSTF  0        0.1133
14676.9    90.00  0.28     Sequence
 HLA-DQA10501-DQB10201  376      NSASFSTFKCYGVSP  TFKCYGVSP  6        0.1293
12340.1    85.00  0.38     Sequence
 HLA-DQA10501-DQB10201  377      SASFSTFKCYGVSPT  FKCYGVSPT  6        0.1561
9240.1    75.00  0.29     Sequence
 HLA-DQA10501-DQB10201  378      ASFSTFKCYGVSPTK  FKCYGVSPT  5        0.1413
10837.9    80.00  0.29     Sequence
 HLA-DQA10501-DQB10201  379      SFSTFKCYGVSPTKL  CYGVSPTKL  6        0.2562
3126.3    46.00  0.62     Sequence
 HLA-DQA10501-DQB10201  380      FSTFKCYGVSPTKLN  CYGVSPTKL  5        0.2455
3509.7    49.00  0.67     Sequence
 HLA-DQA10501-DQB10201  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.2455
3510.2    49.00  0.72     Sequence
```

```
 HLA-DQA10501-DQB10201  382      TFKCYGVSPTKLNDL  CYGVSPTKL  3        0.2453
3519.9    49.00  0.68     Sequence
 HLA-DQA10501-DQB10201  383      FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.2292
4188.4    55.00  0.70     Sequence
 HLA-DQA10501-DQB10201  384      KCYGVSPTKLNDLCF  CYGVSPTKL  1        0.2276
4262.5    55.00  0.49     Sequence
 HLA-DQA10501-DQB10201  385      CYGVSPTKLNDLCFT  CYGVSPTKL  0        0.2153
4865.4    60.00  0.32     Sequence
 HLA-DQA10501-DQB10201  386      YGVSPTKLNDLCFTN  TKLNDLCFT  5        0.1686
8066.0    75.00  0.34     Sequence
 HLA-DQA10501-DQB10201  387      GVSPTKLNDLCFTNV  LNDLCFTNV  6        0.1904
6373.3    65.00  0.31     Sequence
 HLA-DQA10501-DQB10201  388      VSPTKLNDLCFTNVY  LNDLCFTNV  5        0.2057
5398.2    65.00  0.26     Sequence
 HLA-DQA10501-DQB10201  389      SPTKLNDLCFTNVYA  DLCFTNVYA  6        0.2263
4319.5    55.00  0.30     Sequence
 HLA-DQA10501-DQB10201  390      PTKLNDLCFTNVYAD  DLCFTNVYA  5        0.2470
3454.1    49.00  0.26     Sequence
 HLA-DQA10501-DQB10201  391      TKLNDLCFTNVYADS  CFTNVYADS  6        0.2907
2152.4    37.00  0.25     Sequence
 HLA-DQA10501-DQB10201  392      KLNDLCFTNVYADSF  FTNVYADSF  6        0.5874
86.9     1.60  0.78     Sequence         SB
 HLA-DQA10501-DQB10201  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.6121
66.5     1.10  0.74     Sequence         SB
 HLA-DQA10501-DQB10201  394      NDLCFTNVYADSFVI  FTNVYADSF  4        0.6090
68.7     1.10  0.72     Sequence         SB
 HLA-DQA10501-DQB10201  395      DLCFTNVYADSFVIR  FTNVYADSF  3        0.5814
92.7     1.70  0.72     Sequence         SB
 HLA-DQA10501-DQB10201  396      LCFTNVYADSFVIRG  FTNVYADSF  2        0.5524
126.8     3.00  0.74     Sequence         WB
 HLA-DQA10501-DQB10201  397      CFTNVYADSFVIRGD  FTNVYADSF  1        0.5173
185.5     4.50  0.68     Sequence         WB
 HLA-DQA10501-DQB10201  398      FTNVYADSFVIRGDE  FTNVYADSF  0        0.4599
345.0     8.50  0.61     Sequence         WB
 HLA-DQA10501-DQB10201  399      TNVYADSFVIRGDEV  SFVIRGDEV  6        0.4884
253.5     6.50  0.70     Sequence         WB
 HLA-DQA10501-DQB10201  400      NVYADSFVIRGDEVR  SFVIRGDEV  5        0.4692
312.2     8.00  0.70     Sequence         WB
 HLA-DQA10501-DQB10201  401      VYADSFVIRGDEVRQ  SFVIRGDEV  4        0.4703
308.5     8.00  0.64     Sequence         WB
 HLA-DQA10501-DQB10201  402      YADSFVIRGDEVRQI  SFVIRGDEV  3        0.4812
273.9     7.00  0.55     Sequence         WB
 HLA-DQA10501-DQB10201  403      ADSFVIRGDEVRQIA  SFVIRGDEV  2        0.4660
323.2     8.00  0.52     Sequence         WB
 HLA-DQA10501-DQB10201  404      DSFVIRGDEVRQIAP  SFVIRGDEV  1        0.4533
370.6     9.50  0.50     Sequence         WB
 HLA-DQA10501-DQB10201  405      SFVIRGDEVRQIAPG  SFVIRGDEV  0        0.4050
624.9    15.00  0.44     Sequence
 HLA-DQA10501-DQB10201  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.3019
1907.7    35.00  0.28     Sequence
 HLA-DQA10501-DQB10201  407      VIRGDEVRQIAPGQT  VRQIAPGQT  6        0.2660
2811.9    44.00  0.34     Sequence
 HLA-DQA10501-DQB10201  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.2367
3863.0    55.00  0.40     Sequence
 HLA-DQA10501-DQB10201  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.2141
4931.5    60.00  0.50     Sequence
 HLA-DQA10501-DQB10201  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.2103
5140.2    60.00  0.51     Sequence
 HLA-DQA10501-DQB10201  411      DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.2035
5527.1    65.00  0.49     Sequence
 HLA-DQA10501-DQB10201  412      EVRQIAPGQTGTIAD  VRQIAPGQT  1        0.1776
7314.9    70.00  0.44     Sequence
 HLA-DQA10501-DQB10201  413      VRQIAPGQTGTIADY  GQTGTIADY  6        0.1571
9133.5    75.00  0.30     Sequence
 HLA-DQA10501-DQB10201  414      RQIAPGQTGTIADYN  QTGTIADYN  6        0.2081
5261.2    60.00  0.58     Sequence
```

```
 HLA-DQA10501-DQB10201  415      QIAPGQTGTIADYNY  QTGTIADYN  5        0.2533
3227.5    47.00  0.44     Sequence
 HLA-DQA10501-DQB10201  416      IAPGQTGTIADYNYK  QTGTIADYN  4        0.2193
4659.0    60.00  0.46     Sequence
 HLA-DQA10501-DQB10201  417      APGQTGTIADYNYKL  QTGTIADYN  3        0.2257
4350.0    55.00  0.45     Sequence
 HLA-DQA10501-DQB10201  418      PGQTGTIADYNYKLP  QTGTIADYN  2        0.2424
3631.9    50.00  0.34     Sequence
 HLA-DQA10501-DQB10201  419      GQTGTIADYNYKLPD  QTGTIADYN  1        0.2544
3186.8    47.00  0.28     Sequence
 HLA-DQA10501-DQB10201  420      QTGTIADYNYKLPDD  DYNYKLPDD  6        0.2706
2676.2    43.00  0.22     Sequence
 HLA-DQA10501-DQB10201  421      TGTIADYNYKLPDDF  YNYKLPDDF  6        0.4214
523.6    13.00  0.62     Sequence
 HLA-DQA10501-DQB10201  422      GTIADYNYKLPDDFT  YNYKLPDDF  5        0.4169
549.4    14.00  0.60     Sequence
 HLA-DQA10501-DQB10201  423      TIADYNYKLPDDFTG  YNYKLPDDF  4        0.3897
737.7    17.00  0.60     Sequence
 HLA-DQA10501-DQB10201  424      IADYNYKLPDDFTGC  YNYKLPDDF  3        0.3699
913.9    21.00  0.63     Sequence
 HLA-DQA10501-DQB10201  425      ADYNYKLPDDFTGCV  YNYKLPDDF  2        0.3425
1228.6    26.00  0.67     Sequence
 HLA-DQA10501-DQB10201  426      DYNYKLPDDFTGCVI  YNYKLPDDF  1        0.3372
1301.9    27.00  0.54     Sequence
 HLA-DQA10501-DQB10201  427      YNYKLPDDFTGCVIA  YNYKLPDDF  0        0.2697
2700.6    43.00  0.45     Sequence
 HLA-DQA10501-DQB10201  428      NYKLPDDFTGCVIAW  DFTGCVIAW  6        0.2390
3766.2    55.00  0.40     Sequence
 HLA-DQA10501-DQB10201  429      YKLPDDFTGCVIAWN  FTGCVIAWN  6        0.2662
2806.9    44.00  0.32     Sequence
 HLA-DQA10501-DQB10201  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.2672
2775.9    43.00  0.28     Sequence
 HLA-DQA10501-DQB10201  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.2541
3199.6    47.00  0.28     Sequence
 HLA-DQA10501-DQB10201  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.2329
4022.5    55.00  0.31     Sequence
 HLA-DQA10501-DQB10201  433      DDFTGCVIAWNSNNL  VIAWNSNNL  6        0.2542
3194.3    47.00  0.30     Sequence
 HLA-DQA10501-DQB10201  434      DFTGCVIAWNSNNLD  IAWNSNNLD  6        0.3055
1833.5    34.00  0.40     Sequence
 HLA-DQA10501-DQB10201  435      FTGCVIAWNSNNLDS  IAWNSNNLD  5        0.2895
2180.5    38.00  0.41     Sequence
 HLA-DQA10501-DQB10201  436      TGCVIAWNSNNLDSK  IAWNSNNLD  4        0.2511
3304.1    48.00  0.46     Sequence
 HLA-DQA10501-DQB10201  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3        0.2444
3551.6    50.00  0.47     Sequence
 HLA-DQA10501-DQB10201  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2        0.2351
3926.7    55.00  0.50     Sequence
 HLA-DQA10501-DQB10201  439      VIAWNSNNLDSKVGG  IAWNSNNLD  1        0.2179
4732.2    60.00  0.50     Sequence
 HLA-DQA10501-DQB10201  440      IAWNSNNLDSKVGGN  IAWNSNNLD  0        0.1443
10492.4    80.00  0.49     Sequence
 HLA-DQA10501-DQB10201  441      AWNSNNLDSKVGGNY  WNSNNLDSK  1        0.0715
23065.9    95.00  0.47     Sequence
 HLA-DQA10501-DQB10201  442      WNSNNLDSKVGGNYN  WNSNNLDSK  0        0.0552
27525.3   100.00  0.34     Sequence
 HLA-DQA10501-DQB10201  443      NSNNLDSKVGGNYNY  DSKVGGNYN  5        0.0400
32422.2   100.00  0.31     Sequence
 HLA-DQA10501-DQB10201  444      SNNLDSKVGGNYNYL  KVGGNYNYL  6        0.0783
21435.3    95.00  0.63     Sequence
 HLA-DQA10501-DQB10201  445      NNLDSKVGGNYNYLY  VGGNYNYLY  6        0.1614
8718.5    75.00  0.57     Sequence
 HLA-DQA10501-DQB10201  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.1547
9372.0    75.00  0.52     Sequence
 HLA-DQA10501-DQB10201  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4        0.1815
7016.9    70.00  0.36     Sequence
```

```
 HLA-DQA10501-DQB10201  448      DSKVGGNYNYLYRLF  NYNYLYRLF  6        0.2516
3286.1    48.00  0.42     Sequence
 HLA-DQA10501-DQB10201  449      SKVGGNYNYLYRLFR  NYNYLYRLF  5        0.2323
4050.6    55.00  0.32     Sequence
 HLA-DQA10501-DQB10201  450      KVGGNYNYLYRLFRK  NYNYLYRLF  4        0.2022
5608.3    65.00  0.31     Sequence
 HLA-DQA10501-DQB10201  451      VGGNYNYLYRLFRKS  NYNYLYRLF  3        0.1773
7339.9    70.00  0.33     Sequence
 HLA-DQA10501-DQB10201  452      GGNYNYLYRLFRKSN  NYNYLYRLF  2        0.1491
9957.5    80.00  0.39     Sequence
 HLA-DQA10501-DQB10201  453      GNYNYLYRLFRKSNL  NYNYLYRLF  1        0.1501
9860.1    80.00  0.31     Sequence
 HLA-DQA10501-DQB10201  454      NYNYLYRLFRKSNLK  NYNYLYRLF  0        0.1215
13423.7    85.00  0.25     Sequence
 HLA-DQA10501-DQB10201  455      YNYLYRLFRKSNLKP  YRLFRKSNL  4        0.1033
16358.7    90.00  0.37     Sequence
 HLA-DQA10501-DQB10201  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6        0.1254
12871.7    85.00  0.34     Sequence
 HLA-DQA10501-DQB10201  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.1368
11377.8    80.00  0.33     Sequence
 HLA-DQA10501-DQB10201  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.1258
12824.7    85.00  0.32     Sequence
 HLA-DQA10501-DQB10201  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.1326
11907.1    85.00  0.33     Sequence
 HLA-DQA10501-DQB10201  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.1147
14447.9    85.00  0.31     Sequence
 HLA-DQA10501-DQB10201  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.1100
15205.6    90.00  0.24     Sequence
 HLA-DQA10501-DQB10201  462      FRKSNLKPFERDIST  RKSNLKPFE  1        0.0988
17173.1    90.00  0.19     Sequence
 HLA-DQA10501-DQB10201  463      RKSNLKPFERDISTE  PFERDISTE  6        0.1238
13094.4    85.00  0.45     Sequence
 HLA-DQA10501-DQB10201  464      KSNLKPFERDISTEI  FERDISTEI  6        0.2523
3260.2    48.00  0.70     Sequence
 HLA-DQA10501-DQB10201  465      SNLKPFERDISTEIY  ERDISTEIY  6        0.4074
609.3    15.00  0.64     Sequence
 HLA-DQA10501-DQB10201  466      NLKPFERDISTEIYQ  ERDISTEIY  5        0.3837
786.9    18.00  0.60     Sequence
 HLA-DQA10501-DQB10201  467      LKPFERDISTEIYQA  ERDISTEIY  4        0.3855
771.4    18.00  0.53     Sequence
 HLA-DQA10501-DQB10201  468      KPFERDISTEIYQAG  ERDISTEIY  3        0.3590
1028.2    23.00  0.52     Sequence
 HLA-DQA10501-DQB10201  469      PFERDISTEIYQAGS  ERDISTEIY  2        0.3443
1205.7    25.00  0.55     Sequence
 HLA-DQA10501-DQB10201  470      FERDISTEIYQAGST  ERDISTEIY  1        0.3229
1518.9    30.00  0.51     Sequence
 HLA-DQA10501-DQB10201  471      ERDISTEIYQAGSTP  ERDISTEIY  0        0.2811
2387.0    40.00  0.32     Sequence
 HLA-DQA10501-DQB10201  472      RDISTEIYQAGSTPC  EIYQAGSTP  5        0.2467
3464.9    49.00  0.32     Sequence
 HLA-DQA10501-DQB10201  473      DISTEIYQAGSTPCN  EIYQAGSTP  4        0.2322
4052.7    55.00  0.35     Sequence
 HLA-DQA10501-DQB10201  474      ISTEIYQAGSTPCNG  EIYQAGSTP  3        0.2015
5648.3    65.00  0.40     Sequence
 HLA-DQA10501-DQB10201  475      STEIYQAGSTPCNGV  EIYQAGSTP  2        0.1848
6768.5    70.00  0.38     Sequence
 HLA-DQA10501-DQB10201  476      TEIYQAGSTPCNGVK  EIYQAGSTP  1        0.1622
8650.1    75.00  0.39     Sequence
 HLA-DQA10501-DQB10201  477      EIYQAGSTPCNGVKG  EIYQAGSTP  0        0.1261
12781.3    85.00  0.37     Sequence
 HLA-DQA10501-DQB10201  478      IYQAGSTPCNGVKGF  IYQAGSTPC  0        0.0760
21966.6    95.00  0.38     Sequence
 HLA-DQA10501-DQB10201  479      YQAGSTPCNGVKGFN  QAGSTPCNG  1        0.0454
30601.0    100.00  0.40     Sequence
 HLA-DQA10501-DQB10201  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.0389
32826.3    100.00  0.26     Sequence
```

```
 HLA-DQA10501-DQB10201  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.0381
33100.2   100.00  0.28      Sequence
 HLA-DQA10501-DQB10201  482      GSTPCNGVKGFNCYF  GVKGFNCYF  6        0.1124
14819.7    90.00  0.71      Sequence
 HLA-DQA10501-DQB10201  483      STPCNGVKGFNCYFP  GVKGFNCYF  5        0.1898
6414.8    65.00  0.51     Sequence
 HLA-DQA10501-DQB10201  484      TPCNGVKGFNCYFPL  VKGFNCYFP  5        0.2277
4254.9    55.00  0.31     Sequence
 HLA-DQA10501-DQB10201  485      PCNGVKGFNCYFPLQ  VKGFNCYFP  4        0.2514
3291.9    48.00  0.28     Sequence
 HLA-DQA10501-DQB10201  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.2817
2373.6    40.00  0.28     Sequence
 HLA-DQA10501-DQB10201  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.2888
2197.7    38.00  0.26     Sequence
 HLA-DQA10501-DQB10201  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.2628
2912.7    45.00  0.30     Sequence
 HLA-DQA10501-DQB10201  489      VKGFNCYFPLQSYGF  YFPLQSYGF  6        0.2689
2724.6    43.00  0.33     Sequence
 HLA-DQA10501-DQB10201  490      KGFNCYFPLQSYGFQ  YFPLQSYGF  5        0.2426
3624.2    50.00  0.32     Sequence
 HLA-DQA10501-DQB10201  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.2426
3623.5    50.00  0.31     Sequence
 HLA-DQA10501-DQB10201  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.2322
4051.9    55.00  0.31     Sequence
 HLA-DQA10501-DQB10201  493      NCYFPLQSYGFQPTY  YFPLQSYGF  2        0.2372
3841.1    55.00  0.23     Sequence
 HLA-DQA10501-DQB10201  494      CYFPLQSYGFQPTYG  SYGFQPTYG  6        0.2600
3002.0    45.00  0.34     Sequence
 HLA-DQA10501-DQB10201  495      YFPLQSYGFQPTYGV  SYGFQPTYG  5        0.2594
3019.2    46.00  0.33     Sequence
 HLA-DQA10501-DQB10201  496      FPLQSYGFQPTYGVG  SYGFQPTYG  4        0.2228
4487.6    60.00  0.41     Sequence
 HLA-DQA10501-DQB10201  497      PLQSYGFQPTYGVGY  SYGFQPTYG  3        0.2176
4749.2    60.00  0.38     Sequence
 HLA-DQA10501-DQB10201  498      LQSYGFQPTYGVGYQ  SYGFQPTYG  2        0.2047
5460.7    65.00  0.43     Sequence
 HLA-DQA10501-DQB10201  499      QSYGFQPTYGVGYQP  SYGFQPTYG  1        0.2269
4295.3    55.00  0.28     Sequence
 HLA-DQA10501-DQB10201  500      SYGFQPTYGVGYQPY  TYGVGYQPY  6        0.3114
1720.9    32.00  0.53     Sequence
 HLA-DQA10501-DQB10201  501      YGFQPTYGVGYQPYR  TYGVGYQPY  5        0.2914
2137.5    37.00  0.51     Sequence
 HLA-DQA10501-DQB10201  502      GFQPTYGVGYQPYRV  TYGVGYQPY  4        0.3072
1800.9    33.00  0.40     Sequence
 HLA-DQA10501-DQB10201  503      FQPTYGVGYQPYRVV  TYGVGYQPY  3        0.3034
1875.4    34.00  0.41     Sequence
 HLA-DQA10501-DQB10201  504      QPTYGVGYQPYRVVV  TYGVGYQPY  2        0.2752
2546.0    41.00  0.40     Sequence
 HLA-DQA10501-DQB10201  505      PTYGVGYQPYRVVVL  TYGVGYQPY  1        0.2826
2350.8    39.00  0.29     Sequence
 HLA-DQA10501-DQB10201  506      TYGVGYQPYRVVVLS  GVGYQPYRV  2        0.2536
3216.9    47.00  0.28     Sequence
 HLA-DQA10501-DQB10201  507      YGVGYQPYRVVVLSF  PYRVVVLSF  6        0.3232
1514.8    30.00  0.60     Sequence
 HLA-DQA10501-DQB10201  508      GVGYQPYRVVVLSFE  YRVVVLSFE  6        0.3901
734.6    17.00  0.46     Sequence
 HLA-DQA10501-DQB10201  509      VGYQPYRVVVLSFEL  YRVVVLSFE  5        0.3964
686.2    16.00  0.46     Sequence
 HLA-DQA10501-DQB10201  510      GYQPYRVVVLSFELL  YRVVVLSFE  4        0.4198
532.4    13.00  0.40     Sequence
 HLA-DQA10501-DQB10201  511      YQPYRVVVLSFELLH  YRVVVLSFE  3        0.4171
548.0    14.00  0.31     Sequence
 HLA-DQA10501-DQB10201  512      QPYRVVVLSFELLHA  YRVVVLSFE  2        0.4334
459.5    12.00  0.27     Sequence
 HLA-DQA10501-DQB10201  513      PYRVVVLSFELLHAP  VLSFELLHA  5        0.4302
476.0    12.00  0.25     Sequence
```

```
 HLA-DQA10501-DQB10201  514      YRVVVLSFELLHAPA  VLSFELLHA  4        0.4253
501.8    13.00  0.24     Sequence
 HLA-DQA10501-DQB10201  515      RVVVLSFELLHAPAT  VLSFELLHA  3        0.3883
748.7    18.00  0.25     Sequence
 HLA-DQA10501-DQB10201  516      VVVLSFELLHAPATV  VLSFELLHA  2        0.4079
605.4    15.00  0.24     Sequence
 HLA-DQA10501-DQB10201  517      VVLSFELLHAPATVC  ELLHAPATV  5        0.3764
851.3    20.00  0.21     Sequence
 HLA-DQA10501-DQB10201  518      VLSFELLHAPATVCG  ELLHAPATV  4        0.3314
1385.9    28.00  0.25     Sequence
 HLA-DQA10501-DQB10201  519      LSFELLHAPATVCGP  ELLHAPATV  3        0.3037
1871.0    34.00  0.31     Sequence
 HLA-DQA10501-DQB10201  520      SFELLHAPATVCGPK  ELLHAPATV  2        0.2696
2706.0    43.00  0.35     Sequence
 HLA-DQA10501-DQB10201  521      FELLHAPATVCGPKK  ELLHAPATV  1        0.2234
4461.2    60.00  0.48     Sequence
 HLA-DQA10501-DQB10201  522      ELLHAPATVCGPKKS  ELLHAPATV  0        0.1646
8421.3    75.00  0.50     Sequence
 HLA-DQA10501-DQB10201  523      LLHAPATVCGPKKST  LLHAPATVC  0        0.0774
21635.2    95.00  0.28     Sequence
 HLA-DQA10501-DQB10201  524      LHAPATVCGPKKSTN  PATVCGPKK  3        0.0535
28035.4   100.00  0.37     Sequence
 HLA-DQA10501-DQB10201  525      HAPATVCGPKKSTNL  PATVCGPKK  2        0.0400
32426.4   100.00  0.50     Sequence
 HLA-DQA10501-DQB10201  526      APATVCGPKKSTNLV  PATVCGPKK  1        0.0298
36229.5   100.00  0.64     Sequence
 HLA-DQA10501-DQB10201  527      PATVCGPKKSTNLVK  PATVCGPKK  0        0.0245
38350.4   100.00  0.51     Sequence
 HLA-DQA10501-DQB10201  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5        0.0157
42184.1   100.00  0.31     Sequence
 HLA-DQA10501-DQB10201  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.0131
43403.6   100.00  0.28     Sequence
 HLA-DQA10501-DQB10201  530      VCGPKKSTNLVKNKC  STNLVKNKC  6        0.0193
40559.4   100.00  0.43     Sequence
 HLA-DQA10501-DQB10201  531      CGPKKSTNLVKNKCV  TNLVKNKCV  6        0.0292
36463.5   100.00  0.46     Sequence
 HLA-DQA10501-DQB10201  532      GPKKSTNLVKNKCVN  TNLVKNKCV  5        0.0270
37313.2   100.00  0.41     Sequence
 HLA-DQA10501-DQB10201  533      PKKSTNLVKNKCVNF  LVKNKCVNF  6        0.0575
26841.0   100.00  0.56     Sequence
 HLA-DQA10501-DQB10201  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.0624
25446.2   100.00  0.44     Sequence
 HLA-DQA10501-DQB10201  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.0730
22705.9    95.00  0.38     Sequence
 HLA-DQA10501-DQB10201  536      STNLVKNKCVNFNFN  LVKNKCVNF  3        0.0733
22626.6    95.00  0.33     Sequence
 HLA-DQA10501-DQB10201  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2        0.0650
24740.9    95.00  0.35     Sequence
 HLA-DQA10501-DQB10201  538      NLVKNKCVNFNFNGL  CVNFNFNGL  6        0.1015
16680.1    90.00  0.46     Sequence
 HLA-DQA10501-DQB10201  539      LVKNKCVNFNFNGLT  VNFNFNGLT  6        0.1379
11242.9    80.00  0.42     Sequence
 HLA-DQA10501-DQB10201  540      VKNKCVNFNFNGLTG  VNFNFNGLT  5        0.1438
10544.8    80.00  0.34     Sequence
 HLA-DQA10501-DQB10201  541      KNKCVNFNFNGLTGT  FNFNGLTGT  6        0.1543
9413.7    75.00  0.28     Sequence
 HLA-DQA10501-DQB10201  542      NKCVNFNFNGLTGTG  FNFNGLTGT  5        0.1512
9742.0    80.00  0.23     Sequence
 HLA-DQA10501-DQB10201  543      KCVNFNFNGLTGTGV  FNGLTGTGV  6        0.2420
3645.0    50.00  0.68     Sequence
 HLA-DQA10501-DQB10201  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5        0.2592
3025.8    46.00  0.64     Sequence
 HLA-DQA10501-DQB10201  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.2583
3055.5    46.00  0.58     Sequence
 HLA-DQA10501-DQB10201  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3        0.2806
2401.6    40.00  0.45     Sequence
```

```
 HLA-DQA10501-DQB10201  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.2685
2736.1    43.00  0.44     Sequence
 HLA-DQA10501-DQB10201  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.2376
3823.8    55.00  0.35     Sequence
 HLA-DQA10501-DQB10201  549      FNGLTGTGVLTESNK  LTGTGVLTE  3        0.2004
5720.0    65.00  0.35     Sequence
 HLA-DQA10501-DQB10201  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.1507
9791.1    80.00  0.46     Sequence
 HLA-DQA10501-DQB10201  551      GLTGTGVLTESNKKF  LTGTGVLTE  1        0.1310
12119.5    85.00  0.44     Sequence
 HLA-DQA10501-DQB10201  552      LTGTGVLTESNKKFL  LTGTGVLTE  0        0.1037
16285.3    90.00  0.35     Sequence
 HLA-DQA10501-DQB10201  553      TGTGVLTESNKKFLP  GTGVLTESN  1        0.0756
22072.4    95.00  0.28     Sequence
 HLA-DQA10501-DQB10201  554      GTGVLTESNKKFLPF  VLTESNKKF  3        0.0730
22694.3    95.00  0.24     Sequence
 HLA-DQA10501-DQB10201  555      TGVLTESNKKFLPFQ  VLTESNKKF  2        0.0644
24899.6    95.00  0.28     Sequence
 HLA-DQA10501-DQB10201  556      GVLTESNKKFLPFQQ  NKKFLPFQQ  6        0.0729
22726.3    95.00  0.34     Sequence
 HLA-DQA10501-DQB10201  557      VLTESNKKFLPFQQF  KKFLPFQQF  6        0.1410
10879.0    80.00  0.64     Sequence
 HLA-DQA10501-DQB10201  558      LTESNKKFLPFQQFG  KKFLPFQQF  5        0.1322
11962.8    85.00  0.50     Sequence
 HLA-DQA10501-DQB10201  559      TESNKKFLPFQQFGR  KKFLPFQQF  4        0.1225
13278.5    85.00  0.41     Sequence
 HLA-DQA10501-DQB10201  560      ESNKKFLPFQQFGRD  KKFLPFQQF  3        0.1286
12437.1    85.00  0.39     Sequence
 HLA-DQA10501-DQB10201  561      SNKKFLPFQQFGRDI  PFQQFGRDI  6        0.1720
7778.8    70.00  0.42     Sequence
 HLA-DQA10501-DQB10201  562      NKKFLPFQQFGRDIA  FQQFGRDIA  6        0.2290
4198.0    55.00  0.51     Sequence
 HLA-DQA10501-DQB10201  563      KKFLPFQQFGRDIAD  FQQFGRDIA  5        0.2549
3171.6    47.00  0.50     Sequence
 HLA-DQA10501-DQB10201  564      KFLPFQQFGRDIADT  FQQFGRDIA  4        0.2850
2289.5    39.00  0.43     Sequence
 HLA-DQA10501-DQB10201  565      FLPFQQFGRDIADTT  FGRDIADTT  6        0.3483
1153.7    25.00  0.41     Sequence
 HLA-DQA10501-DQB10201  566      LPFQQFGRDIADTTD  FGRDIADTT  5        0.3619
996.6    22.00  0.46     Sequence
 HLA-DQA10501-DQB10201  567      PFQQFGRDIADTTDA  FGRDIADTT  4        0.3571
1049.0    23.00  0.47     Sequence
 HLA-DQA10501-DQB10201  568      FQQFGRDIADTTDAV  FGRDIADTT  3        0.3904
731.6    17.00  0.34     Sequence
 HLA-DQA10501-DQB10201  569      QQFGRDIADTTDAVR  FGRDIADTT  2        0.3570
1051.1    23.00  0.29     Sequence
 HLA-DQA10501-DQB10201  570      QFGRDIADTTDAVRD  DIADTTDAV  4        0.3508
1123.0    24.00  0.35     Sequence
 HLA-DQA10501-DQB10201  571      FGRDIADTTDAVRDP  DIADTTDAV  3        0.3356
1323.9    27.00  0.48     Sequence
 HLA-DQA10501-DQB10201  572      GRDIADTTDAVRDPQ  DIADTTDAV  2        0.2950
2054.9    36.00  0.47     Sequence
 HLA-DQA10501-DQB10201  573      RDIADTTDAVRDPQT  DIADTTDAV  1        0.2801
2414.1    40.00  0.43     Sequence
 HLA-DQA10501-DQB10201  574      DIADTTDAVRDPQTL  DIADTTDAV  0        0.2567
3110.5    46.00  0.35     Sequence
 HLA-DQA10501-DQB10201  575      IADTTDAVRDPQTLE  DAVRDPQTL  5        0.2045
5473.0    65.00  0.20     Sequence
 HLA-DQA10501-DQB10201  576      ADTTDAVRDPQTLEI  VRDPQTLEI  6        0.2337
3988.2    55.00  0.32     Sequence
 HLA-DQA10501-DQB10201  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5        0.2511
3304.7    48.00  0.29     Sequence
 HLA-DQA10501-DQB10201  578      TTDAVRDPQTLEILD  VRDPQTLEI  4        0.2689
2725.4    43.00  0.23     Sequence
 HLA-DQA10501-DQB10201  579      TDAVRDPQTLEILDI  PQTLEILDI  6        0.3688
924.8    21.00  0.51     Sequence
```

```
 HLA-DQA10501-DQB10201  580      DAVRDPQTLEILDIT  PQTLEILDI  5        0.3774
842.5    19.00  0.39     Sequence
 HLA-DQA10501-DQB10201  581      AVRDPQTLEILDITP  PQTLEILDI  4        0.4223
518.4    13.00  0.29     Sequence
 HLA-DQA10501-DQB10201  582      VRDPQTLEILDITPC  PQTLEILDI  3        0.4221
519.7    13.00  0.26     Sequence
 HLA-DQA10501-DQB10201  583      RDPQTLEILDITPCS  QTLEILDIT  3        0.4281
486.7    12.00  0.27     Sequence
 HLA-DQA10501-DQB10201  584      DPQTLEILDITPCSF  ILDITPCSF  6        0.5015
219.9     5.50  0.40     Sequence         WB
 HLA-DQA10501-DQB10201  585      PQTLEILDITPCSFG  ILDITPCSF  5        0.4667
320.8     8.00  0.41     Sequence         WB
 HLA-DQA10501-DQB10201  586      QTLEILDITPCSFGG  ILDITPCSF  4        0.4314
469.5    12.00  0.44     Sequence
 HLA-DQA10501-DQB10201  587      TLEILDITPCSFGGV  ILDITPCSF  3        0.3967
683.7    16.00  0.50     Sequence
 HLA-DQA10501-DQB10201  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.3453
1192.3    25.00  0.62     Sequence
 HLA-DQA10501-DQB10201  589      EILDITPCSFGGVSV  ILDITPCSF  1        0.3063
1817.4    34.00  0.70     Sequence
 HLA-DQA10501-DQB10201  590      ILDITPCSFGGVSVI  ILDITPCSF  0        0.2462
3485.3    49.00  0.73     Sequence
 HLA-DQA10501-DQB10201  591      LDITPCSFGGVSVIT  SFGGVSVIT  6        0.2168
4788.8    60.00  0.64     Sequence
 HLA-DQA10501-DQB10201  592      DITPCSFGGVSVITP  FGGVSVITP  6        0.3243
1497.1    30.00  0.54     Sequence
 HLA-DQA10501-DQB10201  593      ITPCSFGGVSVITPG  FGGVSVITP  5        0.3003
1939.9    35.00  0.51     Sequence
 HLA-DQA10501-DQB10201  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.2882
2210.8    38.00  0.51     Sequence
 HLA-DQA10501-DQB10201  595      PCSFGGVSVITPGTN  FGGVSVITP  3        0.2772
2490.4    41.00  0.48     Sequence
 HLA-DQA10501-DQB10201  596      CSFGGVSVITPGTNT  FGGVSVITP  2        0.2647
2852.1    44.00  0.49     Sequence
 HLA-DQA10501-DQB10201  597      SFGGVSVITPGTNTS  FGGVSVITP  1        0.2368
3858.3    55.00  0.56     Sequence
 HLA-DQA10501-DQB10201  598      FGGVSVITPGTNTSN  FGGVSVITP  0        0.1690
8030.7    75.00  0.56     Sequence
 HLA-DQA10501-DQB10201  599      GGVSVITPGTNTSNQ  VSVITPGTN  2        0.0844
20058.0    95.00  0.38     Sequence
 HLA-DQA10501-DQB10201  600      GVSVITPGTNTSNQV  PGTNTSNQV  6        0.0955
17789.6    90.00  0.41     Sequence
 HLA-DQA10501-DQB10201  601      VSVITPGTNTSNQVA  PGTNTSNQV  5        0.0905
18778.7    95.00  0.46     Sequence
 HLA-DQA10501-DQB10201  602      SVITPGTNTSNQVAV  PGTNTSNQV  4        0.0875
19403.9    95.00  0.48     Sequence
 HLA-DQA10501-DQB10201  603      VITPGTNTSNQVAVL  NTSNQVAVL  6        0.1721
7766.6    70.00  0.60     Sequence
 HLA-DQA10501-DQB10201  604      ITPGTNTSNQVAVLY  TSNQVAVLY  6        0.2733
2598.0    42.00  0.55     Sequence
 HLA-DQA10501-DQB10201  605      TPGTNTSNQVAVLYQ  TSNQVAVLY  5        0.2631
2901.2    45.00  0.45     Sequence
 HLA-DQA10501-DQB10201  606      PGTNTSNQVAVLYQG  TSNQVAVLY  4        0.2315
4083.4    55.00  0.42     Sequence
 HLA-DQA10501-DQB10201  607      GTNTSNQVAVLYQGV  TSNQVAVLY  3        0.2408
3694.9    55.00  0.35     Sequence
 HLA-DQA10501-DQB10201  608      TNTSNQVAVLYQGVN  TSNQVAVLY  2        0.2352
3922.5    55.00  0.29     Sequence
 HLA-DQA10501-DQB10201  609      NTSNQVAVLYQGVNC  TSNQVAVLY  1        0.2262
4327.6    55.00  0.27     Sequence
 HLA-DQA10501-DQB10201  610      TSNQVAVLYQGVNCT  VLYQGVNCT  6        0.2233
4465.6    60.00  0.23     Sequence
 HLA-DQA10501-DQB10201  611      SNQVAVLYQGVNCTE  LYQGVNCTE  6        0.2549
3169.5    47.00  0.38     Sequence
 HLA-DQA10501-DQB10201  612      NQVAVLYQGVNCTEV  YQGVNCTEV  6        0.3413
1245.2    26.00  0.47     Sequence
```

```
 HLA-DQA10501-DQB10201  613      QVAVLYQGVNCTEVP  YQGVNCTEV  5        0.3673
939.7    21.00  0.47     Sequence
 HLA-DQA10501-DQB10201  614      VAVLYQGVNCTEVPV  YQGVNCTEV  4        0.3621
994.7    22.00  0.50     Sequence
 HLA-DQA10501-DQB10201  615      AVLYQGVNCTEVPVA  YQGVNCTEV  3        0.3643
970.4    22.00  0.41     Sequence
 HLA-DQA10501-DQB10201  616      VLYQGVNCTEVPVAI  YQGVNCTEV  2        0.3472
1168.7    25.00  0.42     Sequence
 HLA-DQA10501-DQB10201  617      LYQGVNCTEVPVAIH  YQGVNCTEV  1        0.3072
1801.3    33.00  0.39     Sequence
 HLA-DQA10501-DQB10201  618      YQGVNCTEVPVAIHA  VNCTEVPVA  3        0.2519
3275.2    48.00  0.33     Sequence
 HLA-DQA10501-DQB10201  619      QGVNCTEVPVAIHAD  VNCTEVPVA  2        0.2104
5130.5    60.00  0.38     Sequence
 HLA-DQA10501-DQB10201  620      GVNCTEVPVAIHADQ  VPVAIHADQ  6        0.2288
4206.0    55.00  0.31     Sequence
 HLA-DQA10501-DQB10201  621      VNCTEVPVAIHADQL  PVAIHADQL  6        0.5061
209.4     5.00  0.79     Sequence         WB
 HLA-DQA10501-DQB10201  622      NCTEVPVAIHADQLT  PVAIHADQL  5        0.5499
130.3     3.00  0.69     Sequence         WB
 HLA-DQA10501-DQB10201  623      CTEVPVAIHADQLTP  PVAIHADQL  4        0.5643
111.5     2.50  0.68     Sequence         WB
 HLA-DQA10501-DQB10201  624      TEVPVAIHADQLTPT  PVAIHADQL  3        0.5622
114.0     2.50  0.63     Sequence         WB
 HLA-DQA10501-DQB10201  625      EVPVAIHADQLTPTW  PVAIHADQL  2        0.5657
109.9     2.50  0.55     Sequence         WB
 HLA-DQA10501-DQB10201  626      VPVAIHADQLTPTWR  PVAIHADQL  1        0.5348
153.5     3.50  0.52     Sequence         WB
 HLA-DQA10501-DQB10201  627      PVAIHADQLTPTWRV  PVAIHADQL  0        0.4865
258.8     6.50  0.44     Sequence         WB
 HLA-DQA10501-DQB10201  628      VAIHADQLTPTWRVY  VAIHADQLT  0        0.3349
1333.9    27.00  0.31     Sequence
 HLA-DQA10501-DQB10201  629      AIHADQLTPTWRVYS  IHADQLTPT  1        0.2288
4203.5    55.00  0.42     Sequence
 HLA-DQA10501-DQB10201  630      IHADQLTPTWRVYST  HADQLTPTW  1        0.1763
7425.7    70.00  0.32     Sequence
 HLA-DQA10501-DQB10201  631      HADQLTPTWRVYSTG  HADQLTPTW  0        0.1155
14335.8    85.00  0.34     Sequence
 HLA-DQA10501-DQB10201  632      ADQLTPTWRVYSTGS  TWRVYSTGS  6        0.0819
20620.0    95.00  0.35     Sequence
 HLA-DQA10501-DQB10201  633      DQLTPTWRVYSTGSN  WRVYSTGSN  6        0.1065
15789.2    90.00  0.45     Sequence
 HLA-DQA10501-DQB10201  634      QLTPTWRVYSTGSNV  RVYSTGSNV  6        0.1513
9724.5    80.00  0.47     Sequence
 HLA-DQA10501-DQB10201  635      LTPTWRVYSTGSNVF  VYSTGSNVF  6        0.2529
3238.8    47.00  0.56     Sequence
 HLA-DQA10501-DQB10201  636      TPTWRVYSTGSNVFQ  VYSTGSNVF  5        0.2591
3031.7    46.00  0.44     Sequence
 HLA-DQA10501-DQB10201  637      PTWRVYSTGSNVFQT  VYSTGSNVF  4        0.2607
2977.0    45.00  0.41     Sequence
 HLA-DQA10501-DQB10201  638      TWRVYSTGSNVFQTR  VYSTGSNVF  3        0.2599
3004.4    45.00  0.37     Sequence
 HLA-DQA10501-DQB10201  639      WRVYSTGSNVFQTRA  VYSTGSNVF  2        0.2541
3197.6    47.00  0.32     Sequence
 HLA-DQA10501-DQB10201  640      RVYSTGSNVFQTRAG  VYSTGSNVF  1        0.2182
4719.0    60.00  0.35     Sequence
 HLA-DQA10501-DQB10201  641      VYSTGSNVFQTRAGC  VYSTGSNVF  0        0.1870
6612.4    70.00  0.36     Sequence
 HLA-DQA10501-DQB10201  642      YSTGSNVFQTRAGCL  VFQTRAGCL  6        0.1967
5953.7    65.00  0.48     Sequence
 HLA-DQA10501-DQB10201  643      STGSNVFQTRAGCLI  FQTRAGCLI  6        0.2451
3525.7    50.00  0.49     Sequence
 HLA-DQA10501-DQB10201  644      TGSNVFQTRAGCLIG  FQTRAGCLI  5        0.2249
4385.3    55.00  0.48     Sequence
 HLA-DQA10501-DQB10201  645      GSNVFQTRAGCLIGA  FQTRAGCLI  4        0.2208
4584.4    60.00  0.46     Sequence
```

```
 HLA-DQA10501-DQB10201  646      SNVFQTRAGCLIGAE  FQTRAGCLI  3        0.2292
4188.8    55.00  0.43     Sequence
 HLA-DQA10501-DQB10201  647      NVFQTRAGCLIGAEY  AGCLIGAEY  6        0.3150
1654.2    32.00  0.49     Sequence
 HLA-DQA10501-DQB10201  648      VFQTRAGCLIGAEYV  AGCLIGAEY  5        0.3400
1262.3    26.00  0.44     Sequence
 HLA-DQA10501-DQB10201  649      FQTRAGCLIGAEYVN  AGCLIGAEY  4        0.3202
1564.2    30.00  0.43     Sequence
 HLA-DQA10501-DQB10201  650      QTRAGCLIGAEYVNN  AGCLIGAEY  3        0.3006
1934.7    35.00  0.43     Sequence
 HLA-DQA10501-DQB10201  651      TRAGCLIGAEYVNNS  AGCLIGAEY  2        0.2915
2134.7    37.00  0.41     Sequence
 HLA-DQA10501-DQB10201  652      RAGCLIGAEYVNNSY  AGCLIGAEY  1        0.2956
2040.9    36.00  0.33     Sequence
 HLA-DQA10501-DQB10201  653      AGCLIGAEYVNNSYE  AEYVNNSYE  6        0.2951
2053.7    36.00  0.24     Sequence
 HLA-DQA10501-DQB10201  654      GCLIGAEYVNNSYEC  AEYVNNSYE  5        0.2910
2146.4    37.00  0.28     Sequence
 HLA-DQA10501-DQB10201  655      CLIGAEYVNNSYECD  YVNNSYECD  6        0.3506
1125.7    24.00  0.43     Sequence
 HLA-DQA10501-DQB10201  656      LIGAEYVNNSYECDI  YVNNSYECD  5        0.4313
470.4    12.00  0.35     Sequence
 HLA-DQA10501-DQB10201  657      IGAEYVNNSYECDIP  YVNNSYECD  4        0.4424
416.8    11.00  0.37     Sequence
 HLA-DQA10501-DQB10201  658      GAEYVNNSYECDIPI  YVNNSYECD  3        0.4413
421.9    11.00  0.37     Sequence
 HLA-DQA10501-DQB10201  659      AEYVNNSYECDIPIG  YVNNSYECD  2        0.4197
533.2    13.00  0.37     Sequence
 HLA-DQA10501-DQB10201  660      EYVNNSYECDIPIGA  YVNNSYECD  1        0.3997
661.8    16.00  0.35     Sequence
 HLA-DQA10501-DQB10201  661      YVNNSYECDIPIGAG  VNNSYECDI  1        0.3486
1150.4    25.00  0.29     Sequence
 HLA-DQA10501-DQB10201  662      VNNSYECDIPIGAGI  VNNSYECDI  0        0.2466
3469.3    49.00  0.28     Sequence
 HLA-DQA10501-DQB10201  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.2009
5690.6    65.00  0.37     Sequence
 HLA-DQA10501-DQB10201  664      NSYECDIPIGAGICA  YECDIPIGA  2        0.1939
6133.8    65.00  0.35     Sequence
 HLA-DQA10501-DQB10201  665      SYECDIPIGAGICAS  PIGAGICAS  6        0.2154
4861.9    60.00  0.32     Sequence
 HLA-DQA10501-DQB10201  666      YECDIPIGAGICASY  PIGAGICAS  5        0.2064
5362.0    65.00  0.38     Sequence
 HLA-DQA10501-DQB10201  667      ECDIPIGAGICASYQ  GAGICASYQ  6        0.2215
4550.2    60.00  0.38     Sequence
 HLA-DQA10501-DQB10201  668      CDIPIGAGICASYQT  GAGICASYQ  5        0.2222
4519.1    60.00  0.38     Sequence
 HLA-DQA10501-DQB10201  669      DIPIGAGICASYQTQ  GAGICASYQ  4        0.2153
4867.9    60.00  0.36     Sequence
 HLA-DQA10501-DQB10201  670      IPIGAGICASYQTQT  GAGICASYQ  3        0.1985
5834.7    65.00  0.36     Sequence
 HLA-DQA10501-DQB10201  671      PIGAGICASYQTQTN  GAGICASYQ  2        0.1750
7526.0    70.00  0.37     Sequence
 HLA-DQA10501-DQB10201  672      IGAGICASYQTQTNS  GAGICASYQ  1        0.1456
10349.0    80.00  0.41     Sequence
 HLA-DQA10501-DQB10201  673      GAGICASYQTQTNSP  GAGICASYQ  0        0.1223
13310.7    85.00  0.30     Sequence
 HLA-DQA10501-DQB10201  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.0941
18066.0    90.00  0.22     Sequence
 HLA-DQA10501-DQB10201  675      GICASYQTQTNSPRR  SYQTQTNSP  4        0.0747
22281.2    95.00  0.22     Sequence
 HLA-DQA10501-DQB10201  676      ICASYQTQTNSPRRA  SYQTQTNSP  3        0.0655
24615.1    95.00  0.23     Sequence
 HLA-DQA10501-DQB10201  677      CASYQTQTNSPRRAR  SYQTQTNSP  2        0.0523
28392.9   100.00  0.27     Sequence
 HLA-DQA10501-DQB10201  678      ASYQTQTNSPRRARS  SYQTQTNSP  1        0.0466
30210.8   100.00  0.32     Sequence
```

```
 HLA-DQA10501-DQB10201  679      SYQTQTNSPRRARSV  TQTNSPRRA  3        0.0412
32018.8   100.00  0.34     Sequence
 HLA-DQA10501-DQB10201  680      YQTQTNSPRRARSVA  TQTNSPRRA  2        0.0336
34768.7   100.00  0.45     Sequence
 HLA-DQA10501-DQB10201  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.0485
29571.4   100.00  0.52     Sequence
 HLA-DQA10501-DQB10201  682      TQTNSPRRARSVASQ  RRARSVASQ  6        0.0764
21884.3    95.00  0.48     Sequence
 HLA-DQA10501-DQB10201  683      QTNSPRRARSVASQS  RARSVASQS  6        0.0994
17064.9    90.00  0.48     Sequence
 HLA-DQA10501-DQB10201  684      TNSPRRARSVASQSI  ARSVASQSI  6        0.2053
5423.0    65.00  0.72    Sequence
 HLA-DQA10501-DQB10201  685      NSPRRARSVASQSII  ARSVASQSI  5        0.2149
4890.2    60.00  0.61    Sequence
 HLA-DQA10501-DQB10201  686      SPRRARSVASQSIIA  ARSVASQSI  4        0.2286
4214.9    55.00  0.43    Sequence
 HLA-DQA10501-DQB10201  687      PRRARSVASQSIIAY  ARSVASQSI  3        0.2630
2903.7    45.00  0.28    Sequence
 HLA-DQA10501-DQB10201  688      RRARSVASQSIIAYT  ARSVASQSI  2        0.2547
3178.0    47.00  0.28    Sequence
 HLA-DQA10501-DQB10201  689      RARSVASQSIIAYTM  SQSIIAYTM  6        0.2914
2135.7    37.00  0.34    Sequence
 HLA-DQA10501-DQB10201  690      ARSVASQSIIAYTMS  SQSIIAYTM  5        0.2698
2699.6    43.00  0.29    Sequence
 HLA-DQA10501-DQB10201  691      RSVASQSIIAYTMSL  SIIAYTMSL  6        0.2935
2087.9    37.00  0.34    Sequence
 HLA-DQA10501-DQB10201  692      SVASQSIIAYTMSLG  SIIAYTMSL  5        0.2767
2504.5    41.00  0.31    Sequence
 HLA-DQA10501-DQB10201  693      VASQSIIAYTMSLGA  IAYTMSLGA  6        0.2756
2535.1    41.00  0.25    Sequence
 HLA-DQA10501-DQB10201  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.2817
2373.4    40.00  0.23    Sequence
 HLA-DQA10501-DQB10201  695      SQSIIAYTMSLGAEN  YTMSLGAEN  6        0.3026
1892.0    34.00  0.25    Sequence
 HLA-DQA10501-DQB10201  696      QSIIAYTMSLGAENS  TMSLGAENS  6        0.3292
1419.7    28.00  0.33    Sequence
 HLA-DQA10501-DQB10201  697      SIIAYTMSLGAENSV  TMSLGAENS  5        0.3572
1048.5    23.00  0.31    Sequence
 HLA-DQA10501-DQB10201  698      IIAYTMSLGAENSVA  TMSLGAENS  4        0.3418
1238.2    26.00  0.31    Sequence
 HLA-DQA10501-DQB10201  699      IAYTMSLGAENSVAY  TMSLGAENS  3        0.3395
1269.0    26.00  0.32    Sequence
 HLA-DQA10501-DQB10201  700      AYTMSLGAENSVAYS  TMSLGAENS  2        0.3213
1545.6    30.00  0.34    Sequence
 HLA-DQA10501-DQB10201  701      YTMSLGAENSVAYSN  TMSLGAENS  1        0.2916
2131.9    37.00  0.35    Sequence
 HLA-DQA10501-DQB10201  702      TMSLGAENSVAYSNN  MSLGAENSV  1        0.2327
4032.6    55.00  0.36    Sequence
 HLA-DQA10501-DQB10201  703      MSLGAENSVAYSNNS  MSLGAENSV  0        0.1637
8505.6    75.00  0.34    Sequence
 HLA-DQA10501-DQB10201  704      SLGAENSVAYSNNSI  SVAYSNNSI  6        0.1454
10364.5    80.00  0.40     Sequence
 HLA-DQA10501-DQB10201  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.1616
8699.9    75.00  0.44    Sequence
 HLA-DQA10501-DQB10201  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.1904
6375.4    65.00  0.35    Sequence
 HLA-DQA10501-DQB10201  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.2256
4354.8    55.00  0.32    Sequence
 HLA-DQA10501-DQB10201  708      ENSVAYSNNSIAIPT  VAYSNNSIA  3        0.2203
4613.3    60.00  0.27    Sequence
 HLA-DQA10501-DQB10201  709      NSVAYSNNSIAIPTN  YSNNSIAIP  4        0.2119
5051.0    60.00  0.23    Sequence
 HLA-DQA10501-DQB10201  710      SVAYSNNSIAIPTNF  NSIAIPTNF  6        0.2404
3711.6    55.00  0.35    Sequence
 HLA-DQA10501-DQB10201  711      VAYSNNSIAIPTNFT  NSIAIPTNF  5        0.2185
4701.4    60.00  0.31    Sequence
```

```
 HLA-DQA10501-DQB10201  712      AYSNNSIAIPTNFTI  NSIAIPTNF  4        0.2000
5745.1    65.00  0.34     Sequence
 HLA-DQA10501-DQB10201  713      YSNNSIAIPTNFTIS  NSIAIPTNF  3        0.1743
7588.7    70.00  0.40     Sequence
 HLA-DQA10501-DQB10201  714      SNNSIAIPTNFTISV  NSIAIPTNF  2        0.1665
8252.9    75.00  0.35     Sequence
 HLA-DQA10501-DQB10201  715      NNSIAIPTNFTISVT  PTNFTISVT  6        0.1704
7914.3    75.00  0.25     Sequence
 HLA-DQA10501-DQB10201  716      NSIAIPTNFTISVTT  TNFTISVTT  6        0.1709
7865.2    75.00  0.27     Sequence
 HLA-DQA10501-DQB10201  717      SIAIPTNFTISVTTE  NFTISVTTE  6        0.2420
3646.6    50.00  0.57     Sequence
 HLA-DQA10501-DQB10201  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.3573
1047.5    23.00  0.61     Sequence
 HLA-DQA10501-DQB10201  719      AIPTNFTISVTTEIL  TISVTTEIL  6        0.4229
514.7    13.00  0.42     Sequence
 HLA-DQA10501-DQB10201  720      IPTNFTISVTTEILP  TISVTTEIL  5        0.4548
364.7     9.00  0.38     Sequence          WB
 HLA-DQA10501-DQB10201  721      PTNFTISVTTEILPV  TISVTTEIL  4        0.4626
335.1     8.50  0.32     Sequence          WB
 HLA-DQA10501-DQB10201  722      TNFTISVTTEILPVS  TISVTTEIL  3        0.4522
375.1     9.50  0.28     Sequence          WB
 HLA-DQA10501-DQB10201  723      NFTISVTTEILPVSM  TTEILPVSM  6        0.4597
345.7     8.50  0.20     Sequence          WB
 HLA-DQA10501-DQB10201  724      FTISVTTEILPVSMT  TISVTTEIL  1        0.4241
508.5    13.00  0.28     Sequence
 HLA-DQA10501-DQB10201  725      TISVTTEILPVSMTK  TTEILPVSM  4        0.3535
1091.5    24.00  0.27     Sequence
 HLA-DQA10501-DQB10201  726      ISVTTEILPVSMTKT  TTEILPVSM  3        0.3076
1792.3    33.00  0.35     Sequence
 HLA-DQA10501-DQB10201  727      SVTTEILPVSMTKTS  TTEILPVSM  2        0.2745
2565.5    42.00  0.44     Sequence
 HLA-DQA10501-DQB10201  728      VTTEILPVSMTKTSV  TTEILPVSM  1        0.2319
4067.3    55.00  0.54     Sequence
 HLA-DQA10501-DQB10201  729      TTEILPVSMTKTSVD  TTEILPVSM  0        0.1926
6223.1    65.00  0.42     Sequence
 HLA-DQA10501-DQB10201  730      TEILPVSMTKTSVDC  VSMTKTSVD  5        0.1422
10736.0    80.00  0.29     Sequence
 HLA-DQA10501-DQB10201  731      EILPVSMTKTSVDCT  MTKTSVDCT  6        0.1789
7217.4    70.00  0.41     Sequence
 HLA-DQA10501-DQB10201  732      ILPVSMTKTSVDCTM  TKTSVDCTM  6        0.2375
3827.3    55.00  0.41     Sequence
 HLA-DQA10501-DQB10201  733      LPVSMTKTSVDCTMY  TKTSVDCTM  5        0.2524
3258.8    48.00  0.35     Sequence
 HLA-DQA10501-DQB10201  734      PVSMTKTSVDCTMYI  TKTSVDCTM  4        0.2679
2754.4    43.00  0.34     Sequence
 HLA-DQA10501-DQB10201  735      VSMTKTSVDCTMYIC  TKTSVDCTM  3        0.2598
3006.2    46.00  0.34     Sequence
 HLA-DQA10501-DQB10201  736      SMTKTSVDCTMYICG  TKTSVDCTM  2        0.2386
3780.6    55.00  0.33     Sequence
 HLA-DQA10501-DQB10201  737      MTKTSVDCTMYICGD  TKTSVDCTM  1        0.2260
4335.8    55.00  0.28     Sequence
 HLA-DQA10501-DQB10201  738      TKTSVDCTMYICGDS  TSVDCTMYI  2        0.1941
6121.6    65.00  0.27     Sequence
 HLA-DQA10501-DQB10201  739      KTSVDCTMYICGDST  TMYICGDST  6        0.3102
1743.3    33.00  0.64     Sequence
 HLA-DQA10501-DQB10201  740      TSVDCTMYICGDSTE  TMYICGDST  5        0.3412
1246.1    26.00  0.61     Sequence
 HLA-DQA10501-DQB10201  741      SVDCTMYICGDSTEC  TMYICGDST  4        0.3646
967.9    22.00  0.55     Sequence
 HLA-DQA10501-DQB10201  742      VDCTMYICGDSTECS  TMYICGDST  3        0.3657
956.2    21.00  0.50     Sequence
 HLA-DQA10501-DQB10201  743      DCTMYICGDSTECSN  TMYICGDST  2        0.3560
1062.4    23.00  0.49     Sequence
 HLA-DQA10501-DQB10201  744      CTMYICGDSTECSNL  TMYICGDST  1        0.3370
1304.3    27.00  0.46     Sequence
```

```
 HLA-DQA10501-DQB10201  745      TMYICGDSTECSNLL  TMYICGDST  0        0.3171
1618.2    31.00  0.41     Sequence
 HLA-DQA10501-DQB10201  746      MYICGDSTECSNLLL  YICGDSTEC  1        0.2415
3666.8    55.00  0.31     Sequence
 HLA-DQA10501-DQB10201  747      YICGDSTECSNLLLQ  YICGDSTEC  0        0.1929
6205.2    65.00  0.28     Sequence
 HLA-DQA10501-DQB10201  748      ICGDSTECSNLLLQY  ECSNLLLQY  6        0.1749
7537.9    70.00  0.31     Sequence
 HLA-DQA10501-DQB10201  749      CGDSTECSNLLLQYG  ECSNLLLQY  5        0.1511
9749.0    80.00  0.27     Sequence
 HLA-DQA10501-DQB10201  750      GDSTECSNLLLQYGS  ECSNLLLQY  4        0.1436
10574.9    80.00  0.25     Sequence
 HLA-DQA10501-DQB10201  751      DSTECSNLLLQYGSF  NLLLQYGSF  6        0.1676
8152.8    75.00  0.34     Sequence
 HLA-DQA10501-DQB10201  752      STECSNLLLQYGSFC  LLLQYGSFC  6        0.1731
7683.3    70.00  0.31     Sequence
 HLA-DQA10501-DQB10201  753      TECSNLLLQYGSFCT  LLLQYGSFC  5        0.1857
6706.8    70.00  0.25     Sequence
 HLA-DQA10501-DQB10201  754      ECSNLLLQYGSFCTQ  LQYGSFCTQ  6        0.1892
6452.8    70.00  0.20     Sequence
 HLA-DQA10501-DQB10201  755      CSNLLLQYGSFCTQL  QYGSFCTQL  6        0.2503
3333.3    48.00  0.40     Sequence
 HLA-DQA10501-DQB10201  756      SNLLLQYGSFCTQLN  YGSFCTQLN  6        0.3061
1822.9    34.00  0.41     Sequence
 HLA-DQA10501-DQB10201  757      NLLLQYGSFCTQLNR  YGSFCTQLN  5        0.2834
2330.8    39.00  0.41     Sequence
 HLA-DQA10501-DQB10201  758      LLLQYGSFCTQLNRA  YGSFCTQLN  4        0.2727
2615.8    42.00  0.38     Sequence
 HLA-DQA10501-DQB10201  759      LLQYGSFCTQLNRAL  YGSFCTQLN  3        0.2577
3076.6    46.00  0.41     Sequence
 HLA-DQA10501-DQB10201  760      LQYGSFCTQLNRALT  YGSFCTQLN  2        0.2362
3881.7    55.00  0.41     Sequence
 HLA-DQA10501-DQB10201  761      QYGSFCTQLNRALTG  YGSFCTQLN  1        0.2144
4912.8    60.00  0.39     Sequence
 HLA-DQA10501-DQB10201  762      YGSFCTQLNRALTGI  YGSFCTQLN  0        0.1914
6300.5    65.00  0.28     Sequence
 HLA-DQA10501-DQB10201  763      GSFCTQLNRALTGIA  QLNRALTGI  5        0.1576
9085.0    75.00  0.32     Sequence
 HLA-DQA10501-DQB10201  764      SFCTQLNRALTGIAV  NRALTGIAV  6        0.2130
4987.3    60.00  0.47     Sequence
 HLA-DQA10501-DQB10201  765      FCTQLNRALTGIAVE  RALTGIAVE  6        0.3009
1927.4    35.00  0.47     Sequence
 HLA-DQA10501-DQB10201  766      CTQLNRALTGIAVEQ  ALTGIAVEQ  6        0.3670
943.0    21.00  0.51     Sequence
 HLA-DQA10501-DQB10201  767      TQLNRALTGIAVEQD  LTGIAVEQD  6        0.5819
92.1     1.70  0.64     Sequence          SB
 HLA-DQA10501-DQB10201  768      QLNRALTGIAVEQDK  LTGIAVEQD  5        0.5510
128.8     3.00  0.65     Sequence          WB
 HLA-DQA10501-DQB10201  769      LNRALTGIAVEQDKN  LTGIAVEQD  4        0.5384
147.6     3.50  0.64     Sequence          WB
 HLA-DQA10501-DQB10201  770      NRALTGIAVEQDKNT  LTGIAVEQD  3        0.5208
178.6     4.50  0.65     Sequence          WB
 HLA-DQA10501-DQB10201  771      RALTGIAVEQDKNTQ  LTGIAVEQD  2        0.5024
217.9     5.50  0.67     Sequence          WB
 HLA-DQA10501-DQB10201  772      ALTGIAVEQDKNTQE  LTGIAVEQD  1        0.4620
337.2     8.50  0.72     Sequence          WB
 HLA-DQA10501-DQB10201  773      LTGIAVEQDKNTQEV  LTGIAVEQD  0        0.3528
1099.8    24.00  0.76     Sequence
 HLA-DQA10501-DQB10201  774      TGIAVEQDKNTQEVF  QDKNTQEVF  6        0.1700
7942.1    75.00  0.34     Sequence
 HLA-DQA10501-DQB10201  775      GIAVEQDKNTQEVFA  DKNTQEVFA  6        0.1897
6417.8    65.00  0.39     Sequence
 HLA-DQA10501-DQB10201  776      IAVEQDKNTQEVFAQ  DKNTQEVFA  5        0.1732
7676.4    70.00  0.38     Sequence
 HLA-DQA10501-DQB10201  777      AVEQDKNTQEVFAQV  NTQEVFAQV  6        0.2072
5311.7    60.00  0.29     Sequence
```

```
 HLA-DQA10501-DQB10201  778      VEQDKNTQEVFAQVK  TQEVFAQVK  6        0.2143
4917.6    60.00  0.40     Sequence
 HLA-DQA10501-DQB10201  779      EQDKNTQEVFAQVKQ  TQEVFAQVK  5        0.2168
4787.0    60.00  0.31     Sequence
 HLA-DQA10501-DQB10201  780      QDKNTQEVFAQVKQI  EVFAQVKQI  6        0.2727
2614.3    42.00  0.47     Sequence
 HLA-DQA10501-DQB10201  781      DKNTQEVFAQVKQIY  EVFAQVKQI  5        0.3146
1661.4    32.00  0.38     Sequence
 HLA-DQA10501-DQB10201  782      KNTQEVFAQVKQIYK  EVFAQVKQI  4        0.2784
2460.1    41.00  0.38     Sequence
 HLA-DQA10501-DQB10201  783      NTQEVFAQVKQIYKT  EVFAQVKQI  3        0.2628
2910.4    45.00  0.37     Sequence
 HLA-DQA10501-DQB10201  784      TQEVFAQVKQIYKTP  EVFAQVKQI  2        0.2505
3324.1    48.00  0.38     Sequence
 HLA-DQA10501-DQB10201  785      QEVFAQVKQIYKTPP  EVFAQVKQI  1        0.2251
4378.0    55.00  0.40     Sequence
 HLA-DQA10501-DQB10201  786      EVFAQVKQIYKTPPI  VFAQVKQIY  1        0.2016
5643.9    65.00  0.40     Sequence
 HLA-DQA10501-DQB10201  787      VFAQVKQIYKTPPIK  VFAQVKQIY  0        0.1405
10933.6    80.00  0.46     Sequence
 HLA-DQA10501-DQB10201  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6        0.1058
15921.6    90.00  0.30     Sequence
 HLA-DQA10501-DQB10201  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.1030
16413.2    90.00  0.39     Sequence
 HLA-DQA10501-DQB10201  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.0954
17812.3    90.00  0.37     Sequence
 HLA-DQA10501-DQB10201  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.0893
19034.6    95.00  0.40     Sequence
 HLA-DQA10501-DQB10201  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.0854
19837.0    95.00  0.37     Sequence
 HLA-DQA10501-DQB10201  793      QIYKTPPIKDFGGFN  PIKDFGGFN  6        0.0861
19702.0    95.00  0.28     Sequence
 HLA-DQA10501-DQB10201  794      IYKTPPIKDFGGFNF  IKDFGGFNF  6        0.1294
12324.5    85.00  0.52     Sequence
 HLA-DQA10501-DQB10201  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.1185
13875.4    85.00  0.50     Sequence
 HLA-DQA10501-DQB10201  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.1270
12654.6    85.00  0.40     Sequence
 HLA-DQA10501-DQB10201  797      TPPIKDFGGFNFSQI  FGGFNFSQI  6        0.2422
3639.3    50.00  0.70     Sequence
 HLA-DQA10501-DQB10201  798      PPIKDFGGFNFSQIL  FGGFNFSQI  5        0.2884
2206.9    38.00  0.47     Sequence
 HLA-DQA10501-DQB10201  799      PIKDFGGFNFSQILP  FGGFNFSQI  4        0.3379
1291.9    27.00  0.37     Sequence
 HLA-DQA10501-DQB10201  800      IKDFGGFNFSQILPD  FNFSQILPD  6        0.4419
419.5    11.00  0.41     Sequence
 HLA-DQA10501-DQB10201  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.4778
284.4     7.00  0.38     Sequence         WB
 HLA-DQA10501-DQB10201  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.4879
254.9     6.50  0.28     Sequence         WB
 HLA-DQA10501-DQB10201  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.4468
397.7    10.00  0.26     Sequence
 HLA-DQA10501-DQB10201  804      GGFNFSQILPDPSKP  FSQILPDPS  4        0.4163
553.3    14.00  0.34     Sequence
 HLA-DQA10501-DQB10201  805      GFNFSQILPDPSKPS  FSQILPDPS  3        0.3803
816.5    19.00  0.41     Sequence
 HLA-DQA10501-DQB10201  806      FNFSQILPDPSKPSK  FSQILPDPS  2        0.3342
1344.6    27.00  0.50     Sequence
 HLA-DQA10501-DQB10201  807      NFSQILPDPSKPSKR  FSQILPDPS  1        0.2435
3586.5    50.00  0.74     Sequence
 HLA-DQA10501-DQB10201  808      FSQILPDPSKPSKRS  FSQILPDPS  0        0.1616
8702.8    75.00  0.85     Sequence
 HLA-DQA10501-DQB10201  809      SQILPDPSKPSKRSF  QILPDPSKP  1        0.0313
35649.0    100.00  0.49     Sequence
 HLA-DQA10501-DQB10201  810      QILPDPSKPSKRSFI  QILPDPSKP  0        0.0216
39574.5   100.00  0.44     Sequence
```

```
 HLA-DQA10501-DQB10201  811      ILPDPSKPSKRSFIE  KPSKRSFIE  6         0.0138
43081.3   100.00  0.38     Sequence
 HLA-DQA10501-DQB10201  812      LPDPSKPSKRSFIED  PSKRSFIED  6         0.0496
29222.5   100.00  0.75     Sequence
 HLA-DQA10501-DQB10201  813      PDPSKPSKRSFIEDL  SKRSFIEDL  6         0.1986
5831.0    65.00  0.79     Sequence
 HLA-DQA10501-DQB10201  814      DPSKPSKRSFIEDLL  KRSFIEDLL  6         0.4324
464.4    12.00  0.75     Sequence
 HLA-DQA10501-DQB10201  815      PSKPSKRSFIEDLLF  KRSFIEDLL  5         0.4918
244.3     6.00  0.50     Sequence         WB
 HLA-DQA10501-DQB10201  816      SKPSKRSFIEDLLFN  KRSFIEDLL  4         0.4605
342.8     8.50  0.51     Sequence         WB
 HLA-DQA10501-DQB10201  817      KPSKRSFIEDLLFNK  KRSFIEDLL  3         0.4223
518.2    13.00  0.50     Sequence
 HLA-DQA10501-DQB10201  818      PSKRSFIEDLLFNKV  KRSFIEDLL  2         0.4184
540.9    13.00  0.48     Sequence
 HLA-DQA10501-DQB10201  819      SKRSFIEDLLFNKVT  KRSFIEDLL  1         0.3913
725.1    17.00  0.47     Sequence
 HLA-DQA10501-DQB10201  820      KRSFIEDLLFNKVTL  KRSFIEDLL  0         0.3246
1491.7    29.00  0.38     Sequence
 HLA-DQA10501-DQB10201  821      RSFIEDLLFNKVTLA  RSFIEDLLF  0         0.2515
3290.3    48.00  0.32     Sequence
 HLA-DQA10501-DQB10201  822      SFIEDLLFNKVTLAD  LFNKVTLAD  6         0.2260
4333.0    55.00  0.26     Sequence
 HLA-DQA10501-DQB10201  823      FIEDLLFNKVTLADA  FNKVTLADA  6         0.2861
2263.5    39.00  0.54     Sequence
 HLA-DQA10501-DQB10201  824      IEDLLFNKVTLADAG  FNKVTLADA  5         0.2584
3054.6    46.00  0.56     Sequence
 HLA-DQA10501-DQB10201  825      EDLLFNKVTLADAGF  FNKVTLADA  4         0.3000
1946.3    35.00  0.39     Sequence
 HLA-DQA10501-DQB10201  826      DLLFNKVTLADAGFI  VTLADAGFI  6         0.3663
949.7    21.00  0.44     Sequence
 HLA-DQA10501-DQB10201  827      LLFNKVTLADAGFIK  VTLADAGFI  5         0.3304
1400.6    28.00  0.44     Sequence
 HLA-DQA10501-DQB10201  828      LFNKVTLADAGFIKQ  VTLADAGFI  4         0.3067
1810.0    33.00  0.44     Sequence
 HLA-DQA10501-DQB10201  829      FNKVTLADAGFIKQY  VTLADAGFI  3         0.2905
2156.2    37.00  0.49     Sequence
 HLA-DQA10501-DQB10201  830      NKVTLADAGFIKQYG  VTLADAGFI  2         0.2446
3544.6    50.00  0.54     Sequence
 HLA-DQA10501-DQB10201  831      KVTLADAGFIKQYGD  VTLADAGFI  1         0.2321
4057.2    55.00  0.49     Sequence
 HLA-DQA10501-DQB10201  832      VTLADAGFIKQYGDC  VTLADAGFI  0         0.2006
5704.4    65.00  0.47     Sequence
 HLA-DQA10501-DQB10201  833      TLADAGFIKQYGDCL  FIKQYGDCL  6         0.3465
1177.3    25.00  0.70     Sequence
 HLA-DQA10501-DQB10201  834      LADAGFIKQYGDCLG  FIKQYGDCL  5         0.3546
1077.9    23.00  0.68     Sequence
 HLA-DQA10501-DQB10201  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4         0.3709
904.1    20.00  0.66     Sequence
 HLA-DQA10501-DQB10201  836      DAGFIKQYGDCLGDI  FIKQYGDCL  3         0.4068
612.8    15.00  0.54     Sequence
 HLA-DQA10501-DQB10201  837      AGFIKQYGDCLGDIA  FIKQYGDCL  2         0.4310
471.7    12.00  0.41     Sequence
 HLA-DQA10501-DQB10201  838      GFIKQYGDCLGDIAA  FIKQYGDCL  1         0.4229
514.9    13.00  0.35     Sequence
 HLA-DQA10501-DQB10201  839      FIKQYGDCLGDIAAR  YGDCLGDIA  4         0.3925
715.3    17.00  0.41     Sequence
 HLA-DQA10501-DQB10201  840      IKQYGDCLGDIAARD  YGDCLGDIA  3         0.3623
991.9    22.00  0.53     Sequence
 HLA-DQA10501-DQB10201  841      KQYGDCLGDIAARDL  LGDIAARDL  6         0.4118
580.8    14.00  0.35     Sequence
 HLA-DQA10501-DQB10201  842      QYGDCLGDIAARDLI  LGDIAARDL  5         0.4010
652.7    16.00  0.38     Sequence
 HLA-DQA10501-DQB10201  843      YGDCLGDIAARDLIC  LGDIAARDL  4         0.3768
848.3    19.00  0.39     Sequence
```

```
 HLA-DQA10501-DQB10201  844       GDCLGDIAARDLICA  LGDIAARDL  3         0.3488
1148.2    24.00  0.41     Sequence
 HLA-DQA10501-DQB10201  845       DCLGDIAARDLICAQ  LGDIAARDL  2         0.3397
1266.8    26.00  0.38     Sequence
 HLA-DQA10501-DQB10201  846       CLGDIAARDLICAQK  LGDIAARDL  1         0.3018
1908.3    35.00  0.38     Sequence
 HLA-DQA10501-DQB10201  847       LGDIAARDLICAQKF  RDLICAQKF  6         0.3343
1342.8    27.00  0.38     Sequence
 HLA-DQA10501-DQB10201  848       GDIAARDLICAQKFN  RDLICAQKF  5         0.2837
2322.0    39.00  0.43     Sequence
 HLA-DQA10501-DQB10201  849       DIAARDLICAQKFNG  RDLICAQKF  4         0.2496
3359.2    48.00  0.44     Sequence
 HLA-DQA10501-DQB10201  850       IAARDLICAQKFNGL  RDLICAQKF  3         0.2216
4548.8    60.00  0.51     Sequence
 HLA-DQA10501-DQB10201  851       AARDLICAQKFNGLT  RDLICAQKF  2         0.1918
6278.3    65.00  0.62     Sequence
 HLA-DQA10501-DQB10201  852       ARDLICAQKFNGLTV  RDLICAQKF  1         0.1721
7765.9    70.00  0.58     Sequence
 HLA-DQA10501-DQB10201  853       RDLICAQKFNGLTVL  QKFNGLTVL  6         0.1767
7392.8    70.00  0.39     Sequence
 HLA-DQA10501-DQB10201  854       DLICAQKFNGLTVLP  KFNGLTVLP  6         0.2316
4080.0    55.00  0.43     Sequence
 HLA-DQA10501-DQB10201  855       LICAQKFNGLTVLPP  FNGLTVLPP  6         0.3617
998.6    22.00  0.54     Sequence
 HLA-DQA10501-DQB10201  856       ICAQKFNGLTVLPPL  FNGLTVLPP  5         0.4018
647.3    16.00  0.44     Sequence
 HLA-DQA10501-DQB10201  857       CAQKFNGLTVLPPLL  FNGLTVLPP  4         0.4330
461.7    12.00  0.32     Sequence
 HLA-DQA10501-DQB10201  858       AQKFNGLTVLPPLLT  GLTVLPPLL  5         0.4305
474.2    12.00  0.30     Sequence
 HLA-DQA10501-DQB10201  859       QKFNGLTVLPPLLTD  GLTVLPPLL  4         0.4254
501.1    13.00  0.34     Sequence
 HLA-DQA10501-DQB10201  860       KFNGLTVLPPLLTDE  GLTVLPPLL  3         0.4052
623.6    15.00  0.37     Sequence
 HLA-DQA10501-DQB10201  861       FNGLTVLPPLLTDEM  GLTVLPPLL  2         0.4083
603.2    15.00  0.31     Sequence
 HLA-DQA10501-DQB10201  862       NGLTVLPPLLTDEMI  PPLLTDEMI  6         0.4036
634.7    15.00  0.28     Sequence
 HLA-DQA10501-DQB10201  863       GLTVLPPLLTDEMIA  PPLLTDEMI  5         0.3861
766.7    18.00  0.25     Sequence
 HLA-DQA10501-DQB10201  864       LTVLPPLLTDEMIAQ  PPLLTDEMI  4         0.3470
1170.3    25.00  0.31     Sequence
 HLA-DQA10501-DQB10201  865       TVLPPLLTDEMIAQY  PPLLTDEMI  3         0.3452
1193.3    25.00  0.31     Sequence
 HLA-DQA10501-DQB10201  866       VLPPLLTDEMIAQYT  PPLLTDEMI  2         0.3509
1122.5    24.00  0.25     Sequence
 HLA-DQA10501-DQB10201  867       LPPLLTDEMIAQYTS  PPLLTDEMI  1         0.3206
1557.1    30.00  0.26     Sequence
 HLA-DQA10501-DQB10201  868       PPLLTDEMIAQYTSA  TDEMIAQYT  4         0.3070
1805.1    33.00  0.28     Sequence
 HLA-DQA10501-DQB10201  869       PLLTDEMIAQYTSAL  MIAQYTSAL  6         0.3225
1525.4    30.00  0.34     Sequence
 HLA-DQA10501-DQB10201  870       LLTDEMIAQYTSALL  IAQYTSALL  6         0.3983
671.7    16.00  0.53     Sequence
 HLA-DQA10501-DQB10201  871       LTDEMIAQYTSALLA  IAQYTSALL  5         0.4149
561.8    14.00  0.31     Sequence
 HLA-DQA10501-DQB10201  872       TDEMIAQYTSALLAG  IAQYTSALL  4         0.3787
830.6    19.00  0.32     Sequence
 HLA-DQA10501-DQB10201  873       DEMIAQYTSALLAGT  IAQYTSALL  3         0.3615
1001.0    22.00  0.31     Sequence
 HLA-DQA10501-DQB10201  874       EMIAQYTSALLAGTI  IAQYTSALL  2         0.3562
1059.3    23.00  0.28     Sequence
 HLA-DQA10501-DQB10201  875       MIAQYTSALLAGTIT  AQYTSALLA  2         0.3269
1454.4    29.00  0.25     Sequence
 HLA-DQA10501-DQB10201  876       IAQYTSALLAGTITS  AQYTSALLA  1         0.2855
2276.9    39.00  0.28     Sequence
```

```
 HLA-DQA10501-DQB10201  877      AQYTSALLAGTITSG  TSALLAGTI  3        0.2295
4171.8    55.00  0.27     Sequence
 HLA-DQA10501-DQB10201  878      QYTSALLAGTITSGW  LAGTITSGW  6        0.2496
3358.2    48.00  0.40     Sequence
 HLA-DQA10501-DQB10201  879      YTSALLAGTITSGWT  LAGTITSGW  5        0.2511
3305.6    48.00  0.45     Sequence
 HLA-DQA10501-DQB10201  880      TSALLAGTITSGWTF  LAGTITSGW  4        0.2458
3497.5    49.00  0.53     Sequence
 HLA-DQA10501-DQB10201  881      SALLAGTITSGWTFG  LAGTITSGW  3        0.2206
4593.9    60.00  0.57     Sequence
 HLA-DQA10501-DQB10201  882      ALLAGTITSGWTFGA  LAGTITSGW  2        0.2052
5430.3    65.00  0.62     Sequence
 HLA-DQA10501-DQB10201  883      LLAGTITSGWTFGAG  LAGTITSGW  1        0.1867
6632.6    70.00  0.60     Sequence
 HLA-DQA10501-DQB10201  884      LAGTITSGWTFGAGA  LAGTITSGW  0        0.1544
9410.7    75.00  0.49     Sequence
 HLA-DQA10501-DQB10201  885      AGTITSGWTFGAGAA  SGWTFGAGA  5        0.1103
15167.3    90.00  0.23     Sequence
 HLA-DQA10501-DQB10201  886      GTITSGWTFGAGAAL  WTFGAGAAL  6        0.2619
2940.0    45.00  0.79     Sequence
 HLA-DQA10501-DQB10201  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.3329
1363.7    28.00  0.50     Sequence
 HLA-DQA10501-DQB10201  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.4258
499.2    13.00  0.48     Sequence
 HLA-DQA10501-DQB10201  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.4485
390.5    10.00  0.43     Sequence
 HLA-DQA10501-DQB10201  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.4665
321.4     8.00  0.37     Sequence          WB
 HLA-DQA10501-DQB10201  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.4820
271.6     7.00  0.29     Sequence          WB
 HLA-DQA10501-DQB10201  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.4825
270.3     7.00  0.29     Sequence          WB
 HLA-DQA10501-DQB10201  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.4425
416.3    11.00  0.31     Sequence
 HLA-DQA10501-DQB10201  894      FGAGAALQIPFAMQM  GAALQIPFA  3        0.4186
539.3    13.00  0.37     Sequence
 HLA-DQA10501-DQB10201  895      GAGAALQIPFAMQMA  GAALQIPFA  2        0.3595
1022.1    22.00  0.46     Sequence
 HLA-DQA10501-DQB10201  896      AGAALQIPFAMQMAY  GAALQIPFA  1        0.3507
1124.4    24.00  0.40     Sequence
 HLA-DQA10501-DQB10201  897      GAALQIPFAMQMAYR  GAALQIPFA  0        0.3264
1463.5    29.00  0.31     Sequence
 HLA-DQA10501-DQB10201  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.3293
1418.4    28.00  0.38     Sequence
 HLA-DQA10501-DQB10201  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.3020
1905.0    35.00  0.39     Sequence
 HLA-DQA10501-DQB10201  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.2724
2624.4    42.00  0.41     Sequence
 HLA-DQA10501-DQB10201  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.2829
2341.2    39.00  0.38     Sequence
 HLA-DQA10501-DQB10201  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.2626
2916.6    45.00  0.41     Sequence
 HLA-DQA10501-DQB10201  903      PFAMQMAYRFNGIGV  FAMQMAYRF  1        0.2683
2742.4    43.00  0.29     Sequence
 HLA-DQA10501-DQB10201  904      FAMQMAYRFNGIGVT  FAMQMAYRF  0        0.2470
3453.1    49.00  0.24     Sequence
 HLA-DQA10501-DQB10201  905      AMQMAYRFNGIGVTQ  RFNGIGVTQ  6        0.2560
3132.2    47.00  0.37     Sequence
 HLA-DQA10501-DQB10201  906      MQMAYRFNGIGVTQN  FNGIGVTQN  6        0.2928
2104.1    37.00  0.38     Sequence
 HLA-DQA10501-DQB10201  907      QMAYRFNGIGVTQNV  FNGIGVTQN  5        0.2972
2007.1    36.00  0.38     Sequence
 HLA-DQA10501-DQB10201  908      MAYRFNGIGVTQNVL  FNGIGVTQN  4        0.3176
1609.3    31.00  0.36     Sequence
 HLA-DQA10501-DQB10201  909      AYRFNGIGVTQNVLY  FNGIGVTQN  3        0.3184
1594.8    31.00  0.36     Sequence
```

```
 HLA-DQA10501-DQB10201  910      YRFNGIGVTQNVLYE  FNGIGVTQN  2        0.3023
1898.3    35.00  0.33     Sequence
 HLA-DQA10501-DQB10201  911      RFNGIGVTQNVLYEN  FNGIGVTQN  1        0.2763
2516.5    41.00  0.26     Sequence
 HLA-DQA10501-DQB10201  912      FNGIGVTQNVLYENQ  TQNVLYENQ  6        0.2730
2606.0    42.00  0.29     Sequence
 HLA-DQA10501-DQB10201  913      NGIGVTQNVLYENQK  TQNVLYENQ  5        0.2253
4366.5    55.00  0.34     Sequence
 HLA-DQA10501-DQB10201  914      GIGVTQNVLYENQKL  NVLYENQKL  6        0.2404
3710.5    55.00  0.28     Sequence
 HLA-DQA10501-DQB10201  915      IGVTQNVLYENQKLI  TQNVLYENQ  3        0.2245
4406.0    55.00  0.29     Sequence
 HLA-DQA10501-DQB10201  916      GVTQNVLYENQKLIA  TQNVLYENQ  2        0.2271
4283.8    55.00  0.26     Sequence
 HLA-DQA10501-DQB10201  917      VTQNVLYENQKLIAN  NVLYENQKL  3        0.2088
5222.7    60.00  0.29     Sequence
 HLA-DQA10501-DQB10201  918      TQNVLYENQKLIANQ  NVLYENQKL  2        0.1800
7133.9    70.00  0.34     Sequence
 HLA-DQA10501-DQB10201  919      QNVLYENQKLIANQF  NQKLIANQF  6        0.2623
2927.4    45.00  0.65     Sequence
 HLA-DQA10501-DQB10201  920      NVLYENQKLIANQFN  NQKLIANQF  5        0.2620
2937.6    45.00  0.56     Sequence
 HLA-DQA10501-DQB10201  921      VLYENQKLIANQFNS  NQKLIANQF  4        0.2372
3838.5    55.00  0.61     Sequence
 HLA-DQA10501-DQB10201  922      LYENQKLIANQFNSA  NQKLIANQF  3        0.2404
3708.8    55.00  0.50     Sequence
 HLA-DQA10501-DQB10201  923      YENQKLIANQFNSAI  NQKLIANQF  2        0.2361
3887.5    55.00  0.43     Sequence
 HLA-DQA10501-DQB10201  924      ENQKLIANQFNSAIG  NQKLIANQF  1        0.2108
5108.4    60.00  0.40     Sequence
 HLA-DQA10501-DQB10201  925      NQKLIANQFNSAIGK  NQKLIANQF  0        0.1781
7277.8    70.00  0.25     Sequence
 HLA-DQA10501-DQB10201  926      QKLIANQFNSAIGKI  QFNSAIGKI  6        0.1720
7775.3    70.00  0.26     Sequence
 HLA-DQA10501-DQB10201  927      KLIANQFNSAIGKIQ  QFNSAIGKI  5        0.1610
8758.5    75.00  0.24     Sequence
 HLA-DQA10501-DQB10201  928      LIANQFNSAIGKIQD  FNSAIGKIQ  5        0.1708
7879.1    75.00  0.31     Sequence
 HLA-DQA10501-DQB10201  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4        0.1548
9369.1    75.00  0.41     Sequence
 HLA-DQA10501-DQB10201  930      ANQFNSAIGKIQDSL  AIGKIQDSL  6        0.2000
5742.2    65.00  0.41     Sequence
 HLA-DQA10501-DQB10201  931      NQFNSAIGKIQDSLS  AIGKIQDSL  5        0.2103
5137.0    60.00  0.36     Sequence
 HLA-DQA10501-DQB10201  932      QFNSAIGKIQDSLSS  AIGKIQDSL  4        0.1972
5923.4    65.00  0.39     Sequence
 HLA-DQA10501-DQB10201  933      FNSAIGKIQDSLSST  AIGKIQDSL  3        0.1804
7103.1    70.00  0.41     Sequence
 HLA-DQA10501-DQB10201  934      NSAIGKIQDSLSSTA  AIGKIQDSL  2        0.1664
8262.7    75.00  0.34     Sequence
 HLA-DQA10501-DQB10201  935      SAIGKIQDSLSSTAS  AIGKIQDSL  1        0.1567
9175.7    75.00  0.32     Sequence
 HLA-DQA10501-DQB10201  936      AIGKIQDSLSSTASA  IGKIQDSLS  1        0.1391
11101.7    80.00  0.31     Sequence
 HLA-DQA10501-DQB10201  937      IGKIQDSLSSTASAL  SLSSTASAL  6        0.1450
10416.6    80.00  0.46     Sequence
 HLA-DQA10501-DQB10201  938      GKIQDSLSSTASALG  SLSSTASAL  5        0.1458
10326.4    80.00  0.40     Sequence
 HLA-DQA10501-DQB10201  939      KIQDSLSSTASALGK  SLSSTASAL  4        0.1274
12598.3    85.00  0.39     Sequence
 HLA-DQA10501-DQB10201  940      IQDSLSSTASALGKL  SLSSTASAL  3        0.1279
12528.0    85.00  0.35     Sequence
 HLA-DQA10501-DQB10201  941      QDSLSSTASALGKLQ  SLSSTASAL  2        0.1207
13544.8    85.00  0.31     Sequence
 HLA-DQA10501-DQB10201  942      DSLSSTASALGKLQD  TASALGKLQ  5        0.1312
12089.2    85.00  0.20     Sequence
```

```
 HLA-DQA10501-DQB10201  943       SLSSTASALGKLQDV  SALGKLQDV  6         0.1477
10109.5    80.00  0.31      Sequence
 HLA-DQA10501-DQB10201  944       LSSTASALGKLQDVV  ALGKLQDVV  6         0.1684
8084.5    75.00  0.36      Sequence
 HLA-DQA10501-DQB10201  945       SSTASALGKLQDVVN  ALGKLQDVV  5         0.1716
7810.2    75.00  0.30      Sequence
 HLA-DQA10501-DQB10201  946       STASALGKLQDVVNQ  ALGKLQDVV  4         0.1668
8221.8    75.00  0.28      Sequence
 HLA-DQA10501-DQB10201  947       TASALGKLQDVVNQN  ALGKLQDVV  3         0.1682
8104.6    75.00  0.24      Sequence
 HLA-DQA10501-DQB10201  948       ASALGKLQDVVNQNA  LQDVVNQNA  6         0.1999
5749.3    65.00  0.38      Sequence
 HLA-DQA10501-DQB10201  949       SALGKLQDVVNQNAQ  LQDVVNQNA  5         0.1868
6623.5    70.00  0.40      Sequence
 HLA-DQA10501-DQB10201  950       ALGKLQDVVNQNAQA  LQDVVNQNA  4         0.1984
5845.4    65.00  0.34      Sequence
 HLA-DQA10501-DQB10201  951       LGKLQDVVNQNAQAL  VVNQNAQAL  6         0.2469
3456.4    49.00  0.51      Sequence
 HLA-DQA10501-DQB10201  952       GKLQDVVNQNAQALN  VVNQNAQAL  5         0.2461
3487.8    49.00  0.44      Sequence
 HLA-DQA10501-DQB10201  953       KLQDVVNQNAQALNT  VVNQNAQAL  4         0.2434
3590.7    50.00  0.38      Sequence
 HLA-DQA10501-DQB10201  954       LQDVVNQNAQALNTL  VVNQNAQAL  3         0.2595
3016.2    46.00  0.33      Sequence
 HLA-DQA10501-DQB10201  955       QDVVNQNAQALNTLV  VVNQNAQAL  2         0.2509
3311.4    48.00  0.30      Sequence
 HLA-DQA10501-DQB10201  956       DVVNQNAQALNTLVK  VVNQNAQAL  1         0.2185
4701.8    60.00  0.30      Sequence
 HLA-DQA10501-DQB10201  957       VVNQNAQALNTLVKQ  VVNQNAQAL  0         0.1891
6462.1    70.00  0.17      Sequence
 HLA-DQA10501-DQB10201  958       VNQNAQALNTLVKQL  ALNTLVKQL  6         0.1764
7415.1    70.00  0.19      Sequence
 HLA-DQA10501-DQB10201  959       NQNAQALNTLVKQLS  LNTLVKQLS  6         0.1822
6966.7    70.00  0.29      Sequence
 HLA-DQA10501-DQB10201  960       QNAQALNTLVKQLSS  LNTLVKQLS  5         0.1629
8578.8    75.00  0.32      Sequence
 HLA-DQA10501-DQB10201  961       NAQALNTLVKQLSSN  LNTLVKQLS  4         0.1403
10955.8    80.00  0.35      Sequence
 HLA-DQA10501-DQB10201  962       AQALNTLVKQLSSNF  LVKQLSSNF  6         0.1607
8784.9    75.00  0.35      Sequence
 HLA-DQA10501-DQB10201  963       QALNTLVKQLSSNFG  LVKQLSSNF  5         0.1638
8493.6    75.00  0.31      Sequence
 HLA-DQA10501-DQB10201  964       ALNTLVKQLSSNFGA  LVKQLSSNF  4         0.1532
9533.9    80.00  0.35      Sequence
 HLA-DQA10501-DQB10201  965       LNTLVKQLSSNFGAI  LVKQLSSNF  3         0.1431
10627.9    80.00  0.39      Sequence
 HLA-DQA10501-DQB10201  966       NTLVKQLSSNFGAIS  LVKQLSSNF  2         0.1473
10152.7    80.00  0.29      Sequence
 HLA-DQA10501-DQB10201  967       TLVKQLSSNFGAISS  LVKQLSSNF  1         0.1455
10362.3    80.00  0.26      Sequence
 HLA-DQA10501-DQB10201  968       LVKQLSSNFGAISSV  SNFGAISSV  6         0.1886
6500.7    70.00  0.42      Sequence
 HLA-DQA10501-DQB10201  969       VKQLSSNFGAISSVL  NFGAISSVL  6         0.3090
1766.7    33.00  0.70      Sequence
 HLA-DQA10501-DQB10201  970       KQLSSNFGAISSVLN  FGAISSVLN  6         0.3764
851.2    20.00  0.44      Sequence
 HLA-DQA10501-DQB10201  971       QLSSNFGAISSVLND  FGAISSVLN  5         0.4005
656.0    16.00  0.44      Sequence
 HLA-DQA10501-DQB10201  972       LSSNFGAISSVLNDI  FGAISSVLN  4         0.4338
457.8    12.00  0.37      Sequence
 HLA-DQA10501-DQB10201  973       SSNFGAISSVLNDIL  ISSVLNDIL  6         0.5029
216.7     5.50  0.47      Sequence         WB
 HLA-DQA10501-DQB10201  974       SNFGAISSVLNDILS  ISSVLNDIL  5         0.4783
282.6     7.00  0.46      Sequence         WB
 HLA-DQA10501-DQB10201  975       NFGAISSVLNDILSR  ISSVLNDIL  4         0.4439
410.2    11.00  0.48      Sequence
```

```
 HLA-DQA10501-DQB10201  976      FGAISSVLNDILSRL  ISSVLNDIL  3        0.4191
536.5    13.00  0.54     Sequence
 HLA-DQA10501-DQB10201  977      GAISSVLNDILSRLD  ISSVLNDIL  2        0.3771
845.1    19.00  0.52     Sequence
 HLA-DQA10501-DQB10201  978      AISSVLNDILSRLDK  ISSVLNDIL  1        0.3448
1199.3    25.00  0.55     Sequence
 HLA-DQA10501-DQB10201  979      ISSVLNDILSRLDKV  ISSVLNDIL  0        0.3038
1867.8    34.00  0.34     Sequence
 HLA-DQA10501-DQB10201  980      SSVLNDILSRLDKVE  DILSRLDKV  5        0.2433
3594.0    50.00  0.29     Sequence
 HLA-DQA10501-DQB10201  981      SVLNDILSRLDKVEA  DILSRLDKV  4        0.2496
3359.5    48.00  0.28     Sequence
 HLA-DQA10501-DQB10201  982      VLNDILSRLDKVEAE  SRLDKVEAE  6        0.2914
2135.9    37.00  0.34     Sequence
 HLA-DQA10501-DQB10201  983      LNDILSRLDKVEAEV  SRLDKVEAE  5        0.3294
1415.5    28.00  0.33     Sequence
 HLA-DQA10501-DQB10201  984      NDILSRLDKVEAEVQ  LDKVEAEVQ  6        0.3527
1100.4    24.00  0.34     Sequence
 HLA-DQA10501-DQB10201  985      DILSRLDKVEAEVQI  LDKVEAEVQ  5        0.3645
969.1    22.00  0.34     Sequence
 HLA-DQA10501-DQB10201  986      ILSRLDKVEAEVQID  KVEAEVQID  6        0.4064
615.8    15.00  0.31     Sequence
 HLA-DQA10501-DQB10201  987      LSRLDKVEAEVQIDR  KVEAEVQID  5        0.3924
716.2    17.00  0.29     Sequence
 HLA-DQA10501-DQB10201  988      SRLDKVEAEVQIDRL  EAEVQIDRL  6        0.5530
126.0     3.00  0.64     Sequence         WB
 HLA-DQA10501-DQB10201  989      RLDKVEAEVQIDRLI  EAEVQIDRL  5        0.5499
130.3     3.00  0.60     Sequence         WB
 HLA-DQA10501-DQB10201  990      LDKVEAEVQIDRLIT  EAEVQIDRL  4        0.5338
155.2     3.50  0.58     Sequence         WB
 HLA-DQA10501-DQB10201  991      DKVEAEVQIDRLITG  EAEVQIDRL  3        0.5035
215.3     5.50  0.59     Sequence         WB
 HLA-DQA10501-DQB10201  992      KVEAEVQIDRLITGR  EAEVQIDRL  2        0.4624
335.9     8.50  0.61     Sequence         WB
 HLA-DQA10501-DQB10201  993      VEAEVQIDRLITGRL  EAEVQIDRL  1        0.4377
438.7    11.00  0.63     Sequence
 HLA-DQA10501-DQB10201  994      EAEVQIDRLITGRLQ  EAEVQIDRL  0        0.3788
829.8    19.00  0.50     Sequence
 HLA-DQA10501-DQB10201  995      AEVQIDRLITGRLQS  DRLITGRLQ  5        0.2257
4348.6    55.00  0.20     Sequence
 HLA-DQA10501-DQB10201  996      EVQIDRLITGRLQSL  LITGRLQSL  6        0.2174
4756.1    60.00  0.27     Sequence
 HLA-DQA10501-DQB10201  997      VQIDRLITGRLQSLQ  LITGRLQSL  5        0.1851
6746.1    70.00  0.31     Sequence
 HLA-DQA10501-DQB10201  998      QIDRLITGRLQSLQT  TGRLQSLQT  6        0.2078
5278.5    60.00  0.35     Sequence
 HLA-DQA10501-DQB10201  999      IDRLITGRLQSLQTY  TGRLQSLQT  5        0.2214
4555.8    60.00  0.34     Sequence
 HLA-DQA10501-DQB10201 1000      DRLITGRLQSLQTYV  TGRLQSLQT  4        0.2306
4126.6    55.00  0.29     Sequence
 HLA-DQA10501-DQB10201 1001      RLITGRLQSLQTYVT  RLQSLQTYV  5        0.2278
4253.2    55.00  0.23     Sequence
 HLA-DQA10501-DQB10201 1002      LITGRLQSLQTYVTQ  TGRLQSLQT  2        0.2124
5021.5    60.00  0.25     Sequence
 HLA-DQA10501-DQB10201 1003      ITGRLQSLQTYVTQQ  RLQSLQTYV  3        0.1967
5949.3    65.00  0.19     Sequence
 HLA-DQA10501-DQB10201 1004      TGRLQSLQTYVTQQL  LQTYVTQQL  6        0.3022
1899.9    35.00  0.69     Sequence
 HLA-DQA10501-DQB10201 1005      GRLQSLQTYVTQQLI  LQTYVTQQL  5        0.3323
1372.8    28.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1006      RLQSLQTYVTQQLIR  LQTYVTQQL  4        0.2965
2021.4    36.00  0.45     Sequence
 HLA-DQA10501-DQB10201 1007      LQSLQTYVTQQLIRA  LQTYVTQQL  3        0.3047
1849.9    34.00  0.32     Sequence
 HLA-DQA10501-DQB10201 1008      QSLQTYVTQQLIRAA  LQTYVTQQL  2        0.2870
2239.9    38.00  0.32     Sequence
```

```
 HLA-DQA10501-DQB10201 1009      SLQTYVTQQLIRAAE  LQTYVTQQL  1        0.2860
2264.2    39.00  0.26     Sequence
 HLA-DQA10501-DQB10201 1010      LQTYVTQQLIRAAEI  QQLIRAAEI  6        0.3942
702.5    17.00  0.61     Sequence
 HLA-DQA10501-DQB10201 1011      QTYVTQQLIRAAEIR  QQLIRAAEI  5        0.3699
914.0    21.00  0.60     Sequence
 HLA-DQA10501-DQB10201 1012      TYVTQQLIRAAEIRA  QQLIRAAEI  4        0.3796
822.8    19.00  0.47     Sequence
 HLA-DQA10501-DQB10201 1013      YVTQQLIRAAEIRAS  QQLIRAAEI  3        0.3666
947.3    21.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1014      VTQQLIRAAEIRASA  QQLIRAAEI  2        0.3441
1208.1    25.00  0.42     Sequence
 HLA-DQA10501-DQB10201 1015      TQQLIRAAEIRASAN  QQLIRAAEI  1        0.3206
1557.5    30.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1016      QQLIRAAEIRASANL  LIRAAEIRA  2        0.2931
2096.4    37.00  0.34     Sequence
 HLA-DQA10501-DQB10201 1017      QLIRAAEIRASANLA  EIRASANLA  6        0.2905
2156.7    37.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1018      LIRAAEIRASANLAA  EIRASANLA  5        0.2754
2541.2    41.00  0.47     Sequence
 HLA-DQA10501-DQB10201 1019      IRAAEIRASANLAAI  EIRASANLA  4        0.2808
2397.1    40.00  0.48     Sequence
 HLA-DQA10501-DQB10201 1020      RAAEIRASANLAAIK  EIRASANLA  3        0.2506
3323.8    48.00  0.47     Sequence
 HLA-DQA10501-DQB10201 1021      AAEIRASANLAAIKM  SANLAAIKM  6        0.2940
2076.5    37.00  0.39     Sequence
 HLA-DQA10501-DQB10201 1022      AEIRASANLAAIKMS  EIRASANLA  1        0.2660
2813.1    44.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1023      EIRASANLAAIKMSE  SANLAAIKM  4        0.2565
3117.3    46.00  0.34     Sequence
 HLA-DQA10501-DQB10201 1024      IRASANLAAIKMSEC  SANLAAIKM  3        0.2360
3891.8    55.00  0.35     Sequence
 HLA-DQA10501-DQB10201 1025      RASANLAAIKMSECV  SANLAAIKM  2        0.2473
3441.7    49.00  0.24     Sequence
 HLA-DQA10501-DQB10201 1026      ASANLAAIKMSECVL  AIKMSECVL  6        0.2830
2340.6    39.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1027      SANLAAIKMSECVLG  AIKMSECVL  5        0.2544
3189.9    47.00  0.28     Sequence
 HLA-DQA10501-DQB10201 1028      ANLAAIKMSECVLGQ  AIKMSECVL  4        0.2378
3814.8    55.00  0.30     Sequence
 HLA-DQA10501-DQB10201 1029      NLAAIKMSECVLGQS  AIKMSECVL  3        0.2203
4612.6    60.00  0.28     Sequence
 HLA-DQA10501-DQB10201 1030      LAAIKMSECVLGQSK  AIKMSECVL  2        0.1896
6429.2    70.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1031      AAIKMSECVLGQSKR  AIKMSECVL  1        0.1603
8822.8    75.00  0.47     Sequence
 HLA-DQA10501-DQB10201 1032      AIKMSECVLGQSKRV  AIKMSECVL  0        0.1257
12832.3    85.00  0.40     Sequence
 HLA-DQA10501-DQB10201 1033      IKMSECVLGQSKRVD  SECVLGQSK  3        0.0982
17283.8    90.00  0.25     Sequence
 HLA-DQA10501-DQB10201 1034      KMSECVLGQSKRVDF  LGQSKRVDF  6        0.1039
16246.7    90.00  0.29     Sequence
 HLA-DQA10501-DQB10201 1035      MSECVLGQSKRVDFC  LGQSKRVDF  5        0.1096
15266.9    90.00  0.22     Sequence
 HLA-DQA10501-DQB10201 1036      SECVLGQSKRVDFCG  GQSKRVDFC  5        0.0951
17862.7    90.00  0.20     Sequence
 HLA-DQA10501-DQB10201 1037      ECVLGQSKRVDFCGK  GQSKRVDFC  4        0.0824
20507.0    95.00  0.20     Sequence
 HLA-DQA10501-DQB10201 1038      CVLGQSKRVDFCGKG  GQSKRVDFC  3        0.0719
22963.8    95.00  0.18     Sequence
 HLA-DQA10501-DQB10201 1039      VLGQSKRVDFCGKGY  RVDFCGKGY  6        0.0829
20399.9    95.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1040      LGQSKRVDFCGKGYH  RVDFCGKGY  5        0.0703
23364.0    95.00  0.41     Sequence
 HLA-DQA10501-DQB10201 1041      GQSKRVDFCGKGYHL  RVDFCGKGY  4        0.0682
23903.8    95.00  0.41     Sequence
```

```
 HLA-DQA10501-DQB10201 1042      QSKRVDFCGKGYHLM  RVDFCGKGY  3        0.0643
24944.1    95.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1043      SKRVDFCGKGYHLMS  RVDFCGKGY  2        0.0622
25520.6   100.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1044      KRVDFCGKGYHLMSF  GKGYHLMSF  6        0.1168
14127.5    85.00  0.62     Sequence
 HLA-DQA10501-DQB10201 1045      RVDFCGKGYHLMSFP  GKGYHLMSF  5        0.1513
9727.8    80.00  0.47     Sequence
 HLA-DQA10501-DQB10201 1046      VDFCGKGYHLMSFPQ  GKGYHLMSF  4        0.1476
10129.0    80.00  0.40     Sequence
 HLA-DQA10501-DQB10201 1047      DFCGKGYHLMSFPQS  YHLMSFPQS  6        0.1957
6015.4    65.00  0.50     Sequence
 HLA-DQA10501-DQB10201 1048      FCGKGYHLMSFPQSA  HLMSFPQSA  6        0.2303
4139.9    55.00  0.36     Sequence
 HLA-DQA10501-DQB10201 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.2471
3450.8    49.00  0.40     Sequence
 HLA-DQA10501-DQB10201 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.2338
3983.3    55.00  0.40     Sequence
 HLA-DQA10501-DQB10201 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.2222
4518.3    60.00  0.39     Sequence
 HLA-DQA10501-DQB10201 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.2251
4376.6    55.00  0.36     Sequence
 HLA-DQA10501-DQB10201 1053      YHLMSFPQSAPHGVV  HLMSFPQSA  1        0.2070
5323.5    60.00  0.35     Sequence
 HLA-DQA10501-DQB10201 1054      HLMSFPQSAPHGVVF  FPQSAPHGV  4        0.1630
8571.4    75.00  0.28     Sequence
 HLA-DQA10501-DQB10201 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.1554
9307.5    75.00  0.32     Sequence
 HLA-DQA10501-DQB10201 1056      MSFPQSAPHGVVFLH  FPQSAPHGV  2        0.1438
10552.1    80.00  0.32     Sequence
 HLA-DQA10501-DQB10201 1057      SFPQSAPHGVVFLHV  PHGVVFLHV  6        0.2521
3269.5    48.00  0.63     Sequence
 HLA-DQA10501-DQB10201 1058      FPQSAPHGVVFLHVT  PHGVVFLHV  5        0.2314
4088.5    55.00  0.54     Sequence
 HLA-DQA10501-DQB10201 1059      PQSAPHGVVFLHVTY  PHGVVFLHV  4        0.2312
4096.4    55.00  0.56     Sequence
 HLA-DQA10501-DQB10201 1060      QSAPHGVVFLHVTYV  PHGVVFLHV  3        0.2405
3704.9    55.00  0.45     Sequence
 HLA-DQA10501-DQB10201 1061      SAPHGVVFLHVTYVP  VFLHVTYVP  6        0.3065
1814.9    34.00  0.32     Sequence
 HLA-DQA10501-DQB10201 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.3567
1054.1    23.00  0.46     Sequence
 HLA-DQA10501-DQB10201 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.3575
1045.5    23.00  0.36     Sequence
 HLA-DQA10501-DQB10201 1064      HGVVFLHVTYVPAQE  HVTYVPAQE  6        0.4625
335.5     8.50  0.55     Sequence         WB
 HLA-DQA10501-DQB10201 1065      GVVFLHVTYVPAQEK  HVTYVPAQE  5        0.4692
312.2     8.00  0.47     Sequence         WB
 HLA-DQA10501-DQB10201 1066      VVFLHVTYVPAQEKN  HVTYVPAQE  4        0.4581
352.0     9.00  0.46     Sequence         WB
 HLA-DQA10501-DQB10201 1067      VFLHVTYVPAQEKNF  HVTYVPAQE  3        0.4604
343.3     8.50  0.51     Sequence         WB
 HLA-DQA10501-DQB10201 1068      FLHVTYVPAQEKNFT  HVTYVPAQE  2        0.4325
464.2    12.00  0.52     Sequence
 HLA-DQA10501-DQB10201 1069      LHVTYVPAQEKNFTT  HVTYVPAQE  1        0.3835
788.7    18.00  0.53     Sequence
 HLA-DQA10501-DQB10201 1070      HVTYVPAQEKNFTTA  HVTYVPAQE  0        0.3241
1500.1    30.00  0.50     Sequence
 HLA-DQA10501-DQB10201 1071      VTYVPAQEKNFTTAP  VTYVPAQEK  0        0.1869
6619.4    70.00  0.50     Sequence
 HLA-DQA10501-DQB10201 1072      TYVPAQEKNFTTAPA  YVPAQEKNF  1        0.1139
14573.4    90.00  0.42     Sequence
 HLA-DQA10501-DQB10201 1073      YVPAQEKNFTTAPAI  KNFTTAPAI  6        0.1676
8158.5    75.00  0.59     Sequence
 HLA-DQA10501-DQB10201 1074      VPAQEKNFTTAPAIC  NFTTAPAIC  6        0.2141
4932.5    60.00  0.44     Sequence
```

```
 HLA-DQA10501-DQB10201 1075      PAQEKNFTTAPAICH  NFTTAPAIC  5        0.2310
4106.2    55.00  0.41     Sequence
 HLA-DQA10501-DQB10201 1076      AQEKNFTTAPAICHD  NFTTAPAIC  4        0.2529
3240.9    47.00  0.39     Sequence
 HLA-DQA10501-DQB10201 1077      QEKNFTTAPAICHDG  NFTTAPAIC  3        0.2362
3880.5    55.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1078      EKNFTTAPAICHDGK  NFTTAPAIC  2        0.2202
4615.1    60.00  0.40     Sequence
 HLA-DQA10501-DQB10201 1079      KNFTTAPAICHDGKA  NFTTAPAIC  1        0.1967
5949.7    65.00  0.39     Sequence
 HLA-DQA10501-DQB10201 1080      NFTTAPAICHDGKAH  NFTTAPAIC  0        0.1591
8937.0    75.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1081      FTTAPAICHDGKAHF  FTTAPAICH  0        0.1094
15311.8    90.00  0.26     Sequence
 HLA-DQA10501-DQB10201 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.0856
19813.6    95.00  0.25     Sequence
 HLA-DQA10501-DQB10201 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.0704
23346.3    95.00  0.25     Sequence
 HLA-DQA10501-DQB10201 1084      APAICHDGKAHFPRE  DGKAHFPRE  6        0.0858
19764.2    95.00  0.22     Sequence
 HLA-DQA10501-DQB10201 1085      PAICHDGKAHFPREG  DGKAHFPRE  5        0.0763
21892.1    95.00  0.22     Sequence
 HLA-DQA10501-DQB10201 1086      AICHDGKAHFPREGV  KAHFPREGV  6        0.0928
18317.8    90.00  0.34     Sequence
 HLA-DQA10501-DQB10201 1087      ICHDGKAHFPREGVF  AHFPREGVF  6        0.1170
14093.3    85.00  0.33     Sequence
 HLA-DQA10501-DQB10201 1088      CHDGKAHFPREGVFV  HFPREGVFV  6        0.1464
10258.3    80.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1089      HDGKAHFPREGVFVS  HFPREGVFV  5        0.1422
10739.2    80.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1090      DGKAHFPREGVFVSN  HFPREGVFV  4        0.1555
9292.9    75.00  0.28     Sequence
 HLA-DQA10501-DQB10201 1091      GKAHFPREGVFVSNG  HFPREGVFV  3        0.1504
9827.4    80.00  0.26     Sequence
 HLA-DQA10501-DQB10201 1092      KAHFPREGVFVSNGT  EGVFVSNGT  6        0.1794
7173.9    70.00  0.35     Sequence
 HLA-DQA10501-DQB10201 1093      AHFPREGVFVSNGTH  EGVFVSNGT  5        0.1648
8409.3    75.00  0.36     Sequence
 HLA-DQA10501-DQB10201 1094      HFPREGVFVSNGTHW  VFVSNGTHW  6        0.1889
6476.8    70.00  0.34     Sequence
 HLA-DQA10501-DQB10201 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6        0.2575
3082.5    46.00  0.43     Sequence
 HLA-DQA10501-DQB10201 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.2641
2871.0    44.00  0.48     Sequence
 HLA-DQA10501-DQB10201 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.2552
3160.6    47.00  0.47     Sequence
 HLA-DQA10501-DQB10201 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.2443
3554.8    50.00  0.46     Sequence
 HLA-DQA10501-DQB10201 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.2257
4348.1    55.00  0.51     Sequence
 HLA-DQA10501-DQB10201 1100      VFVSNGTHWFVTQRN  THWFVTQRN  6        0.2566
3112.5    46.00  0.28     Sequence
 HLA-DQA10501-DQB10201 1101      FVSNGTHWFVTQRNF  THWFVTQRN  5        0.2398
3732.4    55.00  0.39     Sequence
 HLA-DQA10501-DQB10201 1102      VSNGTHWFVTQRNFY  WFVTQRNFY  6        0.2687
2730.3    43.00  0.40     Sequence
 HLA-DQA10501-DQB10201 1103      SNGTHWFVTQRNFYE  WFVTQRNFY  5        0.2790
2443.8    40.00  0.37     Sequence
 HLA-DQA10501-DQB10201 1104      NGTHWFVTQRNFYEP  WFVTQRNFY  4        0.2939
2079.7    37.00  0.40     Sequence
 HLA-DQA10501-DQB10201 1105      GTHWFVTQRNFYEPQ  WFVTQRNFY  3        0.2885
2203.4    38.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1106      THWFVTQRNFYEPQI  WFVTQRNFY  2        0.3245
1493.1    29.00  0.30     Sequence
 HLA-DQA10501-DQB10201 1107      HWFVTQRNFYEPQII  RNFYEPQII  6        0.4019
646.2    16.00  0.49     Sequence
```

```
 HLA-DQA10501-DQB10201 1108      WFVTQRNFYEPQIIT  RNFYEPQII  5        0.3736
877.9    20.00  0.49     Sequence
 HLA-DQA10501-DQB10201 1109      FVTQRNFYEPQIITT  RNFYEPQII  4        0.3300
1406.8    28.00  0.57     Sequence
 HLA-DQA10501-DQB10201 1110      VTQRNFYEPQIITTD  RNFYEPQII  3        0.3258
1471.8    29.00  0.62     Sequence
 HLA-DQA10501-DQB10201 1111      TQRNFYEPQIITTDN  RNFYEPQII  2        0.3116
1717.7    32.00  0.61     Sequence
 HLA-DQA10501-DQB10201 1112      QRNFYEPQIITTDNT  RNFYEPQII  1        0.3148
1659.5    32.00  0.48     Sequence
 HLA-DQA10501-DQB10201 1113      RNFYEPQIITTDNTF  QIITTDNTF  6        0.3385
1283.8    27.00  0.35     Sequence
 HLA-DQA10501-DQB10201 1114      NFYEPQIITTDNTFV  QIITTDNTF  5        0.3557
1065.2    23.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1115      FYEPQIITTDNTFVS  QIITTDNTF  4        0.3482
1155.2    25.00  0.34     Sequence
 HLA-DQA10501-DQB10201 1116      YEPQIITTDNTFVSG  QIITTDNTF  3        0.3263
1464.9    29.00  0.35     Sequence
 HLA-DQA10501-DQB10201 1117      EPQIITTDNTFVSGN  QIITTDNTF  2        0.3012
1922.1    35.00  0.36     Sequence
 HLA-DQA10501-DQB10201 1118      PQIITTDNTFVSGNC  IITTDNTFV  2        0.2770
2496.2    41.00  0.32     Sequence
 HLA-DQA10501-DQB10201 1119      QIITTDNTFVSGNCD  IITTDNTFV  1        0.2692
2715.1    43.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1120      IITTDNTFVSGNCDV  TFVSGNCDV  6        0.2363
3877.7    55.00  0.32     Sequence
 HLA-DQA10501-DQB10201 1121      ITTDNTFVSGNCDVV  FVSGNCDVV  6        0.2644
2859.9    44.00  0.47     Sequence
 HLA-DQA10501-DQB10201 1122      TTDNTFVSGNCDVVI  VSGNCDVVI  6        0.3284
1430.9    29.00  0.42     Sequence
 HLA-DQA10501-DQB10201 1123      TDNTFVSGNCDVVIG  VSGNCDVVI  5        0.3109
1729.9    33.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1124      DNTFVSGNCDVVIGI  VSGNCDVVI  4        0.3087
1770.9    33.00  0.35     Sequence
 HLA-DQA10501-DQB10201 1125      NTFVSGNCDVVIGIV  VSGNCDVVI  3        0.2959
2035.2    36.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1126      TFVSGNCDVVIGIVN  VSGNCDVVI  2        0.2736
2589.2    42.00  0.41     Sequence
 HLA-DQA10501-DQB10201 1127      FVSGNCDVVIGIVNN  VSGNCDVVI  1        0.2399
3729.3    55.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1128      VSGNCDVVIGIVNNT  VVIGIVNNT  6        0.2020
5622.5    65.00  0.39     Sequence
 HLA-DQA10501-DQB10201 1129      SGNCDVVIGIVNNTV  VIGIVNNTV  6        0.2553
3156.8    47.00  0.61     Sequence
 HLA-DQA10501-DQB10201 1130      GNCDVVIGIVNNTVY  VIGIVNNTV  5        0.2548
3173.9    47.00  0.55     Sequence
 HLA-DQA10501-DQB10201 1131      NCDVVIGIVNNTVYD  VIGIVNNTV  4        0.2658
2818.2    44.00  0.52     Sequence
 HLA-DQA10501-DQB10201 1132      CDVVIGIVNNTVYDP  VIGIVNNTV  3        0.3131
1689.5    32.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1133      DVVIGIVNNTVYDPL  VNNTVYDPL  6        0.4183
541.0    13.00  0.52     Sequence
 HLA-DQA10501-DQB10201 1134      VVIGIVNNTVYDPLQ  VNNTVYDPL  5        0.3883
749.2    18.00  0.49     Sequence
 HLA-DQA10501-DQB10201 1135      VIGIVNNTVYDPLQP  VNNTVYDPL  4        0.3991
666.1    16.00  0.50     Sequence
 HLA-DQA10501-DQB10201 1136      IGIVNNTVYDPLQPE  VNNTVYDPL  3        0.4097
593.9    15.00  0.49     Sequence
 HLA-DQA10501-DQB10201 1137      GIVNNTVYDPLQPEL  VNNTVYDPL  2        0.4507
381.0     9.50  0.34     Sequence         WB
 HLA-DQA10501-DQB10201 1138      IVNNTVYDPLQPELD  VNNTVYDPL  1        0.4710
306.1     7.50  0.19     Sequence         WB
 HLA-DQA10501-DQB10201 1139      VNNTVYDPLQPELDS  YDPLQPELD  5        0.4356
448.9    11.00  0.29     Sequence
 HLA-DQA10501-DQB10201 1140      NNTVYDPLQPELDSF  YDPLQPELD  4        0.4315
469.4    12.00  0.34     Sequence
```

```
 HLA-DQA10501-DQB10201 1141      NTVYDPLQPELDSFK  VYDPLQPEL  2        0.3977
676.1    16.00  0.32     Sequence
 HLA-DQA10501-DQB10201 1142      TVYDPLQPELDSFKE  YDPLQPELD  2        0.3729
884.9    20.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1143      VYDPLQPELDSFKEE  YDPLQPELD  1        0.3172
1615.5    31.00  0.41     Sequence
 HLA-DQA10501-DQB10201 1144      YDPLQPELDSFKEEL  ELDSFKEEL  6        0.3492
1143.2    24.00  0.50     Sequence
 HLA-DQA10501-DQB10201 1145      DPLQPELDSFKEELD  ELDSFKEEL  5        0.3786
832.1    19.00  0.52     Sequence
 HLA-DQA10501-DQB10201 1146      PLQPELDSFKEELDK  ELDSFKEEL  4        0.3441
1208.5    25.00  0.52     Sequence
 HLA-DQA10501-DQB10201 1147      LQPELDSFKEELDKY  ELDSFKEEL  3        0.3570
1050.7    23.00  0.46     Sequence
 HLA-DQA10501-DQB10201 1148      QPELDSFKEELDKYF  ELDSFKEEL  2        0.3638
976.5    22.00  0.35     Sequence
 HLA-DQA10501-DQB10201 1149      PELDSFKEELDKYFK  ELDSFKEEL  1        0.3351
1331.6    27.00  0.37     Sequence
 HLA-DQA10501-DQB10201 1150      ELDSFKEELDKYFKN  ELDSFKEEL  0        0.2937
2083.8    37.00  0.34     Sequence
 HLA-DQA10501-DQB10201 1151      LDSFKEELDKYFKNH  FKEELDKYF  3        0.1903
6378.2    65.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1152      DSFKEELDKYFKNHT  FKEELDKYF  2        0.1441
10517.9    80.00  0.50     Sequence
 HLA-DQA10501-DQB10201 1153      SFKEELDKYFKNHTS  FKEELDKYF  1        0.1168
14130.7    85.00  0.54     Sequence
 HLA-DQA10501-DQB10201 1154      FKEELDKYFKNHTSP  FKEELDKYF  0        0.0807
20872.1    95.00  0.49     Sequence
 HLA-DQA10501-DQB10201 1155      KEELDKYFKNHTSPD  YFKNHTSPD  6        0.0571
26957.7   100.00  0.35     Sequence
 HLA-DQA10501-DQB10201 1156      EELDKYFKNHTSPDV  FKNHTSPDV  6        0.1074
15641.8    90.00  0.58     Sequence
 HLA-DQA10501-DQB10201 1157      ELDKYFKNHTSPDVD  KNHTSPDVD  6        0.1549
9358.0    75.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1158      LDKYFKNHTSPDVDL  NHTSPDVDL  6        0.2021
5611.8    65.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1159      DKYFKNHTSPDVDLG  KNHTSPDVD  4        0.1963
5977.6    65.00  0.33     Sequence
 HLA-DQA10501-DQB10201 1160      KYFKNHTSPDVDLGD  KNHTSPDVD  3        0.2070
5324.3    60.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1161      YFKNHTSPDVDLGDI  KNHTSPDVD  2        0.2140
4937.9    60.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1162      FKNHTSPDVDLGDIS  PDVDLGDIS  6        0.2256
4355.1    55.00  0.34     Sequence
 HLA-DQA10501-DQB10201 1163      KNHTSPDVDLGDISG  PDVDLGDIS  5        0.2088
5222.1    60.00  0.35     Sequence
 HLA-DQA10501-DQB10201 1164      NHTSPDVDLGDISGI  PDVDLGDIS  4        0.2103
5139.1    60.00  0.36     Sequence
 HLA-DQA10501-DQB10201 1165      HTSPDVDLGDISGIN  PDVDLGDIS  3        0.2035
5530.1    65.00  0.34     Sequence
 HLA-DQA10501-DQB10201 1166      TSPDVDLGDISGINA  LGDISGINA  6        0.2827
2348.5    39.00  0.50     Sequence
 HLA-DQA10501-DQB10201 1167      SPDVDLGDISGINAS  LGDISGINA  5        0.2657
2821.2    44.00  0.48     Sequence
 HLA-DQA10501-DQB10201 1168      PDVDLGDISGINASF  LGDISGINA  4        0.3264
1462.3    29.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1169      DVDLGDISGINASFV  ISGINASFV  6        0.4853
262.1     6.50  0.62     Sequence          WB
 HLA-DQA10501-DQB10201 1170      VDLGDISGINASFVN  ISGINASFV  5        0.4726
300.7     7.50  0.65     Sequence          WB
 HLA-DQA10501-DQB10201 1171      DLGDISGINASFVNI  ISGINASFV  4        0.4728
300.0     7.50  0.65     Sequence          WB
 HLA-DQA10501-DQB10201 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.4593
347.3     9.00  0.62     Sequence          WB
 HLA-DQA10501-DQB10201 1173      GDISGINASFVNIQK  ISGINASFV  2        0.4314
469.8    12.00  0.66     Sequence
```

```
 HLA-DQA10501-DQB10201 1174      DISGINASFVNIQKE  ISGINASFV  1        0.4301
476.6    12.00  0.51     Sequence
 HLA-DQA10501-DQB10201 1175      ISGINASFVNIQKEI  ISGINASFV  0        0.3819
802.3    19.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1176      SGINASFVNIQKEID  FVNIQKEID  6        0.3792
826.1    19.00  0.32     Sequence
 HLA-DQA10501-DQB10201 1177      GINASFVNIQKEIDR  FVNIQKEID  5        0.3567
1054.1    23.00  0.37     Sequence
 HLA-DQA10501-DQB10201 1178      INASFVNIQKEIDRL  FVNIQKEID  4        0.3743
871.7    20.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1179      NASFVNIQKEIDRLN  FVNIQKEID  3        0.3481
1156.8    25.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1180      ASFVNIQKEIDRLNE  FVNIQKEID  2        0.3230
1518.0    30.00  0.47     Sequence
 HLA-DQA10501-DQB10201 1181      SFVNIQKEIDRLNEV  FVNIQKEID  1        0.3079
1786.2    33.00  0.41     Sequence
 HLA-DQA10501-DQB10201 1182      FVNIQKEIDRLNEVA  EIDRLNEVA  6        0.3116
1716.2    32.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1183      VNIQKEIDRLNEVAK  EIDRLNEVA  5        0.2578
3072.4    46.00  0.43     Sequence
 HLA-DQA10501-DQB10201 1184      NIQKEIDRLNEVAKN  EIDRLNEVA  4        0.2418
3653.0    50.00  0.43     Sequence
 HLA-DQA10501-DQB10201 1185      IQKEIDRLNEVAKNL  EIDRLNEVA  3        0.2447
3542.4    50.00  0.40     Sequence
 HLA-DQA10501-DQB10201 1186      QKEIDRLNEVAKNLN  EIDRLNEVA  2        0.2300
4150.1    55.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1187      KEIDRLNEVAKNLNE  EIDRLNEVA  1        0.2116
5068.3    60.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1188      EIDRLNEVAKNLNES  EIDRLNEVA  0        0.1770
7362.8    70.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1189      IDRLNEVAKNLNESL  VAKNLNESL  6        0.1997
5763.1    65.00  0.52     Sequence
 HLA-DQA10501-DQB10201 1190      DRLNEVAKNLNESLI  VAKNLNESL  5        0.2038
5510.4    65.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.2346
3949.0    55.00  0.38     Sequence
 HLA-DQA10501-DQB10201 1192      LNEVAKNLNESLIDL  VAKNLNESL  3        0.2655
2827.4    44.00  0.30     Sequence
 HLA-DQA10501-DQB10201 1193      NEVAKNLNESLIDLQ  LNESLIDLQ  6        0.2784
2458.5    41.00  0.34     Sequence
 HLA-DQA10501-DQB10201 1194      EVAKNLNESLIDLQE  NESLIDLQE  6        0.3174
1613.3    31.00  0.32     Sequence
 HLA-DQA10501-DQB10201 1195      VAKNLNESLIDLQEL  ESLIDLQEL  6        0.4721
302.5     7.50  0.70     Sequence         WB
 HLA-DQA10501-DQB10201 1196      AKNLNESLIDLQELG  ESLIDLQEL  5        0.4405
425.7    11.00  0.65     Sequence
 HLA-DQA10501-DQB10201 1197      KNLNESLIDLQELGK  ESLIDLQEL  4        0.3939
704.6    17.00  0.62     Sequence
 HLA-DQA10501-DQB10201 1198      NLNESLIDLQELGKY  ESLIDLQEL  3        0.3872
758.1    18.00  0.63     Sequence
 HLA-DQA10501-DQB10201 1199      LNESLIDLQELGKYE  ESLIDLQEL  2        0.3655
958.6    21.00  0.66     Sequence
 HLA-DQA10501-DQB10201 1200      NESLIDLQELGKYEQ  ESLIDLQEL  1        0.3323
1371.9    28.00  0.68     Sequence
 HLA-DQA10501-DQB10201 1201      ESLIDLQELGKYEQY  ESLIDLQEL  0        0.2771
2493.3    41.00  0.56     Sequence
 HLA-DQA10501-DQB10201 1202      SLIDLQELGKYEQYI  ELGKYEQYI  6        0.1823
6956.7    70.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1203      LIDLQELGKYEQYIK  ELGKYEQYI  5        0.1463
10270.6    80.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1204      IDLQELGKYEQYIKW  ELGKYEQYI  4        0.1492
9949.7    80.00  0.34     Sequence
 HLA-DQA10501-DQB10201 1205      DLQELGKYEQYIKWP  ELGKYEQYI  3        0.1523
9625.5    80.00  0.40     Sequence
 HLA-DQA10501-DQB10201 1206      LQELGKYEQYIKWPW  ELGKYEQYI  2        0.1533
9518.8    80.00  0.37     Sequence
```

```
 HLA-DQA10501-DQB10201 1207      QELGKYEQYIKWPWY  EQYIKWPWY  6        0.1795
7173.6    70.00  0.35     Sequence
 HLA-DQA10501-DQB10201 1208      ELGKYEQYIKWPWYI  EQYIKWPWY  5        0.1790
7206.1    70.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1209      LGKYEQYIKWPWYIW  EQYIKWPWY  4        0.1878
6552.6    70.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1210      GKYEQYIKWPWYIWL  EQYIKWPWY  3        0.1944
6100.3    65.00  0.29     Sequence
 HLA-DQA10501-DQB10201 1211      KYEQYIKWPWYIWLG  EQYIKWPWY  2        0.1782
7272.7    70.00  0.31     Sequence
 HLA-DQA10501-DQB10201 1212      YEQYIKWPWYIWLGF  WPWYIWLGF  6        0.2716
2647.5    42.00  0.47     Sequence
 HLA-DQA10501-DQB10201 1213      EQYIKWPWYIWLGFI  PWYIWLGFI  6        0.3320
1377.1    28.00  0.41     Sequence
 HLA-DQA10501-DQB10201 1214      QYIKWPWYIWLGFIA  PWYIWLGFI  5        0.3266
1459.7    29.00  0.36     Sequence
 HLA-DQA10501-DQB10201 1215      YIKWPWYIWLGFIAG  PWYIWLGFI  4        0.3232
1514.2    30.00  0.32     Sequence
 HLA-DQA10501-DQB10201 1216      IKWPWYIWLGFIAGL  IWLGFIAGL  6        0.3567
1054.0    23.00  0.25     Sequence
 HLA-DQA10501-DQB10201 1217      KWPWYIWLGFIAGLI  WLGFIAGLI  6        0.5006
222.2     5.50  0.66     Sequence         WB
 HLA-DQA10501-DQB10201 1218      WPWYIWLGFIAGLIA  WLGFIAGLI  5        0.4838
266.5     6.50  0.60     Sequence         WB
 HLA-DQA10501-DQB10201 1219      PWYIWLGFIAGLIAI  WLGFIAGLI  4        0.4641
329.7     8.50  0.62     Sequence         WB
 HLA-DQA10501-DQB10201 1220      WYIWLGFIAGLIAIV  WLGFIAGLI  3        0.4750
293.1     7.50  0.53     Sequence         WB
 HLA-DQA10501-DQB10201 1221      YIWLGFIAGLIAIVM  IAGLIAIVM  6        0.5030
216.5     5.50  0.38     Sequence         WB
 HLA-DQA10501-DQB10201 1222      IWLGFIAGLIAIVMV  IAGLIAIVM  5        0.4614
339.6     8.50  0.33     Sequence         WB
 HLA-DQA10501-DQB10201 1223      WLGFIAGLIAIVMVT  IAGLIAIVM  4        0.4167
550.7    14.00  0.40     Sequence
 HLA-DQA10501-DQB10201 1224      LGFIAGLIAIVMVTI  IAGLIAIVM  3        0.3580
1039.6    23.00  0.56     Sequence
 HLA-DQA10501-DQB10201 1225      GFIAGLIAIVMVTIM  IAGLIAIVM  2        0.3362
1316.0    27.00  0.59     Sequence
 HLA-DQA10501-DQB10201 1226      FIAGLIAIVMVTIML  IAGLIAIVM  1        0.3146
1661.8    32.00  0.58     Sequence
 HLA-DQA10501-DQB10201 1227      IAGLIAIVMVTIMLC  IAGLIAIVM  0        0.2271
4283.5    55.00  0.61     Sequence
 HLA-DQA10501-DQB10201 1228      AGLIAIVMVTIMLCC  IAIVMVTIM  3        0.1385
11169.4    80.00  0.26     Sequence
 HLA-DQA10501-DQB10201 1229      GLIAIVMVTIMLCCM  MVTIMLCCM  6        0.1789
7213.3    70.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1230      LIAIVMVTIMLCCMT  MVTIMLCCM  5        0.1683
8089.9    75.00  0.39     Sequence
 HLA-DQA10501-DQB10201 1231      IAIVMVTIMLCCMTS  MVTIMLCCM  4        0.1604
8817.5    75.00  0.40     Sequence
 HLA-DQA10501-DQB10201 1232      AIVMVTIMLCCMTSC  MVTIMLCCM  3        0.1608
8776.0    75.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1233      IVMVTIMLCCMTSCC  MVTIMLCCM  2        0.1549
9351.9    75.00  0.47     Sequence
 HLA-DQA10501-DQB10201 1234      VMVTIMLCCMTSCCS  MVTIMLCCM  1        0.1459
10316.2    80.00  0.44     Sequence
 HLA-DQA10501-DQB10201 1235      MVTIMLCCMTSCCSC  MVTIMLCCM  0        0.1286
12435.1    85.00  0.42     Sequence
 HLA-DQA10501-DQB10201 1236      VTIMLCCMTSCCSCL  IMLCCMTSC  2        0.0986
17198.9    90.00  0.23     Sequence
 HLA-DQA10501-DQB10201 1237      TIMLCCMTSCCSCLK  IMLCCMTSC  1        0.0879
19312.4    95.00  0.21     Sequence
 HLA-DQA10501-DQB10201 1238      IMLCCMTSCCSCLKG  IMLCCMTSC  0        0.0744
22356.0    95.00  0.22     Sequence
 HLA-DQA10501-DQB10201 1239      MLCCMTSCCSCLKGC  MTSCCSCLK  4        0.0569
27002.3   100.00  0.34     Sequence
```

```
 HLA-DQA10501-DQB10201 1240      LCCMTSCCSCLKGCC  MTSCCSCLK  3        0.0500
29116.8   100.00  0.43      Sequence
 HLA-DQA10501-DQB10201 1241      CCMTSCCSCLKGCCS  MTSCCSCLK  2        0.0465
30217.3   100.00  0.43      Sequence
 HLA-DQA10501-DQB10201 1242      CMTSCCSCLKGCCSC  MTSCCSCLK  1        0.0415
31902.6   100.00  0.43      Sequence
 HLA-DQA10501-DQB10201 1243      MTSCCSCLKGCCSCG  MTSCCSCLK  0        0.0321
35335.6   100.00  0.43      Sequence
 HLA-DQA10501-DQB10201 1244      TSCCSCLKGCCSCGS  LKGCCSCGS  6        0.0299
36188.0   100.00  0.43      Sequence
 HLA-DQA10501-DQB10201 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5        0.0308
35834.6   100.00  0.39      Sequence
 HLA-DQA10501-DQB10201 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.0298
36233.1   100.00  0.40      Sequence
 HLA-DQA10501-DQB10201 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.0254
37968.1   100.00  0.40      Sequence
 HLA-DQA10501-DQB10201 1248      SCLKGCCSCGSCCKF  CSCGSCCKF  6        0.0291
36484.9   100.00  0.31      Sequence
 HLA-DQA10501-DQB10201 1249      CLKGCCSCGSCCKFD  CSCGSCCKF  5        0.0290
36546.1   100.00  0.31      Sequence
 HLA-DQA10501-DQB10201 1250      LKGCCSCGSCCKFDE  CSCGSCCKF  4        0.0307
35884.7   100.00  0.31      Sequence
 HLA-DQA10501-DQB10201 1251      KGCCSCGSCCKFDED  GSCCKFDED  6        0.0614
25743.0   100.00  0.49      Sequence
 HLA-DQA10501-DQB10201 1252      GCCSCGSCCKFDEDD  GSCCKFDED  5        0.0778
21550.4    95.00  0.40      Sequence
 HLA-DQA10501-DQB10201 1253      CCSCGSCCKFDEDDS  GSCCKFDED  4        0.0819
20616.2    95.00  0.30      Sequence
 HLA-DQA10501-DQB10201 1254      CSCGSCCKFDEDDSE  CKFDEDDSE  6        0.1645
8433.2    75.00  0.56      Sequence
 HLA-DQA10501-DQB10201 1255      SCGSCCKFDEDDSEP  CKFDEDDSE  5        0.2157
4847.3    60.00  0.52      Sequence
 HLA-DQA10501-DQB10201 1256      CGSCCKFDEDDSEPV  CKFDEDDSE  4        0.2588
3039.8    46.00  0.39      Sequence
 HLA-DQA10501-DQB10201 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.2782
2465.0    41.00  0.33      Sequence
 HLA-DQA10501-DQB10201 1258      SCCKFDEDDSEPVLK  CKFDEDDSE  2        0.2578
3071.9    46.00  0.37      Sequence
 HLA-DQA10501-DQB10201 1259      CCKFDEDDSEPVLKG  CKFDEDDSE  1        0.2385
3785.2    55.00  0.35      Sequence
 HLA-DQA10501-DQB10201 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.2184
4705.7    60.00  0.37      Sequence
 HLA-DQA10501-DQB10201 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.1632
8554.0    75.00  0.55      Sequence
 HLA-DQA10501-DQB10201 1262      FDEDDSEPVLKGVKL  FDEDDSEPV  0        0.1428
10660.1    80.00  0.36      Sequence
 HLA-DQA10501-DQB10201 1263      DEDDSEPVLKGVKLH  EPVLKGVKL  5        0.0925
18377.5    90.00  0.43      Sequence
 HLA-DQA10501-DQB10201 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.1078
15569.5    90.00  0.37      Sequence
 HLA-DQA10501-DQB10201 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.1294
12328.5    85.00  0.40      Sequence
 HLA-DQA10501-DQB10301    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.1365
11413.9    90.00  0.34      Sequence
 HLA-DQA10501-DQB10301    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.1307
12161.5    90.00  0.32      Sequence
 HLA-DQA10501-DQB10301    3      PIKEMFVFLVLLPLV  IKEMFVFLV  1        0.1330
11852.7    90.00  0.26      Sequence
 HLA-DQA10501-DQB10301    4      IKEMFVFLVLLPLVS  VFLVLLPLV  5        0.1605
8801.7    80.00  0.25      Sequence
 HLA-DQA10501-DQB10301    5      KEMFVFLVLLPLVSS  FLVLLPLVS  5        0.1658
8311.8    80.00  0.34      Sequence
 HLA-DQA10501-DQB10301    6      EMFVFLVLLPLVSSQ  FLVLLPLVS  4        0.1658
8311.1    80.00  0.34      Sequence
 HLA-DQA10501-DQB10301    7      MFVFLVLLPLVSSQC  FLVLLPLVS  3        0.1692
8012.6    80.00  0.29      Sequence
```

```
 HLA-DQA10501-DQB10301    8       FVFLVLLPLVSSQCV  FLVLLPLVS  2         0.1714
7825.2    80.00  0.25      Sequence
 HLA-DQA10501-DQB10301    9       VFLVLLPLVSSQCVN  FLVLLPLVS  1         0.1784
7252.9    75.00  0.19      Sequence
 HLA-DQA10501-DQB10301   10       FLVLLPLVSSQCVNF  LVSSQCVNF  6         0.1860
6683.4    75.00  0.20      Sequence
 HLA-DQA10501-DQB10301   11       LVLLPLVSSQCVNFT  VSSQCVNFT  6         0.2344
3956.9    60.00  0.31      Sequence
 HLA-DQA10501-DQB10301   12       VLLPLVSSQCVNFTN  VSSQCVNFT  5         0.2930
2099.8    43.00  0.46      Sequence
 HLA-DQA10501-DQB10301   13       LLPLVSSQCVNFTNR  VSSQCVNFT  4         0.2927
2106.9    43.00  0.49      Sequence
 HLA-DQA10501-DQB10301   14       LPLVSSQCVNFTNRT  VSSQCVNFT  3         0.2948
2058.4    43.00  0.47      Sequence
 HLA-DQA10501-DQB10301   15       PLVSSQCVNFTNRTQ  VSSQCVNFT  2         0.2745
2566.1    48.00  0.47      Sequence
 HLA-DQA10501-DQB10301   16       LVSSQCVNFTNRTQL  VSSQCVNFT  1         0.2549
3170.1    55.00  0.47      Sequence
 HLA-DQA10501-DQB10301   17       VSSQCVNFTNRTQLP  VSSQCVNFT  0         0.2336
3994.8    60.00  0.44      Sequence
 HLA-DQA10501-DQB10301   18       SSQCVNFTNRTQLPS  SSQCVNFTN  0         0.1803
7107.0    75.00  0.17      Sequence
 HLA-DQA10501-DQB10301   19       SQCVNFTNRTQLPSA  TNRTQLPSA  6         0.1842
6811.5    75.00  0.25      Sequence
 HLA-DQA10501-DQB10301   20       QCVNFTNRTQLPSAY  TNRTQLPSA  5         0.2708
2670.9    48.00  0.35      Sequence
 HLA-DQA10501-DQB10301   21       CVNFTNRTQLPSAYT  NRTQLPSAY  5         0.3313
1387.4    35.00  0.35      Sequence
 HLA-DQA10501-DQB10301   22       VNFTNRTQLPSAYTN  NRTQLPSAY  4         0.3491
1144.1    31.00  0.34      Sequence
 HLA-DQA10501-DQB10301   23       NFTNRTQLPSAYTNS  NRTQLPSAY  3         0.3511
1120.2    31.00  0.32      Sequence
 HLA-DQA10501-DQB10301   24       FTNRTQLPSAYTNSF  NRTQLPSAY  2         0.3615
1001.0    29.00  0.31      Sequence
 HLA-DQA10501-DQB10301   25       TNRTQLPSAYTNSFT  NRTQLPSAY  1         0.3513
1117.1    31.00  0.26      Sequence
 HLA-DQA10501-DQB10301   26       NRTQLPSAYTNSFTR  LPSAYTNSF  4         0.3372
1301.1    33.00  0.19      Sequence
 HLA-DQA10501-DQB10301   27       RTQLPSAYTNSFTRG  LPSAYTNSF  3         0.2872
2235.1    44.00  0.26      Sequence
 HLA-DQA10501-DQB10301   28       TQLPSAYTNSFTRGV  LPSAYTNSF  2         0.2559
3137.9    55.00  0.22      Sequence
 HLA-DQA10501-DQB10301   29       QLPSAYTNSFTRGVY  YTNSFTRGV  5         0.2606
2981.1    55.00  0.29      Sequence
 HLA-DQA10501-DQB10301   30       LPSAYTNSFTRGVYY  YTNSFTRGV  4         0.2948
2058.5    43.00  0.25      Sequence
 HLA-DQA10501-DQB10301   31       PSAYTNSFTRGVYYP  YTNSFTRGV  3         0.3015
1915.3    41.00  0.28      Sequence
 HLA-DQA10501-DQB10301   32       SAYTNSFTRGVYYPD  FTRGVYYPD  6         0.3184
1594.6    37.00  0.28      Sequence
 HLA-DQA10501-DQB10301   33       AYTNSFTRGVYYPDK  FTRGVYYPD  5         0.3295
1414.5    35.00  0.34      Sequence
 HLA-DQA10501-DQB10301   34       YTNSFTRGVYYPDKV  FTRGVYYPD  4         0.3329
1363.7    34.00  0.34      Sequence
 HLA-DQA10501-DQB10301   35       TNSFTRGVYYPDKVF  FTRGVYYPD  3         0.3182
1598.8    37.00  0.35      Sequence
 HLA-DQA10501-DQB10301   36       NSFTRGVYYPDKVFR  FTRGVYYPD  2         0.2824
2354.1    46.00  0.34      Sequence
 HLA-DQA10501-DQB10301   37       SFTRGVYYPDKVFRS  YYPDKVFRS  6         0.2711
2659.8    48.00  0.23      Sequence
 HLA-DQA10501-DQB10301   38       FTRGVYYPDKVFRSS  YYPDKVFRS  5         0.2739
2582.1    48.00  0.42      Sequence
 HLA-DQA10501-DQB10301   39       TRGVYYPDKVFRSSV  YYPDKVFRS  4         0.2615
2953.7    55.00  0.51      Sequence
 HLA-DQA10501-DQB10301   40       RGVYYPDKVFRSSVL  YYPDKVFRS  3         0.2643
2864.4    50.00  0.48      Sequence
```

```
 HLA-DQA10501-DQB10301   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.2616
2950.4    55.00  0.42     Sequence
 HLA-DQA10501-DQB10301   42      VYYPDKVFRSSVLHS  VFRSSVLHS  6        0.3032
1880.6    41.00  0.38     Sequence
 HLA-DQA10501-DQB10301   43      YYPDKVFRSSVLHST  VFRSSVLHS  5        0.4519
376.1    15.00  0.49     Sequence
 HLA-DQA10501-DQB10301   44      YPDKVFRSSVLHSTQ  VFRSSVLHS  4        0.4601
344.2    14.00  0.44     Sequence
 HLA-DQA10501-DQB10301   45      PDKVFRSSVLHSTQD  FRSSVLHST  4        0.4575
354.0    15.00  0.43     Sequence
 HLA-DQA10501-DQB10301   46      DKVFRSSVLHSTQDL  FRSSVLHST  3        0.4544
366.1    15.00  0.44     Sequence
 HLA-DQA10501-DQB10301   47      KVFRSSVLHSTQDLF  FRSSVLHST  2        0.4428
415.1    16.00  0.41     Sequence
 HLA-DQA10501-DQB10301   48      VFRSSVLHSTQDLFL  FRSSVLHST  1        0.4360
446.8    17.00  0.41     Sequence
 HLA-DQA10501-DQB10301   49      FRSSVLHSTQDLFLP  FRSSVLHST  0        0.3888
744.6    24.00  0.44     Sequence
 HLA-DQA10501-DQB10301   50      RSSVLHSTQDLFLPF  LHSTQDLFL  4        0.2379
3813.3    60.00  0.29     Sequence
 HLA-DQA10501-DQB10301   51      SSVLHSTQDLFLPFF  LHSTQDLFL  3        0.2015
5649.2    70.00  0.31     Sequence
 HLA-DQA10501-DQB10301   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2        0.2062
5370.4    70.00  0.28     Sequence
 HLA-DQA10501-DQB10301   53      VLHSTQDLFLPFFSN  QDLFLPFFS  5        0.2028
5571.6    70.00  0.25     Sequence
 HLA-DQA10501-DQB10301   54      LHSTQDLFLPFFSNV  QDLFLPFFS  4        0.1952
6048.0    70.00  0.29     Sequence
 HLA-DQA10501-DQB10301   55      HSTQDLFLPFFSNVT  QDLFLPFFS  3        0.2131
4982.4    65.00  0.25     Sequence
 HLA-DQA10501-DQB10301   56      STQDLFLPFFSNVTW  FLPFFSNVT  5        0.2157
4846.1    65.00  0.33     Sequence
 HLA-DQA10501-DQB10301   57      TQDLFLPFFSNVTWF  FLPFFSNVT  4        0.2366
3867.5    60.00  0.32     Sequence
 HLA-DQA10501-DQB10301   58      QDLFLPFFSNVTWFH  PFFSNVTWF  5        0.2601
2996.8    55.00  0.25     Sequence
 HLA-DQA10501-DQB10301   59      DLFLPFFSNVTWFHA  FFSNVTWFH  5        0.3081
1783.3    40.00  0.31     Sequence
 HLA-DQA10501-DQB10301   60      LFLPFFSNVTWFHAI  FFSNVTWFH  4        0.3334
1355.9    34.00  0.26     Sequence
 HLA-DQA10501-DQB10301   61      FLPFFSNVTWFHAIH  FFSNVTWFH  3        0.3420
1236.3    32.00  0.25     Sequence
 HLA-DQA10501-DQB10301   62      LPFFSNVTWFHAIHV  FSNVTWFHA  3        0.3268
1457.0    36.00  0.29     Sequence
 HLA-DQA10501-DQB10301   63      PFFSNVTWFHAIHVS  FSNVTWFHA  2        0.3538
1087.0    30.00  0.23     Sequence
 HLA-DQA10501-DQB10301   64      FFSNVTWFHAIHVSG  TWFHAIHVS  5        0.4045
628.5    22.00  0.26     Sequence
 HLA-DQA10501-DQB10301   65      FSNVTWFHAIHVSGT  FHAIHVSGT  6        0.4597
345.7    14.00  0.34     Sequence
 HLA-DQA10501-DQB10301   66      SNVTWFHAIHVSGTN  FHAIHVSGT  5        0.5438
139.2     6.50  0.46     Sequence         WB
 HLA-DQA10501-DQB10301   67      NVTWFHAIHVSGTNG  FHAIHVSGT  4        0.5559
122.1     6.00  0.44     Sequence         WB
 HLA-DQA10501-DQB10301   68      VTWFHAIHVSGTNGT  FHAIHVSGT  3        0.5733
101.2     5.00  0.38     Sequence         WB
 HLA-DQA10501-DQB10301   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.5763
97.9     4.50  0.34     Sequence         WB
 HLA-DQA10501-DQB10301   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1        0.5651
110.5     5.50  0.31     Sequence         WB
 HLA-DQA10501-DQB10301   71      FHAIHVSGTNGTKRF  IHVSGTNGT  3        0.5372
149.6     7.00  0.28     Sequence         WB
 HLA-DQA10501-DQB10301   72      HAIHVSGTNGTKRFD  IHVSGTNGT  2        0.4722
302.0    13.00  0.41     Sequence
 HLA-DQA10501-DQB10301   73      AIHVSGTNGTKRFDN  IHVSGTNGT  1        0.3774
842.2    26.00  0.41     Sequence
```

```
 HLA-DQA10501-DQB10301   74      IHVSGTNGTKRFDNP  IHVSGTNGT  0        0.3432
1220.0    32.00  0.38     Sequence
 HLA-DQA10501-DQB10301   75      HVSGTNGTKRFDNPV  TNGTKRFDN  4        0.2465
3473.7    55.00  0.22     Sequence
 HLA-DQA10501-DQB10301   76      VSGTNGTKRFDNPVL  TNGTKRFDN  3        0.2100
5156.3    65.00  0.34     Sequence
 HLA-DQA10501-DQB10301   77      SGTNGTKRFDNPVLP  TNGTKRFDN  2        0.1700
7950.0    80.00  0.41     Sequence
 HLA-DQA10501-DQB10301   78      GTNGTKRFDNPVLPF  TNGTKRFDN  1        0.1790
7208.2    75.00  0.33     Sequence
 HLA-DQA10501-DQB10301   79      TNGTKRFDNPVLPFN  TNGTKRFDN  0        0.1728
7710.1    80.00  0.23     Sequence
 HLA-DQA10501-DQB10301   80      NGTKRFDNPVLPFND  DNPVLPFND  6        0.1668
8226.9    80.00  0.25     Sequence
 HLA-DQA10501-DQB10301   81      GTKRFDNPVLPFNDG  DNPVLPFND  5        0.1805
7089.0    75.00  0.34     Sequence
 HLA-DQA10501-DQB10301   82      TKRFDNPVLPFNDGV  DNPVLPFND  4        0.1780
7289.3    75.00  0.34     Sequence
 HLA-DQA10501-DQB10301   83      KRFDNPVLPFNDGVY  DNPVLPFND  3        0.1787
7235.0    75.00  0.32     Sequence
 HLA-DQA10501-DQB10301   84      RFDNPVLPFNDGVYF  DNPVLPFND  2        0.1918
6276.3    75.00  0.28     Sequence
 HLA-DQA10501-DQB10301   85      FDNPVLPFNDGVYFA  PFNDGVYFA  6        0.2213
4561.7    65.00  0.20     Sequence
 HLA-DQA10501-DQB10301   86      DNPVLPFNDGVYFAS  FNDGVYFAS  6        0.4348
452.5    17.00  0.50     Sequence
 HLA-DQA10501-DQB10301   87      NPVLPFNDGVYFAST  FNDGVYFAS  5        0.5577
119.7     5.50  0.62     Sequence         WB
 HLA-DQA10501-DQB10301   88      PVLPFNDGVYFASTE  FNDGVYFAS  4        0.5718
102.8     5.00  0.60     Sequence         WB
 HLA-DQA10501-DQB10301   89      VLPFNDGVYFASTEK  FNDGVYFAS  3        0.5768
97.4     4.50  0.57     Sequence         WB
 HLA-DQA10501-DQB10301   90      LPFNDGVYFASTEKS  FNDGVYFAS  2        0.5834
90.7     4.50  0.55     Sequence         WB
 HLA-DQA10501-DQB10301   91      PFNDGVYFASTEKSN  FNDGVYFAS  1        0.5888
85.5     4.00  0.49     Sequence         WB
 HLA-DQA10501-DQB10301   92      FNDGVYFASTEKSNI  FNDGVYFAS  0        0.5685
106.6     5.00  0.44     Sequence         WB
 HLA-DQA10501-DQB10301   93      NDGVYFASTEKSNII  VYFASTEKS  3        0.4523
374.6    15.00  0.38     Sequence
 HLA-DQA10501-DQB10301   94      DGVYFASTEKSNIIR  VYFASTEKS  2        0.4102
590.6    21.00  0.37     Sequence
 HLA-DQA10501-DQB10301   95      GVYFASTEKSNIIRG  VYFASTEKS  1        0.4015
648.9    22.00  0.30     Sequence
 HLA-DQA10501-DQB10301   96      VYFASTEKSNIIRGW  TEKSNIIRG  5        0.3925
715.4    23.00  0.31     Sequence
 HLA-DQA10501-DQB10301   97      YFASTEKSNIIRGWI  TEKSNIIRG  4        0.3725
888.1    27.00  0.41     Sequence
 HLA-DQA10501-DQB10301   98      FASTEKSNIIRGWIF  TEKSNIIRG  3        0.3557
1065.1    30.00  0.44     Sequence
 HLA-DQA10501-DQB10301   99      ASTEKSNIIRGWIFG  TEKSNIIRG  2        0.3517
1112.2    31.00  0.39     Sequence
 HLA-DQA10501-DQB10301  100      STEKSNIIRGWIFGT  IIRGWIFGT  6        0.3486
1150.9    31.00  0.27     Sequence
 HLA-DQA10501-DQB10301  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5        0.4189
537.6    20.00  0.44     Sequence
 HLA-DQA10501-DQB10301  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.4486
390.0    16.00  0.40     Sequence
 HLA-DQA10501-DQB10301  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3        0.4516
377.4    15.00  0.38     Sequence
 HLA-DQA10501-DQB10301  104      SNIIRGWIFGTTLDS  IIRGWIFGT  2        0.4568
356.9    15.00  0.35     Sequence
 HLA-DQA10501-DQB10301  105      NIIRGWIFGTTLDSK  IRGWIFGTT  2        0.4539
368.1    15.00  0.28     Sequence
 HLA-DQA10501-DQB10301  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.4463
399.9    16.00  0.23     Sequence
```

```
 HLA-DQA10501-DQB10301  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3        0.4196
533.5    19.00  0.25     Sequence
 HLA-DQA10501-DQB10301  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2        0.3309
1393.3    35.00  0.29     Sequence
 HLA-DQA10501-DQB10301  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1        0.2973
2004.7    42.00  0.31     Sequence
 HLA-DQA10501-DQB10301  110      WIFGTTLDSKTQSLL  WIFGTTLDS  0        0.2653
2833.9    50.00  0.28     Sequence
 HLA-DQA10501-DQB10301  111      IFGTTLDSKTQSLLI  TLDSKTQSL  4        0.2323
4051.6    60.00  0.29     Sequence
 HLA-DQA10501-DQB10301  112      FGTTLDSKTQSLLIV  TLDSKTQSL  3        0.1935
6163.4    70.00  0.36     Sequence
 HLA-DQA10501-DQB10301  113      GTTLDSKTQSLLIVN  TLDSKTQSL  2        0.1925
6225.8    70.00  0.31     Sequence
 HLA-DQA10501-DQB10301  114      TTLDSKTQSLLIVNN  KTQSLLIVN  5        0.2151
4876.9    65.00  0.25     Sequence
 HLA-DQA10501-DQB10301  115      TLDSKTQSLLIVNNA  TQSLLIVNN  5        0.2234
4458.2    65.00  0.23     Sequence
 HLA-DQA10501-DQB10301  116      LDSKTQSLLIVNNAT  QSLLIVNNA  5        0.2262
4327.1    65.00  0.29     Sequence
 HLA-DQA10501-DQB10301  117      DSKTQSLLIVNNATN  QSLLIVNNA  4        0.2282
4232.6    60.00  0.26     Sequence
 HLA-DQA10501-DQB10301  118      SKTQSLLIVNNATNV  QSLLIVNNA  3        0.2233
4462.7    65.00  0.28     Sequence
 HLA-DQA10501-DQB10301  119      KTQSLLIVNNATNVV  QSLLIVNNA  2        0.2338
3984.4    60.00  0.21     Sequence
 HLA-DQA10501-DQB10301  120      TQSLLIVNNATNVVI  VNNATNVVI  6        0.2608
2974.5    55.00  0.29     Sequence
 HLA-DQA10501-DQB10301  121      QSLLIVNNATNVVIK  VNNATNVVI  5        0.3343
1343.2    34.00  0.32     Sequence
 HLA-DQA10501-DQB10301  122      SLLIVNNATNVVIKV  VNNATNVVI  4        0.3367
1308.5    33.00  0.31     Sequence
 HLA-DQA10501-DQB10301  123      LLIVNNATNVVIKVC  VNNATNVVI  3        0.3430
1222.8    32.00  0.29     Sequence
 HLA-DQA10501-DQB10301  124      LIVNNATNVVIKVCE  NNATNVVIK  3        0.3547
1077.5    30.00  0.27     Sequence
 HLA-DQA10501-DQB10301  125      IVNNATNVVIKVCEF  NNATNVVIK  2        0.3621
993.9    29.00  0.25     Sequence
 HLA-DQA10501-DQB10301  126      VNNATNVVIKVCEFQ  NNATNVVIK  1        0.3452
1193.1    32.00  0.25     Sequence
 HLA-DQA10501-DQB10301  127      NNATNVVIKVCEFQF  ATNVVIKVC  2        0.3174
1612.7    38.00  0.19     Sequence
 HLA-DQA10501-DQB10301  128      NATNVVIKVCEFQFC  ATNVVIKVC  1        0.2774
2485.0    47.00  0.23     Sequence
 HLA-DQA10501-DQB10301  129      ATNVVIKVCEFQFCN  IKVCEFQFC  5        0.2738
2584.3    48.00  0.36     Sequence
 HLA-DQA10501-DQB10301  130      TNVVIKVCEFQFCNY  IKVCEFQFC  4        0.2595
3016.8    55.00  0.38     Sequence
 HLA-DQA10501-DQB10301  131      NVVIKVCEFQFCNYP  IKVCEFQFC  3        0.2244
4409.5    65.00  0.46     Sequence
 HLA-DQA10501-DQB10301  132      VVIKVCEFQFCNYPF  IKVCEFQFC  2        0.2005
5713.4    70.00  0.45     Sequence
 HLA-DQA10501-DQB10301  133      VIKVCEFQFCNYPFL  IKVCEFQFC  1        0.1998
5756.4    70.00  0.38     Sequence
 HLA-DQA10501-DQB10301  134      IKVCEFQFCNYPFLG  IKVCEFQFC  0        0.1926
6222.3    70.00  0.35     Sequence
 HLA-DQA10501-DQB10301  135      KVCEFQFCNYPFLGV  FQFCNYPFL  4        0.1955
6032.3    70.00  0.28     Sequence
 HLA-DQA10501-DQB10301  136      VCEFQFCNYPFLGVY  QFCNYPFLG  4        0.2090
5212.4    70.00  0.25     Sequence
 HLA-DQA10501-DQB10301  137      CEFQFCNYPFLGVYY  QFCNYPFLG  3        0.2390
3766.7    60.00  0.19     Sequence
 HLA-DQA10501-DQB10301  138      EFQFCNYPFLGVYYH  NYPFLGVYY  5        0.2507
3320.2    55.00  0.16     Sequence
 HLA-DQA10501-DQB10301  139      FQFCNYPFLGVYYHK  PFLGVYYHK  6        0.2620
2936.6    55.00  0.28     Sequence
```

```
 HLA-DQA10501-DQB10301  140      QFCNYPFLGVYYHKN  PFLGVYYHK  5        0.2756
2533.7    47.00  0.38     Sequence
 HLA-DQA10501-DQB10301  141      FCNYPFLGVYYHKNN  PFLGVYYHK  4        0.2797
2424.0    46.00  0.38     Sequence
 HLA-DQA10501-DQB10301  142      CNYPFLGVYYHKNNK  PFLGVYYHK  3        0.2641
2871.8    50.00  0.41     Sequence
 HLA-DQA10501-DQB10301  143      NYPFLGVYYHKNNKS  PFLGVYYHK  2        0.2566
3113.7    55.00  0.38     Sequence
 HLA-DQA10501-DQB10301  144      YPFLGVYYHKNNKSW  PFLGVYYHK  1        0.2368
3857.2    60.00  0.25     Sequence
 HLA-DQA10501-DQB10301  145      PFLGVYYHKNNKSWM  VYYHKNNKS  4        0.2177
4740.4    65.00  0.22     Sequence
 HLA-DQA10501-DQB10301  146      FLGVYYHKNNKSWME  VYYHKNNKS  3        0.1939
6132.0    70.00  0.26     Sequence
 HLA-DQA10501-DQB10301  147      LGVYYHKNNKSWMES  VYYHKNNKS  2        0.1751
7517.1    75.00  0.26     Sequence
 HLA-DQA10501-DQB10301  148      GVYYHKNNKSWMESE  VYYHKNNKS  1        0.1877
6562.1    75.00  0.23     Sequence
 HLA-DQA10501-DQB10301  149      VYYHKNNKSWMESEF  KNNKSWMES  4        0.1917
6279.9    75.00  0.22     Sequence
 HLA-DQA10501-DQB10301  150      YYHKNNKSWMESEFR  KNNKSWMES  3        0.1810
7057.9    75.00  0.24     Sequence
 HLA-DQA10501-DQB10301  151      YHKNNKSWMESEFRV  KNNKSWMES  2        0.1685
8077.9    80.00  0.23     Sequence
 HLA-DQA10501-DQB10301  152      HKNNKSWMESEFRVY  WMESEFRVY  6        0.1784
7257.9    75.00  0.22     Sequence
 HLA-DQA10501-DQB10301  153      KNNKSWMESEFRVYS  WMESEFRVY  5        0.1771
7359.7    75.00  0.29     Sequence
 HLA-DQA10501-DQB10301  154      NNKSWMESEFRVYSS  WMESEFRVY  4        0.2065
5353.3    70.00  0.26     Sequence
 HLA-DQA10501-DQB10301  155      NKSWMESEFRVYSSA  ESEFRVYSS  5        0.2536
3215.3    55.00  0.40     Sequence
 HLA-DQA10501-DQB10301  156      KSWMESEFRVYSSAN  ESEFRVYSS  4        0.2638
2880.6    50.00  0.38     Sequence
 HLA-DQA10501-DQB10301  157      SWMESEFRVYSSANN  ESEFRVYSS  3        0.3036
1873.0    41.00  0.29     Sequence
 HLA-DQA10501-DQB10301  158      WMESEFRVYSSANNC  ESEFRVYSS  2        0.3132
1687.0    38.00  0.28     Sequence
 HLA-DQA10501-DQB10301  159      MESEFRVYSSANNCT  VYSSANNCT  6        0.3668
944.6    28.00  0.34     Sequence
 HLA-DQA10501-DQB10301  160      ESEFRVYSSANNCTF  VYSSANNCT  5        0.4049
625.7    22.00  0.41     Sequence
 HLA-DQA10501-DQB10301  161      SEFRVYSSANNCTFE  VYSSANNCT  4        0.3987
669.3    22.00  0.42     Sequence
 HLA-DQA10501-DQB10301  162      EFRVYSSANNCTFEY  VYSSANNCT  3        0.3861
766.7    25.00  0.42     Sequence
 HLA-DQA10501-DQB10301  163      FRVYSSANNCTFEYV  VYSSANNCT  2        0.3785
832.2    26.00  0.41     Sequence
 HLA-DQA10501-DQB10301  164      RVYSSANNCTFEYVS  VYSSANNCT  1        0.3248
1488.5    36.00  0.29     Sequence
 HLA-DQA10501-DQB10301  165      VYSSANNCTFEYVSQ  VYSSANNCT  0        0.3180
1602.5    37.00  0.25     Sequence
 HLA-DQA10501-DQB10301  166      YSSANNCTFEYVSQP  ANNCTFEYV  3        0.2485
3398.6    55.00  0.40     Sequence
 HLA-DQA10501-DQB10301  167      SSANNCTFEYVSQPF  ANNCTFEYV  2        0.2208
4587.5    65.00  0.37     Sequence
 HLA-DQA10501-DQB10301  168      SANNCTFEYVSQPFL  ANNCTFEYV  1        0.2241
4423.6    65.00  0.31     Sequence
 HLA-DQA10501-DQB10301  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.2200
4627.3    65.00  0.19     Sequence
 HLA-DQA10501-DQB10301  170      NNCTFEYVSQPFLMD  EYVSQPFLM  5        0.2122
5032.3    65.00  0.34     Sequence
 HLA-DQA10501-DQB10301  171      NCTFEYVSQPFLMDL  EYVSQPFLM  4        0.2079
5274.8    70.00  0.32     Sequence
 HLA-DQA10501-DQB10301  172      CTFEYVSQPFLMDLE  EYVSQPFLM  3        0.2033
5542.3    70.00  0.34     Sequence
```

```
 HLA-DQA10501-DQB10301  173       TFEYVSQPFLMDLEG  EYVSQPFLM  2         0.1873
6589.3    75.00  0.33     Sequence
 HLA-DQA10501-DQB10301  174       FEYVSQPFLMDLEGK  EYVSQPFLM  1         0.1574
9105.6    85.00  0.32     Sequence
 HLA-DQA10501-DQB10301  175       EYVSQPFLMDLEGKQ  EYVSQPFLM  0         0.1250
12924.3    90.00  0.30     Sequence
 HLA-DQA10501-DQB10301  176       YVSQPFLMDLEGKQG  PFLMDLEGK  4         0.1027
16461.5    95.00  0.20     Sequence
 HLA-DQA10501-DQB10301  177       VSQPFLMDLEGKQGN  LMDLEGKQG  5         0.0936
18163.8    100.00  0.23    Sequence
 HLA-DQA10501-DQB10301  178       SQPFLMDLEGKQGNF  LMDLEGKQG  4         0.1052
16026.6    95.00  0.23     Sequence
 HLA-DQA10501-DQB10301  179       QPFLMDLEGKQGNFK  LEGKQGNFK  6         0.1423
10725.2    85.00  0.29     Sequence
 HLA-DQA10501-DQB10301  180       PFLMDLEGKQGNFKN  LEGKQGNFK  5         0.1558
9269.8    85.00  0.30     Sequence
 HLA-DQA10501-DQB10301  181       FLMDLEGKQGNFKNL  LEGKQGNFK  4         0.1687
8061.5    80.00  0.27     Sequence
 HLA-DQA10501-DQB10301  182       LMDLEGKQGNFKNLS  GKQGNFKNL  5         0.1985
5836.3    70.00  0.23     Sequence
 HLA-DQA10501-DQB10301  183       MDLEGKQGNFKNLSE  KQGNFKNLS  5         0.2020
5623.2    70.00  0.27     Sequence
 HLA-DQA10501-DQB10301  184       DLEGKQGNFKNLSEF  KQGNFKNLS  4         0.1996
5770.9    70.00  0.28     Sequence
 HLA-DQA10501-DQB10301  185       LEGKQGNFKNLSEFV  KQGNFKNLS  3         0.2051
5434.4    70.00  0.26     Sequence
 HLA-DQA10501-DQB10301  186       EGKQGNFKNLSEFVF  KQGNFKNLS  2         0.2194
4655.8    65.00  0.22     Sequence
 HLA-DQA10501-DQB10301  187       GKQGNFKNLSEFVFK  KNLSEFVFK  6         0.2239
4435.6    65.00  0.15     Sequence
 HLA-DQA10501-DQB10301  188       KQGNFKNLSEFVFKN  KNLSEFVFK  5         0.2236
4446.8    65.00  0.23     Sequence
 HLA-DQA10501-DQB10301  189       QGNFKNLSEFVFKNI  KNLSEFVFK  4         0.2139
4943.0    65.00  0.29     Sequence
 HLA-DQA10501-DQB10301  190       GNFKNLSEFVFKNID  KNLSEFVFK  3         0.2060
5382.4    70.00  0.28     Sequence
 HLA-DQA10501-DQB10301  191       NFKNLSEFVFKNIDG  NLSEFVFKN  3         0.1961
5988.8    70.00  0.25     Sequence
 HLA-DQA10501-DQB10301  192       FKNLSEFVFKNIDGY  NLSEFVFKN  2         0.2020
5619.4    70.00  0.22     Sequence
 HLA-DQA10501-DQB10301  193       KNLSEFVFKNIDGYF  FVFKNIDGY  5         0.1843
6807.6    75.00  0.31     Sequence
 HLA-DQA10501-DQB10301  194       NLSEFVFKNIDGYFK  FVFKNIDGY  4         0.2040
5499.0    70.00  0.27     Sequence
 HLA-DQA10501-DQB10301  195       LSEFVFKNIDGYFKI  FVFKNIDGY  3         0.2202
4615.0    65.00  0.25     Sequence
 HLA-DQA10501-DQB10301  196       SEFVFKNIDGYFKIY  FVFKNIDGY  2         0.2309
4113.2    60.00  0.22     Sequence
 HLA-DQA10501-DQB10301  197       EFVFKNIDGYFKIYS  NIDGYFKIY  5         0.2559
3137.9    55.00  0.22     Sequence
 HLA-DQA10501-DQB10301  198       FVFKNIDGYFKIYSK  IDGYFKIYS  5         0.2668
2787.5    49.00  0.19     Sequence
 HLA-DQA10501-DQB10301  199       VFKNIDGYFKIYSKH  DGYFKIYSK  5         0.2507
3319.3    55.00  0.22     Sequence
 HLA-DQA10501-DQB10301  200       FKNIDGYFKIYSKHT  DGYFKIYSK  4         0.2562
3126.6    55.00  0.23     Sequence
 HLA-DQA10501-DQB10301  201       KNIDGYFKIYSKHTP  DGYFKIYSK  3         0.2424
3630.6    60.00  0.25     Sequence
 HLA-DQA10501-DQB10301  202       NIDGYFKIYSKHTPI  DGYFKIYSK  2         0.2483
3406.7    55.00  0.20     Sequence
 HLA-DQA10501-DQB10301  203       IDGYFKIYSKHTPIN  IYSKHTPIN  6         0.2405
3706.7    60.00  0.19     Sequence
 HLA-DQA10501-DQB10301  204       DGYFKIYSKHTPINL  IYSKHTPIN  5         0.2271
4283.6    60.00  0.26     Sequence
 HLA-DQA10501-DQB10301  205       GYFKIYSKHTPINLV  SKHTPINLV  6         0.2700
2694.3    49.00  0.25     Sequence
```

```
 HLA-DQA10501-DQB10301  206      YFKIYSKHTPINLVR  SKHTPINLV  5        0.2938
2080.8    43.00  0.40     Sequence
 HLA-DQA10501-DQB10301  207      FKIYSKHTPINLVRD  SKHTPINLV  4        0.2826
2349.4    46.00  0.43     Sequence
 HLA-DQA10501-DQB10301  208      KIYSKHTPINLVRDL  SKHTPINLV  3        0.2618
2941.7    55.00  0.49     Sequence
 HLA-DQA10501-DQB10301  209      IYSKHTPINLVRDLP  SKHTPINLV  2        0.2599
3003.1    55.00  0.50     Sequence
 HLA-DQA10501-DQB10301  210      YSKHTPINLVRDLPQ  SKHTPINLV  1        0.2367
3861.6    60.00  0.50     Sequence
 HLA-DQA10501-DQB10301  211      SKHTPINLVRDLPQG  SKHTPINLV  0        0.2082
5257.1    70.00  0.48     Sequence
 HLA-DQA10501-DQB10301  212      KHTPINLVRDLPQGF  NLVRDLPQG  5        0.1697
7975.1    80.00  0.20     Sequence
 HLA-DQA10501-DQB10301  213      HTPINLVRDLPQGFS  LVRDLPQGF  5        0.2147
4896.6    65.00  0.29     Sequence
 HLA-DQA10501-DQB10301  214      TPINLVRDLPQGFSA  VRDLPQGFS  5        0.2488
3386.4    55.00  0.23     Sequence
 HLA-DQA10501-DQB10301  215      PINLVRDLPQGFSAL  VRDLPQGFS  4        0.2599
3005.1    55.00  0.22     Sequence
 HLA-DQA10501-DQB10301  216      INLVRDLPQGFSALE  VRDLPQGFS  3        0.2553
3158.5    55.00  0.25     Sequence
 HLA-DQA10501-DQB10301  217      NLVRDLPQGFSALEP  VRDLPQGFS  2        0.2589
3035.9    55.00  0.22     Sequence
 HLA-DQA10501-DQB10301  218      LVRDLPQGFSALEPL  PQGFSALEP  5        0.2620
2936.2    55.00  0.23     Sequence
 HLA-DQA10501-DQB10301  219      VRDLPQGFSALEPLV  PQGFSALEP  4        0.2673
2773.8    49.00  0.19     Sequence
 HLA-DQA10501-DQB10301  220      RDLPQGFSALEPLVD  GFSALEPLV  5        0.2760
2524.0    47.00  0.25     Sequence
 HLA-DQA10501-DQB10301  221      DLPQGFSALEPLVDL  GFSALEPLV  4        0.2676
2765.2    49.00  0.26     Sequence
 HLA-DQA10501-DQB10301  222      LPQGFSALEPLVDLP  GFSALEPLV  3        0.2558
3139.1    55.00  0.28     Sequence
 HLA-DQA10501-DQB10301  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.2496
3356.9    55.00  0.29     Sequence
 HLA-DQA10501-DQB10301  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.2415
3667.6    60.00  0.28     Sequence
 HLA-DQA10501-DQB10301  225      GFSALEPLVDLPIGI  FSALEPLVD  1        0.2261
4330.6    65.00  0.28     Sequence
 HLA-DQA10501-DQB10301  226      FSALEPLVDLPIGIN  FSALEPLVD  0        0.1897
6421.6    75.00  0.32     Sequence
 HLA-DQA10501-DQB10301  227      SALEPLVDLPIGINI  PLVDLPIGI  4        0.1332
11837.9    90.00  0.28     Sequence
 HLA-DQA10501-DQB10301  228      ALEPLVDLPIGINIT  PLVDLPIGI  3        0.1657
8323.7    80.00  0.20     Sequence
 HLA-DQA10501-DQB10301  229      LEPLVDLPIGINITR  DLPIGINIT  5        0.1994
5781.4    70.00  0.32     Sequence
 HLA-DQA10501-DQB10301  230      EPLVDLPIGINITRF  DLPIGINIT  4        0.2230
4477.0    65.00  0.28     Sequence
 HLA-DQA10501-DQB10301  231      PLVDLPIGINITRFQ  DLPIGINIT  3        0.2271
4285.3    60.00  0.27     Sequence
 HLA-DQA10501-DQB10301  232      LVDLPIGINITRFQT  PIGINITRF  4        0.2321
4057.3    60.00  0.25     Sequence
 HLA-DQA10501-DQB10301  233      VDLPIGINITRFQTL  PIGINITRF  3        0.2328
4028.7    60.00  0.22     Sequence
 HLA-DQA10501-DQB10301  234      DLPIGINITRFQTLL  INITRFQTL  5        0.2268
4300.1    60.00  0.20     Sequence
 HLA-DQA10501-DQB10301  235      LPIGINITRFQTLLA  INITRFQTL  4        0.2179
4729.8    65.00  0.26     Sequence
 HLA-DQA10501-DQB10301  236      PIGINITRFQTLLAL  INITRFQTL  3        0.2014
5654.6    70.00  0.29     Sequence
 HLA-DQA10501-DQB10301  237      IGINITRFQTLLALH  INITRFQTL  2        0.1925
6226.3    70.00  0.25     Sequence
 HLA-DQA10501-DQB10301  238      GINITRFQTLLALHR  INITRFQTL  1        0.1947
6084.3    70.00  0.22     Sequence
```

```
 HLA-DQA10501-DQB10301  239      INITRFQTLLALHRS  FQTLLALHR  5        0.1888
6485.5    75.00  0.20     Sequence
 HLA-DQA10501-DQB10301  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.1700
7943.4    80.00  0.26     Sequence
 HLA-DQA10501-DQB10301  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.1634
8532.7    80.00  0.27     Sequence
 HLA-DQA10501-DQB10301  242      TRFQTLLALHRSYLT  FQTLLALHR  2        0.1864
6652.2    75.00  0.17     Sequence
 HLA-DQA10501-DQB10301  243      RFQTLLALHRSYLTP  LALHRSYLT  5        0.1981
5864.2    70.00  0.21     Sequence
 HLA-DQA10501-DQB10301  244      FQTLLALHRSYLTPG  LHRSYLTPG  6        0.1950
6060.9    70.00  0.28     Sequence
 HLA-DQA10501-DQB10301  245      QTLLALHRSYLTPGD  LHRSYLTPG  5        0.1851
6747.1    75.00  0.40     Sequence
 HLA-DQA10501-DQB10301  246      TLLALHRSYLTPGDS  LHRSYLTPG  4        0.2078
5279.5    70.00  0.35     Sequence
 HLA-DQA10501-DQB10301  247      LLALHRSYLTPGDSS  RSYLTPGDS  5        0.2783
2462.1    47.00  0.23     Sequence
 HLA-DQA10501-DQB10301  248      LALHRSYLTPGDSSS  RSYLTPGDS  4        0.3031
1882.9    41.00  0.21     Sequence
 HLA-DQA10501-DQB10301  249      ALHRSYLTPGDSSSG  LTPGDSSSG  6        0.3548
1075.5    30.00  0.39     Sequence
 HLA-DQA10501-DQB10301  250      LHRSYLTPGDSSSGW  LTPGDSSSG  5        0.3859
768.8     25.00  0.48    Sequence
 HLA-DQA10501-DQB10301  251      HRSYLTPGDSSSGWT  LTPGDSSSG  4        0.4024
642.9     22.00  0.44    Sequence
 HLA-DQA10501-DQB10301  252      RSYLTPGDSSSGWTA  LTPGDSSSG  3        0.4317
468.4     18.00  0.37    Sequence
 HLA-DQA10501-DQB10301  253      SYLTPGDSSSGWTAG  PGDSSSGWT  4        0.4445
407.7     16.00  0.34    Sequence
 HLA-DQA10501-DQB10301  254      YLTPGDSSSGWTAGA  PGDSSSGWT  3        0.4343
455.4     18.00  0.33    Sequence
 HLA-DQA10501-DQB10301  255      LTPGDSSSGWTAGAA  SSSGWTAGA  5        0.5087
203.5      9.00  0.25    Sequence         WB
 HLA-DQA10501-DQB10301  256      TPGDSSSGWTAGAAA  SSGWTAGAA  5        0.5532
125.7      6.00  0.40    Sequence         WB
 HLA-DQA10501-DQB10301  257      PGDSSSGWTAGAAAY  SSGWTAGAA  4        0.5902
84.2      4.00  0.37    Sequence         WB
 HLA-DQA10501-DQB10301  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.6417
48.2      1.70  0.29    Sequence         SB
 HLA-DQA10501-DQB10301  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.6703
35.4      1.10  0.31    Sequence         SB
 HLA-DQA10501-DQB10301  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.6918
28.1      0.70  0.26    Sequence         SB
 HLA-DQA10501-DQB10301  261      SSGWTAGAAAYYVGY  TAGAAAYYV  4        0.7013
25.3      0.60  0.23    Sequence         SB
 HLA-DQA10501-DQB10301  262      SGWTAGAAAYYVGYL  AGAAAYYVG  4        0.6907
28.4      0.70  0.25    Sequence         SB
 HLA-DQA10501-DQB10301  263      GWTAGAAAYYVGYLQ  AGAAAYYVG  3        0.6793
32.1      0.90  0.28    Sequence         SB
 HLA-DQA10501-DQB10301  264      WTAGAAAYYVGYLQP  AGAAAYYVG  2        0.6599
39.7      1.30  0.26    Sequence         SB
 HLA-DQA10501-DQB10301  265      TAGAAAYYVGYLQPR  AGAAAYYVG  1        0.5986
77.0      3.50  0.29    Sequence         WB
 HLA-DQA10501-DQB10301  266      AGAAAYYVGYLQPRT  AGAAAYYVG  0        0.5147
190.7      8.50  0.38    Sequence         WB
 HLA-DQA10501-DQB10301  267      GAAAYYVGYLQPRTF  YYVGYLQPR  4        0.4261
497.2     19.00  0.28    Sequence
 HLA-DQA10501-DQB10301  268      AAAYYVGYLQPRTFL  YYVGYLQPR  3        0.3798
820.8     26.00  0.32    Sequence
 HLA-DQA10501-DQB10301  269      AAYYVGYLQPRTFLL  YYVGYLQPR  2        0.3433
1218.1    32.00  0.29     Sequence
 HLA-DQA10501-DQB10301  270      AYYVGYLQPRTFLLK  VGYLQPRTF  3        0.3024
1897.6    41.00  0.31     Sequence
 HLA-DQA10501-DQB10301  271      YYVGYLQPRTFLLKY  VGYLQPRTF  2        0.2660
2812.9    50.00  0.29     Sequence
```

```
 HLA-DQA10501-DQB10301  272      YVGYLQPRTFLLKYN  VGYLQPRTF  1        0.2191
4673.7    65.00  0.23     Sequence
 HLA-DQA10501-DQB10301  273      VGYLQPRTFLLKYNE  PRTFLLKYN  5        0.2088
5220.8    70.00  0.35     Sequence
 HLA-DQA10501-DQB10301  274      GYLQPRTFLLKYNEN  PRTFLLKYN  4        0.1905
6368.1    75.00  0.42     Sequence
 HLA-DQA10501-DQB10301  275      YLQPRTFLLKYNENG  PRTFLLKYN  3        0.1707
7885.1    80.00  0.41     Sequence
 HLA-DQA10501-DQB10301  276      LQPRTFLLKYNENGT  PRTFLLKYN  2        0.1638
8498.2    80.00  0.33     Sequence
 HLA-DQA10501-DQB10301  277      QPRTFLLKYNENGTI  PRTFLLKYN  1        0.1691
8019.7    80.00  0.29     Sequence
 HLA-DQA10501-DQB10301  278      PRTFLLKYNENGTIT  LKYNENGTI  5        0.2205
4601.8    65.00  0.22     Sequence
 HLA-DQA10501-DQB10301  279      RTFLLKYNENGTITD  LKYNENGTI  4        0.2321
4056.3    60.00  0.20     Sequence
 HLA-DQA10501-DQB10301  280      TFLLKYNENGTITDA  NENGTITDA  6        0.2982
1985.6    42.00  0.35     Sequence
 HLA-DQA10501-DQB10301  281      FLLKYNENGTITDAV  NENGTITDA  5        0.3830
792.6    25.00  0.45     Sequence
 HLA-DQA10501-DQB10301  282      LLKYNENGTITDAVD  NENGTITDA  4        0.4005
656.2    22.00  0.43     Sequence
 HLA-DQA10501-DQB10301  283      LKYNENGTITDAVDC  NENGTITDA  3        0.4061
617.4    21.00  0.41     Sequence
 HLA-DQA10501-DQB10301  284      KYNENGTITDAVDCA  NENGTITDA  2        0.4087
600.2    21.00  0.39     Sequence
 HLA-DQA10501-DQB10301  285      YNENGTITDAVDCAL  NENGTITDA  1        0.4114
582.9    21.00  0.33     Sequence
 HLA-DQA10501-DQB10301  286      NENGTITDAVDCALD  NENGTITDA  0        0.3791
827.2    26.00  0.31     Sequence
 HLA-DQA10501-DQB10301  287      ENGTITDAVDCALDP  ITDAVDCAL  4        0.3450
1196.6    32.00  0.28     Sequence
 HLA-DQA10501-DQB10301  288      NGTITDAVDCALDPL  ITDAVDCAL  3        0.2874
2230.1    44.00  0.35     Sequence
 HLA-DQA10501-DQB10301  289      GTITDAVDCALDPLS  ITDAVDCAL  2        0.2575
3082.8    55.00  0.28     Sequence
 HLA-DQA10501-DQB10301  290      TITDAVDCALDPLSE  VDCALDPLS  5        0.2537
3213.9    55.00  0.31     Sequence
 HLA-DQA10501-DQB10301  291      ITDAVDCALDPLSET  VDCALDPLS  4        0.2449
3533.9    55.00  0.32     Sequence
 HLA-DQA10501-DQB10301  292      TDAVDCALDPLSETK  VDCALDPLS  3        0.2284
4223.1    60.00  0.35     Sequence
 HLA-DQA10501-DQB10301  293      DAVDCALDPLSETKC  VDCALDPLS  2        0.2047
5458.9    70.00  0.36     Sequence
 HLA-DQA10501-DQB10301  294      AVDCALDPLSETKCT  VDCALDPLS  1        0.1950
6062.0    70.00  0.31     Sequence
 HLA-DQA10501-DQB10301  295      VDCALDPLSETKCTL  VDCALDPLS  0        0.1754
7493.4    75.00  0.25     Sequence
 HLA-DQA10501-DQB10301  296      DCALDPLSETKCTLK  CALDPLSET  1        0.1398
11021.9    90.00  0.26     Sequence
 HLA-DQA10501-DQB10301  297      CALDPLSETKCTLKS  CALDPLSET  0        0.1297
12285.1    90.00  0.22     Sequence
 HLA-DQA10501-DQB10301  298      ALDPLSETKCTLKSF  SETKCTLKS  5        0.1456
10341.3    85.00  0.26     Sequence
 HLA-DQA10501-DQB10301  299      LDPLSETKCTLKSFT  ETKCTLKSF  5        0.1564
9207.1    85.00  0.26     Sequence
 HLA-DQA10501-DQB10301  300      DPLSETKCTLKSFTV  TKCTLKSFT  5        0.1909
6335.0    75.00  0.23     Sequence
 HLA-DQA10501-DQB10301  301      PLSETKCTLKSFTVE  TKCTLKSFT  4        0.1995
5771.9    70.00  0.17     Sequence
 HLA-DQA10501-DQB10301  302      LSETKCTLKSFTVEK  TKCTLKSFT  3        0.1913
6312.6    75.00  0.19     Sequence
 HLA-DQA10501-DQB10301  303      SETKCTLKSFTVEKG  LKSFTVEKG  6        0.2090
5210.8    70.00  0.29     Sequence
 HLA-DQA10501-DQB10301  304      ETKCTLKSFTVEKGI  LKSFTVEKG  5        0.2270
4286.6    60.00  0.42     Sequence
```

```
 HLA-DQA10501-DQB10301  305       TKCTLKSFTVEKGIY  LKSFTVEKG  4        0.2317
4077.2    60.00  0.45     Sequence
 HLA-DQA10501-DQB10301  306       KCTLKSFTVEKGIYQ  LKSFTVEKG  3        0.2532
3229.3    55.00  0.40     Sequence
 HLA-DQA10501-DQB10301  307       CTLKSFTVEKGIYQT  LKSFTVEKG  2        0.2604
2987.8    55.00  0.36     Sequence
 HLA-DQA10501-DQB10301  308       TLKSFTVEKGIYQTS  VEKGIYQTS  6        0.3433
1218.6    32.00  0.45     Sequence
 HLA-DQA10501-DQB10301  309       LKSFTVEKGIYQTSN  VEKGIYQTS  5        0.4026
641.2    22.00  0.61     Sequence
 HLA-DQA10501-DQB10301  310       KSFTVEKGIYQTSNF  VEKGIYQTS  4        0.4080
605.2    21.00  0.63     Sequence
 HLA-DQA10501-DQB10301  311       SFTVEKGIYQTSNFR  VEKGIYQTS  3        0.3986
670.0    23.00  0.63     Sequence
 HLA-DQA10501-DQB10301  312       FTVEKGIYQTSNFRV  VEKGIYQTS  2        0.3839
785.6    25.00  0.56     Sequence
 HLA-DQA10501-DQB10301  313       TVEKGIYQTSNFRVQ  VEKGIYQTS  1        0.3382
1287.5    33.00  0.49     Sequence
 HLA-DQA10501-DQB10301  314       VEKGIYQTSNFRVQP  VEKGIYQTS  0        0.3111
1725.8    39.00  0.46     Sequence
 HLA-DQA10501-DQB10301  315       EKGIYQTSNFRVQPT  TSNFRVQPT  6        0.2491
3375.7    55.00  0.23     Sequence
 HLA-DQA10501-DQB10301  316       KGIYQTSNFRVQPTE  TSNFRVQPT  5        0.2793
2435.0    46.00  0.50     Sequence
 HLA-DQA10501-DQB10301  317       GIYQTSNFRVQPTES  TSNFRVQPT  4        0.3050
1844.1    40.00  0.44     Sequence
 HLA-DQA10501-DQB10301  318       IYQTSNFRVQPTESI  NFRVQPTES  5        0.3814
807.2    25.00  0.29     Sequence
 HLA-DQA10501-DQB10301  319       YQTSNFRVQPTESIV  NFRVQPTES  4        0.3854
772.3    25.00  0.28     Sequence
 HLA-DQA10501-DQB10301  320       QTSNFRVQPTESIVR  NFRVQPTES  3        0.3809
810.8    25.00  0.28     Sequence
 HLA-DQA10501-DQB10301  321       TSNFRVQPTESIVRF  NFRVQPTES  2        0.3859
768.7    25.00  0.28     Sequence
 HLA-DQA10501-DQB10301  322       SNFRVQPTESIVRFP  VQPTESIVR  4        0.3679
933.9    28.00  0.26     Sequence
 HLA-DQA10501-DQB10301  323       NFRVQPTESIVRFPN  VQPTESIVR  3        0.3630
984.1    28.00  0.23     Sequence
 HLA-DQA10501-DQB10301  324       FRVQPTESIVRFPNI  PTESIVRFP  4        0.3143
1667.0    38.00  0.23     Sequence
 HLA-DQA10501-DQB10301  325       RVQPTESIVRFPNIT  PTESIVRFP  3        0.2198
4633.7    65.00  0.31     Sequence
 HLA-DQA10501-DQB10301  326       VQPTESIVRFPNITN  PTESIVRFP  2        0.2081
5260.3    70.00  0.31     Sequence
 HLA-DQA10501-DQB10301  327       QPTESIVRFPNITNL  PTESIVRFP  1        0.1813
7029.8    75.00  0.26     Sequence
 HLA-DQA10501-DQB10301  328       PTESIVRFPNITNLC  PTESIVRFP  0        0.1812
7039.0    75.00  0.20     Sequence
 HLA-DQA10501-DQB10301  329       TESIVRFPNITNLCP  RFPNITNLC  5        0.1705
7903.1    80.00  0.17     Sequence
 HLA-DQA10501-DQB10301  330       ESIVRFPNITNLCPF  RFPNITNLC  4        0.1544
9403.4    85.00  0.23     Sequence
 HLA-DQA10501-DQB10301  331       SIVRFPNITNLCPFG  RFPNITNLC  3        0.1536
9492.7    85.00  0.23     Sequence
 HLA-DQA10501-DQB10301  332       IVRFPNITNLCPFGE  RFPNITNLC  2        0.1586
8985.6    80.00  0.19     Sequence
 HLA-DQA10501-DQB10301  333       VRFPNITNLCPFGEV  ITNLCPFGE  5        0.2033
5540.8    70.00  0.33     Sequence
 HLA-DQA10501-DQB10301  334       RFPNITNLCPFGEVF  TNLCPFGEV  5        0.2388
3774.5    60.00  0.36     Sequence
 HLA-DQA10501-DQB10301  335       FPNITNLCPFGEVFN  TNLCPFGEV  4        0.2490
3379.1    55.00  0.34     Sequence
 HLA-DQA10501-DQB10301  336       PNITNLCPFGEVFNA  CPFGEVFNA  6        0.2769
2498.0    47.00  0.31     Sequence
 HLA-DQA10501-DQB10301  337       NITNLCPFGEVFNAT  CPFGEVFNA  5        0.4449
405.8    16.00  0.41     Sequence
```

```
 HLA-DQA10501-DQB10301  338      ITNLCPFGEVFNATR  CPFGEVFNA  4        0.4713
305.0    13.00  0.36     Sequence
 HLA-DQA10501-DQB10301  339      TNLCPFGEVFNATRF  CPFGEVFNA  3        0.4976
229.4    10.00  0.32     Sequence
 HLA-DQA10501-DQB10301  340      NLCPFGEVFNATRFA  PFGEVFNAT  3        0.4936
239.5    11.00  0.38     Sequence
 HLA-DQA10501-DQB10301  341      LCPFGEVFNATRFAS  PFGEVFNAT  2        0.5178
184.4     8.50  0.31     Sequence         WB
 HLA-DQA10501-DQB10301  342      CPFGEVFNATRFASV  VFNATRFAS  5        0.5626
113.6     5.50  0.35     Sequence         WB
 HLA-DQA10501-DQB10301  343      PFGEVFNATRFASVY  VFNATRFAS  4        0.5610
115.5     5.50  0.36     Sequence         WB
 HLA-DQA10501-DQB10301  344      FGEVFNATRFASVYA  VFNATRFAS  3        0.5300
161.6     7.50  0.45     Sequence         WB
 HLA-DQA10501-DQB10301  345      GEVFNATRFASVYAW  VFNATRFAS  2        0.5382
147.9     7.00  0.35     Sequence         WB
 HLA-DQA10501-DQB10301  346      EVFNATRFASVYAWN  VFNATRFAS  1        0.5217
176.9     8.00  0.31     Sequence         WB
 HLA-DQA10501-DQB10301  347      VFNATRFASVYAWNR  VFNATRFAS  0        0.5242
172.1     8.00  0.26     Sequence         WB
 HLA-DQA10501-DQB10301  348      FNATRFASVYAWNRK  RFASVYAWN  4        0.4733
298.4    13.00  0.22     Sequence
 HLA-DQA10501-DQB10301  349      NATRFASVYAWNRKR  RFASVYAWN  3        0.4083
603.3    21.00  0.28     Sequence
 HLA-DQA10501-DQB10301  350      ATRFASVYAWNRKRI  RFASVYAWN  2        0.3750
864.6    26.00  0.28     Sequence
 HLA-DQA10501-DQB10301  351      TRFASVYAWNRKRIS  RFASVYAWN  1        0.3564
1057.2    30.00  0.28     Sequence
 HLA-DQA10501-DQB10301  352      RFASVYAWNRKRISN  RFASVYAWN  0        0.3097
1752.9    39.00  0.30     Sequence
 HLA-DQA10501-DQB10301  353      FASVYAWNRKRISNC  YAWNRKRIS  4        0.2538
3208.7    55.00  0.22     Sequence
 HLA-DQA10501-DQB10301  354      ASVYAWNRKRISNCV  WNRKRISNC  5        0.2119
5050.3    65.00  0.26     Sequence
 HLA-DQA10501-DQB10301  355      SVYAWNRKRISNCVA  WNRKRISNC  4        0.2228
4487.2    65.00  0.25     Sequence
 HLA-DQA10501-DQB10301  356      VYAWNRKRISNCVAD  WNRKRISNC  3        0.2377
3819.1    60.00  0.21     Sequence
 HLA-DQA10501-DQB10301  357      YAWNRKRISNCVADY  NRKRISNCV  3        0.2313
4095.2    60.00  0.20     Sequence
 HLA-DQA10501-DQB10301  358      AWNRKRISNCVADYS  ISNCVADYS  6        0.3091
1764.9    39.00  0.44     Sequence
 HLA-DQA10501-DQB10301  359      WNRKRISNCVADYSV  ISNCVADYS  5        0.3375
1296.7    33.00  0.51     Sequence
 HLA-DQA10501-DQB10301  360      NRKRISNCVADYSVL  ISNCVADYS  4        0.3382
1287.7    33.00  0.50     Sequence
 HLA-DQA10501-DQB10301  361      RKRISNCVADYSVLY  ISNCVADYS  3        0.3297
1411.3    35.00  0.49     Sequence
 HLA-DQA10501-DQB10301  362      KRISNCVADYSVLYN  ISNCVADYS  2        0.3373
1299.5    33.00  0.44     Sequence
 HLA-DQA10501-DQB10301  363      RISNCVADYSVLYNS  ISNCVADYS  1        0.3544
1080.2    30.00  0.35     Sequence
 HLA-DQA10501-DQB10301  364      ISNCVADYSVLYNSA  ADYSVLYNS  5        0.3641
973.1    28.00  0.22     Sequence
 HLA-DQA10501-DQB10301  365      SNCVADYSVLYNSAS  ADYSVLYNS  4        0.3105
1737.8    39.00  0.36     Sequence
 HLA-DQA10501-DQB10301  366      NCVADYSVLYNSASF  ADYSVLYNS  3        0.3303
1402.4    35.00  0.37     Sequence
 HLA-DQA10501-DQB10301  367      CVADYSVLYNSASFS  ADYSVLYNS  2        0.3603
1013.6    29.00  0.26     Sequence
 HLA-DQA10501-DQB10301  368      VADYSVLYNSASFST  LYNSASFST  6        0.4716
304.2    13.00  0.32     Sequence
 HLA-DQA10501-DQB10301  369      ADYSVLYNSASFSTF  LYNSASFST  5        0.5631
113.0     5.50  0.43     Sequence         WB
 HLA-DQA10501-DQB10301  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.5745
99.9      4.50 0.44     Sequence         WB
```

```
 HLA-DQA10501-DQB10301  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.5756
98.7     4.50  0.44     Sequence         WB
 HLA-DQA10501-DQB10301  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.5594
117.5     5.50  0.41     Sequence         WB
 HLA-DQA10501-DQB10301  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.5381
148.0     7.00  0.39     Sequence         WB
 HLA-DQA10501-DQB10301  374      LYNSASFSTFKCYGV  LYNSASFST  0        0.4939
239.0    11.00  0.37     Sequence
 HLA-DQA10501-DQB10301  375      YNSASFSTFKCYGVS  YNSASFSTF  0        0.4103
589.9    21.00  0.32     Sequence
 HLA-DQA10501-DQB10301  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.3169
1621.7    38.00  0.28     Sequence
 HLA-DQA10501-DQB10301  377      SASFSTFKCYGVSPT  FSTFKCYGV  3        0.3498
1136.1    31.00  0.25     Sequence
 HLA-DQA10501-DQB10301  378      ASFSTFKCYGVSPTK  FKCYGVSPT  5        0.3838
786.3    25.00  0.25     Sequence
 HLA-DQA10501-DQB10301  379      SFSTFKCYGVSPTKL  KCYGVSPTK  5        0.4024
643.0    22.00  0.23     Sequence
 HLA-DQA10501-DQB10301  380      FSTFKCYGVSPTKLN  CYGVSPTKL  5        0.4429
415.0    16.00  0.25     Sequence
 HLA-DQA10501-DQB10301  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.4349
452.5    17.00  0.26     Sequence
 HLA-DQA10501-DQB10301  382      TFKCYGVSPTKLNDL  CYGVSPTKL  3        0.4246
505.7    19.00  0.26     Sequence
 HLA-DQA10501-DQB10301  383      FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.4017
647.8    22.00  0.26     Sequence
 HLA-DQA10501-DQB10301  384      KCYGVSPTKLNDLCF  YGVSPTKLN  2        0.3355
1325.5    34.00  0.31     Sequence
 HLA-DQA10501-DQB10301  385      CYGVSPTKLNDLCFT  YGVSPTKLN  1        0.3067
1809.5    40.00  0.32     Sequence
 HLA-DQA10501-DQB10301  386      YGVSPTKLNDLCFTN  YGVSPTKLN  0        0.2709
2666.1    48.00  0.35     Sequence
 HLA-DQA10501-DQB10301  387      GVSPTKLNDLCFTNV  TKLNDLCFT  4        0.1525
9601.2    85.00  0.26     Sequence
 HLA-DQA10501-DQB10301  388      VSPTKLNDLCFTNVY  NDLCFTNVY  6        0.1809
7062.5    75.00  0.23     Sequence
 HLA-DQA10501-DQB10301  389      SPTKLNDLCFTNVYA  NDLCFTNVY  5        0.1842
6816.4    75.00  0.30     Sequence
 HLA-DQA10501-DQB10301  390      PTKLNDLCFTNVYAD  LCFTNVYAD  6        0.2026
5585.1    70.00  0.24     Sequence
 HLA-DQA10501-DQB10301  391      TKLNDLCFTNVYADS  LCFTNVYAD  5        0.2082
5257.5    70.00  0.31     Sequence
 HLA-DQA10501-DQB10301  392      KLNDLCFTNVYADSF  LCFTNVYAD  4        0.2420
3646.1    60.00  0.28     Sequence
 HLA-DQA10501-DQB10301  393      LNDLCFTNVYADSFV  LCFTNVYAD  3        0.2518
3279.9    55.00  0.22     Sequence
 HLA-DQA10501-DQB10301  394      NDLCFTNVYADSFVI  LCFTNVYAD  2        0.2622
2931.2    55.00  0.19     Sequence
 HLA-DQA10501-DQB10301  395      DLCFTNVYADSFVIR  NVYADSFVI  5        0.2578
3074.0    55.00  0.29     Sequence
 HLA-DQA10501-DQB10301  396      LCFTNVYADSFVIRG  YADSFVIRG  6        0.2755
2536.5    47.00  0.32     Sequence
 HLA-DQA10501-DQB10301  397      CFTNVYADSFVIRGD  YADSFVIRG  5        0.2879
2219.3    44.00  0.38     Sequence
 HLA-DQA10501-DQB10301  398      FTNVYADSFVIRGDE  YADSFVIRG  4        0.2840
2315.4    45.00  0.35     Sequence
 HLA-DQA10501-DQB10301  399      TNVYADSFVIRGDEV  YADSFVIRG  3        0.2769
2499.2    47.00  0.39     Sequence
 HLA-DQA10501-DQB10301  400      NVYADSFVIRGDEVR  YADSFVIRG  2        0.2787
2451.6    47.00  0.31     Sequence
 HLA-DQA10501-DQB10301  401      VYADSFVIRGDEVRQ  YADSFVIRG  1        0.2625
2919.3    55.00  0.28     Sequence
 HLA-DQA10501-DQB10301  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.2624
2923.7    55.00  0.28     Sequence
 HLA-DQA10501-DQB10301  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.2735
2593.8    48.00  0.47     Sequence
```

```
 HLA-DQA10501-DQB10301  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4         0.2721
2632.0    48.00  0.49     Sequence
 HLA-DQA10501-DQB10301  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3         0.2664
2799.9    50.00  0.47     Sequence
 HLA-DQA10501-DQB10301  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2         0.2452
3522.3    55.00  0.37     Sequence
 HLA-DQA10501-DQB10301  407      VIRGDEVRQIAPGQT  VRQIAPGQT  6         0.2791
2441.0    46.00  0.22     Sequence
 HLA-DQA10501-DQB10301  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5         0.4016
648.8    22.00  0.31     Sequence
 HLA-DQA10501-DQB10301  409      RGDEVRQIAPGQTGT  RQIAPGQTG  5         0.4292
481.0    18.00  0.34     Sequence
 HLA-DQA10501-DQB10301  410      GDEVRQIAPGQTGTI  IAPGQTGTI  6         0.5441
138.8     6.50  0.41     Sequence        WB
 HLA-DQA10501-DQB10301  411      DEVRQIAPGQTGTIA  IAPGQTGTI  5         0.5980
77.4     3.50  0.51     Sequence        WB
 HLA-DQA10501-DQB10301  412      EVRQIAPGQTGTIAD  IAPGQTGTI  4         0.5967
78.6     3.50  0.51     Sequence        WB
 HLA-DQA10501-DQB10301  413      VRQIAPGQTGTIADY  IAPGQTGTI  3         0.5925
82.2     4.00  0.51     Sequence        WB
 HLA-DQA10501-DQB10301  414      RQIAPGQTGTIADYN  IAPGQTGTI  2         0.5911
83.4     4.00  0.43     Sequence        WB
 HLA-DQA10501-DQB10301  415      QIAPGQTGTIADYNY  IAPGQTGTI  1         0.5613
115.2     5.50  0.47     Sequence        WB
 HLA-DQA10501-DQB10301  416      IAPGQTGTIADYNYK  IAPGQTGTI  0         0.5311
159.7     7.50  0.43     Sequence        WB
 HLA-DQA10501-DQB10301  417      APGQTGTIADYNYKL  GQTGTIADY  2         0.3946
699.1    23.00  0.34     Sequence
 HLA-DQA10501-DQB10301  418      PGQTGTIADYNYKLP  GQTGTIADY  1         0.3383
1286.8    33.00  0.33     Sequence
 HLA-DQA10501-DQB10301  419      GQTGTIADYNYKLPD  GQTGTIADY  0         0.3205
1559.7    37.00  0.31     Sequence
 HLA-DQA10501-DQB10301  420      QTGTIADYNYKLPDD  QTGTIADYN  0         0.2695
2708.3    49.00  0.32     Sequence
 HLA-DQA10501-DQB10301  421      TGTIADYNYKLPDDF  GTIADYNYK  1         0.1917
6284.8    75.00  0.31     Sequence
 HLA-DQA10501-DQB10301  422      GTIADYNYKLPDDFT  YNYKLPDDF  5         0.1799
7137.3    75.00  0.25     Sequence
 HLA-DQA10501-DQB10301  423      TIADYNYKLPDDFTG  YNYKLPDDF  4         0.1397
11029.8    90.00  0.28     Sequence
 HLA-DQA10501-DQB10301  424      IADYNYKLPDDFTGC  YNYKLPDDF  3         0.1334
11804.9    90.00  0.31     Sequence
 HLA-DQA10501-DQB10301  425      ADYNYKLPDDFTGCV  YNYKLPDDF  2         0.1026
16468.0    95.00  0.28     Sequence
 HLA-DQA10501-DQB10301  426      DYNYKLPDDFTGCVI  YKLPDDFTG  3         0.1564
9202.0    85.00  0.12     Sequence
 HLA-DQA10501-DQB10301  427      YNYKLPDDFTGCVIA  PDDFTGCVI  5         0.2138
4947.6    65.00  0.22     Sequence
 HLA-DQA10501-DQB10301  428      NYKLPDDFTGCVIAW  DFTGCVIAW  6         0.2678
2757.8    49.00  0.32     Sequence
 HLA-DQA10501-DQB10301  429      YKLPDDFTGCVIAWN  FTGCVIAWN  6         0.4732
298.8    13.00  0.52     Sequence
 HLA-DQA10501-DQB10301  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5         0.5084
204.2     9.50  0.56     Sequence        WB
 HLA-DQA10501-DQB10301  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4         0.5267
167.6     8.00  0.51     Sequence        WB
 HLA-DQA10501-DQB10301  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3         0.5256
169.4     8.00  0.51     Sequence        WB
 HLA-DQA10501-DQB10301  433      DDFTGCVIAWNSNNL  FTGCVIAWN  2         0.5141
192.1     9.00  0.47     Sequence        WB
 HLA-DQA10501-DQB10301  434      DFTGCVIAWNSNNLD  FTGCVIAWN  1         0.4984
227.5    10.00  0.43     Sequence
 HLA-DQA10501-DQB10301  435      FTGCVIAWNSNNLDS  FTGCVIAWN  0         0.4659
323.2    14.00  0.39     Sequence
 HLA-DQA10501-DQB10301  436      TGCVIAWNSNNLDSK  IAWNSNNLD  4         0.2903
2161.6    44.00  0.22     Sequence
```

```
 HLA-DQA10501-DQB10301  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3         0.2499
3346.9    55.00  0.30     Sequence
 HLA-DQA10501-DQB10301  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2         0.1878
6554.0    75.00  0.25     Sequence
 HLA-DQA10501-DQB10301  439      VIAWNSNNLDSKVGG  IAWNSNNLD  1         0.1798
7147.8    75.00  0.19     Sequence
 HLA-DQA10501-DQB10301  440      IAWNSNNLDSKVGGN  NLDSKVGGN  6         0.1968
5947.3    70.00  0.34     Sequence
 HLA-DQA10501-DQB10301  441      AWNSNNLDSKVGGNY  NLDSKVGGN  5         0.2124
5019.7    65.00  0.56     Sequence
 HLA-DQA10501-DQB10301  442      WNSNNLDSKVGGNYN  NLDSKVGGN  4         0.2275
4264.1    60.00  0.50     Sequence
 HLA-DQA10501-DQB10301  443      NSNNLDSKVGGNYNY  NLDSKVGGN  3         0.2387
3777.5    60.00  0.42     Sequence
 HLA-DQA10501-DQB10301  444      SNNLDSKVGGNYNYL  NLDSKVGGN  2         0.2695
2708.8    49.00  0.31     Sequence
 HLA-DQA10501-DQB10301  445      NNLDSKVGGNYNYLY  KVGGNYNYL  5         0.2930
2099.5    43.00  0.29     Sequence
 HLA-DQA10501-DQB10301  446      NLDSKVGGNYNYLYR  KVGGNYNYL  4         0.2874
2230.3    44.00  0.29     Sequence
 HLA-DQA10501-DQB10301  447      LDSKVGGNYNYLYRL  KVGGNYNYL  3         0.2707
2672.1    48.00  0.40     Sequence
 HLA-DQA10501-DQB10301  448      DSKVGGNYNYLYRLF  KVGGNYNYL  2         0.2640
2873.3    50.00  0.41     Sequence
 HLA-DQA10501-DQB10301  449      SKVGGNYNYLYRLFR  KVGGNYNYL  1         0.2442
3558.4    55.00  0.37     Sequence
 HLA-DQA10501-DQB10301  450      KVGGNYNYLYRLFRK  KVGGNYNYL  0         0.2210
4575.7    65.00  0.34     Sequence
 HLA-DQA10501-DQB10301  451      VGGNYNYLYRLFRKS  YNYLYRLFR  4         0.1910
6330.0    75.00  0.17     Sequence
 HLA-DQA10501-DQB10301  452      GGNYNYLYRLFRKSN  YLYRLFRKS  5         0.1539
9461.6    85.00  0.28     Sequence
 HLA-DQA10501-DQB10301  453      GNYNYLYRLFRKSNL  YLYRLFRKS  4         0.1369
11368.2    90.00  0.29     Sequence
 HLA-DQA10501-DQB10301  454      NYNYLYRLFRKSNLK  YLYRLFRKS  3         0.1439
10533.9    85.00  0.23     Sequence
 HLA-DQA10501-DQB10301  455      YNYLYRLFRKSNLKP  YLYRLFRKS  2         0.1268
12674.2    90.00  0.28     Sequence
 HLA-DQA10501-DQB10301  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6         0.1325
11916.3    90.00  0.34     Sequence
 HLA-DQA10501-DQB10301  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5         0.1368
11377.6    90.00  0.41     Sequence
 HLA-DQA10501-DQB10301  458      LYRLFRKSNLKPFER  FRKSNLKPF  4         0.1307
12151.1    90.00  0.44     Sequence
 HLA-DQA10501-DQB10301  459      YRLFRKSNLKPFERD  FRKSNLKPF  3         0.1297
12288.9    90.00  0.38     Sequence
 HLA-DQA10501-DQB10301  460      RLFRKSNLKPFERDI  FRKSNLKPF  2         0.1152
14377.0    95.00  0.32     Sequence
 HLA-DQA10501-DQB10301  461      LFRKSNLKPFERDIS  FRKSNLKPF  1         0.1131
14704.8    95.00  0.25     Sequence
 HLA-DQA10501-DQB10301  462      FRKSNLKPFERDIST  LKPFERDIS  5         0.1177
13989.8    95.00  0.19     Sequence
 HLA-DQA10501-DQB10301  463      RKSNLKPFERDISTE  LKPFERDIS  4         0.0950
17896.6   100.00  0.28     Sequence
 HLA-DQA10501-DQB10301  464      KSNLKPFERDISTEI  LKPFERDIS  3         0.1148
14439.6    95.00  0.26     Sequence
 HLA-DQA10501-DQB10301  465      SNLKPFERDISTEIY  FERDISTEI  5         0.1376
11285.8    90.00  0.26     Sequence
 HLA-DQA10501-DQB10301  466      NLKPFERDISTEIYQ  FERDISTEI  4         0.1522
9630.7    85.00  0.20     Sequence
 HLA-DQA10501-DQB10301  467      LKPFERDISTEIYQA  FERDISTEI  3         0.1585
8994.1    80.00  0.18     Sequence
 HLA-DQA10501-DQB10301  468      KPFERDISTEIYQAG  DISTEIYQA  5         0.1995
5777.6    70.00  0.28     Sequence
 HLA-DQA10501-DQB10301  469      PFERDISTEIYQAGS  ISTEIYQAG  5         0.2213
4560.1    65.00  0.35     Sequence
```

```
 HLA-DQA10501-DQB10301  470      FERDISTEIYQAGST  ISTEIYQAG  4         0.3176
1609.5    37.00  0.28     Sequence
 HLA-DQA10501-DQB10301  471      ERDISTEIYQAGSTP  TEIYQAGST  5         0.3518
1110.9    31.00  0.30     Sequence
 HLA-DQA10501-DQB10301  472      RDISTEIYQAGSTPC  IYQAGSTPC  6         0.4080
605.3    21.00  0.28     Sequence
 HLA-DQA10501-DQB10301  473      DISTEIYQAGSTPCN  YQAGSTPCN  6         0.5485
132.3     6.50  0.39     Sequence         WB
 HLA-DQA10501-DQB10301  474      ISTEIYQAGSTPCNG  YQAGSTPCN  5         0.5774
96.8     4.50  0.46     Sequence         WB
 HLA-DQA10501-DQB10301  475      STEIYQAGSTPCNGV  YQAGSTPCN  4         0.5971
78.2     3.50  0.44     Sequence         WB
 HLA-DQA10501-DQB10301  476      TEIYQAGSTPCNGVK  YQAGSTPCN  3         0.5908
83.7     4.00  0.44     Sequence         WB
 HLA-DQA10501-DQB10301  477      EIYQAGSTPCNGVKG  YQAGSTPCN  2         0.5510
128.8     6.00  0.37     Sequence         WB
 HLA-DQA10501-DQB10301  478      IYQAGSTPCNGVKGF  YQAGSTPCN  1         0.5454
136.9     6.50  0.32     Sequence         WB
 HLA-DQA10501-DQB10301  479      YQAGSTPCNGVKGFN  YQAGSTPCN  0         0.5213
177.5     8.00  0.31     Sequence         WB
 HLA-DQA10501-DQB10301  480      QAGSTPCNGVKGFNC  QAGSTPCNG  0         0.4176
545.1    20.00  0.30     Sequence
 HLA-DQA10501-DQB10301  481      AGSTPCNGVKGFNCY  PCNGVKGFN  4         0.3982
672.9    23.00  0.27     Sequence
 HLA-DQA10501-DQB10301  482      GSTPCNGVKGFNCYF  PCNGVKGFN  3         0.3491
1144.2    31.00  0.31     Sequence
 HLA-DQA10501-DQB10301  483      STPCNGVKGFNCYFP  CNGVKGFNC  3         0.3363
1314.5    34.00  0.28     Sequence
 HLA-DQA10501-DQB10301  484      TPCNGVKGFNCYFPL  CNGVKGFNC  2         0.3108
1732.2    39.00  0.31     Sequence
 HLA-DQA10501-DQB10301  485      PCNGVKGFNCYFPLQ  CNGVKGFNC  1         0.2921
2120.8    43.00  0.31     Sequence
 HLA-DQA10501-DQB10301  486      CNGVKGFNCYFPLQS  CNGVKGFNC  0         0.2632
2898.0    50.00  0.27     Sequence
 HLA-DQA10501-DQB10301  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5         0.2709
2666.5    48.00  0.20     Sequence
 HLA-DQA10501-DQB10301  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4         0.2455
3508.7    55.00  0.26     Sequence
 HLA-DQA10501-DQB10301  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3         0.2540
3202.3    55.00  0.22     Sequence
 HLA-DQA10501-DQB10301  490      KGFNCYFPLQSYGFQ  FNCYFPLQS  2         0.2288
4205.2    60.00  0.25     Sequence
 HLA-DQA10501-DQB10301  491      GFNCYFPLQSYGFQP  CYFPLQSYG  3         0.2378
3817.6    60.00  0.20     Sequence
 HLA-DQA10501-DQB10301  492      FNCYFPLQSYGFQPT  PLQSYGFQP  5         0.2660
2812.2    50.00  0.24     Sequence
 HLA-DQA10501-DQB10301  493      NCYFPLQSYGFQPTY  LQSYGFQPT  5         0.2693
2713.5    49.00  0.28     Sequence
 HLA-DQA10501-DQB10301  494      CYFPLQSYGFQPTYG  LQSYGFQPT  4         0.2829
2341.6    45.00  0.25     Sequence
 HLA-DQA10501-DQB10301  495      YFPLQSYGFQPTYGV  SYGFQPTYG  5         0.3306
1398.2    35.00  0.35     Sequence
 HLA-DQA10501-DQB10301  496      FPLQSYGFQPTYGVG  SYGFQPTYG  4         0.3357
1323.3    34.00  0.34     Sequence
 HLA-DQA10501-DQB10301  497      PLQSYGFQPTYGVGY  SYGFQPTYG  3         0.3569
1051.8    30.00  0.31     Sequence
 HLA-DQA10501-DQB10301  498      LQSYGFQPTYGVGYQ  SYGFQPTYG  2         0.3572
1047.8    29.00  0.28     Sequence
 HLA-DQA10501-DQB10301  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4         0.3641
973.4    28.00  0.25     Sequence
 HLA-DQA10501-DQB10301  500      SYGFQPTYGVGYQPY  PTYGVGYQP  5         0.4369
442.5    17.00  0.35     Sequence
 HLA-DQA10501-DQB10301  501      YGFQPTYGVGYQPYR  PTYGVGYQP  4         0.4468
397.7    16.00  0.37     Sequence
 HLA-DQA10501-DQB10301  502      GFQPTYGVGYQPYRV  PTYGVGYQP  3         0.4428
415.1    16.00  0.39     Sequence
```

```
 HLA-DQA10501-DQB10301  503      FQPTYGVGYQPYRVV  PTYGVGYQP  2        0.4479
393.1    16.00  0.29     Sequence
 HLA-DQA10501-DQB10301  504      QPTYGVGYQPYRVVV  PTYGVGYQP  1        0.4366
443.9    17.00  0.29     Sequence
 HLA-DQA10501-DQB10301  505      PTYGVGYQPYRVVVL  PTYGVGYQP  0        0.4412
422.4    17.00  0.25     Sequence
 HLA-DQA10501-DQB10301  506      TYGVGYQPYRVVVLS  YQPYRVVVL  5        0.4246
505.4    19.00  0.17     Sequence
 HLA-DQA10501-DQB10301  507      YGVGYQPYRVVVLSF  YQPYRVVVL  4        0.3666
946.9    28.00  0.23     Sequence
 HLA-DQA10501-DQB10301  508      GVGYQPYRVVVLSFE  YQPYRVVVL  3        0.3429
1223.6    32.00  0.25     Sequence
 HLA-DQA10501-DQB10301  509      VGYQPYRVVVLSFEL  PYRVVVLSF  4        0.3202
1564.6    37.00  0.26     Sequence
 HLA-DQA10501-DQB10301  510      GYQPYRVVVLSFELL  PYRVVVLSF  3        0.2888
2198.3    44.00  0.29     Sequence
 HLA-DQA10501-DQB10301  511      YQPYRVVVLSFELLH  PYRVVVLSF  2        0.2635
2888.2    50.00  0.25     Sequence
 HLA-DQA10501-DQB10301  512      QPYRVVVLSFELLHA  PYRVVVLSF  1        0.1860
6682.0    75.00  0.18     Sequence
 HLA-DQA10501-DQB10301  513      PYRVVVLSFELLHAP  VLSFELLHA  5        0.1993
5786.8    70.00  0.28     Sequence
 HLA-DQA10501-DQB10301  514      YRVVVLSFELLHAPA  VLSFELLHA  4        0.2259
4341.0    65.00  0.26     Sequence
 HLA-DQA10501-DQB10301  515      RVVVLSFELLHAPAT  FELLHAPAT  6        0.3312
1389.5    35.00  0.32     Sequence
 HLA-DQA10501-DQB10301  516      VVVLSFELLHAPATV  FELLHAPAT  5        0.3910
727.4    24.00  0.41     Sequence
 HLA-DQA10501-DQB10301  517      VVLSFELLHAPATVC  FELLHAPAT  4        0.4376
439.3    17.00  0.31     Sequence
 HLA-DQA10501-DQB10301  518      VLSFELLHAPATVCG  LLHAPATVC  5        0.4715
304.3    13.00  0.31     Sequence
 HLA-DQA10501-DQB10301  519      LSFELLHAPATVCGP  LLHAPATVC  4        0.5004
222.7    10.00  0.28     Sequence
 HLA-DQA10501-DQB10301  520      SFELLHAPATVCGPK  LLHAPATVC  3        0.5091
202.7     9.00  0.26     Sequence         WB
 HLA-DQA10501-DQB10301  521      FELLHAPATVCGPKK  HAPATVCGP  4        0.4977
229.4    10.00  0.25     Sequence
 HLA-DQA10501-DQB10301  522      ELLHAPATVCGPKKS  HAPATVCGP  3        0.4348
452.5    17.00  0.34     Sequence
 HLA-DQA10501-DQB10301  523      LLHAPATVCGPKKST  HAPATVCGP  2        0.4294
479.8    18.00  0.30     Sequence
 HLA-DQA10501-DQB10301  524      LHAPATVCGPKKSTN  HAPATVCGP  1        0.4266
494.8    19.00  0.30     Sequence
 HLA-DQA10501-DQB10301  525      HAPATVCGPKKSTNL  HAPATVCGP  0        0.3982
673.1    23.00  0.31     Sequence
 HLA-DQA10501-DQB10301  526      APATVCGPKKSTNLV  VCGPKKSTN  4        0.3578
1041.0    29.00  0.23     Sequence
 HLA-DQA10501-DQB10301  527      PATVCGPKKSTNLVK  VCGPKKSTN  3        0.3349
1334.9    34.00  0.25     Sequence
 HLA-DQA10501-DQB10301  528      ATVCGPKKSTNLVKN  VCGPKKSTN  2        0.3085
1776.0    39.00  0.20     Sequence
 HLA-DQA10501-DQB10301  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.2705
2678.2    49.00  0.16     Sequence
 HLA-DQA10501-DQB10301  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3        0.2203
4610.5    65.00  0.21     Sequence
 HLA-DQA10501-DQB10301  531      CGPKKSTNLVKNKCV  KKSTNLVKN  3        0.1858
6698.1    75.00  0.27     Sequence
 HLA-DQA10501-DQB10301  532      GPKKSTNLVKNKCVN  KKSTNLVKN  2        0.1753
7501.2    75.00  0.28     Sequence
 HLA-DQA10501-DQB10301  533      PKKSTNLVKNKCVNF  KKSTNLVKN  1        0.1566
9182.5    85.00  0.28     Sequence
 HLA-DQA10501-DQB10301  534      KKSTNLVKNKCVNFN  VKNKCVNFN  6        0.1734
7655.5    80.00  0.31     Sequence
 HLA-DQA10501-DQB10301  535      KSTNLVKNKCVNFNF  VKNKCVNFN  5        0.2027
5576.3    70.00  0.47     Sequence
```

```
 HLA-DQA10501-DQB10301  536      STNLVKNKCVNFNFN  VKNKCVNFN  4        0.2094
5186.0    65.00  0.44     Sequence
 HLA-DQA10501-DQB10301  537      TNLVKNKCVNFNFNG  VKNKCVNFN  3        0.2071
5319.5    70.00  0.41     Sequence
 HLA-DQA10501-DQB10301  538      NLVKNKCVNFNFNGL  VKNKCVNFN  2        0.1915
6296.4    75.00  0.46     Sequence
 HLA-DQA10501-DQB10301  539      LVKNKCVNFNFNGLT  VKNKCVNFN  1        0.1906
6358.2    75.00  0.36     Sequence
 HLA-DQA10501-DQB10301  540      VKNKCVNFNFNGLTG  VKNKCVNFN  0        0.2002
5733.7    70.00  0.25     Sequence
 HLA-DQA10501-DQB10301  541      KNKCVNFNFNGLTGT  FNFNGLTGT  6        0.2364
3872.2    60.00  0.32     Sequence
 HLA-DQA10501-DQB10301  542      NKCVNFNFNGLTGTG  NFNGLTGTG  6        0.3154
1647.1    38.00  0.31     Sequence
 HLA-DQA10501-DQB10301  543      KCVNFNFNGLTGTGV  NFNGLTGTG  5        0.4228
515.7    19.00  0.44     Sequence
 HLA-DQA10501-DQB10301  544      CVNFNFNGLTGTGVL  NFNGLTGTG  4        0.4545
366.0    15.00  0.38     Sequence
 HLA-DQA10501-DQB10301  545      VNFNFNGLTGTGVLT  NFNGLTGTG  3        0.4670
319.6    14.00  0.34     Sequence
 HLA-DQA10501-DQB10301  546      NFNFNGLTGTGVLTE  NFNGLTGTG  2        0.5034
215.6     9.50  0.22     Sequence         WB
 HLA-DQA10501-DQB10301  547      FNFNGLTGTGVLTES  TGTGVLTES  6        0.5429
140.5     6.50  0.26     Sequence         WB
 HLA-DQA10501-DQB10301  548      NFNGLTGTGVLTESN  TGTGVLTES  5        0.5857
88.5      4.00  0.49     Sequence         WB
 HLA-DQA10501-DQB10301  549      FNGLTGTGVLTESNK  TGTGVLTES  4        0.5729
101.6     5.00  0.51     Sequence         WB
 HLA-DQA10501-DQB10301  550      NGLTGTGVLTESNKK  TGTGVLTES  3        0.5563
121.7     6.00  0.54     Sequence         WB
 HLA-DQA10501-DQB10301  551      GLTGTGVLTESNKKF  TGTGVLTES  2        0.5380
148.2     7.00  0.53     Sequence         WB
 HLA-DQA10501-DQB10301  552      LTGTGVLTESNKKFL  TGTGVLTES  1        0.5163
187.4     8.50  0.47     Sequence         WB
 HLA-DQA10501-DQB10301  553      TGTGVLTESNKKFLP  TGTGVLTES  0        0.4417
420.0    17.00  0.52     Sequence
 HLA-DQA10501-DQB10301  554      GTGVLTESNKKFLPF  XGTGVLTES -1        0.3082
1781.8    40.00  0.23     Sequence
 HLA-DQA10501-DQB10301  555      TGVLTESNKKFLPFQ  LTESNKKFL  3        0.1395
11054.9    90.00  0.20     Sequence
 HLA-DQA10501-DQB10301  556      GVLTESNKKFLPFQQ  TESNKKFLP  3        0.1098
15234.1    95.00  0.25     Sequence
 HLA-DQA10501-DQB10301  557      VLTESNKKFLPFQQF  NKKFLPFQQ  5        0.1159
14260.5    95.00  0.31     Sequence
 HLA-DQA10501-DQB10301  558      LTESNKKFLPFQQFG  NKKFLPFQQ  4        0.1100
15203.9    95.00  0.29     Sequence
 HLA-DQA10501-DQB10301  559      TESNKKFLPFQQFGR  NKKFLPFQQ  3        0.1107
15093.0    95.00  0.25     Sequence
 HLA-DQA10501-DQB10301  560      ESNKKFLPFQQFGRD  NKKFLPFQQ  2        0.0994
17062.1    95.00  0.21     Sequence
 HLA-DQA10501-DQB10301  561      SNKKFLPFQQFGRDI  KFLPFQQFG  3        0.1014
16695.1    95.00  0.15     Sequence
 HLA-DQA10501-DQB10301  562      NKKFLPFQQFGRDIA  PFQQFGRDI  5        0.1548
9362.2    85.00  0.17     Sequence
 HLA-DQA10501-DQB10301  563      KKFLPFQQFGRDIAD  QQFGRDIAD  6        0.1621
8652.3    80.00  0.20     Sequence
 HLA-DQA10501-DQB10301  564      KFLPFQQFGRDIADT  QQFGRDIAD  5        0.1822
6966.9    75.00  0.23     Sequence
 HLA-DQA10501-DQB10301  565      FLPFQQFGRDIADTT  QFGRDIADT  5        0.2181
4721.7    65.00  0.31     Sequence
 HLA-DQA10501-DQB10301  566      LPFQQFGRDIADTTD  QFGRDIADT  4        0.2177
4744.0    65.00  0.34     Sequence
 HLA-DQA10501-DQB10301  567      PFQQFGRDIADTTDA  QFGRDIADT  3        0.2301
4149.1    60.00  0.31     Sequence
 HLA-DQA10501-DQB10301  568      FQQFGRDIADTTDAV  QFGRDIADT  2        0.2398
3735.4    60.00  0.28     Sequence
```

```
 HLA-DQA10501-DQB10301  569      QQFGRDIADTTDAVR  QFGRDIADT  1        0.2047
5460.2    70.00  0.22     Sequence
 HLA-DQA10501-DQB10301  570      QFGRDIADTTDAVRD  QFGRDIADT  0        0.2034
5536.3    70.00  0.20     Sequence
 HLA-DQA10501-DQB10301  571      FGRDIADTTDAVRDP  RDIADTTDA  2        0.1969
5942.0    70.00  0.19     Sequence
 HLA-DQA10501-DQB10301  572      GRDIADTTDAVRDPQ  ADTTDAVRD  4        0.1632
8556.0    80.00  0.21     Sequence
 HLA-DQA10501-DQB10301  573      RDIADTTDAVRDPQT  ADTTDAVRD  3        0.1583
9019.5    80.00  0.22     Sequence
 HLA-DQA10501-DQB10301  574      DIADTTDAVRDPQTL  TDAVRDPQT  5        0.1637
8506.1    80.00  0.20     Sequence
 HLA-DQA10501-DQB10301  575      IADTTDAVRDPQTLE  TDAVRDPQT  4        0.1606
8799.9    80.00  0.25     Sequence
 HLA-DQA10501-DQB10301  576      ADTTDAVRDPQTLEI  DAVRDPQTL  4        0.1603
8826.5    80.00  0.25     Sequence
 HLA-DQA10501-DQB10301  577      DTTDAVRDPQTLEIL  DAVRDPQTL  3        0.1733
7666.8    80.00  0.23     Sequence
 HLA-DQA10501-DQB10301  578      TTDAVRDPQTLEILD  DAVRDPQTL  2        0.1724
7744.8    80.00  0.22     Sequence
 HLA-DQA10501-DQB10301  579      TDAVRDPQTLEILDI  VRDPQTLEI  3        0.1646
8426.3    80.00  0.19     Sequence
 HLA-DQA10501-DQB10301  580      DAVRDPQTLEILDIT  PQTLEILDI  5        0.1653
8357.1    80.00  0.29     Sequence
 HLA-DQA10501-DQB10301  581      AVRDPQTLEILDITP  PQTLEILDI  4        0.1549
9359.7    85.00  0.35     Sequence
 HLA-DQA10501-DQB10301  582      VRDPQTLEILDITPC  PQTLEILDI  3        0.1527
9585.6    85.00  0.34     Sequence
 HLA-DQA10501-DQB10301  583      RDPQTLEILDITPCS  LEILDITPC  5        0.1533
9517.3    85.00  0.28     Sequence
 HLA-DQA10501-DQB10301  584      DPQTLEILDITPCSF  LEILDITPC  4        0.1861
6678.4    75.00  0.23     Sequence
 HLA-DQA10501-DQB10301  585      PQTLEILDITPCSFG  ILDITPCSF  5        0.2380
3807.0    60.00  0.26     Sequence
 HLA-DQA10501-DQB10301  586      QTLEILDITPCSFGG  LDITPCSFG  5        0.2487
3391.5    55.00  0.28     Sequence
 HLA-DQA10501-DQB10301  587      TLEILDITPCSFGGV  ITPCSFGGV  6        0.3074
1796.7    40.00  0.33     Sequence
 HLA-DQA10501-DQB10301  588      LEILDITPCSFGGVS  ITPCSFGGV  5        0.3351
1331.4    34.00  0.42     Sequence
 HLA-DQA10501-DQB10301  589      EILDITPCSFGGVSV  ITPCSFGGV  4        0.3824
798.0    25.00  0.37     Sequence
 HLA-DQA10501-DQB10301  590      ILDITPCSFGGVSVI  ITPCSFGGV  3        0.4414
421.7    17.00  0.25     Sequence
 HLA-DQA10501-DQB10301  591      LDITPCSFGGVSVIT  CSFGGVSVI  5        0.5124
195.5     9.00  0.34     Sequence         WB
 HLA-DQA10501-DQB10301  592      DITPCSFGGVSVITP  SFGGVSVIT  5        0.5627
113.5     5.50  0.29     Sequence         WB
 HLA-DQA10501-DQB10301  593      ITPCSFGGVSVITPG  FGGVSVITP  5        0.5800
94.1     4.50  0.25     Sequence         WB
 HLA-DQA10501-DQB10301  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.5847
89.4     4.00  0.27     Sequence         WB
 HLA-DQA10501-DQB10301  595      PCSFGGVSVITPGTN  FGGVSVITP  3        0.5874
86.8     4.00  0.24     Sequence         WB
 HLA-DQA10501-DQB10301  596      CSFGGVSVITPGTNT  GGVSVITPG  3        0.5815
92.6     4.50  0.22     Sequence         WB
 HLA-DQA10501-DQB10301  597      SFGGVSVITPGTNTS  GGVSVITPG  2        0.5696
105.3     5.00  0.21     Sequence         WB
 HLA-DQA10501-DQB10301  598      FGGVSVITPGTNTSN  ITPGTNTSN  6        0.5721
102.5     5.00  0.33     Sequence         WB
 HLA-DQA10501-DQB10301  599      GGVSVITPGTNTSNQ  ITPGTNTSN  5        0.5285
164.4     7.50  0.46     Sequence         WB
 HLA-DQA10501-DQB10301  600      GVSVITPGTNTSNQV  ITPGTNTSN  4        0.5073
206.7     9.50  0.50     Sequence         WB
 HLA-DQA10501-DQB10301  601      VSVITPGTNTSNQVA  ITPGTNTSN  3        0.4825
270.2    12.00  0.47     Sequence
```

```
 HLA-DQA10501-DQB10301  602      SVITPGTNTSNQVAV  ITPGTNTSN  2        0.4318
467.4    18.00  0.47     Sequence
 HLA-DQA10501-DQB10301  603      VITPGTNTSNQVAVL  ITPGTNTSN  1        0.3868
760.9    24.00  0.38     Sequence
 HLA-DQA10501-DQB10301  604      ITPGTNTSNQVAVLY  ITPGTNTSN  0        0.3709
903.4    27.00  0.29     Sequence
 HLA-DQA10501-DQB10301  605      TPGTNTSNQVAVLYQ  NTSNQVAVL  4        0.3208
1553.7    37.00  0.19     Sequence
 HLA-DQA10501-DQB10301  606      PGTNTSNQVAVLYQG  NQVAVLYQG  6        0.3946
699.8    23.00  0.40     Sequence
 HLA-DQA10501-DQB10301  607      GTNTSNQVAVLYQGV  NQVAVLYQG  5        0.4263
496.6    19.00  0.51     Sequence
 HLA-DQA10501-DQB10301  608      TNTSNQVAVLYQGVN  NQVAVLYQG  4        0.4254
501.4    19.00  0.56     Sequence
 HLA-DQA10501-DQB10301  609      NTSNQVAVLYQGVNC  NQVAVLYQG  3        0.4182
541.9    20.00  0.61     Sequence
 HLA-DQA10501-DQB10301  610      TSNQVAVLYQGVNCT  NQVAVLYQG  2        0.4120
579.2    21.00  0.51     Sequence
 HLA-DQA10501-DQB10301  611      SNQVAVLYQGVNCTE  NQVAVLYQG  1        0.3813
807.3    25.00  0.41     Sequence
 HLA-DQA10501-DQB10301  612      NQVAVLYQGVNCTEV  NQVAVLYQG  0        0.3808
811.7    25.00  0.31     Sequence
 HLA-DQA10501-DQB10301  613      QVAVLYQGVNCTEVP  YQGVNCTEV  5        0.3307
1396.8    35.00  0.33     Sequence
 HLA-DQA10501-DQB10301  614      VAVLYQGVNCTEVPV  YQGVNCTEV  4        0.3154
1647.4    38.00  0.34     Sequence
 HLA-DQA10501-DQB10301  615      AVLYQGVNCTEVPVA  YQGVNCTEV  3        0.3166
1627.4    38.00  0.32     Sequence
 HLA-DQA10501-DQB10301  616      VLYQGVNCTEVPVAI  VNCTEVPVA  5        0.3445
1202.3    32.00  0.26     Sequence
 HLA-DQA10501-DQB10301  617      LYQGVNCTEVPVAIH  VNCTEVPVA  4        0.3367
1308.6    34.00  0.22     Sequence
 HLA-DQA10501-DQB10301  618      YQGVNCTEVPVAIHA  VNCTEVPVA  3        0.3457
1187.8    32.00  0.25     Sequence
 HLA-DQA10501-DQB10301  619      QGVNCTEVPVAIHAD  NCTEVPVAI  3        0.3291
1420.2    35.00  0.22     Sequence
 HLA-DQA10501-DQB10301  620      GVNCTEVPVAIHADQ  NCTEVPVAI  2        0.3213
1546.3    37.00  0.20     Sequence
 HLA-DQA10501-DQB10301  621      VNCTEVPVAIHADQL  NCTEVPVAI  1        0.3131
1690.1    38.00  0.21     Sequence
 HLA-DQA10501-DQB10301  622      NCTEVPVAIHADQLT  PVAIHADQL  5        0.3066
1812.8    40.00  0.13     Sequence
 HLA-DQA10501-DQB10301  623      CTEVPVAIHADQLTP  PVAIHADQL  4        0.2906
2155.7    44.00  0.17     Sequence
 HLA-DQA10501-DQB10301  624      TEVPVAIHADQLTPT  IHADQLTPT  6        0.2890
2192.9    44.00  0.25     Sequence
 HLA-DQA10501-DQB10301  625      EVPVAIHADQLTPTW  IHADQLTPT  5        0.2718
2642.2    48.00  0.35     Sequence
 HLA-DQA10501-DQB10301  626      VPVAIHADQLTPTWR  IHADQLTPT  4        0.2627
2913.2    55.00  0.36     Sequence
 HLA-DQA10501-DQB10301  627      PVAIHADQLTPTWRV  IHADQLTPT  3        0.2589
3037.4    55.00  0.37     Sequence
 HLA-DQA10501-DQB10301  628      VAIHADQLTPTWRVY  IHADQLTPT  2        0.2519
3276.4    55.00  0.32     Sequence
 HLA-DQA10501-DQB10301  629      AIHADQLTPTWRVYS  IHADQLTPT  1        0.2090
5209.0    70.00  0.29     Sequence
 HLA-DQA10501-DQB10301  630      IHADQLTPTWRVYST  IHADQLTPT  0        0.2116
5064.0    65.00  0.21     Sequence
 HLA-DQA10501-DQB10301  631      HADQLTPTWRVYSTG  TPTWRVYST  5        0.2018
5632.7    70.00  0.22     Sequence
 HLA-DQA10501-DQB10301  632      ADQLTPTWRVYSTGS  TPTWRVYST  4        0.2118
5056.9    65.00  0.27     Sequence
 HLA-DQA10501-DQB10301  633      DQLTPTWRVYSTGSN  TWRVYSTGS  5        0.2816
2375.7    46.00  0.25     Sequence
 HLA-DQA10501-DQB10301  634      QLTPTWRVYSTGSNV  WRVYSTGSN  5        0.3202
1564.3    37.00  0.23     Sequence
```

```
 HLA-DQA10501-DQB10301  635      LTPTWRVYSTGSNVF  RVYSTGSNV  5        0.3777
839.7    26.00  0.19     Sequence
 HLA-DQA10501-DQB10301  636      TPTWRVYSTGSNVFQ  VYSTGSNVF  5        0.3767
848.5    26.00  0.23     Sequence
 HLA-DQA10501-DQB10301  637      PTWRVYSTGSNVFQT  STGSNVFQT  6        0.4196
533.9    20.00  0.28     Sequence
 HLA-DQA10501-DQB10301  638      TWRVYSTGSNVFQTR  STGSNVFQT  5        0.4907
247.2    11.00  0.47     Sequence
 HLA-DQA10501-DQB10301  639      WRVYSTGSNVFQTRA  STGSNVFQT  4        0.5018
219.4    10.00  0.50     Sequence
 HLA-DQA10501-DQB10301  640      RVYSTGSNVFQTRAG  STGSNVFQT  3        0.4640
330.0    14.00  0.50     Sequence
 HLA-DQA10501-DQB10301  641      VYSTGSNVFQTRAGC  STGSNVFQT  2        0.4556
361.3    15.00  0.54     Sequence
 HLA-DQA10501-DQB10301  642      YSTGSNVFQTRAGCL  STGSNVFQT  1        0.4173
547.3    20.00  0.50     Sequence
 HLA-DQA10501-DQB10301  643      STGSNVFQTRAGCLI  STGSNVFQT  0        0.3924
716.5    24.00  0.44     Sequence
 HLA-DQA10501-DQB10301  644      TGSNVFQTRAGCLIG  QTRAGCLIG  6        0.3641
973.0    28.00  0.23     Sequence
 HLA-DQA10501-DQB10301  645      GSNVFQTRAGCLIGA  TRAGCLIGA  6        0.3988
668.1    22.00  0.38     Sequence
 HLA-DQA10501-DQB10301  646      SNVFQTRAGCLIGAE  TRAGCLIGA  5        0.5257
169.4     8.00  0.46     Sequence         WB
 HLA-DQA10501-DQB10301  647      NVFQTRAGCLIGAEY  TRAGCLIGA  4        0.5377
148.6     7.00  0.43     Sequence         WB
 HLA-DQA10501-DQB10301  648      VFQTRAGCLIGAEYV  TRAGCLIGA  3        0.5453
136.9     6.50  0.41     Sequence         WB
 HLA-DQA10501-DQB10301  649      FQTRAGCLIGAEYVN  TRAGCLIGA  2        0.5509
128.9     6.00  0.37     Sequence         WB
 HLA-DQA10501-DQB10301  650      QTRAGCLIGAEYVNN  TRAGCLIGA  1        0.5294
162.7     7.50  0.28     Sequence         WB
 HLA-DQA10501-DQB10301  651      TRAGCLIGAEYVNNS  TRAGCLIGA  0        0.5189
182.3     8.50  0.26     Sequence         WB
 HLA-DQA10501-DQB10301  652      RAGCLIGAEYVNNSY  IGAEYVNNS  5        0.5022
218.3    10.00  0.20     Sequence
 HLA-DQA10501-DQB10301  653      AGCLIGAEYVNNSYE  IGAEYVNNS  4        0.4027
640.6    22.00  0.37     Sequence
 HLA-DQA10501-DQB10301  654      GCLIGAEYVNNSYEC  IGAEYVNNS  3        0.3697
915.3    27.00  0.43     Sequence
 HLA-DQA10501-DQB10301  655      CLIGAEYVNNSYECD  IGAEYVNNS  2        0.3277
1442.0    35.00  0.41     Sequence
 HLA-DQA10501-DQB10301  656      LIGAEYVNNSYECDI  IGAEYVNNS  1        0.2724
2623.6    48.00  0.44     Sequence
 HLA-DQA10501-DQB10301  657      IGAEYVNNSYECDIP  IGAEYVNNS  0        0.2509
3310.1    55.00  0.41     Sequence
 HLA-DQA10501-DQB10301  658      GAEYVNNSYECDIPI  VNNSYECDI  4        0.2158
4840.5    65.00  0.25     Sequence
 HLA-DQA10501-DQB10301  659      AEYVNNSYECDIPIG  SYECDIPIG  6        0.1885
6505.3    75.00  0.34     Sequence
 HLA-DQA10501-DQB10301  660      EYVNNSYECDIPIGA  SYECDIPIG  5        0.2312
4096.7    60.00  0.43     Sequence
 HLA-DQA10501-DQB10301  661      YVNNSYECDIPIGAG  SYECDIPIG  4        0.2634
2891.5    50.00  0.34     Sequence
 HLA-DQA10501-DQB10301  662      VNNSYECDIPIGAGI  SYECDIPIG  3        0.2849
2291.6    45.00  0.26     Sequence
 HLA-DQA10501-DQB10301  663      NNSYECDIPIGAGIC  ECDIPIGAG  4        0.3182
1598.4    37.00  0.20     Sequence
 HLA-DQA10501-DQB10301  664      NSYECDIPIGAGICA  IPIGAGICA  6        0.3898
736.4    24.00  0.22     Sequence
 HLA-DQA10501-DQB10301  665      SYECDIPIGAGICAS  PIGAGICAS  6        0.5456
136.6     6.50  0.37     Sequence         WB
 HLA-DQA10501-DQB10301  666      YECDIPIGAGICASY  PIGAGICAS  5        0.6536
42.4     1.40  0.50     Sequence         SB
 HLA-DQA10501-DQB10301  667      ECDIPIGAGICASYQ  PIGAGICAS  4        0.6667
36.8     1.10  0.46     Sequence         SB
```

```
 HLA-DQA10501-DQB10301  668      CDIPIGAGICASYQT  PIGAGICAS  3        0.6825
31.0     0.80  0.43     Sequence         SB
 HLA-DQA10501-DQB10301  669      DIPIGAGICASYQTQ  PIGAGICAS  2        0.6831
30.8     0.80  0.40     Sequence         SB
 HLA-DQA10501-DQB10301  670      IPIGAGICASYQTQT  PIGAGICAS  1        0.6746
33.8     1.00  0.40     Sequence         SB
 HLA-DQA10501-DQB10301  671      PIGAGICASYQTQTN  PIGAGICAS  0        0.6451
46.5     1.70  0.39     Sequence         SB
 HLA-DQA10501-DQB10301  672      IGAGICASYQTQTNS  IGAGICASY  0        0.5669
108.4     5.00  0.29     Sequence         WB
 HLA-DQA10501-DQB10301  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.4264
495.9    19.00  0.36     Sequence
 HLA-DQA10501-DQB10301  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.3505
1127.2    31.00  0.32     Sequence
 HLA-DQA10501-DQB10301  675      GICASYQTQTNSPRR  ICASYQTQT  1        0.2548
3175.7    55.00  0.32     Sequence
 HLA-DQA10501-DQB10301  676      ICASYQTQTNSPRRA  ICASYQTQT  0        0.2138
4947.7    65.00  0.28     Sequence
 HLA-DQA10501-DQB10301  677      CASYQTQTNSPRRAR  TQTNSPRRA  5        0.1965
5965.7    70.00  0.29     Sequence
 HLA-DQA10501-DQB10301  678      ASYQTQTNSPRRARS  TQTNSPRRA  4        0.1978
5884.3    70.00  0.35     Sequence
 HLA-DQA10501-DQB10301  679      SYQTQTNSPRRARSV  TQTNSPRRA  3        0.2842
2309.9    45.00  0.18     Sequence
 HLA-DQA10501-DQB10301  680      YQTQTNSPRRARSVA  NSPRRARSV  5        0.3146
1662.4    38.00  0.30     Sequence
 HLA-DQA10501-DQB10301  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.4176
545.3    20.00  0.47     Sequence
 HLA-DQA10501-DQB10301  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.4918
244.3    11.00  0.62     Sequence
 HLA-DQA10501-DQB10301  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.5025
217.6    10.00  0.59     Sequence
 HLA-DQA10501-DQB10301  684      TNSPRRARSVASQSI  PRRARSVAS  3        0.5183
183.4     8.50  0.52     Sequence         WB
 HLA-DQA10501-DQB10301  685      NSPRRARSVASQSII  PRRARSVAS  2        0.5037
214.9     9.50  0.47     Sequence         WB
 HLA-DQA10501-DQB10301  686      SPRRARSVASQSIIA  PRRARSVAS  1        0.4804
276.5    12.00  0.40     Sequence
 HLA-DQA10501-DQB10301  687      PRRARSVASQSIIAY  SVASQSIIA  5        0.4781
283.3    12.00  0.19     Sequence
 HLA-DQA10501-DQB10301  688      RRARSVASQSIIAYT  SVASQSIIA  4        0.4754
291.8    13.00  0.20     Sequence
 HLA-DQA10501-DQB10301  689      RARSVASQSIIAYTM  ASQSIIAYT  5        0.5143
191.6     8.50  0.41     Sequence         WB
 HLA-DQA10501-DQB10301  690      ARSVASQSIIAYTMS  ASQSIIAYT  4        0.5027
217.1    10.00  0.43     Sequence
 HLA-DQA10501-DQB10301  691      RSVASQSIIAYTMSL  ASQSIIAYT  3        0.4870
257.3    11.00  0.49     Sequence
 HLA-DQA10501-DQB10301  692      SVASQSIIAYTMSLG  ASQSIIAYT  2        0.4881
254.2    11.00  0.49     Sequence
 HLA-DQA10501-DQB10301  693      VASQSIIAYTMSLGA  ASQSIIAYT  1        0.4869
257.6    11.00  0.38     Sequence
 HLA-DQA10501-DQB10301  694      ASQSIIAYTMSLGAE  ASQSIIAYT  0        0.4510
379.9    15.00  0.31     Sequence
 HLA-DQA10501-DQB10301  695      SQSIIAYTMSLGAEN  IAYTMSLGA  4        0.4362
445.9    17.00  0.28     Sequence
 HLA-DQA10501-DQB10301  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.4152
560.0    20.00  0.25     Sequence
 HLA-DQA10501-DQB10301  697      SIIAYTMSLGAENSV  MSLGAENSV  6        0.4593
347.5    14.00  0.31     Sequence
 HLA-DQA10501-DQB10301  698      IIAYTMSLGAENSVA  MSLGAENSV  5        0.4938
239.1    11.00  0.41     Sequence
 HLA-DQA10501-DQB10301  699      IAYTMSLGAENSVAY  MSLGAENSV  4        0.5153
189.5     8.50  0.35     Sequence         WB
 HLA-DQA10501-DQB10301  700      AYTMSLGAENSVAYS  MSLGAENSV  3        0.5189
182.3     8.50  0.37     Sequence         WB
```

```
 HLA-DQA10501-DQB10301  701      YTMSLGAENSVAYSN  MSLGAENSV  2        0.5573
120.3     5.50  0.28     Sequence        WB
 HLA-DQA10501-DQB10301  702      TMSLGAENSVAYSNN  AENSVAYSN  5        0.5355
152.3     7.00  0.24     Sequence        WB
 HLA-DQA10501-DQB10301  703      MSLGAENSVAYSNNS  AENSVAYSN  4        0.5247
171.2     8.00  0.30     Sequence        WB
 HLA-DQA10501-DQB10301  704      SLGAENSVAYSNNSI  AENSVAYSN  3        0.5023
218.1    10.00  0.37     Sequence
 HLA-DQA10501-DQB10301  705      LGAENSVAYSNNSIA  AENSVAYSN  2        0.4960
233.4    11.00  0.35     Sequence
 HLA-DQA10501-DQB10301  706      GAENSVAYSNNSIAI  NSVAYSNNS  3        0.4912
245.9    11.00  0.24     Sequence
 HLA-DQA10501-DQB10301  707      AENSVAYSNNSIAIP  AENSVAYSN  0        0.4749
293.4    13.00  0.28     Sequence
 HLA-DQA10501-DQB10301  708      ENSVAYSNNSIAIPT  SNNSIAIPT  6        0.4543
366.5    15.00  0.26     Sequence
 HLA-DQA10501-DQB10301  709      NSVAYSNNSIAIPTN  SNNSIAIPT  5        0.4788
281.2    12.00  0.33     Sequence
 HLA-DQA10501-DQB10301  710      SVAYSNNSIAIPTNF  SNNSIAIPT  4        0.4962
233.0    11.00  0.30     Sequence
 HLA-DQA10501-DQB10301  711      VAYSNNSIAIPTNFT  SNNSIAIPT  3        0.5052
211.4     9.50  0.28     Sequence        WB
 HLA-DQA10501-DQB10301  712      AYSNNSIAIPTNFTI  NSIAIPTNF  4        0.4915
245.2    11.00  0.24     Sequence
 HLA-DQA10501-DQB10301  713      YSNNSIAIPTNFTIS  NSIAIPTNF  3        0.4758
290.6    13.00  0.27     Sequence
 HLA-DQA10501-DQB10301  714      SNNSIAIPTNFTISV  NSIAIPTNF  2        0.4274
490.2    18.00  0.27     Sequence
 HLA-DQA10501-DQB10301  715      NNSIAIPTNFTISVT  NSIAIPTNF  1        0.3804
815.7    25.00  0.24     Sequence
 HLA-DQA10501-DQB10301  716      NSIAIPTNFTISVTT  PTNFTISVT  5        0.3776
840.4    26.00  0.25     Sequence
 HLA-DQA10501-DQB10301  717      SIAIPTNFTISVTTE  PTNFTISVT  4        0.3431
1220.9    32.00  0.32     Sequence
 HLA-DQA10501-DQB10301  718      IAIPTNFTISVTTEI  PTNFTISVT  3        0.3402
1260.2    33.00  0.35     Sequence
 HLA-DQA10501-DQB10301  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.3537
1089.0    30.00  0.38     Sequence
 HLA-DQA10501-DQB10301  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.3535
1091.4    30.00  0.40     Sequence
 HLA-DQA10501-DQB10301  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.3451
1195.3    32.00  0.38     Sequence
 HLA-DQA10501-DQB10301  722      TNFTISVTTEILPVS  FTISVTTEI  2        0.3254
1479.5    36.00  0.38     Sequence
 HLA-DQA10501-DQB10301  723      NFTISVTTEILPVSM  FTISVTTEI  1        0.3137
1679.3    38.00  0.35     Sequence
 HLA-DQA10501-DQB10301  724      FTISVTTEILPVSMT  FTISVTTEI  0        0.3458
1186.4    32.00  0.19     Sequence
 HLA-DQA10501-DQB10301  725      TISVTTEILPVSMTK  TEILPVSMT  5        0.3349
1334.2    34.00  0.29     Sequence
 HLA-DQA10501-DQB10301  726      ISVTTEILPVSMTKT  TEILPVSMT  4        0.3396
1268.8    33.00  0.28     Sequence
 HLA-DQA10501-DQB10301  727      SVTTEILPVSMTKTS  TEILPVSMT  3        0.3339
1349.0    34.00  0.29     Sequence
 HLA-DQA10501-DQB10301  728      VTTEILPVSMTKTSV  TEILPVSMT  2        0.3355
1325.7    34.00  0.28     Sequence
 HLA-DQA10501-DQB10301  729      TTEILPVSMTKTSVD  ILPVSMTKT  3        0.3361
1317.9    34.00  0.23     Sequence
 HLA-DQA10501-DQB10301  730      TEILPVSMTKTSVDC  ILPVSMTKT  2        0.3223
1528.9    36.00  0.22     Sequence
 HLA-DQA10501-DQB10301  731      EILPVSMTKTSVDCT  VSMTKTSVD  4        0.2654
2831.6    50.00  0.23     Sequence
 HLA-DQA10501-DQB10301  732      ILPVSMTKTSVDCTM  VSMTKTSVD  3        0.2667
2792.4    50.00  0.25     Sequence
 HLA-DQA10501-DQB10301  733      LPVSMTKTSVDCTMY  MTKTSVDCT  4        0.2630
2904.3    50.00  0.28     Sequence
```

```
 HLA-DQA10501-DQB10301  734      PVSMTKTSVDCTMYI  MTKTSVDCT  3        0.2507
3318.5    55.00  0.29     Sequence
 HLA-DQA10501-DQB10301  735      VSMTKTSVDCTMYIC  MTKTSVDCT  2        0.2377
3821.3    60.00  0.25     Sequence
 HLA-DQA10501-DQB10301  736      SMTKTSVDCTMYICG  MTKTSVDCT  1        0.2035
5529.6    70.00  0.28     Sequence
 HLA-DQA10501-DQB10301  737      MTKTSVDCTMYICGD  MTKTSVDCT  0        0.1941
6121.4    70.00  0.23     Sequence
 HLA-DQA10501-DQB10301  738      TKTSVDCTMYICGDS  SVDCTMYIC  3        0.1739
7621.3    80.00  0.16     Sequence
 HLA-DQA10501-DQB10301  739      KTSVDCTMYICGDST  CTMYICGDS  5        0.1749
7538.1    80.00  0.19     Sequence
 HLA-DQA10501-DQB10301  740      TSVDCTMYICGDSTE  CTMYICGDS  4        0.1756
7477.6    75.00  0.19     Sequence
 HLA-DQA10501-DQB10301  741      SVDCTMYICGDSTEC  YICGDSTEC  6        0.1879
6549.6    75.00  0.22     Sequence
 HLA-DQA10501-DQB10301  742      VDCTMYICGDSTECS  YICGDSTEC  5        0.2704
2681.5    49.00  0.34     Sequence
 HLA-DQA10501-DQB10301  743      DCTMYICGDSTECSN  ICGDSTECS  5        0.2956
2041.5    42.00  0.31     Sequence
 HLA-DQA10501-DQB10301  744      CTMYICGDSTECSNL  ICGDSTECS  4        0.3034
1877.1    41.00  0.29     Sequence
 HLA-DQA10501-DQB10301  745      TMYICGDSTECSNLL  ICGDSTECS  3        0.2986
1977.2    42.00  0.30     Sequence
 HLA-DQA10501-DQB10301  746      MYICGDSTECSNLLL  ICGDSTECS  2        0.2824
2354.7    46.00  0.31     Sequence
 HLA-DQA10501-DQB10301  747      YICGDSTECSNLLLQ  ICGDSTECS  1        0.2664
2798.7    50.00  0.28     Sequence
 HLA-DQA10501-DQB10301  748      ICGDSTECSNLLLQY  ICGDSTECS  0        0.2311
4100.8    60.00  0.28     Sequence
 HLA-DQA10501-DQB10301  749      CGDSTECSNLLLQYG  CSNLLLQYG  6        0.1920
6263.8    75.00  0.22     Sequence
 HLA-DQA10501-DQB10301  750      GDSTECSNLLLQYGS  CSNLLLQYG  5        0.2018
5632.6    70.00  0.41     Sequence
 HLA-DQA10501-DQB10301  751      DSTECSNLLLQYGSF  CSNLLLQYG  4        0.2347
3946.7    60.00  0.38     Sequence
 HLA-DQA10501-DQB10301  752      STECSNLLLQYGSFC  CSNLLLQYG  3        0.2470
3455.0    55.00  0.39     Sequence
 HLA-DQA10501-DQB10301  753      TECSNLLLQYGSFCT  CSNLLLQYG  2        0.2610
2968.1    55.00  0.35     Sequence
 HLA-DQA10501-DQB10301  754      ECSNLLLQYGSFCTQ  LQYGSFCTQ  6        0.2950
2054.2    43.00  0.26     Sequence
 HLA-DQA10501-DQB10301  755      CSNLLLQYGSFCTQL  LQYGSFCTQ  5        0.3130
1691.0    38.00  0.38     Sequence
 HLA-DQA10501-DQB10301  756      SNLLLQYGSFCTQLN  LQYGSFCTQ  4        0.3080
1786.0    40.00  0.38     Sequence
 HLA-DQA10501-DQB10301  757      NLLLQYGSFCTQLNR  LQYGSFCTQ  3        0.3064
1815.8    40.00  0.34     Sequence
 HLA-DQA10501-DQB10301  758      LLLQYGSFCTQLNRA  LQYGSFCTQ  2        0.2938
2082.3    43.00  0.29     Sequence
 HLA-DQA10501-DQB10301  759      LLQYGSFCTQLNRAL  YGSFCTQLN  3        0.2951
2053.0    43.00  0.25     Sequence
 HLA-DQA10501-DQB10301  760      LQYGSFCTQLNRALT  YGSFCTQLN  2        0.2729
2609.8    48.00  0.28     Sequence
 HLA-DQA10501-DQB10301  761      QYGSFCTQLNRALTG  YGSFCTQLN  1        0.2822
2361.2    46.00  0.23     Sequence
 HLA-DQA10501-DQB10301  762      YGSFCTQLNRALTGI  TQLNRALTG  5        0.2845
2302.9    45.00  0.19     Sequence
 HLA-DQA10501-DQB10301  763      GSFCTQLNRALTGIA  LNRALTGIA  6        0.2970
2011.7    42.00  0.29     Sequence
 HLA-DQA10501-DQB10301  764      SFCTQLNRALTGIAV  LNRALTGIA  5        0.4151
560.0    20.00  0.42     Sequence
 HLA-DQA10501-DQB10301  765      FCTQLNRALTGIAVE  LNRALTGIA  4        0.4310
471.8    18.00  0.38     Sequence
 HLA-DQA10501-DQB10301  766      CTQLNRALTGIAVEQ  LNRALTGIA  3        0.4189
537.9    20.00  0.35     Sequence
```

```
 HLA-DQA10501-DQB10301  767      TQLNRALTGIAVEQD  LNRALTGIA  2        0.4206
527.9    19.00  0.31     Sequence
 HLA-DQA10501-DQB10301  768      QLNRALTGIAVEQDK  ALTGIAVEQ  4        0.4069
612.3    21.00  0.22     Sequence
 HLA-DQA10501-DQB10301  769      LNRALTGIAVEQDKN  ALTGIAVEQ  3        0.3998
660.9    22.00  0.21     Sequence
 HLA-DQA10501-DQB10301  770      NRALTGIAVEQDKNT  ALTGIAVEQ  2        0.3546
1078.0    30.00  0.22     Sequence
 HLA-DQA10501-DQB10301  771      RALTGIAVEQDKNTQ  LTGIAVEQD  2        0.2478
3425.8    55.00  0.21     Sequence
 HLA-DQA10501-DQB10301  772      ALTGIAVEQDKNTQE  TGIAVEQDK  2        0.2016
5646.4    70.00  0.25     Sequence
 HLA-DQA10501-DQB10301  773      LTGIAVEQDKNTQEV  LTGIAVEQD  0        0.1638
8499.7    80.00  0.30     Sequence
 HLA-DQA10501-DQB10301  774      TGIAVEQDKNTQEVF  TGIAVEQDK  0        0.1226
13276.2    90.00  0.32     Sequence
 HLA-DQA10501-DQB10301  775      GIAVEQDKNTQEVFA  EQDKNTQEV  4        0.0869
19519.8   100.00  0.25     Sequence
 HLA-DQA10501-DQB10301  776      IAVEQDKNTQEVFAQ  KNTQEVFAQ  6        0.1384
11189.1    90.00  0.38     Sequence
 HLA-DQA10501-DQB10301  777      AVEQDKNTQEVFAQV  KNTQEVFAQ  5        0.1646
8423.7    80.00  0.41     Sequence
 HLA-DQA10501-DQB10301  778      VEQDKNTQEVFAQVK  KNTQEVFAQ  4        0.1969
5938.6    70.00  0.33     Sequence
 HLA-DQA10501-DQB10301  779      EQDKNTQEVFAQVKQ  KNTQEVFAQ  3        0.1997
5761.0    70.00  0.29     Sequence
 HLA-DQA10501-DQB10301  780      QDKNTQEVFAQVKQI  EVFAQVKQI  6        0.2214
4556.9    65.00  0.23     Sequence
 HLA-DQA10501-DQB10301  781      DKNTQEVFAQVKQIY  EVFAQVKQI  5        0.2790
2443.9    46.00  0.38     Sequence
 HLA-DQA10501-DQB10301  782      KNTQEVFAQVKQIYK  EVFAQVKQI  4        0.2991
1965.1    42.00  0.33     Sequence
 HLA-DQA10501-DQB10301  783      NTQEVFAQVKQIYKT  EVFAQVKQI  3        0.3031
1881.7    41.00  0.30     Sequence
 HLA-DQA10501-DQB10301  784      TQEVFAQVKQIYKTP  EVFAQVKQI  2        0.2977
1995.1    42.00  0.23     Sequence
 HLA-DQA10501-DQB10301  785      QEVFAQVKQIYKTPP  AQVKQIYKT  4        0.2880
2215.8    44.00  0.21     Sequence
 HLA-DQA10501-DQB10301  786      EVFAQVKQIYKTPPI  AQVKQIYKT  3        0.2949
2056.1    43.00  0.19     Sequence
 HLA-DQA10501-DQB10301  787      VFAQVKQIYKTPPIK  AQVKQIYKT  2        0.2858
2268.9    45.00  0.20     Sequence
 HLA-DQA10501-DQB10301  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6        0.2308
4117.7    60.00  0.21     Sequence
 HLA-DQA10501-DQB10301  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.2203
4612.0    65.00  0.37     Sequence
 HLA-DQA10501-DQB10301  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.2039
5506.4    70.00  0.42     Sequence
 HLA-DQA10501-DQB10301  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.1956
6026.2    70.00  0.40     Sequence
 HLA-DQA10501-DQB10301  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.1911
6323.5    75.00  0.37     Sequence
 HLA-DQA10501-DQB10301  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.1662
8278.8    80.00  0.33     Sequence
 HLA-DQA10501-DQB10301  794      IYKTPPIKDFGGFNF  IYKTPPIKD  0        0.1796
7164.1    75.00  0.22     Sequence
 HLA-DQA10501-DQB10301  795      YKTPPIKDFGGFNFS  KDFGGFNFS  6        0.2479
3422.1    55.00  0.28     Sequence
 HLA-DQA10501-DQB10301  796      KTPPIKDFGGFNFSQ  KDFGGFNFS  5        0.2709
2667.6    48.00  0.38     Sequence
 HLA-DQA10501-DQB10301  797      TPPIKDFGGFNFSQI  KDFGGFNFS  4        0.3326
1367.8    34.00  0.31     Sequence
 HLA-DQA10501-DQB10301  798      PPIKDFGGFNFSQIL  KDFGGFNFS  3        0.3551
1072.9    30.00  0.30     Sequence
 HLA-DQA10501-DQB10301  799      PIKDFGGFNFSQILP  KDFGGFNFS  2        0.3600
1017.1    29.00  0.29     Sequence
```

```
 HLA-DQA10501-DQB10301  800      IKDFGGFNFSQILPD  FNFSQILPD  6        0.3699
913.5    27.00  0.26     Sequence
 HLA-DQA10501-DQB10301  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.3585
1034.2    29.00  0.33     Sequence
 HLA-DQA10501-DQB10301  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.3452
1194.1    32.00  0.35     Sequence
 HLA-DQA10501-DQB10301  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.3362
1315.5    34.00  0.38     Sequence
 HLA-DQA10501-DQB10301  804      GGFNFSQILPDPSKP  FSQILPDPS  4        0.2665
2796.7    50.00  0.32     Sequence
 HLA-DQA10501-DQB10301  805      GFNFSQILPDPSKPS  FSQILPDPS  3        0.2678
2758.1    49.00  0.31     Sequence
 HLA-DQA10501-DQB10301  806      FNFSQILPDPSKPSK  FSQILPDPS  2        0.2448
3537.2    55.00  0.27     Sequence
 HLA-DQA10501-DQB10301  807      NFSQILPDPSKPSKR  FSQILPDPS  1        0.2289
4202.6    60.00  0.23     Sequence
 HLA-DQA10501-DQB10301  808      FSQILPDPSKPSKRS  PDPSKPSKR  5        0.2274
4271.9    60.00  0.30     Sequence
 HLA-DQA10501-DQB10301  809      SQILPDPSKPSKRSF  PDPSKPSKR  4        0.2159
4836.5    65.00  0.38     Sequence
 HLA-DQA10501-DQB10301  810      QILPDPSKPSKRSFI  PDPSKPSKR  3        0.2138
4949.0    65.00  0.40     Sequence
 HLA-DQA10501-DQB10301  811      ILPDPSKPSKRSFIE  PDPSKPSKR  2        0.2225
4500.8    65.00  0.35     Sequence
 HLA-DQA10501-DQB10301  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.1923
6241.3    70.00  0.29     Sequence
 HLA-DQA10501-DQB10301  813      PDPSKPSKRSFIEDL  SKPSKRSFI  3        0.1846
6784.0    75.00  0.32     Sequence
 HLA-DQA10501-DQB10301  814      DPSKPSKRSFIEDLL  SKPSKRSFI  2        0.1553
9318.7    85.00  0.37     Sequence
 HLA-DQA10501-DQB10301  815      PSKPSKRSFIEDLLF  SKPSKRSFI  1        0.1524
9610.0    85.00  0.34     Sequence
 HLA-DQA10501-DQB10301  816      SKPSKRSFIEDLLFN  SKPSKRSFI  0        0.1382
11212.4    90.00  0.32     Sequence
 HLA-DQA10501-DQB10301  817      KPSKRSFIEDLLFNK  SFIEDLLFN  5        0.1091
15353.4    95.00  0.22     Sequence
 HLA-DQA10501-DQB10301  818      PSKRSFIEDLLFNKV  SFIEDLLFN  4        0.1207
13547.8    95.00  0.21     Sequence
 HLA-DQA10501-DQB10301  819      SKRSFIEDLLFNKVT  IEDLLFNKV  5        0.1370
11357.7    90.00  0.34     Sequence
 HLA-DQA10501-DQB10301  820      KRSFIEDLLFNKVTL  IEDLLFNKV  4        0.1372
11330.3    90.00  0.35     Sequence
 HLA-DQA10501-DQB10301  821      RSFIEDLLFNKVTLA  LLFNKVTLA  6        0.1951
6057.0    70.00  0.35     Sequence
 HLA-DQA10501-DQB10301  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5        0.2316
4079.5    60.00  0.42     Sequence
 HLA-DQA10501-DQB10301  823      FIEDLLFNKVTLADA  LLFNKVTLA  4        0.2617
2947.0    55.00  0.31     Sequence
 HLA-DQA10501-DQB10301  824      IEDLLFNKVTLADAG  FNKVTLADA  5        0.2986
1975.7    42.00  0.31     Sequence
 HLA-DQA10501-DQB10301  825      EDLLFNKVTLADAGF  FNKVTLADA  4        0.3302
1404.6    35.00  0.27     Sequence
 HLA-DQA10501-DQB10301  826      DLLFNKVTLADAGFI  VTLADAGFI  6        0.3717
896.5    27.00  0.28     Sequence
 HLA-DQA10501-DQB10301  827      LLFNKVTLADAGFIK  VTLADAGFI  5        0.4095
595.4    21.00  0.41     Sequence
 HLA-DQA10501-DQB10301  828      LFNKVTLADAGFIKQ  VTLADAGFI  4        0.4089
599.3    21.00  0.43     Sequence
 HLA-DQA10501-DQB10301  829      FNKVTLADAGFIKQY  VTLADAGFI  3        0.4418
419.6    17.00  0.34     Sequence
 HLA-DQA10501-DQB10301  830      NKVTLADAGFIKQYG  ADAGFIKQY  5        0.4429
414.8    16.00  0.32     Sequence
 HLA-DQA10501-DQB10301  831      KVTLADAGFIKQYGD  ADAGFIKQY  4        0.4328
462.9    18.00  0.34     Sequence
 HLA-DQA10501-DQB10301  832      VTLADAGFIKQYGDC  ADAGFIKQY  3        0.4244
506.9    19.00  0.37     Sequence
```

```
 HLA-DQA10501-DQB10301  833      TLADAGFIKQYGDCL  ADAGFIKQY  2        0.3810
810.2    25.00  0.35     Sequence
 HLA-DQA10501-DQB10301  834      LADAGFIKQYGDCLG  ADAGFIKQY  1        0.3365
1312.0    34.00  0.32     Sequence
 HLA-DQA10501-DQB10301  835      ADAGFIKQYGDCLGD  ADAGFIKQY  0        0.3003
1939.7    41.00  0.22     Sequence
 HLA-DQA10501-DQB10301  836      DAGFIKQYGDCLGDI  KQYGDCLGD  5        0.2715
2648.4    48.00  0.35     Sequence
 HLA-DQA10501-DQB10301  837      AGFIKQYGDCLGDIA  KQYGDCLGD  4        0.2630
2905.0    50.00  0.35     Sequence
 HLA-DQA10501-DQB10301  838      GFIKQYGDCLGDIAA  KQYGDCLGD  3        0.2606
2980.2    55.00  0.33     Sequence
 HLA-DQA10501-DQB10301  839      FIKQYGDCLGDIAAR  DCLGDIAAR  6        0.2605
2984.5    55.00  0.24     Sequence
 HLA-DQA10501-DQB10301  840      IKQYGDCLGDIAARD  DCLGDIAAR  5        0.2676
2764.6    49.00  0.38     Sequence
 HLA-DQA10501-DQB10301  841      KQYGDCLGDIAARDL  DCLGDIAAR  4        0.2594
3021.7    55.00  0.40     Sequence
 HLA-DQA10501-DQB10301  842      QYGDCLGDIAARDLI  DCLGDIAAR  3        0.2810
2391.9    46.00  0.32     Sequence
 HLA-DQA10501-DQB10301  843      YGDCLGDIAARDLIC  DCLGDIAAR  2        0.2794
2433.5    46.00  0.32     Sequence
 HLA-DQA10501-DQB10301  844      GDCLGDIAARDLICA  IAARDLICA  6        0.2801
2413.5    46.00  0.23     Sequence
 HLA-DQA10501-DQB10301  845      DCLGDIAARDLICAQ  IAARDLICA  5        0.2803
2407.8    46.00  0.29     Sequence
 HLA-DQA10501-DQB10301  846      CLGDIAARDLICAQK  IAARDLICA  4        0.2695
2708.8    49.00  0.31     Sequence
 HLA-DQA10501-DQB10301  847      LGDIAARDLICAQKF  IAARDLICA  3        0.2601
2999.1    55.00  0.35     Sequence
 HLA-DQA10501-DQB10301  848      GDIAARDLICAQKFN  IAARDLICA  2        0.2531
3234.8    55.00  0.36     Sequence
 HLA-DQA10501-DQB10301  849      DIAARDLICAQKFNG  IAARDLICA  1        0.2175
4752.4    65.00  0.32     Sequence
 HLA-DQA10501-DQB10301  850      IAARDLICAQKFNGL  LICAQKFNG  5        0.2406
3700.7    60.00  0.24     Sequence
 HLA-DQA10501-DQB10301  851      AARDLICAQKFNGLT  ICAQKFNGL  5        0.2238
4439.1    65.00  0.40     Sequence
 HLA-DQA10501-DQB10301  852      ARDLICAQKFNGLTV  ICAQKFNGL  4        0.2505
3325.3    55.00  0.37     Sequence
 HLA-DQA10501-DQB10301  853      RDLICAQKFNGLTVL  ICAQKFNGL  3        0.2687
2729.9    49.00  0.37     Sequence
 HLA-DQA10501-DQB10301  854      DLICAQKFNGLTVLP  ICAQKFNGL  2        0.2794
2431.7    46.00  0.31     Sequence
 HLA-DQA10501-DQB10301  855      LICAQKFNGLTVLPP  KFNGLTVLP  5        0.3795
823.3    26.00  0.28     Sequence
 HLA-DQA10501-DQB10301  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.3903
732.9    24.00  0.32     Sequence
 HLA-DQA10501-DQB10301  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.3843
781.6    25.00  0.37     Sequence
 HLA-DQA10501-DQB10301  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.3873
756.6    24.00  0.34     Sequence
 HLA-DQA10501-DQB10301  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.3690
922.3    27.00  0.32     Sequence
 HLA-DQA10501-DQB10301  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1        0.3588
1030.0    29.00  0.33     Sequence
 HLA-DQA10501-DQB10301  861      FNGLTVLPPLLTDEM  FNGLTVLPP  0        0.3288
1425.6    35.00  0.33     Sequence
 HLA-DQA10501-DQB10301  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.1644
8439.3    80.00  0.29     Sequence
 HLA-DQA10501-DQB10301  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.1333
11813.6    90.00  0.31     Sequence
 HLA-DQA10501-DQB10301  864      LTVLPPLLTDEMIAQ  LTVLPPLLT  0        0.1170
14095.7    95.00  0.29     Sequence
 HLA-DQA10501-DQB10301  865      TVLPPLLTDEMIAQY  PLLTDEMIA  4        0.0794
21176.9   100.00  0.22     Sequence
```

```
 HLA-DQA10501-DQB10301  866      VLPPLLTDEMIAQYT  LTDEMIAQY  5        0.1260
12790.2    90.00  0.28     Sequence
 HLA-DQA10501-DQB10301  867      LPPLLTDEMIAQYTS  TDEMIAQYT  5        0.1475
10131.1    85.00  0.31     Sequence
 HLA-DQA10501-DQB10301  868      PPLLTDEMIAQYTSA  EMIAQYTSA  6        0.1995
5776.2    70.00  0.34     Sequence
 HLA-DQA10501-DQB10301  869      PLLTDEMIAQYTSAL  EMIAQYTSA  5        0.2588
3041.5    55.00  0.46     Sequence
 HLA-DQA10501-DQB10301  870      LLTDEMIAQYTSALL  EMIAQYTSA  4        0.2872
2235.7    44.00  0.38     Sequence
 HLA-DQA10501-DQB10301  871      LTDEMIAQYTSALLA  AQYTSALLA  6        0.3665
948.3    28.00  0.30    Sequence
 HLA-DQA10501-DQB10301  872      TDEMIAQYTSALLAG  AQYTSALLA  5        0.4400
428.2    17.00  0.32    Sequence
 HLA-DQA10501-DQB10301  873      DEMIAQYTSALLAGT  YTSALLAGT  6        0.5343
154.3     7.00  0.44    Sequence         WB
 HLA-DQA10501-DQB10301  874      EMIAQYTSALLAGTI  YTSALLAGT  5        0.6156
64.0     3.00  0.49    Sequence         WB
 HLA-DQA10501-DQB10301  875      MIAQYTSALLAGTIT  YTSALLAGT  4        0.6519
43.2     1.50  0.43    Sequence         SB
 HLA-DQA10501-DQB10301  876      IAQYTSALLAGTITS  YTSALLAGT  3        0.6631
38.3     1.20  0.38    Sequence         SB
 HLA-DQA10501-DQB10301  877      AQYTSALLAGTITSG  LLAGTITSG  6        0.7162
21.5     0.40  0.46    Sequence         SB
 HLA-DQA10501-DQB10301  878      QYTSALLAGTITSGW  LLAGTITSG  5        0.7322
18.1     0.25  0.57    Sequence         SB
 HLA-DQA10501-DQB10301  879      YTSALLAGTITSGWT  LLAGTITSG  4        0.7320
18.2     0.25  0.56    Sequence         SB
 HLA-DQA10501-DQB10301  880      TSALLAGTITSGWTF  LLAGTITSG  3        0.7111
22.8     0.50  0.65    Sequence         SB
 HLA-DQA10501-DQB10301  881      SALLAGTITSGWTFG  LLAGTITSG  2        0.6812
31.5     0.90  0.60    Sequence         SB
 HLA-DQA10501-DQB10301  882      ALLAGTITSGWTFGA  LLAGTITSG  1        0.6453
46.4     1.70  0.50    Sequence         SB
 HLA-DQA10501-DQB10301  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.6358
51.5     1.90  0.31    Sequence         SB
 HLA-DQA10501-DQB10301  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.6009
75.1     3.50  0.41    Sequence         WB
 HLA-DQA10501-DQB10301  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.5999
75.9     3.50  0.41    Sequence         WB
 HLA-DQA10501-DQB10301  886      GTITSGWTFGAGAAL  ITSGWTFGA  2        0.6362
51.2     1.90  0.22    Sequence         SB
 HLA-DQA10501-DQB10301  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.6629
38.4     1.20  0.15    Sequence         SB
 HLA-DQA10501-DQB10301  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.7061
24.0     0.50  0.34    Sequence         SB
 HLA-DQA10501-DQB10301  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.7483
15.2     0.15  0.48    Sequence         SB
 HLA-DQA10501-DQB10301  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.7607
13.3     0.09  0.48    Sequence         SB
 HLA-DQA10501-DQB10301  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.7610
13.3     0.08  0.49    Sequence         SB
 HLA-DQA10501-DQB10301  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.7489
15.1     0.15  0.45    Sequence         SB
 HLA-DQA10501-DQB10301  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.7173
21.3     0.40  0.38    Sequence         SB
 HLA-DQA10501-DQB10301  894      FGAGAALQIPFAMQM  FGAGAALQI  0        0.6740
34.0     1.00  0.35    Sequence         SB
 HLA-DQA10501-DQB10301  895      GAGAALQIPFAMQMA  GAGAALQIP  0        0.6000
75.8     3.50  0.29    Sequence         WB
 HLA-DQA10501-DQB10301  896      AGAALQIPFAMQMAY  GAALQIPFA  1        0.4896
250.3    11.00  0.30    Sequence
 HLA-DQA10501-DQB10301  897      GAALQIPFAMQMAYR  GAALQIPFA  0        0.4104
589.3    21.00  0.34    Sequence
 HLA-DQA10501-DQB10301  898      AALQIPFAMQMAYRF  AALQIPFAM  0        0.3443
1206.0    32.00  0.20     Sequence
```

```
 HLA-DQA10501-DQB10301  899      ALQIPFAMQMAYRFN  IPFAMQMAY  3         0.2815
2377.5    46.00  0.18     Sequence
 HLA-DQA10501-DQB10301  900      LQIPFAMQMAYRFNG  MQMAYRFNG  6         0.2855
2277.0    45.00  0.26     Sequence
 HLA-DQA10501-DQB10301  901      QIPFAMQMAYRFNGI  MQMAYRFNG  5         0.2937
2084.7    43.00  0.34     Sequence
 HLA-DQA10501-DQB10301  902      IPFAMQMAYRFNGIG  MQMAYRFNG  4         0.2906
2156.0    44.00  0.34     Sequence
 HLA-DQA10501-DQB10301  903      PFAMQMAYRFNGIGV  MQMAYRFNG  3         0.2760
2522.9    47.00  0.35     Sequence
 HLA-DQA10501-DQB10301  904      FAMQMAYRFNGIGVT  MQMAYRFNG  2         0.3110
1727.4    39.00  0.18     Sequence
 HLA-DQA10501-DQB10301  905      AMQMAYRFNGIGVTQ  YRFNGIGVT  5         0.3366
1310.3    34.00  0.22     Sequence
 HLA-DQA10501-DQB10301  906      MQMAYRFNGIGVTQN  FNGIGVTQN  6         0.4124
577.2    21.00  0.32     Sequence
 HLA-DQA10501-DQB10301  907      QMAYRFNGIGVTQNV  FNGIGVTQN  5         0.4551
363.5    15.00  0.34     Sequence
 HLA-DQA10501-DQB10301  908      MAYRFNGIGVTQNVL  NGIGVTQNV  5         0.5000
223.6    10.00  0.34     Sequence
 HLA-DQA10501-DQB10301  909      AYRFNGIGVTQNVLY  NGIGVTQNV  4         0.4935
239.8    11.00  0.35     Sequence
 HLA-DQA10501-DQB10301  910      YRFNGIGVTQNVLYE  NGIGVTQNV  3         0.4905
247.8    11.00  0.34     Sequence
 HLA-DQA10501-DQB10301  911      RFNGIGVTQNVLYEN  NGIGVTQNV  2         0.4587
349.6    14.00  0.34     Sequence
 HLA-DQA10501-DQB10301  912      FNGIGVTQNVLYENQ  NGIGVTQNV  1         0.4313
470.1    18.00  0.33     Sequence
 HLA-DQA10501-DQB10301  913      NGIGVTQNVLYENQK  NGIGVTQNV  0         0.3247
1489.8    36.00  0.47     Sequence
 HLA-DQA10501-DQB10301  914      GIGVTQNVLYENQKL  VTQNVLYEN  3         0.2122
5035.6    65.00  0.22     Sequence
 HLA-DQA10501-DQB10301  915      IGVTQNVLYENQKLI  VTQNVLYEN  2         0.1367
11391.6    90.00  0.38     Sequence
 HLA-DQA10501-DQB10301  916      GVTQNVLYENQKLIA  VTQNVLYEN  1         0.1181
13936.0    95.00  0.37     Sequence
 HLA-DQA10501-DQB10301  917      VTQNVLYENQKLIAN  YENQKLIAN  6         0.1832
6885.5    75.00  0.32     Sequence
 HLA-DQA10501-DQB10301  918      TQNVLYENQKLIANQ  YENQKLIAN  5         0.1939
6135.5    70.00  0.47     Sequence
 HLA-DQA10501-DQB10301  919      QNVLYENQKLIANQF  YENQKLIAN  4         0.2154
4861.0    65.00  0.42     Sequence
 HLA-DQA10501-DQB10301  920      NVLYENQKLIANQFN  YENQKLIAN  3         0.2220
4527.9    65.00  0.37     Sequence
 HLA-DQA10501-DQB10301  921      VLYENQKLIANQFNS  YENQKLIAN  2         0.2242
4419.6    65.00  0.34     Sequence
 HLA-DQA10501-DQB10301  922      LYENQKLIANQFNSA  LIANQFNSA  6         0.2561
3129.2    55.00  0.22     Sequence
 HLA-DQA10501-DQB10301  923      YENQKLIANQFNSAI  LIANQFNSA  5         0.2567
3109.2    55.00  0.29     Sequence
 HLA-DQA10501-DQB10301  924      ENQKLIANQFNSAIG  LIANQFNSA  4         0.2317
4076.1    60.00  0.31     Sequence
 HLA-DQA10501-DQB10301  925      NQKLIANQFNSAIGK  LIANQFNSA  3         0.2642
2868.0    50.00  0.27     Sequence
 HLA-DQA10501-DQB10301  926      QKLIANQFNSAIGKI  ANQFNSAIG  4         0.2864
2254.9    45.00  0.17     Sequence
 HLA-DQA10501-DQB10301  927      KLIANQFNSAIGKIQ  QFNSAIGKI  5         0.3498
1136.1    31.00  0.32     Sequence
 HLA-DQA10501-DQB10301  928      LIANQFNSAIGKIQD  QFNSAIGKI  4         0.3676
937.2    28.00  0.28     Sequence
 HLA-DQA10501-DQB10301  929      IANQFNSAIGKIQDS  SAIGKIQDS  6         0.4338
457.5    18.00  0.34     Sequence
 HLA-DQA10501-DQB10301  930      ANQFNSAIGKIQDSL  SAIGKIQDS  5         0.5285
164.3     7.50  0.54     Sequence         WB
 HLA-DQA10501-DQB10301  931      NQFNSAIGKIQDSLS  SAIGKIQDS  4         0.5409
143.6     6.50  0.55     Sequence         WB
```

```
 HLA-DQA10501-DQB10301  932      QFNSAIGKIQDSLSS  SAIGKIQDS  3         0.5392
146.4     7.00  0.52     Sequence         WB
 HLA-DQA10501-DQB10301  933      FNSAIGKIQDSLSST  SAIGKIQDS  2         0.5301
161.5     7.50  0.52     Sequence         WB
 HLA-DQA10501-DQB10301  934      NSAIGKIQDSLSSTA  SAIGKIQDS  1         0.4932
240.6    11.00  0.47     Sequence
 HLA-DQA10501-DQB10301  935      SAIGKIQDSLSSTAS  SAIGKIQDS  0         0.4761
289.6    13.00  0.38     Sequence
 HLA-DQA10501-DQB10301  936      AIGKIQDSLSSTASA  IQDSLSSTA  4         0.4235
511.5    19.00  0.44     Sequence
 HLA-DQA10501-DQB10301  937      IGKIQDSLSSTASAL  IQDSLSSTA  3         0.3806
814.0    25.00  0.45     Sequence
 HLA-DQA10501-DQB10301  938      GKIQDSLSSTASALG  IQDSLSSTA  2         0.3758
857.5    26.00  0.37     Sequence
 HLA-DQA10501-DQB10301  939      KIQDSLSSTASALGK  LSSTASALG  5         0.4017
647.7    22.00  0.20     Sequence
 HLA-DQA10501-DQB10301  940      IQDSLSSTASALGKL  SSTASALGK  5         0.4096
594.9    21.00  0.25     Sequence
 HLA-DQA10501-DQB10301  941      QDSLSSTASALGKLQ  SSTASALGK  4         0.3897
737.2    24.00  0.27     Sequence
 HLA-DQA10501-DQB10301  942      DSLSSTASALGKLQD  SSTASALGK  3         0.4012
651.1    22.00  0.22     Sequence
 HLA-DQA10501-DQB10301  943      SLSSTASALGKLQDV  SSTASALGK  2         0.4169
549.6    20.00  0.22     Sequence
 HLA-DQA10501-DQB10301  944      LSSTASALGKLQDVV  SALGKLQDV  5         0.4290
482.3    18.00  0.41     Sequence
 HLA-DQA10501-DQB10301  945      SSTASALGKLQDVVN  SALGKLQDV  4         0.4114
583.1    21.00  0.47     Sequence
 HLA-DQA10501-DQB10301  946      STASALGKLQDVVNQ  SALGKLQDV  3         0.3840
784.4    25.00  0.53     Sequence
 HLA-DQA10501-DQB10301  947      TASALGKLQDVVNQN  SALGKLQDV  2         0.3517
1113.1    31.00  0.49     Sequence
 HLA-DQA10501-DQB10301  948      ASALGKLQDVVNQNA  SALGKLQDV  1         0.2799
2419.8    46.00  0.50     Sequence
 HLA-DQA10501-DQB10301  949      SALGKLQDVVNQNAQ  SALGKLQDV  0         0.2477
3427.0    55.00  0.44     Sequence
 HLA-DQA10501-DQB10301  950      ALGKLQDVVNQNAQA  XALGKLQDV -1         0.1777
7313.2    75.00  0.19     Sequence
 HLA-DQA10501-DQB10301  951      LGKLQDVVNQNAQAL  VVNQNAQAL  6         0.1485
10023.8    85.00  0.22     Sequence
 HLA-DQA10501-DQB10301  952      GKLQDVVNQNAQALN  VVNQNAQAL  5         0.1905
6364.0    75.00  0.28     Sequence
 HLA-DQA10501-DQB10301  953      KLQDVVNQNAQALNT  NQNAQALNT  6         0.2598
3005.8    55.00  0.38     Sequence
 HLA-DQA10501-DQB10301  954      LQDVVNQNAQALNTL  NQNAQALNT  5         0.3223
1528.8    36.00  0.51     Sequence
 HLA-DQA10501-DQB10301  955      QDVVNQNAQALNTLV  NQNAQALNT  4         0.3321
1375.9    34.00  0.44     Sequence
 HLA-DQA10501-DQB10301  956      DVVNQNAQALNTLVK  NQNAQALNT  3         0.3365
1312.1    34.00  0.38     Sequence
 HLA-DQA10501-DQB10301  957      VVNQNAQALNTLVKQ  NQNAQALNT  2         0.3288
1425.5    35.00  0.37     Sequence
 HLA-DQA10501-DQB10301  958      VNQNAQALNTLVKQL  NQNAQALNT  1         0.2985
1978.9    42.00  0.32     Sequence
 HLA-DQA10501-DQB10301  959      NQNAQALNTLVKQLS  NAQALNTLV  2         0.2692
2715.3    49.00  0.23     Sequence
 HLA-DQA10501-DQB10301  960      QNAQALNTLVKQLSS  NAQALNTLV  1         0.2280
4241.9    60.00  0.25     Sequence
 HLA-DQA10501-DQB10301  961      NAQALNTLVKQLSSN  NAQALNTLV  0         0.2035
5528.8    70.00  0.28     Sequence
 HLA-DQA10501-DQB10301  962      AQALNTLVKQLSSNF  LNTLVKQLS  3         0.1762
7431.3    75.00  0.19     Sequence
 HLA-DQA10501-DQB10301  963      QALNTLVKQLSSNFG  VKQLSSNFG  6         0.1833
6877.2    75.00  0.28     Sequence
 HLA-DQA10501-DQB10301  964      ALNTLVKQLSSNFGA  VKQLSSNFG  5         0.2116
5067.8    65.00  0.35     Sequence
```

```
 HLA-DQA10501-DQB10301  965      LNTLVKQLSSNFGAI  VKQLSSNFG  4        0.2389
3770.8    60.00  0.29     Sequence
 HLA-DQA10501-DQB10301  966      NTLVKQLSSNFGAIS  VKQLSSNFG  3        0.2553
3158.2    55.00  0.23     Sequence
 HLA-DQA10501-DQB10301  967      TLVKQLSSNFGAISS  VKQLSSNFG  2        0.3065
1814.7    40.00  0.16     Sequence
 HLA-DQA10501-DQB10301  968      LVKQLSSNFGAISSV  SNFGAISSV  6        0.3676
936.7    28.00  0.28     Sequence
 HLA-DQA10501-DQB10301  969      VKQLSSNFGAISSVL  SNFGAISSV  5        0.4687
313.6    13.00  0.41     Sequence
 HLA-DQA10501-DQB10301  970      KQLSSNFGAISSVLN  SNFGAISSV  4        0.4962
232.9    11.00  0.32     Sequence
 HLA-DQA10501-DQB10301  971      QLSSNFGAISSVLND  SNFGAISSV  3        0.5049
212.0     9.50  0.32     Sequence         WB
 HLA-DQA10501-DQB10301  972      LSSNFGAISSVLNDI  SNFGAISSV  2        0.5006
222.3    10.00  0.31     Sequence
 HLA-DQA10501-DQB10301  973      SSNFGAISSVLNDIL  SNFGAISSV  1        0.4897
250.0    11.00  0.26     Sequence
 HLA-DQA10501-DQB10301  974      SNFGAISSVLNDILS  SNFGAISSV  0        0.4697
310.4    13.00  0.26     Sequence
 HLA-DQA10501-DQB10301  975      NFGAISSVLNDILSR  FGAISSVLN  1        0.4346
453.9    18.00  0.23     Sequence
 HLA-DQA10501-DQB10301  976      FGAISSVLNDILSRL  FGAISSVLN  0        0.2995
1957.9    42.00  0.34     Sequence
 HLA-DQA10501-DQB10301  977      GAISSVLNDILSRLD  GAISSVLND  0        0.1959
6007.0    70.00  0.22     Sequence
 HLA-DQA10501-DQB10301  978      AISSVLNDILSRLDK  AISSVLNDI  0        0.1460
10296.5    85.00  0.27     Sequence
 HLA-DQA10501-DQB10301  979      ISSVLNDILSRLDKV  LNDILSRLD  4        0.1208
13531.7    95.00  0.25     Sequence
 HLA-DQA10501-DQB10301  980      SSVLNDILSRLDKVE  LNDILSRLD  3        0.1137
14612.5    95.00  0.25     Sequence
 HLA-DQA10501-DQB10301  981      SVLNDILSRLDKVEA  DILSRLDKV  4        0.1008
16797.8    95.00  0.31     Sequence
 HLA-DQA10501-DQB10301  982      VLNDILSRLDKVEAE  LSRLDKVEA  5        0.1161
14230.9    95.00  0.23     Sequence
 HLA-DQA10501-DQB10301  983      LNDILSRLDKVEAEV  SRLDKVEAE  5        0.1280
12519.2    90.00  0.26     Sequence
 HLA-DQA10501-DQB10301  984      NDILSRLDKVEAEVQ  SRLDKVEAE  4        0.1331
11849.5    90.00  0.27     Sequence
 HLA-DQA10501-DQB10301  985      DILSRLDKVEAEVQI  SRLDKVEAE  3        0.1421
10743.2    85.00  0.22     Sequence
 HLA-DQA10501-DQB10301  986      ILSRLDKVEAEVQID  KVEAEVQID  6        0.1742
7594.2    80.00  0.26     Sequence
 HLA-DQA10501-DQB10301  987      LSRLDKVEAEVQIDR  KVEAEVQID  5        0.2030
5558.7    70.00  0.38     Sequence
 HLA-DQA10501-DQB10301  988      SRLDKVEAEVQIDRL  KVEAEVQID  4        0.2041
5492.5    70.00  0.41     Sequence
 HLA-DQA10501-DQB10301  989      RLDKVEAEVQIDRLI  KVEAEVQID  3        0.2010
5684.5    70.00  0.38     Sequence
 HLA-DQA10501-DQB10301  990      LDKVEAEVQIDRLIT  KVEAEVQID  2        0.2021
5613.8    70.00  0.37     Sequence
 HLA-DQA10501-DQB10301  991      DKVEAEVQIDRLITG  KVEAEVQID  1        0.1977
5888.2    70.00  0.35     Sequence
 HLA-DQA10501-DQB10301  992      KVEAEVQIDRLITGR  KVEAEVQID  0        0.1844
6799.3    75.00  0.28     Sequence
 HLA-DQA10501-DQB10301  993      VEAEVQIDRLITGRL  VQIDRLITG  4        0.1838
6844.7    75.00  0.31     Sequence
 HLA-DQA10501-DQB10301  994      EAEVQIDRLITGRLQ  VQIDRLITG  3        0.1640
8475.3    80.00  0.35     Sequence
 HLA-DQA10501-DQB10301  995      AEVQIDRLITGRLQS  LITGRLQSX  7        0.1985
5836.4    70.00  0.20     Sequence
 HLA-DQA10501-DQB10301  996      EVQIDRLITGRLQSL  LITGRLQSL  6        0.2928
2103.7    43.00  0.52     Sequence
 HLA-DQA10501-DQB10301  997      VQIDRLITGRLQSLQ  LITGRLQSL  5        0.3275
1445.8    35.00  0.65     Sequence
```

```
 HLA-DQA10501-DQB10301  998      QIDRLITGRLQSLQT  LITGRLQSL  4        0.3366
1310.8    34.00  0.67     Sequence
 HLA-DQA10501-DQB10301  999      IDRLITGRLQSLQTY  LITGRLQSL  3        0.3406
1255.2    33.00  0.60     Sequence
 HLA-DQA10501-DQB10301 1000      DRLITGRLQSLQTYV  LITGRLQSL  2        0.3334
1356.3    34.00  0.48     Sequence
 HLA-DQA10501-DQB10301 1001      RLITGRLQSLQTYVT  LITGRLQSL  1        0.3165
1627.7    38.00  0.39     Sequence
 HLA-DQA10501-DQB10301 1002      LITGRLQSLQTYVTQ  LITGRLQSL  0        0.2881
2213.0    44.00  0.35     Sequence
 HLA-DQA10501-DQB10301 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.2309
4112.4    60.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.1916
6292.1    75.00  0.35     Sequence
 HLA-DQA10501-DQB10301 1005      GRLQSLQTYVTQQLI  LQSLQTYVT  2        0.1679
8124.8    80.00  0.30     Sequence
 HLA-DQA10501-DQB10301 1006      RLQSLQTYVTQQLIR  LQSLQTYVT  1        0.1480
10077.5    85.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1007      LQSLQTYVTQQLIRA  LQSLQTYVT  0        0.1529
9565.7    85.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1008      QSLQTYVTQQLIRAA  VTQQLIRAA  6        0.1788
7226.6    75.00  0.29     Sequence
 HLA-DQA10501-DQB10301 1009      SLQTYVTQQLIRAAE  VTQQLIRAA  5        0.2139
4942.7    65.00  0.48     Sequence
 HLA-DQA10501-DQB10301 1010      LQTYVTQQLIRAAEI  VTQQLIRAA  4        0.2647
2853.5    50.00  0.43     Sequence
 HLA-DQA10501-DQB10301 1011      QTYVTQQLIRAAEIR  VTQQLIRAA  3        0.2983
1983.5    42.00  0.35     Sequence
 HLA-DQA10501-DQB10301 1012      TYVTQQLIRAAEIRA  VTQQLIRAA  2        0.3232
1514.0    36.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1013      YVTQQLIRAAEIRAS  IRAAEIRAS  6        0.5168
186.4     8.50  0.57     Sequence         WB
 HLA-DQA10501-DQB10301 1014      VTQQLIRAAEIRASA  IRAAEIRAS  5        0.6375
50.5     1.90  0.69     Sequence         SB
 HLA-DQA10501-DQB10301 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.6495
44.4     1.50  0.67     Sequence         SB
 HLA-DQA10501-DQB10301 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.6522
43.1     1.50  0.66     Sequence         SB
 HLA-DQA10501-DQB10301 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.6541
42.2     1.40  0.61     Sequence         SB
 HLA-DQA10501-DQB10301 1018      LIRAAEIRASANLAA  IRAAEIRAS  1        0.6715
34.9     1.00  0.49     Sequence         SB
 HLA-DQA10501-DQB10301 1019      IRAAEIRASANLAAI  IRAAEIRAS  0        0.6569
40.9     1.30  0.39     Sequence         SB
 HLA-DQA10501-DQB10301 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.6084
69.2     3.00  0.31     Sequence         WB
 HLA-DQA10501-DQB10301 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.5769
97.3     4.50  0.31     Sequence         WB
 HLA-DQA10501-DQB10301 1022      AEIRASANLAAIKMS  RASANLAAI  3        0.5749
99.5     4.50  0.21     Sequence         WB
 HLA-DQA10501-DQB10301 1023      EIRASANLAAIKMSE  ANLAAIKMS  5        0.5804
93.7     4.50  0.29     Sequence         WB
 HLA-DQA10501-DQB10301 1024      IRASANLAAIKMSEC  ANLAAIKMS  4        0.5658
109.8     5.00  0.37     Sequence         WB
 HLA-DQA10501-DQB10301 1025      RASANLAAIKMSECV  ANLAAIKMS  3        0.5168
186.4     8.50  0.48     Sequence         WB
 HLA-DQA10501-DQB10301 1026      ASANLAAIKMSECVL  ANLAAIKMS  2        0.4993
225.4    10.00  0.49     Sequence
 HLA-DQA10501-DQB10301 1027      SANLAAIKMSECVLG  ANLAAIKMS  1        0.4683
315.0    13.00  0.46     Sequence
 HLA-DQA10501-DQB10301 1028      ANLAAIKMSECVLGQ  ANLAAIKMS  0        0.4494
386.6    16.00  0.40     Sequence
 HLA-DQA10501-DQB10301 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.3783
834.1    26.00  0.42     Sequence
 HLA-DQA10501-DQB10301 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.3365
1312.2    34.00  0.41     Sequence
```

```
 HLA-DQA10501-DQB10301 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.3149
1657.3    38.00  0.40     Sequence
 HLA-DQA10501-DQB10301 1032      AIKMSECVLGQSKRV  MSECVLGQS  3        0.2988
1971.8    42.00  0.27     Sequence
 HLA-DQA10501-DQB10301 1033      IKMSECVLGQSKRVD  CVLGQSKRV  5        0.3050
1843.8    40.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.2790
2443.3    46.00  0.34     Sequence
 HLA-DQA10501-DQB10301 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.2862
2259.3    45.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.2705
2677.3    49.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1037      ECVLGQSKRVDFCGK  CVLGQSKRV  1        0.2567
3110.9    55.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1038      CVLGQSKRVDFCGKG  CVLGQSKRV  0        0.2373
3837.3    60.00  0.27     Sequence
 HLA-DQA10501-DQB10301 1039      VLGQSKRVDFCGKGY  GQSKRVDFC  2        0.1865
6648.0    75.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1040      LGQSKRVDFCGKGYH  GQSKRVDFC  1        0.1900
6397.1    75.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1041      GQSKRVDFCGKGYHL  VDFCGKGYH  5        0.2206
4596.1    65.00  0.18     Sequence
 HLA-DQA10501-DQB10301 1042      QSKRVDFCGKGYHLM  DFCGKGYHL  5        0.3097
1752.5    39.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1043      SKRVDFCGKGYHLMS  DFCGKGYHL  4        0.3350
1333.1    34.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1044      KRVDFCGKGYHLMSF  CGKGYHLMS  5        0.3865
763.1    24.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1045      RVDFCGKGYHLMSFP  CGKGYHLMS  4        0.3917
721.4    24.00  0.24     Sequence
 HLA-DQA10501-DQB10301 1046      VDFCGKGYHLMSFPQ  CGKGYHLMS  3        0.3918
721.3    24.00  0.23     Sequence
 HLA-DQA10501-DQB10301 1047      DFCGKGYHLMSFPQS  GKGYHLMSF  3        0.3776
840.9    26.00  0.18     Sequence
 HLA-DQA10501-DQB10301 1048      FCGKGYHLMSFPQSA  HLMSFPQSA  6        0.3978
675.9    23.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.3880
751.0    24.00  0.45     Sequence
 HLA-DQA10501-DQB10301 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.3778
838.9    26.00  0.47     Sequence
 HLA-DQA10501-DQB10301 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.3618
997.2    29.00  0.50     Sequence
 HLA-DQA10501-DQB10301 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.3731
882.8    27.00  0.41     Sequence
 HLA-DQA10501-DQB10301 1053      YHLMSFPQSAPHGVV  FPQSAPHGV  5        0.4415
421.0    17.00  0.24     Sequence
 HLA-DQA10501-DQB10301 1054      HLMSFPQSAPHGVVF  PQSAPHGVV  5        0.4495
386.3    16.00  0.23     Sequence
 HLA-DQA10501-DQB10301 1055      LMSFPQSAPHGVVFL  PQSAPHGVV  4        0.4433
413.1    16.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1056      MSFPQSAPHGVVFLH  PQSAPHGVV  3        0.4373
440.6    17.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1057      SFPQSAPHGVVFLHV  APHGVVFLH  5        0.4657
324.1    14.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1058      FPQSAPHGVVFLHVT  APHGVVFLH  4        0.4742
295.7    13.00  0.29     Sequence
 HLA-DQA10501-DQB10301 1059      PQSAPHGVVFLHVTY  APHGVVFLH  3        0.4544
366.4    15.00  0.29     Sequence
 HLA-DQA10501-DQB10301 1060      QSAPHGVVFLHVTYV  APHGVVFLH  2        0.4078
606.3    21.00  0.33     Sequence
 HLA-DQA10501-DQB10301 1061      SAPHGVVFLHVTYVP  APHGVVFLH  1        0.3930
712.0    23.00  0.29     Sequence
 HLA-DQA10501-DQB10301 1062      APHGVVFLHVTYVPA  APHGVVFLH  0        0.3695
917.7    27.00  0.27     Sequence
 HLA-DQA10501-DQB10301 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.3349
1335.0    34.00  0.17     Sequence
```

```
 HLA-DQA10501-DQB10301 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.3013
1919.2    41.00  0.23     Sequence
 HLA-DQA10501-DQB10301 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.2950
2054.2    43.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1066      VVFLHVTYVPAQEKN  VTYVPAQEK  5        0.2941
2074.5    43.00  0.26     Sequence
 HLA-DQA10501-DQB10301 1067      VFLHVTYVPAQEKNF  VTYVPAQEK  4        0.2919
2125.3    43.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1068      FLHVTYVPAQEKNFT  VTYVPAQEK  3        0.2743
2571.6    48.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1069      LHVTYVPAQEKNFTT  VTYVPAQEK  2        0.2413
3672.7    60.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1070      HVTYVPAQEKNFTTA  VTYVPAQEK  1        0.2193
4659.2    65.00  0.23     Sequence
 HLA-DQA10501-DQB10301 1071      VTYVPAQEKNFTTAP  VPAQEKNFT  3        0.1984
5846.9    70.00  0.19     Sequence
 HLA-DQA10501-DQB10301 1072      TYVPAQEKNFTTAPA  PAQEKNFTT  3        0.1911
6323.7    75.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1073      YVPAQEKNFTTAPAI  EKNFTTAPA  5        0.2324
4043.2    60.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1074      VPAQEKNFTTAPAIC  KNFTTAPAI  5        0.2957
2039.0    42.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.4221
519.3    19.00  0.47     Sequence
 HLA-DQA10501-DQB10301 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.4441
409.3    16.00  0.47     Sequence
 HLA-DQA10501-DQB10301 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.4490
388.3    16.00  0.44     Sequence
 HLA-DQA10501-DQB10301 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.4580
352.3    15.00  0.43     Sequence
 HLA-DQA10501-DQB10301 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.4736
297.5    13.00  0.38     Sequence
 HLA-DQA10501-DQB10301 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.4679
316.4    13.00  0.35     Sequence
 HLA-DQA10501-DQB10301 1081      FTTAPAICHDGKAHF  FTTAPAICH  0        0.4403
426.5    17.00  0.34     Sequence
 HLA-DQA10501-DQB10301 1082      TTAPAICHDGKAHFP  CHDGKAHFP  6        0.3604
1012.8    29.00  0.33     Sequence
 HLA-DQA10501-DQB10301 1083      TAPAICHDGKAHFPR  CHDGKAHFP  5        0.4009
653.2    22.00  0.51     Sequence
 HLA-DQA10501-DQB10301 1084      APAICHDGKAHFPRE  CHDGKAHFP  4        0.3900
735.2    24.00  0.51     Sequence
 HLA-DQA10501-DQB10301 1085      PAICHDGKAHFPREG  CHDGKAHFP  3        0.3907
729.4    24.00  0.48     Sequence
 HLA-DQA10501-DQB10301 1086      AICHDGKAHFPREGV  CHDGKAHFP  2        0.3744
870.6    26.00  0.43     Sequence
 HLA-DQA10501-DQB10301 1087      ICHDGKAHFPREGVF  CHDGKAHFP  1        0.3628
987.0    29.00  0.38     Sequence
 HLA-DQA10501-DQB10301 1088      CHDGKAHFPREGVFV  CHDGKAHFP  0        0.3474
1165.4    31.00  0.34     Sequence
 HLA-DQA10501-DQB10301 1089      HDGKAHFPREGVFVS  GKAHFPREG  2        0.3071
1803.1    40.00  0.23     Sequence
 HLA-DQA10501-DQB10301 1090      DGKAHFPREGVFVSN  PREGVFVSN  6        0.3361
1317.2    34.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1091      GKAHFPREGVFVSNG  PREGVFVSN  5        0.3739
875.2    27.00  0.37     Sequence
 HLA-DQA10501-DQB10301 1092      KAHFPREGVFVSNGT  PREGVFVSN  4        0.3831
792.3    25.00  0.35     Sequence
 HLA-DQA10501-DQB10301 1093      AHFPREGVFVSNGTH  PREGVFVSN  3        0.3762
853.3    26.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1094      HFPREGVFVSNGTHW  PREGVFVSN  2        0.3784
833.4    26.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1095      FPREGVFVSNGTHWF  REGVFVSNG  2        0.3808
812.0    25.00  0.26     Sequence
 HLA-DQA10501-DQB10301 1096      PREGVFVSNGTHWFV  VSNGTHWFV  6        0.3819
802.7    25.00  0.20     Sequence
```

```
 HLA-DQA10501-DQB10301 1097      REGVFVSNGTHWFVT  VSNGTHWFV  5        0.4153
558.8    20.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1098      EGVFVSNGTHWFVTQ  VSNGTHWFV  4        0.4199
531.8    19.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1099      GVFVSNGTHWFVTQR  VSNGTHWFV  3        0.4026
641.3    22.00  0.36     Sequence
 HLA-DQA10501-DQB10301 1100      VFVSNGTHWFVTQRN  VSNGTHWFV  2        0.3746
868.5    26.00  0.38     Sequence
 HLA-DQA10501-DQB10301 1101      FVSNGTHWFVTQRNF  VSNGTHWFV  1        0.3520
1108.5    30.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1102      VSNGTHWFVTQRNFY  SNGTHWFVT  1        0.3204
1560.5    37.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1103      SNGTHWFVTQRNFYE  SNGTHWFVT  0        0.2579
3070.4    55.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1104      NGTHWFVTQRNFYEP  THWFVTQRN  2        0.1851
6750.6    75.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1105      GTHWFVTQRNFYEPQ  WFVTQRNFY  3        0.1523
9622.4    85.00  0.20     Sequence
 HLA-DQA10501-DQB10301 1106      THWFVTQRNFYEPQI  THWFVTQRN  0        0.1248
12954.5    90.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1107      HWFVTQRNFYEPQII  RNFYEPQII  6        0.1491
9958.3    85.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1108      WFVTQRNFYEPQIIT  RNFYEPQII  5        0.1924
6236.1    70.00  0.30     Sequence
 HLA-DQA10501-DQB10301 1109      FVTQRNFYEPQIITT  RNFYEPQII  4        0.2200
4626.2    65.00  0.26     Sequence
 HLA-DQA10501-DQB10301 1110      VTQRNFYEPQIITTD  FYEPQIITT  5        0.2392
3757.7    60.00  0.33     Sequence
 HLA-DQA10501-DQB10301 1111      TQRNFYEPQIITTDN  FYEPQIITT  4        0.2400
3726.5    60.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1112      QRNFYEPQIITTDNT  FYEPQIITT  3        0.2368
3859.0    60.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1113      RNFYEPQIITTDNTF  FYEPQIITT  2        0.2380
3807.1    60.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1114      NFYEPQIITTDNTFV  YEPQIITTD  2        0.2121
5041.0    65.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1115      FYEPQIITTDNTFVS  YEPQIITTD  1        0.1706
7893.9    80.00  0.24     Sequence
 HLA-DQA10501-DQB10301 1116      YEPQIITTDNTFVSG  ITTDNTFVS  5        0.1498
9885.5    85.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1117      EPQIITTDNTFVSGN  ITTDNTFVS  4        0.1440
10530.3    85.00  0.29     Sequence
 HLA-DQA10501-DQB10301 1118      PQIITTDNTFVSGNC  TDNTFVSGN  5        0.1667
8234.6    80.00  0.27     Sequence
 HLA-DQA10501-DQB10301 1119      QIITTDNTFVSGNCD  TDNTFVSGN  4        0.2023
5601.7    70.00  0.20     Sequence
 HLA-DQA10501-DQB10301 1120      IITTDNTFVSGNCDV  TDNTFVSGN  3        0.2309
4111.4    60.00  0.19     Sequence
 HLA-DQA10501-DQB10301 1121      ITTDNTFVSGNCDVV  FVSGNCDVV  6        0.3505
1126.7    31.00  0.41     Sequence
 HLA-DQA10501-DQB10301 1122      TTDNTFVSGNCDVVI  FVSGNCDVV  5        0.3821
800.9    25.00  0.44     Sequence
 HLA-DQA10501-DQB10301 1123      TDNTFVSGNCDVVIG  FVSGNCDVV  4        0.4184
540.5    20.00  0.36     Sequence
 HLA-DQA10501-DQB10301 1124      DNTFVSGNCDVVIGI  SGNCDVVIG  5        0.4330
461.7    18.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1125      NTFVSGNCDVVIGIV  SGNCDVVIG  4        0.4364
445.2    17.00  0.34     Sequence
 HLA-DQA10501-DQB10301 1126      TFVSGNCDVVIGIVN  SGNCDVVIG  3        0.4430
414.2    16.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1127      FVSGNCDVVIGIVNN  SGNCDVVIG  2        0.4319
467.0    18.00  0.29     Sequence
 HLA-DQA10501-DQB10301 1128      VSGNCDVVIGIVNNT  VVIGIVNNT  6        0.4328
462.5    18.00  0.39     Sequence
 HLA-DQA10501-DQB10301 1129      SGNCDVVIGIVNNTV  VVIGIVNNT  5        0.5232
173.9     8.00  0.62     Sequence          WB
```

```
 HLA-DQA10501-DQB10301 1130      GNCDVVIGIVNNTVY  VVIGIVNNT  4        0.5073
206.6     9.50  0.69     Sequence         WB
 HLA-DQA10501-DQB10301 1131      NCDVVIGIVNNTVYD  VVIGIVNNT  3        0.4979
228.8    10.00  0.72     Sequence
 HLA-DQA10501-DQB10301 1132      CDVVIGIVNNTVYDP  VVIGIVNNT  2        0.4695
310.9    13.00  0.68     Sequence
 HLA-DQA10501-DQB10301 1133      DVVIGIVNNTVYDPL  VVIGIVNNT  1        0.4265
495.2    19.00  0.57     Sequence
 HLA-DQA10501-DQB10301 1134      VVIGIVNNTVYDPLQ  VVIGIVNNT  0        0.4015
649.3    22.00  0.56     Sequence
 HLA-DQA10501-DQB10301 1135      VIGIVNNTVYDPLQP  XVIGIVNNT -1        0.2626
2916.7    55.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1136      IGIVNNTVYDPLQPE  NTVYDPLQP  5        0.1642
8458.6    80.00  0.19     Sequence
 HLA-DQA10501-DQB10301 1137      GIVNNTVYDPLQPEL  NTVYDPLQP  4        0.1395
11052.6    90.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1138      IVNNTVYDPLQPELD  YDPLQPELD  6        0.1431
10625.6    85.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1139      VNNTVYDPLQPELDS  YDPLQPELD  5        0.1442
10500.0    85.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1140      NNTVYDPLQPELDSF  YDPLQPELD  4        0.1440
10528.9    85.00  0.33     Sequence
 HLA-DQA10501-DQB10301 1141      NTVYDPLQPELDSFK  YDPLQPELD  3        0.1392
11094.4    90.00  0.35     Sequence
 HLA-DQA10501-DQB10301 1142      TVYDPLQPELDSFKE  YDPLQPELD  2        0.1105
15128.8    95.00  0.34     Sequence
 HLA-DQA10501-DQB10301 1143      VYDPLQPELDSFKEE  YDPLQPELD  1        0.0923
18422.1   100.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1144      YDPLQPELDSFKEEL  YDPLQPELD  0        0.0814
20722.0   100.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1145      DPLQPELDSFKEELD  LQPELDSFK  2        0.0615
25716.9   100.00  0.16     Sequence
 HLA-DQA10501-DQB10301 1146      PLQPELDSFKEELDK  LDSFKEELD  5        0.0591
26369.7   100.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1147      LQPELDSFKEELDKY  LDSFKEELD  4        0.0548
27628.6   100.00  0.26     Sequence
 HLA-DQA10501-DQB10301 1148      QPELDSFKEELDKYF  LDSFKEELD  3        0.0543
27788.4   100.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.0585
26557.3   100.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1150      ELDSFKEELDKYFKN  FKEELDKYF  4        0.0653
24660.4   100.00  0.17     Sequence
 HLA-DQA10501-DQB10301 1151      LDSFKEELDKYFKNH  EELDKYFKN  5        0.0666
24324.1   100.00  0.26     Sequence
 HLA-DQA10501-DQB10301 1152      DSFKEELDKYFKNHT  EELDKYFKN  4        0.0607
25925.6   100.00  0.30     Sequence
 HLA-DQA10501-DQB10301 1153      SFKEELDKYFKNHTS  EELDKYFKN  3        0.0647
24821.6   100.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1154      FKEELDKYFKNHTSP  DKYFKNHTS  5        0.0829
20384.7   100.00  0.24     Sequence
 HLA-DQA10501-DQB10301 1155      KEELDKYFKNHTSPD  DKYFKNHTS  4        0.0976
17398.4    95.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1156      EELDKYFKNHTSPDV  YFKNHTSPD  5        0.1416
10800.8    85.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.1802
7117.4    75.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1158      LDKYFKNHTSPDVDL  KNHTSPDVD  5        0.1996
5771.3    70.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1159      DKYFKNHTSPDVDLG  KNHTSPDVD  4        0.2233
4464.0    65.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1160      KYFKNHTSPDVDLGD  HTSPDVDLG  5        0.2325
4042.5    60.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1161      YFKNHTSPDVDLGDI  HTSPDVDLG  4        0.2333
4004.0    60.00  0.24     Sequence
 HLA-DQA10501-DQB10301 1162      FKNHTSPDVDLGDIS  HTSPDVDLG  3        0.2362
3881.4    60.00  0.22     Sequence
```

```
 HLA-DQA10501-DQB10301 1163      KNHTSPDVDLGDISG  HTSPDVDLG  2        0.2136
4959.6    65.00  0.23     Sequence
 HLA-DQA10501-DQB10301 1164      NHTSPDVDLGDISGI  VDLGDISGI  6        0.2840
2315.2    45.00  0.47     Sequence
 HLA-DQA10501-DQB10301 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.3249
1486.1    36.00  0.62     Sequence
 HLA-DQA10501-DQB10301 1166      TSPDVDLGDISGINA  VDLGDISGI  4        0.3343
1343.0    34.00  0.62     Sequence
 HLA-DQA10501-DQB10301 1167      SPDVDLGDISGINAS  VDLGDISGI  3        0.3910
727.2    24.00  0.46     Sequence
 HLA-DQA10501-DQB10301 1168      PDVDLGDISGINASF  VDLGDISGI  2        0.4098
593.3    21.00  0.35     Sequence
 HLA-DQA10501-DQB10301 1169      DVDLGDISGINASFV  ISGINASFV  6        0.4786
281.8    12.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1170      VDLGDISGINASFVN  ISGINASFV  5        0.5058
209.9     9.50  0.36     Sequence          WB
 HLA-DQA10501-DQB10301 1171      DLGDISGINASFVNI  ISGINASFV  4        0.4875
256.1    11.00  0.40     Sequence
 HLA-DQA10501-DQB10301 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.4747
293.9    13.00  0.40     Sequence
 HLA-DQA10501-DQB10301 1173      GDISGINASFVNIQK  INASFVNIQ  5        0.4712
305.5    13.00  0.29     Sequence
 HLA-DQA10501-DQB10301 1174      DISGINASFVNIQKE  INASFVNIQ  4        0.4373
440.8    17.00  0.35     Sequence
 HLA-DQA10501-DQB10301 1175      ISGINASFVNIQKEI  INASFVNIQ  3        0.4069
612.2    21.00  0.37     Sequence
 HLA-DQA10501-DQB10301 1176      SGINASFVNIQKEID  INASFVNIQ  2        0.3146
1662.6    38.00  0.46     Sequence
 HLA-DQA10501-DQB10301 1177      GINASFVNIQKEIDR  INASFVNIQ  1        0.2495
3363.5    55.00  0.43     Sequence
 HLA-DQA10501-DQB10301 1178      INASFVNIQKEIDRL  INASFVNIQ  0        0.2259
4340.3    65.00  0.41     Sequence
 HLA-DQA10501-DQB10301 1179      NASFVNIQKEIDRLN  ASFVNIQKE  1        0.1441
10521.3    85.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1180      ASFVNIQKEIDRLNE  ASFVNIQKE  0        0.1126
14790.7    95.00  0.23     Sequence
 HLA-DQA10501-DQB10301 1181      SFVNIQKEIDRLNEV  KEIDRLNEV  6        0.1195
13716.6    95.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1182      FVNIQKEIDRLNEVA  KEIDRLNEV  5        0.1383
11202.7    90.00  0.38     Sequence
 HLA-DQA10501-DQB10301 1183      VNIQKEIDRLNEVAK  KEIDRLNEV  4        0.1310
12113.7    90.00  0.40     Sequence
 HLA-DQA10501-DQB10301 1184      NIQKEIDRLNEVAKN  KEIDRLNEV  3        0.1380
11234.4    90.00  0.34     Sequence
 HLA-DQA10501-DQB10301 1185      IQKEIDRLNEVAKNL  DRLNEVAKN  5        0.1673
8185.4    80.00  0.35     Sequence
 HLA-DQA10501-DQB10301 1186      QKEIDRLNEVAKNLN  DRLNEVAKN  4        0.1702
7927.6    80.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1187      KEIDRLNEVAKNLNE  DRLNEVAKN  3        0.1682
8098.2    80.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1188      EIDRLNEVAKNLNES  DRLNEVAKN  2        0.1774
7333.6    75.00  0.19     Sequence
 HLA-DQA10501-DQB10301 1189      IDRLNEVAKNLNESL  EVAKNLNES  5        0.1864
6653.7    75.00  0.27     Sequence
 HLA-DQA10501-DQB10301 1190      DRLNEVAKNLNESLI  EVAKNLNES  4        0.1901
6395.7    75.00  0.26     Sequence
 HLA-DQA10501-DQB10301 1191      RLNEVAKNLNESLID  EVAKNLNES  3        0.1956
6022.6    70.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1192      LNEVAKNLNESLIDL  EVAKNLNES  2        0.1913
6313.4    75.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1193      NEVAKNLNESLIDLQ  EVAKNLNES  1        0.1796
7159.8    75.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1194      EVAKNLNESLIDLQE  LNESLIDLQ  5        0.1682
8102.5    80.00  0.29     Sequence
 HLA-DQA10501-DQB10301 1195      VAKNLNESLIDLQEL  LNESLIDLQ  4        0.1462
10282.6    85.00  0.37     Sequence
```

```
 HLA-DQA10501-DQB10301 1196      AKNLNESLIDLQELG  LNESLIDLQ  3        0.1286
12442.1    90.00  0.38     Sequence
 HLA-DQA10501-DQB10301 1197      KNLNESLIDLQELGK  LNESLIDLQ  2        0.1073
15653.0    95.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1198      NLNESLIDLQELGKY  LNESLIDLQ  1        0.1064
15812.3    95.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1199      LNESLIDLQELGKYE  IDLQELGKY  5        0.1078
15572.6    95.00  0.20     Sequence
 HLA-DQA10501-DQB10301 1200      NESLIDLQELGKYEQ  IDLQELGKY  4        0.0936
18166.4   100.00  0.23     Sequence
 HLA-DQA10501-DQB10301 1201      ESLIDLQELGKYEQY  QELGKYEQY  6        0.0995
17046.8    95.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1202      SLIDLQELGKYEQYI  QELGKYEQY  5        0.1112
15015.5    95.00  0.44     Sequence
 HLA-DQA10501-DQB10301 1203      LIDLQELGKYEQYIK  QELGKYEQY  4        0.1118
14917.2    95.00  0.41     Sequence
 HLA-DQA10501-DQB10301 1204      IDLQELGKYEQYIKW  QELGKYEQY  3        0.1134
14654.8    95.00  0.38     Sequence
 HLA-DQA10501-DQB10301 1205      DLQELGKYEQYIKWP  QELGKYEQY  2        0.1029
16417.4    95.00  0.38     Sequence
 HLA-DQA10501-DQB10301 1206      LQELGKYEQYIKWPW  QELGKYEQY  1        0.1062
15845.7    95.00  0.30     Sequence
 HLA-DQA10501-DQB10301 1207      QELGKYEQYIKWPWY  QELGKYEQY  0        0.1104
15150.1    95.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1208      ELGKYEQYIKWPWYI  EQYIKWPWY  5        0.1152
14381.6    95.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1209      LGKYEQYIKWPWYIW  QYIKWPWYI  5        0.1400
10987.5    90.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1210      GKYEQYIKWPWYIWL  QYIKWPWYI  4        0.1441
10512.5    85.00  0.24     Sequence
 HLA-DQA10501-DQB10301 1211      KYEQYIKWPWYIWLG  KWPWYIWLG  6        0.1710
7856.7    80.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1212      YEQYIKWPWYIWLGF  KWPWYIWLG  5        0.2014
5657.7    70.00  0.35     Sequence
 HLA-DQA10501-DQB10301 1213      EQYIKWPWYIWLGFI  KWPWYIWLG  4        0.2278
4249.5    60.00  0.35     Sequence
 HLA-DQA10501-DQB10301 1214      QYIKWPWYIWLGFIA  KWPWYIWLG  3        0.3085
1775.5    39.00  0.22     Sequence
 HLA-DQA10501-DQB10301 1215      YIKWPWYIWLGFIAG  WYIWLGFIA  5        0.3619
996.1    29.00  0.19     Sequence
 HLA-DQA10501-DQB10301 1216      IKWPWYIWLGFIAGL  IWLGFIAGL  6        0.4171
548.2    20.00  0.41     Sequence
 HLA-DQA10501-DQB10301 1217      KWPWYIWLGFIAGLI  IWLGFIAGL  5        0.4902
248.6    11.00  0.49     Sequence
 HLA-DQA10501-DQB10301 1218      WPWYIWLGFIAGLIA  IWLGFIAGL  4        0.5223
175.7     8.00  0.44     Sequence         WB
 HLA-DQA10501-DQB10301 1219      PWYIWLGFIAGLIAI  IWLGFIAGL  3        0.5280
165.1     7.50  0.39     Sequence         WB
 HLA-DQA10501-DQB10301 1220      WYIWLGFIAGLIAIV  FIAGLIAIV  6        0.5885
85.9     4.00  0.36     Sequence         WB
 HLA-DQA10501-DQB10301 1221      YIWLGFIAGLIAIVM  FIAGLIAIV  5        0.5794
94.7     4.50  0.47     Sequence         WB
 HLA-DQA10501-DQB10301 1222      IWLGFIAGLIAIVMV  FIAGLIAIV  4        0.5705
104.3     5.00  0.50     Sequence         WB
 HLA-DQA10501-DQB10301 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3        0.5516
128.0     6.00  0.55     Sequence         WB
 HLA-DQA10501-DQB10301 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.5151
190.0     8.50  0.55     Sequence         WB
 HLA-DQA10501-DQB10301 1225      GFIAGLIAIVMVTIM  FIAGLIAIV  1        0.4853
262.0    12.00  0.51     Sequence
 HLA-DQA10501-DQB10301 1226      FIAGLIAIVMVTIML  FIAGLIAIV  0        0.4500
384.3    16.00  0.52     Sequence
 HLA-DQA10501-DQB10301 1227      IAGLIAIVMVTIMLC  GLIAIVMVT  2        0.2852
2284.4    45.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1228      AGLIAIVMVTIMLCC  GLIAIVMVT  1        0.2358
3899.8    60.00  0.34     Sequence
```

```
 HLA-DQA10501-DQB10301 1229      GLIAIVMVTIMLCCM  GLIAIVMVT  0         0.2007
5702.4    70.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3         0.1536
9484.9    85.00  0.21     Sequence
 HLA-DQA10501-DQB10301 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2         0.1611
8745.7    80.00  0.19     Sequence
 HLA-DQA10501-DQB10301 1232      AIVMVTIMLCCMTSC  IMLCCMTSC  6         0.1915
6298.0    75.00  0.23     Sequence
 HLA-DQA10501-DQB10301 1233      IVMVTIMLCCMTSCC  IMLCCMTSC  5         0.2052
5430.6    70.00  0.29     Sequence
 HLA-DQA10501-DQB10301 1234      VMVTIMLCCMTSCCS  IMLCCMTSC  4         0.2079
5274.7    70.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1235      MVTIMLCCMTSCCSC  IMLCCMTSC  3         0.2057
5402.1    70.00  0.34     Sequence
 HLA-DQA10501-DQB10301 1236      VTIMLCCMTSCCSCL  IMLCCMTSC  2         0.2085
5241.0    70.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1237      TIMLCCMTSCCSCLK  IMLCCMTSC  1         0.2111
5096.1    65.00  0.23     Sequence
 HLA-DQA10501-DQB10301 1238      IMLCCMTSCCSCLKG  TSCCSCLKG  6         0.2051
5436.0    70.00  0.15     Sequence
 HLA-DQA10501-DQB10301 1239      MLCCMTSCCSCLKGC  TSCCSCLKG  5         0.1894
6438.3    75.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1240      LCCMTSCCSCLKGCC  TSCCSCLKG  4         0.1997
5759.4    70.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1241      CCMTSCCSCLKGCCS  TSCCSCLKG  3         0.2109
5106.9    65.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1242      CMTSCCSCLKGCCSC  TSCCSCLKG  2         0.2201
4619.0    65.00  0.23     Sequence
 HLA-DQA10501-DQB10301 1243      MTSCCSCLKGCCSCG  CLKGCCSCG  6         0.2325
4042.4    60.00  0.19     Sequence
 HLA-DQA10501-DQB10301 1244      TSCCSCLKGCCSCGS  CLKGCCSCG  5         0.2607
2977.2    55.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5         0.2719
2639.3    48.00  0.34     Sequence
 HLA-DQA10501-DQB10301 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4         0.2776
2481.0    47.00  0.38     Sequence
 HLA-DQA10501-DQB10301 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3         0.2810
2389.9    46.00  0.36     Sequence
 HLA-DQA10501-DQB10301 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2         0.2863
2258.7    45.00  0.33     Sequence
 HLA-DQA10501-DQB10301 1249      CLKGCCSCGSCCKFD  LKGCCSCGS  1         0.2835
2327.4    45.00  0.27     Sequence
 HLA-DQA10501-DQB10301 1250      LKGCCSCGSCCKFDE  LKGCCSCGS  0         0.2726
2617.0    48.00  0.26     Sequence
 HLA-DQA10501-DQB10301 1251      KGCCSCGSCCKFDED  CSCGSCCKF  3         0.2288
4206.7    60.00  0.32     Sequence
 HLA-DQA10501-DQB10301 1252      GCCSCGSCCKFDEDD  CSCGSCCKF  2         0.2180
4729.1    65.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1253      CCSCGSCCKFDEDDS  CSCGSCCKF  1         0.2006
5708.1    70.00  0.29     Sequence
 HLA-DQA10501-DQB10301 1254      CSCGSCCKFDEDDSE  CSCGSCCKF  0         0.1717
7797.8    80.00  0.31     Sequence
 HLA-DQA10501-DQB10301 1255      SCGSCCKFDEDDSEP  SCGSCCKFD  0         0.1198
13682.8    95.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1256      CGSCCKFDEDDSEPV  GSCCKFDED  1         0.0830
20365.7   100.00  0.23     Sequence
 HLA-DQA10501-DQB10301 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5         0.0703
23372.6   100.00  0.19     Sequence
 HLA-DQA10501-DQB10301 1258      SCCKFDEDDSEPVLK  EDDSEPVLK  6         0.0891
19062.5   100.00  0.37     Sequence
 HLA-DQA10501-DQB10301 1259      CCKFDEDDSEPVLKG  EDDSEPVLK  5         0.1539
9460.2    85.00  0.39     Sequence
 HLA-DQA10501-DQB10301 1260      CKFDEDDSEPVLKGV  DDSEPVLKG  5         0.1750
7530.6    80.00  0.34     Sequence
 HLA-DQA10501-DQB10301 1261      KFDEDDSEPVLKGVK  DDSEPVLKG  4         0.2073
5305.3    70.00  0.32     Sequence
```

```
 HLA-DQA10501-DQB10301 1262      FDEDDSEPVLKGVKL  DDSEPVLKG  3        0.2304
4132.0    60.00  0.28     Sequence
 HLA-DQA10501-DQB10301 1263      DEDDSEPVLKGVKLH  DDSEPVLKG  2        0.2486
3393.3    55.00  0.25     Sequence
 HLA-DQA10501-DQB10301 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.2774
2486.5    47.00  0.19     Sequence
 HLA-DQA10501-DQB10301 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.3625
990.0    29.00  0.39     Sequence
 HLA-DQA10301-DQB10302    1      PSPIKEMFVFLVLLP  EMFVFLVLL  5        0.2035
5531.9    55.00  0.44     Sequence
 HLA-DQA10301-DQB10302    2      SPIKEMFVFLVLLPL  EMFVFLVLL  4        0.2204
4605.4    46.00  0.32     Sequence
 HLA-DQA10301-DQB10302    3      PIKEMFVFLVLLPLV  EMFVFLVLL  3        0.2064
5360.2    55.00  0.33     Sequence
 HLA-DQA10301-DQB10302    4      IKEMFVFLVLLPLVS  EMFVFLVLL  2        0.1989
5814.5    55.00  0.33     Sequence
 HLA-DQA10301-DQB10302    5      KEMFVFLVLLPLVSS  EMFVFLVLL  1        0.1830
6903.5    60.00  0.38     Sequence
 HLA-DQA10301-DQB10302    6      EMFVFLVLLPLVSSQ  VLLPLVSSQ  6        0.1972
5920.9    55.00  0.31     Sequence
 HLA-DQA10301-DQB10302    7      MFVFLVLLPLVSSQC  VLLPLVSSQ  5        0.1850
6757.3    60.00  0.48     Sequence
 HLA-DQA10301-DQB10302    8      FVFLVLLPLVSSQCV  VLLPLVSSQ  4        0.1829
6909.1    60.00  0.40     Sequence
 HLA-DQA10301-DQB10302    9      VFLVLLPLVSSQCVN  VLLPLVSSQ  3        0.1600
8855.5    70.00  0.47     Sequence
 HLA-DQA10301-DQB10302   10      FLVLLPLVSSQCVNF  VLLPLVSSQ  2        0.1608
8774.0    70.00  0.50     Sequence
 HLA-DQA10301-DQB10302   11      LVLLPLVSSQCVNFT  VLLPLVSSQ  1        0.1695
7989.0    65.00  0.46     Sequence
 HLA-DQA10301-DQB10302   12      VLLPLVSSQCVNFTN  VLLPLVSSQ  0        0.1539
9462.3    75.00  0.40     Sequence
 HLA-DQA10301-DQB10302   13      LLPLVSSQCVNFTNR  VSSQCVNFT  4        0.1169
14118.5    85.00  0.28     Sequence
 HLA-DQA10301-DQB10302   14      LPLVSSQCVNFTNRT  VSSQCVNFT  3        0.1011
16747.9    90.00  0.28     Sequence
 HLA-DQA10301-DQB10302   15      PLVSSQCVNFTNRTQ  CVNFTNRTQ  6        0.1001
16923.1    90.00  0.23     Sequence
 HLA-DQA10301-DQB10302   16      LVSSQCVNFTNRTQL  CVNFTNRTQ  5        0.1127
14778.0    90.00  0.30     Sequence
 HLA-DQA10301-DQB10302   17      VSSQCVNFTNRTQLP  CVNFTNRTQ  4        0.1017
16637.9    90.00  0.30     Sequence
 HLA-DQA10301-DQB10302   18      SSQCVNFTNRTQLPS  CVNFTNRTQ  3        0.0936
18158.7    95.00  0.28     Sequence
 HLA-DQA10301-DQB10302   19      SQCVNFTNRTQLPSA  TNRTQLPSA  6        0.1037
16278.9    90.00  0.28     Sequence
 HLA-DQA10301-DQB10302   20      QCVNFTNRTQLPSAY  TNRTQLPSA  5        0.1026
16478.1    90.00  0.31     Sequence
 HLA-DQA10301-DQB10302   21      CVNFTNRTQLPSAYT  TNRTQLPSA  4        0.1050
16050.3    90.00  0.28     Sequence
 HLA-DQA10301-DQB10302   22      VNFTNRTQLPSAYTN  TQLPSAYTN  6        0.1213
13465.4    85.00  0.34     Sequence
 HLA-DQA10301-DQB10302   23      NFTNRTQLPSAYTNS  TQLPSAYTN  5        0.1145
14479.9    85.00  0.42     Sequence
 HLA-DQA10301-DQB10302   24      FTNRTQLPSAYTNSF  LPSAYTNSF  6        0.1513
9729.9    75.00  0.28     Sequence
 HLA-DQA10301-DQB10302   25      TNRTQLPSAYTNSFT  LPSAYTNSF  5        0.1545
9400.7    75.00  0.32     Sequence
 HLA-DQA10301-DQB10302   26      NRTQLPSAYTNSFTR  LPSAYTNSF  4        0.1480
10084.2    75.00  0.25     Sequence
 HLA-DQA10301-DQB10302   27      RTQLPSAYTNSFTRG  SAYTNSFTR  5        0.1512
9743.4    75.00  0.22     Sequence
 HLA-DQA10301-DQB10302   28      TQLPSAYTNSFTRGV  YTNSFTRGV  6        0.1569
9154.5    70.00  0.22     Sequence
 HLA-DQA10301-DQB10302   29      QLPSAYTNSFTRGVY  YTNSFTRGV  5        0.1584
9009.6    70.00  0.28     Sequence
```

```
 HLA-DQA10301-DQB10302   30      LPSAYTNSFTRGVYY  YTNSFTRGV  4        0.1656
8333.3    70.00  0.25     Sequence
 HLA-DQA10301-DQB10302   31      PSAYTNSFTRGVYYP  NSFTRGVYY  5        0.1595
8902.2    70.00  0.25     Sequence
 HLA-DQA10301-DQB10302   32      SAYTNSFTRGVYYPD  FTRGVYYPD  6        0.2101
5149.9    49.00  0.39     Sequence
 HLA-DQA10301-DQB10302   33      AYTNSFTRGVYYPDK  FTRGVYYPD  5        0.1908
6346.5    60.00  0.40     Sequence
 HLA-DQA10301-DQB10302   34      YTNSFTRGVYYPDKV  FTRGVYYPD  4        0.1996
5765.8    55.00  0.35     Sequence
 HLA-DQA10301-DQB10302   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.1982
5858.3    55.00  0.40     Sequence
 HLA-DQA10301-DQB10302   36      NSFTRGVYYPDKVFR  FTRGVYYPD  2        0.1770
7369.9    65.00  0.40     Sequence
 HLA-DQA10301-DQB10302   37      SFTRGVYYPDKVFRS  FTRGVYYPD  1        0.1635
8520.4    70.00  0.44     Sequence
 HLA-DQA10301-DQB10302   38      FTRGVYYPDKVFRSS  FTRGVYYPD  0        0.1409
10880.8    80.00  0.46     Sequence
 HLA-DQA10301-DQB10302   39      TRGVYYPDKVFRSSV  PDKVFRSSV  6        0.0991
17113.9    90.00  0.25     Sequence
 HLA-DQA10301-DQB10302   40      RGVYYPDKVFRSSVL  DKVFRSSVL  6        0.1355
11542.6    80.00  0.40     Sequence
 HLA-DQA10301-DQB10302   41      GVYYPDKVFRSSVLH  DKVFRSSVL  5        0.1343
11692.0    80.00  0.44     Sequence
 HLA-DQA10301-DQB10302   42      VYYPDKVFRSSVLHS  VFRSSVLHS  6        0.1612
8742.6    70.00  0.35     Sequence
 HLA-DQA10301-DQB10302   43      YYPDKVFRSSVLHST  VFRSSVLHS  5        0.1999
5750.8    55.00  0.37     Sequence
 HLA-DQA10301-DQB10302   44      YPDKVFRSSVLHSTQ  VFRSSVLHS  4        0.1939
6138.0    60.00  0.33     Sequence
 HLA-DQA10301-DQB10302   45      PDKVFRSSVLHSTQD  VFRSSVLHS  3        0.2184
4708.9    46.00  0.28     Sequence
 HLA-DQA10301-DQB10302   46      DKVFRSSVLHSTQDL  SSVLHSTQD  5        0.2210
4577.5    45.00  0.19     Sequence
 HLA-DQA10301-DQB10302   47      KVFRSSVLHSTQDLF  SVLHSTQDL  5        0.2388
3775.9    39.00  0.22     Sequence
 HLA-DQA10301-DQB10302   48      VFRSSVLHSTQDLFL  SVLHSTQDL  4        0.2262
4325.7    43.00  0.20     Sequence
 HLA-DQA10301-DQB10302   49      FRSSVLHSTQDLFLP  SVLHSTQDL  3        0.2136
4955.8    48.00  0.20     Sequence
 HLA-DQA10301-DQB10302   50      RSSVLHSTQDLFLPF  SVLHSTQDL  2        0.2367
3862.6    40.00  0.19     Sequence
 HLA-DQA10301-DQB10302   51      SSVLHSTQDLFLPFF  TQDLFLPFF  6        0.3054
1836.1    20.00  0.40     Sequence
 HLA-DQA10301-DQB10302   52      SVLHSTQDLFLPFFS  TQDLFLPFF  5        0.2997
1952.4    21.00  0.38     Sequence
 HLA-DQA10301-DQB10302   53      VLHSTQDLFLPFFSN  TQDLFLPFF  4        0.3051
1842.8    20.00  0.29     Sequence
 HLA-DQA10301-DQB10302   54      LHSTQDLFLPFFSNV  TQDLFLPFF  3        0.2847
2296.9    25.00  0.29     Sequence
 HLA-DQA10301-DQB10302   55      HSTQDLFLPFFSNVT  TQDLFLPFF  2        0.2746
2562.3    28.00  0.29     Sequence
 HLA-DQA10301-DQB10302   56      STQDLFLPFFSNVTW  TQDLFLPFF  1        0.2815
2378.6    26.00  0.27     Sequence
 HLA-DQA10301-DQB10302   57      TQDLFLPFFSNVTWF  TQDLFLPFF  0        0.2900
2169.9    24.00  0.25     Sequence
 HLA-DQA10301-DQB10302   58      QDLFLPFFSNVTWFH  FFSNVTWFH  6        0.2570
3098.2    33.00  0.16     Sequence
 HLA-DQA10301-DQB10302   59      DLFLPFFSNVTWFHA  FFSNVTWFH  5        0.2559
3136.9    33.00  0.23     Sequence
 HLA-DQA10301-DQB10302   60      LFLPFFSNVTWFHAI  FFSNVTWFH  4        0.2462
3485.5    36.00  0.26     Sequence
 HLA-DQA10301-DQB10302   61      FLPFFSNVTWFHAIH  FFSNVTWFH  3        0.2248
4391.3    44.00  0.26     Sequence
 HLA-DQA10301-DQB10302   62      LPFFSNVTWFHAIHV  FFSNVTWFH  2        0.2279
4246.2    43.00  0.23     Sequence
```

```
 HLA-DQA10301-DQB10302   63      PFFSNVTWFHAIHVS  VTWFHAIHV  5         0.2461
3487.6    36.00  0.22     Sequence
 HLA-DQA10301-DQB10302   64      FFSNVTWFHAIHVSG  TWFHAIHVS  5         0.2710
2664.5    29.00  0.31     Sequence
 HLA-DQA10301-DQB10302   65      FSNVTWFHAIHVSGT  TWFHAIHVS  4         0.2771
2493.0    27.00  0.28     Sequence
 HLA-DQA10301-DQB10302   66      SNVTWFHAIHVSGTN  FHAIHVSGT  5         0.2627
2914.6    31.00  0.32     Sequence
 HLA-DQA10301-DQB10302   67      NVTWFHAIHVSGTNG  FHAIHVSGT  4         0.2496
3358.3    35.00  0.31     Sequence
 HLA-DQA10301-DQB10302   68      VTWFHAIHVSGTNGT  FHAIHVSGT  3         0.2349
3936.5    40.00  0.29     Sequence
 HLA-DQA10301-DQB10302   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2         0.2132
4979.2    48.00  0.35     Sequence
 HLA-DQA10301-DQB10302   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1         0.1770
7367.0    65.00  0.45     Sequence
 HLA-DQA10301-DQB10302   71      FHAIHVSGTNGTKRF  FHAIHVSGT  0         0.1317
12019.9    80.00  0.44     Sequence
 HLA-DQA10301-DQB10302   72      HAIHVSGTNGTKRFD  HAIHVSGTN  0         0.0769
21750.5    95.00  0.20     Sequence
 HLA-DQA10301-DQB10302   73      AIHVSGTNGTKRFDN  VSGTNGTKR  3         0.0650
24754.5   100.00  0.26     Sequence
 HLA-DQA10301-DQB10302   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2         0.0600
26110.0   100.00  0.28     Sequence
 HLA-DQA10301-DQB10302   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1         0.0564
27155.3   100.00  0.27     Sequence
 HLA-DQA10301-DQB10302   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6         0.0786
21354.5    95.00  0.34     Sequence
 HLA-DQA10301-DQB10302   77      SGTNGTKRFDNPVLP  TKRFDNPVL  5         0.0840
20158.1    95.00  0.41     Sequence
 HLA-DQA10301-DQB10302   78      GTNGTKRFDNPVLPF  RFDNPVLPF  6         0.2533
3225.2    34.00  0.51     Sequence
 HLA-DQA10301-DQB10302   79      TNGTKRFDNPVLPFN  RFDNPVLPF  5         0.2453
3519.0    37.00  0.56     Sequence
 HLA-DQA10301-DQB10302   80      NGTKRFDNPVLPFND  RFDNPVLPF  4         0.2965
2022.0    22.00  0.41     Sequence
 HLA-DQA10301-DQB10302   81      GTKRFDNPVLPFNDG  RFDNPVLPF  3         0.2909
2148.0    23.00  0.37     Sequence
 HLA-DQA10301-DQB10302   82      TKRFDNPVLPFNDGV  RFDNPVLPF  2         0.2901
2166.5    24.00  0.35     Sequence
 HLA-DQA10301-DQB10302   83      KRFDNPVLPFNDGVY  RFDNPVLPF  1         0.2860
2265.2    25.00  0.36     Sequence
 HLA-DQA10301-DQB10302   84      RFDNPVLPFNDGVYF  DNPVLPFND  2         0.2833
2331.9    25.00  0.32     Sequence
 HLA-DQA10301-DQB10302   85      FDNPVLPFNDGVYFA  DNPVLPFND  1         0.2388
3775.9    39.00  0.41     Sequence
 HLA-DQA10301-DQB10302   86      DNPVLPFNDGVYFAS  FNDGVYFAS  6         0.2804
2406.8    26.00  0.34     Sequence
 HLA-DQA10301-DQB10302   87      NPVLPFNDGVYFAST  FNDGVYFAS  5         0.2568
3105.3    33.00  0.42     Sequence
 HLA-DQA10301-DQB10302   88      PVLPFNDGVYFASTE  DGVYFASTE  6         0.4397
429.3     3.50  0.64    Sequence         WB
 HLA-DQA10301-DQB10302   89      VLPFNDGVYFASTEK  DGVYFASTE  5         0.4490
388.3     3.00  0.71    Sequence         WB
 HLA-DQA10301-DQB10302   90      LPFNDGVYFASTEKS  DGVYFASTE  4         0.4788
281.2     1.60  0.60    Sequence         SB
 HLA-DQA10301-DQB10302   91      PFNDGVYFASTEKSN  DGVYFASTE  3         0.4561
359.7     2.50  0.63    Sequence         WB
 HLA-DQA10301-DQB10302   92      FNDGVYFASTEKSNI  DGVYFASTE  2         0.4385
434.8     3.50  0.63    Sequence         WB
 HLA-DQA10301-DQB10302   93      NDGVYFASTEKSNII  DGVYFASTE  1         0.4169
549.7     4.50  0.67    Sequence         WB
 HLA-DQA10301-DQB10302   94      DGVYFASTEKSNIIR  DGVYFASTE  0         0.3838
786.1     7.50  0.68    Sequence         WB
 HLA-DQA10301-DQB10302   95      GVYFASTEKSNIIRG  VYFASTEKS  1         0.1984
5843.4    55.00  0.50     Sequence
```

```
 HLA-DQA10301-DQB10302   96      VYFASTEKSNIIRGW  VYFASTEKS  0         0.1826
6933.7    60.00  0.49      Sequence
 HLA-DQA10301-DQB10302   97      YFASTEKSNIIRGWI  EKSNIIRGW  5         0.1163
14209.5    85.00  0.26      Sequence
 HLA-DQA10301-DQB10302   98      FASTEKSNIIRGWIF  SNIIRGWIF  6         0.1713
7837.2    65.00  0.34      Sequence
 HLA-DQA10301-DQB10302   99      ASTEKSNIIRGWIFG  SNIIRGWIF  5         0.1736
7643.0    65.00  0.40      Sequence
 HLA-DQA10301-DQB10302  100      STEKSNIIRGWIFGT  SNIIRGWIF  4         0.1825
6938.5    60.00  0.32      Sequence
 HLA-DQA10301-DQB10302  101      TEKSNIIRGWIFGTT  SNIIRGWIF  3         0.1778
7300.4    65.00  0.31      Sequence
 HLA-DQA10301-DQB10302  102      EKSNIIRGWIFGTTL  SNIIRGWIF  2         0.1947
6080.4    55.00  0.25      Sequence
 HLA-DQA10301-DQB10302  103      KSNIIRGWIFGTTLD  RGWIFGTTL  5         0.2231
4473.8    44.00  0.29      Sequence
 HLA-DQA10301-DQB10302  104      SNIIRGWIFGTTLDS  GWIFGTTLD  5         0.2479
3421.9    36.00  0.30      Sequence
 HLA-DQA10301-DQB10302  105      NIIRGWIFGTTLDSK  GWIFGTTLD  4         0.2262
4325.6    43.00  0.29      Sequence
 HLA-DQA10301-DQB10302  106      IIRGWIFGTTLDSKT  GWIFGTTLD  3         0.2109
5104.5    49.00  0.29      Sequence
 HLA-DQA10301-DQB10302  107      IRGWIFGTTLDSKTQ  GWIFGTTLD  2         0.1917
6283.5    60.00  0.31      Sequence
 HLA-DQA10301-DQB10302  108      RGWIFGTTLDSKTQS  GWIFGTTLD  1         0.1788
7226.5    65.00  0.32      Sequence
 HLA-DQA10301-DQB10302  109      GWIFGTTLDSKTQSL  TLDSKTQSL  6         0.1848
6766.9    60.00  0.31      Sequence
 HLA-DQA10301-DQB10302  110      WIFGTTLDSKTQSLL  TLDSKTQSL  5         0.1652
8373.1    70.00  0.38      Sequence
 HLA-DQA10301-DQB10302  111      IFGTTLDSKTQSLLI  DSKTQSLLI  6         0.1842
6813.0    60.00  0.37      Sequence
 HLA-DQA10301-DQB10302  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5         0.1755
7486.5    65.00  0.38      Sequence
 HLA-DQA10301-DQB10302  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4         0.1773
7341.4    65.00  0.34      Sequence
 HLA-DQA10301-DQB10302  114      TTLDSKTQSLLIVNN  DSKTQSLLI  3         0.1938
6143.2    60.00  0.22      Sequence
 HLA-DQA10301-DQB10302  115      TLDSKTQSLLIVNNA  TQSLLIVNN  5         0.2145
4912.1    48.00  0.32      Sequence
 HLA-DQA10301-DQB10302  116      LDSKTQSLLIVNNAT  TQSLLIVNN  4         0.2007
5701.7    55.00  0.26      Sequence
 HLA-DQA10301-DQB10302  117      DSKTQSLLIVNNATN  TQSLLIVNN  3         0.1883
6516.4    60.00  0.25      Sequence
 HLA-DQA10301-DQB10302  118      SKTQSLLIVNNATNV  TQSLLIVNN  2         0.1736
7645.4    65.00  0.28      Sequence
 HLA-DQA10301-DQB10302  119      KTQSLLIVNNATNVV  TQSLLIVNN  1         0.1818
6995.5    60.00  0.21      Sequence
 HLA-DQA10301-DQB10302  120      TQSLLIVNNATNVVI  VNNATNVVI  6         0.2444
3553.3    37.00  0.38      Sequence
 HLA-DQA10301-DQB10302  121      QSLLIVNNATNVVIK  VNNATNVVI  5         0.2326
4035.0    41.00  0.28      Sequence
 HLA-DQA10301-DQB10302  122      SLLIVNNATNVVIKV  NNATNVVIK  5         0.2422
3636.7    38.00  0.37      Sequence
 HLA-DQA10301-DQB10302  123      LLIVNNATNVVIKVC  NNATNVVIK  4         0.2334
4003.2    41.00  0.34      Sequence
 HLA-DQA10301-DQB10302  124      LIVNNATNVVIKVCE  NNATNVVIK  3         0.2644
2861.0    31.00  0.23      Sequence
 HLA-DQA10301-DQB10302  125      IVNNATNVVIKVCEF  TNVVIKVCE  5         0.2752
2546.8    27.00  0.30      Sequence
 HLA-DQA10301-DQB10302  126      VNNATNVVIKVCEFQ  TNVVIKVCE  4         0.2574
3087.2    33.00  0.31      Sequence
 HLA-DQA10301-DQB10302  127      NNATNVVIKVCEFQF  TNVVIKVCE  3         0.2529
3240.6    34.00  0.34      Sequence
 HLA-DQA10301-DQB10302  128      NATNVVIKVCEFQFC  TNVVIKVCE  2         0.2483
3404.3    36.00  0.37      Sequence
```

```
 HLA-DQA10301-DQB10302  129      ATNVVIKVCEFQFCN  TNVVIKVCE  1        0.2244
4409.9    44.00  0.38     Sequence
 HLA-DQA10301-DQB10302  130      TNVVIKVCEFQFCNY  TNVVIKVCE  0        0.2067
5344.8    55.00  0.41     Sequence
 HLA-DQA10301-DQB10302  131      NVVIKVCEFQFCNYP  NVVIKVCEF  0        0.1546
9391.0    75.00  0.22     Sequence
 HLA-DQA10301-DQB10302  132      VVIKVCEFQFCNYPF  EFQFCNYPF  6        0.1897
6422.1    60.00  0.40     Sequence
 HLA-DQA10301-DQB10302  133      VIKVCEFQFCNYPFL  EFQFCNYPF  5        0.1887
6492.7    60.00  0.44     Sequence
 HLA-DQA10301-DQB10302  134      IKVCEFQFCNYPFLG  EFQFCNYPF  4        0.1637
8505.3    70.00  0.41     Sequence
 HLA-DQA10301-DQB10302  135      KVCEFQFCNYPFLGV  EFQFCNYPF  3        0.1613
8728.4    70.00  0.41     Sequence
 HLA-DQA10301-DQB10302  136      VCEFQFCNYPFLGVY  EFQFCNYPF  2        0.1580
9044.1    70.00  0.38     Sequence
 HLA-DQA10301-DQB10302  137      CEFQFCNYPFLGVYY  EFQFCNYPF  1        0.1527
9586.1    75.00  0.34     Sequence
 HLA-DQA10301-DQB10302  138      EFQFCNYPFLGVYYH  YPFLGVYYH  6        0.1723
7751.3    65.00  0.29     Sequence
 HLA-DQA10301-DQB10302  139      FQFCNYPFLGVYYHK  YPFLGVYYH  5        0.1273
12613.4    85.00  0.38     Sequence
 HLA-DQA10301-DQB10302  140      QFCNYPFLGVYYHKN  YPFLGVYYH  4        0.1254
12874.2    85.00  0.29     Sequence
 HLA-DQA10301-DQB10302  141      FCNYPFLGVYYHKNN  YPFLGVYYH  3        0.1142
14527.6    85.00  0.29     Sequence
 HLA-DQA10301-DQB10302  142      CNYPFLGVYYHKNNK  YPFLGVYYH  2        0.1003
16891.9    90.00  0.37     Sequence
 HLA-DQA10301-DQB10302  143      NYPFLGVYYHKNNKS  YPFLGVYYH  1        0.0958
17742.9    90.00  0.40     Sequence
 HLA-DQA10301-DQB10302  144      YPFLGVYYHKNNKSW  YPFLGVYYH  0        0.0885
19193.5    95.00  0.35     Sequence
 HLA-DQA10301-DQB10302  145      PFLGVYYHKNNKSWM  FLGVYYHKN  1        0.0640
25027.6   100.00  0.43     Sequence
 HLA-DQA10301-DQB10302  146      FLGVYYHKNNKSWME  HKNNKSWME  6        0.0988
17169.7    90.00  0.49     Sequence
 HLA-DQA10301-DQB10302  147      LGVYYHKNNKSWMES  HKNNKSWME  5        0.1257
12837.7    85.00  0.69     Sequence
 HLA-DQA10301-DQB10302  148      GVYYHKNNKSWMESE  NNKSWMESE  6        0.2261
4330.0    43.00  0.59     Sequence
 HLA-DQA10301-DQB10302  149      VYYHKNNKSWMESEF  NNKSWMESE  5        0.2571
3097.2    33.00  0.69     Sequence
 HLA-DQA10301-DQB10302  150      YYHKNNKSWMESEFR  NNKSWMESE  4        0.2457
3502.2    36.00  0.60     Sequence
 HLA-DQA10301-DQB10302  151      YHKNNKSWMESEFRV  NNKSWMESE  3        0.2589
3037.4    32.00  0.57     Sequence
 HLA-DQA10301-DQB10302  152      HKNNKSWMESEFRVY  NNKSWMESE  2        0.3095
1756.4    19.00  0.36     Sequence
 HLA-DQA10301-DQB10302  153      KNNKSWMESEFRVYS  NNKSWMESE  1        0.2886
2201.2    24.00  0.38     Sequence
 HLA-DQA10301-DQB10302  154      NNKSWMESEFRVYSS  NNKSWMESE  0        0.2917
2128.8    23.00  0.26     Sequence
 HLA-DQA10301-DQB10302  155      NKSWMESEFRVYSSA  ESEFRVYSS  5        0.2677
2761.2    30.00  0.30     Sequence
 HLA-DQA10301-DQB10302  156      KSWMESEFRVYSSAN  EFRVYSSAN  6        0.3213
1546.3    17.00  0.38     Sequence
 HLA-DQA10301-DQB10302  157      SWMESEFRVYSSANN  EFRVYSSAN  5        0.3061
1822.3    20.00  0.41     Sequence
 HLA-DQA10301-DQB10302  158      WMESEFRVYSSANNC  EFRVYSSAN  4        0.2873
2232.3    24.00  0.40     Sequence
 HLA-DQA10301-DQB10302  159      MESEFRVYSSANNCT  EFRVYSSAN  3        0.2693
2712.3    29.00  0.40     Sequence
 HLA-DQA10301-DQB10302  160      ESEFRVYSSANNCTF  EFRVYSSAN  2        0.2840
2314.8    25.00  0.32     Sequence
 HLA-DQA10301-DQB10302  161      SEFRVYSSANNCTFE  EFRVYSSAN  1        0.2678
2758.7    30.00  0.30     Sequence
```

```
 HLA-DQA10301-DQB10302  162      EFRVYSSANNCTFEY  SSANNCTFE  5         0.2780
2469.5    27.00  0.22     Sequence
 HLA-DQA10301-DQB10302  163      FRVYSSANNCTFEYV  SSANNCTFE  4         0.2628
2912.6    31.00  0.25     Sequence
 HLA-DQA10301-DQB10302  164      RVYSSANNCTFEYVS  SSANNCTFE  3         0.2474
3440.0    36.00  0.23     Sequence
 HLA-DQA10301-DQB10302  165      VYSSANNCTFEYVSQ  SSANNCTFE  2         0.2323
4049.0    41.00  0.25     Sequence
 HLA-DQA10301-DQB10302  166      YSSANNCTFEYVSQP  SSANNCTFE  1         0.2180
4728.3    46.00  0.24     Sequence
 HLA-DQA10301-DQB10302  167      SSANNCTFEYVSQPF  TFEYVSQPF  6         0.3323
1372.6    15.00  0.47     Sequence
 HLA-DQA10301-DQB10302  168      SANNCTFEYVSQPFL  TFEYVSQPF  5         0.3105
1737.1    19.00  0.44     Sequence
 HLA-DQA10301-DQB10302  169      ANNCTFEYVSQPFLM  TFEYVSQPF  4         0.2991
1965.3    21.00  0.40     Sequence
 HLA-DQA10301-DQB10302  170      NNCTFEYVSQPFLMD  TFEYVSQPF  3         0.3034
1876.0    20.00  0.43     Sequence
 HLA-DQA10301-DQB10302  171      NCTFEYVSQPFLMDL  TFEYVSQPF  2         0.2993
1962.2    21.00  0.38     Sequence
 HLA-DQA10301-DQB10302  172      CTFEYVSQPFLMDLE  TFEYVSQPF  1         0.3192
1581.8    17.00  0.31     Sequence
 HLA-DQA10301-DQB10302  173      TFEYVSQPFLMDLEG  SQPFLMDLE  5         0.3131
1689.1    18.00  0.27     Sequence
 HLA-DQA10301-DQB10302  174      FEYVSQPFLMDLEGK  SQPFLMDLE  4         0.2454
3513.7    37.00  0.34     Sequence
 HLA-DQA10301-DQB10302  175      EYVSQPFLMDLEGKQ  SQPFLMDLE  3         0.2205
4599.7    45.00  0.39     Sequence
 HLA-DQA10301-DQB10302  176      YVSQPFLMDLEGKQG  SQPFLMDLE  2         0.1936
6152.6    60.00  0.43     Sequence
 HLA-DQA10301-DQB10302  177      VSQPFLMDLEGKQGN  SQPFLMDLE  1         0.1731
7687.0    65.00  0.47     Sequence
 HLA-DQA10301-DQB10302  178      SQPFLMDLEGKQGNF  SQPFLMDLE  0         0.1547
9377.7    75.00  0.46     Sequence
 HLA-DQA10301-DQB10302  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2         0.0997
16997.6    90.00  0.25     Sequence
 HLA-DQA10301-DQB10302  180      PFLMDLEGKQGNFKN  FLMDLEGKQ  1         0.0734
22597.3    95.00  0.29     Sequence
 HLA-DQA10301-DQB10302  181      FLMDLEGKQGNFKNL  FLMDLEGKQ  0         0.0543
27786.6   100.00  0.29     Sequence
 HLA-DQA10301-DQB10302  182      LMDLEGKQGNFKNLS  KQGNFKNLS  6         0.0419
31772.1   100.00  0.20     Sequence
 HLA-DQA10301-DQB10302  183      MDLEGKQGNFKNLSE  QGNFKNLSE  6         0.0947
17948.5    95.00  0.61     Sequence
 HLA-DQA10301-DQB10302  184      DLEGKQGNFKNLSEF  QGNFKNLSE  5         0.2059
5387.6    55.00  0.52     Sequence
 HLA-DQA10301-DQB10302  185      LEGKQGNFKNLSEFV  GNFKNLSEF  5         0.2060
5381.7    55.00  0.31     Sequence
 HLA-DQA10301-DQB10302  186      EGKQGNFKNLSEFVF  QGNFKNLSE  3         0.2411
3680.4    38.00  0.28     Sequence
 HLA-DQA10301-DQB10302  187      GKQGNFKNLSEFVFK  QGNFKNLSE  2         0.2222
4516.4    45.00  0.28     Sequence
 HLA-DQA10301-DQB10302  188      KQGNFKNLSEFVFKN  QGNFKNLSE  1         0.2184
4709.1    46.00  0.28     Sequence
 HLA-DQA10301-DQB10302  189      QGNFKNLSEFVFKNI  GNFKNLSEF  1         0.2090
5207.8    50.00  0.24     Sequence
 HLA-DQA10301-DQB10302  190      GNFKNLSEFVFKNID  GNFKNLSEF  0         0.1977
5887.6    55.00  0.20     Sequence
 HLA-DQA10301-DQB10302  191      NFKNLSEFVFKNIDG  SEFVFKNID  5         0.1635
8529.4    70.00  0.25     Sequence
 HLA-DQA10301-DQB10302  192      FKNLSEFVFKNIDGY  FVFKNIDGY  6         0.1896
6428.0    60.00  0.25     Sequence
 HLA-DQA10301-DQB10302  193      KNLSEFVFKNIDGYF  FVFKNIDGY  5         0.1829
6910.4    60.00  0.32     Sequence
 HLA-DQA10301-DQB10302  194      NLSEFVFKNIDGYFK  FVFKNIDGY  4         0.1746
7557.3    65.00  0.31     Sequence
```

```
 HLA-DQA10301-DQB10302  195      LSEFVFKNIDGYFKI  FVFKNIDGY  3        0.1806
7083.9    65.00  0.27     Sequence
 HLA-DQA10301-DQB10302  196      SEFVFKNIDGYFKIY  FVFKNIDGY  2        0.1749
7538.6    65.00  0.26     Sequence
 HLA-DQA10301-DQB10302  197      EFVFKNIDGYFKIYS  FVFKNIDGY  1        0.1597
8886.8    70.00  0.31     Sequence
 HLA-DQA10301-DQB10302  198      FVFKNIDGYFKIYSK  FVFKNIDGY  0        0.1580
9049.6    70.00  0.25     Sequence
 HLA-DQA10301-DQB10302  199      VFKNIDGYFKIYSKH  DGYFKIYSK  5        0.1279
12527.2    85.00  0.32     Sequence
 HLA-DQA10301-DQB10302  200      FKNIDGYFKIYSKHT  DGYFKIYSK  4        0.1159
14265.4    85.00  0.31     Sequence
 HLA-DQA10301-DQB10302  201      KNIDGYFKIYSKHTP  DGYFKIYSK  3        0.1121
14860.3    90.00  0.31     Sequence
 HLA-DQA10301-DQB10302  202      NIDGYFKIYSKHTPI  DGYFKIYSK  2        0.1038
16262.7    90.00  0.34     Sequence
 HLA-DQA10301-DQB10302  203      IDGYFKIYSKHTPIN  DGYFKIYSK  1        0.0955
17799.4    90.00  0.38     Sequence
 HLA-DQA10301-DQB10302  204      DGYFKIYSKHTPINL  DGYFKIYSK  0        0.0884
19211.1    95.00  0.31     Sequence
 HLA-DQA10301-DQB10302  205      GYFKIYSKHTPINLV  SKHTPINLV  6        0.0880
19298.8    95.00  0.34     Sequence
 HLA-DQA10301-DQB10302  206      YFKIYSKHTPINLVR  SKHTPINLV  5        0.0785
21385.0    95.00  0.38     Sequence
 HLA-DQA10301-DQB10302  207      FKIYSKHTPINLVRD  HTPINLVRD  6        0.1175
14023.6    85.00  0.45     Sequence
 HLA-DQA10301-DQB10302  208      KIYSKHTPINLVRDL  HTPINLVRD  5        0.1570
9143.6    70.00  0.44     Sequence
 HLA-DQA10301-DQB10302  209      IYSKHTPINLVRDLP  HTPINLVRD  4        0.1487
10010.5    75.00  0.41     Sequence
 HLA-DQA10301-DQB10302  210      YSKHTPINLVRDLPQ  HTPINLVRD  3        0.1525
9604.9    75.00  0.34     Sequence
 HLA-DQA10301-DQB10302  211      SKHTPINLVRDLPQG  HTPINLVRD  2        0.1510
9758.1    75.00  0.31     Sequence
 HLA-DQA10301-DQB10302  212      KHTPINLVRDLPQGF  HTPINLVRD  1        0.1785
7245.0    65.00  0.24     Sequence
 HLA-DQA10301-DQB10302  213      HTPINLVRDLPQGFS  LVRDLPQGF  5        0.1761
7438.6    65.00  0.29     Sequence
 HLA-DQA10301-DQB10302  214      TPINLVRDLPQGFSA  VRDLPQGFS  5        0.1854
6723.4    60.00  0.19     Sequence
 HLA-DQA10301-DQB10302  215      PINLVRDLPQGFSAL  RDLPQGFSA  5        0.1932
6185.2    60.00  0.25     Sequence
 HLA-DQA10301-DQB10302  216      INLVRDLPQGFSALE  LPQGFSALE  6        0.2134
4967.9    48.00  0.22     Sequence
 HLA-DQA10301-DQB10302  217      NLVRDLPQGFSALEP  LPQGFSALE  5        0.2410
3686.9    38.00  0.31     Sequence
 HLA-DQA10301-DQB10302  218      LVRDLPQGFSALEPL  QGFSALEPL  6        0.3320
1376.3    15.00  0.41     Sequence
 HLA-DQA10301-DQB10302  219      VRDLPQGFSALEPLV  QGFSALEPL  5        0.3173
1614.8    17.00  0.38     Sequence
 HLA-DQA10301-DQB10302  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.3809
810.8     8.00  0.33     Sequence        WB
 HLA-DQA10301-DQB10302  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.3930
711.6     6.50  0.42     Sequence        WB
 HLA-DQA10301-DQB10302  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.3693
920.0     9.00  0.43     Sequence        WB
 HLA-DQA10301-DQB10302  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.3540
1085.5    11.00  0.43     Sequence
 HLA-DQA10301-DQB10302  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.3276
1443.4    15.00  0.47     Sequence
 HLA-DQA10301-DQB10302  225      GFSALEPLVDLPIGI  FSALEPLVD  1        0.2724
2625.3    28.00  0.63     Sequence
 HLA-DQA10301-DQB10302  226      FSALEPLVDLPIGIN  FSALEPLVD  0        0.2567
3109.2    33.00  0.57     Sequence
 HLA-DQA10301-DQB10302  227      SALEPLVDLPIGINI  LVDLPIGIN  5        0.1852
6737.6    60.00  0.33     Sequence
```

```
 HLA-DQA10301-DQB10302  228      ALEPLVDLPIGINIT  DLPIGINIT  6        0.2255
4360.4    44.00  0.44     Sequence
 HLA-DQA10301-DQB10302  229      LEPLVDLPIGINITR  DLPIGINIT  5        0.2069
5328.4    55.00  0.51     Sequence
 HLA-DQA10301-DQB10302  230      EPLVDLPIGINITRF  DLPIGINIT  4        0.2257
4348.3    43.00  0.42     Sequence
 HLA-DQA10301-DQB10302  231      PLVDLPIGINITRFQ  DLPIGINIT  3        0.2614
2955.1    31.00  0.29     Sequence
 HLA-DQA10301-DQB10302  232      LVDLPIGINITRFQT  IGINITRFQ  5        0.2586
3046.8    32.00  0.33     Sequence
 HLA-DQA10301-DQB10302  233      VDLPIGINITRFQTL  IGINITRFQ  4        0.2647
2852.9    30.00  0.27     Sequence
 HLA-DQA10301-DQB10302  234      DLPIGINITRFQTLL  IGINITRFQ  3        0.2389
3770.1    39.00  0.29     Sequence
 HLA-DQA10301-DQB10302  235      LPIGINITRFQTLLA  IGINITRFQ  2        0.2030
5557.4    55.00  0.33     Sequence
 HLA-DQA10301-DQB10302  236      PIGINITRFQTLLAL  IGINITRFQ  1        0.2304
4132.0    42.00  0.22     Sequence
 HLA-DQA10301-DQB10302  237      IGINITRFQTLLALH  TRFQTLLAL  5        0.2084
5244.2    50.00  0.29     Sequence
 HLA-DQA10301-DQB10302  238      GINITRFQTLLALHR  TRFQTLLAL  4        0.1803
7107.6    65.00  0.31     Sequence
 HLA-DQA10301-DQB10302  239      INITRFQTLLALHRS  TRFQTLLAL  3        0.1785
7247.4    65.00  0.28     Sequence
 HLA-DQA10301-DQB10302  240      NITRFQTLLALHRSY  TRFQTLLAL  2        0.1953
6045.0    55.00  0.20     Sequence
 HLA-DQA10301-DQB10302  241      ITRFQTLLALHRSYL  TLLALHRSY  5        0.1818
6997.0    60.00  0.25     Sequence
 HLA-DQA10301-DQB10302  242      TRFQTLLALHRSYLT  TLLALHRSY  4        0.1672
8194.8    70.00  0.24     Sequence
 HLA-DQA10301-DQB10302  243      RFQTLLALHRSYLTP  TLLALHRSY  3        0.1475
10133.6    75.00  0.30     Sequence
 HLA-DQA10301-DQB10302  244      FQTLLALHRSYLTPG  TLLALHRSY  2        0.1463
10268.8    75.00  0.31     Sequence
 HLA-DQA10301-DQB10302  245      QTLLALHRSYLTPGD  TLLALHRSY  1        0.1433
10602.0    75.00  0.30     Sequence
 HLA-DQA10301-DQB10302  246      TLLALHRSYLTPGDS  HRSYLTPGD  5        0.1488
9995.1    75.00  0.22     Sequence
 HLA-DQA10301-DQB10302  247      LLALHRSYLTPGDSS  HRSYLTPGD  4        0.1341
11717.7    80.00  0.22     Sequence
 HLA-DQA10301-DQB10302  248      LALHRSYLTPGDSSS  HRSYLTPGD  3        0.1253
12893.4    85.00  0.21     Sequence
 HLA-DQA10301-DQB10302  249      ALHRSYLTPGDSSSG  HRSYLTPGD  2        0.1140
14568.8    85.00  0.23     Sequence
 HLA-DQA10301-DQB10302  250      LHRSYLTPGDSSSGW  HRSYLTPGD  1        0.1054
15977.4    90.00  0.25     Sequence
 HLA-DQA10301-DQB10302  251      HRSYLTPGDSSSGWT  PGDSSSGWT  6        0.1129
14736.7    85.00  0.26     Sequence
 HLA-DQA10301-DQB10302  252      RSYLTPGDSSSGWTA  PGDSSSGWT  5        0.1396
11043.6    80.00  0.38     Sequence
 HLA-DQA10301-DQB10302  253      SYLTPGDSSSGWTAG  GDSSSGWTA  5        0.1665
8253.0    70.00  0.38     Sequence
 HLA-DQA10301-DQB10302  254      YLTPGDSSSGWTAGA  GDSSSGWTA  4        0.1618
8685.4    70.00  0.35     Sequence
 HLA-DQA10301-DQB10302  255      LTPGDSSSGWTAGAA  GDSSSGWTA  3        0.1737
7636.6    65.00  0.29     Sequence
 HLA-DQA10301-DQB10302  256      TPGDSSSGWTAGAAA  SGWTAGAAA  6        0.2043
5481.4    55.00  0.28     Sequence
 HLA-DQA10301-DQB10302  257      PGDSSSGWTAGAAAY  SGWTAGAAA  5        0.2619
2938.2    31.00  0.29     Sequence
 HLA-DQA10301-DQB10302  258      GDSSSGWTAGAAAYY  GWTAGAAAY  5        0.2876
2224.9    24.00  0.38     Sequence
 HLA-DQA10301-DQB10302  259      DSSSGWTAGAAAYYV  TAGAAAYYV  6        0.3230
1518.4    16.00  0.32     Sequence
 HLA-DQA10301-DQB10302  260      SSSGWTAGAAAYYVG  TAGAAAYYV  5        0.3119
1711.3    19.00  0.38     Sequence
```

```
 HLA-DQA10301-DQB10302  261       SSGWTAGAAAYYVGY  TAGAAAYYV  4         0.3033
1878.4    20.00  0.35     Sequence
 HLA-DQA10301-DQB10302  262       SGWTAGAAAYYVGYL  TAGAAAYYV  3         0.2940
2076.9    23.00  0.34     Sequence
 HLA-DQA10301-DQB10302  263       GWTAGAAAYYVGYLQ  TAGAAAYYV  2         0.2978
1993.6    22.00  0.28     Sequence
 HLA-DQA10301-DQB10302  264       WTAGAAAYYVGYLQP  AAYYVGYLQ  5         0.3394
1271.1    13.00  0.38     Sequence
 HLA-DQA10301-DQB10302  265       TAGAAAYYVGYLQPR  AAYYVGYLQ  4         0.3017
1910.7    21.00  0.38     Sequence
 HLA-DQA10301-DQB10302  266       AGAAAYYVGYLQPRT  AAYYVGYLQ  3         0.2679
2754.7    30.00  0.43     Sequence
 HLA-DQA10301-DQB10302  267       GAAAYYVGYLQPRTF  AAYYVGYLQ  2         0.2679
2754.6    30.00  0.44     Sequence
 HLA-DQA10301-DQB10302  268       AAAYYVGYLQPRTFL  AAYYVGYLQ  1         0.2591
3029.0    32.00  0.46     Sequence
 HLA-DQA10301-DQB10302  269       AAYYVGYLQPRTFLL  AAYYVGYLQ  0         0.2386
3784.2    39.00  0.45     Sequence
 HLA-DQA10301-DQB10302  270       AYYVGYLQPRTFLLK  AYYVGYLQP  0         0.1840
6828.5    60.00  0.28     Sequence
 HLA-DQA10301-DQB10302  271       YYVGYLQPRTFLLKY  YVGYLQPRT  1         0.1218
13384.4    85.00  0.21     Sequence
 HLA-DQA10301-DQB10302  272       YVGYLQPRTFLLKYN  YVGYLQPRT  0         0.0974
17437.1    90.00  0.21     Sequence
 HLA-DQA10301-DQB10302  273       VGYLQPRTFLLKYNE  RTFLLKYNE  6         0.1832
6890.4    60.00  0.62     Sequence
 HLA-DQA10301-DQB10302  274       GYLQPRTFLLKYNEN  RTFLLKYNE  5         0.2125
5017.4    49.00  0.64     Sequence
 HLA-DQA10301-DQB10302  275       YLQPRTFLLKYNENG  RTFLLKYNE  4         0.1895
6432.9    60.00  0.62     Sequence
 HLA-DQA10301-DQB10302  276       LQPRTFLLKYNENGT  RTFLLKYNE  3         0.1768
7386.1    65.00  0.63     Sequence
 HLA-DQA10301-DQB10302  277       QPRTFLLKYNENGTI  RTFLLKYNE  2         0.1720
7774.6    65.00  0.60     Sequence
 HLA-DQA10301-DQB10302  278       PRTFLLKYNENGTIT  RTFLLKYNE  1         0.1639
8486.6    70.00  0.61     Sequence
 HLA-DQA10301-DQB10302  279       RTFLLKYNENGTITD  YNENGTITD  6         0.2240
4428.3    44.00  0.43     Sequence
 HLA-DQA10301-DQB10302  280       TFLLKYNENGTITDA  YNENGTITD  5         0.2212
4568.0    45.00  0.62     Sequence
 HLA-DQA10301-DQB10302  281       FLLKYNENGTITDAV  ENGTITDAV  6         0.3458
1185.4    12.00  0.52     Sequence
 HLA-DQA10301-DQB10302  282       LLKYNENGTITDAVD  ENGTITDAV  5         0.3663
949.8     9.50  0.54    Sequence          WB
 HLA-DQA10301-DQB10302  283       LKYNENGTITDAVDC  ENGTITDAV  4         0.3770
845.8     8.00  0.50    Sequence          WB
 HLA-DQA10301-DQB10302  284       KYNENGTITDAVDCA  ENGTITDAV  3         0.3781
836.4     8.00  0.46    Sequence          WB
 HLA-DQA10301-DQB10302  285       YNENGTITDAVDCAL  ENGTITDAV  2         0.3751
863.6     8.50  0.43    Sequence          WB
 HLA-DQA10301-DQB10302  286       NENGTITDAVDCALD  ENGTITDAV  1         0.3615
1000.8    10.00  0.42     Sequence
 HLA-DQA10301-DQB10302  287       ENGTITDAVDCALDP  ENGTITDAV  0         0.3642
971.5     9.50  0.32    Sequence          WB
 HLA-DQA10301-DQB10302  288       NGTITDAVDCALDPL  AVDCALDPL  6         0.3693
919.9     9.00  0.36    Sequence          WB
 HLA-DQA10301-DQB10302  289       GTITDAVDCALDPLS  AVDCALDPL  5         0.3536
1089.9    11.00  0.34     Sequence
 HLA-DQA10301-DQB10302  290       TITDAVDCALDPLSE  DCALDPLSE  6         0.4560
359.8     2.50  0.43    Sequence          WB
 HLA-DQA10301-DQB10302  291       ITDAVDCALDPLSET  DCALDPLSE  5         0.4544
366.4     2.50  0.48    Sequence          WB
 HLA-DQA10301-DQB10302  292       TDAVDCALDPLSETK  DCALDPLSE  4         0.4337
458.4     3.50  0.47    Sequence          WB
 HLA-DQA10301-DQB10302  293       DAVDCALDPLSETKC  DCALDPLSE  3         0.4162
553.4     5.00  0.50    Sequence          WB
```

```
 HLA-DQA10301-DQB10302  294      AVDCALDPLSETKCT  DCALDPLSE  2        0.3631
983.6    10.00  0.60     Sequence
 HLA-DQA10301-DQB10302  295      VDCALDPLSETKCTL  DCALDPLSE  1        0.3167
1624.1    18.00  0.71     Sequence
 HLA-DQA10301-DQB10302  296      DCALDPLSETKCTLK  DCALDPLSE  0        0.2731
2605.7    28.00  0.78     Sequence
 HLA-DQA10301-DQB10302  297      CALDPLSETKCTLKS  ALDPLSETK  1        0.1006
16828.9    90.00  0.35     Sequence
 HLA-DQA10301-DQB10302  298      ALDPLSETKCTLKSF  ETKCTLKSF  6        0.1427
10674.1    75.00  0.38     Sequence
 HLA-DQA10301-DQB10302  299      LDPLSETKCTLKSFT  ETKCTLKSF  5        0.1288
12412.5    80.00  0.41     Sequence
 HLA-DQA10301-DQB10302  300      DPLSETKCTLKSFTV  ETKCTLKSF  4        0.1248
12952.0    85.00  0.40     Sequence
 HLA-DQA10301-DQB10302  301      PLSETKCTLKSFTVE  CTLKSFTVE  6        0.1535
9502.2    75.00  0.36     Sequence
 HLA-DQA10301-DQB10302  302      LSETKCTLKSFTVEK  CTLKSFTVE  5        0.1595
8905.1    70.00  0.41     Sequence
 HLA-DQA10301-DQB10302  303      SETKCTLKSFTVEKG  CTLKSFTVE  4        0.1661
8290.9    70.00  0.32     Sequence
 HLA-DQA10301-DQB10302  304      ETKCTLKSFTVEKGI  CTLKSFTVE  3        0.1578
9070.4    70.00  0.33     Sequence
 HLA-DQA10301-DQB10302  305      TKCTLKSFTVEKGIY  CTLKSFTVE  2        0.1382
11213.1    80.00  0.40     Sequence
 HLA-DQA10301-DQB10302  306      KCTLKSFTVEKGIYQ  CTLKSFTVE  1        0.1319
11998.0    80.00  0.40     Sequence
 HLA-DQA10301-DQB10302  307      CTLKSFTVEKGIYQT  CTLKSFTVE  0        0.1402
10971.1    80.00  0.30     Sequence
 HLA-DQA10301-DQB10302  308      TLKSFTVEKGIYQTS  TVEKGIYQT  5        0.1184
13889.1    85.00  0.31     Sequence
 HLA-DQA10301-DQB10302  309      LKSFTVEKGIYQTSN  TVEKGIYQT  4        0.1222
13321.5    85.00  0.30     Sequence
 HLA-DQA10301-DQB10302  310      KSFTVEKGIYQTSNF  EKGIYQTSN  5        0.1435
10581.3    75.00  0.38     Sequence
 HLA-DQA10301-DQB10302  311      SFTVEKGIYQTSNFR  EKGIYQTSN  4        0.1272
12622.3    85.00  0.31     Sequence
 HLA-DQA10301-DQB10302  312      FTVEKGIYQTSNFRV  EKGIYQTSN  3        0.1305
12176.5    80.00  0.26     Sequence
 HLA-DQA10301-DQB10302  313      TVEKGIYQTSNFRVQ  YQTSNFRVQ  6        0.1434
10599.4    75.00  0.23     Sequence
 HLA-DQA10301-DQB10302  314      VEKGIYQTSNFRVQP  YQTSNFRVQ  5        0.1425
10699.6    80.00  0.33     Sequence
 HLA-DQA10301-DQB10302  315      EKGIYQTSNFRVQPT  TSNFRVQPT  6        0.2080
5268.5    50.00  0.41     Sequence
 HLA-DQA10301-DQB10302  316      KGIYQTSNFRVQPTE  TSNFRVQPT  5        0.2587
3042.0    32.00  0.47     Sequence
 HLA-DQA10301-DQB10302  317      GIYQTSNFRVQPTES  TSNFRVQPT  4        0.2775
2484.0    27.00  0.37     Sequence
 HLA-DQA10301-DQB10302  318      IYQTSNFRVQPTESI  TSNFRVQPT  3        0.2826
2350.9    25.00  0.29     Sequence
 HLA-DQA10301-DQB10302  319      YQTSNFRVQPTESIV  TSNFRVQPT  2        0.2728
2613.9    28.00  0.29     Sequence
 HLA-DQA10301-DQB10302  320      QTSNFRVQPTESIVR  TSNFRVQPT  1        0.2525
3255.7    34.00  0.28     Sequence
 HLA-DQA10301-DQB10302  321      TSNFRVQPTESIVRF  SNFRVQPTE  1        0.2632
2898.3    31.00  0.21     Sequence
 HLA-DQA10301-DQB10302  322      SNFRVQPTESIVRFP  PTESIVRFP  6        0.2596
3012.2    32.00  0.26     Sequence
 HLA-DQA10301-DQB10302  323      NFRVQPTESIVRFPN  PTESIVRFP  5        0.2499
3346.1    35.00  0.30     Sequence
 HLA-DQA10301-DQB10302  324      FRVQPTESIVRFPNI  PTESIVRFP  4        0.2344
3959.2    40.00  0.29     Sequence
 HLA-DQA10301-DQB10302  325      RVQPTESIVRFPNIT  PTESIVRFP  3        0.2117
5059.5    49.00  0.32     Sequence
 HLA-DQA10301-DQB10302  326      VQPTESIVRFPNITN  PTESIVRFP  2        0.2041
5496.8    55.00  0.31     Sequence
```

```
 HLA-DQA10301-DQB10302  327      QPTESIVRFPNITNL  PTESIVRFP  1        0.1945
6095.2    55.00  0.31     Sequence
 HLA-DQA10301-DQB10302  328      PTESIVRFPNITNLC  PTESIVRFP  0        0.1687
8058.1    65.00  0.31     Sequence
 HLA-DQA10301-DQB10302  329      TESIVRFPNITNLCP  TESIVRFPN  0        0.1453
10379.4    75.00  0.28     Sequence
 HLA-DQA10301-DQB10302  330      ESIVRFPNITNLCPF  PNITNLCPF  6        0.1749
7538.3    65.00  0.31     Sequence
 HLA-DQA10301-DQB10302  331      SIVRFPNITNLCPFG  PNITNLCPF  5        0.1462
10282.7    75.00  0.32     Sequence
 HLA-DQA10301-DQB10302  332      IVRFPNITNLCPFGE  ITNLCPFGE  6        0.2273
4276.3    43.00  0.46     Sequence
 HLA-DQA10301-DQB10302  333      VRFPNITNLCPFGEV  ITNLCPFGE  5        0.2830
2339.9    25.00  0.54     Sequence
 HLA-DQA10301-DQB10302  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.2817
2372.1    26.00  0.52     Sequence
 HLA-DQA10301-DQB10302  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.2652
2837.5    30.00  0.52     Sequence
 HLA-DQA10301-DQB10302  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.2535
3218.5    34.00  0.55     Sequence
 HLA-DQA10301-DQB10302  337      NITNLCPFGEVFNAT  ITNLCPFGE  1        0.2419
3651.0    38.00  0.51     Sequence
 HLA-DQA10301-DQB10302  338      ITNLCPFGEVFNATR  ITNLCPFGE  0        0.2265
4312.5    43.00  0.47     Sequence
 HLA-DQA10301-DQB10302  339      TNLCPFGEVFNATRF  GEVFNATRF  6        0.2339
3980.2    41.00  0.35     Sequence
 HLA-DQA10301-DQB10302  340      NLCPFGEVFNATRFA  GEVFNATRF  5        0.2542
3194.1    34.00  0.37     Sequence
 HLA-DQA10301-DQB10302  341      LCPFGEVFNATRFAS  EVFNATRFA  5        0.2565
3117.7    33.00  0.35     Sequence
 HLA-DQA10301-DQB10302  342      CPFGEVFNATRFASV  EVFNATRFA  4        0.2584
3051.7    32.00  0.30     Sequence
 HLA-DQA10301-DQB10302  343      PFGEVFNATRFASVY  EVFNATRFA  3        0.2572
3092.7    33.00  0.32     Sequence
 HLA-DQA10301-DQB10302  344      FGEVFNATRFASVYA  EVFNATRFA  2        0.2501
3340.7    35.00  0.29     Sequence
 HLA-DQA10301-DQB10302  345      GEVFNATRFASVYAW  TRFASVYAW  6        0.3058
1828.6    20.00  0.32     Sequence
 HLA-DQA10301-DQB10302  346      EVFNATRFASVYAWN  TRFASVYAW  5        0.3014
1918.0    21.00  0.44     Sequence
 HLA-DQA10301-DQB10302  347      VFNATRFASVYAWNR  TRFASVYAW  4        0.3097
1753.2    19.00  0.39     Sequence
 HLA-DQA10301-DQB10302  348      FNATRFASVYAWNRK  TRFASVYAW  3        0.2908
2151.0    23.00  0.35     Sequence
 HLA-DQA10301-DQB10302  349      NATRFASVYAWNRKR  TRFASVYAW  2        0.2741
2576.0    28.00  0.38     Sequence
 HLA-DQA10301-DQB10302  350      ATRFASVYAWNRKRI  TRFASVYAW  1        0.2695
2708.9    29.00  0.40     Sequence
 HLA-DQA10301-DQB10302  351      TRFASVYAWNRKRIS  TRFASVYAW  0        0.2577
3077.4    33.00  0.41     Sequence
 HLA-DQA10301-DQB10302  352      RFASVYAWNRKRISN  FASVYAWNR  1        0.1874
6584.9    60.00  0.45     Sequence
 HLA-DQA10301-DQB10302  353      FASVYAWNRKRISNC  FASVYAWNR  0        0.1676
8152.2    70.00  0.42     Sequence
 HLA-DQA10301-DQB10302  354      ASVYAWNRKRISNCV  WNRKRISNC  5        0.1032
16370.6    90.00  0.26     Sequence
 HLA-DQA10301-DQB10302  355      SVYAWNRKRISNCVA  RKRISNCVA  6        0.0984
17233.9    90.00  0.25     Sequence
 HLA-DQA10301-DQB10302  356      VYAWNRKRISNCVAD  KRISNCVAD  6        0.1331
11846.1    80.00  0.27     Sequence
 HLA-DQA10301-DQB10302  357      YAWNRKRISNCVADY  KRISNCVAD  5        0.1811
7043.6    65.00  0.35     Sequence
 HLA-DQA10301-DQB10302  358      AWNRKRISNCVADYS  KRISNCVAD  4        0.1913
6308.7    60.00  0.28     Sequence
 HLA-DQA10301-DQB10302  359      WNRKRISNCVADYSV  SNCVADYSV  6        0.2281
4238.4    43.00  0.28     Sequence
```

```
 HLA-DQA10301-DQB10302  360      NRKRISNCVADYSVL  SNCVADYSV  5        0.2481
3413.4    36.00  0.28     Sequence
 HLA-DQA10301-DQB10302  361      RKRISNCVADYSVLY  SNCVADYSV  4        0.2395
3746.5    39.00  0.25     Sequence
 HLA-DQA10301-DQB10302  362      KRISNCVADYSVLYN  VADYSVLYN  6        0.2723
2625.8    28.00  0.31     Sequence
 HLA-DQA10301-DQB10302  363      RISNCVADYSVLYNS  VADYSVLYN  5        0.2682
2746.6    29.00  0.41     Sequence
 HLA-DQA10301-DQB10302  364      ISNCVADYSVLYNSA  VADYSVLYN  4        0.2931
2097.4    23.00  0.29     Sequence
 HLA-DQA10301-DQB10302  365      SNCVADYSVLYNSAS  VADYSVLYN  3        0.2810
2390.0    26.00  0.27     Sequence
 HLA-DQA10301-DQB10302  366      NCVADYSVLYNSASF  SVLYNSASF  6        0.3025
1894.0    21.00  0.22     Sequence
 HLA-DQA10301-DQB10302  367      CVADYSVLYNSASFS  SVLYNSASF  5        0.3068
1808.3    20.00  0.26     Sequence
 HLA-DQA10301-DQB10302  368      VADYSVLYNSASFST  VLYNSASFS  5        0.3200
1568.4    17.00  0.23     Sequence
 HLA-DQA10301-DQB10302  369      ADYSVLYNSASFSTF  LYNSASFST  5        0.3432
1219.4    13.00  0.17     Sequence
 HLA-DQA10301-DQB10302  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.3114
1720.1    19.00  0.19     Sequence
 HLA-DQA10301-DQB10302  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.2924
2114.3    23.00  0.19     Sequence
 HLA-DQA10301-DQB10302  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.2913
2137.7    23.00  0.19     Sequence
 HLA-DQA10301-DQB10302  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.2534
3223.6    34.00  0.25     Sequence
 HLA-DQA10301-DQB10302  374      LYNSASFSTFKCYGV  YNSASFSTF  1        0.2219
4531.4    45.00  0.34     Sequence
 HLA-DQA10301-DQB10302  375      YNSASFSTFKCYGVS  YNSASFSTF  0        0.1930
6195.1    60.00  0.34     Sequence
 HLA-DQA10301-DQB10302  376      NSASFSTFKCYGVSP  SASFSTFKC  1        0.1500
9869.8    75.00  0.28     Sequence
 HLA-DQA10301-DQB10302  377      SASFSTFKCYGVSPT  FKCYGVSPT  6        0.2023
5602.8    55.00  0.41     Sequence
 HLA-DQA10301-DQB10302  378      ASFSTFKCYGVSPTK  FKCYGVSPT  5        0.1781
7275.3    65.00  0.43     Sequence
 HLA-DQA10301-DQB10302  379      SFSTFKCYGVSPTKL  FKCYGVSPT  4        0.1796
7162.2    65.00  0.38     Sequence
 HLA-DQA10301-DQB10302  380      FSTFKCYGVSPTKLN  FKCYGVSPT  3        0.1730
7690.0    65.00  0.36     Sequence
 HLA-DQA10301-DQB10302  381      STFKCYGVSPTKLND  FKCYGVSPT  2        0.1655
8344.7    70.00  0.35     Sequence
 HLA-DQA10301-DQB10302  382      TFKCYGVSPTKLNDL  FKCYGVSPT  1        0.1536
9488.1    75.00  0.35     Sequence
 HLA-DQA10301-DQB10302  383      FKCYGVSPTKLNDLC  FKCYGVSPT  0        0.1376
11287.8    80.00  0.34     Sequence
 HLA-DQA10301-DQB10302  384      KCYGVSPTKLNDLCF  CYGVSPTKL  1        0.1102
15171.4    90.00  0.35     Sequence
 HLA-DQA10301-DQB10302  385      CYGVSPTKLNDLCFT  CYGVSPTKL  0        0.1021
16568.6    90.00  0.34     Sequence
 HLA-DQA10301-DQB10302  386      YGVSPTKLNDLCFTN  TKLNDLCFT  5        0.0759
21986.4    95.00  0.19     Sequence
 HLA-DQA10301-DQB10302  387      GVSPTKLNDLCFTNV  LNDLCFTNV  6        0.0960
17693.3    90.00  0.38     Sequence
 HLA-DQA10301-DQB10302  388      VSPTKLNDLCFTNVY  LNDLCFTNV  5        0.1136
14627.6    85.00  0.34     Sequence
 HLA-DQA10301-DQB10302  389      SPTKLNDLCFTNVYA  DLCFTNVYA  6        0.1510
9757.7    75.00  0.34     Sequence
 HLA-DQA10301-DQB10302  390      PTKLNDLCFTNVYAD  LCFTNVYAD  6        0.2681
2749.7    29.00  0.55     Sequence
 HLA-DQA10301-DQB10302  391      TKLNDLCFTNVYADS  LCFTNVYAD  5        0.3160
1637.5    18.00  0.65     Sequence
 HLA-DQA10301-DQB10302  392      KLNDLCFTNVYADSF  LCFTNVYAD  4        0.3897
737.2     7.00  0.44     Sequence          WB
```

```
 HLA-DQA10301-DQB10302  393      LNDLCFTNVYADSFV  LCFTNVYAD  3         0.3828
794.7     7.50  0.43     Sequence         WB
 HLA-DQA10301-DQB10302  394      NDLCFTNVYADSFVI  LCFTNVYAD  2         0.3724
889.5     8.50  0.43     Sequence         WB
 HLA-DQA10301-DQB10302  395      DLCFTNVYADSFVIR  LCFTNVYAD  1         0.3550
1074.0    11.00  0.46     Sequence
 HLA-DQA10301-DQB10302  396      LCFTNVYADSFVIRG  LCFTNVYAD  0         0.3340
1348.2    14.00  0.38     Sequence
 HLA-DQA10301-DQB10302  397      CFTNVYADSFVIRGD  FTNVYADSF  1         0.3205
1559.9    17.00  0.28     Sequence
 HLA-DQA10301-DQB10302  398      FTNVYADSFVIRGDE  ADSFVIRGD  5         0.3716
896.8     9.00  0.31     Sequence         WB
 HLA-DQA10301-DQB10302  399      TNVYADSFVIRGDEV  DSFVIRGDE  5         0.3775
841.8     8.00  0.44     Sequence         WB
 HLA-DQA10301-DQB10302  400      NVYADSFVIRGDEVR  DSFVIRGDE  4         0.3511
1120.0    12.00  0.41     Sequence
 HLA-DQA10301-DQB10302  401      VYADSFVIRGDEVRQ  DSFVIRGDE  3         0.3368
1307.8    14.00  0.41     Sequence
 HLA-DQA10301-DQB10302  402      YADSFVIRGDEVRQI  DSFVIRGDE  2         0.3219
1536.1    16.00  0.43     Sequence
 HLA-DQA10301-DQB10302  403      ADSFVIRGDEVRQIA  DSFVIRGDE  1         0.2998
1950.9    21.00  0.44     Sequence
 HLA-DQA10301-DQB10302  404      DSFVIRGDEVRQIAP  DSFVIRGDE  0         0.2657
2822.3    30.00  0.51     Sequence
 HLA-DQA10301-DQB10302  405      SFVIRGDEVRQIAPG  RGDEVRQIA  4         0.1863
6662.2    60.00  0.22     Sequence
 HLA-DQA10301-DQB10302  406      FVIRGDEVRQIAPGQ  EVRQIAPGQ  6         0.1841
6824.9    60.00  0.23     Sequence
 HLA-DQA10301-DQB10302  407      VIRGDEVRQIAPGQT  EVRQIAPGQ  5         0.1922
6247.6    60.00  0.28     Sequence
 HLA-DQA10301-DQB10302  408      IRGDEVRQIAPGQTG  EVRQIAPGQ  4         0.2116
5067.8    49.00  0.27     Sequence
 HLA-DQA10301-DQB10302  409      RGDEVRQIAPGQTGT  EVRQIAPGQ  3         0.1942
6115.4    60.00  0.28     Sequence
 HLA-DQA10301-DQB10302  410      GDEVRQIAPGQTGTI  EVRQIAPGQ  2         0.1810
7055.2    65.00  0.30     Sequence
 HLA-DQA10301-DQB10302  411      DEVRQIAPGQTGTIA  EVRQIAPGQ  1         0.1692
8016.5    65.00  0.28     Sequence
 HLA-DQA10301-DQB10302  412      EVRQIAPGQTGTIAD  PGQTGTIAD  6         0.1607
8785.8    70.00  0.29     Sequence
 HLA-DQA10301-DQB10302  413      VRQIAPGQTGTIADY  PGQTGTIAD  5         0.1599
8864.2    70.00  0.47     Sequence
 HLA-DQA10301-DQB10302  414      RQIAPGQTGTIADYN  PGQTGTIAD  4         0.1781
7276.0    65.00  0.29     Sequence
 HLA-DQA10301-DQB10302  415      QIAPGQTGTIADYNY  QTGTIADYN  5         0.1962
5983.3    55.00  0.45     Sequence
 HLA-DQA10301-DQB10302  416      IAPGQTGTIADYNYK  QTGTIADYN  4         0.1753
7503.4    65.00  0.43     Sequence
 HLA-DQA10301-DQB10302  417      APGQTGTIADYNYKL  QTGTIADYN  3         0.1691
8026.7    65.00  0.40     Sequence
 HLA-DQA10301-DQB10302  418      PGQTGTIADYNYKLP  QTGTIADYN  2         0.1584
9004.0    70.00  0.42     Sequence
 HLA-DQA10301-DQB10302  419      GQTGTIADYNYKLPD  QTGTIADYN  1         0.1529
9565.2    75.00  0.40     Sequence
 HLA-DQA10301-DQB10302  420      QTGTIADYNYKLPDD  QTGTIADYN  0         0.1661
8287.1    70.00  0.28     Sequence
 HLA-DQA10301-DQB10302  421      TGTIADYNYKLPDDF  DYNYKLPDD  5         0.1664
8263.9    70.00  0.35     Sequence
 HLA-DQA10301-DQB10302  422      GTIADYNYKLPDDFT  DYNYKLPDD  4         0.1523
9618.0    75.00  0.34     Sequence
 HLA-DQA10301-DQB10302  423      TIADYNYKLPDDFTG  DYNYKLPDD  3         0.1443
10488.2    75.00  0.34     Sequence
 HLA-DQA10301-DQB10302  424      IADYNYKLPDDFTGC  DYNYKLPDD  2         0.1383
11191.2    80.00  0.36     Sequence
 HLA-DQA10301-DQB10302  425      ADYNYKLPDDFTGCV  DYNYKLPDD  1         0.1338
11751.0    80.00  0.35     Sequence
```

```
 HLA-DQA10301-DQB10302  426      DYNYKLPDDFTGCVI  PDDFTGCVI  6        0.1636
8515.1    70.00  0.37     Sequence
 HLA-DQA10301-DQB10302  427      YNYKLPDDFTGCVIA  DDFTGCVIA  6        0.2427
3616.7    37.00  0.50     Sequence
 HLA-DQA10301-DQB10302  428      NYKLPDDFTGCVIAW  DDFTGCVIA  5        0.2853
2283.4    25.00  0.46     Sequence
 HLA-DQA10301-DQB10302  429      YKLPDDFTGCVIAWN  DDFTGCVIA  4        0.3477
1161.6    12.00  0.33     Sequence
 HLA-DQA10301-DQB10302  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.3895
739.3     7.00  0.27     Sequence         WB
 HLA-DQA10301-DQB10302  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.3821
801.2     7.50  0.26     Sequence         WB
 HLA-DQA10301-DQB10302  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.3704
908.5     9.00  0.25     Sequence         WB
 HLA-DQA10301-DQB10302  433      DDFTGCVIAWNSNNL  FTGCVIAWN  2        0.3589
1029.0    11.00  0.27     Sequence
 HLA-DQA10301-DQB10302  434      DFTGCVIAWNSNNLD  FTGCVIAWN  1        0.3185
1593.0    17.00  0.31     Sequence
 HLA-DQA10301-DQB10302  435      FTGCVIAWNSNNLDS  TGCVIAWNS  1        0.2932
2095.4    23.00  0.28     Sequence
 HLA-DQA10301-DQB10302  436      TGCVIAWNSNNLDSK  TGCVIAWNS  0        0.2441
3565.0    37.00  0.29     Sequence
 HLA-DQA10301-DQB10302  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3        0.1906
6360.7    60.00  0.36     Sequence
 HLA-DQA10301-DQB10302  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2        0.1735
7650.4    65.00  0.41     Sequence
 HLA-DQA10301-DQB10302  439      VIAWNSNNLDSKVGG  IAWNSNNLD  1        0.1593
8925.9    70.00  0.47     Sequence
 HLA-DQA10301-DQB10302  440      IAWNSNNLDSKVGGN  IAWNSNNLD  0        0.1405
10931.0    80.00  0.48     Sequence
 HLA-DQA10301-DQB10302  441      AWNSNNLDSKVGGNY  WNSNNLDSK  1        0.1049
16078.8    90.00  0.25     Sequence
 HLA-DQA10301-DQB10302  442      WNSNNLDSKVGGNYN  DSKVGGNYN  6        0.0959
17723.7    90.00  0.25     Sequence
 HLA-DQA10301-DQB10302  443      NSNNLDSKVGGNYNY  DSKVGGNYN  5        0.0858
19765.0    95.00  0.41     Sequence
 HLA-DQA10301-DQB10302  444      SNNLDSKVGGNYNYL  DSKVGGNYN  4        0.0882
19248.8    95.00  0.34     Sequence
 HLA-DQA10301-DQB10302  445      NNLDSKVGGNYNYLY  VGGNYNYLY  6        0.1174
14031.8    85.00  0.37     Sequence
 HLA-DQA10301-DQB10302  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.1137
14619.2    85.00  0.39     Sequence
 HLA-DQA10301-DQB10302  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4        0.1185
13878.7    85.00  0.31     Sequence
 HLA-DQA10301-DQB10302  448      DSKVGGNYNYLYRLF  GNYNYLYRL  5        0.1363
11441.8    80.00  0.32     Sequence
 HLA-DQA10301-DQB10302  449      SKVGGNYNYLYRLFR  GNYNYLYRL  4        0.1131
14711.5    85.00  0.30     Sequence
 HLA-DQA10301-DQB10302  450      KVGGNYNYLYRLFRK  VGGNYNYLY  1        0.1007
16811.1    90.00  0.28     Sequence
 HLA-DQA10301-DQB10302  451      VGGNYNYLYRLFRKS  GNYNYLYRL  2        0.0966
17572.1    90.00  0.25     Sequence
 HLA-DQA10301-DQB10302  452      GGNYNYLYRLFRKSN  GNYNYLYRL  1        0.0838
20192.4    95.00  0.28     Sequence
 HLA-DQA10301-DQB10302  453      GNYNYLYRLFRKSNL  GNYNYLYRL  0        0.0773
21658.2    95.00  0.29     Sequence
 HLA-DQA10301-DQB10302  454      NYNYLYRLFRKSNLK  NYNYLYRLF  0        0.0659
24503.0   100.00  0.24     Sequence
 HLA-DQA10301-DQB10302  455      YNYLYRLFRKSNLKP  NYLYRLFRK  1        0.0503
29025.6   100.00  0.25     Sequence
 HLA-DQA10301-DQB10302  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6        0.0859
19739.8    95.00  0.50     Sequence
 HLA-DQA10301-DQB10302  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.0960
17699.0    90.00  0.44     Sequence
 HLA-DQA10301-DQB10302  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.0881
19267.8    95.00  0.43     Sequence
```

```
 HLA-DQA10301-DQB10302  459      YRLFRKSNLKPFERD  SNLKPFERD  6        0.1328
11878.7    80.00  0.31     Sequence
 HLA-DQA10301-DQB10302  460      RLFRKSNLKPFERDI  SNLKPFERD  5        0.1299
12262.0    80.00  0.34     Sequence
 HLA-DQA10301-DQB10302  461      LFRKSNLKPFERDIS  SNLKPFERD  4        0.1246
12980.5    85.00  0.33     Sequence
 HLA-DQA10301-DQB10302  462      FRKSNLKPFERDIST  SNLKPFERD  3        0.1215
13429.5    85.00  0.32     Sequence
 HLA-DQA10301-DQB10302  463      RKSNLKPFERDISTE  PFERDISTE  6        0.1792
7190.5    65.00  0.47     Sequence
 HLA-DQA10301-DQB10302  464      KSNLKPFERDISTEI  PFERDISTE  5        0.2676
2762.9    30.00  0.57     Sequence
 HLA-DQA10301-DQB10302  465      SNLKPFERDISTEIY  ERDISTEIY  6        0.3798
821.3     8.00  0.48    Sequence         WB
 HLA-DQA10301-DQB10302  466      NLKPFERDISTEIYQ  ERDISTEIY  5        0.3656
956.8     9.50  0.48    Sequence         WB
 HLA-DQA10301-DQB10302  467      LKPFERDISTEIYQA  ERDISTEIY  4        0.3713
900.4     9.00  0.38    Sequence         WB
 HLA-DQA10301-DQB10302  468      KPFERDISTEIYQAG  ERDISTEIY  3        0.3614
1001.5    10.00  0.35     Sequence
 HLA-DQA10301-DQB10302  469      PFERDISTEIYQAGS  ERDISTEIY  2        0.3516
1114.2    12.00  0.37     Sequence
 HLA-DQA10301-DQB10302  470      FERDISTEIYQAGST  ERDISTEIY  1        0.3455
1190.3    13.00  0.35     Sequence
 HLA-DQA10301-DQB10302  471      ERDISTEIYQAGSTP  ERDISTEIY  0        0.3137
1678.7    18.00  0.31     Sequence
 HLA-DQA10301-DQB10302  472      RDISTEIYQAGSTPC  TEIYQAGST  4        0.2800
2417.3    26.00  0.23     Sequence
 HLA-DQA10301-DQB10302  473      DISTEIYQAGSTPCN  TEIYQAGST  3        0.2501
3338.9    35.00  0.25     Sequence
 HLA-DQA10301-DQB10302  474      ISTEIYQAGSTPCNG  TEIYQAGST  2        0.2184
4705.2    46.00  0.29     Sequence
 HLA-DQA10301-DQB10302  475      STEIYQAGSTPCNGV  TEIYQAGST  1        0.2055
5411.6    55.00  0.30     Sequence
 HLA-DQA10301-DQB10302  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.1909
6340.9    60.00  0.37     Sequence
 HLA-DQA10301-DQB10302  477      EIYQAGSTPCNGVKG  IYQAGSTPC  1        0.1583
9022.5    70.00  0.46     Sequence
 HLA-DQA10301-DQB10302  478      IYQAGSTPCNGVKGF  IYQAGSTPC  0        0.1169
14121.4    85.00  0.39     Sequence
 HLA-DQA10301-DQB10302  479      YQAGSTPCNGVKGFN  TPCNGVKGF  5        0.0680
23958.2   100.00  0.35     Sequence
 HLA-DQA10301-DQB10302  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.0788
21309.3    95.00  0.27     Sequence
 HLA-DQA10301-DQB10302  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.1064
15812.1    90.00  0.38     Sequence
 HLA-DQA10301-DQB10302  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.1124
14812.6    90.00  0.34     Sequence
 HLA-DQA10301-DQB10302  483      STPCNGVKGFNCYFP  CNGVKGFNC  3        0.1122
14858.5    90.00  0.31     Sequence
 HLA-DQA10301-DQB10302  484      TPCNGVKGFNCYFPL  KGFNCYFPL  6        0.1457
10331.2    75.00  0.26     Sequence
 HLA-DQA10301-DQB10302  485      PCNGVKGFNCYFPLQ  KGFNCYFPL  5        0.1360
11479.2    80.00  0.28     Sequence
 HLA-DQA10301-DQB10302  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.1755
7484.1    65.00  0.31     Sequence
 HLA-DQA10301-DQB10302  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.2193
4658.7    46.00  0.32     Sequence
 HLA-DQA10301-DQB10302  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.1986
5833.6    55.00  0.31     Sequence
 HLA-DQA10301-DQB10302  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3        0.2121
5037.9    49.00  0.29     Sequence
 HLA-DQA10301-DQB10302  490      KGFNCYFPLQSYGFQ  FNCYFPLQS  2        0.1989
5809.8    55.00  0.30     Sequence
 HLA-DQA10301-DQB10302  491      GFNCYFPLQSYGFQP  FNCYFPLQS  1        0.1839
6835.5    60.00  0.32     Sequence
```

```
 HLA-DQA10301-DQB10302  492      FNCYFPLQSYGFQPT  FNCYFPLQS  0         0.1957
6013.9    55.00  0.25     Sequence
 HLA-DQA10301-DQB10302  493      NCYFPLQSYGFQPTY  LQSYGFQPT  5         0.1760
7446.1    65.00  0.35     Sequence
 HLA-DQA10301-DQB10302  494      CYFPLQSYGFQPTYG  LQSYGFQPT  4         0.1498
9888.3    75.00  0.38     Sequence
 HLA-DQA10301-DQB10302  495      YFPLQSYGFQPTYGV  LQSYGFQPT  3         0.1532
9530.4    75.00  0.30     Sequence
 HLA-DQA10301-DQB10302  496      FPLQSYGFQPTYGVG  LQSYGFQPT  2         0.1383
11191.2    80.00  0.32     Sequence
 HLA-DQA10301-DQB10302  497      PLQSYGFQPTYGVGY  LQSYGFQPT  1         0.1276
12576.0    85.00  0.31     Sequence
 HLA-DQA10301-DQB10302  498      LQSYGFQPTYGVGYQ  LQSYGFQPT  0         0.1194
13737.5    85.00  0.26     Sequence
 HLA-DQA10301-DQB10302  499      QSYGFQPTYGVGYQP  QPTYGVGYQ  5         0.1236
13128.2    85.00  0.31     Sequence
 HLA-DQA10301-DQB10302  500      SYGFQPTYGVGYQPY  TYGVGYQPY  6         0.2218
4538.9    45.00  0.49     Sequence
 HLA-DQA10301-DQB10302  501      YGFQPTYGVGYQPYR  TYGVGYQPY  5         0.1992
5796.0    55.00  0.52     Sequence
 HLA-DQA10301-DQB10302  502      GFQPTYGVGYQPYRV  TYGVGYQPY  4         0.2005
5713.1    55.00  0.49     Sequence
 HLA-DQA10301-DQB10302  503      FQPTYGVGYQPYRVV  TYGVGYQPY  3         0.2042
5491.3    55.00  0.46     Sequence
 HLA-DQA10301-DQB10302  504      QPTYGVGYQPYRVVV  TYGVGYQPY  2         0.2017
5641.4    55.00  0.44     Sequence
 HLA-DQA10301-DQB10302  505      PTYGVGYQPYRVVVL  TYGVGYQPY  1         0.2047
5458.7    55.00  0.38     Sequence
 HLA-DQA10301-DQB10302  506      TYGVGYQPYRVVVLS  TYGVGYQPY  0         0.2145
4907.3    48.00  0.33     Sequence
 HLA-DQA10301-DQB10302  507      YGVGYQPYRVVVLSF  PYRVVVLSF  6         0.2773
2489.7    27.00  0.47     Sequence
 HLA-DQA10301-DQB10302  508      GVGYQPYRVVVLSFE  YRVVVLSFE  6         0.3529
1098.8    11.00  0.42     Sequence
 HLA-DQA10301-DQB10302  509      VGYQPYRVVVLSFEL  YRVVVLSFE  5         0.3632
982.4    10.00  0.47     Sequence
 HLA-DQA10301-DQB10302  510      GYQPYRVVVLSFELL  YRVVVLSFE  4         0.3400
1263.1    13.00  0.44     Sequence
 HLA-DQA10301-DQB10302  511      YQPYRVVVLSFELLH  YRVVVLSFE  3         0.3256
1475.5    16.00  0.44     Sequence
 HLA-DQA10301-DQB10302  512      QPYRVVVLSFELLHA  YRVVVLSFE  2         0.3047
1849.9    20.00  0.46     Sequence
 HLA-DQA10301-DQB10302  513      PYRVVVLSFELLHAP  YRVVVLSFE  1         0.2936
2085.8    23.00  0.45     Sequence
 HLA-DQA10301-DQB10302  514      YRVVVLSFELLHAPA  YRVVVLSFE  0         0.2701
2690.3    29.00  0.40     Sequence
 HLA-DQA10301-DQB10302  515      RVVVLSFELLHAPAT  SFELLHAPA  5         0.2236
4448.9    44.00  0.28     Sequence
 HLA-DQA10301-DQB10302  516      VVVLSFELLHAPATV  FELLHAPAT  5         0.2215
4553.6    45.00  0.28     Sequence
 HLA-DQA10301-DQB10302  517      VVLSFELLHAPATVC  FELLHAPAT  4         0.2178
4738.1    47.00  0.22     Sequence
 HLA-DQA10301-DQB10302  518      VLSFELLHAPATVCG  FELLHAPAT  3         0.2083
5252.9    50.00  0.19     Sequence
 HLA-DQA10301-DQB10302  519      LSFELLHAPATVCGP  FELLHAPAT  2         0.2071
5318.5    55.00  0.19     Sequence
 HLA-DQA10301-DQB10302  520      SFELLHAPATVCGPK  FELLHAPAT  1         0.1771
7359.7    65.00  0.26     Sequence
 HLA-DQA10301-DQB10302  521      FELLHAPATVCGPKK  FELLHAPAT  0         0.1523
9621.9    75.00  0.29     Sequence
 HLA-DQA10301-DQB10302  522      ELLHAPATVCGPKKS  HAPATVCGP  3         0.1265
12721.8    85.00  0.23     Sequence
 HLA-DQA10301-DQB10302  523      LLHAPATVCGPKKST  HAPATVCGP  2         0.0987
17179.0    90.00  0.32     Sequence
 HLA-DQA10301-DQB10302  524      LHAPATVCGPKKSTN  HAPATVCGP  1         0.0773
21661.0    95.00  0.42     Sequence
```

```
 HLA-DQA10301-DQB10302  525      HAPATVCGPKKSTNL  HAPATVCGP  0        0.0589
26436.3   100.00  0.46     Sequence
 HLA-DQA10301-DQB10302  526      APATVCGPKKSTNLV  ATVCGPKKS  2        0.0321
35319.6   100.00  0.22     Sequence
 HLA-DQA10301-DQB10302  527      PATVCGPKKSTNLVK  ATVCGPKKS  1        0.0295
36333.2   100.00  0.23     Sequence
 HLA-DQA10301-DQB10302  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5        0.0325
35172.0   100.00  0.28     Sequence
 HLA-DQA10301-DQB10302  529      TVCGPKKSTNLVKNK  KKSTNLVKN  5        0.0291
36499.4   100.00  0.37     Sequence
 HLA-DQA10301-DQB10302  530      VCGPKKSTNLVKNKC  KSTNLVKNK  5        0.0395
32599.1   100.00  0.21     Sequence
 HLA-DQA10301-DQB10302  531      CGPKKSTNLVKNKCV  TNLVKNKCV  6        0.0511
28764.2   100.00  0.31     Sequence
 HLA-DQA10301-DQB10302  532      GPKKSTNLVKNKCVN  TNLVKNKCV  5        0.0474
29950.4   100.00  0.29     Sequence
 HLA-DQA10301-DQB10302  533      PKKSTNLVKNKCVNF  TNLVKNKCV  4        0.0490
29410.6   100.00  0.26     Sequence
 HLA-DQA10301-DQB10302  534      KKSTNLVKNKCVNFN  VKNKCVNFN  6        0.0582
26624.9   100.00  0.29     Sequence
 HLA-DQA10301-DQB10302  535      KSTNLVKNKCVNFNF  VKNKCVNFN  5        0.0804
20941.3    95.00  0.41     Sequence
 HLA-DQA10301-DQB10302  536      STNLVKNKCVNFNFN  VKNKCVNFN  4        0.0822
20549.8    95.00  0.28     Sequence
 HLA-DQA10301-DQB10302  537      TNLVKNKCVNFNFNG  VKNKCVNFN  3        0.0772
21687.0    95.00  0.29     Sequence
 HLA-DQA10301-DQB10302  538      NLVKNKCVNFNFNGL  CVNFNFNGL  6        0.1035
16313.5    90.00  0.20     Sequence
 HLA-DQA10301-DQB10302  539      LVKNKCVNFNFNGLT  VNFNFNGLT  6        0.1386
11157.8    80.00  0.33     Sequence
 HLA-DQA10301-DQB10302  540      VKNKCVNFNFNGLTG  VNFNFNGLT  5        0.1463
10272.0    75.00  0.37     Sequence
 HLA-DQA10301-DQB10302  541      KNKCVNFNFNGLTGT  FNFNGLTGT  6        0.1844
6798.8    60.00  0.37     Sequence
 HLA-DQA10301-DQB10302  542      NKCVNFNFNGLTGTG  FNFNGLTGT  5        0.1748
7546.9    65.00  0.44     Sequence
 HLA-DQA10301-DQB10302  543      KCVNFNFNGLTGTGV  FNFNGLTGT  4        0.1842
6817.4    60.00  0.30     Sequence
 HLA-DQA10301-DQB10302  544      CVNFNFNGLTGTGVL  FNFNGLTGT  3        0.1938
6140.4    60.00  0.22     Sequence
 HLA-DQA10301-DQB10302  545      VNFNFNGLTGTGVLT  FNFNGLTGT  2        0.1726
7725.1    65.00  0.30     Sequence
 HLA-DQA10301-DQB10302  546      NFNFNGLTGTGVLTE  LTGTGVLTE  6        0.3811
809.8     8.00  0.69     Sequence         WB
 HLA-DQA10301-DQB10302  547      FNFNGLTGTGVLTES  LTGTGVLTE  5        0.4611
340.8     2.50  0.83     Sequence         WB
 HLA-DQA10301-DQB10302  548      NFNGLTGTGVLTESN  LTGTGVLTE  4        0.4518
376.6     3.00  0.80     Sequence         WB
 HLA-DQA10301-DQB10302  549      FNGLTGTGVLTESNK  LTGTGVLTE  3        0.4266
494.6     4.00  0.80     Sequence         WB
 HLA-DQA10301-DQB10302  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.4126
575.8     5.00  0.81     Sequence         WB
 HLA-DQA10301-DQB10302  551      GLTGTGVLTESNKKF  LTGTGVLTE  1        0.4002
658.2     6.00  0.81     Sequence         WB
 HLA-DQA10301-DQB10302  552      LTGTGVLTESNKKFL  LTGTGVLTE  0        0.3812
808.8     8.00  0.80     Sequence         WB
 HLA-DQA10301-DQB10302  553      TGTGVLTESNKKFLP  GTGVLTESN  1        0.1787
7235.5    65.00  0.38     Sequence
 HLA-DQA10301-DQB10302  554      GTGVLTESNKKFLPF  ESNKKFLPF  6        0.1566
9188.8    70.00  0.31     Sequence
 HLA-DQA10301-DQB10302  555      TGVLTESNKKFLPFQ  ESNKKFLPF  5        0.1350
11599.9    80.00  0.32     Sequence
 HLA-DQA10301-DQB10302  556      GVLTESNKKFLPFQQ  ESNKKFLPF  4        0.1510
9760.8    75.00  0.31     Sequence
 HLA-DQA10301-DQB10302  557      VLTESNKKFLPFQQF  NKKFLPFQQ  5        0.2361
3887.9    40.00  0.35     Sequence
```

```
 HLA-DQA10301-DQB10302  558      LTESNKKFLPFQQFG  NKKFLPFQQ  4        0.2094
5186.9    50.00  0.34     Sequence
 HLA-DQA10301-DQB10302  559      TESNKKFLPFQQFGR  NKKFLPFQQ  3        0.1889
6473.2    60.00  0.34     Sequence
 HLA-DQA10301-DQB10302  560      ESNKKFLPFQQFGRD  NKKFLPFQQ  2        0.1848
6773.1    60.00  0.33     Sequence
 HLA-DQA10301-DQB10302  561      SNKKFLPFQQFGRDI  NKKFLPFQQ  1        0.1589
8960.7    70.00  0.31     Sequence
 HLA-DQA10301-DQB10302  562      NKKFLPFQQFGRDIA  NKKFLPFQQ  0        0.1536
9489.2    75.00  0.28     Sequence
 HLA-DQA10301-DQB10302  563      KKFLPFQQFGRDIAD  QQFGRDIAD  6        0.1618
8681.6    70.00  0.30     Sequence
 HLA-DQA10301-DQB10302  564      KFLPFQQFGRDIADT  QQFGRDIAD  5        0.1595
8901.0    70.00  0.41     Sequence
 HLA-DQA10301-DQB10302  565      FLPFQQFGRDIADTT  QQFGRDIAD  4        0.1890
6469.1    60.00  0.29     Sequence
 HLA-DQA10301-DQB10302  566      LPFQQFGRDIADTTD  QQFGRDIAD  3        0.2013
5661.0    55.00  0.25     Sequence
 HLA-DQA10301-DQB10302  567      PFQQFGRDIADTTDA  GRDIADTTD  5        0.2242
4419.9    44.00  0.22     Sequence
 HLA-DQA10301-DQB10302  568      FQQFGRDIADTTDAV  RDIADTTDA  5        0.2638
2880.8    31.00  0.25     Sequence
 HLA-DQA10301-DQB10302  569      QQFGRDIADTTDAVR  RDIADTTDA  4        0.2534
3223.1    34.00  0.22     Sequence
 HLA-DQA10301-DQB10302  570      QFGRDIADTTDAVRD  ADTTDAVRD  6        0.3190
1585.1    17.00  0.41     Sequence
 HLA-DQA10301-DQB10302  571      FGRDIADTTDAVRDP  ADTTDAVRD  5        0.3223
1529.6    16.00  0.49     Sequence
 HLA-DQA10301-DQB10302  572      GRDIADTTDAVRDPQ  ADTTDAVRD  4        0.3172
1615.8    17.00  0.43     Sequence
 HLA-DQA10301-DQB10302  573      RDIADTTDAVRDPQT  ADTTDAVRD  3        0.3117
1715.9    19.00  0.38     Sequence
 HLA-DQA10301-DQB10302  574      DIADTTDAVRDPQTL  ADTTDAVRD  2        0.3070
1804.5    20.00  0.38     Sequence
 HLA-DQA10301-DQB10302  575      IADTTDAVRDPQTLE  ADTTDAVRD  1        0.2873
2233.3    24.00  0.38     Sequence
 HLA-DQA10301-DQB10302  576      ADTTDAVRDPQTLEI  ADTTDAVRD  0        0.2833
2331.5    25.00  0.31     Sequence
 HLA-DQA10301-DQB10302  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5        0.2667
2792.3    30.00  0.17     Sequence
 HLA-DQA10301-DQB10302  578      TTDAVRDPQTLEILD  AVRDPQTLE  3        0.2498
3349.6    35.00  0.19     Sequence
 HLA-DQA10301-DQB10302  579      TDAVRDPQTLEILDI  AVRDPQTLE  2        0.2428
3615.4    37.00  0.19     Sequence
 HLA-DQA10301-DQB10302  580      DAVRDPQTLEILDIT  AVRDPQTLE  1        0.2330
4020.7    41.00  0.17     Sequence
 HLA-DQA10301-DQB10302  581      AVRDPQTLEILDITP  VRDPQTLEI  1        0.2182
4719.2    46.00  0.18     Sequence
 HLA-DQA10301-DQB10302  582      VRDPQTLEILDITPC  LEILDITPC  6        0.2511
3303.6    35.00  0.25     Sequence
 HLA-DQA10301-DQB10302  583      RDPQTLEILDITPCS  LEILDITPC  5        0.2432
3597.4    37.00  0.32     Sequence
 HLA-DQA10301-DQB10302  584      DPQTLEILDITPCSF  LEILDITPC  4        0.2787
2451.2    26.00  0.31     Sequence
 HLA-DQA10301-DQB10302  585      PQTLEILDITPCSFG  LEILDITPC  3        0.2505
3324.8    35.00  0.31     Sequence
 HLA-DQA10301-DQB10302  586      QTLEILDITPCSFGG  LEILDITPC  2        0.2361
3886.2    40.00  0.31     Sequence
 HLA-DQA10301-DQB10302  587      TLEILDITPCSFGGV  LEILDITPC  1        0.2172
4770.1    47.00  0.34     Sequence
 HLA-DQA10301-DQB10302  588      LEILDITPCSFGGVS  LEILDITPC  0        0.2096
5175.5    50.00  0.31     Sequence
 HLA-DQA10301-DQB10302  589      EILDITPCSFGGVSV  ILDITPCSF  1        0.1808
7066.0    65.00  0.30     Sequence
 HLA-DQA10301-DQB10302  590      ILDITPCSFGGVSVI  CSFGGVSVI  6        0.1703
7917.3    65.00  0.26     Sequence
```

```
 HLA-DQA10301-DQB10302  591      LDITPCSFGGVSVIT  CSFGGVSVI  5         0.1672
8190.6    70.00  0.32     Sequence
 HLA-DQA10301-DQB10302  592      DITPCSFGGVSVITP  FGGVSVITP  6         0.2376
3823.1    39.00  0.41     Sequence
 HLA-DQA10301-DQB10302  593      ITPCSFGGVSVITPG  FGGVSVITP  5         0.2632
2898.7    31.00  0.48     Sequence
 HLA-DQA10301-DQB10302  594      TPCSFGGVSVITPGT  FGGVSVITP  4         0.2517
3283.2    35.00  0.43     Sequence
 HLA-DQA10301-DQB10302  595      PCSFGGVSVITPGTN  FGGVSVITP  3         0.2509
3312.0    35.00  0.38     Sequence
 HLA-DQA10301-DQB10302  596      CSFGGVSVITPGTNT  FGGVSVITP  2         0.2381
3803.2    39.00  0.38     Sequence
 HLA-DQA10301-DQB10302  597      SFGGVSVITPGTNTS  FGGVSVITP  1         0.2274
4269.1    43.00  0.41     Sequence
 HLA-DQA10301-DQB10302  598      FGGVSVITPGTNTSN  FGGVSVITP  0         0.1998
5758.7    55.00  0.46     Sequence
 HLA-DQA10301-DQB10302  599      GGVSVITPGTNTSNQ  GGVSVITPG  0         0.1533
9523.4    75.00  0.28     Sequence
 HLA-DQA10301-DQB10302  600      GVSVITPGTNTSNQV  TPGTNTSNQ  5         0.1304
12198.2    80.00  0.34     Sequence
 HLA-DQA10301-DQB10302  601      VSVITPGTNTSNQVA  GTNTSNQVA  6         0.1510
9759.4    75.00  0.31     Sequence
 HLA-DQA10301-DQB10302  602      SVITPGTNTSNQVAV  GTNTSNQVA  5         0.1899
6409.9    60.00  0.38     Sequence
 HLA-DQA10301-DQB10302  603      VITPGTNTSNQVAVL  NTSNQVAVL  6         0.2339
3978.8    41.00  0.39     Sequence
 HLA-DQA10301-DQB10302  604      ITPGTNTSNQVAVLY  NTSNQVAVL  5         0.2679
2754.0    30.00  0.47     Sequence
 HLA-DQA10301-DQB10302  605      TPGTNTSNQVAVLYQ  SNQVAVLYQ  6         0.3119
1711.0    19.00  0.41     Sequence
 HLA-DQA10301-DQB10302  606      PGTNTSNQVAVLYQG  SNQVAVLYQ  5         0.3056
1832.5    20.00  0.50     Sequence
 HLA-DQA10301-DQB10302  607      GTNTSNQVAVLYQGV  SNQVAVLYQ  4         0.3005
1935.2    21.00  0.44     Sequence
 HLA-DQA10301-DQB10302  608      TNTSNQVAVLYQGVN  SNQVAVLYQ  3         0.2917
2130.4    23.00  0.46     Sequence
 HLA-DQA10301-DQB10302  609      NTSNQVAVLYQGVNC  SNQVAVLYQ  2         0.2773
2488.2    27.00  0.50     Sequence
 HLA-DQA10301-DQB10302  610      TSNQVAVLYQGVNCT  SNQVAVLYQ  1         0.2548
3173.9    34.00  0.53     Sequence
 HLA-DQA10301-DQB10302  611      SNQVAVLYQGVNCTE  SNQVAVLYQ  0         0.2352
3926.4    40.00  0.46     Sequence
 HLA-DQA10301-DQB10302  612      NQVAVLYQGVNCTEV  LYQGVNCTE  5         0.1966
5960.5    55.00  0.26     Sequence
 HLA-DQA10301-DQB10302  613      QVAVLYQGVNCTEVP  LYQGVNCTE  4         0.2135
4964.5    48.00  0.19     Sequence
 HLA-DQA10301-DQB10302  614      VAVLYQGVNCTEVPV  QGVNCTEVP  5         0.2126
5011.4    48.00  0.30     Sequence
 HLA-DQA10301-DQB10302  615      AVLYQGVNCTEVPVA  QGVNCTEVP  4         0.2273
4272.6    43.00  0.25     Sequence
 HLA-DQA10301-DQB10302  616      VLYQGVNCTEVPVAI  VNCTEVPVA  5         0.2236
4450.1    44.00  0.31     Sequence
 HLA-DQA10301-DQB10302  617      LYQGVNCTEVPVAIH  VNCTEVPVA  4         0.2165
4803.6    47.00  0.28     Sequence
 HLA-DQA10301-DQB10302  618      YQGVNCTEVPVAIHA  CTEVPVAIH  5         0.2163
4815.3    47.00  0.23     Sequence
 HLA-DQA10301-DQB10302  619      QGVNCTEVPVAIHAD  EVPVAIHAD  6         0.2790
2443.6    26.00  0.40     Sequence
 HLA-DQA10301-DQB10302  620      GVNCTEVPVAIHADQ  EVPVAIHAD  5         0.2754
2541.5    27.00  0.47     Sequence
 HLA-DQA10301-DQB10302  621      VNCTEVPVAIHADQL  EVPVAIHAD  4         0.2887
2199.1    24.00  0.40     Sequence
 HLA-DQA10301-DQB10302  622      NCTEVPVAIHADQLT  EVPVAIHAD  3         0.2853
2283.1    25.00  0.40     Sequence
 HLA-DQA10301-DQB10302  623      CTEVPVAIHADQLTP  EVPVAIHAD  2         0.2788
2447.9    26.00  0.38     Sequence
```

```
 HLA-DQA10301-DQB10302  624      TEVPVAIHADQLTPT  EVPVAIHAD  1        0.2793
2434.1    26.00  0.42     Sequence
 HLA-DQA10301-DQB10302  625      EVPVAIHADQLTPTW  EVPVAIHAD  0        0.2602
2993.2    32.00  0.41     Sequence
 HLA-DQA10301-DQB10302  626      VPVAIHADQLTPTWR  PVAIHADQL  1        0.1752
7512.5    65.00  0.28     Sequence
 HLA-DQA10301-DQB10302  627      PVAIHADQLTPTWRV  DQLTPTWRV  6        0.1744
7572.9    65.00  0.25     Sequence
 HLA-DQA10301-DQB10302  628      VAIHADQLTPTWRVY  DQLTPTWRV  5        0.1701
7933.4    65.00  0.32     Sequence
 HLA-DQA10301-DQB10302  629      AIHADQLTPTWRVYS  DQLTPTWRV  4        0.1496
9913.2    75.00  0.32     Sequence
 HLA-DQA10301-DQB10302  630      IHADQLTPTWRVYST  DQLTPTWRV  3        0.1405
10928.8    80.00  0.34     Sequence
 HLA-DQA10301-DQB10302  631      HADQLTPTWRVYSTG  DQLTPTWRV  2        0.1274
12597.9    85.00  0.37     Sequence
 HLA-DQA10301-DQB10302  632      ADQLTPTWRVYSTGS  TWRVYSTGS  6        0.1467
10223.8    75.00  0.28     Sequence
 HLA-DQA10301-DQB10302  633      DQLTPTWRVYSTGSN  TWRVYSTGS  5        0.1719
7787.7    65.00  0.34     Sequence
 HLA-DQA10301-DQB10302  634      QLTPTWRVYSTGSNV  WRVYSTGSN  5        0.1613
8726.0    70.00  0.38     Sequence
 HLA-DQA10301-DQB10302  635      LTPTWRVYSTGSNVF  VYSTGSNVF  6        0.2280
4241.8    43.00  0.35     Sequence
 HLA-DQA10301-DQB10302  636      TPTWRVYSTGSNVFQ  VYSTGSNVF  5        0.2125
5015.4    48.00  0.33     Sequence
 HLA-DQA10301-DQB10302  637      PTWRVYSTGSNVFQT  VYSTGSNVF  4        0.2195
4652.9    46.00  0.23     Sequence
 HLA-DQA10301-DQB10302  638      TWRVYSTGSNVFQTR  STGSNVFQT  5        0.2181
4723.4    46.00  0.31     Sequence
 HLA-DQA10301-DQB10302  639      WRVYSTGSNVFQTRA  STGSNVFQT  4        0.2028
5570.1    55.00  0.31     Sequence
 HLA-DQA10301-DQB10302  640      RVYSTGSNVFQTRAG  STGSNVFQT  3        0.1850
6756.6    60.00  0.34     Sequence
 HLA-DQA10301-DQB10302  641      VYSTGSNVFQTRAGC  STGSNVFQT  2        0.1700
7947.1    65.00  0.36     Sequence
 HLA-DQA10301-DQB10302  642      YSTGSNVFQTRAGCL  STGSNVFQT  1        0.1437
10559.2    75.00  0.38     Sequence
 HLA-DQA10301-DQB10302  643      STGSNVFQTRAGCLI  STGSNVFQT  0        0.1375
11294.6    80.00  0.35     Sequence
 HLA-DQA10301-DQB10302  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.1170
14099.4    85.00  0.26     Sequence
 HLA-DQA10301-DQB10302  645      GSNVFQTRAGCLIGA  QTRAGCLIG  5        0.1133
14681.0    85.00  0.22     Sequence
 HLA-DQA10301-DQB10302  646      SNVFQTRAGCLIGAE  RAGCLIGAE  6        0.3040
1864.6    20.00  0.64     Sequence
 HLA-DQA10301-DQB10302  647      NVFQTRAGCLIGAEY  RAGCLIGAE  5        0.3616
1000.1    10.00  0.71     Sequence
 HLA-DQA10301-DQB10302  648      VFQTRAGCLIGAEYV  RAGCLIGAE  4        0.3649
964.9      9.50  0.68     Sequence         WB
 HLA-DQA10301-DQB10302  649      FQTRAGCLIGAEYVN  RAGCLIGAE  3        0.3506
1126.5    12.00  0.69     Sequence
 HLA-DQA10301-DQB10302  650      QTRAGCLIGAEYVNN  RAGCLIGAE  2        0.3456
1188.0    13.00  0.68     Sequence
 HLA-DQA10301-DQB10302  651      TRAGCLIGAEYVNNS  RAGCLIGAE  1        0.3331
1360.1    15.00  0.68     Sequence
 HLA-DQA10301-DQB10302  652      RAGCLIGAEYVNNSY  RAGCLIGAE  0        0.3150
1654.3    18.00  0.61     Sequence
 HLA-DQA10301-DQB10302  653      AGCLIGAEYVNNSYE  AEYVNNSYE  6        0.2494
3363.7    35.00  0.43     Sequence
 HLA-DQA10301-DQB10302  654      GCLIGAEYVNNSYEC  AEYVNNSYE  5        0.2689
2725.0    29.00  0.49     Sequence
 HLA-DQA10301-DQB10302  655      CLIGAEYVNNSYECD  AEYVNNSYE  4        0.2761
2520.7    27.00  0.40     Sequence
 HLA-DQA10301-DQB10302  656      LIGAEYVNNSYECDI  AEYVNNSYE  3        0.2779
2471.4    27.00  0.36     Sequence
```

```
 HLA-DQA10301-DQB10302  657      IGAEYVNNSYECDIP  AEYVNNSYE  2        0.2683
2742.5    29.00  0.37     Sequence
 HLA-DQA10301-DQB10302  658      GAEYVNNSYECDIPI  AEYVNNSYE  1        0.2722
2629.2    28.00  0.32     Sequence
 HLA-DQA10301-DQB10302  659      AEYVNNSYECDIPIG  AEYVNNSYE  0        0.2656
2825.8    30.00  0.36     Sequence
 HLA-DQA10301-DQB10302  660      EYVNNSYECDIPIGA  YVNNSYECD  1        0.2260
4333.9    43.00  0.31     Sequence
 HLA-DQA10301-DQB10302  661      YVNNSYECDIPIGAG  ECDIPIGAG  6        0.2030
5558.6    55.00  0.28     Sequence
 HLA-DQA10301-DQB10302  662      VNNSYECDIPIGAGI  ECDIPIGAG  5        0.1644
8442.8    70.00  0.40     Sequence
 HLA-DQA10301-DQB10302  663      NNSYECDIPIGAGIC  DIPIGAGIC  6        0.2218
4534.5    45.00  0.39     Sequence
 HLA-DQA10301-DQB10302  664      NSYECDIPIGAGICA  DIPIGAGIC  5        0.2134
4968.2    48.00  0.44     Sequence
 HLA-DQA10301-DQB10302  665      SYECDIPIGAGICAS  DIPIGAGIC  4        0.2173
4763.7    47.00  0.34     Sequence
 HLA-DQA10301-DQB10302  666      YECDIPIGAGICASY  DIPIGAGIC  3        0.2262
4324.5    43.00  0.31     Sequence
 HLA-DQA10301-DQB10302  667      ECDIPIGAGICASYQ  GAGICASYQ  6        0.2533
3226.2    34.00  0.25     Sequence
 HLA-DQA10301-DQB10302  668      CDIPIGAGICASYQT  GAGICASYQ  5        0.2746
2562.0    28.00  0.44     Sequence
 HLA-DQA10301-DQB10302  669      DIPIGAGICASYQTQ  GAGICASYQ  4        0.2741
2575.6    28.00  0.39     Sequence
 HLA-DQA10301-DQB10302  670      IPIGAGICASYQTQT  GAGICASYQ  3        0.2462
3482.3    36.00  0.44     Sequence
 HLA-DQA10301-DQB10302  671      PIGAGICASYQTQTN  GAGICASYQ  2        0.2371
3842.6    39.00  0.43     Sequence
 HLA-DQA10301-DQB10302  672      IGAGICASYQTQTNS  GAGICASYQ  1        0.2217
4540.8    45.00  0.46     Sequence
 HLA-DQA10301-DQB10302  673      GAGICASYQTQTNSP  GAGICASYQ  0        0.1996
5766.3    55.00  0.46     Sequence
 HLA-DQA10301-DQB10302  674      AGICASYQTQTNSPR  GICASYQTQ  1        0.1529
9558.5    75.00  0.36     Sequence
 HLA-DQA10301-DQB10302  675      GICASYQTQTNSPRR  GICASYQTQ  0        0.1124
14817.4    90.00  0.40     Sequence
 HLA-DQA10301-DQB10302  676      ICASYQTQTNSPRRA  CASYQTQTN  1        0.0810
20821.6    95.00  0.25     Sequence
 HLA-DQA10301-DQB10302  677      CASYQTQTNSPRRAR  CASYQTQTN  0        0.0668
24263.2   100.00  0.23     Sequence
 HLA-DQA10301-DQB10302  678      ASYQTQTNSPRRARS  TQTNSPRRA  4        0.0591
26366.9   100.00  0.28     Sequence
 HLA-DQA10301-DQB10302  679      SYQTQTNSPRRARSV  TQTNSPRRA  3        0.0581
26657.8   100.00  0.31     Sequence
 HLA-DQA10301-DQB10302  680      YQTQTNSPRRARSVA  TQTNSPRRA  2        0.0569
27021.0   100.00  0.33     Sequence
 HLA-DQA10301-DQB10302  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.0798
21080.9    95.00  0.42     Sequence
 HLA-DQA10301-DQB10302  682      TQTNSPRRARSVASQ  RRARSVASQ  6        0.1530
9550.5    75.00  0.42     Sequence
 HLA-DQA10301-DQB10302  683      QTNSPRRARSVASQS  RRARSVASQ  5        0.2040
5497.6    55.00  0.42     Sequence
 HLA-DQA10301-DQB10302  684      TNSPRRARSVASQSI  RARSVASQS  5        0.2526
3250.2    34.00  0.35     Sequence
 HLA-DQA10301-DQB10302  685      NSPRRARSVASQSII  RARSVASQS  4        0.2410
3683.9    38.00  0.30     Sequence
 HLA-DQA10301-DQB10302  686      SPRRARSVASQSIIA  RARSVASQS  3        0.2383
3795.7    39.00  0.29     Sequence
 HLA-DQA10301-DQB10302  687      PRRARSVASQSIIAY  RARSVASQS  2        0.2622
2928.9    31.00  0.23     Sequence
 HLA-DQA10301-DQB10302  688      RRARSVASQSIIAYT  VASQSIIAY  5        0.2593
3024.4    32.00  0.25     Sequence
 HLA-DQA10301-DQB10302  689      RARSVASQSIIAYTM  SQSIIAYTM  6        0.3029
1886.9    20.00  0.34     Sequence
```

```
 HLA-DQA10301-DQB10302  690      ARSVASQSIIAYTMS  SQSIIAYTM  5        0.3095
1756.6    19.00  0.44     Sequence
 HLA-DQA10301-DQB10302  691      RSVASQSIIAYTMSL  SQSIIAYTM  4        0.2993
1960.5    21.00  0.41     Sequence
 HLA-DQA10301-DQB10302  692      SVASQSIIAYTMSLG  SQSIIAYTM  3        0.2899
2172.3    24.00  0.37     Sequence
 HLA-DQA10301-DQB10302  693      VASQSIIAYTMSLGA  SQSIIAYTM  2        0.2988
1973.1    21.00  0.31     Sequence
 HLA-DQA10301-DQB10302  694      ASQSIIAYTMSLGAE  AYTMSLGAE  6        0.3991
666.1     6.00  0.39     Sequence         WB
 HLA-DQA10301-DQB10302  695      SQSIIAYTMSLGAEN  AYTMSLGAE  5        0.4032
637.4     6.00  0.47     Sequence         WB
 HLA-DQA10301-DQB10302  696      QSIIAYTMSLGAENS  AYTMSLGAE  4        0.3776
841.1     8.00  0.56     Sequence         WB
 HLA-DQA10301-DQB10302  697      SIIAYTMSLGAENSV  AYTMSLGAE  3        0.3635
979.2    10.00  0.56     Sequence
 HLA-DQA10301-DQB10302  698      IIAYTMSLGAENSVA  AYTMSLGAE  2        0.3592
1025.6    11.00  0.52     Sequence
 HLA-DQA10301-DQB10302  699      IAYTMSLGAENSVAY  AYTMSLGAE  1        0.3642
972.2     9.50  0.44     Sequence         WB
 HLA-DQA10301-DQB10302  700      AYTMSLGAENSVAYS  AYTMSLGAE  0        0.3437
1213.6    13.00  0.37     Sequence
 HLA-DQA10301-DQB10302  701      YTMSLGAENSVAYSN  SLGAENSVA  3        0.3009
1927.6    21.00  0.23     Sequence
 HLA-DQA10301-DQB10302  702      TMSLGAENSVAYSNN  SLGAENSVA  2        0.2769
2500.1    27.00  0.25     Sequence
 HLA-DQA10301-DQB10302  703      MSLGAENSVAYSNNS  SLGAENSVA  1        0.2604
2987.4    32.00  0.28     Sequence
 HLA-DQA10301-DQB10302  704      SLGAENSVAYSNNSI  SLGAENSVA  0        0.2613
2959.0    32.00  0.22     Sequence
 HLA-DQA10301-DQB10302  705      LGAENSVAYSNNSIA  GAENSVAYS  1        0.2624
2924.2    31.00  0.23     Sequence
 HLA-DQA10301-DQB10302  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.2820
2365.6    26.00  0.31     Sequence
 HLA-DQA10301-DQB10302  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.2807
2398.9    26.00  0.29     Sequence
 HLA-DQA10301-DQB10302  708      ENSVAYSNNSIAIPT  YSNNSIAIP  5        0.3078
1789.8    19.00  0.25     Sequence
 HLA-DQA10301-DQB10302  709      NSVAYSNNSIAIPTN  SNNSIAIPT  5        0.2945
2065.2    22.00  0.32     Sequence
 HLA-DQA10301-DQB10302  710      SVAYSNNSIAIPTNF  SNNSIAIPT  4        0.3066
1812.4    20.00  0.32     Sequence
 HLA-DQA10301-DQB10302  711      VAYSNNSIAIPTNFT  SNNSIAIPT  3        0.2920
2122.1    23.00  0.34     Sequence
 HLA-DQA10301-DQB10302  712      AYSNNSIAIPTNFTI  SNNSIAIPT  2        0.2730
2607.0    28.00  0.38     Sequence
 HLA-DQA10301-DQB10302  713      YSNNSIAIPTNFTIS  SNNSIAIPT  1        0.2514
3292.2    35.00  0.40     Sequence
 HLA-DQA10301-DQB10302  714      SNNSIAIPTNFTISV  SNNSIAIPT  0        0.2133
4971.5    48.00  0.41     Sequence
 HLA-DQA10301-DQB10302  715      NNSIAIPTNFTISVT  NNSIAIPTN  0        0.1848
6767.9    60.00  0.19     Sequence
 HLA-DQA10301-DQB10302  716      NSIAIPTNFTISVTT  TNFTISVTT  6        0.2483
3404.6    36.00  0.56     Sequence
 HLA-DQA10301-DQB10302  717      SIAIPTNFTISVTTE  NFTISVTTE  6        0.3991
666.4     6.00  0.56     Sequence         WB
 HLA-DQA10301-DQB10302  718      IAIPTNFTISVTTEI  NFTISVTTE  5        0.4526
373.5     3.00  0.63     Sequence         WB
 HLA-DQA10301-DQB10302  719      AIPTNFTISVTTEIL  NFTISVTTE  4        0.4369
442.5     3.50  0.63     Sequence         WB
 HLA-DQA10301-DQB10302  720      IPTNFTISVTTEILP  NFTISVTTE  3        0.4279
487.6     4.00  0.63     Sequence         WB
 HLA-DQA10301-DQB10302  721      PTNFTISVTTEILPV  NFTISVTTE  2        0.4187
539.0     4.50  0.62     Sequence         WB
 HLA-DQA10301-DQB10302  722      TNFTISVTTEILPVS  NFTISVTTE  1        0.4002
658.5     6.00  0.63     Sequence         WB
```

```
 HLA-DQA10301-DQB10302  723      NFTISVTTEILPVSM  NFTISVTTE  0        0.3893
740.6     7.00  0.56     Sequence         WB
 HLA-DQA10301-DQB10302  724      FTISVTTEILPVSMT  TTEILPVSM  5        0.2934
2090.5    23.00  0.29     Sequence
 HLA-DQA10301-DQB10302  725      TISVTTEILPVSMTK  TTEILPVSM  4        0.2332
4008.8    41.00  0.38     Sequence
 HLA-DQA10301-DQB10302  726      ISVTTEILPVSMTKT  TTEILPVSM  3        0.2157
4846.6    47.00  0.37     Sequence
 HLA-DQA10301-DQB10302  727      SVTTEILPVSMTKTS  TTEILPVSM  2        0.1994
5779.0    55.00  0.38     Sequence
 HLA-DQA10301-DQB10302  728      VTTEILPVSMTKTSV  TTEILPVSM  1        0.1827
6924.2    60.00  0.44     Sequence
 HLA-DQA10301-DQB10302  729      TTEILPVSMTKTSVD  TTEILPVSM  0        0.1717
7803.1    65.00  0.33     Sequence
 HLA-DQA10301-DQB10302  730      TEILPVSMTKTSVDC  VSMTKTSVD  5        0.1489
9982.8    75.00  0.43     Sequence
 HLA-DQA10301-DQB10302  731      EILPVSMTKTSVDCT  VSMTKTSVD  4        0.1310
12114.0    80.00  0.48     Sequence
 HLA-DQA10301-DQB10302  732      ILPVSMTKTSVDCTM  VSMTKTSVD  3        0.1248
12958.4    85.00  0.47     Sequence
 HLA-DQA10301-DQB10302  733      LPVSMTKTSVDCTMY  VSMTKTSVD  2        0.1197
13696.3    85.00  0.43     Sequence
 HLA-DQA10301-DQB10302  734      PVSMTKTSVDCTMYI  VSMTKTSVD  1        0.1286
12436.7    80.00  0.34     Sequence
 HLA-DQA10301-DQB10302  735      VSMTKTSVDCTMYIC  SVDCTMYIC  6        0.1521
9648.0    75.00  0.31     Sequence
 HLA-DQA10301-DQB10302  736      SMTKTSVDCTMYICG  SVDCTMYIC  5        0.1380
11232.2    80.00  0.38     Sequence
 HLA-DQA10301-DQB10302  737      MTKTSVDCTMYICGD  DCTMYICGD  6        0.2145
4908.3    48.00  0.43     Sequence
 HLA-DQA10301-DQB10302  738      TKTSVDCTMYICGDS  DCTMYICGD  5        0.2229
4480.9    45.00  0.52     Sequence
 HLA-DQA10301-DQB10302  739      KTSVDCTMYICGDST  DCTMYICGD  4        0.2440
3569.0    37.00  0.41     Sequence
 HLA-DQA10301-DQB10302  740      TSVDCTMYICGDSTE  DCTMYICGD  3        0.2532
3229.9    34.00  0.37     Sequence
 HLA-DQA10301-DQB10302  741      SVDCTMYICGDSTEC  DCTMYICGD  2        0.2441
3564.7    37.00  0.37     Sequence
 HLA-DQA10301-DQB10302  742      VDCTMYICGDSTECS  DCTMYICGD  1        0.2249
4387.4    44.00  0.38     Sequence
 HLA-DQA10301-DQB10302  743      DCTMYICGDSTECSN  DCTMYICGD  0        0.2035
5528.3    55.00  0.38     Sequence
 HLA-DQA10301-DQB10302  744      CTMYICGDSTECSNL  TMYICGDST  1        0.1464
10254.0    75.00  0.29     Sequence
 HLA-DQA10301-DQB10302  745      TMYICGDSTECSNLL  TMYICGDST  0        0.1600
8851.7    70.00  0.25     Sequence
 HLA-DQA10301-DQB10302  746      MYICGDSTECSNLLL  DSTECSNLL  5        0.1429
10658.8    75.00  0.19     Sequence
 HLA-DQA10301-DQB10302  747      YICGDSTECSNLLLQ  TECSNLLLQ  6        0.1749
7533.2    65.00  0.45     Sequence
 HLA-DQA10301-DQB10302  748      ICGDSTECSNLLLQY  TECSNLLLQ  5        0.2207
4593.2    45.00  0.49     Sequence
 HLA-DQA10301-DQB10302  749      CGDSTECSNLLLQYG  TECSNLLLQ  4        0.1986
5829.8    55.00  0.48     Sequence
 HLA-DQA10301-DQB10302  750      GDSTECSNLLLQYGS  TECSNLLLQ  3        0.1944
6104.0    60.00  0.46     Sequence
 HLA-DQA10301-DQB10302  751      DSTECSNLLLQYGSF  TECSNLLLQ  2        0.2179
4732.2    46.00  0.39     Sequence
 HLA-DQA10301-DQB10302  752      STECSNLLLQYGSFC  TECSNLLLQ  1        0.1916
6286.8    60.00  0.41     Sequence
 HLA-DQA10301-DQB10302  753      TECSNLLLQYGSFCT  TECSNLLLQ  0        0.1888
6485.0    60.00  0.35     Sequence
 HLA-DQA10301-DQB10302  754      ECSNLLLQYGSFCTQ  ECSNLLLQY  0        0.1586
8985.4    70.00  0.18     Sequence
 HLA-DQA10301-DQB10302  755      CSNLLLQYGSFCTQL  LQYGSFCTQ  5        0.1379
11247.9    80.00  0.19     Sequence
```

```
 HLA-DQA10301-DQB10302  756      SNLLLQYGSFCTQLN  YGSFCTQLN  6        0.1632
8554.5    70.00  0.24     Sequence
 HLA-DQA10301-DQB10302  757      NLLLQYGSFCTQLNR  YGSFCTQLN  5        0.1470
10190.4    75.00  0.31     Sequence
 HLA-DQA10301-DQB10302  758      LLLQYGSFCTQLNRA  YGSFCTQLN  4        0.1424
10706.9    80.00  0.26     Sequence
 HLA-DQA10301-DQB10302  759      LLQYGSFCTQLNRAL  YGSFCTQLN  3        0.1417
10787.7    80.00  0.23     Sequence
 HLA-DQA10301-DQB10302  760      LQYGSFCTQLNRALT  YGSFCTQLN  2        0.1276
12574.7    85.00  0.26     Sequence
 HLA-DQA10301-DQB10302  761      QYGSFCTQLNRALTG  YGSFCTQLN  1        0.1369
11367.1    80.00  0.26     Sequence
 HLA-DQA10301-DQB10302  762      YGSFCTQLNRALTGI  TQLNRALTG  5        0.1294
12332.3    80.00  0.22     Sequence
 HLA-DQA10301-DQB10302  763      GSFCTQLNRALTGIA  LNRALTGIA  6        0.1628
8590.7    70.00  0.44     Sequence
 HLA-DQA10301-DQB10302  764      SFCTQLNRALTGIAV  LNRALTGIA  5        0.1966
5956.8    55.00  0.42     Sequence
 HLA-DQA10301-DQB10302  765      FCTQLNRALTGIAVE  RALTGIAVE  6        0.4419
419.2     3.50  0.69    Sequence         WB
 HLA-DQA10301-DQB10302  766      CTQLNRALTGIAVEQ  RALTGIAVE  5        0.4747
293.9     1.80  0.76    Sequence         SB
 HLA-DQA10301-DQB10302  767      TQLNRALTGIAVEQD  RALTGIAVE  4        0.5070
207.2     1.00  0.63    Sequence         SB
 HLA-DQA10301-DQB10302  768      QLNRALTGIAVEQDK  RALTGIAVE  3        0.5008
221.6     1.10  0.61    Sequence         SB
 HLA-DQA10301-DQB10302  769      LNRALTGIAVEQDKN  RALTGIAVE  2        0.4872
256.7     1.40  0.62    Sequence         SB
 HLA-DQA10301-DQB10302  770      NRALTGIAVEQDKNT  RALTGIAVE  1        0.4751
292.9     1.80  0.62    Sequence         SB
 HLA-DQA10301-DQB10302  771      RALTGIAVEQDKNTQ  RALTGIAVE  0        0.4478
393.4     3.00  0.61    Sequence         WB
 HLA-DQA10301-DQB10302  772      ALTGIAVEQDKNTQE  LTGIAVEQD  1        0.2863
2257.7    25.00  0.60     Sequence
 HLA-DQA10301-DQB10302  773      LTGIAVEQDKNTQEV  LTGIAVEQD  0        0.2500
3342.9    35.00  0.62     Sequence
 HLA-DQA10301-DQB10302  774      TGIAVEQDKNTQEVF  EQDKNTQEV  5        0.2244
4411.2    44.00  0.41     Sequence
 HLA-DQA10301-DQB10302  775      GIAVEQDKNTQEVFA  EQDKNTQEV  4        0.2151
4875.2    48.00  0.34     Sequence
 HLA-DQA10301-DQB10302  776      IAVEQDKNTQEVFAQ  EQDKNTQEV  3        0.2226
4495.4    45.00  0.25     Sequence
 HLA-DQA10301-DQB10302  777      AVEQDKNTQEVFAQV  KNTQEVFAQ  5        0.2541
3197.9    34.00  0.37     Sequence
 HLA-DQA10301-DQB10302  778      VEQDKNTQEVFAQVK  KNTQEVFAQ  4        0.2747
2560.7    28.00  0.25     Sequence
 HLA-DQA10301-DQB10302  779      EQDKNTQEVFAQVKQ  TQEVFAQVK  5        0.2568
3105.5    33.00  0.28     Sequence
 HLA-DQA10301-DQB10302  780      QDKNTQEVFAQVKQI  TQEVFAQVK  4        0.2439
3570.2    37.00  0.28     Sequence
 HLA-DQA10301-DQB10302  781      DKNTQEVFAQVKQIY  TQEVFAQVK  3        0.2167
4794.4    47.00  0.32     Sequence
 HLA-DQA10301-DQB10302  782      KNTQEVFAQVKQIYK  TQEVFAQVK  2        0.1928
6212.0    60.00  0.34     Sequence
 HLA-DQA10301-DQB10302  783      NTQEVFAQVKQIYKT  TQEVFAQVK  1        0.1762
7426.9    65.00  0.38     Sequence
 HLA-DQA10301-DQB10302  784      TQEVFAQVKQIYKTP  TQEVFAQVK  0        0.1520
9651.8    75.00  0.38     Sequence
 HLA-DQA10301-DQB10302  785      QEVFAQVKQIYKTPP  EVFAQVKQI  1        0.1168
14131.1    85.00  0.37     Sequence
 HLA-DQA10301-DQB10302  786      EVFAQVKQIYKTPPI  EVFAQVKQI  0        0.0998
16987.5    90.00  0.40     Sequence
 HLA-DQA10301-DQB10302  787      VFAQVKQIYKTPPIK  AQVKQIYKT  2        0.0675
24092.1   100.00  0.28     Sequence
 HLA-DQA10301-DQB10302  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6        0.0854
19837.4    95.00  0.35     Sequence
```

```
 HLA-DQA10301-DQB10302  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.1245
13003.4    85.00  0.47     Sequence
 HLA-DQA10301-DQB10302  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.1106
15108.5    90.00  0.47     Sequence
 HLA-DQA10301-DQB10302  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.1009
16778.6    90.00  0.49     Sequence
 HLA-DQA10301-DQB10302  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.1003
16896.2    90.00  0.49     Sequence
 HLA-DQA10301-DQB10302  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.1005
16849.9    90.00  0.44     Sequence
 HLA-DQA10301-DQB10302  794      IYKTPPIKDFGGFNF  IKDFGGFNF  6        0.1193
13759.2    85.00  0.34     Sequence
 HLA-DQA10301-DQB10302  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.1180
13941.6    85.00  0.43     Sequence
 HLA-DQA10301-DQB10302  796      KTPPIKDFGGFNFSQ  DFGGFNFSQ  6        0.1941
6124.1    60.00  0.55     Sequence
 HLA-DQA10301-DQB10302  797      TPPIKDFGGFNFSQI  DFGGFNFSQ  5        0.2291
4191.6    42.00  0.60     Sequence
 HLA-DQA10301-DQB10302  798      PPIKDFGGFNFSQIL  DFGGFNFSQ  4        0.2505
3324.3    35.00  0.46     Sequence
 HLA-DQA10301-DQB10302  799      PIKDFGGFNFSQILP  DFGGFNFSQ  3        0.2494
3364.1    35.00  0.42     Sequence
 HLA-DQA10301-DQB10302  800      IKDFGGFNFSQILPD  FNFSQILPD  6        0.4281
486.8     4.00  0.52    Sequence         WB
 HLA-DQA10301-DQB10302  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.4316
468.5     4.00  0.65    Sequence         WB
 HLA-DQA10301-DQB10302  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.4201
531.1     4.50  0.63    Sequence         WB
 HLA-DQA10301-DQB10302  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.3832
791.5     7.50  0.72    Sequence         WB
 HLA-DQA10301-DQB10302  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.3702
911.1     9.00  0.74    Sequence         WB
 HLA-DQA10301-DQB10302  805      GFNFSQILPDPSKPS  FNFSQILPD  1        0.3620
995.6    10.00  0.77    Sequence
 HLA-DQA10301-DQB10302  806      FNFSQILPDPSKPSK  FNFSQILPD  0        0.3394
1270.7    13.00  0.78     Sequence
 HLA-DQA10301-DQB10302  807      NFSQILPDPSKPSKR  FSQILPDPS  1        0.1334
11805.5    80.00  0.47     Sequence
 HLA-DQA10301-DQB10302  808      FSQILPDPSKPSKRS  FSQILPDPS  0        0.0799
21053.8    95.00  0.50     Sequence
 HLA-DQA10301-DQB10302  809      SQILPDPSKPSKRSF  QILPDPSKP  1        0.0448
30793.6   100.00  0.19     Sequence
 HLA-DQA10301-DQB10302  810      QILPDPSKPSKRSFI  QILPDPSKP  0        0.0368
33566.2   100.00  0.19     Sequence
 HLA-DQA10301-DQB10302  811      ILPDPSKPSKRSFIE  KPSKRSFIE  6        0.0796
21142.1    95.00  0.56     Sequence
 HLA-DQA10301-DQB10302  812      LPDPSKPSKRSFIED  KPSKRSFIE  5        0.1388
11135.9    80.00  0.67     Sequence
 HLA-DQA10301-DQB10302  813      PDPSKPSKRSFIEDL  SKRSFIEDL  6        0.1950
6060.5    55.00  0.49     Sequence
 HLA-DQA10301-DQB10302  814      DPSKPSKRSFIEDLL  SKRSFIEDL  5        0.1860
6681.3    60.00  0.47     Sequence
 HLA-DQA10301-DQB10302  815      PSKPSKRSFIEDLLF  SKRSFIEDL  4        0.2231
4473.6    44.00  0.35     Sequence
 HLA-DQA10301-DQB10302  816      SKPSKRSFIEDLLFN  SKRSFIEDL  3        0.2025
5587.4    55.00  0.35     Sequence
 HLA-DQA10301-DQB10302  817      KPSKRSFIEDLLFNK  SKRSFIEDL  2        0.1889
6474.9    60.00  0.38     Sequence
 HLA-DQA10301-DQB10302  818      PSKRSFIEDLLFNKV  SKRSFIEDL  1        0.1941
6120.9    60.00  0.32     Sequence
 HLA-DQA10301-DQB10302  819      SKRSFIEDLLFNKVT  SKRSFIEDL  0        0.1924
6238.2    60.00  0.24     Sequence
 HLA-DQA10301-DQB10302  820      KRSFIEDLLFNKVTL  EDLLFNKVT  5        0.1855
6717.9    60.00  0.27     Sequence
 HLA-DQA10301-DQB10302  821      RSFIEDLLFNKVTLA  EDLLFNKVT  4        0.1812
7040.1    65.00  0.25     Sequence
```

```
 HLA-DQA10301-DQB10302  822      SFIEDLLFNKVTLAD  LFNKVTLAD  6        0.2258
4345.1    43.00  0.28     Sequence
 HLA-DQA10301-DQB10302  823      FIEDLLFNKVTLADA  LFNKVTLAD  5        0.2504
3328.3    35.00  0.22     Sequence
 HLA-DQA10301-DQB10302  824      IEDLLFNKVTLADAG  FNKVTLADA  5        0.2394
3750.4    39.00  0.29     Sequence
 HLA-DQA10301-DQB10302  825      EDLLFNKVTLADAGF  FNKVTLADA  4        0.2405
3704.7    38.00  0.28     Sequence
 HLA-DQA10301-DQB10302  826      DLLFNKVTLADAGFI  FNKVTLADA  3        0.2259
4338.7    43.00  0.28     Sequence
 HLA-DQA10301-DQB10302  827      LLFNKVTLADAGFIK  FNKVTLADA  2        0.2002
5728.8    55.00  0.29     Sequence
 HLA-DQA10301-DQB10302  828      LFNKVTLADAGFIKQ  LADAGFIKQ  6        0.2297
4164.2    42.00  0.29     Sequence
 HLA-DQA10301-DQB10302  829      FNKVTLADAGFIKQY  LADAGFIKQ  5        0.2452
3522.4    37.00  0.45     Sequence
 HLA-DQA10301-DQB10302  830      NKVTLADAGFIKQYG  LADAGFIKQ  4        0.2309
4109.8    42.00  0.46     Sequence
 HLA-DQA10301-DQB10302  831      KVTLADAGFIKQYGD  LADAGFIKQ  3        0.2334
4002.4    41.00  0.44     Sequence
 HLA-DQA10301-DQB10302  832      VTLADAGFIKQYGDC  LADAGFIKQ  2        0.2338
3983.3    41.00  0.44     Sequence
 HLA-DQA10301-DQB10302  833      TLADAGFIKQYGDCL  LADAGFIKQ  1        0.2175
4753.6    47.00  0.47     Sequence
 HLA-DQA10301-DQB10302  834      LADAGFIKQYGDCLG  LADAGFIKQ  0        0.2013
5663.5    55.00  0.47     Sequence
 HLA-DQA10301-DQB10302  835      ADAGFIKQYGDCLGD  AGFIKQYGD  2        0.1426
10692.6    80.00  0.26     Sequence
 HLA-DQA10301-DQB10302  836      DAGFIKQYGDCLGDI  AGFIKQYGD  1        0.1212
13467.8    85.00  0.31     Sequence
 HLA-DQA10301-DQB10302  837      AGFIKQYGDCLGDIA  AGFIKQYGD  0        0.1168
14134.8    85.00  0.23     Sequence
 HLA-DQA10301-DQB10302  838      GFIKQYGDCLGDIAA  YGDCLGDIA  5        0.1414
10830.4    80.00  0.32     Sequence
 HLA-DQA10301-DQB10302  839      FIKQYGDCLGDIAAR  GDCLGDIAA  5        0.1612
8736.9    70.00  0.31     Sequence
 HLA-DQA10301-DQB10302  840      IKQYGDCLGDIAARD  CLGDIAARD  6        0.2262
4324.2    43.00  0.32     Sequence
 HLA-DQA10301-DQB10302  841      KQYGDCLGDIAARDL  CLGDIAARD  5        0.2770
2497.1    27.00  0.34     Sequence
 HLA-DQA10301-DQB10302  842      QYGDCLGDIAARDLI  LGDIAARDL  5        0.2774
2485.2    27.00  0.31     Sequence
 HLA-DQA10301-DQB10302  843      YGDCLGDIAARDLIC  CLGDIAARD  3        0.2745
2564.9    28.00  0.26     Sequence
 HLA-DQA10301-DQB10302  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.2627
2915.3    31.00  0.27     Sequence
 HLA-DQA10301-DQB10302  845      DCLGDIAARDLICAQ  CLGDIAARD  1        0.2797
2425.0    26.00  0.22     Sequence
 HLA-DQA10301-DQB10302  846      CLGDIAARDLICAQK  AARDLICAQ  5        0.2488
3388.2    35.00  0.35     Sequence
 HLA-DQA10301-DQB10302  847      LGDIAARDLICAQKF  RDLICAQKF  6        0.3273
1448.0    15.00  0.35     Sequence
 HLA-DQA10301-DQB10302  848      GDIAARDLICAQKFN  RDLICAQKF  5        0.3026
1893.4    21.00  0.38     Sequence
 HLA-DQA10301-DQB10302  849      DIAARDLICAQKFNG  RDLICAQKF  4        0.2850
2288.8    25.00  0.40     Sequence
 HLA-DQA10301-DQB10302  850      IAARDLICAQKFNGL  RDLICAQKF  3        0.2663
2803.6    30.00  0.42     Sequence
 HLA-DQA10301-DQB10302  851      AARDLICAQKFNGLT  RDLICAQKF  2        0.2481
3412.9    36.00  0.44     Sequence
 HLA-DQA10301-DQB10302  852      ARDLICAQKFNGLTV  RDLICAQKF  1        0.2207
4592.7    45.00  0.52     Sequence
 HLA-DQA10301-DQB10302  853      RDLICAQKFNGLTVL  RDLICAQKF  0        0.2361
3887.6    40.00  0.33     Sequence
 HLA-DQA10301-DQB10302  854      DLICAQKFNGLTVLP  QKFNGLTVL  5        0.1636
8518.7    70.00  0.50     Sequence
```

```
 HLA-DQA10301-DQB10302  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.2682
2746.1    29.00  0.49     Sequence
 HLA-DQA10301-DQB10302  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.2822
2360.1    26.00  0.52     Sequence
 HLA-DQA10301-DQB10302  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.2684
2740.6    29.00  0.48     Sequence
 HLA-DQA10301-DQB10302  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.2530
3237.9    34.00  0.49     Sequence
 HLA-DQA10301-DQB10302  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.2584
3051.7    32.00  0.44     Sequence
 HLA-DQA10301-DQB10302  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1        0.2519
3274.6    34.00  0.40     Sequence
 HLA-DQA10301-DQB10302  861      FNGLTVLPPLLTDEM  FNGLTVLPP  0        0.2327
4033.4    41.00  0.38     Sequence
 HLA-DQA10301-DQB10302  862      NGLTVLPPLLTDEMI  VLPPLLTDE  4        0.1798
7147.4    65.00  0.29     Sequence
 HLA-DQA10301-DQB10302  863      GLTVLPPLLTDEMIA  VLPPLLTDE  3        0.1500
9862.2    75.00  0.36     Sequence
 HLA-DQA10301-DQB10302  864      LTVLPPLLTDEMIAQ  VLPPLLTDE  2        0.1583
9016.1    70.00  0.28     Sequence
 HLA-DQA10301-DQB10302  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.2030
5557.2    55.00  0.24     Sequence
 HLA-DQA10301-DQB10302  866      VLPPLLTDEMIAQYT  TDEMIAQYT  6        0.2461
3488.5    36.00  0.40     Sequence
 HLA-DQA10301-DQB10302  867      LPPLLTDEMIAQYTS  TDEMIAQYT  5        0.2465
3472.5    36.00  0.40     Sequence
 HLA-DQA10301-DQB10302  868      PPLLTDEMIAQYTSA  TDEMIAQYT  4        0.2752
2546.3    27.00  0.29     Sequence
 HLA-DQA10301-DQB10302  869      PLLTDEMIAQYTSAL  TDEMIAQYT  3        0.2631
2900.9    31.00  0.28     Sequence
 HLA-DQA10301-DQB10302  870      LLTDEMIAQYTSALL  TDEMIAQYT  2        0.2721
2634.0    28.00  0.22     Sequence
 HLA-DQA10301-DQB10302  871      LTDEMIAQYTSALLA  AQYTSALLA  6        0.2930
2100.2    23.00  0.28     Sequence
 HLA-DQA10301-DQB10302  872      TDEMIAQYTSALLAG  AQYTSALLA  5        0.3164
1630.8    18.00  0.41     Sequence
 HLA-DQA10301-DQB10302  873      DEMIAQYTSALLAGT  AQYTSALLA  4        0.2984
1981.6    21.00  0.38     Sequence
 HLA-DQA10301-DQB10302  874      EMIAQYTSALLAGTI  AQYTSALLA  3        0.2858
2269.3    25.00  0.40     Sequence
 HLA-DQA10301-DQB10302  875      MIAQYTSALLAGTIT  AQYTSALLA  2        0.2610
2969.6    32.00  0.42     Sequence
 HLA-DQA10301-DQB10302  876      IAQYTSALLAGTITS  AQYTSALLA  1        0.2560
3134.7    33.00  0.41     Sequence
 HLA-DQA10301-DQB10302  877      AQYTSALLAGTITSG  AQYTSALLA  0        0.2450
3530.8    37.00  0.37     Sequence
 HLA-DQA10301-DQB10302  878      QYTSALLAGTITSGW  YTSALLAGT  1        0.2238
4440.8    44.00  0.19     Sequence
 HLA-DQA10301-DQB10302  879      YTSALLAGTITSGWT  LAGTITSGW  5        0.2134
4967.5    48.00  0.25     Sequence
 HLA-DQA10301-DQB10302  880      TSALLAGTITSGWTF  AGTITSGWT  5        0.2285
4218.7    42.00  0.26     Sequence
 HLA-DQA10301-DQB10302  881      SALLAGTITSGWTFG  LAGTITSGW  3        0.2246
4403.2    44.00  0.25     Sequence
 HLA-DQA10301-DQB10302  882      ALLAGTITSGWTFGA  LAGTITSGW  2        0.2287
4209.8    42.00  0.23     Sequence
 HLA-DQA10301-DQB10302  883      LLAGTITSGWTFGAG  LAGTITSGW  1        0.2238
4440.1    44.00  0.22     Sequence
 HLA-DQA10301-DQB10302  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.2166
4798.7    47.00  0.17     Sequence
 HLA-DQA10301-DQB10302  885      AGTITSGWTFGAGAA  GWTFGAGAA  6        0.2421
3642.6    38.00  0.25     Sequence
 HLA-DQA10301-DQB10302  886      GTITSGWTFGAGAAL  GWTFGAGAA  5        0.3260
1468.6    16.00  0.28     Sequence
 HLA-DQA10301-DQB10302  887      TITSGWTFGAGAALQ  TFGAGAALQ  6        0.4110
585.6     5.00  0.46     Sequence          WB
```

```
 HLA-DQA10301-DQB10302  888       ITSGWTFGAGAALQI  TFGAGAALQ  5         0.4749
293.4     1.80  0.62     Sequence         SB
 HLA-DQA10301-DQB10302  889       TSGWTFGAGAALQIP  TFGAGAALQ  4         0.4628
334.6     2.50  0.58     Sequence         WB
 HLA-DQA10301-DQB10302  890       SGWTFGAGAALQIPF  TFGAGAALQ  3         0.5013
220.4     1.10  0.47     Sequence         SB
 HLA-DQA10301-DQB10302  891       GWTFGAGAALQIPFA  TFGAGAALQ  2         0.4829
269.2     1.50  0.47     Sequence         SB
 HLA-DQA10301-DQB10302  892       WTFGAGAALQIPFAM  TFGAGAALQ  1         0.4740
296.2     1.80  0.51     Sequence         SB
 HLA-DQA10301-DQB10302  893       TFGAGAALQIPFAMQ  TFGAGAALQ  0         0.4319
467.2     4.00  0.47     Sequence         WB
 HLA-DQA10301-DQB10302  894       FGAGAALQIPFAMQM  GAGAALQIP  1         0.3401
1261.0    13.00  0.21     Sequence
 HLA-DQA10301-DQB10302  895       GAGAALQIPFAMQMA  GAGAALQIP  0         0.2783
2462.0    27.00  0.31     Sequence
 HLA-DQA10301-DQB10302  896       AGAALQIPFAMQMAY  AGAALQIPF  0         0.2605
2983.5    32.00  0.25     Sequence
 HLA-DQA10301-DQB10302  897       GAALQIPFAMQMAYR  ALQIPFAMQ  2         0.1979
5877.5    55.00  0.16     Sequence
 HLA-DQA10301-DQB10302  898       AALQIPFAMQMAYRF  FAMQMAYRF  6         0.2398
3735.1    39.00  0.28     Sequence
 HLA-DQA10301-DQB10302  899       ALQIPFAMQMAYRFN  FAMQMAYRF  5         0.2138
4944.4    48.00  0.25     Sequence
 HLA-DQA10301-DQB10302  900       LQIPFAMQMAYRFNG  FAMQMAYRF  4         0.1910
6334.1    60.00  0.30     Sequence
 HLA-DQA10301-DQB10302  901       QIPFAMQMAYRFNGI  FAMQMAYRF  3         0.1795
7167.6    65.00  0.31     Sequence
 HLA-DQA10301-DQB10302  902       IPFAMQMAYRFNGIG  FAMQMAYRF  2         0.1608
8781.6    70.00  0.31     Sequence
 HLA-DQA10301-DQB10302  903       PFAMQMAYRFNGIGV  FAMQMAYRF  1         0.1731
7685.3    65.00  0.31     Sequence
 HLA-DQA10301-DQB10302  904       FAMQMAYRFNGIGVT  YRFNGIGVT  6         0.2172
4768.8    47.00  0.42     Sequence
 HLA-DQA10301-DQB10302  905       AMQMAYRFNGIGVTQ  YRFNGIGVT  5         0.2024
5596.3    55.00  0.56     Sequence
 HLA-DQA10301-DQB10302  906       MQMAYRFNGIGVTQN  FNGIGVTQN  6         0.2594
3021.9    32.00  0.43     Sequence
 HLA-DQA10301-DQB10302  907       QMAYRFNGIGVTQNV  FNGIGVTQN  5         0.2715
2649.5    28.00  0.54     Sequence
 HLA-DQA10301-DQB10302  908       MAYRFNGIGVTQNVL  FNGIGVTQN  4         0.2766
2506.3    27.00  0.48     Sequence
 HLA-DQA10301-DQB10302  909       AYRFNGIGVTQNVLY  FNGIGVTQN  3         0.2726
2617.3    28.00  0.45     Sequence
 HLA-DQA10301-DQB10302  910       YRFNGIGVTQNVLYE  FNGIGVTQN  2         0.2835
2326.5    25.00  0.41     Sequence
 HLA-DQA10301-DQB10302  911       RFNGIGVTQNVLYEN  FNGIGVTQN  1         0.2605
2984.2    32.00  0.36     Sequence
 HLA-DQA10301-DQB10302  912       FNGIGVTQNVLYENQ  FNGIGVTQN  0         0.2479
3420.9    36.00  0.36     Sequence
 HLA-DQA10301-DQB10302  913       NGIGVTQNVLYENQK  GVTQNVLYE  3         0.1894
6442.4    60.00  0.28     Sequence
 HLA-DQA10301-DQB10302  914       GIGVTQNVLYENQKL  GVTQNVLYE  2         0.1874
6585.2    60.00  0.32     Sequence
 HLA-DQA10301-DQB10302  915       IGVTQNVLYENQKLI  GVTQNVLYE  1         0.1722
7760.6    65.00  0.36     Sequence
 HLA-DQA10301-DQB10302  916       GVTQNVLYENQKLIA  GVTQNVLYE  0         0.1644
8438.0    70.00  0.33     Sequence
 HLA-DQA10301-DQB10302  917       VTQNVLYENQKLIAN  TQNVLYENQ  1         0.1413
10844.5    80.00  0.19     Sequence
 HLA-DQA10301-DQB10302  918       TQNVLYENQKLIANQ  ENQKLIANQ  6         0.1671
8200.3    70.00  0.37     Sequence
 HLA-DQA10301-DQB10302  919       QNVLYENQKLIANQF  ENQKLIANQ  5         0.2291
4190.8    42.00  0.47     Sequence
 HLA-DQA10301-DQB10302  920       NVLYENQKLIANQFN  ENQKLIANQ  4         0.2162
4817.7    47.00  0.41     Sequence
```

```
 HLA-DQA10301-DQB10302  921      VLYENQKLIANQFNS  ENQKLIANQ  3        0.2032
5547.3    55.00  0.40     Sequence
 HLA-DQA10301-DQB10302  922      LYENQKLIANQFNSA  ENQKLIANQ  2        0.2050
5438.9    55.00  0.35     Sequence
 HLA-DQA10301-DQB10302  923      YENQKLIANQFNSAI  ENQKLIANQ  1        0.1992
5790.6    55.00  0.34     Sequence
 HLA-DQA10301-DQB10302  924      ENQKLIANQFNSAIG  ENQKLIANQ  0        0.1817
6998.8    60.00  0.29     Sequence
 HLA-DQA10301-DQB10302  925      NQKLIANQFNSAIGK  NQKLIANQF  0        0.1446
10455.7    75.00  0.18     Sequence
 HLA-DQA10301-DQB10302  926      QKLIANQFNSAIGKI  NQFNSAIGK  5        0.1414
10822.5    80.00  0.28     Sequence
 HLA-DQA10301-DQB10302  927      KLIANQFNSAIGKIQ  FNSAIGKIQ  6        0.1509
9769.2    75.00  0.25     Sequence
 HLA-DQA10301-DQB10302  928      LIANQFNSAIGKIQD  FNSAIGKIQ  5        0.1866
6637.2    60.00  0.33     Sequence
 HLA-DQA10301-DQB10302  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4        0.1857
6707.4    60.00  0.30     Sequence
 HLA-DQA10301-DQB10302  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.2278
4252.3    43.00  0.22     Sequence
 HLA-DQA10301-DQB10302  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.2182
4717.6    46.00  0.22     Sequence
 HLA-DQA10301-DQB10302  932      QFNSAIGKIQDSLSS  FNSAIGKIQ  1        0.2052
5429.4    55.00  0.24     Sequence
 HLA-DQA10301-DQB10302  933      FNSAIGKIQDSLSST  NSAIGKIQD  1        0.1876
6567.7    60.00  0.25     Sequence
 HLA-DQA10301-DQB10302  934      NSAIGKIQDSLSSTA  IQDSLSSTA  6        0.1965
5967.5    55.00  0.30     Sequence
 HLA-DQA10301-DQB10302  935      SAIGKIQDSLSSTAS  IQDSLSSTA  5        0.2062
5368.3    55.00  0.38     Sequence
 HLA-DQA10301-DQB10302  936      AIGKIQDSLSSTASA  DSLSSTASA  6        0.2428
3613.3    37.00  0.42     Sequence
 HLA-DQA10301-DQB10302  937      IGKIQDSLSSTASAL  DSLSSTASA  5        0.2781
2466.1    27.00  0.38     Sequence
 HLA-DQA10301-DQB10302  938      GKIQDSLSSTASALG  SLSSTASAL  5        0.2718
2640.7    28.00  0.40     Sequence
 HLA-DQA10301-DQB10302  939      KIQDSLSSTASALGK  SLSSTASAL  4        0.2577
3075.5    33.00  0.35     Sequence
 HLA-DQA10301-DQB10302  940      IQDSLSSTASALGKL  SLSSTASAL  3        0.2520
3270.6    34.00  0.32     Sequence
 HLA-DQA10301-DQB10302  941      QDSLSSTASALGKLQ  SLSSTASAL  2        0.2371
3846.0    39.00  0.34     Sequence
 HLA-DQA10301-DQB10302  942      DSLSSTASALGKLQD  SLSSTASAL  1        0.2315
4085.3    41.00  0.31     Sequence
 HLA-DQA10301-DQB10302  943      SLSSTASALGKLQDV  SLSSTASAL  0        0.1994
5780.6    55.00  0.31     Sequence
 HLA-DQA10301-DQB10302  944      LSSTASALGKLQDVV  TASALGKLQ  3        0.1851
6748.9    60.00  0.28     Sequence
 HLA-DQA10301-DQB10302  945      SSTASALGKLQDVVN  TASALGKLQ  2        0.1689
8043.1    65.00  0.29     Sequence
 HLA-DQA10301-DQB10302  946      STASALGKLQDVVNQ  TASALGKLQ  1        0.1601
8840.0    70.00  0.28     Sequence
 HLA-DQA10301-DQB10302  947      TASALGKLQDVVNQN  TASALGKLQ  0        0.1504
9819.4    75.00  0.24     Sequence
 HLA-DQA10301-DQB10302  948      ASALGKLQDVVNQNA  ASALGKLQD  0        0.1399
11006.0    80.00  0.20     Sequence
 HLA-DQA10301-DQB10302  949      SALGKLQDVVNQNAQ  LQDVVNQNA  5        0.1342
11705.0    80.00  0.20     Sequence
 HLA-DQA10301-DQB10302  950      ALGKLQDVVNQNAQA  QDVVNQNAQ  5        0.1389
11120.7    80.00  0.29     Sequence
 HLA-DQA10301-DQB10302  951      LGKLQDVVNQNAQAL  VVNQNAQAL  6        0.1931
6189.0    60.00  0.43     Sequence
 HLA-DQA10301-DQB10302  952      GKLQDVVNQNAQALN  VVNQNAQAL  5        0.1897
6421.3    60.00  0.42     Sequence
 HLA-DQA10301-DQB10302  953      KLQDVVNQNAQALNT  VVNQNAQAL  4        0.2017
5640.5    55.00  0.34     Sequence
```

```
 HLA-DQA10301-DQB10302  954      LQDVVNQNAQALNTL  NQNAQALNT  5        0.2257
4351.2    44.00  0.31     Sequence
 HLA-DQA10301-DQB10302  955      QDVVNQNAQALNTLV  VVNQNAQAL  2        0.2296
4167.5    42.00  0.22     Sequence
 HLA-DQA10301-DQB10302  956      DVVNQNAQALNTLVK  VVNQNAQAL  1        0.2058
5395.0    55.00  0.25     Sequence
 HLA-DQA10301-DQB10302  957      VVNQNAQALNTLVKQ  QALNTLVKQ  6        0.2145
4909.8    48.00  0.29     Sequence
 HLA-DQA10301-DQB10302  958      VNQNAQALNTLVKQL  QALNTLVKQ  5        0.2069
5329.9    55.00  0.38     Sequence
 HLA-DQA10301-DQB10302  959      NQNAQALNTLVKQLS  QALNTLVKQ  4        0.1933
6172.4    60.00  0.37     Sequence
 HLA-DQA10301-DQB10302  960      QNAQALNTLVKQLSS  QALNTLVKQ  3        0.1795
7172.3    65.00  0.41     Sequence
 HLA-DQA10301-DQB10302  961      NAQALNTLVKQLSSN  QALNTLVKQ  2        0.1579
9060.4    70.00  0.46     Sequence
 HLA-DQA10301-DQB10302  962      AQALNTLVKQLSSNF  QALNTLVKQ  1        0.1488
9992.0    75.00  0.46     Sequence
 HLA-DQA10301-DQB10302  963      QALNTLVKQLSSNFG  QALNTLVKQ  0        0.1289
12396.8    80.00  0.42     Sequence
 HLA-DQA10301-DQB10302  964      ALNTLVKQLSSNFGA  ALNTLVKQL  0        0.0915
18575.0    95.00  0.24     Sequence
 HLA-DQA10301-DQB10302  965      LNTLVKQLSSNFGAI  KQLSSNFGA  5        0.0987
17180.5    90.00  0.26     Sequence
 HLA-DQA10301-DQB10302  966      NTLVKQLSSNFGAIS  LSSNFGAIS  6        0.1143
14523.5    85.00  0.38     Sequence
 HLA-DQA10301-DQB10302  967      TLVKQLSSNFGAISS  SSNFGAISS  6        0.1673
8184.6    70.00  0.45     Sequence
 HLA-DQA10301-DQB10302  968      LVKQLSSNFGAISSV  SSNFGAISS  5        0.2118
5054.0    49.00  0.41     Sequence
 HLA-DQA10301-DQB10302  969      VKQLSSNFGAISSVL  SNFGAISSV  5        0.2549
3170.6    34.00  0.26     Sequence
 HLA-DQA10301-DQB10302  970      KQLSSNFGAISSVLN  NFGAISSVL  5        0.2876
2225.6    24.00  0.32     Sequence
 HLA-DQA10301-DQB10302  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.3218
1538.1    17.00  0.27     Sequence
 HLA-DQA10301-DQB10302  972      LSSNFGAISSVLNDI  GAISSVLND  5        0.3597
1020.5    10.00  0.28     Sequence
 HLA-DQA10301-DQB10302  973      SSNFGAISSVLNDIL  GAISSVLND  4        0.3413
1244.5    13.00  0.28     Sequence
 HLA-DQA10301-DQB10302  974      SNFGAISSVLNDILS  GAISSVLND  3        0.3254
1479.4    16.00  0.29     Sequence
 HLA-DQA10301-DQB10302  975      NFGAISSVLNDILSR  GAISSVLND  2        0.2958
2036.8    22.00  0.37     Sequence
 HLA-DQA10301-DQB10302  976      FGAISSVLNDILSRL  GAISSVLND  1        0.2650
2843.7    30.00  0.43     Sequence
 HLA-DQA10301-DQB10302  977      GAISSVLNDILSRLD  GAISSVLND  0        0.2770
2496.9    27.00  0.37     Sequence
 HLA-DQA10301-DQB10302  978      AISSVLNDILSRLDK  LNDILSRLD  5        0.2122
5031.2    49.00  0.49     Sequence
 HLA-DQA10301-DQB10302  979      ISSVLNDILSRLDKV  LNDILSRLD  4        0.1865
6645.8    60.00  0.53     Sequence
 HLA-DQA10301-DQB10302  980      SSVLNDILSRLDKVE  LNDILSRLD  3        0.1866
6642.0    60.00  0.47     Sequence
 HLA-DQA10301-DQB10302  981      SVLNDILSRLDKVEA  LNDILSRLD  2        0.1848
6773.2    60.00  0.47     Sequence
 HLA-DQA10301-DQB10302  982      VLNDILSRLDKVEAE  SRLDKVEAE  6        0.2439
3570.6    37.00  0.45     Sequence
 HLA-DQA10301-DQB10302  983      LNDILSRLDKVEAEV  SRLDKVEAE  5        0.2671
2777.9    30.00  0.60     Sequence
 HLA-DQA10301-DQB10302  984      NDILSRLDKVEAEVQ  SRLDKVEAE  4        0.2796
2427.5    26.00  0.45     Sequence
 HLA-DQA10301-DQB10302  985      DILSRLDKVEAEVQI  LDKVEAEVQ  5        0.3141
1671.1    18.00  0.46     Sequence
 HLA-DQA10301-DQB10302  986      ILSRLDKVEAEVQID  KVEAEVQID  6        0.3933
709.2     6.50  0.43     Sequence         WB
```

```
 HLA-DQA10301-DQB10302  987      LSRLDKVEAEVQIDR  KVEAEVQID  5        0.4094
596.0     5.50  0.54     Sequence         WB
 HLA-DQA10301-DQB10302  988      SRLDKVEAEVQIDRL  KVEAEVQID  4        0.4414
421.7     3.50  0.40     Sequence         WB
 HLA-DQA10301-DQB10302  989      RLDKVEAEVQIDRLI  KVEAEVQID  3        0.4267
494.2     4.00  0.42     Sequence         WB
 HLA-DQA10301-DQB10302  990      LDKVEAEVQIDRLIT  KVEAEVQID  2        0.4168
550.3     4.50  0.44     Sequence         WB
 HLA-DQA10301-DQB10302  991      DKVEAEVQIDRLITG  KVEAEVQID  1        0.3947
698.6     6.50  0.47     Sequence         WB
 HLA-DQA10301-DQB10302  992      KVEAEVQIDRLITGR  KVEAEVQID  0        0.3415
1242.8    13.00  0.47     Sequence
 HLA-DQA10301-DQB10302  993      VEAEVQIDRLITGRL  EAEVQIDRL  1        0.2746
2561.5    28.00  0.57     Sequence
 HLA-DQA10301-DQB10302  994      EAEVQIDRLITGRLQ  EAEVQIDRL  0        0.2604
2986.7    32.00  0.40     Sequence
 HLA-DQA10301-DQB10302  995      AEVQIDRLITGRLQS  DRLITGRLQ  5        0.2063
5365.0    55.00  0.57     Sequence
 HLA-DQA10301-DQB10302  996      EVQIDRLITGRLQSL  DRLITGRLQ  4        0.1994
5783.7    55.00  0.56     Sequence
 HLA-DQA10301-DQB10302  997      VQIDRLITGRLQSLQ  DRLITGRLQ  3        0.1922
6250.8    60.00  0.56     Sequence
 HLA-DQA10301-DQB10302  998      QIDRLITGRLQSLQT  DRLITGRLQ  2        0.2007
5698.6    55.00  0.47     Sequence
 HLA-DQA10301-DQB10302  999      IDRLITGRLQSLQTY  DRLITGRLQ  1        0.2173
4762.0    47.00  0.38     Sequence
 HLA-DQA10301-DQB10302 1000      DRLITGRLQSLQTYV  DRLITGRLQ  0        0.2029
5564.2    55.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1001      RLITGRLQSLQTYVT  LQSLQTYVT  6        0.1745
7570.4    65.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.2006
5706.0    55.00  0.37     Sequence
 HLA-DQA10301-DQB10302 1003      ITGRLQSLQTYVTQQ  SLQTYVTQQ  6        0.2156
4853.3    47.00  0.26     Sequence
 HLA-DQA10301-DQB10302 1004      TGRLQSLQTYVTQQL  SLQTYVTQQ  5        0.2266
4307.6    43.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1005      GRLQSLQTYVTQQLI  SLQTYVTQQ  4        0.2257
4347.8    43.00  0.29     Sequence
 HLA-DQA10301-DQB10302 1006      RLQSLQTYVTQQLIR  SLQTYVTQQ  3        0.2030
5561.6    55.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1007      LQSLQTYVTQQLIRA  SLQTYVTQQ  2        0.1912
6316.3    60.00  0.32     Sequence
 HLA-DQA10301-DQB10302 1008      QSLQTYVTQQLIRAA  SLQTYVTQQ  1        0.1773
7342.5    65.00  0.35     Sequence
 HLA-DQA10301-DQB10302 1009      SLQTYVTQQLIRAAE  TQQLIRAAE  6        0.1932
6179.5    60.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1010      LQTYVTQQLIRAAEI  TQQLIRAAE  5        0.2242
4420.6    44.00  0.38     Sequence
 HLA-DQA10301-DQB10302 1011      QTYVTQQLIRAAEIR  QQLIRAAEI  5        0.2104
5129.5    49.00  0.37     Sequence
 HLA-DQA10301-DQB10302 1012      TYVTQQLIRAAEIRA  TQQLIRAAE  3        0.2006
5705.5    55.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1013      YVTQQLIRAAEIRAS  TQQLIRAAE  2        0.2164
4809.0    47.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1014      VTQQLIRAAEIRASA  IRAAEIRAS  5        0.2463
3481.1    36.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.2688
2728.7    29.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1016      QQLIRAAEIRASANL  AAEIRASAN  5        0.2813
2382.3    26.00  0.41     Sequence
 HLA-DQA10301-DQB10302 1017      QLIRAAEIRASANLA  AAEIRASAN  4        0.2990
1968.2    21.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1018      LIRAAEIRASANLAA  EIRASANLA  5        0.3036
1873.3    20.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1019      IRAAEIRASANLAAI  EIRASANLA  4        0.3348
1335.6    14.00  0.20     Sequence
```

```
 HLA-DQA10301-DQB10302 1020      RAAEIRASANLAAIK  EIRASANLA  3        0.3149
1656.1    18.00  0.19     Sequence
 HLA-DQA10301-DQB10302 1021      AAEIRASANLAAIKM  EIRASANLA  2        0.3141
1671.2    18.00  0.17     Sequence
 HLA-DQA10301-DQB10302 1022      AEIRASANLAAIKMS  EIRASANLA  1        0.2976
1996.9    22.00  0.21     Sequence
 HLA-DQA10301-DQB10302 1023      EIRASANLAAIKMSE  RASANLAAI  2        0.3021
1903.8    21.00  0.16     Sequence
 HLA-DQA10301-DQB10302 1024      IRASANLAAIKMSEC  NLAAIKMSE  5        0.2852
2285.8    25.00  0.30     Sequence
 HLA-DQA10301-DQB10302 1025      RASANLAAIKMSECV  NLAAIKMSE  4        0.2757
2532.7    27.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1026      ASANLAAIKMSECVL  NLAAIKMSE  3        0.2481
3412.5    36.00  0.33     Sequence
 HLA-DQA10301-DQB10302 1027      SANLAAIKMSECVLG  NLAAIKMSE  2        0.2287
4208.7    42.00  0.42     Sequence
 HLA-DQA10301-DQB10302 1028      ANLAAIKMSECVLGQ  NLAAIKMSE  1        0.2034
5535.7    55.00  0.47     Sequence
 HLA-DQA10301-DQB10302 1029      NLAAIKMSECVLGQS  NLAAIKMSE  0        0.1907
6348.8    60.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1030      LAAIKMSECVLGQSK  KMSECVLGQ  4        0.1485
10023.4    75.00  0.19     Sequence
 HLA-DQA10301-DQB10302 1031      AAIKMSECVLGQSKR  KMSECVLGQ  3        0.1304
12198.0    80.00  0.23     Sequence
 HLA-DQA10301-DQB10302 1032      AIKMSECVLGQSKRV  KMSECVLGQ  2        0.1075
15622.2    90.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1033      IKMSECVLGQSKRVD  KMSECVLGQ  1        0.1139
14574.3    85.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1034      KMSECVLGQSKRVDF  VLGQSKRVD  5        0.1167
14141.4    85.00  0.32     Sequence
 HLA-DQA10301-DQB10302 1035      MSECVLGQSKRVDFC  VLGQSKRVD  4        0.1106
15116.0    90.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1036      SECVLGQSKRVDFCG  VLGQSKRVD  3        0.0951
17875.9    90.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1037      ECVLGQSKRVDFCGK  VLGQSKRVD  2        0.0790
21268.5    95.00  0.37     Sequence
 HLA-DQA10301-DQB10302 1038      CVLGQSKRVDFCGKG  VLGQSKRVD  1        0.0656
24577.0    100.00  0.41     Sequence
 HLA-DQA10301-DQB10302 1039      VLGQSKRVDFCGKGY  VLGQSKRVD  0        0.0709
23221.9    100.00  0.32     Sequence
 HLA-DQA10301-DQB10302 1040      LGQSKRVDFCGKGYH  GQSKRVDFC  1        0.0564
27159.7    100.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1041      GQSKRVDFCGKGYHL  GQSKRVDFC  0        0.0512
28746.2    100.00  0.27     Sequence
 HLA-DQA10301-DQB10302 1042      QSKRVDFCGKGYHLM  FCGKGYHLM  6        0.0570
26991.5    100.00  0.35     Sequence
 HLA-DQA10301-DQB10302 1043      SKRVDFCGKGYHLMS  FCGKGYHLM  5        0.0539
27892.9    100.00  0.36     Sequence
 HLA-DQA10301-DQB10302 1044      KRVDFCGKGYHLMSF  GKGYHLMSF  6        0.1070
15716.4    90.00  0.46     Sequence
 HLA-DQA10301-DQB10302 1045      RVDFCGKGYHLMSFP  GKGYHLMSF  5        0.1172
14066.9    85.00  0.47     Sequence
 HLA-DQA10301-DQB10302 1046      VDFCGKGYHLMSFPQ  GYHLMSFPQ  6        0.1569
9156.4    70.00  0.40     Sequence
 HLA-DQA10301-DQB10302 1047      DFCGKGYHLMSFPQS  GYHLMSFPQ  5        0.1868
6625.0    60.00  0.46     Sequence
 HLA-DQA10301-DQB10302 1048      FCGKGYHLMSFPQSA  GYHLMSFPQ  4        0.2155
4859.0    47.00  0.33     Sequence
 HLA-DQA10301-DQB10302 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.2141
4928.3    48.00  0.32     Sequence
 HLA-DQA10301-DQB10302 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.2172
4765.8    47.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.2031
5555.1    55.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.1946
6088.9    55.00  0.29     Sequence
```

```
 HLA-DQA10301-DQB10302 1053      YHLMSFPQSAPHGVV  HLMSFPQSA  1        0.1744
7573.2    65.00  0.32     Sequence
 HLA-DQA10301-DQB10302 1054      HLMSFPQSAPHGVVF  HLMSFPQSA  0        0.1782
7270.1    65.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1055      LMSFPQSAPHGVVFL  SAPHGVVFL  6        0.1847
6776.9    60.00  0.35     Sequence
 HLA-DQA10301-DQB10302 1056      MSFPQSAPHGVVFLH  SAPHGVVFL  5        0.1778
7301.0    65.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1057      SFPQSAPHGVVFLHV  APHGVVFLH  5        0.1976
5895.1    55.00  0.26     Sequence
 HLA-DQA10301-DQB10302 1058      FPQSAPHGVVFLHVT  PHGVVFLHV  5        0.1987
5821.8    55.00  0.21     Sequence
 HLA-DQA10301-DQB10302 1059      PQSAPHGVVFLHVTY  APHGVVFLH  3        0.1974
5909.6    55.00  0.19     Sequence
 HLA-DQA10301-DQB10302 1060      QSAPHGVVFLHVTYV  APHGVVFLH  2        0.1860
6685.5    60.00  0.17     Sequence
 HLA-DQA10301-DQB10302 1061      SAPHGVVFLHVTYVP  APHGVVFLH  1        0.1755
7487.4    65.00  0.16     Sequence
 HLA-DQA10301-DQB10302 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.2220
4525.9    45.00  0.35     Sequence
 HLA-DQA10301-DQB10302 1063      PHGVVFLHVTYVPAQ  LHVTYVPAQ  6        0.2210
4574.1    45.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1064      HGVVFLHVTYVPAQE  HVTYVPAQE  6        0.3124
1702.2    18.00  0.38     Sequence
 HLA-DQA10301-DQB10302 1065      GVVFLHVTYVPAQEK  HVTYVPAQE  5        0.3682
930.6     9.00  0.46     Sequence          WB
 HLA-DQA10301-DQB10302 1066      VVFLHVTYVPAQEKN  HVTYVPAQE  4        0.3572
1048.5    11.00  0.41     Sequence
 HLA-DQA10301-DQB10302 1067      VFLHVTYVPAQEKNF  HVTYVPAQE  3        0.3568
1053.3    11.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1068      FLHVTYVPAQEKNFT  HVTYVPAQE  2        0.3385
1284.1    14.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1069      LHVTYVPAQEKNFTT  HVTYVPAQE  1        0.3160
1637.9    18.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1070      HVTYVPAQEKNFTTA  HVTYVPAQE  0        0.2745
2564.0    28.00  0.49     Sequence
 HLA-DQA10301-DQB10302 1071      VTYVPAQEKNFTTAP  VTYVPAQEK  0        0.1965
5966.4    55.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1072      TYVPAQEKNFTTAPA  EKNFTTAPA  6        0.1709
7868.0    65.00  0.41     Sequence
 HLA-DQA10301-DQB10302 1073      YVPAQEKNFTTAPAI  EKNFTTAPA  5        0.2105
5127.9    49.00  0.40     Sequence
 HLA-DQA10301-DQB10302 1074      VPAQEKNFTTAPAIC  KNFTTAPAI  5        0.2176
4748.5    47.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1075      PAQEKNFTTAPAICH  KNFTTAPAI  4        0.2430
3605.2    37.00  0.22     Sequence
 HLA-DQA10301-DQB10302 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.2643
2864.7    31.00  0.23     Sequence
 HLA-DQA10301-DQB10302 1077      QEKNFTTAPAICHDG  TTAPAICHD  5        0.2537
3214.1    34.00  0.20     Sequence
 HLA-DQA10301-DQB10302 1078      EKNFTTAPAICHDGK  KNFTTAPAI  1        0.2306
4123.6    42.00  0.23     Sequence
 HLA-DQA10301-DQB10302 1079      KNFTTAPAICHDGKA  TTAPAICHD  3        0.2003
5724.7    55.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1080      NFTTAPAICHDGKAH  TTAPAICHD  2        0.1727
7718.3    65.00  0.38     Sequence
 HLA-DQA10301-DQB10302 1081      FTTAPAICHDGKAHF  TTAPAICHD  1        0.1483
10048.8    75.00  0.46     Sequence
 HLA-DQA10301-DQB10302 1082      TTAPAICHDGKAHFP  TTAPAICHD  0        0.1131
14711.5    85.00  0.54     Sequence
 HLA-DQA10301-DQB10302 1083      TAPAICHDGKAHFPR  CHDGKAHFP  5        0.0642
24961.6   100.00  0.26     Sequence
 HLA-DQA10301-DQB10302 1084      APAICHDGKAHFPRE  DGKAHFPRE  6        0.1371
11347.9    80.00  0.57     Sequence
 HLA-DQA10301-DQB10302 1085      PAICHDGKAHFPREG  DGKAHFPRE  5        0.1353
11572.1    80.00  0.64     Sequence
```

```
 HLA-DQA10301-DQB10302 1086      AICHDGKAHFPREGV  DGKAHFPRE  4         0.1453
10383.6    75.00  0.61     Sequence
 HLA-DQA10301-DQB10302 1087      ICHDGKAHFPREGVF  DGKAHFPRE  3         0.1475
10138.1    75.00  0.57     Sequence
 HLA-DQA10301-DQB10302 1088      CHDGKAHFPREGVFV  DGKAHFPRE  2         0.1404
10943.2    80.00  0.57     Sequence
 HLA-DQA10301-DQB10302 1089      HDGKAHFPREGVFVS  DGKAHFPRE  1         0.1665
8256.2    70.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1090      DGKAHFPREGVFVSN  FPREGVFVS  5         0.1664
8265.8    70.00  0.36     Sequence
 HLA-DQA10301-DQB10302 1091      GKAHFPREGVFVSNG  FPREGVFVS  4         0.1446
10463.6    75.00  0.38     Sequence
 HLA-DQA10301-DQB10302 1092      KAHFPREGVFVSNGT  REGVFVSNG  5         0.1930
6193.0    60.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1093      AHFPREGVFVSNGTH  EGVFVSNGT  5         0.1861
6676.3    60.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1094      HFPREGVFVSNGTHW  EGVFVSNGT  4         0.1936
6154.0    60.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1095      FPREGVFVSNGTHWF  EGVFVSNGT  3         0.2151
4880.3    48.00  0.20     Sequence
 HLA-DQA10301-DQB10302 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5         0.1959
6001.0    55.00  0.26     Sequence
 HLA-DQA10301-DQB10302 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4         0.1922
6248.1    60.00  0.23     Sequence
 HLA-DQA10301-DQB10302 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3         0.1834
6875.4    60.00  0.22     Sequence
 HLA-DQA10301-DQB10302 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2         0.1474
10144.2    75.00  0.26     Sequence
 HLA-DQA10301-DQB10302 1100      VFVSNGTHWFVTQRN  THWFVTQRN  6         0.1791
7199.8    65.00  0.36     Sequence
 HLA-DQA10301-DQB10302 1101      FVSNGTHWFVTQRNF  THWFVTQRN  5         0.2049
5447.0    55.00  0.50     Sequence
 HLA-DQA10301-DQB10302 1102      VSNGTHWFVTQRNFY  THWFVTQRN  4         0.1987
5826.5    55.00  0.47     Sequence
 HLA-DQA10301-DQB10302 1103      SNGTHWFVTQRNFYE  THWFVTQRN  3         0.2016
5641.9    55.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1104      NGTHWFVTQRNFYEP  THWFVTQRN  2         0.2005
5714.7    55.00  0.41     Sequence
 HLA-DQA10301-DQB10302 1105      GTHWFVTQRNFYEPQ  THWFVTQRN  1         0.2070
5322.4    55.00  0.35     Sequence
 HLA-DQA10301-DQB10302 1106      THWFVTQRNFYEPQI  THWFVTQRN  0         0.2040
5498.4    55.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1107      HWFVTQRNFYEPQII  RNFYEPQII  6         0.2367
3861.5    40.00  0.33     Sequence
 HLA-DQA10301-DQB10302 1108      WFVTQRNFYEPQIIT  RNFYEPQII  5         0.2139
4943.1    48.00  0.42     Sequence
 HLA-DQA10301-DQB10302 1109      FVTQRNFYEPQIITT  RNFYEPQII  4         0.2153
4864.7    47.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1110      VTQRNFYEPQIITTD  FYEPQIITT  5         0.2167
4791.6    47.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1111      TQRNFYEPQIITTDN  RNFYEPQII  2         0.2056
5407.1    55.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1112      QRNFYEPQIITTDNT  RNFYEPQII  1         0.1873
6591.6    60.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1113      RNFYEPQIITTDNTF  FYEPQIITT  2         0.2085
5237.4    50.00  0.22     Sequence
 HLA-DQA10301-DQB10302 1114      NFYEPQIITTDNTFV  FYEPQIITT  1         0.1820
6974.9    60.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1115      FYEPQIITTDNTFVS  YEPQIITTD  1         0.1731
7680.9    65.00  0.17     Sequence
 HLA-DQA10301-DQB10302 1116      YEPQIITTDNTFVSG  ITTDNTFVS  5         0.1860
6679.5    60.00  0.19     Sequence
 HLA-DQA10301-DQB10302 1117      EPQIITTDNTFVSGN  TDNTFVSGN  6         0.1838
6845.2    60.00  0.22     Sequence
 HLA-DQA10301-DQB10302 1118      PQIITTDNTFVSGNC  TDNTFVSGN  5         0.2102
5143.0    49.00  0.29     Sequence
```

```
 HLA-DQA10301-DQB10302 1119      QIITTDNTFVSGNCD  NTFVSGNCD  6        0.2474
3440.3    36.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1120      IITTDNTFVSGNCDV  NTFVSGNCD  5        0.2681
2748.3    29.00  0.40     Sequence
 HLA-DQA10301-DQB10302 1121      ITTDNTFVSGNCDVV  NTFVSGNCD  4        0.2581
3063.7    33.00  0.38     Sequence
 HLA-DQA10301-DQB10302 1122      TTDNTFVSGNCDVVI  NTFVSGNCD  3        0.2689
2724.7    29.00  0.32     Sequence
 HLA-DQA10301-DQB10302 1123      TDNTFVSGNCDVVIG  NTFVSGNCD  2        0.2604
2986.6    32.00  0.35     Sequence
 HLA-DQA10301-DQB10302 1124      DNTFVSGNCDVVIGI  NTFVSGNCD  1        0.2551
3164.7    33.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1125      NTFVSGNCDVVIGIV  NTFVSGNCD  0        0.2345
3953.5    40.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1126      TFVSGNCDVVIGIVN  NCDVVIGIV  5        0.1990
5804.7    55.00  0.24     Sequence
 HLA-DQA10301-DQB10302 1127      FVSGNCDVVIGIVNN  NCDVVIGIV  4        0.2017
5636.5    55.00  0.19     Sequence
 HLA-DQA10301-DQB10302 1128      VSGNCDVVIGIVNNT  DVVIGIVNN  5        0.2071
5318.5    55.00  0.33     Sequence
 HLA-DQA10301-DQB10302 1129      SGNCDVVIGIVNNTV  DVVIGIVNN  4        0.2176
4747.8    47.00  0.26     Sequence
 HLA-DQA10301-DQB10302 1130      GNCDVVIGIVNNTVY  VIGIVNNTV  5        0.2251
4375.3    44.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1131      NCDVVIGIVNNTVYD  DVVIGIVNN  2        0.2210
4576.8    45.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1132      CDVVIGIVNNTVYDP  DVVIGIVNN  1        0.2252
4370.8    44.00  0.23     Sequence
 HLA-DQA10301-DQB10302 1133      DVVIGIVNNTVYDPL  IVNNTVYDP  5        0.2448
3538.0    37.00  0.21     Sequence
 HLA-DQA10301-DQB10302 1134      VVIGIVNNTVYDPLQ  IVNNTVYDP  4        0.2145
4909.3    48.00  0.22     Sequence
 HLA-DQA10301-DQB10302 1135      VIGIVNNTVYDPLQP  IVNNTVYDP  3        0.2065
5353.7    55.00  0.23     Sequence
 HLA-DQA10301-DQB10302 1136      IGIVNNTVYDPLQPE  TVYDPLQPE  6        0.3272
1450.8    16.00  0.51     Sequence
 HLA-DQA10301-DQB10302 1137      GIVNNTVYDPLQPEL  TVYDPLQPE  5        0.3372
1301.0    14.00  0.55     Sequence
 HLA-DQA10301-DQB10302 1138      IVNNTVYDPLQPELD  TVYDPLQPE  4        0.3389
1277.7    14.00  0.52     Sequence
 HLA-DQA10301-DQB10302 1139      VNNTVYDPLQPELDS  TVYDPLQPE  3        0.3190
1584.6    17.00  0.56     Sequence
 HLA-DQA10301-DQB10302 1140      NNTVYDPLQPELDSF  TVYDPLQPE  2        0.3141
1671.0    18.00  0.55     Sequence
 HLA-DQA10301-DQB10302 1141      NTVYDPLQPELDSFK  TVYDPLQPE  1        0.2936
2085.2    23.00  0.58     Sequence
 HLA-DQA10301-DQB10302 1142      TVYDPLQPELDSFKE  TVYDPLQPE  0        0.2986
1977.0    21.00  0.47     Sequence
 HLA-DQA10301-DQB10302 1143      VYDPLQPELDSFKEE  QPELDSFKE  5        0.2697
2703.1    29.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1144      YDPLQPELDSFKEEL  QPELDSFKE  4        0.2838
2319.9    25.00  0.41     Sequence
 HLA-DQA10301-DQB10302 1145      DPLQPELDSFKEELD  QPELDSFKE  3        0.2800
2417.4    26.00  0.42     Sequence
 HLA-DQA10301-DQB10302 1146      PLQPELDSFKEELDK  QPELDSFKE  2        0.2588
3039.9    32.00  0.41     Sequence
 HLA-DQA10301-DQB10302 1147      LQPELDSFKEELDKY  QPELDSFKE  1        0.2534
3222.1    34.00  0.38     Sequence
 HLA-DQA10301-DQB10302 1148      QPELDSFKEELDKYF  QPELDSFKE  0        0.2373
3835.9    39.00  0.35     Sequence
 HLA-DQA10301-DQB10302 1149      PELDSFKEELDKYFK  ELDSFKEEL  1        0.1875
6577.5    60.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1150      ELDSFKEELDKYFKN  ELDSFKEEL  0        0.1326
11913.4    80.00  0.41     Sequence
 HLA-DQA10301-DQB10302 1151      LDSFKEELDKYFKNH  LDSFKEELD  0        0.0803
20964.7    95.00  0.28     Sequence
```

```
 HLA-DQA10301-DQB10302 1152      DSFKEELDKYFKNHT  SFKEELDKY  1         0.0638
25061.7   100.00  0.29     Sequence
 HLA-DQA10301-DQB10302 1153      SFKEELDKYFKNHTS  SFKEELDKY  0         0.0587
26497.3   100.00  0.27     Sequence
 HLA-DQA10301-DQB10302 1154      FKEELDKYFKNHTSP  DKYFKNHTS  5         0.0549
27607.6   100.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1155      KEELDKYFKNHTSPD  YFKNHTSPD  6         0.0885
19196.8    95.00  0.46     Sequence
 HLA-DQA10301-DQB10302 1156      EELDKYFKNHTSPDV  YFKNHTSPD  5         0.1207
13548.7    85.00  0.54     Sequence
 HLA-DQA10301-DQB10302 1157      ELDKYFKNHTSPDVD  YFKNHTSPD  4         0.1370
11352.6    80.00  0.41     Sequence
 HLA-DQA10301-DQB10302 1158      LDKYFKNHTSPDVDL  KNHTSPDVD  5         0.1520
9655.7    75.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1159      DKYFKNHTSPDVDLG  YFKNHTSPD  2         0.1449
10426.8    75.00  0.32     Sequence
 HLA-DQA10301-DQB10302 1160      KYFKNHTSPDVDLGD  KNHTSPDVD  3         0.1402
10969.1    80.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1161      YFKNHTSPDVDLGDI  KNHTSPDVD  2         0.1642
8457.5    70.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1162      FKNHTSPDVDLGDIS  SPDVDLGDI  5         0.1545
9395.6    75.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1163      KNHTSPDVDLGDISG  SPDVDLGDI  4         0.1640
8481.7    70.00  0.26     Sequence
 HLA-DQA10301-DQB10302 1164      NHTSPDVDLGDISGI  SPDVDLGDI  3         0.1654
8355.4    70.00  0.22     Sequence
 HLA-DQA10301-DQB10302 1165      HTSPDVDLGDISGIN  DLGDISGIN  6         0.1781
7282.4    65.00  0.19     Sequence
 HLA-DQA10301-DQB10302 1166      TSPDVDLGDISGINA  DLGDISGIN  5         0.1970
5933.8    55.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1167      SPDVDLGDISGINAS  LGDISGINA  5         0.2234
4460.7    44.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1168      PDVDLGDISGINASF  GDISGINAS  5         0.2940
2078.0    23.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1169      DVDLGDISGINASFV  DISGINASF  5         0.3242
1498.6    16.00  0.29     Sequence
 HLA-DQA10301-DQB10302 1170      VDLGDISGINASFVN  ISGINASFV  5         0.3212
1547.6    17.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1171      DLGDISGINASFVNI  ISGINASFV  4         0.3100
1747.0    19.00  0.29     Sequence
 HLA-DQA10301-DQB10302 1172      LGDISGINASFVNIQ  ISGINASFV  3         0.3099
1748.7    19.00  0.24     Sequence
 HLA-DQA10301-DQB10302 1173      GDISGINASFVNIQK  INASFVNIQ  5         0.2935
2087.8    23.00  0.23     Sequence
 HLA-DQA10301-DQB10302 1174      DISGINASFVNIQKE  ASFVNIQKE  6         0.4105
588.6     5.00  0.51     Sequence         WB
 HLA-DQA10301-DQB10302 1175      ISGINASFVNIQKEI  ASFVNIQKE  5         0.4136
569.3     5.00  0.71     Sequence         WB
 HLA-DQA10301-DQB10302 1176      SGINASFVNIQKEID  ASFVNIQKE  4         0.4219
520.4     4.50  0.67     Sequence         WB
 HLA-DQA10301-DQB10302 1177      GINASFVNIQKEIDR  ASFVNIQKE  3         0.3956
692.3     6.50  0.69     Sequence         WB
 HLA-DQA10301-DQB10302 1178      INASFVNIQKEIDRL  ASFVNIQKE  2         0.3948
697.6     6.50  0.71     Sequence         WB
 HLA-DQA10301-DQB10302 1179      NASFVNIQKEIDRLN  ASFVNIQKE  1         0.3747
867.1     8.50  0.75     Sequence         WB
 HLA-DQA10301-DQB10302 1180      ASFVNIQKEIDRLNE  ASFVNIQKE  0         0.3528
1099.9    11.00  0.75     Sequence
 HLA-DQA10301-DQB10302 1181      SFVNIQKEIDRLNEV  FVNIQKEID  1         0.1916
6287.2    60.00  0.40     Sequence
 HLA-DQA10301-DQB10302 1182      FVNIQKEIDRLNEVA  EIDRLNEVA  6         0.2069
5332.5    55.00  0.37     Sequence
 HLA-DQA10301-DQB10302 1183      VNIQKEIDRLNEVAK  EIDRLNEVA  5         0.1613
8729.7    70.00  0.51     Sequence
 HLA-DQA10301-DQB10302 1184      NIQKEIDRLNEVAKN  EIDRLNEVA  4         0.1678
8138.0    70.00  0.38     Sequence
```

```
 HLA-DQA10301-DQB10302 1185      IQKEIDRLNEVAKNL  DRLNEVAKN  5        0.1883
6520.2    60.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1186      QKEIDRLNEVAKNLN  DRLNEVAKN  4        0.1869
6615.6    60.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1187      KEIDRLNEVAKNLNE  DRLNEVAKN  3        0.2054
5415.0    55.00  0.26     Sequence
 HLA-DQA10301-DQB10302 1188      EIDRLNEVAKNLNES  NEVAKNLNE  5        0.2327
4034.0    41.00  0.29     Sequence
 HLA-DQA10301-DQB10302 1189      IDRLNEVAKNLNESL  NEVAKNLNE  4        0.2305
4127.5    42.00  0.26     Sequence
 HLA-DQA10301-DQB10302 1190      DRLNEVAKNLNESLI  NEVAKNLNE  3        0.2155
4859.0    47.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1191      RLNEVAKNLNESLID  NEVAKNLNE  2        0.2225
4504.4    45.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1192      LNEVAKNLNESLIDL  KNLNESLID  5        0.2241
4423.0    44.00  0.32     Sequence
 HLA-DQA10301-DQB10302 1193      NEVAKNLNESLIDLQ  LNESLIDLQ  6        0.2878
2220.4    24.00  0.35     Sequence
 HLA-DQA10301-DQB10302 1194      EVAKNLNESLIDLQE  LNESLIDLQ  5        0.3572
1047.8    11.00  0.45     Sequence
 HLA-DQA10301-DQB10302 1195      VAKNLNESLIDLQEL  ESLIDLQEL  6        0.4758
290.7     1.70  0.40     Sequence         SB
 HLA-DQA10301-DQB10302 1196      AKNLNESLIDLQELG  ESLIDLQEL  5        0.4481
391.9     3.00  0.42     Sequence         WB
 HLA-DQA10301-DQB10302 1197      KNLNESLIDLQELGK  ESLIDLQEL  4        0.4258
498.8     4.00  0.41     Sequence         WB
 HLA-DQA10301-DQB10302 1198      NLNESLIDLQELGKY  ESLIDLQEL  3        0.4148
561.9     5.00  0.41     Sequence         WB
 HLA-DQA10301-DQB10302 1199      LNESLIDLQELGKYE  ESLIDLQEL  2        0.4074
609.3     5.50  0.40     Sequence         WB
 HLA-DQA10301-DQB10302 1200      NESLIDLQELGKYEQ  ESLIDLQEL  1        0.3696
917.1     9.00  0.45     Sequence         WB
 HLA-DQA10301-DQB10302 1201      ESLIDLQELGKYEQY  ESLIDLQEL  0        0.3054
1837.1    20.00  0.51     Sequence
 HLA-DQA10301-DQB10302 1202      SLIDLQELGKYEQYI  DLQELGKYE  3        0.1659
8308.5    70.00  0.32     Sequence
 HLA-DQA10301-DQB10302 1203      LIDLQELGKYEQYIK  DLQELGKYE  2        0.1531
9544.8    75.00  0.36     Sequence
 HLA-DQA10301-DQB10302 1204      IDLQELGKYEQYIKW  DLQELGKYE  1        0.1508
9780.7    75.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1205      DLQELGKYEQYIKWP  DLQELGKYE  0        0.1332
11827.4    80.00  0.33     Sequence
 HLA-DQA10301-DQB10302 1206      LQELGKYEQYIKWPW  ELGKYEQYI  2        0.1099
15226.8    90.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1207      QELGKYEQYIKWPWY  EQYIKWPWY  6        0.1238
13099.8    85.00  0.26     Sequence
 HLA-DQA10301-DQB10302 1208      ELGKYEQYIKWPWYI  EQYIKWPWY  5        0.1201
13641.1    85.00  0.30     Sequence
 HLA-DQA10301-DQB10302 1209      LGKYEQYIKWPWYIW  EQYIKWPWY  4        0.1123
14827.7    90.00  0.30     Sequence
 HLA-DQA10301-DQB10302 1210      GKYEQYIKWPWYIWL  EQYIKWPWY  3        0.1157
14293.8    85.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1211      KYEQYIKWPWYIWLG  EQYIKWPWY  2        0.1182
13911.3    85.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1212      YEQYIKWPWYIWLGF  WPWYIWLGF  6        0.1502
9839.3    75.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1213      EQYIKWPWYIWLGFI  WPWYIWLGF  5        0.1469
10201.7    75.00  0.29     Sequence
 HLA-DQA10301-DQB10302 1214      QYIKWPWYIWLGFIA  WPWYIWLGF  4        0.1493
9938.8    75.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1215      YIKWPWYIWLGFIAG  YIWLGFIAG  6        0.1673
8178.4    70.00  0.23     Sequence
 HLA-DQA10301-DQB10302 1216      IKWPWYIWLGFIAGL  IWLGFIAGL  6        0.1956
6026.1    55.00  0.30     Sequence
 HLA-DQA10301-DQB10302 1217      KWPWYIWLGFIAGLI  IWLGFIAGL  5        0.2357
3902.0    40.00  0.31     Sequence
```

```
 HLA-DQA10301-DQB10302 1218      WPWYIWLGFIAGLIA  WLGFIAGLI  5        0.2652
2836.6    30.00  0.29     Sequence
 HLA-DQA10301-DQB10302 1219      PWYIWLGFIAGLIAI  LGFIAGLIA  5        0.2642
2866.1    31.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1220      WYIWLGFIAGLIAIV  LGFIAGLIA  4        0.2619
2939.7    31.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1221      YIWLGFIAGLIAIVM  LGFIAGLIA  3        0.2743
2569.9    28.00  0.23     Sequence
 HLA-DQA10301-DQB10302 1222      IWLGFIAGLIAIVMV  IAGLIAIVM  5        0.2680
2752.4    29.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1223      WLGFIAGLIAIVMVT  IAGLIAIVM  4        0.2508
3313.4    35.00  0.29     Sequence
 HLA-DQA10301-DQB10302 1224      LGFIAGLIAIVMVTI  IAGLIAIVM  3        0.2250
4382.6    44.00  0.32     Sequence
 HLA-DQA10301-DQB10302 1225      GFIAGLIAIVMVTIM  IAGLIAIVM  2        0.2000
5744.2    55.00  0.38     Sequence
 HLA-DQA10301-DQB10302 1226      FIAGLIAIVMVTIML  IAGLIAIVM  1        0.1800
7128.8    65.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1227      IAGLIAIVMVTIMLC  IAGLIAIVM  0        0.1630
8572.1    70.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1228      AGLIAIVMVTIMLCC  AGLIAIVMV  0        0.1261
12774.1    85.00  0.26     Sequence
 HLA-DQA10301-DQB10302 1229      GLIAIVMVTIMLCCM  GLIAIVMVT  0        0.0922
18438.7    95.00  0.16     Sequence
 HLA-DQA10301-DQB10302 1230      LIAIVMVTIMLCCMT  IAIVMVTIM  1        0.0826
20450.3    95.00  0.27     Sequence
 HLA-DQA10301-DQB10302 1231      IAIVMVTIMLCCMTS  IAIVMVTIM  0        0.0850
19925.8    95.00  0.22     Sequence
 HLA-DQA10301-DQB10302 1232      AIVMVTIMLCCMTSC  IMLCCMTSC  6        0.1067
15767.5    90.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1233      IVMVTIMLCCMTSCC  IMLCCMTSC  5        0.0978
17350.1    90.00  0.29     Sequence
 HLA-DQA10301-DQB10302 1234      VMVTIMLCCMTSCCS  IMLCCMTSC  4        0.0938
18122.6    95.00  0.26     Sequence
 HLA-DQA10301-DQB10302 1235      MVTIMLCCMTSCCSC  IMLCCMTSC  3        0.0850
19926.7    95.00  0.30     Sequence
 HLA-DQA10301-DQB10302 1236      VTIMLCCMTSCCSCL  IMLCCMTSC  2        0.0823
20527.6    95.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1237      TIMLCCMTSCCSCLK  IMLCCMTSC  1        0.0744
22351.2    95.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1238      IMLCCMTSCCSCLKG  IMLCCMTSC  0        0.0681
23927.4   100.00  0.36     Sequence
 HLA-DQA10301-DQB10302 1239      MLCCMTSCCSCLKGC  LCCMTSCCS  1        0.0441
31029.7   100.00  0.23     Sequence
 HLA-DQA10301-DQB10302 1240      LCCMTSCCSCLKGCC  LCCMTSCCS  0        0.0376
33287.0   100.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1241      CCMTSCCSCLKGCCS  SCCSCLKGC  4        0.0295
36352.1   100.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1242      CMTSCCSCLKGCCSC  SCCSCLKGC  3        0.0308
35843.9   100.00  0.21     Sequence
 HLA-DQA10301-DQB10302 1243      MTSCCSCLKGCCSCG  SCCSCLKGC  2        0.0288
36619.7   100.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1244      TSCCSCLKGCCSCGS  LKGCCSCGS  6        0.0299
36190.4   100.00  0.27     Sequence
 HLA-DQA10301-DQB10302 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5        0.0282
36856.2   100.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1246      CCSCLKGCCSCGSCC  GCCSCGSCC  6        0.0326
35140.8   100.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1247      CSCLKGCCSCGSCCK  GCCSCGSCC  5        0.0317
35472.4   100.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1248      SCLKGCCSCGSCCKF  GCCSCGSCC  4        0.0386
32913.5   100.00  0.25     Sequence
 HLA-DQA10301-DQB10302 1249      CLKGCCSCGSCCKFD  SCGSCCKFD  6        0.0503
29004.2   100.00  0.28     Sequence
 HLA-DQA10301-DQB10302 1250      LKGCCSCGSCCKFDE  SCGSCCKFD  5        0.0759
22003.3    95.00  0.34     Sequence
```

```
 HLA-DQA10301-DQB10302 1251      KGCCSCGSCCKFDED  CGSCCKFDE  5        0.0828
20403.4    95.00  0.34     Sequence
 HLA-DQA10301-DQB10302 1252      GCCSCGSCCKFDEDD  SCCKFDEDD  6        0.0979
17337.9    90.00  0.24     Sequence
 HLA-DQA10301-DQB10302 1253      CCSCGSCCKFDEDDS  SCCKFDEDD  5        0.0966
17575.5    90.00  0.30     Sequence
 HLA-DQA10301-DQB10302 1254      CSCGSCCKFDEDDSE  SCCKFDEDD  4        0.1094
15305.5    90.00  0.19     Sequence
 HLA-DQA10301-DQB10302 1255      SCGSCCKFDEDDSEP  CKFDEDDSE  5        0.1180
13943.3    85.00  0.31     Sequence
 HLA-DQA10301-DQB10302 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.1520
9655.1    75.00  0.37     Sequence
 HLA-DQA10301-DQB10302 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.1688
8050.3    65.00  0.35     Sequence
 HLA-DQA10301-DQB10302 1258      SCCKFDEDDSEPVLK  EDDSEPVLK  6        0.2077
5286.3    50.00  0.38     Sequence
 HLA-DQA10301-DQB10302 1259      CCKFDEDDSEPVLKG  EDDSEPVLK  5        0.2384
3791.7    39.00  0.51     Sequence
 HLA-DQA10301-DQB10302 1260      CKFDEDDSEPVLKGV  EDDSEPVLK  4        0.2506
3321.9    35.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1261      KFDEDDSEPVLKGVK  EDDSEPVLK  3        0.2307
4118.5    42.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1262      FDEDDSEPVLKGVKL  EDDSEPVLK  2        0.2260
4336.8    43.00  0.44     Sequence
 HLA-DQA10301-DQB10302 1263      DEDDSEPVLKGVKLH  EDDSEPVLK  1        0.2077
5284.6    50.00  0.50     Sequence
 HLA-DQA10301-DQB10302 1264      EDDSEPVLKGVKLHY  EDDSEPVLK  0        0.1700
7946.2    65.00  0.54     Sequence
 HLA-DQA10301-DQB10302 1265      DDSEPVLKGVKLHYT  DSEPVLKGV  1        0.1168
14131.0    85.00  0.26     Sequence
 HLA-DQA10401-DQB10402    1      PSPIKEMFVFLVLLP  EMFVFLVLL  5        0.2103
5137.2    55.00  0.31     Sequence
 HLA-DQA10401-DQB10402    2      SPIKEMFVFLVLLPL  EMFVFLVLL  4        0.2246
4400.4    46.00  0.22     Sequence
 HLA-DQA10401-DQB10402    3      PIKEMFVFLVLLPLV  FVFLVLLPL  5        0.2279
4244.9    45.00  0.22     Sequence
 HLA-DQA10401-DQB10402    4      IKEMFVFLVLLPLVS  FLVLLPLVS  6        0.2369
3854.1    42.00  0.25     Sequence
 HLA-DQA10401-DQB10402    5      KEMFVFLVLLPLVSS  FLVLLPLVS  5        0.2319
4066.9    44.00  0.27     Sequence
 HLA-DQA10401-DQB10402    6      EMFVFLVLLPLVSSQ  VLLPLVSSQ  6        0.2513
3296.3    37.00  0.29     Sequence
 HLA-DQA10401-DQB10402    7      MFVFLVLLPLVSSQC  VLLPLVSSQ  5        0.2655
2828.9    33.00  0.32     Sequence
 HLA-DQA10401-DQB10402    8      FVFLVLLPLVSSQCV  VLLPLVSSQ  4        0.2624
2924.5    34.00  0.30     Sequence
 HLA-DQA10401-DQB10402    9      VFLVLLPLVSSQCVN  VLLPLVSSQ  3        0.2397
3738.9    41.00  0.32     Sequence
 HLA-DQA10401-DQB10402   10      FLVLLPLVSSQCVNF  VLLPLVSSQ  2        0.2378
3814.7    42.00  0.29     Sequence
 HLA-DQA10401-DQB10402   11      LVLLPLVSSQCVNFT  LLPLVSSQC  2        0.2199
4629.8    48.00  0.25     Sequence
 HLA-DQA10401-DQB10402   12      VLLPLVSSQCVNFTN  LLPLVSSQC  1        0.2009
5686.7    55.00  0.25     Sequence
 HLA-DQA10401-DQB10402   13      LLPLVSSQCVNFTNR  LPLVSSQCV  1        0.1650
8387.5    70.00  0.28     Sequence
 HLA-DQA10401-DQB10402   14      LPLVSSQCVNFTNRT  LPLVSSQCV  0        0.1328
11881.1    80.00  0.29     Sequence
 HLA-DQA10401-DQB10402   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.1082
15501.4    90.00  0.28     Sequence
 HLA-DQA10401-DQB10402   16      LVSSQCVNFTNRTQL  VNFTNRTQL  6        0.1195
13723.8    85.00  0.25     Sequence
 HLA-DQA10401-DQB10402   17      VSSQCVNFTNRTQLP  NFTNRTQLP  6        0.1318
12013.7    80.00  0.34     Sequence
 HLA-DQA10401-DQB10402   18      SSQCVNFTNRTQLPS  NFTNRTQLP  5        0.1275
12585.6    85.00  0.34     Sequence
```

```
 HLA-DQA10401-DQB10402   19      SQCVNFTNRTQLPSA  NFTNRTQLP  4        0.1340
11732.8    80.00  0.25      Sequence
 HLA-DQA10401-DQB10402   20      QCVNFTNRTQLPSAY  NFTNRTQLP  3        0.1413
10844.5    80.00  0.21      Sequence
 HLA-DQA10401-DQB10402   21      CVNFTNRTQLPSAYT  NRTQLPSAY  5        0.1402
10974.8    80.00  0.25      Sequence
 HLA-DQA10401-DQB10402   22      VNFTNRTQLPSAYTN  NRTQLPSAY  4        0.1299
12256.3    80.00  0.25      Sequence
 HLA-DQA10401-DQB10402   23      NFTNRTQLPSAYTNS  NRTQLPSAY  3        0.1212
13467.9    85.00  0.28      Sequence
 HLA-DQA10401-DQB10402   24      FTNRTQLPSAYTNSF  LPSAYTNSF  6        0.1719
7780.0    70.00  0.46      Sequence
 HLA-DQA10401-DQB10402   25      TNRTQLPSAYTNSFT  LPSAYTNSF  5        0.1650
8392.1    70.00  0.52      Sequence
 HLA-DQA10401-DQB10402   26      NRTQLPSAYTNSFTR  LPSAYTNSF  4        0.1546
9384.7    75.00  0.46      Sequence
 HLA-DQA10401-DQB10402   27      RTQLPSAYTNSFTRG  LPSAYTNSF  3        0.1474
10143.6    75.00  0.46      Sequence
 HLA-DQA10401-DQB10402   28      TQLPSAYTNSFTRGV  LPSAYTNSF  2        0.1514
9715.5    75.00  0.40      Sequence
 HLA-DQA10401-DQB10402   29      QLPSAYTNSFTRGVY  LPSAYTNSF  1        0.1684
8084.2    70.00  0.32      Sequence
 HLA-DQA10401-DQB10402   30      LPSAYTNSFTRGVYY  NSFTRGVYY  6        0.1840
6827.2    65.00  0.26      Sequence
 HLA-DQA10401-DQB10402   31      PSAYTNSFTRGVYYP  NSFTRGVYY  5        0.1889
6477.0    60.00  0.31      Sequence
 HLA-DQA10401-DQB10402   32      SAYTNSFTRGVYYPD  FTRGVYYPD  6        0.2235
4452.2    47.00  0.20      Sequence
 HLA-DQA10401-DQB10402   33      AYTNSFTRGVYYPDK  FTRGVYYPD  5        0.2087
5227.9    55.00  0.22      Sequence
 HLA-DQA10401-DQB10402   34      YTNSFTRGVYYPDKV  FTRGVYYPD  4        0.2073
5309.5    55.00  0.22      Sequence
 HLA-DQA10401-DQB10402   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.1937
6147.4    60.00  0.25      Sequence
 HLA-DQA10401-DQB10402   36      NSFTRGVYYPDKVFR  FTRGVYYPD  2        0.1669
8221.2    70.00  0.35      Sequence
 HLA-DQA10401-DQB10402   37      SFTRGVYYPDKVFRS  FTRGVYYPD  1        0.1448
10432.5    75.00  0.38      Sequence
 HLA-DQA10401-DQB10402   38      FTRGVYYPDKVFRSS  FTRGVYYPD  0        0.1235
13148.1    85.00  0.34      Sequence
 HLA-DQA10401-DQB10402   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.0901
18856.3    95.00  0.22      Sequence
 HLA-DQA10401-DQB10402   40      RGVYYPDKVFRSSVL  DKVFRSSVL  6        0.1623
8637.3    70.00  0.50      Sequence
 HLA-DQA10401-DQB10402   41      GVYYPDKVFRSSVLH  DKVFRSSVL  5        0.1547
9375.2    75.00  0.47      Sequence
 HLA-DQA10401-DQB10402   42      VYYPDKVFRSSVLHS  DKVFRSSVL  4        0.1783
7262.5    65.00  0.35      Sequence
 HLA-DQA10401-DQB10402   43      YYPDKVFRSSVLHST  DKVFRSSVL  3        0.1975
5899.5    60.00  0.34      Sequence
 HLA-DQA10401-DQB10402   44      YPDKVFRSSVLHSTQ  DKVFRSSVL  2        0.1906
6356.5    60.00  0.31      Sequence
 HLA-DQA10401-DQB10402   45      PDKVFRSSVLHSTQD  SSVLHSTQD  6        0.2220
4526.4    47.00  0.26      Sequence
 HLA-DQA10401-DQB10402   46      DKVFRSSVLHSTQDL  SSVLHSTQD  5        0.2455
3510.8    39.00  0.28      Sequence
 HLA-DQA10401-DQB10402   47      KVFRSSVLHSTQDLF  SVLHSTQDL  5        0.2611
2966.8    34.00  0.25      Sequence
 HLA-DQA10401-DQB10402   48      VFRSSVLHSTQDLFL  SSVLHSTQD  3        0.2491
3375.0    38.00  0.29      Sequence
 HLA-DQA10401-DQB10402   49      FRSSVLHSTQDLFLP  SVLHSTQDL  3        0.2370
3850.0    42.00  0.28      Sequence
 HLA-DQA10401-DQB10402   50      RSSVLHSTQDLFLPF  SVLHSTQDL  2        0.2285
4221.6    45.00  0.25      Sequence
 HLA-DQA10401-DQB10402   51      SSVLHSTQDLFLPFF  SVLHSTQDL  1        0.2459
3494.7    39.00  0.19      Sequence
```

```
 HLA-DQA10401-DQB10402   52      SVLHSTQDLFLPFFS  TQDLFLPFF  5        0.2424
3629.5    40.00  0.18     Sequence
 HLA-DQA10401-DQB10402   53      VLHSTQDLFLPFFSN  DLFLPFFSN  6        0.2665
2797.0    33.00  0.28     Sequence
 HLA-DQA10401-DQB10402   54      LHSTQDLFLPFFSNV  DLFLPFFSN  5        0.2598
3006.0    35.00  0.31     Sequence
 HLA-DQA10401-DQB10402   55      HSTQDLFLPFFSNVT  DLFLPFFSN  4        0.2573
3089.6    35.00  0.31     Sequence
 HLA-DQA10401-DQB10402   56      STQDLFLPFFSNVTW  DLFLPFFSN  3        0.2523
3261.0    37.00  0.29     Sequence
 HLA-DQA10401-DQB10402   57      TQDLFLPFFSNVTWF  PFFSNVTWF  6        0.3024
1897.0    23.00  0.35     Sequence
 HLA-DQA10401-DQB10402   58      QDLFLPFFSNVTWFH  PFFSNVTWF  5        0.2971
2007.7    24.00  0.35     Sequence
 HLA-DQA10401-DQB10402   59      DLFLPFFSNVTWFHA  PFFSNVTWF  4        0.2854
2279.9    27.00  0.35     Sequence
 HLA-DQA10401-DQB10402   60      LFLPFFSNVTWFHAI  PFFSNVTWF  3        0.2742
2574.5    30.00  0.35     Sequence
 HLA-DQA10401-DQB10402   61      FLPFFSNVTWFHAIH  PFFSNVTWF  2        0.2615
2952.6    34.00  0.35     Sequence
 HLA-DQA10401-DQB10402   62      LPFFSNVTWFHAIHV  PFFSNVTWF  1        0.2481
3415.0    38.00  0.31     Sequence
 HLA-DQA10401-DQB10402   63      PFFSNVTWFHAIHVS  PFFSNVTWF  0        0.2416
3661.4    41.00  0.23     Sequence
 HLA-DQA10401-DQB10402   64      FFSNVTWFHAIHVSG  VTWFHAIHV  4        0.2348
3942.1    43.00  0.27     Sequence
 HLA-DQA10401-DQB10402   65      FSNVTWFHAIHVSGT  VTWFHAIHV  3        0.2146
4906.6    50.00  0.28     Sequence
 HLA-DQA10401-DQB10402   66      SNVTWFHAIHVSGTN  VTWFHAIHV  2        0.1941
6122.3    60.00  0.26     Sequence
 HLA-DQA10401-DQB10402   67      NVTWFHAIHVSGTNG  VTWFHAIHV  1        0.1789
7216.4    65.00  0.28     Sequence
 HLA-DQA10401-DQB10402   68      VTWFHAIHVSGTNGT  VTWFHAIHV  0        0.1640
8477.1    70.00  0.25     Sequence
 HLA-DQA10401-DQB10402   69      TWFHAIHVSGTNGTK  WFHAIHVSG  1        0.1235
13145.4    85.00  0.29     Sequence
 HLA-DQA10401-DQB10402   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1        0.0943
18027.9    90.00  0.35     Sequence
 HLA-DQA10401-DQB10402   71      FHAIHVSGTNGTKRF  SGTNGTKRF  6        0.0871
19476.9    95.00  0.34     Sequence
 HLA-DQA10401-DQB10402   72      HAIHVSGTNGTKRFD  SGTNGTKRF  5        0.0779
21526.4    95.00  0.44     Sequence
 HLA-DQA10401-DQB10402   73      AIHVSGTNGTKRFDN  SGTNGTKRF  4        0.0736
22539.2    95.00  0.44     Sequence
 HLA-DQA10401-DQB10402   74      IHVSGTNGTKRFDNP  SGTNGTKRF  3        0.0728
22756.3    95.00  0.45     Sequence
 HLA-DQA10401-DQB10402   75      HVSGTNGTKRFDNPV  SGTNGTKRF  2        0.0686
23808.3   100.00  0.44     Sequence
 HLA-DQA10401-DQB10402   76      VSGTNGTKRFDNPVL  SGTNGTKRF  1        0.0710
23181.2    95.00  0.39     Sequence
 HLA-DQA10401-DQB10402   77      SGTNGTKRFDNPVLP  KRFDNPVLP  6        0.0771
21713.3    95.00  0.37     Sequence
 HLA-DQA10401-DQB10402   78      GTNGTKRFDNPVLPF  RFDNPVLPF  6        0.2098
5166.4    55.00  0.63     Sequence
 HLA-DQA10401-DQB10402   79      TNGTKRFDNPVLPFN  RFDNPVLPF  5        0.2179
4730.1    49.00  0.64     Sequence
 HLA-DQA10401-DQB10402   80      NGTKRFDNPVLPFND  RFDNPVLPF  4        0.2786
2452.9    29.00  0.51     Sequence
 HLA-DQA10401-DQB10402   81      GTKRFDNPVLPFNDG  RFDNPVLPF  3        0.2753
2542.8    30.00  0.43     Sequence
 HLA-DQA10401-DQB10402   82      TKRFDNPVLPFNDGV  RFDNPVLPF  2        0.2762
2517.1    30.00  0.42     Sequence
 HLA-DQA10401-DQB10402   83      KRFDNPVLPFNDGVY  RFDNPVLPF  1        0.2801
2414.8    29.00  0.40     Sequence
 HLA-DQA10401-DQB10402   84      RFDNPVLPFNDGVYF  RFDNPVLPF  0        0.2752
2546.0    30.00  0.34     Sequence
```

```
 HLA-DQA10401-DQB10402   85      FDNPVLPFNDGVYFA  DNPVLPFND  1         0.2295
4174.4    45.00  0.29     Sequence
 HLA-DQA10401-DQB10402   86      DNPVLPFNDGVYFAS  PFNDGVYFA  5         0.2237
4443.0    47.00  0.28     Sequence
 HLA-DQA10401-DQB10402   87      NPVLPFNDGVYFAST  PFNDGVYFA  4         0.2177
4744.1    49.00  0.26     Sequence
 HLA-DQA10401-DQB10402   88      PVLPFNDGVYFASTE  DGVYFASTE  6         0.3244
1495.6    18.00  0.57     Sequence
 HLA-DQA10401-DQB10402   89      VLPFNDGVYFASTEK  DGVYFASTE  5         0.3131
1689.9    21.00  0.57     Sequence
 HLA-DQA10401-DQB10402   90      LPFNDGVYFASTEKS  DGVYFASTE  4         0.3184
1595.0    19.00  0.54     Sequence
 HLA-DQA10401-DQB10402   91      PFNDGVYFASTEKSN  DGVYFASTE  3         0.3012
1921.2    23.00  0.56     Sequence
 HLA-DQA10401-DQB10402   92      FNDGVYFASTEKSNI  DGVYFASTE  2         0.2906
2155.4    26.00  0.57     Sequence
 HLA-DQA10401-DQB10402   93      NDGVYFASTEKSNII  DGVYFASTE  1         0.2593
3025.0    35.00  0.56     Sequence
 HLA-DQA10401-DQB10402   94      DGVYFASTEKSNIIR  DGVYFASTE  0         0.2256
4352.5    46.00  0.51     Sequence
 HLA-DQA10401-DQB10402   95      GVYFASTEKSNIIRG  VYFASTEKS  1         0.1335
11797.6    80.00  0.44     Sequence
 HLA-DQA10401-DQB10402   96      VYFASTEKSNIIRGW  EKSNIIRGW  6         0.1383
11201.4    80.00  0.32     Sequence
 HLA-DQA10401-DQB10402   97      YFASTEKSNIIRGWI  EKSNIIRGW  5         0.1308
12148.5    80.00  0.38     Sequence
 HLA-DQA10401-DQB10402   98      FASTEKSNIIRGWIF  EKSNIIRGW  4         0.1647
8417.6    70.00  0.32     Sequence
 HLA-DQA10401-DQB10402   99      ASTEKSNIIRGWIFG  EKSNIIRGW  3         0.1521
9648.3    75.00  0.32     Sequence
 HLA-DQA10401-DQB10402  100      STEKSNIIRGWIFGT  EKSNIIRGW  2         0.1425
10694.5    80.00  0.30     Sequence
 HLA-DQA10401-DQB10402  101      TEKSNIIRGWIFGTT  EKSNIIRGW  1         0.1433
10603.0    80.00  0.26     Sequence
 HLA-DQA10401-DQB10402  102      EKSNIIRGWIFGTTL  RGWIFGTTL  6         0.1484
10038.3    75.00  0.23     Sequence
 HLA-DQA10401-DQB10402  103      KSNIIRGWIFGTTLD  GWIFGTTLD  6         0.2141
4933.0    50.00  0.46     Sequence
 HLA-DQA10401-DQB10402  104      SNIIRGWIFGTTLDS  GWIFGTTLD  5         0.2611
2966.4    34.00  0.37     Sequence
 HLA-DQA10401-DQB10402  105      NIIRGWIFGTTLDSK  GWIFGTTLD  4         0.2440
3568.6    40.00  0.34     Sequence
 HLA-DQA10401-DQB10402  106      IIRGWIFGTTLDSKT  GWIFGTTLD  3         0.2360
3889.6    42.00  0.32     Sequence
 HLA-DQA10401-DQB10402  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3         0.2234
4460.2    47.00  0.32     Sequence
 HLA-DQA10401-DQB10402  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2         0.2056
5404.9    55.00  0.32     Sequence
 HLA-DQA10401-DQB10402  109      GWIFGTTLDSKTQSL  TLDSKTQSL  6         0.2203
4610.6    48.00  0.27     Sequence
 HLA-DQA10401-DQB10402  110      WIFGTTLDSKTQSLL  TLDSKTQSL  5         0.1878
6551.1    60.00  0.39     Sequence
 HLA-DQA10401-DQB10402  111      IFGTTLDSKTQSLLI  TLDSKTQSL  4         0.1914
6306.2    60.00  0.34     Sequence
 HLA-DQA10401-DQB10402  112      FGTTLDSKTQSLLIV  TLDSKTQSL  3         0.1892
6452.6    60.00  0.34     Sequence
 HLA-DQA10401-DQB10402  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4         0.1772
7352.9    65.00  0.36     Sequence
 HLA-DQA10401-DQB10402  114      TTLDSKTQSLLIVNN  DSKTQSLLI  3         0.1848
6771.1    65.00  0.31     Sequence
 HLA-DQA10401-DQB10402  115      TLDSKTQSLLIVNNA  QSLLIVNNA  6         0.2193
4663.1    48.00  0.35     Sequence
 HLA-DQA10401-DQB10402  116      LDSKTQSLLIVNNAT  QSLLIVNNA  5         0.2086
5232.1    55.00  0.35     Sequence
 HLA-DQA10401-DQB10402  117      DSKTQSLLIVNNATN  QSLLIVNNA  4         0.1962
5983.3    60.00  0.36     Sequence
```

```
 HLA-DQA10401-DQB10402  118      SKTQSLLIVNNATNV  QSLLIVNNA  3        0.1845
6790.0    65.00  0.40     Sequence
 HLA-DQA10401-DQB10402  119      KTQSLLIVNNATNVV  QSLLIVNNA  2        0.1940
6131.4    60.00  0.26     Sequence
 HLA-DQA10401-DQB10402  120      TQSLLIVNNATNVVI  IVNNATNVV  5        0.2084
5243.8    55.00  0.28     Sequence
 HLA-DQA10401-DQB10402  121      QSLLIVNNATNVVIK  IVNNATNVV  4        0.1928
6206.7    60.00  0.20     Sequence
 HLA-DQA10401-DQB10402  122      SLLIVNNATNVVIKV  NATNVVIKV  6        0.2044
5474.7    55.00  0.31     Sequence
 HLA-DQA10401-DQB10402  123      LLIVNNATNVVIKVC  NATNVVIKV  5        0.2199
4632.7    48.00  0.32     Sequence
 HLA-DQA10401-DQB10402  124      LIVNNATNVVIKVCE  TNVVIKVCE  6        0.2408
3695.2    41.00  0.26     Sequence
 HLA-DQA10401-DQB10402  125      IVNNATNVVIKVCEF  NVVIKVCEF  6        0.2955
2043.1    25.00  0.33     Sequence
 HLA-DQA10401-DQB10402  126      VNNATNVVIKVCEFQ  NVVIKVCEF  5        0.2838
2319.8    28.00  0.35     Sequence
 HLA-DQA10401-DQB10402  127      NNATNVVIKVCEFQF  NVVIKVCEF  4        0.2865
2253.0    27.00  0.34     Sequence
 HLA-DQA10401-DQB10402  128      NATNVVIKVCEFQFC  NVVIKVCEF  3        0.2796
2427.8    29.00  0.35     Sequence
 HLA-DQA10401-DQB10402  129      ATNVVIKVCEFQFCN  NVVIKVCEF  2        0.2603
2989.7    34.00  0.38     Sequence
 HLA-DQA10401-DQB10402  130      TNVVIKVCEFQFCNY  NVVIKVCEF  1        0.2396
3740.4    41.00  0.40     Sequence
 HLA-DQA10401-DQB10402  131      NVVIKVCEFQFCNYP  NVVIKVCEF  0        0.2020
5620.7    55.00  0.41     Sequence
 HLA-DQA10401-DQB10402  132      VVIKVCEFQFCNYPF  EFQFCNYPF  6        0.1894
6438.1    60.00  0.34     Sequence
 HLA-DQA10401-DQB10402  133      VIKVCEFQFCNYPFL  EFQFCNYPF  5        0.1654
8350.2    70.00  0.50     Sequence
 HLA-DQA10401-DQB10402  134      IKVCEFQFCNYPFLG  EFQFCNYPF  4        0.1675
8166.6    70.00  0.49     Sequence
 HLA-DQA10401-DQB10402  135      KVCEFQFCNYPFLGV  EFQFCNYPF  3        0.1673
8181.1    70.00  0.47     Sequence
 HLA-DQA10401-DQB10402  136      VCEFQFCNYPFLGVY  EFQFCNYPF  2        0.1713
7838.9    70.00  0.44     Sequence
 HLA-DQA10401-DQB10402  137      CEFQFCNYPFLGVYY  EFQFCNYPF  1        0.1690
8035.0    70.00  0.41     Sequence
 HLA-DQA10401-DQB10402  138      EFQFCNYPFLGVYYH  YPFLGVYYH  6        0.2219
4532.4    47.00  0.41     Sequence
 HLA-DQA10401-DQB10402  139      FQFCNYPFLGVYYHK  YPFLGVYYH  5        0.1842
6812.8    65.00  0.51     Sequence
 HLA-DQA10401-DQB10402  140      QFCNYPFLGVYYHKN  YPFLGVYYH  4        0.1899
6407.3    60.00  0.47     Sequence
 HLA-DQA10401-DQB10402  141      FCNYPFLGVYYHKNN  YPFLGVYYH  3        0.1812
7039.1    65.00  0.47     Sequence
 HLA-DQA10401-DQB10402  142      CNYPFLGVYYHKNNK  YPFLGVYYH  2        0.1610
8761.9    70.00  0.50     Sequence
 HLA-DQA10401-DQB10402  143      NYPFLGVYYHKNNKS  YPFLGVYYH  1        0.1484
10034.9    75.00  0.52     Sequence
 HLA-DQA10401-DQB10402  144      YPFLGVYYHKNNKSW  YPFLGVYYH  0        0.1249
12937.1    85.00  0.52     Sequence
 HLA-DQA10401-DQB10402  145      PFLGVYYHKNNKSWM  FLGVYYHKN  1        0.0690
23709.4   100.00  0.53     Sequence
 HLA-DQA10401-DQB10402  146      FLGVYYHKNNKSWME  HKNNKSWME  6        0.0963
17635.9    90.00  0.56     Sequence
 HLA-DQA10401-DQB10402  147      LGVYYHKNNKSWMES  HKNNKSWME  5        0.1028
16439.5    90.00  0.62     Sequence
 HLA-DQA10401-DQB10402  148      GVYYHKNNKSWMESE  NNKSWMESE  6        0.1931
6187.2    60.00  0.49     Sequence
 HLA-DQA10401-DQB10402  149      VYYHKNNKSWMESEF  NNKSWMESE  5        0.2385
3785.2    42.00  0.49     Sequence
 HLA-DQA10401-DQB10402  150      YYHKNNKSWMESEFR  NNKSWMESE  4        0.2192
4665.4    48.00  0.44     Sequence
```

```
 HLA-DQA10401-DQB10402  151      YHKNNKSWMESEFRV  NNKSWMESE  3        0.2244
4410.6    47.00  0.41     Sequence
 HLA-DQA10401-DQB10402  152      HKNNKSWMESEFRVY  NNKSWMESE  2        0.2460
3491.3    39.00  0.28     Sequence
 HLA-DQA10401-DQB10402  153      KNNKSWMESEFRVYS  NNKSWMESE  1        0.2416
3663.5    41.00  0.26     Sequence
 HLA-DQA10401-DQB10402  154      NNKSWMESEFRVYSS  WMESEFRVY  4        0.2507
3319.1    38.00  0.24     Sequence
 HLA-DQA10401-DQB10402  155      NKSWMESEFRVYSSA  WMESEFRVY  3        0.2558
3141.1    36.00  0.25     Sequence
 HLA-DQA10401-DQB10402  156      KSWMESEFRVYSSAN  EFRVYSSAN  6        0.2727
2616.3    31.00  0.25     Sequence
 HLA-DQA10401-DQB10402  157      SWMESEFRVYSSANN  EFRVYSSAN  5        0.2663
2802.1    33.00  0.29     Sequence
 HLA-DQA10401-DQB10402  158      WMESEFRVYSSANNC  EFRVYSSAN  4        0.2570
3098.8    36.00  0.32     Sequence
 HLA-DQA10401-DQB10402  159      MESEFRVYSSANNCT  EFRVYSSAN  3        0.2248
4389.5    46.00  0.40     Sequence
 HLA-DQA10401-DQB10402  160      ESEFRVYSSANNCTF  EFRVYSSAN  2        0.2226
4497.1    47.00  0.32     Sequence
 HLA-DQA10401-DQB10402  161      SEFRVYSSANNCTFE  EFRVYSSAN  1        0.2103
5138.3    55.00  0.26     Sequence
 HLA-DQA10401-DQB10402  162      EFRVYSSANNCTFEY  SANNCTFEY  6        0.2397
3739.8    41.00  0.35     Sequence
 HLA-DQA10401-DQB10402  163      FRVYSSANNCTFEYV  SANNCTFEY  5        0.2354
3915.8    43.00  0.40     Sequence
 HLA-DQA10401-DQB10402  164      RVYSSANNCTFEYVS  SANNCTFEY  4        0.2181
4724.2    49.00  0.41     Sequence
 HLA-DQA10401-DQB10402  165      VYSSANNCTFEYVSQ  SANNCTFEY  3        0.2106
5122.0    55.00  0.40     Sequence
 HLA-DQA10401-DQB10402  166      YSSANNCTFEYVSQP  SANNCTFEY  2        0.2196
4646.6    48.00  0.32     Sequence
 HLA-DQA10401-DQB10402  167      SSANNCTFEYVSQPF  TFEYVSQPF  6        0.2898
2174.7    26.00  0.42     Sequence
 HLA-DQA10401-DQB10402  168      SANNCTFEYVSQPFL  TFEYVSQPF  5        0.2791
2439.8    29.00  0.47     Sequence
 HLA-DQA10401-DQB10402  169      ANNCTFEYVSQPFLM  TFEYVSQPF  4        0.2930
2099.1    25.00  0.38     Sequence
 HLA-DQA10401-DQB10402  170      NNCTFEYVSQPFLMD  TFEYVSQPF  3        0.3307
1396.0    17.00  0.28     Sequence
 HLA-DQA10401-DQB10402  171      NCTFEYVSQPFLMDL  TFEYVSQPF  2        0.3461
1182.2    14.00  0.22     Sequence
 HLA-DQA10401-DQB10402  172      CTFEYVSQPFLMDLE  TFEYVSQPF  1        0.3796
822.6     9.00  0.17    Sequence         WB
 HLA-DQA10401-DQB10402  173      TFEYVSQPFLMDLEG  SQPFLMDLE  5        0.3711
902.4    10.00  0.25    Sequence
 HLA-DQA10401-DQB10402  174      FEYVSQPFLMDLEGK  SQPFLMDLE  4        0.3324
1370.7    17.00  0.28     Sequence
 HLA-DQA10401-DQB10402  175      EYVSQPFLMDLEGKQ  SQPFLMDLE  3        0.3021
1902.6    23.00  0.34     Sequence
 HLA-DQA10401-DQB10402  176      YVSQPFLMDLEGKQG  SQPFLMDLE  2        0.2608
2974.8    34.00  0.41     Sequence
 HLA-DQA10401-DQB10402  177      VSQPFLMDLEGKQGN  SQPFLMDLE  1        0.2129
4992.7    55.00  0.43     Sequence
 HLA-DQA10401-DQB10402  178      SQPFLMDLEGKQGNF  SQPFLMDLE  0        0.1866
6637.7    60.00  0.37     Sequence
 HLA-DQA10401-DQB10402  179      QPFLMDLEGKQGNFK  QPFLMDLEG  0        0.1224
13302.9    85.00  0.30     Sequence
 HLA-DQA10401-DQB10402  180      PFLMDLEGKQGNFKN  FLMDLEGKQ  1        0.0906
18751.7    95.00  0.25     Sequence
 HLA-DQA10401-DQB10402  181      FLMDLEGKQGNFKNL  LMDLEGKQG  1        0.0757
22053.3    95.00  0.36     Sequence
 HLA-DQA10401-DQB10402  182      LMDLEGKQGNFKNLS  LMDLEGKQG  0        0.0522
28418.4   100.00  0.32     Sequence
 HLA-DQA10401-DQB10402  183      MDLEGKQGNFKNLSE  QGNFKNLSE  6        0.1085
15461.1    90.00  0.68     Sequence
```

```
 HLA-DQA10401-DQB10402  184      DLEGKQGNFKNLSEF  QGNFKNLSE  5        0.1840
6831.7    65.00  0.52     Sequence
 HLA-DQA10401-DQB10402  185      LEGKQGNFKNLSEFV  QGNFKNLSE  4        0.1892
6455.3    60.00  0.43     Sequence
 HLA-DQA10401-DQB10402  186      EGKQGNFKNLSEFVF  QGNFKNLSE  3        0.2178
4734.9    49.00  0.34     Sequence
 HLA-DQA10401-DQB10402  187      GKQGNFKNLSEFVFK  QGNFKNLSE  2        0.2059
5388.7    55.00  0.31     Sequence
 HLA-DQA10401-DQB10402  188      KQGNFKNLSEFVFKN  QGNFKNLSE  1        0.2118
5057.8    55.00  0.28     Sequence
 HLA-DQA10401-DQB10402  189      QGNFKNLSEFVFKNI  GNFKNLSEF  1        0.2060
5383.5    55.00  0.23     Sequence
 HLA-DQA10401-DQB10402  190      GNFKNLSEFVFKNID  FKNLSEFVF  2        0.2051
5434.1    55.00  0.20     Sequence
 HLA-DQA10401-DQB10402  191      NFKNLSEFVFKNIDG  SEFVFKNID  5        0.1905
6365.1    60.00  0.27     Sequence
 HLA-DQA10401-DQB10402  192      FKNLSEFVFKNIDGY  SEFVFKNID  4        0.1990
5809.1    60.00  0.25     Sequence
 HLA-DQA10401-DQB10402  193      KNLSEFVFKNIDGYF  SEFVFKNID  3        0.1938
6142.4    60.00  0.26     Sequence
 HLA-DQA10401-DQB10402  194      NLSEFVFKNIDGYFK  SEFVFKNID  2        0.1797
7155.7    65.00  0.27     Sequence
 HLA-DQA10401-DQB10402  195      LSEFVFKNIDGYFKI  SEFVFKNID  1        0.1745
7571.0    65.00  0.27     Sequence
 HLA-DQA10401-DQB10402  196      SEFVFKNIDGYFKIY  FVFKNIDGY  2        0.1688
8045.7    70.00  0.26     Sequence
 HLA-DQA10401-DQB10402  197      EFVFKNIDGYFKIYS  NIDGYFKIY  5        0.1632
8548.9    70.00  0.20     Sequence
 HLA-DQA10401-DQB10402  198      FVFKNIDGYFKIYSK  NIDGYFKIY  4        0.1649
8396.1    70.00  0.19     Sequence
 HLA-DQA10401-DQB10402  199      VFKNIDGYFKIYSKH  NIDGYFKIY  3        0.1438
10554.7    80.00  0.23     Sequence
 HLA-DQA10401-DQB10402  200      FKNIDGYFKIYSKHT  NIDGYFKIY  2        0.1366
11405.3    80.00  0.24     Sequence
 HLA-DQA10401-DQB10402  201      KNIDGYFKIYSKHTP  DGYFKIYSK  3        0.1243
13034.9    85.00  0.34     Sequence
 HLA-DQA10401-DQB10402  202      NIDGYFKIYSKHTPI  DGYFKIYSK  2        0.1169
14114.9    85.00  0.37     Sequence
 HLA-DQA10401-DQB10402  203      IDGYFKIYSKHTPIN  DGYFKIYSK  1        0.0987
17190.6    90.00  0.39     Sequence
 HLA-DQA10401-DQB10402  204      DGYFKIYSKHTPINL  DGYFKIYSK  0        0.0818
20635.6    95.00  0.32     Sequence
 HLA-DQA10401-DQB10402  205      GYFKIYSKHTPINLV  SKHTPINLV  6        0.1078
15567.2    90.00  0.49     Sequence
 HLA-DQA10401-DQB10402  206      YFKIYSKHTPINLVR  SKHTPINLV  5        0.1024
16518.5    90.00  0.44     Sequence
 HLA-DQA10401-DQB10402  207      FKIYSKHTPINLVRD  HTPINLVRD  6        0.1525
9604.8    75.00  0.48     Sequence
 HLA-DQA10401-DQB10402  208      KIYSKHTPINLVRDL  HTPINLVRD  5        0.1928
6206.8    60.00  0.44     Sequence
 HLA-DQA10401-DQB10402  209      IYSKHTPINLVRDLP  HTPINLVRD  4        0.2006
5706.1    55.00  0.43     Sequence
 HLA-DQA10401-DQB10402  210      YSKHTPINLVRDLPQ  HTPINLVRD  3        0.2118
5057.1    55.00  0.30     Sequence
 HLA-DQA10401-DQB10402  211      SKHTPINLVRDLPQG  HTPINLVRD  2        0.1953
6041.5    60.00  0.29     Sequence
 HLA-DQA10401-DQB10402  212      KHTPINLVRDLPQGF  HTPINLVRD  1        0.2034
5538.9    55.00  0.23     Sequence
 HLA-DQA10401-DQB10402  213      HTPINLVRDLPQGFS  INLVRDLPQ  3        0.1990
5807.5    60.00  0.21     Sequence
 HLA-DQA10401-DQB10402  214      TPINLVRDLPQGFSA  INLVRDLPQ  2        0.1777
7310.3    65.00  0.27     Sequence
 HLA-DQA10401-DQB10402  215      PINLVRDLPQGFSAL  DLPQGFSAL  6        0.2163
4814.8    50.00  0.38     Sequence
 HLA-DQA10401-DQB10402  216      INLVRDLPQGFSALE  DLPQGFSAL  5        0.2525
3255.3    37.00  0.38     Sequence
```

```
 HLA-DQA10401-DQB10402  217      NLVRDLPQGFSALEP  LPQGFSALE  5        0.2948
2058.3    25.00  0.32     Sequence
 HLA-DQA10401-DQB10402  218      LVRDLPQGFSALEPL  QGFSALEPL  6        0.3942
702.3     7.50  0.41     Sequence        WB
 HLA-DQA10401-DQB10402  219      VRDLPQGFSALEPLV  QGFSALEPL  5        0.3848
777.5     8.50  0.41     Sequence        WB
 HLA-DQA10401-DQB10402  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.4770
286.9     2.50  0.38     Sequence        WB
 HLA-DQA10401-DQB10402  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.4943
237.8     1.50  0.42     Sequence        SB
 HLA-DQA10401-DQB10402  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.4805
276.2     2.00  0.47     Sequence        WB
 HLA-DQA10401-DQB10402  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.4665
321.2     2.50  0.47     Sequence        WB
 HLA-DQA10401-DQB10402  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.4416
420.6     4.00  0.53     Sequence        WB
 HLA-DQA10401-DQB10402  225      GFSALEPLVDLPIGI  FSALEPLVD  1        0.3870
759.3     8.50  0.59     Sequence        WB
 HLA-DQA10401-DQB10402  226      FSALEPLVDLPIGIN  FSALEPLVD  0        0.3486
1150.8    14.00  0.55     Sequence
 HLA-DQA10401-DQB10402  227      SALEPLVDLPIGINI  LVDLPIGIN  5        0.2185
4702.5    49.00  0.21     Sequence
 HLA-DQA10401-DQB10402  228      ALEPLVDLPIGINIT  DLPIGINIT  6        0.2656
2824.5    33.00  0.51     Sequence
 HLA-DQA10401-DQB10402  229      LEPLVDLPIGINITR  DLPIGINIT  5        0.2560
3133.9    36.00  0.56     Sequence
 HLA-DQA10401-DQB10402  230      EPLVDLPIGINITRF  DLPIGINIT  4        0.2812
2386.4    28.00  0.41     Sequence
 HLA-DQA10401-DQB10402  231      PLVDLPIGINITRFQ  DLPIGINIT  3        0.2995
1957.0    24.00  0.31     Sequence
 HLA-DQA10401-DQB10402  232      LVDLPIGINITRFQT  DLPIGINIT  2        0.2926
2107.9    25.00  0.30     Sequence
 HLA-DQA10401-DQB10402  233      VDLPIGINITRFQTL  DLPIGINIT  1        0.2863
2258.4    27.00  0.31     Sequence
 HLA-DQA10401-DQB10402  234      DLPIGINITRFQTLL  DLPIGINIT  0        0.2610
2968.2    34.00  0.25     Sequence
 HLA-DQA10401-DQB10402  235      LPIGINITRFQTLLA  PIGINITRF  1        0.2367
3862.5    42.00  0.31     Sequence
 HLA-DQA10401-DQB10402  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.2612
2962.1    34.00  0.28     Sequence
 HLA-DQA10401-DQB10402  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.2333
4007.9    43.00  0.28     Sequence
 HLA-DQA10401-DQB10402  238      GINITRFQTLLALHR  ITRFQTLLA  3        0.2191
4670.5    49.00  0.25     Sequence
 HLA-DQA10401-DQB10402  239      INITRFQTLLALHRS  ITRFQTLLA  2        0.2255
4356.4    46.00  0.22     Sequence
 HLA-DQA10401-DQB10402  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.2442
3560.8    40.00  0.22     Sequence
 HLA-DQA10401-DQB10402  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.2313
4093.3    44.00  0.23     Sequence
 HLA-DQA10401-DQB10402  242      TRFQTLLALHRSYLT  FQTLLALHR  2        0.2030
5557.6    55.00  0.30     Sequence
 HLA-DQA10401-DQB10402  243      RFQTLLALHRSYLTP  FQTLLALHR  1        0.1907
6350.4    60.00  0.31     Sequence
 HLA-DQA10401-DQB10402  244      FQTLLALHRSYLTPG  TLLALHRSY  2        0.1785
7245.2    65.00  0.25     Sequence
 HLA-DQA10401-DQB10402  245      QTLLALHRSYLTPGD  TLLALHRSY  1        0.1364
11431.4    80.00  0.26     Sequence
 HLA-DQA10401-DQB10402  246      TLLALHRSYLTPGDS  TLLALHRSY  0        0.1220
13360.5    85.00  0.24     Sequence
 HLA-DQA10401-DQB10402  247      LLALHRSYLTPGDSS  ALHRSYLTP  2        0.1073
15657.4    90.00  0.22     Sequence
 HLA-DQA10401-DQB10402  248      LALHRSYLTPGDSSS  ALHRSYLTP  1        0.1046
16115.1    90.00  0.19     Sequence
 HLA-DQA10401-DQB10402  249      ALHRSYLTPGDSSSG  HRSYLTPGD  2        0.0904
18806.4    95.00  0.22     Sequence
```

```
 HLA-DQA10401-DQB10402  250      LHRSYLTPGDSSSGW  SYLTPGDSS  3        0.0808
20863.3    95.00  0.19     Sequence
 HLA-DQA10401-DQB10402  251      HRSYLTPGDSSSGWT  TPGDSSSGW  5        0.0794
21173.0    95.00  0.23     Sequence
 HLA-DQA10401-DQB10402  252      RSYLTPGDSSSGWTA  GDSSSGWTA  6        0.0901
18853.2    95.00  0.25     Sequence
 HLA-DQA10401-DQB10402  253      SYLTPGDSSSGWTAG  DSSSGWTAG  6        0.1041
16211.1    90.00  0.31     Sequence
 HLA-DQA10401-DQB10402  254      YLTPGDSSSGWTAGA  SSSGWTAGA  6        0.1299
12267.4    80.00  0.38     Sequence
 HLA-DQA10401-DQB10402  255      LTPGDSSSGWTAGAA  SSGWTAGAA  6        0.1555
9293.2    75.00  0.34     Sequence
 HLA-DQA10401-DQB10402  256      TPGDSSSGWTAGAAA  SGWTAGAAA  6        0.2287
4208.7    45.00  0.50     Sequence
 HLA-DQA10401-DQB10402  257      PGDSSSGWTAGAAAY  GWTAGAAAY  6        0.3196
1573.8    19.00  0.48     Sequence
 HLA-DQA10401-DQB10402  258      GDSSSGWTAGAAAYY  GWTAGAAAY  5        0.3543
1082.2    13.00  0.43     Sequence
 HLA-DQA10401-DQB10402  259      DSSSGWTAGAAAYYV  GWTAGAAAY  4        0.3797
822.2     9.00  0.37     Sequence         WB
 HLA-DQA10401-DQB10402  260      SSSGWTAGAAAYYVG  GWTAGAAAY  3        0.3734
879.9    10.00  0.32     Sequence
 HLA-DQA10401-DQB10402  261      SSGWTAGAAAYYVGY  GWTAGAAAY  2        0.3704
909.2    11.00  0.26     Sequence
 HLA-DQA10401-DQB10402  262      SGWTAGAAAYYVGYL  GWTAGAAAY  1        0.3625
989.7    12.00  0.23     Sequence
 HLA-DQA10401-DQB10402  263      GWTAGAAAYYVGYLQ  TAGAAAYYV  2        0.3408
1252.0    15.00  0.22     Sequence
 HLA-DQA10401-DQB10402  264      WTAGAAAYYVGYLQP  TAGAAAYYV  1        0.3607
1009.8    12.00  0.22     Sequence
 HLA-DQA10401-DQB10402  265      TAGAAAYYVGYLQPR  AYYVGYLQP  5        0.3160
1637.6    20.00  0.26     Sequence
 HLA-DQA10401-DQB10402  266      AGAAAYYVGYLQPRT  AYYVGYLQP  4        0.2778
2476.1    29.00  0.31     Sequence
 HLA-DQA10401-DQB10402  267      GAAAYYVGYLQPRTF  AYYVGYLQP  3        0.2833
2331.0    28.00  0.30     Sequence
 HLA-DQA10401-DQB10402  268      AAAYYVGYLQPRTFL  AYYVGYLQP  2        0.2689
2725.8    32.00  0.31     Sequence
 HLA-DQA10401-DQB10402  269      AAYYVGYLQPRTFLL  AYYVGYLQP  1        0.2540
3202.4    37.00  0.31     Sequence
 HLA-DQA10401-DQB10402  270      AYYVGYLQPRTFLLK  AYYVGYLQP  0        0.1991
5800.5    60.00  0.34     Sequence
 HLA-DQA10401-DQB10402  271      YYVGYLQPRTFLLKY  VGYLQPRTF  2        0.1473
10160.1    75.00  0.37     Sequence
 HLA-DQA10401-DQB10402  272      YVGYLQPRTFLLKYN  VGYLQPRTF  1        0.1311
12103.1    80.00  0.37     Sequence
 HLA-DQA10401-DQB10402  273      VGYLQPRTFLLKYNE  RTFLLKYNE  6        0.1500
9867.5    75.00  0.38     Sequence
 HLA-DQA10401-DQB10402  274      GYLQPRTFLLKYNEN  RTFLLKYNE  5        0.1645
8434.0    70.00  0.34     Sequence
 HLA-DQA10401-DQB10402  275      YLQPRTFLLKYNENG  RTFLLKYNE  4        0.1558
9270.3    75.00  0.34     Sequence
 HLA-DQA10401-DQB10402  276      LQPRTFLLKYNENGT  RTFLLKYNE  3        0.1427
10679.6    80.00  0.35     Sequence
 HLA-DQA10401-DQB10402  277      QPRTFLLKYNENGTI  RTFLLKYNE  2        0.1324
11940.1    80.00  0.40     Sequence
 HLA-DQA10401-DQB10402  278      PRTFLLKYNENGTIT  RTFLLKYNE  1        0.1205
13577.0    85.00  0.43     Sequence
 HLA-DQA10401-DQB10402  279      RTFLLKYNENGTITD  YNENGTITD  6        0.1481
10073.3    75.00  0.34     Sequence
 HLA-DQA10401-DQB10402  280      TFLLKYNENGTITDA  YNENGTITD  5        0.1545
9396.5    75.00  0.44     Sequence
 HLA-DQA10401-DQB10402  281      FLLKYNENGTITDAV  ENGTITDAV  6        0.2376
3825.6    42.00  0.49     Sequence
 HLA-DQA10401-DQB10402  282      LLKYNENGTITDAVD  ENGTITDAV  5        0.2879
2219.2    27.00  0.41     Sequence
```

```
 HLA-DQA10401-DQB10402  283      LKYNENGTITDAVDC  ENGTITDAV  4        0.2965
2021.2    24.00  0.34     Sequence
 HLA-DQA10401-DQB10402  284      KYNENGTITDAVDCA  ENGTITDAV  3        0.3053
1839.1    22.00  0.28     Sequence
 HLA-DQA10401-DQB10402  285      YNENGTITDAVDCAL  ENGTITDAV  2        0.3143
1667.4    20.00  0.24     Sequence
 HLA-DQA10401-DQB10402  286      NENGTITDAVDCALD  NGTITDAVD  2        0.3094
1758.6    21.00  0.24     Sequence
 HLA-DQA10401-DQB10402  287      ENGTITDAVDCALDP  NGTITDAVD  1        0.3036
1873.1    23.00  0.22     Sequence
 HLA-DQA10401-DQB10402  288      NGTITDAVDCALDPL  DAVDCALDP  5        0.3048
1847.9    22.00  0.18     Sequence
 HLA-DQA10401-DQB10402  289      GTITDAVDCALDPLS  AVDCALDPL  5        0.2932
2094.7    25.00  0.26     Sequence
 HLA-DQA10401-DQB10402  290      TITDAVDCALDPLSE  DCALDPLSE  6        0.3884
748.2     8.00  0.43     Sequence         WB
 HLA-DQA10401-DQB10402  291      ITDAVDCALDPLSET  DCALDPLSE  5        0.3966
684.4     7.50  0.47     Sequence         WB
 HLA-DQA10401-DQB10402  292      TDAVDCALDPLSETK  DCALDPLSE  4        0.3691
921.8    11.00  0.47     Sequence
 HLA-DQA10401-DQB10402  293      DAVDCALDPLSETKC  DCALDPLSE  3        0.3584
1035.2    12.00  0.50     Sequence
 HLA-DQA10401-DQB10402  294      AVDCALDPLSETKCT  DCALDPLSE  2        0.3332
1358.6    16.00  0.53     Sequence
 HLA-DQA10401-DQB10402  295      VDCALDPLSETKCTL  DCALDPLSE  1        0.2902
2163.5    26.00  0.60     Sequence
 HLA-DQA10401-DQB10402  296      DCALDPLSETKCTLK  DCALDPLSE  0        0.2412
3676.8    41.00  0.60     Sequence
 HLA-DQA10401-DQB10402  297      CALDPLSETKCTLKS  CALDPLSET  0        0.1137
14614.3    85.00  0.26     Sequence
 HLA-DQA10401-DQB10402  298      ALDPLSETKCTLKSF  ETKCTLKSF  6        0.0960
17694.4    90.00  0.25     Sequence
 HLA-DQA10401-DQB10402  299      LDPLSETKCTLKSFT  ETKCTLKSF  5        0.0831
20338.8    95.00  0.29     Sequence
 HLA-DQA10401-DQB10402  300      DPLSETKCTLKSFTV  ETKCTLKSF  4        0.0785
21394.8    95.00  0.31     Sequence
 HLA-DQA10401-DQB10402  301      PLSETKCTLKSFTVE  CTLKSFTVE  6        0.1720
7775.0    70.00  0.56     Sequence
 HLA-DQA10401-DQB10402  302      LSETKCTLKSFTVEK  CTLKSFTVE  5        0.2129
4993.2    55.00  0.50     Sequence
 HLA-DQA10401-DQB10402  303      SETKCTLKSFTVEKG  CTLKSFTVE  4        0.2104
5133.9    55.00  0.44     Sequence
 HLA-DQA10401-DQB10402  304      ETKCTLKSFTVEKGI  CTLKSFTVE  3        0.2066
5347.8    55.00  0.40     Sequence
 HLA-DQA10401-DQB10402  305      TKCTLKSFTVEKGIY  CTLKSFTVE  2        0.1967
5955.4    60.00  0.39     Sequence
 HLA-DQA10401-DQB10402  306      KCTLKSFTVEKGIYQ  CTLKSFTVE  1        0.1902
6382.8    60.00  0.32     Sequence
 HLA-DQA10401-DQB10402  307      CTLKSFTVEKGIYQT  CTLKSFTVE  0        0.1824
6944.9    65.00  0.28     Sequence
 HLA-DQA10401-DQB10402  308      TLKSFTVEKGIYQTS  TVEKGIYQT  5        0.1418
10783.5    80.00  0.24     Sequence
 HLA-DQA10401-DQB10402  309      LKSFTVEKGIYQTSN  TVEKGIYQT  4        0.1372
11336.7    80.00  0.31     Sequence
 HLA-DQA10401-DQB10402  310      KSFTVEKGIYQTSNF  TVEKGIYQT  3        0.1530
9550.8    75.00  0.24     Sequence
 HLA-DQA10401-DQB10402  311      SFTVEKGIYQTSNFR  TVEKGIYQT  2        0.1343
11692.5    80.00  0.32     Sequence
 HLA-DQA10401-DQB10402  312      FTVEKGIYQTSNFRV  TVEKGIYQT  1        0.1300
12246.4    80.00  0.28     Sequence
 HLA-DQA10401-DQB10402  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.1219
13373.1    85.00  0.19     Sequence
 HLA-DQA10401-DQB10402  314      VEKGIYQTSNFRVQP  YQTSNFRVQ  5        0.1342
11701.7    80.00  0.31     Sequence
 HLA-DQA10401-DQB10402  315      EKGIYQTSNFRVQPT  TSNFRVQPT  6        0.1593
8921.2    70.00  0.32     Sequence
```

```
 HLA-DQA10401-DQB10402  316      KGIYQTSNFRVQPTE  TSNFRVQPT  5        0.2023
5605.2    55.00  0.35     Sequence
 HLA-DQA10401-DQB10402  317      GIYQTSNFRVQPTES  TSNFRVQPT  4        0.2222
4515.3    47.00  0.26     Sequence
 HLA-DQA10401-DQB10402  318      IYQTSNFRVQPTESI  NFRVQPTES  5        0.2286
4215.4    45.00  0.27     Sequence
 HLA-DQA10401-DQB10402  319      YQTSNFRVQPTESIV  NFRVQPTES  4        0.2183
4714.1    49.00  0.26     Sequence
 HLA-DQA10401-DQB10402  320      QTSNFRVQPTESIVR  NFRVQPTES  3        0.2019
5628.2    55.00  0.24     Sequence
 HLA-DQA10401-DQB10402  321      TSNFRVQPTESIVRF  QPTESIVRF  6        0.2417
3657.7    41.00  0.29     Sequence
 HLA-DQA10401-DQB10402  322      SNFRVQPTESIVRFP  QPTESIVRF  5        0.2500
3345.4    38.00  0.33     Sequence
 HLA-DQA10401-DQB10402  323      NFRVQPTESIVRFPN  QPTESIVRF  4        0.2488
3388.4    38.00  0.34     Sequence
 HLA-DQA10401-DQB10402  324      FRVQPTESIVRFPNI  QPTESIVRF  3        0.2493
3368.1    38.00  0.31     Sequence
 HLA-DQA10401-DQB10402  325      RVQPTESIVRFPNIT  QPTESIVRF  2        0.2271
4281.5    46.00  0.32     Sequence
 HLA-DQA10401-DQB10402  326      VQPTESIVRFPNITN  QPTESIVRF  1        0.2188
4685.4    49.00  0.34     Sequence
 HLA-DQA10401-DQB10402  327      QPTESIVRFPNITNL  QPTESIVRF  0        0.1779
7292.3    65.00  0.31     Sequence
 HLA-DQA10401-DQB10402  328      PTESIVRFPNITNLC  TESIVRFPN  1        0.1485
10031.9    75.00  0.28     Sequence
 HLA-DQA10401-DQB10402  329      TESIVRFPNITNLCP  TESIVRFPN  0        0.1383
11196.1    80.00  0.21     Sequence
 HLA-DQA10401-DQB10402  330      ESIVRFPNITNLCPF  PNITNLCPF  6        0.1844
6797.1    65.00  0.40     Sequence
 HLA-DQA10401-DQB10402  331      SIVRFPNITNLCPFG  PNITNLCPF  5        0.1716
7810.2    70.00  0.45     Sequence
 HLA-DQA10401-DQB10402  332      IVRFPNITNLCPFGE  ITNLCPFGE  6        0.2590
3032.6    35.00  0.47     Sequence
 HLA-DQA10401-DQB10402  333      VRFPNITNLCPFGEV  ITNLCPFGE  5        0.2975
2000.9    24.00  0.51     Sequence
 HLA-DQA10401-DQB10402  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.3220
1534.9    19.00  0.49     Sequence
 HLA-DQA10401-DQB10402  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.3102
1744.1    21.00  0.48     Sequence
 HLA-DQA10401-DQB10402  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.2944
2067.7    25.00  0.44     Sequence
 HLA-DQA10401-DQB10402  337      NITNLCPFGEVFNAT  ITNLCPFGE  1        0.2785
2455.8    29.00  0.44     Sequence
 HLA-DQA10401-DQB10402  338      ITNLCPFGEVFNATR  ITNLCPFGE  0        0.2517
3282.1    37.00  0.37     Sequence
 HLA-DQA10401-DQB10402  339      TNLCPFGEVFNATRF  GEVFNATRF  6        0.2392
3757.9    41.00  0.35     Sequence
 HLA-DQA10401-DQB10402  340      NLCPFGEVFNATRFA  EVFNATRFA  6        0.2641
2870.1    33.00  0.38     Sequence
 HLA-DQA10401-DQB10402  341      LCPFGEVFNATRFAS  EVFNATRFA  5        0.2704
2680.7    31.00  0.34     Sequence
 HLA-DQA10401-DQB10402  342      CPFGEVFNATRFASV  EVFNATRFA  4        0.2677
2759.6    32.00  0.32     Sequence
 HLA-DQA10401-DQB10402  343      PFGEVFNATRFASVY  EVFNATRFA  3        0.2757
2532.5    30.00  0.26     Sequence
 HLA-DQA10401-DQB10402  344      FGEVFNATRFASVYA  EVFNATRFA  2        0.2868
2244.3    27.00  0.25     Sequence
 HLA-DQA10401-DQB10402  345      GEVFNATRFASVYAW  TRFASVYAW  6        0.3432
1220.3    15.00  0.39     Sequence
 HLA-DQA10401-DQB10402  346      EVFNATRFASVYAWN  TRFASVYAW  5        0.3412
1246.7    15.00  0.40     Sequence
 HLA-DQA10401-DQB10402  347      VFNATRFASVYAWNR  TRFASVYAW  4        0.3347
1336.9    16.00  0.36     Sequence
 HLA-DQA10401-DQB10402  348      FNATRFASVYAWNRK  TRFASVYAW  3        0.3120
1710.0    21.00  0.38     Sequence
```

```
 HLA-DQA10401-DQB10402  349      NATRFASVYAWNRKR  TRFASVYAW  2        0.2826
2350.9    28.00  0.41     Sequence
 HLA-DQA10401-DQB10402  350      ATRFASVYAWNRKRI  TRFASVYAW  1        0.2610
2970.0    34.00  0.45     Sequence
 HLA-DQA10401-DQB10402  351      TRFASVYAWNRKRIS  TRFASVYAW  0        0.2293
4182.1    45.00  0.46     Sequence
 HLA-DQA10401-DQB10402  352      RFASVYAWNRKRISN  FASVYAWNR  1        0.1548
9364.7    75.00  0.44     Sequence
 HLA-DQA10401-DQB10402  353      FASVYAWNRKRISNC  FASVYAWNR  0        0.1253
12894.2    85.00  0.47     Sequence
 HLA-DQA10401-DQB10402  354      ASVYAWNRKRISNCV  YAWNRKRIS  3        0.0692
23653.5   100.00  0.29     Sequence
 HLA-DQA10401-DQB10402  355      SVYAWNRKRISNCVA  RKRISNCVA  6        0.0768
21781.3    95.00  0.34     Sequence
 HLA-DQA10401-DQB10402  356      VYAWNRKRISNCVAD  KRISNCVAD  6        0.1204
13588.1    85.00  0.48     Sequence
 HLA-DQA10401-DQB10402  357      YAWNRKRISNCVADY  RISNCVADY  6        0.1645
8436.5    70.00  0.42     Sequence
 HLA-DQA10401-DQB10402  358      AWNRKRISNCVADYS  RISNCVADY  5        0.1770
7370.2    65.00  0.44     Sequence
 HLA-DQA10401-DQB10402  359      WNRKRISNCVADYSV  RISNCVADY  4        0.1930
6195.4    60.00  0.34     Sequence
 HLA-DQA10401-DQB10402  360      NRKRISNCVADYSVL  RISNCVADY  3        0.1940
6130.0    60.00  0.31     Sequence
 HLA-DQA10401-DQB10402  361      RKRISNCVADYSVLY  RISNCVADY  2        0.1991
5802.3    60.00  0.28     Sequence
 HLA-DQA10401-DQB10402  362      KRISNCVADYSVLYN  VADYSVLYN  6        0.2424
3631.2    40.00  0.34     Sequence
 HLA-DQA10401-DQB10402  363      RISNCVADYSVLYNS  VADYSVLYN  5        0.2536
3216.1    37.00  0.44     Sequence
 HLA-DQA10401-DQB10402  364      ISNCVADYSVLYNSA  DYSVLYNSA  6        0.3057
1829.2    22.00  0.37     Sequence
 HLA-DQA10401-DQB10402  365      SNCVADYSVLYNSAS  DYSVLYNSA  5        0.3021
1902.0    23.00  0.44     Sequence
 HLA-DQA10401-DQB10402  366      NCVADYSVLYNSASF  DYSVLYNSA  4        0.3305
1399.9    17.00  0.37     Sequence
 HLA-DQA10401-DQB10402  367      CVADYSVLYNSASFS  DYSVLYNSA  3        0.3291
1421.1    17.00  0.35     Sequence
 HLA-DQA10401-DQB10402  368      VADYSVLYNSASFST  DYSVLYNSA  2        0.3040
1863.3    23.00  0.38     Sequence
 HLA-DQA10401-DQB10402  369      ADYSVLYNSASFSTF  DYSVLYNSA  1        0.2910
2144.5    26.00  0.32     Sequence
 HLA-DQA10401-DQB10402  370      DYSVLYNSASFSTFK  DYSVLYNSA  0        0.2531
3233.5    37.00  0.25     Sequence
 HLA-DQA10401-DQB10402  371      YSVLYNSASFSTFKC  SVLYNSASF  1        0.2191
4672.5    49.00  0.22     Sequence
 HLA-DQA10401-DQB10402  372      SVLYNSASFSTFKCY  YNSASFSTF  3        0.2149
4886.0    50.00  0.21     Sequence
 HLA-DQA10401-DQB10402  373      VLYNSASFSTFKCYG  YNSASFSTF  2        0.1881
6532.6    60.00  0.28     Sequence
 HLA-DQA10401-DQB10402  374      LYNSASFSTFKCYGV  YNSASFSTF  1        0.1679
8128.8    70.00  0.28     Sequence
 HLA-DQA10401-DQB10402  375      YNSASFSTFKCYGVS  ASFSTFKCY  3        0.1527
9583.3    75.00  0.29     Sequence
 HLA-DQA10401-DQB10402  376      NSASFSTFKCYGVSP  ASFSTFKCY  2        0.1287
12426.9    85.00  0.38     Sequence
 HLA-DQA10401-DQB10402  377      SASFSTFKCYGVSPT  ASFSTFKCY  1        0.1432
10616.8    80.00  0.31     Sequence
 HLA-DQA10401-DQB10402  378      ASFSTFKCYGVSPTK  FKCYGVSPT  5        0.1197
13690.2    85.00  0.26     Sequence
 HLA-DQA10401-DQB10402  379      SFSTFKCYGVSPTKL  FKCYGVSPT  4        0.1150
14401.0    85.00  0.29     Sequence
 HLA-DQA10401-DQB10402  380      FSTFKCYGVSPTKLN  CYGVSPTKL  5        0.1332
11831.5    80.00  0.34     Sequence
 HLA-DQA10401-DQB10402  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.1317
12020.4    80.00  0.33     Sequence
```

```
 HLA-DQA10401-DQB10402  382       TFKCYGVSPTKLNDL  CYGVSPTKL  3        0.1320
11989.9    80.00  0.31     Sequence
 HLA-DQA10401-DQB10402  383       FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.1275
12587.5    85.00  0.32     Sequence
 HLA-DQA10401-DQB10402  384       KCYGVSPTKLNDLCF  CYGVSPTKL  1        0.1148
14440.1    85.00  0.28     Sequence
 HLA-DQA10401-DQB10402  385       CYGVSPTKLNDLCFT  PTKLNDLCF  5        0.1097
15258.0    90.00  0.20     Sequence
 HLA-DQA10401-DQB10402  386       YGVSPTKLNDLCFTN  PTKLNDLCF  4        0.0932
18230.2    95.00  0.25     Sequence
 HLA-DQA10401-DQB10402  387       GVSPTKLNDLCFTNV  PTKLNDLCF  3        0.1002
16902.3    90.00  0.25     Sequence
 HLA-DQA10401-DQB10402  388       VSPTKLNDLCFTNVY  NDLCFTNVY  6        0.1282
12492.3    85.00  0.40     Sequence
 HLA-DQA10401-DQB10402  389       SPTKLNDLCFTNVYA  DLCFTNVYA  6        0.1875
6575.3    60.00  0.38     Sequence
 HLA-DQA10401-DQB10402  390       PTKLNDLCFTNVYAD  LCFTNVYAD  6        0.3243
1496.5    18.00  0.54     Sequence
 HLA-DQA10401-DQB10402  391       TKLNDLCFTNVYADS  LCFTNVYAD  5        0.3568
1053.1    12.00  0.55     Sequence
 HLA-DQA10401-DQB10402  392       KLNDLCFTNVYADSF  LCFTNVYAD  4        0.4289
482.8     4.50  0.39    Sequence         WB
 HLA-DQA10401-DQB10402  393       LNDLCFTNVYADSFV  LCFTNVYAD  3        0.4297
478.3     4.50  0.38    Sequence         WB
 HLA-DQA10401-DQB10402  394       NDLCFTNVYADSFVI  LCFTNVYAD  2        0.4188
538.5     5.50  0.37    Sequence         WB
 HLA-DQA10401-DQB10402  395       DLCFTNVYADSFVIR  LCFTNVYAD  1        0.3907
729.4     8.00  0.38    Sequence         WB
 HLA-DQA10401-DQB10402  396       LCFTNVYADSFVIRG  FTNVYADSF  2        0.3602
1014.9    12.00  0.34     Sequence
 HLA-DQA10401-DQB10402  397       CFTNVYADSFVIRGD  FTNVYADSF  1        0.3299
1409.3    17.00  0.36     Sequence
 HLA-DQA10401-DQB10402  398       FTNVYADSFVIRGDE  DSFVIRGDE  6        0.3790
828.4     9.00  0.34    Sequence         WB
 HLA-DQA10401-DQB10402  399       TNVYADSFVIRGDEV  DSFVIRGDE  5        0.3716
896.7    10.00  0.36    Sequence
 HLA-DQA10401-DQB10402  400       NVYADSFVIRGDEVR  DSFVIRGDE  4        0.3425
1228.6    15.00  0.38     Sequence
 HLA-DQA10401-DQB10402  401       VYADSFVIRGDEVRQ  DSFVIRGDE  3        0.3258
1472.9    18.00  0.41     Sequence
 HLA-DQA10401-DQB10402  402       YADSFVIRGDEVRQI  DSFVIRGDE  2        0.3152
1650.7    20.00  0.38     Sequence
 HLA-DQA10401-DQB10402  403       ADSFVIRGDEVRQIA  DSFVIRGDE  1        0.2773
2489.4    29.00  0.38     Sequence
 HLA-DQA10401-DQB10402  404       DSFVIRGDEVRQIAP  DSFVIRGDE  0        0.2389
3771.9    42.00  0.35     Sequence
 HLA-DQA10401-DQB10402  405       SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.1963
5978.7    60.00  0.31     Sequence
 HLA-DQA10401-DQB10402  406       FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.1910
6330.5    60.00  0.31     Sequence
 HLA-DQA10401-DQB10402  407       VIRGDEVRQIAPGQT  DEVRQIAPG  4        0.1913
6309.0    60.00  0.26     Sequence
 HLA-DQA10401-DQB10402  408       IRGDEVRQIAPGQTG  DEVRQIAPG  3        0.1867
6631.7    60.00  0.25     Sequence
 HLA-DQA10401-DQB10402  409       RGDEVRQIAPGQTGT  DEVRQIAPG  2        0.1694
7996.6    70.00  0.25     Sequence
 HLA-DQA10401-DQB10402  410       GDEVRQIAPGQTGTI  DEVRQIAPG  1        0.1646
8423.0    70.00  0.28     Sequence
 HLA-DQA10401-DQB10402  411       DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.1578
9066.7    75.00  0.25     Sequence
 HLA-DQA10401-DQB10402  412       EVRQIAPGQTGTIAD  PGQTGTIAD  6        0.1768
7382.9    65.00  0.44     Sequence
 HLA-DQA10401-DQB10402  413       VRQIAPGQTGTIADY  PGQTGTIAD  5        0.2066
5346.1    55.00  0.46     Sequence
 HLA-DQA10401-DQB10402  414       RQIAPGQTGTIADYN  PGQTGTIAD  4        0.2118
5055.1    55.00  0.38     Sequence
```

```
 HLA-DQA10401-DQB10402  415      QIAPGQTGTIADYNY  PGQTGTIAD  3         0.2217
4539.9    48.00  0.31     Sequence
 HLA-DQA10401-DQB10402  416      IAPGQTGTIADYNYK  PGQTGTIAD  2         0.2063
5364.3    55.00  0.32     Sequence
 HLA-DQA10401-DQB10402  417      APGQTGTIADYNYKL  PGQTGTIAD  1         0.1990
5807.9    60.00  0.28     Sequence
 HLA-DQA10401-DQB10402  418      PGQTGTIADYNYKLP  PGQTGTIAD  0         0.1851
6746.2    65.00  0.24     Sequence
 HLA-DQA10401-DQB10402  419      GQTGTIADYNYKLPD  GQTGTIADY  0         0.1627
8603.6    70.00  0.19     Sequence
 HLA-DQA10401-DQB10402  420      QTGTIADYNYKLPDD  ADYNYKLPD  5         0.1788
7221.2    65.00  0.24     Sequence
 HLA-DQA10401-DQB10402  421      TGTIADYNYKLPDDF  DYNYKLPDD  5         0.1961
5989.3    60.00  0.26     Sequence
 HLA-DQA10401-DQB10402  422      GTIADYNYKLPDDFT  DYNYKLPDD  4         0.1821
6972.0    65.00  0.28     Sequence
 HLA-DQA10401-DQB10402  423      TIADYNYKLPDDFTG  DYNYKLPDD  3         0.1730
7694.2    65.00  0.27     Sequence
 HLA-DQA10401-DQB10402  424      IADYNYKLPDDFTGC  DYNYKLPDD  2         0.1620
8659.8    70.00  0.28     Sequence
 HLA-DQA10401-DQB10402  425      ADYNYKLPDDFTGCV  DYNYKLPDD  1         0.1263
12749.3    85.00  0.30     Sequence
 HLA-DQA10401-DQB10402  426      DYNYKLPDDFTGCVI  PDDFTGCVI  6         0.1347
11635.6    80.00  0.35     Sequence
 HLA-DQA10401-DQB10402  427      YNYKLPDDFTGCVIA  DDFTGCVIA  6         0.2656
2825.2    33.00  0.71     Sequence
 HLA-DQA10401-DQB10402  428      NYKLPDDFTGCVIAW  DDFTGCVIA  5         0.3257
1473.4    18.00  0.50     Sequence
 HLA-DQA10401-DQB10402  429      YKLPDDFTGCVIAWN  DDFTGCVIA  4         0.3674
938.6    11.00  0.38     Sequence
 HLA-DQA10401-DQB10402  430      KLPDDFTGCVIAWNS  DDFTGCVIA  3         0.4073
609.7     6.50  0.29     Sequence          WB
 HLA-DQA10401-DQB10402  431      LPDDFTGCVIAWNSN  DDFTGCVIA  2         0.3930
711.8     7.50  0.31     Sequence          WB
 HLA-DQA10401-DQB10402  432      PDDFTGCVIAWNSNN  DDFTGCVIA  1         0.3785
832.8     9.50  0.28     Sequence          WB
 HLA-DQA10401-DQB10402  433      DDFTGCVIAWNSNNL  DDFTGCVIA  0         0.3589
1029.8    12.00  0.26     Sequence
 HLA-DQA10401-DQB10402  434      DFTGCVIAWNSNNLD  IAWNSNNLD  6         0.3207
1555.5    19.00  0.25     Sequence
 HLA-DQA10401-DQB10402  435      FTGCVIAWNSNNLDS  IAWNSNNLD  5         0.2944
2068.4    25.00  0.39     Sequence
 HLA-DQA10401-DQB10402  436      TGCVIAWNSNNLDSK  IAWNSNNLD  4         0.2316
4080.5    44.00  0.56     Sequence
 HLA-DQA10401-DQB10402  437      GCVIAWNSNNLDSKV  IAWNSNNLD  3         0.2163
4812.6    50.00  0.57     Sequence
 HLA-DQA10401-DQB10402  438      CVIAWNSNNLDSKVG  IAWNSNNLD  2         0.2112
5089.5    55.00  0.57     Sequence
 HLA-DQA10401-DQB10402  439      VIAWNSNNLDSKVGG  IAWNSNNLD  1         0.1934
6165.8    60.00  0.58     Sequence
 HLA-DQA10401-DQB10402  440      IAWNSNNLDSKVGGN  IAWNSNNLD  0         0.1554
9310.1    75.00  0.56     Sequence
 HLA-DQA10401-DQB10402  441      AWNSNNLDSKVGGNY  AWNSNNLDS  0         0.0884
19209.5    95.00  0.23     Sequence
 HLA-DQA10401-DQB10402  442      WNSNNLDSKVGGNYN  DSKVGGNYN  6         0.0759
21992.8    95.00  0.29     Sequence
 HLA-DQA10401-DQB10402  443      NSNNLDSKVGGNYNY  DSKVGGNYN  5         0.0756
22076.5    95.00  0.34     Sequence
 HLA-DQA10401-DQB10402  444      SNNLDSKVGGNYNYL  DSKVGGNYN  4         0.0829
20384.7    95.00  0.32     Sequence
 HLA-DQA10401-DQB10402  445      NNLDSKVGGNYNYLY  VGGNYNYLY  6         0.1075
15621.3    90.00  0.43     Sequence
 HLA-DQA10401-DQB10402  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5         0.0968
17543.0    90.00  0.38     Sequence
 HLA-DQA10401-DQB10402  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4         0.1065
15798.6    90.00  0.31     Sequence
```

```
 HLA-DQA10401-DQB10402  448      DSKVGGNYNYLYRLF  VGGNYNYLY  3        0.1221
13346.9    85.00  0.26     Sequence
 HLA-DQA10401-DQB10402  449      SKVGGNYNYLYRLFR  NYNYLYRLF  5        0.1137
14613.5    85.00  0.29     Sequence
 HLA-DQA10401-DQB10402  450      KVGGNYNYLYRLFRK  VGGNYNYLY  1        0.1109
15059.1    90.00  0.22     Sequence
 HLA-DQA10401-DQB10402  451      VGGNYNYLYRLFRKS  NYNYLYRLF  3        0.1090
15377.7    90.00  0.22     Sequence
 HLA-DQA10401-DQB10402  452      GGNYNYLYRLFRKSN  NYNYLYRLF  2        0.0966
17583.7    90.00  0.24     Sequence
 HLA-DQA10401-DQB10402  453      GNYNYLYRLFRKSNL  NYNYLYRLF  1        0.0956
17767.5    90.00  0.22     Sequence
 HLA-DQA10401-DQB10402  454      NYNYLYRLFRKSNLK  NYNYLYRLF  0        0.0853
19871.6    95.00  0.20     Sequence
 HLA-DQA10401-DQB10402  455      YNYLYRLFRKSNLKP  NYLYRLFRK  1        0.0708
23236.7   100.00  0.20     Sequence
 HLA-DQA10401-DQB10402  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6        0.0885
19185.4    95.00  0.38     Sequence
 HLA-DQA10401-DQB10402  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.0944
17996.4    90.00  0.37     Sequence
 HLA-DQA10401-DQB10402  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.1071
15688.9    90.00  0.29     Sequence
 HLA-DQA10401-DQB10402  459      YRLFRKSNLKPFERD  SNLKPFERD  6        0.1602
8836.3    70.00  0.34     Sequence
 HLA-DQA10401-DQB10402  460      RLFRKSNLKPFERDI  SNLKPFERD  5        0.1702
7932.3    70.00  0.37     Sequence
 HLA-DQA10401-DQB10402  461      LFRKSNLKPFERDIS  SNLKPFERD  4        0.1703
7916.3    70.00  0.38     Sequence
 HLA-DQA10401-DQB10402  462      FRKSNLKPFERDIST  SNLKPFERD  3        0.1640
8480.4    70.00  0.38     Sequence
 HLA-DQA10401-DQB10402  463      RKSNLKPFERDISTE  PFERDISTE  6        0.1798
7143.6    65.00  0.31     Sequence
 HLA-DQA10401-DQB10402  464      KSNLKPFERDISTEI  PFERDISTE  5        0.2214
4556.3    48.00  0.34     Sequence
 HLA-DQA10401-DQB10402  465      SNLKPFERDISTEIY  ERDISTEIY  6        0.3297
1411.3    17.00  0.55     Sequence
 HLA-DQA10401-DQB10402  466      NLKPFERDISTEIYQ  ERDISTEIY  5        0.3391
1275.8    15.00  0.57     Sequence
 HLA-DQA10401-DQB10402  467      LKPFERDISTEIYQA  DISTEIYQA  6        0.4194
534.7     5.50  0.41     Sequence         WB
 HLA-DQA10401-DQB10402  468      KPFERDISTEIYQAG  DISTEIYQA  5        0.4122
577.9     6.00  0.42     Sequence         WB
 HLA-DQA10401-DQB10402  469      PFERDISTEIYQAGS  DISTEIYQA  4        0.4078
606.1     6.50  0.44     Sequence         WB
 HLA-DQA10401-DQB10402  470      FERDISTEIYQAGST  DISTEIYQA  3        0.3937
705.9     7.50  0.46     Sequence         WB
 HLA-DQA10401-DQB10402  471      ERDISTEIYQAGSTP  DISTEIYQA  2        0.3578
1041.5    12.00  0.49     Sequence
 HLA-DQA10401-DQB10402  472      RDISTEIYQAGSTPC  DISTEIYQA  1        0.2967
2018.2    24.00  0.62     Sequence
 HLA-DQA10401-DQB10402  473      DISTEIYQAGSTPCN  DISTEIYQA  0        0.2509
3312.8    38.00  0.62     Sequence
 HLA-DQA10401-DQB10402  474      ISTEIYQAGSTPCNG  QAGSTPCNG  6        0.1596
8887.5    70.00  0.26     Sequence
 HLA-DQA10401-DQB10402  475      STEIYQAGSTPCNGV  QAGSTPCNG  5        0.1529
9562.2    75.00  0.27     Sequence
 HLA-DQA10401-DQB10402  476      TEIYQAGSTPCNGVK  QAGSTPCNG  4        0.1416
10805.1    80.00  0.26     Sequence
 HLA-DQA10401-DQB10402  477      EIYQAGSTPCNGVKG  QAGSTPCNG  3        0.1254
12881.0    85.00  0.29     Sequence
 HLA-DQA10401-DQB10402  478      IYQAGSTPCNGVKGF  QAGSTPCNG  2        0.1133
14667.0    85.00  0.25     Sequence
 HLA-DQA10401-DQB10402  479      YQAGSTPCNGVKGFN  TPCNGVKGF  5        0.0935
18189.4    95.00  0.30     Sequence
 HLA-DQA10401-DQB10402  480      QAGSTPCNGVKGFNC  TPCNGVKGF  4        0.0837
20223.4    95.00  0.36     Sequence
```

```
 HLA-DQA10401-DQB10402  481      AGSTPCNGVKGFNCY  TPCNGVKGF  3        0.0906
18763.9    95.00  0.31     Sequence
 HLA-DQA10401-DQB10402  482      GSTPCNGVKGFNCYF  NGVKGFNCY  5        0.0906
18752.1    95.00  0.32     Sequence
 HLA-DQA10401-DQB10402  483      STPCNGVKGFNCYFP  NGVKGFNCY  4        0.1028
16443.6    90.00  0.30     Sequence
 HLA-DQA10401-DQB10402  484      TPCNGVKGFNCYFPL  NGVKGFNCY  3        0.1166
14155.5    85.00  0.25     Sequence
 HLA-DQA10401-DQB10402  485      PCNGVKGFNCYFPLQ  KGFNCYFPL  5        0.1224
13301.9    85.00  0.29     Sequence
 HLA-DQA10401-DQB10402  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.1670
8207.8    70.00  0.35     Sequence
 HLA-DQA10401-DQB10402  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.1945
6094.9    60.00  0.31     Sequence
 HLA-DQA10401-DQB10402  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.1814
7025.2    65.00  0.31     Sequence
 HLA-DQA10401-DQB10402  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3        0.2043
5485.2    55.00  0.24     Sequence
 HLA-DQA10401-DQB10402  490      KGFNCYFPLQSYGFQ  YFPLQSYGF  5        0.2020
5618.4    55.00  0.24     Sequence
 HLA-DQA10401-DQB10402  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.2043
5482.4    55.00  0.23     Sequence
 HLA-DQA10401-DQB10402  492      FNCYFPLQSYGFQPT  YFPLQSYGF  3        0.1959
6002.0    60.00  0.20     Sequence
 HLA-DQA10401-DQB10402  493      NCYFPLQSYGFQPTY  YFPLQSYGF  2        0.1724
7741.3    70.00  0.25     Sequence
 HLA-DQA10401-DQB10402  494      CYFPLQSYGFQPTYG  YFPLQSYGF  1        0.1558
9262.3    75.00  0.28     Sequence
 HLA-DQA10401-DQB10402  495      YFPLQSYGFQPTYGV  YFPLQSYGF  0        0.1606
8801.3    70.00  0.20     Sequence
 HLA-DQA10401-DQB10402  496      FPLQSYGFQPTYGVG  PLQSYGFQP  1        0.1348
11634.6    80.00  0.25     Sequence
 HLA-DQA10401-DQB10402  497      PLQSYGFQPTYGVGY  YGFQPTYGV  4        0.1246
12985.1    85.00  0.22     Sequence
 HLA-DQA10401-DQB10402  498      LQSYGFQPTYGVGYQ  QPTYGVGYQ  6        0.1396
11037.0    80.00  0.30     Sequence
 HLA-DQA10401-DQB10402  499      QSYGFQPTYGVGYQP  QPTYGVGYQ  5        0.1563
9219.9    75.00  0.31     Sequence
 HLA-DQA10401-DQB10402  500      SYGFQPTYGVGYQPY  TYGVGYQPY  6        0.2358
3900.3    43.00  0.44     Sequence
 HLA-DQA10401-DQB10402  501      YGFQPTYGVGYQPYR  TYGVGYQPY  5        0.2190
4674.0    49.00  0.47     Sequence
 HLA-DQA10401-DQB10402  502      GFQPTYGVGYQPYRV  TYGVGYQPY  4        0.2188
4684.1    49.00  0.48     Sequence
 HLA-DQA10401-DQB10402  503      FQPTYGVGYQPYRVV  TYGVGYQPY  3        0.2209
4582.9    48.00  0.43     Sequence
 HLA-DQA10401-DQB10402  504      QPTYGVGYQPYRVVV  TYGVGYQPY  2        0.1996
5766.3    60.00  0.44     Sequence
 HLA-DQA10401-DQB10402  505      PTYGVGYQPYRVVVL  TYGVGYQPY  1        0.1972
5917.7    60.00  0.42     Sequence
 HLA-DQA10401-DQB10402  506      TYGVGYQPYRVVVLS  TYGVGYQPY  0        0.1947
6083.1    60.00  0.32     Sequence
 HLA-DQA10401-DQB10402  507      YGVGYQPYRVVVLSF  PYRVVVLSF  6        0.2367
3859.2    42.00  0.43     Sequence
 HLA-DQA10401-DQB10402  508      GVGYQPYRVVVLSFE  YRVVVLSFE  6        0.3474
1165.5    14.00  0.49     Sequence
 HLA-DQA10401-DQB10402  509      VGYQPYRVVVLSFEL  YRVVVLSFE  5        0.3826
796.3     9.00  0.44     Sequence         WB
 HLA-DQA10401-DQB10402  510      GYQPYRVVVLSFELL  YRVVVLSFE  4        0.3737
876.7    10.00  0.43     Sequence
 HLA-DQA10401-DQB10402  511      YQPYRVVVLSFELLH  YRVVVLSFE  3        0.3582
1037.0    12.00  0.44     Sequence
 HLA-DQA10401-DQB10402  512      QPYRVVVLSFELLHA  YRVVVLSFE  2        0.3358
1321.9    16.00  0.45     Sequence
 HLA-DQA10401-DQB10402  513      PYRVVVLSFELLHAP  YRVVVLSFE  1        0.3256
1475.7    18.00  0.41     Sequence
```

```
 HLA-DQA10401-DQB10402  514      YRVVVLSFELLHAPA  YRVVVLSFE  0        0.3050
1843.6    22.00  0.34     Sequence
 HLA-DQA10401-DQB10402  515      RVVVLSFELLHAPAT  SFELLHAPA  5        0.2496
3356.8    38.00  0.25     Sequence
 HLA-DQA10401-DQB10402  516      VVVLSFELLHAPATV  SFELLHAPA  4        0.2447
3540.3    40.00  0.22     Sequence
 HLA-DQA10401-DQB10402  517      VVLSFELLHAPATVC  SFELLHAPA  3        0.2467
3463.9    39.00  0.20     Sequence
 HLA-DQA10401-DQB10402  518      VLSFELLHAPATVCG  SFELLHAPA  2        0.2284
4222.7    45.00  0.22     Sequence
 HLA-DQA10401-DQB10402  519      LSFELLHAPATVCGP  ELLHAPATV  3        0.2260
4336.5    46.00  0.23     Sequence
 HLA-DQA10401-DQB10402  520      SFELLHAPATVCGPK  ELLHAPATV  2        0.2103
5137.6    55.00  0.23     Sequence
 HLA-DQA10401-DQB10402  521      FELLHAPATVCGPKK  ELLHAPATV  1        0.1898
6416.1    60.00  0.28     Sequence
 HLA-DQA10401-DQB10402  522      ELLHAPATVCGPKKS  HAPATVCGP  3        0.1440
10522.5    80.00  0.37     Sequence
 HLA-DQA10401-DQB10402  523      LLHAPATVCGPKKST  HAPATVCGP  2        0.1067
15753.0    90.00  0.50     Sequence
 HLA-DQA10401-DQB10402  524      LHAPATVCGPKKSTN  HAPATVCGP  1        0.0894
19007.3    95.00  0.56     Sequence
 HLA-DQA10401-DQB10402  525      HAPATVCGPKKSTNL  HAPATVCGP  0        0.0734
22601.7    95.00  0.56     Sequence
 HLA-DQA10401-DQB10402  526      APATVCGPKKSTNLV  APATVCGPK  0        0.0399
32453.4   100.00  0.22     Sequence
 HLA-DQA10401-DQB10402  527      PATVCGPKKSTNLVK  GPKKSTNLV  5        0.0314
35605.4   100.00  0.25     Sequence
 HLA-DQA10401-DQB10402  528      ATVCGPKKSTNLVKN  KKSTNLVKN  6        0.0333
34872.3   100.00  0.34     Sequence
 HLA-DQA10401-DQB10402  529      TVCGPKKSTNLVKNK  KKSTNLVKN  5        0.0284
36780.1   100.00  0.37     Sequence
 HLA-DQA10401-DQB10402  530      VCGPKKSTNLVKNKC  KKSTNLVKN  4        0.0347
34362.9   100.00  0.28     Sequence
 HLA-DQA10401-DQB10402  531      CGPKKSTNLVKNKCV  TNLVKNKCV  6        0.0400
32445.0   100.00  0.25     Sequence
 HLA-DQA10401-DQB10402  532      GPKKSTNLVKNKCVN  TNLVKNKCV  5        0.0406
32233.6   100.00  0.32     Sequence
 HLA-DQA10401-DQB10402  533      PKKSTNLVKNKCVNF  TNLVKNKCV  4        0.0431
31357.8   100.00  0.31     Sequence
 HLA-DQA10401-DQB10402  534      KKSTNLVKNKCVNFN  VKNKCVNFN  6        0.0482
29681.7   100.00  0.25     Sequence
 HLA-DQA10401-DQB10402  535      KSTNLVKNKCVNFNF  VKNKCVNFN  5        0.0573
26903.8   100.00  0.30     Sequence
 HLA-DQA10401-DQB10402  536      STNLVKNKCVNFNFN  NKCVNFNFN  6        0.0618
25623.6   100.00  0.24     Sequence
 HLA-DQA10401-DQB10402  537      TNLVKNKCVNFNFNG  NKCVNFNFN  5        0.0578
26758.9   100.00  0.22     Sequence
 HLA-DQA10401-DQB10402  538      NLVKNKCVNFNFNGL  CVNFNFNGL  6        0.0617
25655.5   100.00  0.22     Sequence
 HLA-DQA10401-DQB10402  539      LVKNKCVNFNFNGLT  CVNFNFNGL  5        0.0658
24532.9   100.00  0.22     Sequence
 HLA-DQA10401-DQB10402  540      VKNKCVNFNFNGLTG  NFNFNGLTG  6        0.0681
23941.6   100.00  0.29     Sequence
 HLA-DQA10401-DQB10402  541      KNKCVNFNFNGLTGT  FNFNGLTGT  6        0.0736
22540.6    95.00  0.29     Sequence
 HLA-DQA10401-DQB10402  542      NKCVNFNFNGLTGTG  FNFNGLTGT  5        0.0766
21838.9    95.00  0.30     Sequence
 HLA-DQA10401-DQB10402  543      KCVNFNFNGLTGTGV  FNGLTGTGV  6        0.0892
19051.5    95.00  0.29     Sequence
 HLA-DQA10401-DQB10402  544      CVNFNFNGLTGTGVL  NGLTGTGVL  6        0.1732
7677.7    65.00  0.62     Sequence
 HLA-DQA10401-DQB10402  545      VNFNFNGLTGTGVLT  NGLTGTGVL  5        0.1670
8210.8    70.00  0.67     Sequence
 HLA-DQA10401-DQB10402  546      NFNFNGLTGTGVLTE  LTGTGVLTE  6        0.3365
1311.2    16.00  0.71     Sequence
```

```
 HLA-DQA10401-DQB10402  547      FNFNGLTGTGVLTES  LTGTGVLTE  5        0.3725
888.4    10.00  0.69     Sequence
 HLA-DQA10401-DQB10402  548      NFNGLTGTGVLTESN  LTGTGVLTE  4        0.3606
1010.2    12.00  0.68     Sequence
 HLA-DQA10401-DQB10402  549      FNGLTGTGVLTESNK  LTGTGVLTE  3        0.3372
1301.9    16.00  0.67     Sequence
 HLA-DQA10401-DQB10402  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.3104
1739.8    21.00  0.69     Sequence
 HLA-DQA10401-DQB10402  551      GLTGTGVLTESNKKF  LTGTGVLTE  1        0.2850
2288.9    27.00  0.76     Sequence
 HLA-DQA10401-DQB10402  552      LTGTGVLTESNKKFL  LTGTGVLTE  0        0.2500
3341.9    38.00  0.73     Sequence
 HLA-DQA10401-DQB10402  553      TGTGVLTESNKKFLP  GTGVLTESN  1        0.1070
15708.3    90.00  0.38     Sequence
 HLA-DQA10401-DQB10402  554      GTGVLTESNKKFLPF  ESNKKFLPF  6        0.1159
14272.0    85.00  0.43     Sequence
 HLA-DQA10401-DQB10402  555      TGVLTESNKKFLPFQ  ESNKKFLPF  5        0.1122
14847.8    90.00  0.50     Sequence
 HLA-DQA10401-DQB10402  556      GVLTESNKKFLPFQQ  NKKFLPFQQ  6        0.1455
10362.7    75.00  0.32     Sequence
 HLA-DQA10401-DQB10402  557      VLTESNKKFLPFQQF  KKFLPFQQF  6        0.2221
4521.1    47.00  0.40     Sequence
 HLA-DQA10401-DQB10402  558      LTESNKKFLPFQQFG  KKFLPFQQF  5        0.2139
4940.9    50.00  0.36     Sequence
 HLA-DQA10401-DQB10402  559      TESNKKFLPFQQFGR  KKFLPFQQF  4        0.2018
5631.2    55.00  0.35     Sequence
 HLA-DQA10401-DQB10402  560      ESNKKFLPFQQFGRD  KKFLPFQQF  3        0.2036
5523.1    55.00  0.37     Sequence
 HLA-DQA10401-DQB10402  561      SNKKFLPFQQFGRDI  KKFLPFQQF  2        0.1845
6789.9    65.00  0.38     Sequence
 HLA-DQA10401-DQB10402  562      NKKFLPFQQFGRDIA  FQQFGRDIA  6        0.2090
5209.7    55.00  0.24     Sequence
 HLA-DQA10401-DQB10402  563      KKFLPFQQFGRDIAD  FQQFGRDIA  5        0.2333
4004.9    43.00  0.28     Sequence
 HLA-DQA10401-DQB10402  564      KFLPFQQFGRDIADT  FQQFGRDIA  4        0.2283
4226.8    45.00  0.26     Sequence
 HLA-DQA10401-DQB10402  565      FLPFQQFGRDIADTT  FQQFGRDIA  3        0.2398
3733.4    41.00  0.24     Sequence
 HLA-DQA10401-DQB10402  566      LPFQQFGRDIADTTD  FQQFGRDIA  2        0.2357
3902.1    43.00  0.23     Sequence
 HLA-DQA10401-DQB10402  567      PFQQFGRDIADTTDA  FQQFGRDIA  1        0.2487
3390.6    38.00  0.20     Sequence
 HLA-DQA10401-DQB10402  568      FQQFGRDIADTTDAV  DIADTTDAV  6        0.2732
2600.0    31.00  0.28     Sequence
 HLA-DQA10401-DQB10402  569      QQFGRDIADTTDAVR  DIADTTDAV  5        0.2195
4652.8    48.00  0.28     Sequence
 HLA-DQA10401-DQB10402  570      QFGRDIADTTDAVRD  IADTTDAVR  5        0.2481
3414.1    38.00  0.28     Sequence
 HLA-DQA10401-DQB10402  571      FGRDIADTTDAVRDP  ADTTDAVRD  5        0.2611
2964.0    34.00  0.23     Sequence
 HLA-DQA10401-DQB10402  572      GRDIADTTDAVRDPQ  ADTTDAVRD  4        0.2570
3100.3    36.00  0.22     Sequence
 HLA-DQA10401-DQB10402  573      RDIADTTDAVRDPQT  ADTTDAVRD  3        0.2508
3314.7    38.00  0.20     Sequence
 HLA-DQA10401-DQB10402  574      DIADTTDAVRDPQTL  ADTTDAVRD  2        0.2481
3411.7    38.00  0.21     Sequence
 HLA-DQA10401-DQB10402  575      IADTTDAVRDPQTLE  ADTTDAVRD  1        0.2406
3702.0    41.00  0.15     Sequence
 HLA-DQA10401-DQB10402  576      ADTTDAVRDPQTLEI  AVRDPQTLE  5        0.2175
4753.9    49.00  0.22     Sequence
 HLA-DQA10401-DQB10402  577      DTTDAVRDPQTLEIL  AVRDPQTLE  4        0.1995
5777.3    60.00  0.25     Sequence
 HLA-DQA10401-DQB10402  578      TTDAVRDPQTLEILD  DPQTLEILD  6        0.2220
4529.2    47.00  0.25     Sequence
 HLA-DQA10401-DQB10402  579      TDAVRDPQTLEILDI  DPQTLEILD  5        0.2488
3389.2    38.00  0.25     Sequence
```

```
 HLA-DQA10401-DQB10402  580      DAVRDPQTLEILDIT  DPQTLEILD  4        0.2442
3558.4    40.00  0.26     Sequence
 HLA-DQA10401-DQB10402  581      AVRDPQTLEILDITP  DPQTLEILD  3        0.2480
3415.8    38.00  0.25     Sequence
 HLA-DQA10401-DQB10402  582      VRDPQTLEILDITPC  DPQTLEILD  2        0.2420
3645.3    40.00  0.25     Sequence
 HLA-DQA10401-DQB10402  583      RDPQTLEILDITPCS  DPQTLEILD  1        0.2291
4190.7    45.00  0.21     Sequence
 HLA-DQA10401-DQB10402  584      DPQTLEILDITPCSF  ILDITPCSF  6        0.2799
2419.9    29.00  0.38     Sequence
 HLA-DQA10401-DQB10402  585      PQTLEILDITPCSFG  ILDITPCSF  5        0.2535
3219.1    37.00  0.44     Sequence
 HLA-DQA10401-DQB10402  586      QTLEILDITPCSFGG  ILDITPCSF  4        0.2308
4114.4    44.00  0.52     Sequence
 HLA-DQA10401-DQB10402  587      TLEILDITPCSFGGV  ILDITPCSF  3        0.2161
4824.2    50.00  0.55     Sequence
 HLA-DQA10401-DQB10402  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.2021
5613.1    55.00  0.62     Sequence
 HLA-DQA10401-DQB10402  589      EILDITPCSFGGVSV  ILDITPCSF  1        0.1827
6924.4    65.00  0.61     Sequence
 HLA-DQA10401-DQB10402  590      ILDITPCSFGGVSVI  ILDITPCSF  0        0.1863
6662.2    65.00  0.44     Sequence
 HLA-DQA10401-DQB10402  591      LDITPCSFGGVSVIT  CSFGGVSVI  5        0.1548
9367.2    75.00  0.49     Sequence
 HLA-DQA10401-DQB10402  592      DITPCSFGGVSVITP  FGGVSVITP  6        0.2301
4147.9    45.00  0.53     Sequence
 HLA-DQA10401-DQB10402  593      ITPCSFGGVSVITPG  FGGVSVITP  5        0.2371
3845.0    42.00  0.45     Sequence
 HLA-DQA10401-DQB10402  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.2301
4149.1    45.00  0.47     Sequence
 HLA-DQA10401-DQB10402  595      PCSFGGVSVITPGTN  FGGVSVITP  3        0.2343
3962.0    43.00  0.37     Sequence
 HLA-DQA10401-DQB10402  596      CSFGGVSVITPGTNT  FGGVSVITP  2        0.2240
4430.1    47.00  0.41     Sequence
 HLA-DQA10401-DQB10402  597      SFGGVSVITPGTNTS  FGGVSVITP  1        0.1994
5778.3    60.00  0.48     Sequence
 HLA-DQA10401-DQB10402  598      FGGVSVITPGTNTSN  FGGVSVITP  0        0.1731
7683.8    65.00  0.47     Sequence
 HLA-DQA10401-DQB10402  599      GGVSVITPGTNTSNQ  VSVITPGTN  2        0.1035
16316.7    90.00  0.25     Sequence
 HLA-DQA10401-DQB10402  600      GVSVITPGTNTSNQV  PGTNTSNQV  6        0.1194
13741.7    85.00  0.34     Sequence
 HLA-DQA10401-DQB10402  601      VSVITPGTNTSNQVA  GTNTSNQVA  6        0.1459
10314.1    75.00  0.35     Sequence
 HLA-DQA10401-DQB10402  602      SVITPGTNTSNQVAV  GTNTSNQVA  5        0.1613
8726.8    70.00  0.42     Sequence
 HLA-DQA10401-DQB10402  603      VITPGTNTSNQVAVL  NTSNQVAVL  6        0.1898
6411.2    60.00  0.38     Sequence
 HLA-DQA10401-DQB10402  604      ITPGTNTSNQVAVLY  NTSNQVAVL  5        0.2035
5528.5    55.00  0.34     Sequence
 HLA-DQA10401-DQB10402  605      TPGTNTSNQVAVLYQ  NTSNQVAVL  4        0.2107
5115.7    55.00  0.29     Sequence
 HLA-DQA10401-DQB10402  606      PGTNTSNQVAVLYQG  NTSNQVAVL  3        0.2260
4335.5    46.00  0.22     Sequence
 HLA-DQA10401-DQB10402  607      GTNTSNQVAVLYQGV  NQVAVLYQG  5        0.2464
3477.8    39.00  0.22     Sequence
 HLA-DQA10401-DQB10402  608      TNTSNQVAVLYQGVN  NQVAVLYQG  4        0.2384
3789.9    42.00  0.20     Sequence
 HLA-DQA10401-DQB10402  609      NTSNQVAVLYQGVNC  NQVAVLYQG  3        0.2314
4089.3    44.00  0.22     Sequence
 HLA-DQA10401-DQB10402  610      TSNQVAVLYQGVNCT  NQVAVLYQG  2        0.2122
5034.9    55.00  0.24     Sequence
 HLA-DQA10401-DQB10402  611      SNQVAVLYQGVNCTE  LYQGVNCTE  6        0.2151
4875.1    50.00  0.28     Sequence
 HLA-DQA10401-DQB10402  612      NQVAVLYQGVNCTEV  LYQGVNCTE  5        0.2174
4759.3    49.00  0.33     Sequence
```

```
 HLA-DQA10401-DQB10402  613      QVAVLYQGVNCTEVP  LYQGVNCTE  4        0.2253
4366.9    46.00  0.37     Sequence
 HLA-DQA10401-DQB10402  614      VAVLYQGVNCTEVPV  LYQGVNCTE  3        0.2174
4757.5    49.00  0.37     Sequence
 HLA-DQA10401-DQB10402  615      AVLYQGVNCTEVPVA  VNCTEVPVA  6        0.2326
4035.5    44.00  0.25     Sequence
 HLA-DQA10401-DQB10402  616      VLYQGVNCTEVPVAI  VNCTEVPVA  5        0.2285
4219.1    45.00  0.29     Sequence
 HLA-DQA10401-DQB10402  617      LYQGVNCTEVPVAIH  VNCTEVPVA  4        0.2190
4677.0    49.00  0.22     Sequence
 HLA-DQA10401-DQB10402  618      YQGVNCTEVPVAIHA  CTEVPVAIH  5        0.2313
4092.6    44.00  0.28     Sequence
 HLA-DQA10401-DQB10402  619      QGVNCTEVPVAIHAD  EVPVAIHAD  6        0.3032
1880.9    23.00  0.49     Sequence
 HLA-DQA10401-DQB10402  620      GVNCTEVPVAIHADQ  EVPVAIHAD  5        0.3427
1225.8    15.00  0.55     Sequence
 HLA-DQA10401-DQB10402  621      VNCTEVPVAIHADQL  EVPVAIHAD  4        0.3793
825.1     9.00  0.41     Sequence         WB
 HLA-DQA10401-DQB10402  622      NCTEVPVAIHADQLT  EVPVAIHAD  3        0.3689
923.4    11.00  0.44     Sequence
 HLA-DQA10401-DQB10402  623      CTEVPVAIHADQLTP  EVPVAIHAD  2        0.3568
1053.0    12.00  0.46     Sequence
 HLA-DQA10401-DQB10402  624      TEVPVAIHADQLTPT  EVPVAIHAD  1        0.3323
1372.8    17.00  0.47     Sequence
 HLA-DQA10401-DQB10402  625      EVPVAIHADQLTPTW  EVPVAIHAD  0        0.3029
1886.0    23.00  0.39     Sequence
 HLA-DQA10401-DQB10402  626      VPVAIHADQLTPTWR  PVAIHADQL  1        0.2334
3999.8    43.00  0.42     Sequence
 HLA-DQA10401-DQB10402  627      PVAIHADQLTPTWRV  PVAIHADQL  0        0.1898
6412.3    60.00  0.36     Sequence
 HLA-DQA10401-DQB10402  628      VAIHADQLTPTWRVY  DQLTPTWRV  5        0.1535
9495.0    75.00  0.25     Sequence
 HLA-DQA10401-DQB10402  629      AIHADQLTPTWRVYS  DQLTPTWRV  4        0.1379
11248.0    80.00  0.33     Sequence
 HLA-DQA10401-DQB10402  630      IHADQLTPTWRVYST  DQLTPTWRV  3        0.1364
11431.4    80.00  0.31     Sequence
 HLA-DQA10401-DQB10402  631      HADQLTPTWRVYSTG  DQLTPTWRV  2        0.1289
12391.6    85.00  0.30     Sequence
 HLA-DQA10401-DQB10402  632      ADQLTPTWRVYSTGS  DQLTPTWRV  1        0.1195
13721.6    85.00  0.29     Sequence
 HLA-DQA10401-DQB10402  633      DQLTPTWRVYSTGSN  DQLTPTWRV  0        0.1105
15125.7    90.00  0.22     Sequence
 HLA-DQA10401-DQB10402  634      QLTPTWRVYSTGSNV  WRVYSTGSN  5        0.1009
16785.3    90.00  0.25     Sequence
 HLA-DQA10401-DQB10402  635      LTPTWRVYSTGSNVF  VYSTGSNVF  6        0.2088
5221.3    55.00  0.65     Sequence
 HLA-DQA10401-DQB10402  636      TPTWRVYSTGSNVFQ  VYSTGSNVF  5        0.2180
4728.2    49.00  0.65     Sequence
 HLA-DQA10401-DQB10402  637      PTWRVYSTGSNVFQT  VYSTGSNVF  4        0.2465
3473.8    39.00  0.46     Sequence
 HLA-DQA10401-DQB10402  638      TWRVYSTGSNVFQTR  VYSTGSNVF  3        0.2344
3957.0    43.00  0.41     Sequence
 HLA-DQA10401-DQB10402  639      WRVYSTGSNVFQTRA  VYSTGSNVF  2        0.2358
3898.3    43.00  0.38     Sequence
 HLA-DQA10401-DQB10402  640      RVYSTGSNVFQTRAG  VYSTGSNVF  1        0.2244
4409.4    47.00  0.34     Sequence
 HLA-DQA10401-DQB10402  641      VYSTGSNVFQTRAGC  VYSTGSNVF  0        0.2135
4962.1    55.00  0.31     Sequence
 HLA-DQA10401-DQB10402  642      YSTGSNVFQTRAGCL  STGSNVFQT  1        0.1719
7780.5    70.00  0.35     Sequence
 HLA-DQA10401-DQB10402  643      STGSNVFQTRAGCLI  STGSNVFQT  0        0.1459
10312.2    75.00  0.26     Sequence
 HLA-DQA10401-DQB10402  644      TGSNVFQTRAGCLIG  QTRAGCLIG  6        0.1376
11284.0    80.00  0.28     Sequence
 HLA-DQA10401-DQB10402  645      GSNVFQTRAGCLIGA  QTRAGCLIG  5        0.1412
10855.7    80.00  0.26     Sequence
```

```
 HLA-DQA10401-DQB10402  646      SNVFQTRAGCLIGAE  RAGCLIGAE  6         0.2324
4044.0    44.00  0.51     Sequence
 HLA-DQA10401-DQB10402  647      NVFQTRAGCLIGAEY  RAGCLIGAE  5         0.3085
1776.0    22.00  0.44     Sequence
 HLA-DQA10401-DQB10402  648      VFQTRAGCLIGAEYV  RAGCLIGAE  4         0.3234
1511.4    18.00  0.39     Sequence
 HLA-DQA10401-DQB10402  649      FQTRAGCLIGAEYVN  RAGCLIGAE  3         0.3098
1750.6    21.00  0.35     Sequence
 HLA-DQA10401-DQB10402  650      QTRAGCLIGAEYVNN  RAGCLIGAE  2         0.2918
2127.6    26.00  0.35     Sequence
 HLA-DQA10401-DQB10402  651      TRAGCLIGAEYVNNS  RAGCLIGAE  1         0.2779
2471.5    29.00  0.32     Sequence
 HLA-DQA10401-DQB10402  652      RAGCLIGAEYVNNSY  AGCLIGAEY  1         0.2590
3032.9    35.00  0.31     Sequence
 HLA-DQA10401-DQB10402  653      AGCLIGAEYVNNSYE  AEYVNNSYE  6         0.2691
2718.1    32.00  0.37     Sequence
 HLA-DQA10401-DQB10402  654      GCLIGAEYVNNSYEC  AEYVNNSYE  5         0.2736
2590.8    31.00  0.43     Sequence
 HLA-DQA10401-DQB10402  655      CLIGAEYVNNSYECD  AEYVNNSYE  4         0.2833
2332.7    28.00  0.44     Sequence
 HLA-DQA10401-DQB10402  656      LIGAEYVNNSYECDI  AEYVNNSYE  3         0.2776
2479.7    29.00  0.40     Sequence
 HLA-DQA10401-DQB10402  657      IGAEYVNNSYECDIP  AEYVNNSYE  2         0.2672
2774.5    32.00  0.38     Sequence
 HLA-DQA10401-DQB10402  658      GAEYVNNSYECDIPI  AEYVNNSYE  1         0.2524
3259.4    37.00  0.34     Sequence
 HLA-DQA10401-DQB10402  659      AEYVNNSYECDIPIG  AEYVNNSYE  0         0.2277
4254.1    45.00  0.31     Sequence
 HLA-DQA10401-DQB10402  660      EYVNNSYECDIPIGA  YVNNSYECD  1         0.1890
6469.0    60.00  0.41     Sequence
 HLA-DQA10401-DQB10402  661      YVNNSYECDIPIGAG  YVNNSYECD  0         0.1794
7176.8    65.00  0.28     Sequence
 HLA-DQA10401-DQB10402  662      VNNSYECDIPIGAGI  ECDIPIGAG  5         0.1587
8978.5    75.00  0.41     Sequence
 HLA-DQA10401-DQB10402  663      NNSYECDIPIGAGIC  DIPIGAGIC  6         0.2180
4729.7    49.00  0.43     Sequence
 HLA-DQA10401-DQB10402  664      NSYECDIPIGAGICA  DIPIGAGIC  5         0.2233
4465.3    47.00  0.43     Sequence
 HLA-DQA10401-DQB10402  665      SYECDIPIGAGICAS  DIPIGAGIC  4         0.2525
3255.9    37.00  0.32     Sequence
 HLA-DQA10401-DQB10402  666      YECDIPIGAGICASY  DIPIGAGIC  3         0.2722
2629.4    31.00  0.27     Sequence
 HLA-DQA10401-DQB10402  667      ECDIPIGAGICASYQ  PIGAGICAS  4         0.2817
2372.8    28.00  0.23     Sequence
 HLA-DQA10401-DQB10402  668      CDIPIGAGICASYQT  GAGICASYQ  5         0.2903
2161.6    26.00  0.25     Sequence
 HLA-DQA10401-DQB10402  669      DIPIGAGICASYQTQ  GAGICASYQ  4         0.2825
2353.2    28.00  0.26     Sequence
 HLA-DQA10401-DQB10402  670      IPIGAGICASYQTQT  GAGICASYQ  3         0.2440
3566.1    40.00  0.29     Sequence
 HLA-DQA10401-DQB10402  671      PIGAGICASYQTQTN  GAGICASYQ  2         0.2257
4347.3    46.00  0.34     Sequence
 HLA-DQA10401-DQB10402  672      IGAGICASYQTQTNS  GAGICASYQ  1         0.1983
5847.6    60.00  0.37     Sequence
 HLA-DQA10401-DQB10402  673      GAGICASYQTQTNSP  GAGICASYQ  0         0.1653
8360.3    70.00  0.34     Sequence
 HLA-DQA10401-DQB10402  674      AGICASYQTQTNSPR  GICASYQTQ  1         0.1218
13380.6    85.00  0.25     Sequence
 HLA-DQA10401-DQB10402  675      GICASYQTQTNSPRR  CASYQTQTN  2         0.0931
18255.0    95.00  0.28     Sequence
 HLA-DQA10401-DQB10402  676      ICASYQTQTNSPRRA  CASYQTQTN  1         0.0888
19131.1    95.00  0.25     Sequence
 HLA-DQA10401-DQB10402  677      CASYQTQTNSPRRAR  TQTNSPRRA  5         0.0739
22474.4    95.00  0.31     Sequence
 HLA-DQA10401-DQB10402  678      ASYQTQTNSPRRARS  TQTNSPRRA  4         0.0651
24717.8   100.00  0.35     Sequence
```

```
 HLA-DQA10401-DQB10402  679      SYQTQTNSPRRARSV  NSPRRARSV  6        0.0749
22244.6    95.00  0.23     Sequence
 HLA-DQA10401-DQB10402  680      YQTQTNSPRRARSVA  NSPRRARSV  5        0.0768
21787.2    95.00  0.31     Sequence
 HLA-DQA10401-DQB10402  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.0984
17239.3    90.00  0.32     Sequence
 HLA-DQA10401-DQB10402  682      TQTNSPRRARSVASQ  RRARSVASQ  6        0.1384
11180.9    80.00  0.48     Sequence
 HLA-DQA10401-DQB10402  683      QTNSPRRARSVASQS  RRARSVASQ  5        0.1795
7170.0    65.00  0.43     Sequence
 HLA-DQA10401-DQB10402  684      TNSPRRARSVASQSI  ARSVASQSI  6        0.2244
4408.9    47.00  0.40    Sequence
 HLA-DQA10401-DQB10402  685      NSPRRARSVASQSII  ARSVASQSI  5        0.2185
4701.2    49.00  0.40    Sequence
 HLA-DQA10401-DQB10402  686      SPRRARSVASQSIIA  ARSVASQSI  4        0.2336
3994.1    43.00  0.34    Sequence
 HLA-DQA10401-DQB10402  687      PRRARSVASQSIIAY  VASQSIIAY  6        0.2778
2474.0    29.00  0.35    Sequence
 HLA-DQA10401-DQB10402  688      RRARSVASQSIIAYT  VASQSIIAY  5        0.2860
2265.8    27.00  0.38    Sequence
 HLA-DQA10401-DQB10402  689      RARSVASQSIIAYTM  VASQSIIAY  4        0.2987
1973.5    24.00  0.34    Sequence
 HLA-DQA10401-DQB10402  690      ARSVASQSIIAYTMS  VASQSIIAY  3        0.3072
1801.6    22.00  0.31    Sequence
 HLA-DQA10401-DQB10402  691      RSVASQSIIAYTMSL  VASQSIIAY  2        0.3188
1588.0    19.00  0.28    Sequence
 HLA-DQA10401-DQB10402  692      SVASQSIIAYTMSLG  VASQSIIAY  1        0.3045
1854.8    23.00  0.28    Sequence
 HLA-DQA10401-DQB10402  693      VASQSIIAYTMSLGA  IAYTMSLGA  6        0.3098
1750.6    21.00  0.20    Sequence
 HLA-DQA10401-DQB10402  694      ASQSIIAYTMSLGAE  AYTMSLGAE  6        0.3874
755.7     8.50  0.44    Sequence         WB
 HLA-DQA10401-DQB10402  695      SQSIIAYTMSLGAEN  AYTMSLGAE  5        0.3915
723.3     8.00  0.51    Sequence         WB
 HLA-DQA10401-DQB10402  696      QSIIAYTMSLGAENS  AYTMSLGAE  4        0.3980
673.9     7.00  0.49    Sequence         WB
 HLA-DQA10401-DQB10402  697      SIIAYTMSLGAENSV  AYTMSLGAE  3        0.3784
833.5     9.50  0.50    Sequence         WB
 HLA-DQA10401-DQB10402  698      IIAYTMSLGAENSVA  AYTMSLGAE  2        0.3774
842.1     9.50  0.47    Sequence         WB
 HLA-DQA10401-DQB10402  699      IAYTMSLGAENSVAY  AYTMSLGAE  1        0.3644
969.3    11.00  0.40    Sequence
 HLA-DQA10401-DQB10402  700      AYTMSLGAENSVAYS  AYTMSLGAE  0        0.3174
1612.6    20.00  0.30    Sequence
 HLA-DQA10401-DQB10402  701      YTMSLGAENSVAYSN  SLGAENSVA  3        0.2865
2252.2    27.00  0.31    Sequence
 HLA-DQA10401-DQB10402  702      TMSLGAENSVAYSNN  SLGAENSVA  2        0.2626
2919.0    34.00  0.29    Sequence
 HLA-DQA10401-DQB10402  703      MSLGAENSVAYSNNS  SLGAENSVA  1        0.2458
3498.5    39.00  0.28    Sequence
 HLA-DQA10401-DQB10402  704      SLGAENSVAYSNNSI  AENSVAYSN  3        0.2219
4530.0    47.00  0.21    Sequence
 HLA-DQA10401-DQB10402  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.2239
4433.8    47.00  0.31    Sequence
 HLA-DQA10401-DQB10402  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.2297
4165.2    45.00  0.34    Sequence
 HLA-DQA10401-DQB10402  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.2387
3779.2    42.00  0.32    Sequence
 HLA-DQA10401-DQB10402  708      ENSVAYSNNSIAIPT  VAYSNNSIA  3        0.2338
3982.7    43.00  0.31    Sequence
 HLA-DQA10401-DQB10402  709      NSVAYSNNSIAIPTN  VAYSNNSIA  2        0.2291
4192.7    45.00  0.27    Sequence
 HLA-DQA10401-DQB10402  710      SVAYSNNSIAIPTNF  YSNNSIAIP  3        0.2563
3122.3    36.00  0.22    Sequence
 HLA-DQA10401-DQB10402  711      VAYSNNSIAIPTNFT  YSNNSIAIP  2        0.2418
3653.7    41.00  0.23    Sequence
```

```
 HLA-DQA10401-DQB10402  712      AYSNNSIAIPTNFTI  YSNNSIAIP  1        0.2111
5093.2    55.00  0.29     Sequence
 HLA-DQA10401-DQB10402  713      YSNNSIAIPTNFTIS  YSNNSIAIP  0        0.1922
6250.5    60.00  0.28     Sequence
 HLA-DQA10401-DQB10402  714      SNNSIAIPTNFTISV  NSIAIPTNF  2        0.1625
8613.6    70.00  0.28     Sequence
 HLA-DQA10401-DQB10402  715      NNSIAIPTNFTISVT  NSIAIPTNF  1        0.1628
8587.7    70.00  0.23     Sequence
 HLA-DQA10401-DQB10402  716      NSIAIPTNFTISVTT  TNFTISVTT  6        0.1699
7957.5    70.00  0.23     Sequence
 HLA-DQA10401-DQB10402  717      SIAIPTNFTISVTTE  NFTISVTTE  6        0.3875
755.4     8.50  0.77    Sequence         WB
 HLA-DQA10401-DQB10402  718      IAIPTNFTISVTTEI  NFTISVTTE  5        0.4470
396.7     3.50  0.67    Sequence         WB
 HLA-DQA10401-DQB10402  719      AIPTNFTISVTTEIL  NFTISVTTE  4        0.4632
333.1     3.00  0.61    Sequence         WB
 HLA-DQA10401-DQB10402  720      IPTNFTISVTTEILP  NFTISVTTE  3        0.4584
350.8     3.00  0.60    Sequence         WB
 HLA-DQA10401-DQB10402  721      PTNFTISVTTEILPV  NFTISVTTE  2        0.4555
362.0     3.00  0.52    Sequence         WB
 HLA-DQA10401-DQB10402  722      TNFTISVTTEILPVS  NFTISVTTE  1        0.4467
398.2     3.50  0.47    Sequence         WB
 HLA-DQA10401-DQB10402  723      NFTISVTTEILPVSM  NFTISVTTE  0        0.4322
465.8     4.50  0.35    Sequence         WB
 HLA-DQA10401-DQB10402  724      FTISVTTEILPVSMT  SVTTEILPV  3        0.3773
843.4     9.50  0.19    Sequence         WB
 HLA-DQA10401-DQB10402  725      TISVTTEILPVSMTK  SVTTEILPV  2        0.3249
1486.4    18.00  0.26     Sequence
 HLA-DQA10401-DQB10402  726      ISVTTEILPVSMTKT  SVTTEILPV  1        0.3086
1773.4    22.00  0.29     Sequence
 HLA-DQA10401-DQB10402  727      SVTTEILPVSMTKTS  SVTTEILPV  0        0.2820
2366.3    28.00  0.26     Sequence
 HLA-DQA10401-DQB10402  728      VTTEILPVSMTKTSV  TTEILPVSM  1        0.2136
4959.6    55.00  0.31     Sequence
 HLA-DQA10401-DQB10402  729      TTEILPVSMTKTSVD  VSMTKTSVD  6        0.2257
4349.6    46.00  0.37     Sequence
 HLA-DQA10401-DQB10402  730      TEILPVSMTKTSVDC  VSMTKTSVD  5        0.2157
4848.1    50.00  0.52     Sequence
 HLA-DQA10401-DQB10402  731      EILPVSMTKTSVDCT  VSMTKTSVD  4        0.2006
5708.7    55.00  0.57     Sequence
 HLA-DQA10401-DQB10402  732      ILPVSMTKTSVDCTM  VSMTKTSVD  3        0.2029
5565.7    55.00  0.51     Sequence
 HLA-DQA10401-DQB10402  733      LPVSMTKTSVDCTMY  VSMTKTSVD  2        0.1982
5856.6    60.00  0.46     Sequence
 HLA-DQA10401-DQB10402  734      PVSMTKTSVDCTMYI  VSMTKTSVD  1        0.1934
6171.0    60.00  0.37     Sequence
 HLA-DQA10401-DQB10402  735      VSMTKTSVDCTMYIC  VSMTKTSVD  0        0.1837
6851.3    65.00  0.29     Sequence
 HLA-DQA10401-DQB10402  736      SMTKTSVDCTMYICG  KTSVDCTMY  3        0.1410
10878.3    80.00  0.21     Sequence
 HLA-DQA10401-DQB10402  737      MTKTSVDCTMYICGD  DCTMYICGD  6        0.2190
4678.4    49.00  0.47     Sequence
 HLA-DQA10401-DQB10402  738      TKTSVDCTMYICGDS  DCTMYICGD  5        0.2270
4290.7    46.00  0.54     Sequence
 HLA-DQA10401-DQB10402  739      KTSVDCTMYICGDST  DCTMYICGD  4        0.2167
4793.1    49.00  0.53     Sequence
 HLA-DQA10401-DQB10402  740      TSVDCTMYICGDSTE  DCTMYICGD  3        0.2309
4109.6    44.00  0.47     Sequence
 HLA-DQA10401-DQB10402  741      SVDCTMYICGDSTEC  DCTMYICGD  2        0.2298
4162.0    45.00  0.45     Sequence
 HLA-DQA10401-DQB10402  742      VDCTMYICGDSTECS  DCTMYICGD  1        0.2208
4585.3    48.00  0.43     Sequence
 HLA-DQA10401-DQB10402  743      DCTMYICGDSTECSN  DCTMYICGD  0        0.1903
6377.4    60.00  0.37     Sequence
 HLA-DQA10401-DQB10402  744      CTMYICGDSTECSNL  MYICGDSTE  2        0.1481
10073.2    75.00  0.37     Sequence
```

```
 HLA-DQA10401-DQB10402  745      TMYICGDSTECSNLL  MYICGDSTE  1        0.1603
8823.1    70.00  0.31     Sequence
 HLA-DQA10401-DQB10402  746      MYICGDSTECSNLLL  DSTECSNLL  5        0.1534
9512.8    75.00  0.28     Sequence
 HLA-DQA10401-DQB10402  747      YICGDSTECSNLLLQ  TECSNLLLQ  6        0.1599
8862.8    70.00  0.37     Sequence
 HLA-DQA10401-DQB10402  748      ICGDSTECSNLLLQY  ECSNLLLQY  6        0.2305
4130.3    44.00  0.47     Sequence
 HLA-DQA10401-DQB10402  749      CGDSTECSNLLLQYG  ECSNLLLQY  5        0.2271
4285.9    46.00  0.49     Sequence
 HLA-DQA10401-DQB10402  750      GDSTECSNLLLQYGS  ECSNLLLQY  4        0.2228
4487.2    47.00  0.49     Sequence
 HLA-DQA10401-DQB10402  751      DSTECSNLLLQYGSF  ECSNLLLQY  3        0.2422
3636.5    40.00  0.40     Sequence
 HLA-DQA10401-DQB10402  752      STECSNLLLQYGSFC  ECSNLLLQY  2        0.2193
4663.3    48.00  0.44     Sequence
 HLA-DQA10401-DQB10402  753      TECSNLLLQYGSFCT  ECSNLLLQY  1        0.2091
5205.3    55.00  0.41     Sequence
 HLA-DQA10401-DQB10402  754      ECSNLLLQYGSFCTQ  ECSNLLLQY  0        0.1869
6618.0    60.00  0.36     Sequence
 HLA-DQA10401-DQB10402  755      CSNLLLQYGSFCTQL  QYGSFCTQL  6        0.1880
6542.0    60.00  0.38     Sequence
 HLA-DQA10401-DQB10402  756      SNLLLQYGSFCTQLN  QYGSFCTQL  5        0.2161
4827.0    50.00  0.34     Sequence
 HLA-DQA10401-DQB10402  757      NLLLQYGSFCTQLNR  QYGSFCTQL  4        0.2025
5589.4    55.00  0.32     Sequence
 HLA-DQA10401-DQB10402  758      LLLQYGSFCTQLNRA  QYGSFCTQL  3        0.2181
4719.9    49.00  0.25     Sequence
 HLA-DQA10401-DQB10402  759      LLQYGSFCTQLNRAL  SFCTQLNRA  5        0.2164
4807.8    50.00  0.27     Sequence
 HLA-DQA10401-DQB10402  760      LQYGSFCTQLNRALT  SFCTQLNRA  4        0.1979
5876.8    60.00  0.29     Sequence
 HLA-DQA10401-DQB10402  761      QYGSFCTQLNRALTG  SFCTQLNRA  3        0.1952
6047.2    60.00  0.28     Sequence
 HLA-DQA10401-DQB10402  762      YGSFCTQLNRALTGI  SFCTQLNRA  2        0.1811
7047.2    65.00  0.25     Sequence
 HLA-DQA10401-DQB10402  763      GSFCTQLNRALTGIA  LNRALTGIA  6        0.1826
6935.9    65.00  0.26     Sequence
 HLA-DQA10401-DQB10402  764      SFCTQLNRALTGIAV  LNRALTGIA  5        0.1993
5784.5    60.00  0.28     Sequence
 HLA-DQA10401-DQB10402  765      FCTQLNRALTGIAVE  RALTGIAVE  6        0.4655
324.7     2.50  0.80     Sequence          WB
 HLA-DQA10401-DQB10402  766      CTQLNRALTGIAVEQ  RALTGIAVE  5        0.5284
164.5     0.80  0.69     Sequence          SB
 HLA-DQA10401-DQB10402  767      TQLNRALTGIAVEQD  RALTGIAVE  4        0.5792
94.9     0.25   0.55    Sequence          SB
 HLA-DQA10401-DQB10402  768      QLNRALTGIAVEQDK  RALTGIAVE  3        0.5606
116.1     0.40  0.51     Sequence          SB
 HLA-DQA10401-DQB10402  769      LNRALTGIAVEQDKN  RALTGIAVE  2        0.5485
132.3     0.50  0.53     Sequence          SB
 HLA-DQA10401-DQB10402  770      NRALTGIAVEQDKNT  RALTGIAVE  1        0.5299
161.9     0.80  0.51     Sequence          SB
 HLA-DQA10401-DQB10402  771      RALTGIAVEQDKNTQ  RALTGIAVE  0        0.5035
215.3     1.30  0.47     Sequence          SB
 HLA-DQA10401-DQB10402  772      ALTGIAVEQDKNTQE  LTGIAVEQD  1        0.3759
856.0     9.50  0.63     Sequence          WB
 HLA-DQA10401-DQB10402  773      LTGIAVEQDKNTQEV  LTGIAVEQD  0        0.2917
2128.6    26.00  0.65     Sequence
 HLA-DQA10401-DQB10402  774      TGIAVEQDKNTQEVF  EQDKNTQEV  5        0.1970
5932.8    60.00  0.38     Sequence
 HLA-DQA10401-DQB10402  775      GIAVEQDKNTQEVFA  EQDKNTQEV  4        0.1983
5851.6    60.00  0.36     Sequence
 HLA-DQA10401-DQB10402  776      IAVEQDKNTQEVFAQ  EQDKNTQEV  3        0.2178
4736.3    49.00  0.24     Sequence
 HLA-DQA10401-DQB10402  777      AVEQDKNTQEVFAQV  KNTQEVFAQ  5        0.2560
3132.9    36.00  0.29     Sequence
```

```
 HLA-DQA10401-DQB10402  778       VEQDKNTQEVFAQVK  KNTQEVFAQ  4         0.2451
3527.6    39.00  0.25     Sequence
 HLA-DQA10401-DQB10402  779       EQDKNTQEVFAQVKQ  KNTQEVFAQ  3         0.2459
3494.7    39.00  0.25     Sequence
 HLA-DQA10401-DQB10402  780       QDKNTQEVFAQVKQI  EVFAQVKQI  6         0.3141
1670.6    20.00  0.50     Sequence
 HLA-DQA10401-DQB10402  781       DKNTQEVFAQVKQIY  EVFAQVKQI  5         0.3060
1824.4    22.00  0.54     Sequence
 HLA-DQA10401-DQB10402  782       KNTQEVFAQVKQIYK  EVFAQVKQI  4         0.2786
2454.0    29.00  0.54     Sequence
 HLA-DQA10401-DQB10402  783       NTQEVFAQVKQIYKT  EVFAQVKQI  3         0.2660
2811.0    33.00  0.55     Sequence
 HLA-DQA10401-DQB10402  784       TQEVFAQVKQIYKTP  EVFAQVKQI  2         0.2493
3370.5    38.00  0.61     Sequence
 HLA-DQA10401-DQB10402  785       QEVFAQVKQIYKTPP  EVFAQVKQI  1         0.2322
4053.6    44.00  0.62     Sequence
 HLA-DQA10401-DQB10402  786       EVFAQVKQIYKTPPI  EVFAQVKQI  0         0.1879
6549.8    60.00  0.61     Sequence
 HLA-DQA10401-DQB10402  787       VFAQVKQIYKTPPIK  VFAQVKQIY  0         0.0929
18289.8    95.00  0.31     Sequence
 HLA-DQA10401-DQB10402  788       FAQVKQIYKTPPIKD  IYKTPPIKD  6         0.1002
16903.9    90.00  0.44     Sequence
 HLA-DQA10401-DQB10402  789       AQVKQIYKTPPIKDF  IYKTPPIKD  5         0.1439
10533.9    80.00  0.45     Sequence
 HLA-DQA10401-DQB10402  790       QVKQIYKTPPIKDFG  IYKTPPIKD  4         0.1331
11849.8    80.00  0.44     Sequence
 HLA-DQA10401-DQB10402  791       VKQIYKTPPIKDFGG  IYKTPPIKD  3         0.1259
12810.4    85.00  0.43     Sequence
 HLA-DQA10401-DQB10402  792       KQIYKTPPIKDFGGF  IYKTPPIKD  2         0.1204
13592.5    85.00  0.44     Sequence
 HLA-DQA10401-DQB10402  793       QIYKTPPIKDFGGFN  IYKTPPIKD  1         0.1086
15445.7    90.00  0.46     Sequence
 HLA-DQA10401-DQB10402  794       IYKTPPIKDFGGFNF  IKDFGGFNF  6         0.1349
11618.6    80.00  0.37     Sequence
 HLA-DQA10401-DQB10402  795       YKTPPIKDFGGFNFS  IKDFGGFNF  5         0.1309
12134.7    80.00  0.44     Sequence
 HLA-DQA10401-DQB10402  796       KTPPIKDFGGFNFSQ  DFGGFNFSQ  6         0.1763
7418.8    65.00  0.49     Sequence
 HLA-DQA10401-DQB10402  797       TPPIKDFGGFNFSQI  DFGGFNFSQ  5         0.2193
4660.8    48.00  0.45     Sequence
 HLA-DQA10401-DQB10402  798       PPIKDFGGFNFSQIL  DFGGFNFSQ  4         0.2547
3179.4    36.00  0.36     Sequence
 HLA-DQA10401-DQB10402  799       PIKDFGGFNFSQILP  DFGGFNFSQ  3         0.2524
3258.0    37.00  0.34     Sequence
 HLA-DQA10401-DQB10402  800       IKDFGGFNFSQILPD  FNFSQILPD  6         0.3729
884.1    10.00  0.51     Sequence
 HLA-DQA10401-DQB10402  801       KDFGGFNFSQILPDP  FNFSQILPD  5         0.3923
716.8     7.50  0.54    Sequence         WB
 HLA-DQA10401-DQB10402  802       DFGGFNFSQILPDPS  FNFSQILPD  4         0.3907
729.7     8.00  0.50    Sequence         WB
 HLA-DQA10401-DQB10402  803       FGGFNFSQILPDPSK  FNFSQILPD  3         0.3524
1104.4    13.00  0.56     Sequence
 HLA-DQA10401-DQB10402  804       GGFNFSQILPDPSKP  FNFSQILPD  2         0.3098
1750.2    21.00  0.60     Sequence
 HLA-DQA10401-DQB10402  805       GFNFSQILPDPSKPS  FNFSQILPD  1         0.2931
2097.9    25.00  0.64     Sequence
 HLA-DQA10401-DQB10402  806       FNFSQILPDPSKPSK  FNFSQILPD  0         0.2608
2974.9    34.00  0.63     Sequence
 HLA-DQA10401-DQB10402  807       NFSQILPDPSKPSKR  FSQILPDPS  1         0.1312
12088.6    80.00  0.48     Sequence
 HLA-DQA10401-DQB10402  808       FSQILPDPSKPSKRS  FSQILPDPS  0         0.0829
20392.8    95.00  0.55     Sequence
 HLA-DQA10401-DQB10402  809       SQILPDPSKPSKRSF  ILPDPSKPS  2         0.0406
32219.0   100.00  0.20     Sequence
 HLA-DQA10401-DQB10402  810       QILPDPSKPSKRSFI  ILPDPSKPS  1         0.0351
34216.7   100.00  0.22     Sequence
```

```
 HLA-DQA10401-DQB10402  811      ILPDPSKPSKRSFIE  KPSKRSFIE  6        0.0830
20372.1    95.00  0.63     Sequence
 HLA-DQA10401-DQB10402  812      LPDPSKPSKRSFIED  KPSKRSFIE  5        0.1352
11575.7    80.00  0.55     Sequence
 HLA-DQA10401-DQB10402  813      PDPSKPSKRSFIEDL  SKRSFIEDL  6        0.1952
6050.4    60.00  0.32     Sequence
 HLA-DQA10401-DQB10402  814      DPSKPSKRSFIEDLL  SKRSFIEDL  5        0.2038
5511.1    55.00  0.35     Sequence
 HLA-DQA10401-DQB10402  815      PSKPSKRSFIEDLLF  RSFIEDLLF  6        0.2272
4279.9    46.00  0.23     Sequence
 HLA-DQA10401-DQB10402  816      SKPSKRSFIEDLLFN  RSFIEDLLF  5        0.2164
4811.5    50.00  0.25     Sequence
 HLA-DQA10401-DQB10402  817      KPSKRSFIEDLLFNK  RSFIEDLLF  4        0.2035
5531.3    55.00  0.21     Sequence
 HLA-DQA10401-DQB10402  818      PSKRSFIEDLLFNKV  RSFIEDLLF  3        0.2008
5693.9    55.00  0.22     Sequence
 HLA-DQA10401-DQB10402  819      SKRSFIEDLLFNKVT  RSFIEDLLF  2        0.1914
6305.4    60.00  0.25     Sequence
 HLA-DQA10401-DQB10402  820      KRSFIEDLLFNKVTL  IEDLLFNKV  4        0.1869
6616.0    60.00  0.22     Sequence
 HLA-DQA10401-DQB10402  821      RSFIEDLLFNKVTLA  LLFNKVTLA  6        0.2075
5294.2    55.00  0.29     Sequence
 HLA-DQA10401-DQB10402  822      SFIEDLLFNKVTLAD  LFNKVTLAD  6        0.2678
2757.1    32.00  0.41     Sequence
 HLA-DQA10401-DQB10402  823      FIEDLLFNKVTLADA  LFNKVTLAD  5        0.2999
1948.8    24.00  0.38     Sequence
 HLA-DQA10401-DQB10402  824      IEDLLFNKVTLADAG  LFNKVTLAD  4        0.2895
2180.5    26.00  0.37     Sequence
 HLA-DQA10401-DQB10402  825      EDLLFNKVTLADAGF  LFNKVTLAD  3        0.2881
2215.2    27.00  0.39     Sequence
 HLA-DQA10401-DQB10402  826      DLLFNKVTLADAGFI  LFNKVTLAD  2        0.2717
2645.1    31.00  0.37     Sequence
 HLA-DQA10401-DQB10402  827      LLFNKVTLADAGFIK  LFNKVTLAD  1        0.2458
3501.0    39.00  0.37     Sequence
 HLA-DQA10401-DQB10402  828      LFNKVTLADAGFIKQ  LFNKVTLAD  0        0.2203
4613.0    48.00  0.25     Sequence
 HLA-DQA10401-DQB10402  829      FNKVTLADAGFIKQY  LADAGFIKQ  5        0.2215
4551.8    48.00  0.26     Sequence
 HLA-DQA10401-DQB10402  830      NKVTLADAGFIKQYG  ADAGFIKQY  5        0.2205
4599.7    48.00  0.37     Sequence
 HLA-DQA10401-DQB10402  831      KVTLADAGFIKQYGD  ADAGFIKQY  4        0.2426
3622.4    40.00  0.34     Sequence
 HLA-DQA10401-DQB10402  832      VTLADAGFIKQYGDC  ADAGFIKQY  3        0.2369
3854.8    42.00  0.33     Sequence
 HLA-DQA10401-DQB10402  833      TLADAGFIKQYGDCL  ADAGFIKQY  2        0.2222
4518.7    47.00  0.34     Sequence
 HLA-DQA10401-DQB10402  834      LADAGFIKQYGDCLG  ADAGFIKQY  1        0.2065
5355.2    55.00  0.35     Sequence
 HLA-DQA10401-DQB10402  835      ADAGFIKQYGDCLGD  ADAGFIKQY  0        0.1720
7778.0    70.00  0.38     Sequence
 HLA-DQA10401-DQB10402  836      DAGFIKQYGDCLGDI  AGFIKQYGD  1        0.1240
13069.7    85.00  0.23     Sequence
 HLA-DQA10401-DQB10402  837      AGFIKQYGDCLGDIA  QYGDCLGDI  5        0.0984
17237.3    90.00  0.17     Sequence
 HLA-DQA10401-DQB10402  838      GFIKQYGDCLGDIAA  GDCLGDIAA  6        0.1160
14246.6    85.00  0.35     Sequence
 HLA-DQA10401-DQB10402  839      FIKQYGDCLGDIAAR  DCLGDIAAR  6        0.1381
11221.8    80.00  0.35     Sequence
 HLA-DQA10401-DQB10402  840      IKQYGDCLGDIAARD  CLGDIAARD  6        0.2287
4211.8    45.00  0.46     Sequence
 HLA-DQA10401-DQB10402  841      KQYGDCLGDIAARDL  CLGDIAARD  5        0.2791
2439.8    29.00  0.40     Sequence
 HLA-DQA10401-DQB10402  842      QYGDCLGDIAARDLI  CLGDIAARD  4        0.2748
2555.5    30.00  0.38     Sequence
 HLA-DQA10401-DQB10402  843      YGDCLGDIAARDLIC  CLGDIAARD  3        0.2803
2409.1    29.00  0.32     Sequence
```

```
 HLA-DQA10401-DQB10402  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.2683
2744.3    32.00  0.31     Sequence
 HLA-DQA10401-DQB10402  845      DCLGDIAARDLICAQ  LGDIAARDL  2        0.2822
2360.4    28.00  0.25     Sequence
 HLA-DQA10401-DQB10402  846      CLGDIAARDLICAQK  LGDIAARDL  1        0.2662
2805.4    33.00  0.26     Sequence
 HLA-DQA10401-DQB10402  847      LGDIAARDLICAQKF  AARDLICAQ  4        0.2712
2658.3    31.00  0.22     Sequence
 HLA-DQA10401-DQB10402  848      GDIAARDLICAQKFN  RDLICAQKF  5        0.2490
3378.3    38.00  0.33     Sequence
 HLA-DQA10401-DQB10402  849      DIAARDLICAQKFNG  RDLICAQKF  4        0.2266
4307.4    46.00  0.37     Sequence
 HLA-DQA10401-DQB10402  850      IAARDLICAQKFNGL  RDLICAQKF  3        0.2063
5366.7    55.00  0.44     Sequence
 HLA-DQA10401-DQB10402  851      AARDLICAQKFNGLT  RDLICAQKF  2        0.1809
7061.9    65.00  0.51     Sequence
 HLA-DQA10401-DQB10402  852      ARDLICAQKFNGLTV  RDLICAQKF  1        0.1482
10055.3    75.00  0.61     Sequence
 HLA-DQA10401-DQB10402  853      RDLICAQKFNGLTVL  RDLICAQKF  0        0.1543
9417.2    75.00  0.41     Sequence
 HLA-DQA10401-DQB10402  854      DLICAQKFNGLTVLP  QKFNGLTVL  5        0.1360
11484.1    80.00  0.43     Sequence
 HLA-DQA10401-DQB10402  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.2080
5264.6    55.00  0.55     Sequence
 HLA-DQA10401-DQB10402  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.2657
2821.5    33.00  0.49     Sequence
 HLA-DQA10401-DQB10402  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.2727
2614.7    31.00  0.45     Sequence
 HLA-DQA10401-DQB10402  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.2721
2631.5    31.00  0.42     Sequence
 HLA-DQA10401-DQB10402  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.2755
2537.1    30.00  0.38     Sequence
 HLA-DQA10401-DQB10402  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1        0.2902
2164.4    26.00  0.32     Sequence
 HLA-DQA10401-DQB10402  861      FNGLTVLPPLLTDEM  FNGLTVLPP  0        0.2928
2105.2    25.00  0.24     Sequence
 HLA-DQA10401-DQB10402  862      NGLTVLPPLLTDEMI  VLPPLLTDE  4        0.2532
3229.3    37.00  0.23     Sequence
 HLA-DQA10401-DQB10402  863      GLTVLPPLLTDEMIA  VLPPLLTDE  3        0.2433
3593.6    40.00  0.25     Sequence
 HLA-DQA10401-DQB10402  864      LTVLPPLLTDEMIAQ  VLPPLLTDE  2        0.2545
3185.1    36.00  0.22     Sequence
 HLA-DQA10401-DQB10402  865      TVLPPLLTDEMIAQY  LTDEMIAQY  6        0.3144
1666.1    20.00  0.38     Sequence
 HLA-DQA10401-DQB10402  866      VLPPLLTDEMIAQYT  LTDEMIAQY  5        0.3120
1709.4    21.00  0.43     Sequence
 HLA-DQA10401-DQB10402  867      LPPLLTDEMIAQYTS  LTDEMIAQY  4        0.2984
1980.0    24.00  0.44     Sequence
 HLA-DQA10401-DQB10402  868      PPLLTDEMIAQYTSA  LTDEMIAQY  3        0.3143
1667.6    20.00  0.39     Sequence
 HLA-DQA10401-DQB10402  869      PLLTDEMIAQYTSAL  LTDEMIAQY  2        0.3002
1942.3    24.00  0.38     Sequence
 HLA-DQA10401-DQB10402  870      LLTDEMIAQYTSALL  LTDEMIAQY  1        0.2896
2178.1    26.00  0.34     Sequence
 HLA-DQA10401-DQB10402  871      LTDEMIAQYTSALLA  AQYTSALLA  6        0.3181
1601.2    19.00  0.44     Sequence
 HLA-DQA10401-DQB10402  872      TDEMIAQYTSALLAG  AQYTSALLA  5        0.3083
1779.2    22.00  0.47     Sequence
 HLA-DQA10401-DQB10402  873      DEMIAQYTSALLAGT  AQYTSALLA  4        0.3049
1845.4    22.00  0.42     Sequence
 HLA-DQA10401-DQB10402  874      EMIAQYTSALLAGTI  AQYTSALLA  3        0.3151
1652.9    20.00  0.38     Sequence
 HLA-DQA10401-DQB10402  875      MIAQYTSALLAGTIT  AQYTSALLA  2        0.2962
2028.9    24.00  0.40     Sequence
 HLA-DQA10401-DQB10402  876      IAQYTSALLAGTITS  AQYTSALLA  1        0.2997
1952.6    24.00  0.32     Sequence
```

```
 HLA-DQA10401-DQB10402  877      AQYTSALLAGTITSG  AQYTSALLA  0        0.2823
2356.6    28.00  0.28     Sequence
 HLA-DQA10401-DQB10402  878      QYTSALLAGTITSGW  LAGTITSGW  6        0.2519
3277.1    37.00  0.22     Sequence
 HLA-DQA10401-DQB10402  879      YTSALLAGTITSGWT  LAGTITSGW  5        0.2463
3479.7    39.00  0.29     Sequence
 HLA-DQA10401-DQB10402  880      TSALLAGTITSGWTF  LAGTITSGW  4        0.2501
3338.6    38.00  0.30     Sequence
 HLA-DQA10401-DQB10402  881      SALLAGTITSGWTFG  LAGTITSGW  3        0.2331
4015.1    43.00  0.33     Sequence
 HLA-DQA10401-DQB10402  882      ALLAGTITSGWTFGA  LAGTITSGW  2        0.2127
5008.5    55.00  0.29     Sequence
 HLA-DQA10401-DQB10402  883      LLAGTITSGWTFGAG  LAGTITSGW  1        0.1955
6030.3    60.00  0.31     Sequence
 HLA-DQA10401-DQB10402  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.1850
6752.1    65.00  0.22     Sequence
 HLA-DQA10401-DQB10402  885      AGTITSGWTFGAGAA  GWTFGAGAA  6        0.2069
5329.5    55.00  0.38     Sequence
 HLA-DQA10401-DQB10402  886      GTITSGWTFGAGAAL  WTFGAGAAL  6        0.2710
2663.5    31.00  0.41     Sequence
 HLA-DQA10401-DQB10402  887      TITSGWTFGAGAALQ  TFGAGAALQ  6        0.3862
765.6     8.50  0.55     Sequence         WB
 HLA-DQA10401-DQB10402  888      ITSGWTFGAGAALQI  TFGAGAALQ  5        0.4633
332.5     3.00  0.47     Sequence         WB
 HLA-DQA10401-DQB10402  889      TSGWTFGAGAALQIP  TFGAGAALQ  4        0.4682
315.4     2.50  0.49     Sequence         WB
 HLA-DQA10401-DQB10402  890      SGWTFGAGAALQIPF  TFGAGAALQ  3        0.4922
243.4     1.60  0.44     Sequence         SB
 HLA-DQA10401-DQB10402  891      GWTFGAGAALQIPFA  TFGAGAALQ  2        0.4797
278.4     2.00  0.44     Sequence         WB
 HLA-DQA10401-DQB10402  892      WTFGAGAALQIPFAM  TFGAGAALQ  1        0.4730
299.6     2.50  0.41     Sequence         WB
 HLA-DQA10401-DQB10402  893      TFGAGAALQIPFAMQ  TFGAGAALQ  0        0.4319
467.0     4.50  0.35     Sequence         WB
 HLA-DQA10401-DQB10402  894      FGAGAALQIPFAMQM  FGAGAALQI  0        0.3740
874.3    10.00  0.30     Sequence
 HLA-DQA10401-DQB10402  895      GAGAALQIPFAMQMA  QIPFAMQMA  6        0.3160
1637.6    20.00  0.25     Sequence
 HLA-DQA10401-DQB10402  896      AGAALQIPFAMQMAY  QIPFAMQMA  5        0.3132
1687.6    21.00  0.22     Sequence
 HLA-DQA10401-DQB10402  897      GAALQIPFAMQMAYR  QIPFAMQMA  4        0.2839
2317.9    28.00  0.19     Sequence
 HLA-DQA10401-DQB10402  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.3305
1399.9    17.00  0.28     Sequence
 HLA-DQA10401-DQB10402  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.3063
1819.3    22.00  0.34     Sequence
 HLA-DQA10401-DQB10402  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.2855
2277.1    27.00  0.37     Sequence
 HLA-DQA10401-DQB10402  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.2603
2992.6    35.00  0.40     Sequence
 HLA-DQA10401-DQB10402  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.2216
4548.5    48.00  0.49     Sequence
 HLA-DQA10401-DQB10402  903      PFAMQMAYRFNGIGV  FAMQMAYRF  1        0.1852
6740.7    65.00  0.58     Sequence
 HLA-DQA10401-DQB10402  904      FAMQMAYRFNGIGVT  FAMQMAYRF  0        0.1698
7967.4    70.00  0.50     Sequence
 HLA-DQA10401-DQB10402  905      AMQMAYRFNGIGVTQ  YRFNGIGVT  5        0.1165
14178.5    85.00  0.38     Sequence
 HLA-DQA10401-DQB10402  906      MQMAYRFNGIGVTQN  FNGIGVTQN  6        0.2075
5297.8    55.00  0.57     Sequence
 HLA-DQA10401-DQB10402  907      QMAYRFNGIGVTQNV  FNGIGVTQN  5        0.2451
3526.4    39.00  0.55     Sequence
 HLA-DQA10401-DQB10402  908      MAYRFNGIGVTQNVL  FNGIGVTQN  4        0.2486
3393.3    38.00  0.51     Sequence
 HLA-DQA10401-DQB10402  909      AYRFNGIGVTQNVLY  FNGIGVTQN  3        0.2514
3292.2    37.00  0.46     Sequence
```

```
 HLA-DQA10401-DQB10402  910      YRFNGIGVTQNVLYE  FNGIGVTQN  2        0.2883
2208.6    26.00  0.34     Sequence
 HLA-DQA10401-DQB10402  911      RFNGIGVTQNVLYEN  GVTQNVLYE  5        0.3010
1926.1    23.00  0.28     Sequence
 HLA-DQA10401-DQB10402  912      FNGIGVTQNVLYENQ  GVTQNVLYE  4        0.2878
2221.3    27.00  0.27     Sequence
 HLA-DQA10401-DQB10402  913      NGIGVTQNVLYENQK  GVTQNVLYE  3        0.2214
4554.4    48.00  0.37     Sequence
 HLA-DQA10401-DQB10402  914      GIGVTQNVLYENQKL  GVTQNVLYE  2        0.2143
4920.2    50.00  0.35     Sequence
 HLA-DQA10401-DQB10402  915      IGVTQNVLYENQKLI  GVTQNVLYE  1        0.2043
5482.2    55.00  0.38     Sequence
 HLA-DQA10401-DQB10402  916      GVTQNVLYENQKLIA  GVTQNVLYE  0        0.1700
7945.8    70.00  0.35     Sequence
 HLA-DQA10401-DQB10402  917      VTQNVLYENQKLIAN  VTQNVLYEN  0        0.1344
11679.4    80.00  0.23     Sequence
 HLA-DQA10401-DQB10402  918      TQNVLYENQKLIANQ  ENQKLIANQ  6        0.1393
11072.1    80.00  0.31     Sequence
 HLA-DQA10401-DQB10402  919      QNVLYENQKLIANQF  NQKLIANQF  6        0.2220
4524.4    47.00  0.43     Sequence
 HLA-DQA10401-DQB10402  920      NVLYENQKLIANQFN  NQKLIANQF  5        0.2266
4305.2    46.00  0.42     Sequence
 HLA-DQA10401-DQB10402  921      VLYENQKLIANQFNS  NQKLIANQF  4        0.2227
4492.6    47.00  0.43     Sequence
 HLA-DQA10401-DQB10402  922      LYENQKLIANQFNSA  NQKLIANQF  3        0.2236
4451.3    47.00  0.41     Sequence
 HLA-DQA10401-DQB10402  923      YENQKLIANQFNSAI  NQKLIANQF  2        0.2121
5038.7    55.00  0.40     Sequence
 HLA-DQA10401-DQB10402  924      ENQKLIANQFNSAIG  NQKLIANQF  1        0.2144
4914.0    50.00  0.34     Sequence
 HLA-DQA10401-DQB10402  925      NQKLIANQFNSAIGK  NQKLIANQF  0        0.1911
6320.8    60.00  0.25     Sequence
 HLA-DQA10401-DQB10402  926      QKLIANQFNSAIGKI  QFNSAIGKI  6        0.1967
5950.0    60.00  0.32     Sequence
 HLA-DQA10401-DQB10402  927      KLIANQFNSAIGKIQ  QFNSAIGKI  5        0.1879
6548.0    60.00  0.35     Sequence
 HLA-DQA10401-DQB10402  928      LIANQFNSAIGKIQD  QFNSAIGKI  4        0.2109
5104.8    55.00  0.31     Sequence
 HLA-DQA10401-DQB10402  929      IANQFNSAIGKIQDS  QFNSAIGKI  3        0.2116
5066.1    55.00  0.25     Sequence
 HLA-DQA10401-DQB10402  930      ANQFNSAIGKIQDSL  QFNSAIGKI  2        0.2234
4458.2    47.00  0.20     Sequence
 HLA-DQA10401-DQB10402  931      NQFNSAIGKIQDSLS  QFNSAIGKI  1        0.1949
6071.4    60.00  0.18     Sequence
 HLA-DQA10401-DQB10402  932      QFNSAIGKIQDSLSS  NSAIGKIQD  2        0.1849
6765.5    65.00  0.20     Sequence
 HLA-DQA10401-DQB10402  933      FNSAIGKIQDSLSST  NSAIGKIQD  1        0.1563
9218.5    75.00  0.28     Sequence
 HLA-DQA10401-DQB10402  934      NSAIGKIQDSLSSTA  IQDSLSSTA  6        0.1453
10379.1    75.00  0.34     Sequence
 HLA-DQA10401-DQB10402  935      SAIGKIQDSLSSTAS  IQDSLSSTA  5        0.1479
10095.2    75.00  0.37     Sequence
 HLA-DQA10401-DQB10402  936      AIGKIQDSLSSTASA  DSLSSTASA  6        0.2895
2180.5    26.00  0.64     Sequence
 HLA-DQA10401-DQB10402  937      IGKIQDSLSSTASAL  DSLSSTASA  5        0.3553
1069.8    13.00  0.49     Sequence
 HLA-DQA10401-DQB10402  938      GKIQDSLSSTASALG  DSLSSTASA  4        0.3468
1173.2    14.00  0.43     Sequence
 HLA-DQA10401-DQB10402  939      KIQDSLSSTASALGK  DSLSSTASA  3        0.3287
1427.0    17.00  0.40     Sequence
 HLA-DQA10401-DQB10402  940      IQDSLSSTASALGKL  DSLSSTASA  2        0.3282
1434.0    17.00  0.39     Sequence
 HLA-DQA10401-DQB10402  941      QDSLSSTASALGKLQ  DSLSSTASA  1        0.3083
1779.1    22.00  0.38     Sequence
 HLA-DQA10401-DQB10402  942      DSLSSTASALGKLQD  DSLSSTASA  0        0.2925
2110.9    25.00  0.34     Sequence
```

```
 HLA-DQA10401-DQB10402  943       SLSSTASALGKLQDV  SLSSTASAL  0         0.2393
3754.8    41.00  0.29     Sequence
 HLA-DQA10401-DQB10402  944       LSSTASALGKLQDVV  ASALGKLQD  4         0.2085
5237.3    55.00  0.16     Sequence
 HLA-DQA10401-DQB10402  945       SSTASALGKLQDVVN  ASALGKLQD  3         0.1775
7329.4    65.00  0.25     Sequence
 HLA-DQA10401-DQB10402  946       STASALGKLQDVVNQ  ASALGKLQD  2         0.1640
8483.3    70.00  0.31     Sequence
 HLA-DQA10401-DQB10402  947       TASALGKLQDVVNQN  ASALGKLQD  1         0.1623
8633.1    70.00  0.26     Sequence
 HLA-DQA10401-DQB10402  948       ASALGKLQDVVNQNA  KLQDVVNQN  5         0.1593
8920.3    70.00  0.21     Sequence
 HLA-DQA10401-DQB10402  949       SALGKLQDVVNQNAQ  LQDVVNQNA  5         0.1511
9752.5    75.00  0.20     Sequence
 HLA-DQA10401-DQB10402  950       ALGKLQDVVNQNAQA  DVVNQNAQA  6         0.1994
5782.3    60.00  0.46     Sequence
 HLA-DQA10401-DQB10402  951       LGKLQDVVNQNAQAL  DVVNQNAQA  5         0.2452
3521.0    39.00  0.39     Sequence
 HLA-DQA10401-DQB10402  952       GKLQDVVNQNAQALN  VVNQNAQAL  5         0.2455
3510.3    39.00  0.34     Sequence
 HLA-DQA10401-DQB10402  953       KLQDVVNQNAQALNT  VVNQNAQAL  4         0.2436
3582.2    40.00  0.33     Sequence
 HLA-DQA10401-DQB10402  954       LQDVVNQNAQALNTL  VVNQNAQAL  3         0.2449
3532.9    39.00  0.32     Sequence
 HLA-DQA10401-DQB10402  955       QDVVNQNAQALNTLV  VVNQNAQAL  2         0.2385
3788.7    42.00  0.29     Sequence
 HLA-DQA10401-DQB10402  956       DVVNQNAQALNTLVK  VVNQNAQAL  1         0.2280
4243.0    45.00  0.29     Sequence
 HLA-DQA10401-DQB10402  957       VVNQNAQALNTLVKQ  QALNTLVKQ  6         0.2477
3427.0    39.00  0.37     Sequence
 HLA-DQA10401-DQB10402  958       VNQNAQALNTLVKQL  QALNTLVKQ  5         0.2952
2051.4    25.00  0.37     Sequence
 HLA-DQA10401-DQB10402  959       NQNAQALNTLVKQLS  ALNTLVKQL  5         0.2993
1961.9    24.00  0.39     Sequence
 HLA-DQA10401-DQB10402  960       QNAQALNTLVKQLSS  ALNTLVKQL  4         0.2906
2154.5    26.00  0.38     Sequence
 HLA-DQA10401-DQB10402  961       NAQALNTLVKQLSSN  ALNTLVKQL  3         0.2796
2427.6    29.00  0.39     Sequence
 HLA-DQA10401-DQB10402  962       AQALNTLVKQLSSNF  ALNTLVKQL  2         0.2686
2734.2    32.00  0.40     Sequence
 HLA-DQA10401-DQB10402  963       QALNTLVKQLSSNFG  ALNTLVKQL  1         0.2369
3853.0    42.00  0.47     Sequence
 HLA-DQA10401-DQB10402  964       ALNTLVKQLSSNFGA  ALNTLVKQL  0         0.1942
6114.0    60.00  0.49     Sequence
 HLA-DQA10401-DQB10402  965       LNTLVKQLSSNFGAI  QLSSNFGAI  6         0.1519
9668.2    75.00  0.32     Sequence
 HLA-DQA10401-DQB10402  966       NTLVKQLSSNFGAIS  QLSSNFGAI  5         0.1358
11508.3    80.00  0.37     Sequence
 HLA-DQA10401-DQB10402  967       TLVKQLSSNFGAISS  QLSSNFGAI  4         0.1437
10563.0    80.00  0.29     Sequence
 HLA-DQA10401-DQB10402  968       LVKQLSSNFGAISSV  SNFGAISSV  6         0.2099
5161.5    55.00  0.47     Sequence
 HLA-DQA10401-DQB10402  969       VKQLSSNFGAISSVL  SNFGAISSV  5         0.2651
2838.8    33.00  0.35     Sequence
 HLA-DQA10401-DQB10402  970       KQLSSNFGAISSVLN  NFGAISSVL  5         0.3152
1651.8    20.00  0.31     Sequence
 HLA-DQA10401-DQB10402  971       QLSSNFGAISSVLND  FGAISSVLN  5         0.3798
821.0     9.00  0.28     Sequence         WB
 HLA-DQA10401-DQB10402  972       LSSNFGAISSVLNDI  GAISSVLND  5         0.4349
452.4     4.50  0.26     Sequence         WB
 HLA-DQA10401-DQB10402  973       SSNFGAISSVLNDIL  GAISSVLND  4         0.4219
520.8     5.00  0.26     Sequence         WB
 HLA-DQA10401-DQB10402  974       SNFGAISSVLNDILS  GAISSVLND  3         0.4102
590.5     6.00  0.27     Sequence         WB
 HLA-DQA10401-DQB10402  975       NFGAISSVLNDILSR  GAISSVLND  2         0.3729
884.7    10.00  0.33     Sequence
```

```
 HLA-DQA10401-DQB10402  976      FGAISSVLNDILSRL  GAISSVLND  1        0.3485
1151.8    14.00  0.34     Sequence
 HLA-DQA10401-DQB10402  977      GAISSVLNDILSRLD  GAISSVLND  0        0.2930
2100.1    25.00  0.28     Sequence
 HLA-DQA10401-DQB10402  978      AISSVLNDILSRLDK  LNDILSRLD  5        0.2478
3425.5    39.00  0.28     Sequence
 HLA-DQA10401-DQB10402  979      ISSVLNDILSRLDKV  LNDILSRLD  4        0.2263
4321.0    46.00  0.29     Sequence
 HLA-DQA10401-DQB10402  980      SSVLNDILSRLDKVE  LNDILSRLD  3        0.2519
3276.4    37.00  0.25     Sequence
 HLA-DQA10401-DQB10402  981      SVLNDILSRLDKVEA  ILSRLDKVE  5        0.2462
3485.7    39.00  0.28     Sequence
 HLA-DQA10401-DQB10402  982      VLNDILSRLDKVEAE  SRLDKVEAE  6        0.3125
1700.2    21.00  0.44     Sequence
 HLA-DQA10401-DQB10402  983      LNDILSRLDKVEAEV  SRLDKVEAE  5        0.3481
1157.2    14.00  0.49     Sequence
 HLA-DQA10401-DQB10402  984      NDILSRLDKVEAEVQ  SRLDKVEAE  4        0.3496
1138.6    14.00  0.45     Sequence
 HLA-DQA10401-DQB10402  985      DILSRLDKVEAEVQI  SRLDKVEAE  3        0.3617
998.1    12.00  0.39     Sequence
 HLA-DQA10401-DQB10402  986      ILSRLDKVEAEVQID  KVEAEVQID  6        0.4152
559.4     5.50  0.35     Sequence         WB
 HLA-DQA10401-DQB10402  987      LSRLDKVEAEVQIDR  KVEAEVQID  5        0.4096
594.9     6.00  0.44     Sequence         WB
 HLA-DQA10401-DQB10402  988      SRLDKVEAEVQIDRL  KVEAEVQID  4        0.4510
379.9     3.50  0.31     Sequence         WB
 HLA-DQA10401-DQB10402  989      RLDKVEAEVQIDRLI  KVEAEVQID  3        0.4307
473.1     4.50  0.34     Sequence         WB
 HLA-DQA10401-DQB10402  990      LDKVEAEVQIDRLIT  KVEAEVQID  2        0.4128
574.2     6.00  0.37     Sequence         WB
 HLA-DQA10401-DQB10402  991      DKVEAEVQIDRLITG  KVEAEVQID  1        0.3758
857.2     9.50  0.40     Sequence         WB
 HLA-DQA10401-DQB10402  992      KVEAEVQIDRLITGR  EAEVQIDRL  2        0.3253
1481.2    18.00  0.47     Sequence
 HLA-DQA10401-DQB10402  993      VEAEVQIDRLITGRL  EAEVQIDRL  1        0.2730
2605.8    31.00  0.64     Sequence
 HLA-DQA10401-DQB10402  994      EAEVQIDRLITGRLQ  EAEVQIDRL  0        0.2606
2980.5    34.00  0.43     Sequence
 HLA-DQA10401-DQB10402  995      AEVQIDRLITGRLQS  DRLITGRLQ  5        0.2267
4302.1    46.00  0.56     Sequence
 HLA-DQA10401-DQB10402  996      EVQIDRLITGRLQSL  DRLITGRLQ  4        0.2419
3651.9    41.00  0.50     Sequence
 HLA-DQA10401-DQB10402  997      VQIDRLITGRLQSLQ  DRLITGRLQ  3        0.2428
3613.4    40.00  0.48     Sequence
 HLA-DQA10401-DQB10402  998      QIDRLITGRLQSLQT  DRLITGRLQ  2        0.2429
3611.0    40.00  0.41     Sequence
 HLA-DQA10401-DQB10402  999      IDRLITGRLQSLQTY  DRLITGRLQ  1        0.2446
3546.8    40.00  0.35     Sequence
 HLA-DQA10401-DQB10402 1000      DRLITGRLQSLQTYV  DRLITGRLQ  0        0.2246
4399.3    46.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1001      RLITGRLQSLQTYVT  LQSLQTYVT  6        0.1834
6872.4    65.00  0.19     Sequence
 HLA-DQA10401-DQB10402 1002      LITGRLQSLQTYVTQ  QSLQTYVTQ  6        0.1916
6289.2    60.00  0.20     Sequence
 HLA-DQA10401-DQB10402 1003      ITGRLQSLQTYVTQQ  SLQTYVTQQ  6        0.2498
3351.7    38.00  0.52     Sequence
 HLA-DQA10401-DQB10402 1004      TGRLQSLQTYVTQQL  SLQTYVTQQ  5        0.2842
2309.2    28.00  0.55     Sequence
 HLA-DQA10401-DQB10402 1005      GRLQSLQTYVTQQLI  SLQTYVTQQ  4        0.2876
2227.3    27.00  0.50     Sequence
 HLA-DQA10401-DQB10402 1006      RLQSLQTYVTQQLIR  SLQTYVTQQ  3        0.2634
2890.9    34.00  0.49     Sequence
 HLA-DQA10401-DQB10402 1007      LQSLQTYVTQQLIRA  SLQTYVTQQ  2        0.2611
2966.4    34.00  0.49     Sequence
 HLA-DQA10401-DQB10402 1008      QSLQTYVTQQLIRAA  SLQTYVTQQ  1        0.2519
3273.9    37.00  0.41     Sequence
```

```
 HLA-DQA10401-DQB10402 1009      SLQTYVTQQLIRAAE  SLQTYVTQQ  0        0.2583
3055.1    35.00  0.23     Sequence
 HLA-DQA10401-DQB10402 1010      LQTYVTQQLIRAAEI  QQLIRAAEI  6        0.3007
1931.2    23.00  0.39     Sequence
 HLA-DQA10401-DQB10402 1011      QTYVTQQLIRAAEIR  QQLIRAAEI  5        0.2765
2509.1    30.00  0.38     Sequence
 HLA-DQA10401-DQB10402 1012      TYVTQQLIRAAEIRA  QQLIRAAEI  4        0.2755
2538.2    30.00  0.35     Sequence
 HLA-DQA10401-DQB10402 1013      YVTQQLIRAAEIRAS  QQLIRAAEI  3        0.2834
2330.0    28.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1014      VTQQLIRAAEIRASA  QQLIRAAEI  2        0.2837
2322.0    28.00  0.26     Sequence
 HLA-DQA10401-DQB10402 1015      TQQLIRAAEIRASAN  AAEIRASAN  6        0.3020
1904.7    23.00  0.30     Sequence
 HLA-DQA10401-DQB10402 1016      QQLIRAAEIRASANL  AAEIRASAN  5        0.2970
2011.8    24.00  0.35     Sequence
 HLA-DQA10401-DQB10402 1017      QLIRAAEIRASANLA  EIRASANLA  6        0.3198
1571.5    19.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1018      LIRAAEIRASANLAA  EIRASANLA  5        0.3192
1581.6    19.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1019      IRAAEIRASANLAAI  EIRASANLA  4        0.3405
1255.6    15.00  0.25     Sequence
 HLA-DQA10401-DQB10402 1020      RAAEIRASANLAAIK  EIRASANLA  3        0.3091
1764.9    21.00  0.24     Sequence
 HLA-DQA10401-DQB10402 1021      AAEIRASANLAAIKM  EIRASANLA  2        0.3022
1901.5    23.00  0.25     Sequence
 HLA-DQA10401-DQB10402 1022      AEIRASANLAAIKMS  EIRASANLA  1        0.2990
1966.8    24.00  0.20     Sequence
 HLA-DQA10401-DQB10402 1023      EIRASANLAAIKMSE  NLAAIKMSE  6        0.3373
1300.4    16.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1024      IRASANLAAIKMSEC  NLAAIKMSE  5        0.3336
1353.6    16.00  0.33     Sequence
 HLA-DQA10401-DQB10402 1025      RASANLAAIKMSECV  NLAAIKMSE  4        0.3298
1409.9    17.00  0.35     Sequence
 HLA-DQA10401-DQB10402 1026      ASANLAAIKMSECVL  NLAAIKMSE  3        0.3204
1560.6    19.00  0.41     Sequence
 HLA-DQA10401-DQB10402 1027      SANLAAIKMSECVLG  NLAAIKMSE  2        0.3078
1789.8    22.00  0.42     Sequence
 HLA-DQA10401-DQB10402 1028      ANLAAIKMSECVLGQ  NLAAIKMSE  1        0.2604
2986.3    34.00  0.49     Sequence
 HLA-DQA10401-DQB10402 1029      NLAAIKMSECVLGQS  NLAAIKMSE  0        0.2195
4651.2    48.00  0.50     Sequence
 HLA-DQA10401-DQB10402 1030      LAAIKMSECVLGQSK  AAIKMSECV  1        0.1459
10309.9    75.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1031      AAIKMSECVLGQSKR  AAIKMSECV  0        0.1248
12957.0    85.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1032      AIKMSECVLGQSKRV  KMSECVLGQ  2        0.1007
16823.3    90.00  0.27     Sequence
 HLA-DQA10401-DQB10402 1033      IKMSECVLGQSKRVD  VLGQSKRVD  6        0.1035
16324.6    90.00  0.25     Sequence
 HLA-DQA10401-DQB10402 1034      KMSECVLGQSKRVDF  VLGQSKRVD  5        0.1148
14442.5    85.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1035      MSECVLGQSKRVDFC  VLGQSKRVD  4        0.1080
15543.1    90.00  0.35     Sequence
 HLA-DQA10401-DQB10402 1036      SECVLGQSKRVDFCG  VLGQSKRVD  3        0.0972
17459.5    90.00  0.37     Sequence
 HLA-DQA10401-DQB10402 1037      ECVLGQSKRVDFCGK  VLGQSKRVD  2        0.0873
19433.6    95.00  0.41     Sequence
 HLA-DQA10401-DQB10402 1038      CVLGQSKRVDFCGKG  VLGQSKRVD  1        0.0738
22501.9    95.00  0.45     Sequence
 HLA-DQA10401-DQB10402 1039      VLGQSKRVDFCGKGY  VLGQSKRVD  0        0.0628
25356.9   100.00  0.42     Sequence
 HLA-DQA10401-DQB10402 1040      LGQSKRVDFCGKGYH  LGQSKRVDF  0        0.0429
31420.6   100.00  0.25     Sequence
 HLA-DQA10401-DQB10402 1041      GQSKRVDFCGKGYHL  DFCGKGYHL  6        0.0440
31059.6   100.00  0.29     Sequence
```

```
 HLA-DQA10401-DQB10402 1042      QSKRVDFCGKGYHLM  FCGKGYHLM  6        0.0540
27885.3 100.00    0.37     Sequence
 HLA-DQA10401-DQB10402 1043      SKRVDFCGKGYHLMS  FCGKGYHLM  5        0.0571
26964.4 100.00    0.38     Sequence
 HLA-DQA10401-DQB10402 1044      KRVDFCGKGYHLMSF  GKGYHLMSF  6        0.0931
18256.6    95.00  0.43     Sequence
 HLA-DQA10401-DQB10402 1045      RVDFCGKGYHLMSFP  GKGYHLMSF  5        0.1037
16281.4    90.00  0.43     Sequence
 HLA-DQA10401-DQB10402 1046      VDFCGKGYHLMSFPQ  GYHLMSFPQ  6        0.1400
10988.7    80.00  0.41     Sequence
 HLA-DQA10401-DQB10402 1047      DFCGKGYHLMSFPQS  GYHLMSFPQ  5        0.1785
7245.5    65.00   0.43    Sequence
 HLA-DQA10401-DQB10402 1048      FCGKGYHLMSFPQSA  HLMSFPQSA  6        0.2540
3203.1    37.00   0.35    Sequence
 HLA-DQA10401-DQB10402 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.2660
2812.0    33.00   0.40    Sequence
 HLA-DQA10401-DQB10402 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.2584
3052.1    35.00   0.35    Sequence
 HLA-DQA10401-DQB10402 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.2451
3525.5    39.00   0.38    Sequence
 HLA-DQA10401-DQB10402 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.2354
3916.5    43.00   0.38    Sequence
 HLA-DQA10401-DQB10402 1053      YHLMSFPQSAPHGVV  HLMSFPQSA  1        0.2095
5182.4    55.00   0.43    Sequence
 HLA-DQA10401-DQB10402 1054      HLMSFPQSAPHGVVF  HLMSFPQSA  0        0.1677
8147.4    70.00   0.37    Sequence
 HLA-DQA10401-DQB10402 1055      LMSFPQSAPHGVVFL  SAPHGVVFL  6        0.1474
10144.7    75.00  0.33     Sequence
 HLA-DQA10401-DQB10402 1056      MSFPQSAPHGVVFLH  SAPHGVVFL  5        0.1444
10486.9    80.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1057      SFPQSAPHGVVFLHV  SAPHGVVFL  4        0.1616
8697.4    70.00   0.26    Sequence
 HLA-DQA10401-DQB10402 1058      FPQSAPHGVVFLHVT  SAPHGVVFL  3        0.1601
8843.2    70.00   0.22    Sequence
 HLA-DQA10401-DQB10402 1059      PQSAPHGVVFLHVTY  APHGVVFLH  3        0.1508
9783.1    75.00   0.25    Sequence
 HLA-DQA10401-DQB10402 1060      QSAPHGVVFLHVTYV  APHGVVFLH  2        0.1576
9082.6    75.00   0.21    Sequence
 HLA-DQA10401-DQB10402 1061      SAPHGVVFLHVTYVP  VFLHVTYVP  6        0.1747
7554.7    65.00   0.22    Sequence
 HLA-DQA10401-DQB10402 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.2406
3703.1    41.00   0.46    Sequence
 HLA-DQA10401-DQB10402 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.2662
2806.0    33.00   0.45    Sequence
 HLA-DQA10401-DQB10402 1064      HGVVFLHVTYVPAQE  HVTYVPAQE  6        0.4097
593.9     6.00    0.51   Sequence         WB
 HLA-DQA10401-DQB10402 1065      GVVFLHVTYVPAQEK  HVTYVPAQE  5        0.4442
408.8     3.50    0.43   Sequence         WB
 HLA-DQA10401-DQB10402 1066      VVFLHVTYVPAQEKN  HVTYVPAQE  4        0.4358
448.0     4.00    0.40   Sequence         WB
 HLA-DQA10401-DQB10402 1067      VFLHVTYVPAQEKNF  HVTYVPAQE  3        0.4390
432.6     4.00    0.42   Sequence         WB
 HLA-DQA10401-DQB10402 1068      FLHVTYVPAQEKNFT  HVTYVPAQE  2        0.4158
556.2     5.50    0.43   Sequence         WB
 HLA-DQA10401-DQB10402 1069      LHVTYVPAQEKNFTT  HVTYVPAQE  1        0.3623
992.0    12.00    0.50   Sequence
 HLA-DQA10401-DQB10402 1070      HVTYVPAQEKNFTTA  HVTYVPAQE  0        0.3005
1937.1    23.00   0.54    Sequence
 HLA-DQA10401-DQB10402 1071      VTYVPAQEKNFTTAP  VTYVPAQEK  0        0.1506
9799.9    75.00   0.55    Sequence
 HLA-DQA10401-DQB10402 1072      TYVPAQEKNFTTAPA  EKNFTTAPA  6        0.1467
10221.7    75.00  0.64     Sequence
 HLA-DQA10401-DQB10402 1073      YVPAQEKNFTTAPAI  EKNFTTAPA  5        0.1970
5932.7    60.00   0.53    Sequence
 HLA-DQA10401-DQB10402 1074      VPAQEKNFTTAPAIC  KNFTTAPAI  5        0.2499
3347.5    38.00   0.31    Sequence
```

```
 HLA-DQA10401-DQB10402 1075      PAQEKNFTTAPAICH  NFTTAPAIC  5        0.2670
2781.7    32.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1076      AQEKNFTTAPAICHD  NFTTAPAIC  4        0.2916
2131.7    26.00  0.26     Sequence
 HLA-DQA10401-DQB10402 1077      QEKNFTTAPAICHDG  NFTTAPAIC  3        0.2874
2230.5    27.00  0.22     Sequence
 HLA-DQA10401-DQB10402 1078      EKNFTTAPAICHDGK  NFTTAPAIC  2        0.2712
2659.1    31.00  0.22     Sequence
 HLA-DQA10401-DQB10402 1079      KNFTTAPAICHDGKA  NFTTAPAIC  1        0.2463
3481.8    39.00  0.22     Sequence
 HLA-DQA10401-DQB10402 1080      NFTTAPAICHDGKAH  NFTTAPAIC  0        0.2005
5710.5    55.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1081      FTTAPAICHDGKAHF  FTTAPAICH  0        0.1493
9943.1    75.00  0.45     Sequence
 HLA-DQA10401-DQB10402 1082      TTAPAICHDGKAHFP  TTAPAICHD  0        0.0928
18324.1    95.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1083      TAPAICHDGKAHFPR  TAPAICHDG  0        0.0612
25782.6    100.00  0.20     Sequence
 HLA-DQA10401-DQB10402 1084      APAICHDGKAHFPRE  DGKAHFPRE  6        0.1379
11250.1    80.00  0.62     Sequence
 HLA-DQA10401-DQB10402 1085      PAICHDGKAHFPREG  DGKAHFPRE  5        0.1391
11098.2    80.00  0.63     Sequence
 HLA-DQA10401-DQB10402 1086      AICHDGKAHFPREGV  DGKAHFPRE  4        0.1403
10958.2    80.00  0.59     Sequence
 HLA-DQA10401-DQB10402 1087      ICHDGKAHFPREGVF  DGKAHFPRE  3        0.1605
8802.4    70.00  0.55     Sequence
 HLA-DQA10401-DQB10402 1088      CHDGKAHFPREGVFV  DGKAHFPRE  2        0.1464
10261.1    75.00  0.51     Sequence
 HLA-DQA10401-DQB10402 1089      HDGKAHFPREGVFVS  DGKAHFPRE  1        0.1555
9295.5    75.00  0.38     Sequence
 HLA-DQA10401-DQB10402 1090      DGKAHFPREGVFVSN  FPREGVFVS  5        0.1529
9556.7    75.00  0.32     Sequence
 HLA-DQA10401-DQB10402 1091      GKAHFPREGVFVSNG  FPREGVFVS  4        0.1410
10875.6    80.00  0.35     Sequence
 HLA-DQA10401-DQB10402 1092      KAHFPREGVFVSNGT  FPREGVFVS  3        0.1576
9091.5    75.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1093      AHFPREGVFVSNGTH  FPREGVFVS  2        0.1490
9969.4    75.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1094      HFPREGVFVSNGTHW  FPREGVFVS  1        0.1468
10218.3    75.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6        0.1704
7911.9    70.00  0.27     Sequence
 HLA-DQA10401-DQB10402 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.1398
11015.2    80.00  0.37     Sequence
 HLA-DQA10401-DQB10402 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.1359
11492.5    80.00  0.35     Sequence
 HLA-DQA10401-DQB10402 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.1393
11071.5    80.00  0.30     Sequence
 HLA-DQA10401-DQB10402 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.1284
12467.9    85.00  0.30     Sequence
 HLA-DQA10401-DQB10402 1100      VFVSNGTHWFVTQRN  THWFVTQRN  6        0.1684
8089.0    70.00  0.35     Sequence
 HLA-DQA10401-DQB10402 1101      FVSNGTHWFVTQRNF  THWFVTQRN  5        0.1956
6025.6    60.00  0.37     Sequence
 HLA-DQA10401-DQB10402 1102      VSNGTHWFVTQRNFY  THWFVTQRN  4        0.1872
6599.7    60.00  0.36     Sequence
 HLA-DQA10401-DQB10402 1103      SNGTHWFVTQRNFYE  THWFVTQRN  3        0.1978
5882.8    60.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1104      NGTHWFVTQRNFYEP  THWFVTQRN  2        0.1991
5796.7    60.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1105      GTHWFVTQRNFYEPQ  THWFVTQRN  1        0.1927
6212.3    60.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1106      THWFVTQRNFYEPQI  THWFVTQRN  0        0.1977
5890.2    60.00  0.20     Sequence
 HLA-DQA10401-DQB10402 1107      HWFVTQRNFYEPQII  RNFYEPQII  6        0.1942
6114.1    60.00  0.26     Sequence
```

```
 HLA-DQA10401-DQB10402 1108      WFVTQRNFYEPQIIT  RNFYEPQII  5         0.1741
7602.3    65.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1109      FVTQRNFYEPQIITT  RNFYEPQII  4         0.1611
8753.5    70.00  0.32     Sequence
 HLA-DQA10401-DQB10402 1110      VTQRNFYEPQIITTD  RNFYEPQII  3         0.1677
8148.4    70.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1111      TQRNFYEPQIITTDN  YEPQIITTD  5         0.1775
7330.5    65.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1112      QRNFYEPQIITTDNT  YEPQIITTD  4         0.1691
8022.0    70.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1113      RNFYEPQIITTDNTF  YEPQIITTD  3         0.1779
7295.8    65.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1114      NFYEPQIITTDNTFV  YEPQIITTD  2         0.1679
8131.6    70.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1115      FYEPQIITTDNTFVS  YEPQIITTD  1         0.1791
7198.6    65.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1116      YEPQIITTDNTFVSG  ITTDNTFVS  5         0.1738
7627.9    65.00  0.27     Sequence
 HLA-DQA10401-DQB10402 1117      EPQIITTDNTFVSGN  ITTDNTFVS  4         0.1506
9800.6    75.00  0.35     Sequence
 HLA-DQA10401-DQB10402 1118      PQIITTDNTFVSGNC  ITTDNTFVS  3         0.1656
8332.4    70.00  0.32     Sequence
 HLA-DQA10401-DQB10402 1119      QIITTDNTFVSGNCD  NTFVSGNCD  6         0.2226
4496.2    47.00  0.37     Sequence
 HLA-DQA10401-DQB10402 1120      IITTDNTFVSGNCDV  NTFVSGNCD  5         0.2577
3076.2    35.00  0.41     Sequence
 HLA-DQA10401-DQB10402 1121      ITTDNTFVSGNCDVV  NTFVSGNCD  4         0.2603
2992.3    35.00  0.41     Sequence
 HLA-DQA10401-DQB10402 1122      TTDNTFVSGNCDVVI  NTFVSGNCD  3         0.2447
3540.2    40.00  0.44     Sequence
 HLA-DQA10401-DQB10402 1123      TDNTFVSGNCDVVIG  NTFVSGNCD  2         0.2323
4047.9    44.00  0.44     Sequence
 HLA-DQA10401-DQB10402 1124      DNTFVSGNCDVVIGI  NTFVSGNCD  1         0.2257
4349.1    46.00  0.41     Sequence
 HLA-DQA10401-DQB10402 1125      NTFVSGNCDVVIGIV  NTFVSGNCD  0         0.2084
5245.1    55.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1126      TFVSGNCDVVIGIVN  NCDVVIGIV  5         0.1801
7125.8    65.00  0.22     Sequence
 HLA-DQA10401-DQB10402 1127      FVSGNCDVVIGIVNN  DVVIGIVNN  6         0.2112
5090.0    55.00  0.38     Sequence
 HLA-DQA10401-DQB10402 1128      VSGNCDVVIGIVNNT  DVVIGIVNN  5         0.2129
4996.5    55.00  0.38     Sequence
 HLA-DQA10401-DQB10402 1129      SGNCDVVIGIVNNTV  DVVIGIVNN  4         0.2214
4555.4    48.00  0.30     Sequence
 HLA-DQA10401-DQB10402 1130      GNCDVVIGIVNNTVY  DVVIGIVNN  3         0.2387
3777.5    42.00  0.22     Sequence
 HLA-DQA10401-DQB10402 1131      NCDVVIGIVNNTVYD  DVVIGIVNN  2         0.2447
3542.5    40.00  0.20     Sequence
 HLA-DQA10401-DQB10402 1132      CDVVIGIVNNTVYDP  DVVIGIVNN  1         0.2408
3692.2    41.00  0.17     Sequence
 HLA-DQA10401-DQB10402 1133      DVVIGIVNNTVYDPL  IVNNTVYDP  5         0.2364
3873.9    42.00  0.19     Sequence
 HLA-DQA10401-DQB10402 1134      VVIGIVNNTVYDPLQ  IVNNTVYDP  4         0.2172
4767.5    49.00  0.21     Sequence
 HLA-DQA10401-DQB10402 1135      VIGIVNNTVYDPLQP  IVNNTVYDP  3         0.2212
4566.1    48.00  0.19     Sequence
 HLA-DQA10401-DQB10402 1136      IGIVNNTVYDPLQPE  TVYDPLQPE  6         0.2934
2090.1    25.00  0.41     Sequence
 HLA-DQA10401-DQB10402 1137      GIVNNTVYDPLQPEL  TVYDPLQPE  5         0.2925
2110.6    25.00  0.49     Sequence
 HLA-DQA10401-DQB10402 1138      IVNNTVYDPLQPELD  TVYDPLQPE  4         0.3301
1405.1    17.00  0.40     Sequence
 HLA-DQA10401-DQB10402 1139      VNNTVYDPLQPELDS  TVYDPLQPE  3         0.3251
1484.1    18.00  0.41     Sequence
 HLA-DQA10401-DQB10402 1140      NNTVYDPLQPELDSF  TVYDPLQPE  2         0.3203
1561.9    19.00  0.38     Sequence
```

```
 HLA-DQA10401-DQB10402 1141      NTVYDPLQPELDSFK  TVYDPLQPE  1        0.2946
2064.2    25.00  0.42     Sequence
 HLA-DQA10401-DQB10402 1142      TVYDPLQPELDSFKE  TVYDPLQPE  0        0.3129
1693.7    21.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1143      VYDPLQPELDSFKEE  QPELDSFKE  5        0.3282
1434.5    17.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1144      YDPLQPELDSFKEEL  ELDSFKEEL  6        0.4110
585.5     6.00  0.29    Sequence         WB
 HLA-DQA10401-DQB10402 1145      DPLQPELDSFKEELD  ELDSFKEEL  5        0.4149
561.6     5.50  0.31    Sequence         WB
 HLA-DQA10401-DQB10402 1146      PLQPELDSFKEELDK  ELDSFKEEL  4        0.3925
715.8     7.50  0.31    Sequence         WB
 HLA-DQA10401-DQB10402 1147      LQPELDSFKEELDKY  ELDSFKEEL  3        0.3775
841.6     9.50  0.34    Sequence         WB
 HLA-DQA10401-DQB10402 1148      QPELDSFKEELDKYF  ELDSFKEEL  2        0.3493
1141.9    14.00  0.35     Sequence
 HLA-DQA10401-DQB10402 1149      PELDSFKEELDKYFK  ELDSFKEEL  1        0.2931
2097.2    25.00  0.44     Sequence
 HLA-DQA10401-DQB10402 1150      ELDSFKEELDKYFKN  ELDSFKEEL  0        0.2359
3893.3    43.00  0.47     Sequence
 HLA-DQA10401-DQB10402 1151      LDSFKEELDKYFKNH  LDSFKEELD  0        0.1224
13305.5    85.00  0.47     Sequence
 HLA-DQA10401-DQB10402 1152      DSFKEELDKYFKNHT  SFKEELDKY  1        0.0605
25979.5   100.00  0.22     Sequence
 HLA-DQA10401-DQB10402 1153      SFKEELDKYFKNHTS  EELDKYFKN  3        0.0563
27200.0   100.00  0.30     Sequence
 HLA-DQA10401-DQB10402 1154      FKEELDKYFKNHTSP  EELDKYFKN  2        0.0532
28121.1   100.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1155      KEELDKYFKNHTSPD  YFKNHTSPD  6        0.0714
23081.6    95.00  0.40     Sequence
 HLA-DQA10401-DQB10402 1156      EELDKYFKNHTSPDV  YFKNHTSPD  5        0.0864
19629.3    95.00  0.45     Sequence
 HLA-DQA10401-DQB10402 1157      ELDKYFKNHTSPDVD  KNHTSPDVD  6        0.1237
13117.1    85.00  0.44     Sequence
 HLA-DQA10401-DQB10402 1158      LDKYFKNHTSPDVDL  KNHTSPDVD  5        0.1664
8265.8    70.00  0.38     Sequence
 HLA-DQA10401-DQB10402 1159      DKYFKNHTSPDVDLG  KNHTSPDVD  4        0.1514
9718.6    75.00  0.37     Sequence
 HLA-DQA10401-DQB10402 1160      KYFKNHTSPDVDLGD  KNHTSPDVD  3        0.1558
9264.3    75.00  0.36     Sequence
 HLA-DQA10401-DQB10402 1161      YFKNHTSPDVDLGDI  KNHTSPDVD  2        0.1541
9435.1    75.00  0.36     Sequence
 HLA-DQA10401-DQB10402 1162      FKNHTSPDVDLGDIS  KNHTSPDVD  1        0.1347
11644.2    80.00  0.36     Sequence
 HLA-DQA10401-DQB10402 1163      KNHTSPDVDLGDISG  DVDLGDISG  6        0.1322
11962.4    80.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1164      NHTSPDVDLGDISGI  DVDLGDISG  5        0.1239
13085.1    85.00  0.38     Sequence
 HLA-DQA10401-DQB10402 1165      HTSPDVDLGDISGIN  DVDLGDISG  4        0.1372
11332.9    80.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1166      TSPDVDLGDISGINA  LGDISGINA  6        0.1620
8664.6    70.00  0.32     Sequence
 HLA-DQA10401-DQB10402 1167      SPDVDLGDISGINAS  LGDISGINA  5        0.1908
6342.2    60.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1168      PDVDLGDISGINASF  DISGINASF  6        0.2699
2697.4    32.00  0.33     Sequence
 HLA-DQA10401-DQB10402 1169      DVDLGDISGINASFV  DISGINASF  5        0.2845
2301.9    27.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1170      VDLGDISGINASFVN  DISGINASF  4        0.2767
2505.4    30.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1171      DLGDISGINASFVNI  DISGINASF  3        0.2673
2773.7    32.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1172      LGDISGINASFVNIQ  INASFVNIQ  6        0.2847
2296.4    27.00  0.26     Sequence
 HLA-DQA10401-DQB10402 1173      GDISGINASFVNIQK  INASFVNIQ  5        0.2660
2812.9    33.00  0.29     Sequence
```

```
 HLA-DQA10401-DQB10402 1174      DISGINASFVNIQKE  ASFVNIQKE  6        0.4421
418.6     4.00  0.64     Sequence         WB
 HLA-DQA10401-DQB10402 1175      ISGINASFVNIQKEI  ASFVNIQKE  5        0.4514
378.4     3.50  0.65     Sequence         WB
 HLA-DQA10401-DQB10402 1176      SGINASFVNIQKEID  ASFVNIQKE  4        0.4518
376.8     3.50  0.67     Sequence         WB
 HLA-DQA10401-DQB10402 1177      GINASFVNIQKEIDR  ASFVNIQKE  3        0.4255
500.6     5.00  0.65     Sequence         WB
 HLA-DQA10401-DQB10402 1178      INASFVNIQKEIDRL  ASFVNIQKE  2        0.4141
566.3     6.00  0.66     Sequence         WB
 HLA-DQA10401-DQB10402 1179      NASFVNIQKEIDRLN  ASFVNIQKE  1        0.3737
877.1    10.00  0.73     Sequence
 HLA-DQA10401-DQB10402 1180      ASFVNIQKEIDRLNE  ASFVNIQKE  0        0.3251
1484.1    18.00  0.67     Sequence
 HLA-DQA10401-DQB10402 1181      SFVNIQKEIDRLNEV  FVNIQKEID  1        0.1910
6327.7    60.00  0.37     Sequence
 HLA-DQA10401-DQB10402 1182      FVNIQKEIDRLNEVA  EIDRLNEVA  6        0.1838
6841.9    65.00  0.26     Sequence
 HLA-DQA10401-DQB10402 1183      VNIQKEIDRLNEVAK  EIDRLNEVA  5        0.1527
9579.7    75.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1184      NIQKEIDRLNEVAKN  DRLNEVAKN  6        0.1834
6872.8    65.00  0.38     Sequence
 HLA-DQA10401-DQB10402 1185      IQKEIDRLNEVAKNL  DRLNEVAKN  5        0.1990
5804.5    60.00  0.40     Sequence
 HLA-DQA10401-DQB10402 1186      QKEIDRLNEVAKNLN  DRLNEVAKN  4        0.1904
6371.9    60.00  0.40     Sequence
 HLA-DQA10401-DQB10402 1187      KEIDRLNEVAKNLNE  DRLNEVAKN  3        0.2139
4942.5    50.00  0.32     Sequence
 HLA-DQA10401-DQB10402 1188      EIDRLNEVAKNLNES  DRLNEVAKN  2        0.2312
4096.1    44.00  0.25     Sequence
 HLA-DQA10401-DQB10402 1189      IDRLNEVAKNLNESL  NEVAKNLNE  4        0.2241
4426.1    47.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1190      DRLNEVAKNLNESLI  NEVAKNLNE  3        0.2082
5254.6    55.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1191      RLNEVAKNLNESLID  KNLNESLID  6        0.2277
4256.9    45.00  0.26     Sequence
 HLA-DQA10401-DQB10402 1192      LNEVAKNLNESLIDL  KNLNESLID  5        0.2498
3350.3    38.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1193      NEVAKNLNESLIDLQ  KNLNESLID  4        0.2617
2945.3    34.00  0.23     Sequence
 HLA-DQA10401-DQB10402 1194      EVAKNLNESLIDLQE  NESLIDLQE  6        0.3309
1393.9    17.00  0.39     Sequence
 HLA-DQA10401-DQB10402 1195      VAKNLNESLIDLQEL  NESLIDLQE  5        0.4378
438.4     4.00  0.34     Sequence         WB
 HLA-DQA10401-DQB10402 1196      AKNLNESLIDLQELG  ESLIDLQEL  5        0.4115
582.8     6.00  0.34     Sequence         WB
 HLA-DQA10401-DQB10402 1197      KNLNESLIDLQELGK  NESLIDLQE  3        0.3835
788.6     8.50  0.38     Sequence         WB
 HLA-DQA10401-DQB10402 1198      NLNESLIDLQELGKY  NESLIDLQE  2        0.3673
940.1    11.00  0.41     Sequence
 HLA-DQA10401-DQB10402 1199      LNESLIDLQELGKYE  NESLIDLQE  1        0.3488
1147.6    14.00  0.41     Sequence
 HLA-DQA10401-DQB10402 1200      NESLIDLQELGKYEQ  ESLIDLQEL  1        0.3065
1814.1    22.00  0.44     Sequence
 HLA-DQA10401-DQB10402 1201      ESLIDLQELGKYEQY  ESLIDLQEL  0        0.2401
3720.6    41.00  0.40     Sequence
 HLA-DQA10401-DQB10402 1202      SLIDLQELGKYEQYI  QELGKYEQY  5        0.1928
6206.1    60.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1203      LIDLQELGKYEQYIK  QELGKYEQY  4        0.1770
7366.0    65.00  0.33     Sequence
 HLA-DQA10401-DQB10402 1204      IDLQELGKYEQYIKW  QELGKYEQY  3        0.1714
7825.5    70.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1205      DLQELGKYEQYIKWP  QELGKYEQY  2        0.1614
8723.2    70.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1206      LQELGKYEQYIKWPW  QELGKYEQY  1        0.1464
10262.3    75.00  0.31     Sequence
```

```
 HLA-DQA10401-DQB10402 1207      QELGKYEQYIKWPWY  QELGKYEQY  0         0.1262
12759.1    85.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1208      ELGKYEQYIKWPWYI  QYIKWPWYI  6         0.0980
17316.9    90.00  0.22     Sequence
 HLA-DQA10401-DQB10402 1209      LGKYEQYIKWPWYIW  QYIKWPWYI  5         0.0850
19922.8    95.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1210      GKYEQYIKWPWYIWL  IKWPWYIWL  6         0.0972
17461.4    90.00  0.22     Sequence
 HLA-DQA10401-DQB10402 1211      KYEQYIKWPWYIWLG  IKWPWYIWL  5         0.0986
17211.4    90.00  0.22     Sequence
 HLA-DQA10401-DQB10402 1212      YEQYIKWPWYIWLGF  WPWYIWLGF  6         0.1261
12774.5    85.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1213      EQYIKWPWYIWLGFI  WPWYIWLGF  5         0.1267
12698.5    85.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1214      QYIKWPWYIWLGFIA  WPWYIWLGF  4         0.1369
11372.0    80.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1215      YIKWPWYIWLGFIAG  YIWLGFIAG  6         0.1685
8072.4    70.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1216      IKWPWYIWLGFIAGL  YIWLGFIAG  5         0.1920
6259.9    60.00  0.37     Sequence
 HLA-DQA10401-DQB10402 1217      KWPWYIWLGFIAGLI  WLGFIAGLI  6         0.2376
3822.4    42.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1218      WPWYIWLGFIAGLIA  LGFIAGLIA  6         0.2899
2170.2    26.00  0.43     Sequence
 HLA-DQA10401-DQB10402 1219      PWYIWLGFIAGLIAI  LGFIAGLIA  5         0.3059
1826.1    22.00  0.41     Sequence
 HLA-DQA10401-DQB10402 1220      WYIWLGFIAGLIAIV  LGFIAGLIA  4         0.3105
1737.5    21.00  0.38     Sequence
 HLA-DQA10401-DQB10402 1221      YIWLGFIAGLIAIVM  LGFIAGLIA  3         0.3306
1398.4    17.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1222      IWLGFIAGLIAIVMV  IAGLIAIVM  5         0.3411
1247.5    15.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1223      WLGFIAGLIAIVMVT  IAGLIAIVM  4         0.3199
1569.1    19.00  0.32     Sequence
 HLA-DQA10401-DQB10402 1224      LGFIAGLIAIVMVTI  IAGLIAIVM  3         0.2984
1980.0    24.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1225      GFIAGLIAIVMVTIM  IAGLIAIVM  2         0.2787
2450.7    29.00  0.33     Sequence
 HLA-DQA10401-DQB10402 1226      FIAGLIAIVMVTIML  IAGLIAIVM  1         0.2691
2718.8    32.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1227      IAGLIAIVMVTIMLC  AGLIAIVMV  1         0.2431
3601.5    40.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1228      AGLIAIVMVTIMLCC  AGLIAIVMV  0         0.2004
5718.3    55.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1229      GLIAIVMVTIMLCCM  IAIVMVTIM  2         0.1621
8651.1    70.00  0.34     Sequence
 HLA-DQA10401-DQB10402 1230      LIAIVMVTIMLCCMT  IAIVMVTIM  1         0.1576
9087.9    75.00  0.36     Sequence
 HLA-DQA10401-DQB10402 1231      IAIVMVTIMLCCMTS  IAIVMVTIM  0         0.1524
9610.2    75.00  0.28     Sequence
 HLA-DQA10401-DQB10402 1232      AIVMVTIMLCCMTSC  IVMVTIMLC  1         0.1315
12054.5    80.00  0.24     Sequence
 HLA-DQA10401-DQB10402 1233      IVMVTIMLCCMTSCC  IVMVTIMLC  0         0.1182
13918.6    85.00  0.19     Sequence
 HLA-DQA10401-DQB10402 1234      VMVTIMLCCMTSCCS  TIMLCCMTS  3         0.1068
15735.7    90.00  0.20     Sequence
 HLA-DQA10401-DQB10402 1235      MVTIMLCCMTSCCSC  TIMLCCMTS  2         0.1032
16375.2    90.00  0.22     Sequence
 HLA-DQA10401-DQB10402 1236      VTIMLCCMTSCCSCL  TIMLCCMTS  1         0.0962
17647.9    90.00  0.22     Sequence
 HLA-DQA10401-DQB10402 1237      TIMLCCMTSCCSCLK  TIMLCCMTS  0         0.0815
20708.5    95.00  0.19     Sequence
 HLA-DQA10401-DQB10402 1238      IMLCCMTSCCSCLKG  LCCMTSCCS  2         0.0709
23206.1    95.00  0.19     Sequence
 HLA-DQA10401-DQB10402 1239      MLCCMTSCCSCLKGC  LCCMTSCCS  1         0.0631
25265.4   100.00  0.21     Sequence
```

```
 HLA-DQA10401-DQB10402 1240      LCCMTSCCSCLKGCC  CCMTSCCSC  1         0.0556
27404.1   100.00  0.17      Sequence
 HLA-DQA10401-DQB10402 1241      CCMTSCCSCLKGCCS  MTSCCSCLK  2         0.0500
29099.8   100.00  0.22      Sequence
 HLA-DQA10401-DQB10402 1242      CMTSCCSCLKGCCSC  SCLKGCCSC  6         0.0493
29345.5   100.00  0.22      Sequence
 HLA-DQA10401-DQB10402 1243      MTSCCSCLKGCCSCG  SCLKGCCSC  5         0.0420
31723.6   100.00  0.28      Sequence
 HLA-DQA10401-DQB10402 1244      TSCCSCLKGCCSCGS  SCLKGCCSC  4         0.0375
33306.8   100.00  0.28      Sequence
 HLA-DQA10401-DQB10402 1245      SCCSCLKGCCSCGSC  SCLKGCCSC  3         0.0383
33034.0   100.00  0.27      Sequence
 HLA-DQA10401-DQB10402 1246      CCSCLKGCCSCGSCC  SCLKGCCSC  2         0.0382
33054.8   100.00  0.28      Sequence
 HLA-DQA10401-DQB10402 1247      CSCLKGCCSCGSCCK  SCLKGCCSC  1         0.0361
33847.7   100.00  0.26      Sequence
 HLA-DQA10401-DQB10402 1248      SCLKGCCSCGSCCKF  CSCGSCCKF  6         0.0449
30772.7   100.00  0.38      Sequence
 HLA-DQA10401-DQB10402 1249      CLKGCCSCGSCCKFD  CSCGSCCKF  5         0.0526
28306.7   100.00  0.34      Sequence
 HLA-DQA10401-DQB10402 1250      LKGCCSCGSCCKFDE  CGSCCKFDE  6         0.0718
22995.4    95.00  0.36      Sequence
 HLA-DQA10401-DQB10402 1251      KGCCSCGSCCKFDED  CGSCCKFDE  5         0.0935
18176.4    95.00  0.34      Sequence
 HLA-DQA10401-DQB10402 1252      GCCSCGSCCKFDEDD  CGSCCKFDE  4         0.1101
15193.9    90.00  0.26      Sequence
 HLA-DQA10401-DQB10402 1253      CCSCGSCCKFDEDDS  CGSCCKFDE  3         0.1046
16121.9    90.00  0.23      Sequence
 HLA-DQA10401-DQB10402 1254      CSCGSCCKFDEDDSE  CGSCCKFDE  2         0.1084
15467.3    90.00  0.20      Sequence
 HLA-DQA10401-DQB10402 1255      SCGSCCKFDEDDSEP  CKFDEDDSE  5         0.1110
15041.6    90.00  0.28      Sequence
 HLA-DQA10401-DQB10402 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6         0.1336
11775.0    80.00  0.34      Sequence
 HLA-DQA10401-DQB10402 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5         0.1495
9922.8    75.00  0.40     Sequence
 HLA-DQA10401-DQB10402 1258      SCCKFDEDDSEPVLK  EDDSEPVLK  6         0.1707
7889.3    70.00  0.32     Sequence
 HLA-DQA10401-DQB10402 1259      CCKFDEDDSEPVLKG  EDDSEPVLK  5         0.1819
6987.0    65.00  0.35     Sequence
 HLA-DQA10401-DQB10402 1260      CKFDEDDSEPVLKGV  EDDSEPVLK  4         0.2021
5616.0    55.00  0.31     Sequence
 HLA-DQA10401-DQB10402 1261      KFDEDDSEPVLKGVK  EDDSEPVLK  3         0.1856
6709.5    65.00  0.29     Sequence
 HLA-DQA10401-DQB10402 1262      FDEDDSEPVLKGVKL  EDDSEPVLK  2         0.1946
6090.7    60.00  0.22     Sequence
 HLA-DQA10401-DQB10402 1263      DEDDSEPVLKGVKLH  EDDSEPVLK  1         0.1711
7855.8    70.00  0.23     Sequence
 HLA-DQA10401-DQB10402 1264      EDDSEPVLKGVKLHY  EDDSEPVLK  0         0.1516
9694.4    75.00  0.23     Sequence
 HLA-DQA10401-DQB10402 1265      DDSEPVLKGVKLHYT  EPVLKGVKL  3         0.1212
13479.3    85.00  0.25      Sequence
 HLA-DQA10101-DQB10501    1      PSPIKEMFVFLVLLP  KEMFVFLVL  4         0.2670
2781.0    35.00  0.25     Sequence
 HLA-DQA10101-DQB10501    2      SPIKEMFVFLVLLPL  KEMFVFLVL  3         0.2861
2261.5    31.00  0.22     Sequence
 HLA-DQA10101-DQB10501    3      PIKEMFVFLVLLPLV  MFVFLVLLP  4         0.3028
1889.2    28.00  0.21     Sequence
 HLA-DQA10101-DQB10501    4      IKEMFVFLVLLPLVS  FVFLVLLPL  4         0.2994
1960.2    28.00  0.29     Sequence
 HLA-DQA10101-DQB10501    5      KEMFVFLVLLPLVSS  FVFLVLLPL  3         0.2788
2448.3    33.00  0.31     Sequence
 HLA-DQA10101-DQB10501    6      EMFVFLVLLPLVSSQ  FVFLVLLPL  2         0.2665
2798.0    35.00  0.32     Sequence
 HLA-DQA10101-DQB10501    7      MFVFLVLLPLVSSQC  FVFLVLLPL  1         0.2632
2898.9    36.00  0.25     Sequence
```

```
 HLA-DQA10101-DQB10501    8      FVFLVLLPLVSSQCV  VLLPLVSSQ  4        0.2542
3194.4    38.00  0.26     Sequence
 HLA-DQA10101-DQB10501    9      VFLVLLPLVSSQCVN  VLLPLVSSQ  3        0.2173
4760.7    47.00  0.32     Sequence
 HLA-DQA10101-DQB10501   10      FLVLLPLVSSQCVNF  VLLPLVSSQ  2        0.2044
5475.5    55.00  0.35     Sequence
 HLA-DQA10101-DQB10501   11      LVLLPLVSSQCVNFT  VLLPLVSSQ  1        0.1993
5790.0    55.00  0.37     Sequence
 HLA-DQA10101-DQB10501   12      VLLPLVSSQCVNFTN  LVSSQCVNF  4        0.1701
7935.5    60.00  0.28     Sequence
 HLA-DQA10101-DQB10501   13      LLPLVSSQCVNFTNR  LVSSQCVNF  3        0.1374
11307.1    70.00  0.40     Sequence
 HLA-DQA10101-DQB10501   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.1303
12207.5    75.00  0.40     Sequence
 HLA-DQA10101-DQB10501   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.1345
11666.3    75.00  0.30     Sequence
 HLA-DQA10101-DQB10501   16      LVSSQCVNFTNRTQL  QCVNFTNRT  4        0.1521
9647.4    65.00  0.44     Sequence
 HLA-DQA10101-DQB10501   17      VSSQCVNFTNRTQLP  QCVNFTNRT  3        0.1340
11735.6    75.00  0.50     Sequence
 HLA-DQA10101-DQB10501   18      SSQCVNFTNRTQLPS  QCVNFTNRT  2        0.1278
12549.6    75.00  0.49     Sequence
 HLA-DQA10101-DQB10501   19      SQCVNFTNRTQLPSA  QCVNFTNRT  1        0.1225
13282.2    75.00  0.42     Sequence
 HLA-DQA10101-DQB10501   20      QCVNFTNRTQLPSAY  QCVNFTNRT  0        0.1063
15827.0    80.00  0.31     Sequence
 HLA-DQA10101-DQB10501   21      CVNFTNRTQLPSAYT  FTNRTQLPS  3        0.0846
20012.0    90.00  0.30     Sequence
 HLA-DQA10101-DQB10501   22      VNFTNRTQLPSAYTN  FTNRTQLPS  2        0.0655
24601.2    95.00  0.37     Sequence
 HLA-DQA10101-DQB10501   23      NFTNRTQLPSAYTNS  FTNRTQLPS  1        0.0642
24966.8    95.00  0.37     Sequence
 HLA-DQA10101-DQB10501   24      FTNRTQLPSAYTNSF  QLPSAYTNS  5        0.0773
21669.2    90.00  0.26     Sequence
 HLA-DQA10101-DQB10501   25      TNRTQLPSAYTNSFT  LPSAYTNSF  5        0.0900
18882.0    85.00  0.43     Sequence
 HLA-DQA10101-DQB10501   26      NRTQLPSAYTNSFTR  LPSAYTNSF  4        0.1000
16946.2    85.00  0.55     Sequence
 HLA-DQA10101-DQB10501   27      RTQLPSAYTNSFTRG  LPSAYTNSF  3        0.0938
18120.8    85.00  0.54     Sequence
 HLA-DQA10101-DQB10501   28      TQLPSAYTNSFTRGV  LPSAYTNSF  2        0.0942
18051.8    85.00  0.51     Sequence
 HLA-DQA10101-DQB10501   29      QLPSAYTNSFTRGVY  LPSAYTNSF  1        0.0969
17527.5    85.00  0.40     Sequence
 HLA-DQA10101-DQB10501   30      LPSAYTNSFTRGVYY  YTNSFTRGV  4        0.1063
15836.6    80.00  0.38     Sequence
 HLA-DQA10101-DQB10501   31      PSAYTNSFTRGVYYP  YTNSFTRGV  3        0.1199
13656.2    75.00  0.36     Sequence
 HLA-DQA10101-DQB10501   32      SAYTNSFTRGVYYPD  FTRGVYYPD  6        0.1631
8559.0    65.00  0.31     Sequence
 HLA-DQA10101-DQB10501   33      AYTNSFTRGVYYPDK  FTRGVYYPD  5        0.1714
7827.8    60.00  0.32     Sequence
 HLA-DQA10101-DQB10501   34      YTNSFTRGVYYPDKV  TRGVYYPDK  5        0.2504
3329.0    39.00  0.31     Sequence
 HLA-DQA10101-DQB10501   35      TNSFTRGVYYPDKVF  RGVYYPDKV  5        0.3276
1444.2    23.00  0.33     Sequence
 HLA-DQA10101-DQB10501   36      NSFTRGVYYPDKVFR  RGVYYPDKV  4        0.3407
1252.6    21.00  0.40     Sequence
 HLA-DQA10101-DQB10501   37      SFTRGVYYPDKVFRS  RGVYYPDKV  3        0.3276
1444.2    23.00  0.43     Sequence
 HLA-DQA10101-DQB10501   38      FTRGVYYPDKVFRSS  RGVYYPDKV  2        0.3051
1843.1    27.00  0.49     Sequence
 HLA-DQA10101-DQB10501   39      TRGVYYPDKVFRSSV  RGVYYPDKV  1        0.2676
2764.2    35.00  0.54     Sequence
 HLA-DQA10101-DQB10501   40      RGVYYPDKVFRSSVL  RGVYYPDKV  0        0.2356
3906.3    43.00  0.49     Sequence
```

```
 HLA-DQA10101-DQB10501   41      GVYYPDKVFRSSVLH  PDKVFRSSV  4         0.1786
7236.9    60.00  0.37     Sequence
 HLA-DQA10101-DQB10501   42      VYYPDKVFRSSVLHS  PDKVFRSSV  3         0.1587
8980.3    65.00  0.44     Sequence
 HLA-DQA10101-DQB10501   43      YYPDKVFRSSVLHST  PDKVFRSSV  2         0.1547
9377.9    65.00  0.46     Sequence
 HLA-DQA10101-DQB10501   44      YPDKVFRSSVLHSTQ  VFRSSVLHS  4         0.1554
9309.3    65.00  0.44     Sequence
 HLA-DQA10101-DQB10501   45      PDKVFRSSVLHSTQD  VFRSSVLHS  3         0.1441
10518.0    70.00  0.49     Sequence
 HLA-DQA10101-DQB10501   46      DKVFRSSVLHSTQDL  VFRSSVLHS  2         0.1658
8314.6    65.00  0.46     Sequence
 HLA-DQA10101-DQB10501   47      KVFRSSVLHSTQDLF  VLHSTQDLF  6         0.2167
4793.7    47.00  0.25     Sequence
 HLA-DQA10101-DQB10501   48      VFRSSVLHSTQDLFL  VLHSTQDLF  5         0.3552
1070.9    19.00  0.59     Sequence
 HLA-DQA10101-DQB10501   49      FRSSVLHSTQDLFLP  VLHSTQDLF  4         0.4137
568.7    12.00  0.68    Sequence
 HLA-DQA10101-DQB10501   50      RSSVLHSTQDLFLPF  VLHSTQDLF  3         0.4477
393.9     9.00  0.59    Sequence         WB
 HLA-DQA10101-DQB10501   51      SSVLHSTQDLFLPFF  VLHSTQDLF  2         0.4774
285.4     7.00  0.43    Sequence         WB
 HLA-DQA10101-DQB10501   52      SVLHSTQDLFLPFFS  VLHSTQDLF  1         0.4811
274.2     6.50  0.36    Sequence         WB
 HLA-DQA10101-DQB10501   53      VLHSTQDLFLPFFSN  STQDLFLPF  3         0.4481
392.0     9.00  0.41    Sequence         WB
 HLA-DQA10101-DQB10501   54      LHSTQDLFLPFFSNV  STQDLFLPF  2         0.4197
533.2    12.00  0.44    Sequence
 HLA-DQA10101-DQB10501   55      HSTQDLFLPFFSNVT  STQDLFLPF  1         0.3857
770.4    15.00  0.41    Sequence
 HLA-DQA10101-DQB10501   56      STQDLFLPFFSNVTW  LFLPFFSNV  4         0.3926
714.5    14.00  0.39    Sequence
 HLA-DQA10101-DQB10501   57      TQDLFLPFFSNVTWF  LFLPFFSNV  3         0.3818
803.3    16.00  0.43    Sequence
 HLA-DQA10101-DQB10501   58      QDLFLPFFSNVTWFH  LFLPFFSNV  2         0.3564
1057.8    19.00  0.47     Sequence
 HLA-DQA10101-DQB10501   59      DLFLPFFSNVTWFHA  LFLPFFSNV  1         0.3345
1340.5    22.00  0.43     Sequence
 HLA-DQA10101-DQB10501   60      LFLPFFSNVTWFHAI  LFLPFFSNV  0         0.3235
1510.3    24.00  0.32     Sequence
 HLA-DQA10101-DQB10501   61      FLPFFSNVTWFHAIH  SNVTWFHAI  5         0.3122
1706.2    26.00  0.20     Sequence
 HLA-DQA10101-DQB10501   62      LPFFSNVTWFHAIHV  NVTWFHAIH  5         0.3796
822.5    16.00  0.38    Sequence
 HLA-DQA10101-DQB10501   63      PFFSNVTWFHAIHVS  NVTWFHAIH  4         0.4031
637.8    13.00  0.50    Sequence
 HLA-DQA10101-DQB10501   64      FFSNVTWFHAIHVSG  NVTWFHAIH  3         0.4026
641.3    13.00  0.49    Sequence
 HLA-DQA10101-DQB10501   65      FSNVTWFHAIHVSGT  NVTWFHAIH  2         0.3873
756.7    15.00  0.52    Sequence
 HLA-DQA10101-DQB10501   66      SNVTWFHAIHVSGTN  NVTWFHAIH  1         0.3576
1043.9    19.00  0.54     Sequence
 HLA-DQA10101-DQB10501   67      NVTWFHAIHVSGTNG  NVTWFHAIH  0         0.3177
1606.9    25.00  0.47     Sequence
 HLA-DQA10101-DQB10501   68      VTWFHAIHVSGTNGT  XVTWFHAIH -1         0.2512
3301.1    39.00  0.31     Sequence
 HLA-DQA10101-DQB10501   69      TWFHAIHVSGTNGTK  WFHAIHVSG  1         0.1492
9951.4    70.00  0.41     Sequence
 HLA-DQA10101-DQB10501   70      WFHAIHVSGTNGTKR  WFHAIHVSG  0         0.1023
16527.4    85.00  0.38     Sequence
 HLA-DQA10101-DQB10501   71      FHAIHVSGTNGTKRF  FHAIHVSGT  0         0.0421
31689.7   100.00  0.38     Sequence
 HLA-DQA10101-DQB10501   72      HAIHVSGTNGTKRFD  IHVSGTNGT  2         0.0165
41837.8   100.00  0.26     Sequence
 HLA-DQA10101-DQB10501   73      AIHVSGTNGTKRFDN  HVSGTNGTK  2         0.0185
40941.7   100.00  0.20     Sequence
```

```
 HLA-DQA10101-DQB10501   74      IHVSGTNGTKRFDNP  GTNGTKRFD  4         0.0286
36692.7   100.00  0.28     Sequence
 HLA-DQA10101-DQB10501   75      HVSGTNGTKRFDNPV  NGTKRFDNP  5         0.0747
22274.2    90.00  0.38     Sequence
 HLA-DQA10101-DQB10501   76      VSGTNGTKRFDNPVL  GTKRFDNPV  5         0.1835
6866.5    60.00  0.50     Sequence
 HLA-DQA10101-DQB10501   77      SGTNGTKRFDNPVLP  GTKRFDNPV  4         0.2286
4213.9    44.00  0.50     Sequence
 HLA-DQA10101-DQB10501   78      GTNGTKRFDNPVLPF  GTKRFDNPV  3         0.3100
1747.9    26.00  0.38     Sequence
 HLA-DQA10101-DQB10501   79      TNGTKRFDNPVLPFN  RFDNPVLPF  5         0.3290
1422.6    23.00  0.35     Sequence
 HLA-DQA10101-DQB10501   80      NGTKRFDNPVLPFND  RFDNPVLPF  4         0.3255
1477.7    24.00  0.40     Sequence
 HLA-DQA10101-DQB10501   81      GTKRFDNPVLPFNDG  RFDNPVLPF  3         0.3046
1851.2    27.00  0.41     Sequence
 HLA-DQA10101-DQB10501   82      TKRFDNPVLPFNDGV  RFDNPVLPF  2         0.3023
1899.3    28.00  0.35     Sequence
 HLA-DQA10101-DQB10501   83      KRFDNPVLPFNDGVY  PVLPFNDGV  5         0.3909
727.7    15.00  0.51     Sequence
 HLA-DQA10101-DQB10501   84      RFDNPVLPFNDGVYF  PVLPFNDGV  4         0.4341
456.4    10.00  0.65     Sequence
 HLA-DQA10101-DQB10501   85      FDNPVLPFNDGVYFA  PVLPFNDGV  3         0.4242
507.9    11.00  0.75     Sequence
 HLA-DQA10101-DQB10501   86      DNPVLPFNDGVYFAS  PVLPFNDGV  2         0.4206
527.8    12.00  0.71     Sequence
 HLA-DQA10101-DQB10501   87      NPVLPFNDGVYFAST  PVLPFNDGV  1         0.4092
597.0    13.00  0.70     Sequence
 HLA-DQA10101-DQB10501   88      PVLPFNDGVYFASTE  PVLPFNDGV  0         0.3673
939.9    18.00  0.57     Sequence
 HLA-DQA10101-DQB10501   89      VLPFNDGVYFASTEK  XVLPFNDGV -1         0.2737
2587.9    34.00  0.36     Sequence
 HLA-DQA10101-DQB10501   90      LPFNDGVYFASTEKS  FNDGVYFAS  2         0.1711
7852.4    60.00  0.23     Sequence
 HLA-DQA10101-DQB10501   91      PFNDGVYFASTEKSN  NDGVYFAST  2         0.1351
11593.0    75.00  0.27     Sequence
 HLA-DQA10101-DQB10501   92      FNDGVYFASTEKSNI  NDGVYFAST  1         0.1269
12665.4    75.00  0.28     Sequence
 HLA-DQA10101-DQB10501   93      NDGVYFASTEKSNII  DGVYFASTE  1         0.1010
16769.7    85.00  0.28     Sequence
 HLA-DQA10101-DQB10501   94      DGVYFASTEKSNIIR  DGVYFASTE  0         0.0851
19916.6    90.00  0.23     Sequence
 HLA-DQA10101-DQB10501   95      GVYFASTEKSNIIRG  FASTEKSNI  3         0.0644
24900.6    95.00  0.31     Sequence
 HLA-DQA10101-DQB10501   96      VYFASTEKSNIIRGW  FASTEKSNI  2         0.0644
24899.6    95.00  0.33     Sequence
 HLA-DQA10101-DQB10501   97      YFASTEKSNIIRGWI  TEKSNIIRG  4         0.0774
21642.3    90.00  0.31     Sequence
 HLA-DQA10101-DQB10501   98      FASTEKSNIIRGWIF  EKSNIIRGW  4         0.1092
15333.5    80.00  0.34     Sequence
 HLA-DQA10101-DQB10501   99      ASTEKSNIIRGWIFG  EKSNIIRGW  3         0.1538
9464.8    65.00  0.31     Sequence
 HLA-DQA10101-DQB10501  100      STEKSNIIRGWIFGT  IIRGWIFGT  6         0.2554
3154.7    38.00  0.40     Sequence
 HLA-DQA10101-DQB10501  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5         0.3275
1445.4    23.00  0.60     Sequence
 HLA-DQA10101-DQB10501  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4         0.4090
598.5    13.00  0.64     Sequence
 HLA-DQA10101-DQB10501  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3         0.4238
509.9    11.00  0.61     Sequence
 HLA-DQA10101-DQB10501  104      SNIIRGWIFGTTLDS  IIRGWIFGT  2         0.4280
487.5    11.00  0.50     Sequence
 HLA-DQA10101-DQB10501  105      NIIRGWIFGTTLDSK  IIRGWIFGT  1         0.4090
598.8    13.00  0.49     Sequence
 HLA-DQA10101-DQB10501  106      IIRGWIFGTTLDSKT  IIRGWIFGT  0         0.3719
894.5    17.00  0.39     Sequence
```

```
 HLA-DQA10101-DQB10501  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3        0.2967
2017.7    29.00  0.38     Sequence
 HLA-DQA10101-DQB10501  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2        0.2428
3613.4    41.00  0.43     Sequence
 HLA-DQA10101-DQB10501  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1        0.1929
6203.8    55.00  0.49     Sequence
 HLA-DQA10101-DQB10501  110      WIFGTTLDSKTQSLL  WIFGTTLDS  0        0.1669
8217.3    65.00  0.39     Sequence
 HLA-DQA10101-DQB10501  111      IFGTTLDSKTQSLLI  IFGTTLDSK  0        0.0791
21257.3    90.00  0.32     Sequence
 HLA-DQA10101-DQB10501  112      FGTTLDSKTQSLLIV  TTLDSKTQS  2        0.0730
22705.4    90.00  0.27     Sequence
 HLA-DQA10101-DQB10501  113      GTTLDSKTQSLLIVN  TTLDSKTQS  1        0.0736
22559.7    90.00  0.21     Sequence
 HLA-DQA10101-DQB10501  114      TTLDSKTQSLLIVNN  KTQSLLIVN  5        0.0925
18383.1    85.00  0.34     Sequence
 HLA-DQA10101-DQB10501  115      TLDSKTQSLLIVNNA  TQSLLIVNN  5        0.1463
10266.5    70.00  0.38     Sequence
 HLA-DQA10101-DQB10501  116      LDSKTQSLLIVNNAT  TQSLLIVNN  4        0.1604
8813.4    65.00  0.43     Sequence
 HLA-DQA10101-DQB10501  117      DSKTQSLLIVNNATN  TQSLLIVNN  3        0.1620
8660.1    65.00  0.38     Sequence
 HLA-DQA10101-DQB10501  118      SKTQSLLIVNNATNV  TQSLLIVNN  2        0.1898
6416.3    55.00  0.30     Sequence
 HLA-DQA10101-DQB10501  119      KTQSLLIVNNATNVV  LIVNNATNV  5        0.2082
5255.5    50.00  0.31     Sequence
 HLA-DQA10101-DQB10501  120      TQSLLIVNNATNVVI  LIVNNATNV  4        0.2410
3687.6    41.00  0.34     Sequence
 HLA-DQA10101-DQB10501  121      QSLLIVNNATNVVIK  LIVNNATNV  3        0.2223
4512.0    46.00  0.34     Sequence
 HLA-DQA10101-DQB10501  122      SLLIVNNATNVVIKV  LIVNNATNV  2        0.2121
5037.2    48.00  0.36     Sequence
 HLA-DQA10101-DQB10501  123      LLIVNNATNVVIKVC  LIVNNATNV  1        0.1986
5832.2    55.00  0.35     Sequence
 HLA-DQA10101-DQB10501  124      LIVNNATNVVIKVCE  IVNNATNVV  1        0.1647
8410.8    65.00  0.35     Sequence
 HLA-DQA10101-DQB10501  125      IVNNATNVVIKVCEF  NATNVVIKV  3        0.1394
11069.7    70.00  0.19     Sequence
 HLA-DQA10101-DQB10501  126      VNNATNVVIKVCEFQ  NVVIKVCEF  5        0.1411
10868.1    70.00  0.23     Sequence
 HLA-DQA10101-DQB10501  127      NNATNVVIKVCEFQF  NVVIKVCEF  4        0.1564
9209.6    65.00  0.28     Sequence
 HLA-DQA10101-DQB10501  128      NATNVVIKVCEFQFC  NVVIKVCEF  3        0.1841
6824.5    60.00  0.26     Sequence
 HLA-DQA10101-DQB10501  129      ATNVVIKVCEFQFCN  NVVIKVCEF  2        0.1774
7333.8    60.00  0.28     Sequence
 HLA-DQA10101-DQB10501  130      TNVVIKVCEFQFCNY  NVVIKVCEF  1        0.2270
4286.7    45.00  0.16     Sequence
 HLA-DQA10101-DQB10501  131      NVVIKVCEFQFCNYP  VCEFQFCNY  5        0.2502
3338.0    39.00  0.26     Sequence
 HLA-DQA10101-DQB10501  132      VVIKVCEFQFCNYPF  VCEFQFCNY  4        0.3138
1676.2    26.00  0.34     Sequence
 HLA-DQA10101-DQB10501  133      VIKVCEFQFCNYPFL  CEFQFCNYP  4        0.3845
779.9    15.00  0.37     Sequence
 HLA-DQA10101-DQB10501  134      IKVCEFQFCNYPFLG  CEFQFCNYP  3        0.3829
793.9    16.00  0.34     Sequence
 HLA-DQA10101-DQB10501  135      KVCEFQFCNYPFLGV  CEFQFCNYP  2        0.4159
555.3    12.00  0.29     Sequence
 HLA-DQA10101-DQB10501  136      VCEFQFCNYPFLGVY  CEFQFCNYP  1        0.4255
500.7    11.00  0.28     Sequence
 HLA-DQA10101-DQB10501  137      CEFQFCNYPFLGVYY  FCNYPFLGV  4        0.4079
605.6    13.00  0.28     Sequence
 HLA-DQA10101-DQB10501  138      EFQFCNYPFLGVYYH  FCNYPFLGV  3        0.3855
772.1    15.00  0.32     Sequence
 HLA-DQA10101-DQB10501  139      FQFCNYPFLGVYYHK  FCNYPFLGV  2        0.3284
1431.9    23.00  0.37     Sequence
```

```
 HLA-DQA10101-DQB10501  140      QFCNYPFLGVYYHKN  FCNYPFLGV  1        0.2768
2503.1    33.00  0.42     Sequence
 HLA-DQA10101-DQB10501  141      FCNYPFLGVYYHKNN  FCNYPFLGV  0        0.2492
3372.6    39.00  0.34     Sequence
 HLA-DQA10101-DQB10501  142      CNYPFLGVYYHKNNK  PFLGVYYHK  3        0.1775
7329.8    60.00  0.20     Sequence
 HLA-DQA10101-DQB10501  143      NYPFLGVYYHKNNKS  PFLGVYYHK  2        0.1627
8597.5    65.00  0.22     Sequence
 HLA-DQA10101-DQB10501  144      YPFLGVYYHKNNKSW  FLGVYYHKN  2        0.1484
10038.0    70.00  0.22     Sequence
 HLA-DQA10101-DQB10501  145      PFLGVYYHKNNKSWM  GVYYHKNNK  3        0.1296
12305.7    75.00  0.29     Sequence
 HLA-DQA10101-DQB10501  146      FLGVYYHKNNKSWME  GVYYHKNNK  2        0.1268
12685.3    75.00  0.30     Sequence
 HLA-DQA10101-DQB10501  147      LGVYYHKNNKSWMES  GVYYHKNNK  1        0.1110
15036.9    80.00  0.35     Sequence
 HLA-DQA10101-DQB10501  148      GVYYHKNNKSWMESE  NNKSWMESE  6        0.1283
12482.4    75.00  0.26     Sequence
 HLA-DQA10101-DQB10501  149      VYYHKNNKSWMESEF  NNKSWMESE  5        0.2395
3744.2    42.00  0.49     Sequence
 HLA-DQA10101-DQB10501  150      YYHKNNKSWMESEFR  NNKSWMESE  4        0.2698
2698.5    35.00  0.61     Sequence
 HLA-DQA10101-DQB10501  151      YHKNNKSWMESEFRV  NNKSWMESE  3        0.3054
1836.2    27.00  0.58     Sequence
 HLA-DQA10101-DQB10501  152      HKNNKSWMESEFRVY  NNKSWMESE  2        0.3813
807.5    16.00  0.41     Sequence
 HLA-DQA10101-DQB10501  153      KNNKSWMESEFRVYS  NNKSWMESE  1        0.3863
765.3    15.00  0.38     Sequence
 HLA-DQA10101-DQB10501  154      NNKSWMESEFRVYSS  NNKSWMESE  0        0.3915
723.1    15.00  0.30     Sequence
 HLA-DQA10101-DQB10501  155      NKSWMESEFRVYSSA  MESEFRVYS  4        0.3795
823.4    16.00  0.36     Sequence
 HLA-DQA10101-DQB10501  156      KSWMESEFRVYSSAN  MESEFRVYS  3        0.3374
1298.3    22.00  0.47     Sequence
 HLA-DQA10101-DQB10501  157      SWMESEFRVYSSANN  MESEFRVYS  2        0.3198
1570.8    25.00  0.47     Sequence
 HLA-DQA10101-DQB10501  158      WMESEFRVYSSANNC  MESEFRVYS  1        0.2943
2070.8    29.00  0.46     Sequence
 HLA-DQA10101-DQB10501  159      MESEFRVYSSANNCT  MESEFRVYS  0        0.2405
3705.7    41.00  0.34     Sequence
 HLA-DQA10101-DQB10501  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.2249
4389.0    45.00  0.28     Sequence
 HLA-DQA10101-DQB10501  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.1948
6078.0    55.00  0.31     Sequence
 HLA-DQA10101-DQB10501  162      EFRVYSSANNCTFEY  FRVYSSANN  1        0.1811
7046.2    60.00  0.28     Sequence
 HLA-DQA10101-DQB10501  163      FRVYSSANNCTFEYV  FRVYSSANN  0        0.1690
8031.9    60.00  0.20     Sequence
 HLA-DQA10101-DQB10501  164      RVYSSANNCTFEYVS  SANNCTFEY  4        0.1404
10941.6    70.00  0.17     Sequence
 HLA-DQA10101-DQB10501  165      VYSSANNCTFEYVSQ  ANNCTFEYV  4        0.1391
11098.1    70.00  0.19     Sequence
 HLA-DQA10101-DQB10501  166      YSSANNCTFEYVSQP  NCTFEYVSQ  5        0.1555
9296.3    65.00  0.29     Sequence
 HLA-DQA10101-DQB10501  167      SSANNCTFEYVSQPF  NCTFEYVSQ  4        0.2073
5308.7    50.00  0.30     Sequence
 HLA-DQA10101-DQB10501  168      SANNCTFEYVSQPFL  CTFEYVSQP  4        0.2715
2648.7    34.00  0.35     Sequence
 HLA-DQA10101-DQB10501  169      ANNCTFEYVSQPFLM  TFEYVSQPF  4        0.2950
2055.9    29.00  0.28     Sequence
 HLA-DQA10101-DQB10501  170      NNCTFEYVSQPFLMD  TFEYVSQPF  3        0.3164
1630.0    25.00  0.31     Sequence
 HLA-DQA10101-DQB10501  171      NCTFEYVSQPFLMDL  TFEYVSQPF  2        0.3880
750.9    15.00  0.25     Sequence
 HLA-DQA10101-DQB10501  172      CTFEYVSQPFLMDLE  VSQPFLMDL  5        0.4561
359.4     8.50  0.54     Sequence          WB
```

```
 HLA-DQA10101-DQB10501  173      TFEYVSQPFLMDLEG  VSQPFLMDL  4        0.4822
271.1     6.50  0.64     Sequence        WB
 HLA-DQA10101-DQB10501  174      FEYVSQPFLMDLEGK  VSQPFLMDL  3        0.4568
356.7     8.00  0.68     Sequence        WB
 HLA-DQA10101-DQB10501  175      EYVSQPFLMDLEGKQ  VSQPFLMDL  2        0.4408
424.2     9.50  0.69     Sequence        WB
 HLA-DQA10101-DQB10501  176      YVSQPFLMDLEGKQG  VSQPFLMDL  1        0.4019
646.5    13.00  0.68     Sequence
 HLA-DQA10101-DQB10501  177      VSQPFLMDLEGKQGN  VSQPFLMDL  0        0.3350
1332.3    22.00  0.57     Sequence
 HLA-DQA10101-DQB10501  178      SQPFLMDLEGKQGNF  XSQPFLMDL -1        0.2521
3269.0    39.00  0.32     Sequence
 HLA-DQA10101-DQB10501  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2        0.1660
8299.6    65.00  0.32     Sequence
 HLA-DQA10101-DQB10501  180      PFLMDLEGKQGNFKN  FLMDLEGKQ  1        0.1121
14871.2    80.00  0.39     Sequence
 HLA-DQA10101-DQB10501  181      FLMDLEGKQGNFKNL  FLMDLEGKQ  0        0.0954
17818.5    85.00  0.31     Sequence
 HLA-DQA10101-DQB10501  182      LMDLEGKQGNFKNLS  GKQGNFKNL  5        0.0625
25433.5    95.00  0.25     Sequence
 HLA-DQA10101-DQB10501  183      MDLEGKQGNFKNLSE  KQGNFKNLS  5        0.0895
18978.3    85.00  0.42     Sequence
 HLA-DQA10101-DQB10501  184      DLEGKQGNFKNLSEF  KQGNFKNLS  4        0.1098
15240.0    80.00  0.50     Sequence
 HLA-DQA10101-DQB10501  185      LEGKQGNFKNLSEFV  KQGNFKNLS  3        0.1317
12021.6    75.00  0.38     Sequence
 HLA-DQA10101-DQB10501  186      EGKQGNFKNLSEFVF  KQGNFKNLS  2        0.1598
8872.3    65.00  0.25     Sequence
 HLA-DQA10101-DQB10501  187      GKQGNFKNLSEFVFK  NFKNLSEFV  4        0.1564
9204.9    65.00  0.27     Sequence
 HLA-DQA10101-DQB10501  188      KQGNFKNLSEFVFKN  NFKNLSEFV  3        0.1520
9652.5    70.00  0.25     Sequence
 HLA-DQA10101-DQB10501  189      QGNFKNLSEFVFKNI  NLSEFVFKN  5        0.2161
4825.1    47.00  0.38     Sequence
 HLA-DQA10101-DQB10501  190      GNFKNLSEFVFKNID  NLSEFVFKN  4        0.2327
4031.6    43.00  0.41     Sequence
 HLA-DQA10101-DQB10501  191      NFKNLSEFVFKNIDG  NLSEFVFKN  3        0.2293
4181.2    44.00  0.41     Sequence
 HLA-DQA10101-DQB10501  192      FKNLSEFVFKNIDGY  FVFKNIDGY  6        0.3229
1520.1    24.00  0.28     Sequence
 HLA-DQA10101-DQB10501  193      KNLSEFVFKNIDGYF  FVFKNIDGY  5        0.3800
819.2    16.00  0.49     Sequence
 HLA-DQA10101-DQB10501  194      NLSEFVFKNIDGYFK  FVFKNIDGY  4        0.3762
853.9    16.00  0.50     Sequence
 HLA-DQA10101-DQB10501  195      LSEFVFKNIDGYFKI  FVFKNIDGY  3        0.3899
735.5    15.00  0.44     Sequence
 HLA-DQA10101-DQB10501  196      SEFVFKNIDGYFKIY  FVFKNIDGY  2        0.3826
796.0    16.00  0.44     Sequence
 HLA-DQA10101-DQB10501  197      EFVFKNIDGYFKIYS  FVFKNIDGY  1        0.4014
650.0    13.00  0.34     Sequence
 HLA-DQA10101-DQB10501  198      FVFKNIDGYFKIYSK  NIDGYFKIY  4        0.4208
526.8    12.00  0.34     Sequence
 HLA-DQA10101-DQB10501  199      VFKNIDGYFKIYSKH  IDGYFKIYS  4        0.3932
710.1    14.00  0.41     Sequence
 HLA-DQA10101-DQB10501  200      FKNIDGYFKIYSKHT  IDGYFKIYS  3        0.3761
854.2    16.00  0.47     Sequence
 HLA-DQA10101-DQB10501  201      KNIDGYFKIYSKHTP  IDGYFKIYS  2        0.3629
985.5    18.00  0.50     Sequence
 HLA-DQA10101-DQB10501  202      NIDGYFKIYSKHTPI  IDGYFKIYS  1        0.3311
1390.9    23.00  0.51     Sequence
 HLA-DQA10101-DQB10501  203      IDGYFKIYSKHTPIN  IDGYFKIYS  0        0.2853
2281.8    31.00  0.49     Sequence
 HLA-DQA10101-DQB10501  204      DGYFKIYSKHTPINL  XDGYFKIYS -1        0.2318
4071.4    43.00  0.31     Sequence
 HLA-DQA10101-DQB10501  205      GYFKIYSKHTPINLV  YSKHTPINL  5        0.1990
5804.7    55.00  0.36     Sequence
```

```
 HLA-DQA10101-DQB10501  206      YFKIYSKHTPINLVR  YSKHTPINL  4         0.1845
6791.9    60.00  0.45     Sequence
 HLA-DQA10101-DQB10501  207      FKIYSKHTPINLVRD  YSKHTPINL  3         0.1733
7668.5    60.00  0.50     Sequence
 HLA-DQA10101-DQB10501  208      KIYSKHTPINLVRDL  YSKHTPINL  2         0.1693
8006.3    60.00  0.54     Sequence
 HLA-DQA10101-DQB10501  209      IYSKHTPINLVRDLP  YSKHTPINL  1         0.1706
7898.3    60.00  0.49     Sequence
 HLA-DQA10101-DQB10501  210      YSKHTPINLVRDLPQ  PINLVRDLP  5         0.2577
3076.1    37.00  0.38     Sequence
 HLA-DQA10101-DQB10501  211      SKHTPINLVRDLPQG  PINLVRDLP  4         0.2703
2685.0    34.00  0.50     Sequence
 HLA-DQA10101-DQB10501  212      KHTPINLVRDLPQGF  PINLVRDLP  3         0.2952
2050.6    29.00  0.50     Sequence
 HLA-DQA10101-DQB10501  213      HTPINLVRDLPQGFS  PINLVRDLP  2         0.2975
1999.3    29.00  0.50     Sequence
 HLA-DQA10101-DQB10501  214      TPINLVRDLPQGFSA  PINLVRDLP  1         0.2922
2118.0    30.00  0.49     Sequence
 HLA-DQA10101-DQB10501  215      PINLVRDLPQGFSAL  PINLVRDLP  0         0.2811
2389.6    32.00  0.40     Sequence
 HLA-DQA10101-DQB10501  216      INLVRDLPQGFSALE  LVRDLPQGF  2         0.2736
2589.8    34.00  0.22     Sequence
 HLA-DQA10101-DQB10501  217      NLVRDLPQGFSALEP  LPQGFSALE  5         0.2510
3306.2    39.00  0.34     Sequence
 HLA-DQA10101-DQB10501  218      LVRDLPQGFSALEPL  LPQGFSALE  4         0.3554
1069.1    19.00  0.41     Sequence
 HLA-DQA10101-DQB10501  219      VRDLPQGFSALEPLV  LPQGFSALE  3         0.3799
820.4    16.00  0.40     Sequence
 HLA-DQA10101-DQB10501  220      RDLPQGFSALEPLVD  LPQGFSALE  2         0.3818
803.5    16.00  0.38     Sequence
 HLA-DQA10101-DQB10501  221      DLPQGFSALEPLVDL  LPQGFSALE  1         0.4092
597.4    13.00  0.31     Sequence
 HLA-DQA10101-DQB10501  222      LPQGFSALEPLVDLP  PQGFSALEP  1         0.4190
537.0    12.00  0.25     Sequence
 HLA-DQA10101-DQB10501  223      PQGFSALEPLVDLPI  ALEPLVDLP  5         0.5184
183.2     4.50  0.35     Sequence         WB
 HLA-DQA10101-DQB10501  224      QGFSALEPLVDLPIG  ALEPLVDLP  4         0.5152
189.8     5.00  0.44     Sequence         WB
 HLA-DQA10101-DQB10501  225      GFSALEPLVDLPIGI  ALEPLVDLP  3         0.5189
182.2     4.50  0.51     Sequence         WB
 HLA-DQA10101-DQB10501  226      FSALEPLVDLPIGIN  ALEPLVDLP  2         0.5071
207.1     5.00  0.51     Sequence         WB
 HLA-DQA10101-DQB10501  227      SALEPLVDLPIGINI  ALEPLVDLP  1         0.4866
258.5     6.00  0.50     Sequence         WB
 HLA-DQA10101-DQB10501  228      ALEPLVDLPIGINIT  ALEPLVDLP  0         0.4200
531.2    12.00  0.46     Sequence
 HLA-DQA10101-DQB10501  229      LEPLVDLPIGINITR  XLEPLVDLP -1         0.3545
1080.0    19.00  0.37     Sequence
 HLA-DQA10101-DQB10501  230      EPLVDLPIGINITRF  PLVDLPIGI  1         0.2388
3774.1    42.00  0.33     Sequence
 HLA-DQA10101-DQB10501  231      PLVDLPIGINITRFQ  LPIGINITR  4         0.2147
4898.3    48.00  0.34     Sequence
 HLA-DQA10101-DQB10501  232      LVDLPIGINITRFQT  LPIGINITR  3         0.1894
6438.2    55.00  0.40     Sequence
 HLA-DQA10101-DQB10501  233      VDLPIGINITRFQTL  LPIGINITR  2         0.1971
5926.6    55.00  0.43     Sequence
 HLA-DQA10101-DQB10501  234      DLPIGINITRFQTLL  LPIGINITR  1         0.2057
5398.0    50.00  0.38     Sequence
 HLA-DQA10101-DQB10501  235      LPIGINITRFQTLLA  NITRFQTLL  5         0.2170
4776.9    47.00  0.31     Sequence
 HLA-DQA10101-DQB10501  236      PIGINITRFQTLLAL  NITRFQTLL  4         0.2533
3226.2    38.00  0.40     Sequence
 HLA-DQA10101-DQB10501  237      IGINITRFQTLLALH  NITRFQTLL  3         0.2542
3196.8    38.00  0.37     Sequence
 HLA-DQA10101-DQB10501  238      GINITRFQTLLALHR  NITRFQTLL  2         0.2393
3755.9    42.00  0.33     Sequence
```

```
 HLA-DQA10101-DQB10501  239      INITRFQTLLALHRS  NITRFQTLL  1        0.2356
3909.0    43.00  0.31     Sequence
 HLA-DQA10101-DQB10501  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.2227
4491.5    46.00  0.26     Sequence
 HLA-DQA10101-DQB10501  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.2558
3139.8    38.00  0.31     Sequence
 HLA-DQA10101-DQB10501  242      TRFQTLLALHRSYLT  TLLALHRSY  4        0.2679
2754.7    35.00  0.31     Sequence
 HLA-DQA10101-DQB10501  243      RFQTLLALHRSYLTP  TLLALHRSY  3        0.2942
2071.8    29.00  0.34     Sequence
 HLA-DQA10101-DQB10501  244      FQTLLALHRSYLTPG  TLLALHRSY  2        0.3028
1887.8    28.00  0.28     Sequence
 HLA-DQA10101-DQB10501  245      QTLLALHRSYLTPGD  LHRSYLTPG  5        0.3213
1546.1    24.00  0.37     Sequence
 HLA-DQA10101-DQB10501  246      TLLALHRSYLTPGDS  LHRSYLTPG  4        0.3192
1580.9    25.00  0.46     Sequence
 HLA-DQA10101-DQB10501  247      LLALHRSYLTPGDSS  LHRSYLTPG  3        0.2913
2139.0    30.00  0.53     Sequence
 HLA-DQA10101-DQB10501  248      LALHRSYLTPGDSSS  LHRSYLTPG  2        0.2561
3131.5    38.00  0.65     Sequence
 HLA-DQA10101-DQB10501  249      ALHRSYLTPGDSSSG  LHRSYLTPG  1        0.2150
4884.4    48.00  0.69     Sequence
 HLA-DQA10101-DQB10501  250      LHRSYLTPGDSSSGW  LHRSYLTPG  0        0.1514
9722.5    70.00  0.60     Sequence
 HLA-DQA10101-DQB10501  251      HRSYLTPGDSSSGWT  XHRSYLTPG -1        0.0729
22721.8    90.00  0.36     Sequence
 HLA-DQA10101-DQB10501  252      RSYLTPGDSSSGWTA  SYLTPGDSS  1        0.0396
32564.2   100.00  0.34     Sequence
 HLA-DQA10101-DQB10501  253      SYLTPGDSSSGWTAG  YLTPGDSSS  1        0.0318
35452.8   100.00  0.32     Sequence
 HLA-DQA10101-DQB10501  254      YLTPGDSSSGWTAGA  SSSGWTAGA  6        0.0385
32965.9   100.00  0.28     Sequence
 HLA-DQA10101-DQB10501  255      LTPGDSSSGWTAGAA  SSSGWTAGA  5        0.0873
19443.2    85.00  0.59     Sequence
 HLA-DQA10101-DQB10501  256      TPGDSSSGWTAGAAA  SSSGWTAGA  4        0.1316
12041.3    75.00  0.69     Sequence
 HLA-DQA10101-DQB10501  257      PGDSSSGWTAGAAAY  SSSGWTAGA  3        0.1477
10116.7    70.00  0.64     Sequence
 HLA-DQA10101-DQB10501  258      GDSSSGWTAGAAAYY  SSSGWTAGA  2        0.2419
3649.8    41.00  0.39     Sequence
 HLA-DQA10101-DQB10501  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.2693
2713.9    35.00  0.41     Sequence
 HLA-DQA10101-DQB10501  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4        0.2546
3180.3    38.00  0.47     Sequence
 HLA-DQA10101-DQB10501  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.2778
2474.6    33.00  0.36     Sequence
 HLA-DQA10101-DQB10501  262      SGWTAGAAAYYVGYL  GAAAYYVGY  5        0.3384
1285.2    22.00  0.44     Sequence
 HLA-DQA10101-DQB10501  263      GWTAGAAAYYVGYLQ  GAAAYYVGY  4        0.4399
428.2     9.50  0.52    Sequence         WB
 HLA-DQA10101-DQB10501  264      WTAGAAAYYVGYLQP  GAAAYYVGY  3        0.4807
275.6     6.50  0.47    Sequence         WB
 HLA-DQA10101-DQB10501  265      TAGAAAYYVGYLQPR  GAAAYYVGY  2        0.5227
175.0     4.50  0.39    Sequence         WB
 HLA-DQA10101-DQB10501  266      AGAAAYYVGYLQPRT  YYVGYLQPR  5        0.5432
140.1     3.50  0.41    Sequence         WB
 HLA-DQA10101-DQB10501  267      GAAAYYVGYLQPRTF  YYVGYLQPR  4        0.5519
127.5     3.50  0.48    Sequence         WB
 HLA-DQA10101-DQB10501  268      AAAYYVGYLQPRTFL  YYVGYLQPR  3        0.5473
134.0     3.50  0.57    Sequence         WB
 HLA-DQA10101-DQB10501  269      AAYYVGYLQPRTFLL  YYVGYLQPR  2        0.5098
201.1     5.00  0.63    Sequence         WB
 HLA-DQA10101-DQB10501  270      AYYVGYLQPRTFLLK  YYVGYLQPR  1        0.4472
396.0     9.00  0.73    Sequence         WB
 HLA-DQA10101-DQB10501  271      YYVGYLQPRTFLLKY  YYVGYLQPR  0        0.3603
1014.1    18.00  0.61     Sequence
```

```
 HLA-DQA10101-DQB10501  272      YVGYLQPRTFLLKYN  XYVGYLQPR -1        0.2001
5735.6    55.00  0.28     Sequence
 HLA-DQA10101-DQB10501  273      VGYLQPRTFLLKYNE  QPRTFLLKY  4        0.2001
5739.3    55.00  0.45     Sequence
 HLA-DQA10101-DQB10501  274      GYLQPRTFLLKYNEN  QPRTFLLKY  3        0.1926
6219.6    55.00  0.44     Sequence
 HLA-DQA10101-DQB10501  275      YLQPRTFLLKYNENG  QPRTFLLKY  2        0.2142
4927.3    48.00  0.40     Sequence
 HLA-DQA10101-DQB10501  276      LQPRTFLLKYNENGT  QPRTFLLKY  1        0.2305
4128.3    44.00  0.31     Sequence
 HLA-DQA10101-DQB10501  277      QPRTFLLKYNENGTI  FLLKYNENG  4        0.2483
3403.9    39.00  0.43     Sequence
 HLA-DQA10101-DQB10501  278      PRTFLLKYNENGTIT  FLLKYNENG  3        0.2358
3899.6    42.00  0.48     Sequence
 HLA-DQA10101-DQB10501  279      RTFLLKYNENGTITD  FLLKYNENG  2        0.2310
4108.1    44.00  0.50     Sequence
 HLA-DQA10101-DQB10501  280      TFLLKYNENGTITDA  FLLKYNENG  1        0.2034
5535.6    55.00  0.54     Sequence
 HLA-DQA10101-DQB10501  281      FLLKYNENGTITDAV  FLLKYNENG  0        0.1920
6263.5    55.00  0.41     Sequence
 HLA-DQA10101-DQB10501  282      LLKYNENGTITDAVD  NENGTITDA  4        0.1545
9397.5    65.00  0.50     Sequence
 HLA-DQA10101-DQB10501  283      LKYNENGTITDAVDC  NENGTITDA  3        0.1651
8380.9    65.00  0.47     Sequence
 HLA-DQA10101-DQB10501  284      KYNENGTITDAVDCA  NENGTITDA  2        0.1811
7044.4    60.00  0.38     Sequence
 HLA-DQA10101-DQB10501  285      YNENGTITDAVDCAL  TITDAVDCA  5        0.2936
2087.2    30.00  0.50     Sequence
 HLA-DQA10101-DQB10501  286      NENGTITDAVDCALD  TITDAVDCA  4        0.3199
1569.0    25.00  0.60     Sequence
 HLA-DQA10101-DQB10501  287      ENGTITDAVDCALDP  TITDAVDCA  3        0.3381
1288.6    22.00  0.54     Sequence
 HLA-DQA10101-DQB10501  288      NGTITDAVDCALDPL  TITDAVDCA  2        0.3676
936.9    17.00  0.44     Sequence
 HLA-DQA10101-DQB10501  289      GTITDAVDCALDPLS  TITDAVDCA  1        0.3763
852.3    16.00  0.38     Sequence
 HLA-DQA10101-DQB10501  290      TITDAVDCALDPLSE  TITDAVDCA  0        0.3667
946.0    18.00  0.29     Sequence
 HLA-DQA10101-DQB10501  291      ITDAVDCALDPLSET  DAVDCALDP  2        0.3266
1459.1    24.00  0.28     Sequence
 HLA-DQA10101-DQB10501  292      TDAVDCALDPLSETK  AVDCALDPL  2        0.2649
2844.9    36.00  0.40     Sequence
 HLA-DQA10101-DQB10501  293      DAVDCALDPLSETKC  AVDCALDPL  1        0.2409
3688.1    41.00  0.43     Sequence
 HLA-DQA10101-DQB10501  294      AVDCALDPLSETKCT  AVDCALDPL  0        0.1851
6750.2    60.00  0.41     Sequence
 HLA-DQA10101-DQB10501  295      VDCALDPLSETKCTL  CALDPLSET  2        0.1048
16092.1    80.00  0.29     Sequence
 HLA-DQA10101-DQB10501  296      DCALDPLSETKCTLK  CALDPLSET  1        0.0704
23348.6    90.00  0.29     Sequence
 HLA-DQA10101-DQB10501  297      CALDPLSETKCTLKS  ALDPLSETK  1        0.0533
28091.6    95.00  0.32     Sequence
 HLA-DQA10101-DQB10501  298      ALDPLSETKCTLKSF  PLSETKCTL  3        0.0415
31925.1   100.00  0.33     Sequence
 HLA-DQA10101-DQB10501  299      LDPLSETKCTLKSFT  PLSETKCTL  2        0.0380
33152.2   100.00  0.35     Sequence
 HLA-DQA10101-DQB10501  300      DPLSETKCTLKSFTV  PLSETKCTL  1        0.0415
31927.5   100.00  0.28     Sequence
 HLA-DQA10101-DQB10501  301      PLSETKCTLKSFTVE  TKCTLKSFT  4        0.1297
12289.8    75.00  0.22     Sequence
 HLA-DQA10101-DQB10501  302      LSETKCTLKSFTVEK  TLKSFTVEK  6        0.1863
6658.2    55.00  0.40     Sequence
 HLA-DQA10101-DQB10501  303      SETKCTLKSFTVEKG  TLKSFTVEK  5        0.2803
2409.3    32.00  0.69     Sequence
 HLA-DQA10101-DQB10501  304      ETKCTLKSFTVEKGI  TLKSFTVEK  4        0.3482
1155.7    20.00  0.70     Sequence
```

```
 HLA-DQA10101-DQB10501  305      TKCTLKSFTVEKGIY  TLKSFTVEK  3        0.3518
1111.1    20.00  0.71     Sequence
 HLA-DQA10101-DQB10501  306      KCTLKSFTVEKGIYQ  TLKSFTVEK  2        0.3392
1274.0    22.00  0.71     Sequence
 HLA-DQA10101-DQB10501  307      CTLKSFTVEKGIYQT  TLKSFTVEK  1        0.3129
1693.2    26.00  0.73     Sequence
 HLA-DQA10101-DQB10501  308      TLKSFTVEKGIYQTS  TLKSFTVEK  0        0.2434
3590.6    41.00  0.62     Sequence
 HLA-DQA10101-DQB10501  309      LKSFTVEKGIYQTSN  XLKSFTVEK -1        0.1567
9171.2    65.00  0.37     Sequence
 HLA-DQA10101-DQB10501  310      KSFTVEKGIYQTSNF  VEKGIYQTS  4        0.1123
14836.2    80.00  0.37     Sequence
 HLA-DQA10101-DQB10501  311      SFTVEKGIYQTSNFR  VEKGIYQTS  3        0.0960
17694.6    85.00  0.41     Sequence
 HLA-DQA10101-DQB10501  312      FTVEKGIYQTSNFRV  VEKGIYQTS  2        0.1180
13950.5    80.00  0.35     Sequence
 HLA-DQA10101-DQB10501  313      TVEKGIYQTSNFRVQ  VEKGIYQTS  1        0.1499
9879.1    70.00  0.22     Sequence
 HLA-DQA10101-DQB10501  314      VEKGIYQTSNFRVQP  QTSNFRVQP  6        0.2043
5480.6    55.00  0.32     Sequence
 HLA-DQA10101-DQB10501  315      EKGIYQTSNFRVQPT  QTSNFRVQP  5        0.2858
2269.3    31.00  0.56     Sequence
 HLA-DQA10101-DQB10501  316      KGIYQTSNFRVQPTE  QTSNFRVQP  4        0.3448
1199.0    21.00  0.72     Sequence
 HLA-DQA10101-DQB10501  317      GIYQTSNFRVQPTES  QTSNFRVQP  3        0.3355
1326.4    22.00  0.71     Sequence
 HLA-DQA10101-DQB10501  318      IYQTSNFRVQPTESI  QTSNFRVQP  2        0.3443
1204.9    21.00  0.68     Sequence
 HLA-DQA10101-DQB10501  319      YQTSNFRVQPTESIV  QTSNFRVQP  1        0.3239
1503.3    24.00  0.64     Sequence
 HLA-DQA10101-DQB10501  320      QTSNFRVQPTESIVR  QTSNFRVQP  0        0.2677
2761.4    35.00  0.51     Sequence
 HLA-DQA10101-DQB10501  321      TSNFRVQPTESIVRF  XTSNFRVQP -1        0.2117
5062.5    49.00  0.34     Sequence
 HLA-DQA10101-DQB10501  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.1521
9641.6    65.00  0.28     Sequence
 HLA-DQA10101-DQB10501  323      NFRVQPTESIVRFPN  FRVQPTESI  1        0.1292
12359.1    75.00  0.28     Sequence
 HLA-DQA10101-DQB10501  324      FRVQPTESIVRFPNI  TESIVRFPN  5        0.1617
8694.4    65.00  0.22     Sequence
 HLA-DQA10101-DQB10501  325      RVQPTESIVRFPNIT  TESIVRFPN  4        0.1447
10445.6    70.00  0.34     Sequence
 HLA-DQA10101-DQB10501  326      VQPTESIVRFPNITN  TESIVRFPN  3        0.1512
9737.5    70.00  0.26     Sequence
 HLA-DQA10101-DQB10501  327      QPTESIVRFPNITNL  SIVRFPNIT  4        0.1852
6742.6    60.00  0.22     Sequence
 HLA-DQA10101-DQB10501  328      PTESIVRFPNITNLC  IVRFPNITN  4        0.1991
5796.9    55.00  0.31     Sequence
 HLA-DQA10101-DQB10501  329      TESIVRFPNITNLCP  IVRFPNITN  3        0.2108
5111.7    49.00  0.30     Sequence
 HLA-DQA10101-DQB10501  330      ESIVRFPNITNLCPF  IVRFPNITN  2        0.2075
5295.2    50.00  0.32     Sequence
 HLA-DQA10101-DQB10501  331      SIVRFPNITNLCPFG  IVRFPNITN  1        0.1786
7240.3    60.00  0.34     Sequence
 HLA-DQA10101-DQB10501  332      IVRFPNITNLCPFGE  IVRFPNITN  0        0.1670
8206.1    65.00  0.25     Sequence
 HLA-DQA10101-DQB10501  333      VRFPNITNLCPFGEV  PNITNLCPF  3        0.1650
8387.6    65.00  0.17     Sequence
 HLA-DQA10101-DQB10501  334      RFPNITNLCPFGEVF  NLCPFGEVF  6        0.1835
6867.0    60.00  0.24     Sequence
 HLA-DQA10101-DQB10501  335      FPNITNLCPFGEVFN  NLCPFGEVF  5        0.2222
4515.3    46.00  0.47     Sequence
 HLA-DQA10101-DQB10501  336      PNITNLCPFGEVFNA  NLCPFGEVF  4        0.2615
2951.6    36.00  0.56     Sequence
 HLA-DQA10101-DQB10501  337      NITNLCPFGEVFNAT  NLCPFGEVF  3        0.2627
2913.9    36.00  0.56     Sequence
```

```
 HLA-DQA10101-DQB10501  338      ITNLCPFGEVFNATR  NLCPFGEVF  2         0.2513
3298.3    39.00  0.55     Sequence
 HLA-DQA10101-DQB10501  339      TNLCPFGEVFNATRF  NLCPFGEVF  1         0.2447
3540.7    40.00  0.51     Sequence
 HLA-DQA10101-DQB10501  340      NLCPFGEVFNATRFA  NLCPFGEVF  0         0.2314
4087.8    44.00  0.30     Sequence
 HLA-DQA10101-DQB10501  341      LCPFGEVFNATRFAS  FGEVFNATR  3         0.2129
4996.0    48.00  0.33     Sequence
 HLA-DQA10101-DQB10501  342      CPFGEVFNATRFASV  FGEVFNATR  2         0.2365
3869.1    42.00  0.28     Sequence
 HLA-DQA10101-DQB10501  343      PFGEVFNATRFASVY  FGEVFNATR  1         0.2368
3856.4    42.00  0.27     Sequence
 HLA-DQA10101-DQB10501  344      FGEVFNATRFASVYA  FNATRFASV  4         0.2427
3619.6    41.00  0.25     Sequence
 HLA-DQA10101-DQB10501  345      GEVFNATRFASVYAW  NATRFASVY  4         0.2607
2978.7    37.00  0.24     Sequence
 HLA-DQA10101-DQB10501  346      EVFNATRFASVYAWN  NATRFASVY  3         0.2538
3210.2    38.00  0.26     Sequence
 HLA-DQA10101-DQB10501  347      VFNATRFASVYAWNR  NATRFASVY  2         0.2280
4243.9    44.00  0.26     Sequence
 HLA-DQA10101-DQB10501  348      FNATRFASVYAWNRK  NATRFASVY  1         0.2086
5235.2    49.00  0.22     Sequence
 HLA-DQA10101-DQB10501  349      NATRFASVYAWNRKR  ATRFASVYA  1         0.1713
7837.7    60.00  0.20     Sequence
 HLA-DQA10101-DQB10501  350      ATRFASVYAWNRKRI  SVYAWNRKR  5         0.2458
3498.7    40.00  0.32     Sequence
 HLA-DQA10101-DQB10501  351      TRFASVYAWNRKRIS  SVYAWNRKR  4         0.2804
2407.2    32.00  0.44     Sequence
 HLA-DQA10101-DQB10501  352      RFASVYAWNRKRISN  SVYAWNRKR  3         0.2721
2632.1    34.00  0.47     Sequence
 HLA-DQA10101-DQB10501  353      FASVYAWNRKRISNC  SVYAWNRKR  2         0.2808
2395.1    32.00  0.44     Sequence
 HLA-DQA10101-DQB10501  354      ASVYAWNRKRISNCV  SVYAWNRKR  1         0.2652
2836.4    36.00  0.45     Sequence
 HLA-DQA10101-DQB10501  355      SVYAWNRKRISNCVA  SVYAWNRKR  0         0.2459
3494.9    40.00  0.39     Sequence
 HLA-DQA10101-DQB10501  356      VYAWNRKRISNCVAD  XVYAWNRKR -1         0.2071
5321.5    50.00  0.31     Sequence
 HLA-DQA10101-DQB10501  357      YAWNRKRISNCVADY  WNRKRISNC  2         0.1746
7557.1    60.00  0.22     Sequence
 HLA-DQA10101-DQB10501  358      AWNRKRISNCVADYS  RISNCVADY  5         0.1867
6635.9    55.00  0.41     Sequence
 HLA-DQA10101-DQB10501  359      WNRKRISNCVADYSV  RISNCVADY  4         0.2240
4431.7    45.00  0.44     Sequence
 HLA-DQA10101-DQB10501  360      NRKRISNCVADYSVL  RISNCVADY  3         0.2825
2351.4    32.00  0.39     Sequence
 HLA-DQA10101-DQB10501  361      RKRISNCVADYSVLY  RISNCVADY  2         0.3189
1585.8    25.00  0.29     Sequence
 HLA-DQA10101-DQB10501  362      KRISNCVADYSVLYN  CVADYSVLY  5         0.3344
1341.4    22.00  0.37     Sequence
 HLA-DQA10101-DQB10501  363      RISNCVADYSVLYNS  CVADYSVLY  4         0.3271
1452.2    23.00  0.44     Sequence
 HLA-DQA10101-DQB10501  364      ISNCVADYSVLYNSA  CVADYSVLY  3         0.2969
2013.4    29.00  0.50     Sequence
 HLA-DQA10101-DQB10501  365      SNCVADYSVLYNSAS  CVADYSVLY  2         0.2751
2548.5    33.00  0.54     Sequence
 HLA-DQA10101-DQB10501  366      NCVADYSVLYNSASF  CVADYSVLY  1         0.2612
2963.5    37.00  0.49     Sequence
 HLA-DQA10101-DQB10501  367      CVADYSVLYNSASFS  CVADYSVLY  0         0.2430
3606.2    41.00  0.31     Sequence
 HLA-DQA10101-DQB10501  368      VADYSVLYNSASFST  YSVLYNSAS  3         0.2015
5649.6    55.00  0.32     Sequence
 HLA-DQA10101-DQB10501  369      ADYSVLYNSASFSTF  YSVLYNSAS  2         0.1995
5777.8    55.00  0.32     Sequence
 HLA-DQA10101-DQB10501  370      DYSVLYNSASFSTFK  YSVLYNSAS  1         0.1861
6677.3    60.00  0.31     Sequence
```

```
 HLA-DQA10101-DQB10501  371      YSVLYNSASFSTFKC  YSVLYNSAS  0        0.1957
6016.6    55.00  0.22     Sequence
 HLA-DQA10101-DQB10501  372      SVLYNSASFSTFKCY  NSASFSTFK  4        0.1857
6701.1    60.00  0.28     Sequence
 HLA-DQA10101-DQB10501  373      VLYNSASFSTFKCYG  NSASFSTFK  3        0.1574
9110.1    65.00  0.35     Sequence
 HLA-DQA10101-DQB10501  374      LYNSASFSTFKCYGV  SFSTFKCYG  5        0.1934
6167.4    55.00  0.30     Sequence
 HLA-DQA10101-DQB10501  375      YNSASFSTFKCYGVS  SFSTFKCYG  4        0.1969
5941.3    55.00  0.41     Sequence
 HLA-DQA10101-DQB10501  376      NSASFSTFKCYGVSP  SFSTFKCYG  3        0.1968
5947.8    55.00  0.43     Sequence
 HLA-DQA10101-DQB10501  377      SASFSTFKCYGVSPT  SFSTFKCYG  2        0.2318
4069.4    43.00  0.35     Sequence
 HLA-DQA10101-DQB10501  378      ASFSTFKCYGVSPTK  SFSTFKCYG  1        0.2295
4172.6    44.00  0.34     Sequence
 HLA-DQA10101-DQB10501  379      SFSTFKCYGVSPTKL  FKCYGVSPT  4        0.2357
3904.7    42.00  0.29     Sequence
 HLA-DQA10101-DQB10501  380      FSTFKCYGVSPTKLN  FKCYGVSPT  3        0.2117
5059.3    49.00  0.34     Sequence
 HLA-DQA10101-DQB10501  381      STFKCYGVSPTKLND  FKCYGVSPT  2        0.1801
7126.1    60.00  0.38     Sequence
 HLA-DQA10101-DQB10501  382      TFKCYGVSPTKLNDL  FKCYGVSPT  1        0.1662
8281.4    65.00  0.39     Sequence
 HLA-DQA10101-DQB10501  383      FKCYGVSPTKLNDLC  FKCYGVSPT  0        0.1353
11563.3    75.00  0.32     Sequence
 HLA-DQA10101-DQB10501  384      KCYGVSPTKLNDLCF  GVSPTKLND  3        0.0978
17362.5    85.00  0.27     Sequence
 HLA-DQA10101-DQB10501  385      CYGVSPTKLNDLCFT  SPTKLNDLC  4        0.1206
13553.3    75.00  0.28     Sequence
 HLA-DQA10101-DQB10501  386      YGVSPTKLNDLCFTN  SPTKLNDLC  3        0.1157
14305.1    80.00  0.32     Sequence
 HLA-DQA10101-DQB10501  387      GVSPTKLNDLCFTNV  SPTKLNDLC  2        0.1610
8757.4    65.00  0.25     Sequence
 HLA-DQA10101-DQB10501  388      VSPTKLNDLCFTNVY  LNDLCFTNV  5        0.1854
6730.0    60.00  0.29     Sequence
 HLA-DQA10101-DQB10501  389      SPTKLNDLCFTNVYA  LNDLCFTNV  4        0.2058
5395.2    50.00  0.35     Sequence
 HLA-DQA10101-DQB10501  390      PTKLNDLCFTNVYAD  NDLCFTNVY  4        0.2669
2784.4    35.00  0.28     Sequence
 HLA-DQA10101-DQB10501  391      TKLNDLCFTNVYADS  NDLCFTNVY  3        0.2976
1998.1    29.00  0.25     Sequence
 HLA-DQA10101-DQB10501  392      KLNDLCFTNVYADSF  CFTNVYADS  5        0.3876
754.8    15.00  0.22     Sequence
 HLA-DQA10101-DQB10501  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.4999
223.8     5.50  0.51     Sequence         WB
 HLA-DQA10101-DQB10501  394      NDLCFTNVYADSFVI  FTNVYADSF  4        0.5587
118.5     3.00  0.65     Sequence         WB
 HLA-DQA10101-DQB10501  395      DLCFTNVYADSFVIR  FTNVYADSF  3        0.5520
127.3     3.50  0.63     Sequence         WB
 HLA-DQA10101-DQB10501  396      LCFTNVYADSFVIRG  FTNVYADSF  2        0.5309
160.0     4.00  0.60     Sequence         WB
 HLA-DQA10101-DQB10501  397      CFTNVYADSFVIRGD  FTNVYADSF  1        0.4975
229.9     5.50  0.56     Sequence         WB
 HLA-DQA10101-DQB10501  398      FTNVYADSFVIRGDE  FTNVYADSF  0        0.4434
412.7     9.50  0.44     Sequence         WB
 HLA-DQA10101-DQB10501  399      TNVYADSFVIRGDEV  YADSFVIRG  3        0.3682
930.8    17.00  0.37     Sequence
 HLA-DQA10101-DQB10501  400      NVYADSFVIRGDEVR  YADSFVIRG  2        0.2985
1979.1    29.00  0.48     Sequence
 HLA-DQA10101-DQB10501  401      VYADSFVIRGDEVRQ  YADSFVIRG  1        0.2516
3285.4    39.00  0.52     Sequence
 HLA-DQA10101-DQB10501  402      YADSFVIRGDEVRQI  YADSFVIRG  0        0.2256
4355.0    45.00  0.38     Sequence
 HLA-DQA10101-DQB10501  403      ADSFVIRGDEVRQIA  VIRGDEVRQ  4        0.1926
6221.7    55.00  0.31     Sequence
```

```
 HLA-DQA10101-DQB10501  404      DSFVIRGDEVRQIAP  VIRGDEVRQ  3        0.1804
7103.1    60.00  0.36     Sequence
 HLA-DQA10101-DQB10501  405      SFVIRGDEVRQIAPG  VIRGDEVRQ  2        0.1574
9105.5    65.00  0.42     Sequence
 HLA-DQA10101-DQB10501  406      FVIRGDEVRQIAPGQ  VIRGDEVRQ  1        0.1413
10841.8    70.00  0.42     Sequence
 HLA-DQA10101-DQB10501  407      VIRGDEVRQIAPGQT  VIRGDEVRQ  0        0.1122
14854.2    80.00  0.32     Sequence
 HLA-DQA10101-DQB10501  408      IRGDEVRQIAPGQTG  GDEVRQIAP  2        0.0923
18416.1    85.00  0.22     Sequence
 HLA-DQA10101-DQB10501  409      RGDEVRQIAPGQTGT  GDEVRQIAP  1        0.0680
23948.9    95.00  0.31     Sequence
 HLA-DQA10101-DQB10501  410      GDEVRQIAPGQTGTI  DEVRQIAPG  1        0.0633
25213.8    95.00  0.26     Sequence
 HLA-DQA10101-DQB10501  411      DEVRQIAPGQTGTIA  EVRQIAPGQ  1        0.0555
27440.6    95.00  0.31     Sequence
 HLA-DQA10101-DQB10501  412      EVRQIAPGQTGTIAD  EVRQIAPGQ  0        0.0408
32146.9   100.00  0.27     Sequence
 HLA-DQA10101-DQB10501  413      VRQIAPGQTGTIADY  GQTGTIADY  6        0.0693
23616.9    90.00  0.34     Sequence
 HLA-DQA10101-DQB10501  414      RQIAPGQTGTIADYN  GQTGTIADY  5        0.0863
19644.6    85.00  0.54     Sequence
 HLA-DQA10101-DQB10501  415      QIAPGQTGTIADYNY  GQTGTIADY  4        0.1240
13064.6    75.00  0.57     Sequence
 HLA-DQA10101-DQB10501  416      IAPGQTGTIADYNYK  GQTGTIADY  3        0.1242
13037.0    75.00  0.52     Sequence
 HLA-DQA10101-DQB10501  417      APGQTGTIADYNYKL  GQTGTIADY  2        0.1469
10206.8    70.00  0.34     Sequence
 HLA-DQA10101-DQB10501  418      PGQTGTIADYNYKLP  GQTGTIADY  1        0.2035
5532.2    55.00  0.19     Sequence
 HLA-DQA10101-DQB10501  419      GQTGTIADYNYKLPD  TIADYNYKL  4        0.2449
3532.9    40.00  0.18     Sequence
 HLA-DQA10101-DQB10501  420      QTGTIADYNYKLPDD  ADYNYKLPD  5        0.2975
2000.8    29.00  0.44     Sequence
 HLA-DQA10101-DQB10501  421      TGTIADYNYKLPDDF  ADYNYKLPD  4        0.3424
1230.2    21.00  0.54     Sequence
 HLA-DQA10101-DQB10501  422      GTIADYNYKLPDDFT  ADYNYKLPD  3        0.3411
1247.6    21.00  0.51     Sequence
 HLA-DQA10101-DQB10501  423      TIADYNYKLPDDFTG  ADYNYKLPD  2        0.3298
1409.7    23.00  0.50     Sequence
 HLA-DQA10101-DQB10501  424      IADYNYKLPDDFTGC  ADYNYKLPD  1        0.3125
1700.8    26.00  0.51     Sequence
 HLA-DQA10101-DQB10501  425      ADYNYKLPDDFTGCV  ADYNYKLPD  0        0.2685
2735.7    35.00  0.41     Sequence
 HLA-DQA10101-DQB10501  426      DYNYKLPDDFTGCVI  YNYKLPDDF  1        0.2135
4963.2    48.00  0.22     Sequence
 HLA-DQA10101-DQB10501  427      YNYKLPDDFTGCVIA  NYKLPDDFT  1        0.1818
6993.5    60.00  0.20     Sequence
 HLA-DQA10101-DQB10501  428      NYKLPDDFTGCVIAW  DFTGCVIAW  6        0.1973
5916.8    55.00  0.29     Sequence
 HLA-DQA10101-DQB10501  429      YKLPDDFTGCVIAWN  DFTGCVIAW  5        0.2325
4042.5    43.00  0.54     Sequence
 HLA-DQA10101-DQB10501  430      KLPDDFTGCVIAWNS  DFTGCVIAW  4        0.2335
3997.2    43.00  0.66     Sequence
 HLA-DQA10101-DQB10501  431      LPDDFTGCVIAWNSN  DFTGCVIAW  3        0.2275
4265.6    45.00  0.62     Sequence
 HLA-DQA10101-DQB10501  432      PDDFTGCVIAWNSNN  DFTGCVIAW  2        0.2250
4382.8    45.00  0.56     Sequence
 HLA-DQA10101-DQB10501  433      DDFTGCVIAWNSNNL  DFTGCVIAW  1        0.2783
2461.0    33.00  0.39     Sequence
 HLA-DQA10101-DQB10501  434      DFTGCVIAWNSNNLD  CVIAWNSNN  4        0.3100
1746.5    26.00  0.52     Sequence
 HLA-DQA10101-DQB10501  435      FTGCVIAWNSNNLDS  CVIAWNSNN  3        0.3106
1735.3    26.00  0.57     Sequence
 HLA-DQA10101-DQB10501  436      TGCVIAWNSNNLDSK  CVIAWNSNN  2        0.3450
1195.8    21.00  0.52     Sequence
```

```
 HLA-DQA10101-DQB10501  437      GCVIAWNSNNLDSKV  CVIAWNSNN  1        0.3518
1111.7    20.00  0.49     Sequence
 HLA-DQA10101-DQB10501  438      CVIAWNSNNLDSKVG  CVIAWNSNN  0        0.3334
1356.5    22.00  0.44     Sequence
 HLA-DQA10101-DQB10501  439      VIAWNSNNLDSKVGG  WNSNNLDSK  3        0.2748
2555.9    34.00  0.36     Sequence
 HLA-DQA10101-DQB10501  440      IAWNSNNLDSKVGGN  WNSNNLDSK  2        0.2011
5676.4    55.00  0.51     Sequence
 HLA-DQA10101-DQB10501  441      AWNSNNLDSKVGGNY  WNSNNLDSK  1        0.1523
9619.0    65.00  0.62     Sequence
 HLA-DQA10101-DQB10501  442      WNSNNLDSKVGGNYN  WNSNNLDSK  0        0.1051
16039.4    80.00  0.54     Sequence
 HLA-DQA10101-DQB10501  443      NSNNLDSKVGGNYNY  NNLDSKVGG  2        0.0469
30091.7   100.00  0.40     Sequence
 HLA-DQA10101-DQB10501  444      SNNLDSKVGGNYNYL  KVGGNYNYL  6        0.0558
27352.0    95.00  0.26     Sequence
 HLA-DQA10101-DQB10501  445      NNLDSKVGGNYNYLY  KVGGNYNYL  5        0.1063
15823.2    80.00  0.55     Sequence
 HLA-DQA10101-DQB10501  446      NLDSKVGGNYNYLYR  KVGGNYNYL  4        0.1110
15044.4    80.00  0.61     Sequence
 HLA-DQA10101-DQB10501  447      LDSKVGGNYNYLYRL  KVGGNYNYL  3        0.1471
10181.1    70.00  0.45     Sequence
 HLA-DQA10101-DQB10501  448      DSKVGGNYNYLYRLF  KVGGNYNYL  2        0.1791
7199.1    60.00  0.29     Sequence
 HLA-DQA10101-DQB10501  449      SKVGGNYNYLYRLFR  KVGGNYNYL  1        0.1741
7603.6    60.00  0.25     Sequence
 HLA-DQA10101-DQB10501  450      KVGGNYNYLYRLFRK  YNYLYRLFR  5        0.1808
7066.9    60.00  0.21     Sequence
 HLA-DQA10101-DQB10501  451      VGGNYNYLYRLFRKS  YNYLYRLFR  4        0.1864
6657.3    55.00  0.29     Sequence
 HLA-DQA10101-DQB10501  452      GGNYNYLYRLFRKSN  YNYLYRLFR  3        0.1853
6732.3    60.00  0.31     Sequence
 HLA-DQA10101-DQB10501  453      GNYNYLYRLFRKSNL  LYRLFRKSN  5        0.2902
2165.4    30.00  0.34     Sequence
 HLA-DQA10101-DQB10501  454      NYNYLYRLFRKSNLK  LYRLFRKSN  4        0.3159
1638.4    25.00  0.41     Sequence
 HLA-DQA10101-DQB10501  455      YNYLYRLFRKSNLKP  LYRLFRKSN  3        0.3254
1478.9    24.00  0.44     Sequence
 HLA-DQA10101-DQB10501  456      NYLYRLFRKSNLKPF  LYRLFRKSN  2        0.3233
1512.4    24.00  0.47     Sequence
 HLA-DQA10101-DQB10501  457      YLYRLFRKSNLKPFE  LYRLFRKSN  1        0.3069
1807.1    27.00  0.47     Sequence
 HLA-DQA10101-DQB10501  458      LYRLFRKSNLKPFER  YRLFRKSNL  1        0.2659
2814.7    35.00  0.38     Sequence
 HLA-DQA10101-DQB10501  459      YRLFRKSNLKPFERD  YRLFRKSNL  0        0.2186
4697.7    47.00  0.34     Sequence
 HLA-DQA10101-DQB10501  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.1173
14052.9    80.00  0.25     Sequence
 HLA-DQA10101-DQB10501  461      LFRKSNLKPFERDIS  NLKPFERDI  5        0.1442
10499.4    70.00  0.41     Sequence
 HLA-DQA10101-DQB10501  462      FRKSNLKPFERDIST  NLKPFERDI  4        0.1547
9372.7    65.00  0.41     Sequence
 HLA-DQA10101-DQB10501  463      RKSNLKPFERDISTE  NLKPFERDI  3        0.1629
8577.1    65.00  0.44     Sequence
 HLA-DQA10101-DQB10501  464      KSNLKPFERDISTEI  NLKPFERDI  2        0.1916
6291.2    55.00  0.34     Sequence
 HLA-DQA10101-DQB10501  465      SNLKPFERDISTEIY  FERDISTEI  5        0.1985
5835.5    55.00  0.26     Sequence
 HLA-DQA10101-DQB10501  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.1885
6503.7    55.00  0.35     Sequence
 HLA-DQA10101-DQB10501  467      LKPFERDISTEIYQA  FERDISTEI  3        0.1717
7801.5    60.00  0.39     Sequence
 HLA-DQA10101-DQB10501  468      KPFERDISTEIYQAG  FERDISTEI  2        0.1536
9490.5    65.00  0.36     Sequence
 HLA-DQA10101-DQB10501  469      PFERDISTEIYQAGS  FERDISTEI  1        0.1348
11630.1    75.00  0.31     Sequence
```

```
 HLA-DQA10101-DQB10501  470      FERDISTEIYQAGST  RDISTEIYQ  2        0.1123
14842.3    80.00  0.34     Sequence
 HLA-DQA10101-DQB10501  471      ERDISTEIYQAGSTP  STEIYQAGS  4        0.1012
16718.8    85.00  0.28     Sequence
 HLA-DQA10101-DQB10501  472      RDISTEIYQAGSTPC  STEIYQAGS  3        0.0982
17272.6    85.00  0.35     Sequence
 HLA-DQA10101-DQB10501  473      DISTEIYQAGSTPCN  STEIYQAGS  2        0.0937
18149.7    85.00  0.36     Sequence
 HLA-DQA10101-DQB10501  474      ISTEIYQAGSTPCNG  STEIYQAGS  1        0.0810
20803.8    90.00  0.40     Sequence
 HLA-DQA10101-DQB10501  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.0738
22506.0    90.00  0.34     Sequence
 HLA-DQA10101-DQB10501  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.0618
25612.2    95.00  0.38     Sequence
 HLA-DQA10101-DQB10501  477      EIYQAGSTPCNGVKG  IYQAGSTPC  1        0.0485
29591.0    95.00  0.47     Sequence
 HLA-DQA10101-DQB10501  478      IYQAGSTPCNGVKGF  IYQAGSTPC  0        0.0324
35216.2   100.00  0.44     Sequence
 HLA-DQA10101-DQB10501  479      YQAGSTPCNGVKGFN  XYQAGSTPC -1        0.0206
40002.0   100.00  0.22     Sequence
 HLA-DQA10101-DQB10501  480      QAGSTPCNGVKGFNC  PCNGVKGFN  5        0.0421
31721.9   100.00  0.42     Sequence
 HLA-DQA10101-DQB10501  481      AGSTPCNGVKGFNCY  PCNGVKGFN  4        0.0654
24640.9    95.00  0.40     Sequence
 HLA-DQA10101-DQB10501  482      GSTPCNGVKGFNCYF  GVKGFNCYF  6        0.1265
12716.8    75.00  0.34     Sequence
 HLA-DQA10101-DQB10501  483      STPCNGVKGFNCYFP  GVKGFNCYF  5        0.2183
4711.2    47.00  0.60     Sequence
 HLA-DQA10101-DQB10501  484      TPCNGVKGFNCYFPL  GVKGFNCYF  4        0.3294
1416.7    23.00  0.66     Sequence
 HLA-DQA10101-DQB10501  485      PCNGVKGFNCYFPLQ  GVKGFNCYF  3        0.3683
929.8    17.00  0.56    Sequence
 HLA-DQA10101-DQB10501  486      CNGVKGFNCYFPLQS  GVKGFNCYF  2        0.4707
306.9     7.00  0.36    Sequence         WB
 HLA-DQA10101-DQB10501  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.5416
142.5     3.50  0.48    Sequence         WB
 HLA-DQA10101-DQB10501  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.5670
108.3     3.00  0.56    Sequence         WB
 HLA-DQA10101-DQB10501  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3        0.5729
101.6     2.50  0.59    Sequence         WB
 HLA-DQA10101-DQB10501  490      KGFNCYFPLQSYGFQ  FNCYFPLQS  2        0.5500
130.2     3.50  0.65    Sequence         WB
 HLA-DQA10101-DQB10501  491      GFNCYFPLQSYGFQP  FNCYFPLQS  1        0.5253
170.1     4.50  0.64    Sequence         WB
 HLA-DQA10101-DQB10501  492      FNCYFPLQSYGFQPT  FNCYFPLQS  0        0.4913
245.6     6.00  0.55    Sequence         WB
 HLA-DQA10101-DQB10501  493      NCYFPLQSYGFQPTY  PLQSYGFQP  4        0.4305
474.4    11.00  0.22    Sequence
 HLA-DQA10101-DQB10501  494      CYFPLQSYGFQPTYG  PLQSYGFQP  3        0.3648
965.2    18.00  0.29    Sequence
 HLA-DQA10101-DQB10501  495      YFPLQSYGFQPTYGV  PLQSYGFQP  2        0.3671
941.9    18.00  0.31    Sequence
 HLA-DQA10101-DQB10501  496      FPLQSYGFQPTYGVG  LQSYGFQPT  2        0.3341
1345.5    22.00  0.30     Sequence
 HLA-DQA10101-DQB10501  497      PLQSYGFQPTYGVGY  LQSYGFQPT  1        0.2930
2098.8    30.00  0.32     Sequence
 HLA-DQA10101-DQB10501  498      LQSYGFQPTYGVGYQ  QSYGFQPTY  1        0.2458
3499.5    40.00  0.35     Sequence
 HLA-DQA10101-DQB10501  499      QSYGFQPTYGVGYQP  QSYGFQPTY  0        0.1655
8342.7    65.00  0.36     Sequence
 HLA-DQA10101-DQB10501  500      SYGFQPTYGVGYQPY  FQPTYGVGY  3        0.1660
8293.8    65.00  0.21     Sequence
 HLA-DQA10101-DQB10501  501      YGFQPTYGVGYQPYR  TYGVGYQPY  5        0.1752
7513.1    60.00  0.22     Sequence
 HLA-DQA10101-DQB10501  502      GFQPTYGVGYQPYRV  YGVGYQPYR  5        0.2245
4405.9    45.00  0.40     Sequence
```

```
 HLA-DQA10101-DQB10501  503      FQPTYGVGYQPYRVV  YGVGYQPYR  4        0.3053
1837.6    27.00  0.50     Sequence
 HLA-DQA10101-DQB10501  504      QPTYGVGYQPYRVVV  YGVGYQPYR  3        0.3281
1435.5    23.00  0.46     Sequence
 HLA-DQA10101-DQB10501  505      PTYGVGYQPYRVVVL  YGVGYQPYR  2        0.3619
996.2    18.00  0.38     Sequence
 HLA-DQA10101-DQB10501  506      TYGVGYQPYRVVVLS  GYQPYRVVV  4        0.3609
1007.4    18.00  0.38     Sequence
 HLA-DQA10101-DQB10501  507      YGVGYQPYRVVVLSF  GYQPYRVVV  3        0.3293
1417.3    23.00  0.44     Sequence
 HLA-DQA10101-DQB10501  508      GVGYQPYRVVVLSFE  GYQPYRVVV  2        0.2958
2037.9    29.00  0.50     Sequence
 HLA-DQA10101-DQB10501  509      VGYQPYRVVVLSFEL  GYQPYRVVV  1        0.2680
2752.6    35.00  0.52     Sequence
 HLA-DQA10101-DQB10501  510      GYQPYRVVVLSFELL  GYQPYRVVV  0        0.2443
3557.9    40.00  0.29     Sequence
 HLA-DQA10101-DQB10501  511      YQPYRVVVLSFELLH  VVLSFELLH  6        0.3189
1586.0    25.00  0.31     Sequence
 HLA-DQA10101-DQB10501  512      QPYRVVVLSFELLHA  VVLSFELLH  5        0.4008
654.3    14.00  0.56     Sequence
 HLA-DQA10101-DQB10501  513      PYRVVVLSFELLHAP  VVLSFELLH  4        0.4625
335.4     8.00  0.67     Sequence         WB
 HLA-DQA10101-DQB10501  514      YRVVVLSFELLHAPA  VVLSFELLH  3        0.4732
298.9     7.00  0.63     Sequence         WB
 HLA-DQA10101-DQB10501  515      RVVVLSFELLHAPAT  VVLSFELLH  2        0.4665
321.2     7.50  0.63     Sequence         WB
 HLA-DQA10101-DQB10501  516      VVVLSFELLHAPATV  VVLSFELLH  1        0.4595
346.5     8.00  0.56     Sequence         WB
 HLA-DQA10101-DQB10501  517      VVLSFELLHAPATVC  VVLSFELLH  0        0.4352
450.8    10.00  0.47     Sequence
 HLA-DQA10101-DQB10501  518      VLSFELLHAPATVCG  FELLHAPAT  3        0.3521
1107.9    20.00  0.22     Sequence
 HLA-DQA10101-DQB10501  519      LSFELLHAPATVCGP  FELLHAPAT  2        0.2737
2587.8    34.00  0.37     Sequence
 HLA-DQA10101-DQB10501  520      SFELLHAPATVCGPK  FELLHAPAT  1        0.2250
4384.0    45.00  0.40     Sequence
 HLA-DQA10101-DQB10501  521      FELLHAPATVCGPKK  FELLHAPAT  0        0.1802
7116.2    60.00  0.41     Sequence
 HLA-DQA10101-DQB10501  522      ELLHAPATVCGPKKS  ELLHAPATV  0        0.1088
15406.1    80.00  0.41     Sequence
 HLA-DQA10101-DQB10501  523      LLHAPATVCGPKKST  XLLHAPATV -1        0.0496
29231.7    95.00  0.25     Sequence
 HLA-DQA10101-DQB10501  524      LHAPATVCGPKKSTN  LHAPATVCG  0        0.0182
41083.7   100.00  0.23     Sequence
 HLA-DQA10101-DQB10501  525      HAPATVCGPKKSTNL  TVCGPKKST  4        0.0153
42352.0   100.00  0.35     Sequence
 HLA-DQA10101-DQB10501  526      APATVCGPKKSTNLV  TVCGPKKST  3        0.0143
42852.1   100.00  0.40     Sequence
 HLA-DQA10101-DQB10501  527      PATVCGPKKSTNLVK  TVCGPKKST  2        0.0132
43353.4   100.00  0.40     Sequence
 HLA-DQA10101-DQB10501  528      ATVCGPKKSTNLVKN  TVCGPKKST  1        0.0142
42873.9   100.00  0.31     Sequence
 HLA-DQA10101-DQB10501  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.0147
42651.3   100.00  0.29     Sequence
 HLA-DQA10101-DQB10501  530      VCGPKKSTNLVKNKC  KSTNLVKNK  5        0.0184
40956.3   100.00  0.39     Sequence
 HLA-DQA10101-DQB10501  531      CGPKKSTNLVKNKCV  KSTNLVKNK  4        0.0360
33851.0   100.00  0.38     Sequence
 HLA-DQA10101-DQB10501  532      GPKKSTNLVKNKCVN  STNLVKNKC  4        0.0499
29144.2    95.00  0.38     Sequence
 HLA-DQA10101-DQB10501  533      PKKSTNLVKNKCVNF  LVKNKCVNF  6        0.0777
21566.3    90.00  0.37     Sequence
 HLA-DQA10101-DQB10501  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.0880
19297.2    85.00  0.49     Sequence
 HLA-DQA10101-DQB10501  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.1010
16763.0    85.00  0.56     Sequence
```

```
 HLA-DQA10101-DQB10501  536      STNLVKNKCVNFNFN  LVKNKCVNF  3        0.1009
16774.7    85.00  0.51     Sequence
 HLA-DQA10101-DQB10501  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2        0.0966
17583.9    85.00  0.50     Sequence
 HLA-DQA10101-DQB10501  538      NLVKNKCVNFNFNGL  KCVNFNFNG  5        0.1385
11176.1    70.00  0.34     Sequence
 HLA-DQA10101-DQB10501  539      LVKNKCVNFNFNGLT  KCVNFNFNG  4        0.1716
7807.1    60.00  0.44     Sequence
 HLA-DQA10101-DQB10501  540      VKNKCVNFNFNGLTG  KCVNFNFNG  3        0.1601
8846.0    65.00  0.42     Sequence
 HLA-DQA10101-DQB10501  541      KNKCVNFNFNGLTGT  KCVNFNFNG  2        0.1641
8472.6    65.00  0.40     Sequence
 HLA-DQA10101-DQB10501  542      NKCVNFNFNGLTGTG  CVNFNFNGL  2        0.1537
9483.1    65.00  0.33     Sequence
 HLA-DQA10101-DQB10501  543      KCVNFNFNGLTGTGV  CVNFNFNGL  1        0.1477
10110.8    70.00  0.31     Sequence
 HLA-DQA10101-DQB10501  544      CVNFNFNGLTGTGVL  CVNFNFNGL  0        0.1300
12248.3    75.00  0.27     Sequence
 HLA-DQA10101-DQB10501  545      VNFNFNGLTGTGVLT  FNFNGLTGT  2        0.0878
19335.6    85.00  0.20     Sequence
 HLA-DQA10101-DQB10501  546      NFNFNGLTGTGVLTE  GLTGTGVLT  5        0.0866
19593.8    85.00  0.28     Sequence
 HLA-DQA10101-DQB10501  547      FNFNGLTGTGVLTES  GLTGTGVLT  4        0.0901
18856.1    85.00  0.37     Sequence
 HLA-DQA10101-DQB10501  548      NFNGLTGTGVLTESN  GLTGTGVLT  3        0.0795
21144.4    90.00  0.40     Sequence
 HLA-DQA10101-DQB10501  549      FNGLTGTGVLTESNK  GLTGTGVLT  2        0.0709
23214.9    90.00  0.42     Sequence
 HLA-DQA10101-DQB10501  550      NGLTGTGVLTESNKK  GLTGTGVLT  1        0.0581
26665.8    95.00  0.47     Sequence
 HLA-DQA10101-DQB10501  551      GLTGTGVLTESNKKF  GLTGTGVLT  0        0.0506
28911.2    95.00  0.38     Sequence
 HLA-DQA10101-DQB10501  552      LTGTGVLTESNKKFL  TGTGVLTES  1        0.0466
30201.3   100.00  0.20     Sequence
 HLA-DQA10101-DQB10501  553      TGTGVLTESNKKFLP  LTESNKKFL  5        0.0441
31041.5   100.00  0.28     Sequence
 HLA-DQA10101-DQB10501  554      GTGVLTESNKKFLPF  LTESNKKFL  4        0.0703
23371.4    90.00  0.26     Sequence
 HLA-DQA10101-DQB10501  555      TGVLTESNKKFLPFQ  ESNKKFLPF  5        0.0976
17385.3    85.00  0.38     Sequence
 HLA-DQA10101-DQB10501  556      GVLTESNKKFLPFQQ  ESNKKFLPF  4        0.1213
13454.9    75.00  0.36     Sequence
 HLA-DQA10101-DQB10501  557      VLTESNKKFLPFQQF  ESNKKFLPF  3        0.1745
7565.7    60.00  0.22     Sequence
 HLA-DQA10101-DQB10501  558      LTESNKKFLPFQQFG  ESNKKFLPF  2        0.1817
7001.5    60.00  0.17     Sequence
 HLA-DQA10101-DQB10501  559      TESNKKFLPFQQFGR  KFLPFQQFG  5        0.1767
7390.0    60.00  0.22     Sequence
 HLA-DQA10101-DQB10501  560      ESNKKFLPFQQFGRD  KFLPFQQFG  4        0.1802
7118.6    60.00  0.29     Sequence
 HLA-DQA10101-DQB10501  561      SNKKFLPFQQFGRDI  KFLPFQQFG  3        0.1758
7466.3    60.00  0.34     Sequence
 HLA-DQA10101-DQB10501  562      NKKFLPFQQFGRDIA  KFLPFQQFG  2        0.2368
3856.5    42.00  0.19     Sequence
 HLA-DQA10101-DQB10501  563      KKFLPFQQFGRDIAD  FQQFGRDIA  5        0.3283
1433.1    23.00  0.34     Sequence
 HLA-DQA10101-DQB10501  564      KFLPFQQFGRDIADT  FQQFGRDIA  4        0.3683
930.1    17.00  0.41     Sequence
 HLA-DQA10101-DQB10501  565      FLPFQQFGRDIADTT  FQQFGRDIA  3        0.3817
804.1    16.00  0.37     Sequence
 HLA-DQA10101-DQB10501  566      LPFQQFGRDIADTTD  FQQFGRDIA  2        0.3800
819.5    16.00  0.37     Sequence
 HLA-DQA10101-DQB10501  567      PFQQFGRDIADTTDA  FQQFGRDIA  1        0.3655
957.8    18.00  0.35     Sequence
 HLA-DQA10101-DQB10501  568      FQQFGRDIADTTDAV  FQQFGRDIA  0        0.3554
1069.4    19.00  0.32     Sequence
```

```
 HLA-DQA10101-DQB10501  569      QQFGRDIADTTDAVR  FGRDIADTT  2        0.2736
2589.2    34.00  0.30     Sequence
 HLA-DQA10101-DQB10501  570      QFGRDIADTTDAVRD  FGRDIADTT  1        0.1778
7298.9    60.00  0.37     Sequence
 HLA-DQA10101-DQB10501  571      FGRDIADTTDAVRDP  DIADTTDAV  3        0.1295
12314.9    75.00  0.38     Sequence
 HLA-DQA10101-DQB10501  572      GRDIADTTDAVRDPQ  DIADTTDAV  2        0.1141
14548.3    80.00  0.37     Sequence
 HLA-DQA10101-DQB10501  573      RDIADTTDAVRDPQT  TTDAVRDPQ  5        0.1464
10254.4    70.00  0.42     Sequence
 HLA-DQA10101-DQB10501  574      DIADTTDAVRDPQTL  TTDAVRDPQ  4        0.1713
7838.4    60.00  0.62     Sequence
 HLA-DQA10101-DQB10501  575      IADTTDAVRDPQTLE  TTDAVRDPQ  3        0.1698
7965.0    60.00  0.68     Sequence
 HLA-DQA10101-DQB10501  576      ADTTDAVRDPQTLEI  TTDAVRDPQ  2        0.1789
7218.3    60.00  0.60     Sequence
 HLA-DQA10101-DQB10501  577      DTTDAVRDPQTLEIL  TTDAVRDPQ  1        0.1873
6591.3    55.00  0.50     Sequence
 HLA-DQA10101-DQB10501  578      TTDAVRDPQTLEILD  TTDAVRDPQ  0        0.1739
7616.4    60.00  0.41     Sequence
 HLA-DQA10101-DQB10501  579      TDAVRDPQTLEILDI  VRDPQTLEI  3        0.1935
6161.9    55.00  0.14     Sequence
 HLA-DQA10101-DQB10501  580      DAVRDPQTLEILDIT  PQTLEILDI  5        0.2450
3529.8    40.00  0.27     Sequence
 HLA-DQA10101-DQB10501  581      AVRDPQTLEILDITP  PQTLEILDI  4        0.2778
2476.4    33.00  0.29     Sequence
 HLA-DQA10101-DQB10501  582      VRDPQTLEILDITPC  QTLEILDIT  4        0.3225
1526.6    24.00  0.31     Sequence
 HLA-DQA10101-DQB10501  583      RDPQTLEILDITPCS  TLEILDITP  4        0.3275
1445.4    23.00  0.28     Sequence
 HLA-DQA10101-DQB10501  584      DPQTLEILDITPCSF  TLEILDITP  3        0.3283
1432.5    23.00  0.28     Sequence
 HLA-DQA10101-DQB10501  585      PQTLEILDITPCSFG  TLEILDITP  2        0.3036
1872.5    28.00  0.28     Sequence
 HLA-DQA10101-DQB10501  586      QTLEILDITPCSFGG  TLEILDITP  1        0.2718
2639.8    34.00  0.31     Sequence
 HLA-DQA10101-DQB10501  587      TLEILDITPCSFGGV  TLEILDITP  0        0.2124
5023.1    48.00  0.31     Sequence
 HLA-DQA10101-DQB10501  588      LEILDITPCSFGGVS  EILDITPCS  1        0.1576
9089.0    65.00  0.22     Sequence
 HLA-DQA10101-DQB10501  589      EILDITPCSFGGVSV  EILDITPCS  0        0.1021
16563.4    85.00  0.22     Sequence
 HLA-DQA10101-DQB10501  590      ILDITPCSFGGVSVI  TPCSFGGVS  4        0.1607
8790.7    65.00  0.25     Sequence
 HLA-DQA10101-DQB10501  591      LDITPCSFGGVSVIT  PCSFGGVSV  4        0.1703
7922.8    60.00  0.37     Sequence
 HLA-DQA10101-DQB10501  592      DITPCSFGGVSVITP  PCSFGGVSV  3        0.1997
5763.4    55.00  0.31     Sequence
 HLA-DQA10101-DQB10501  593      ITPCSFGGVSVITPG  PCSFGGVSV  2        0.1936
6154.4    55.00  0.31     Sequence
 HLA-DQA10101-DQB10501  594      TPCSFGGVSVITPGT  PCSFGGVSV  1        0.1815
7017.5    60.00  0.30     Sequence
 HLA-DQA10101-DQB10501  595      PCSFGGVSVITPGTN  PCSFGGVSV  0        0.1637
8509.5    65.00  0.30     Sequence
 HLA-DQA10101-DQB10501  596      CSFGGVSVITPGTNT  FGGVSVITP  2        0.1329
11869.2    75.00  0.25     Sequence
 HLA-DQA10101-DQB10501  597      SFGGVSVITPGTNTS  FGGVSVITP  1        0.0784
21396.9    90.00  0.32     Sequence
 HLA-DQA10101-DQB10501  598      FGGVSVITPGTNTSN  FGGVSVITP  0        0.0572
26925.6    95.00  0.31     Sequence
 HLA-DQA10101-DQB10501  599      GGVSVITPGTNTSNQ  VITPGTNTS  4        0.0170
41608.0   100.00  0.28     Sequence
 HLA-DQA10101-DQB10501  600      GVSVITPGTNTSNQV  VITPGTNTS  3        0.0146
42687.8   100.00  0.33     Sequence
 HLA-DQA10101-DQB10501  601      VSVITPGTNTSNQVA  VITPGTNTS  2        0.0156
42233.0   100.00  0.28     Sequence
```

```
 HLA-DQA10101-DQB10501  602      SVITPGTNTSNQVAV  TNTSNQVAV  6        0.0261
37706.9   100.00  0.32     Sequence
 HLA-DQA10101-DQB10501  603      VITPGTNTSNQVAVL  TNTSNQVAV  5        0.0522
28428.2    95.00  0.53     Sequence
 HLA-DQA10101-DQB10501  604      ITPGTNTSNQVAVLY  TNTSNQVAV  4        0.0754
22121.7    90.00  0.52     Sequence
 HLA-DQA10101-DQB10501  605      TPGTNTSNQVAVLYQ  TNTSNQVAV  3        0.0841
20131.0    90.00  0.41     Sequence
 HLA-DQA10101-DQB10501  606      PGTNTSNQVAVLYQG  TNTSNQVAV  2        0.0853
19871.8    90.00  0.34     Sequence
 HLA-DQA10101-DQB10501  607      GTNTSNQVAVLYQGV  TNTSNQVAV  1        0.1085
15461.1    80.00  0.24     Sequence
 HLA-DQA10101-DQB10501  608      TNTSNQVAVLYQGVN  QVAVLYQGV  5        0.1127
14767.3    80.00  0.21     Sequence
 HLA-DQA10101-DQB10501  609      NTSNQVAVLYQGVNC  QVAVLYQGV  4        0.1405
10927.8    70.00  0.26     Sequence
 HLA-DQA10101-DQB10501  610      TSNQVAVLYQGVNCT  AVLYQGVNC  5        0.1572
9127.7    65.00  0.28     Sequence
 HLA-DQA10101-DQB10501  611      SNQVAVLYQGVNCTE  AVLYQGVNC  4        0.2122
5033.8    48.00  0.40     Sequence
 HLA-DQA10101-DQB10501  612      NQVAVLYQGVNCTEV  AVLYQGVNC  3        0.2399
3730.1    41.00  0.36     Sequence
 HLA-DQA10101-DQB10501  613      QVAVLYQGVNCTEVP  AVLYQGVNC  2        0.2499
3346.0    39.00  0.32     Sequence
 HLA-DQA10101-DQB10501  614      VAVLYQGVNCTEVPV  AVLYQGVNC  1        0.2561
3129.8    38.00  0.28     Sequence
 HLA-DQA10101-DQB10501  615      AVLYQGVNCTEVPVA  AVLYQGVNC  0        0.2459
3495.4    40.00  0.26     Sequence
 HLA-DQA10101-DQB10501  616      VLYQGVNCTEVPVAI  LYQGVNCTE  1        0.2237
4442.6    45.00  0.27     Sequence
 HLA-DQA10101-DQB10501  617      LYQGVNCTEVPVAIH  LYQGVNCTE  0        0.1988
5821.6    55.00  0.24     Sequence
 HLA-DQA10101-DQB10501  618      YQGVNCTEVPVAIHA  GVNCTEVPV  2        0.1555
9298.4    65.00  0.26     Sequence
 HLA-DQA10101-DQB10501  619      QGVNCTEVPVAIHAD  GVNCTEVPV  1        0.1425
10696.5    70.00  0.27     Sequence
 HLA-DQA10101-DQB10501  620      GVNCTEVPVAIHADQ  TEVPVAIHA  4        0.1457
10338.3    70.00  0.32     Sequence
 HLA-DQA10101-DQB10501  621      VNCTEVPVAIHADQL  TEVPVAIHA  3        0.1711
7851.4    60.00  0.30     Sequence
 HLA-DQA10101-DQB10501  622      NCTEVPVAIHADQLT  PVAIHADQL  5        0.2138
4946.7    48.00  0.34     Sequence
 HLA-DQA10101-DQB10501  623      CTEVPVAIHADQLTP  PVAIHADQL  4        0.2354
3916.5    43.00  0.41     Sequence
 HLA-DQA10101-DQB10501  624      TEVPVAIHADQLTPT  PVAIHADQL  3        0.2363
3878.8    42.00  0.43     Sequence
 HLA-DQA10101-DQB10501  625      EVPVAIHADQLTPTW  PVAIHADQL  2        0.2315
4082.7    43.00  0.44     Sequence
 HLA-DQA10101-DQB10501  626      VPVAIHADQLTPTWR  PVAIHADQL  1        0.2053
5421.6    50.00  0.47     Sequence
 HLA-DQA10101-DQB10501  627      PVAIHADQLTPTWRV  PVAIHADQL  0        0.1649
8394.5    65.00  0.41     Sequence
 HLA-DQA10101-DQB10501  628      VAIHADQLTPTWRVY  IHADQLTPT  2        0.1278
12544.4    75.00  0.22     Sequence
 HLA-DQA10101-DQB10501  629      AIHADQLTPTWRVYS  IHADQLTPT  1        0.1028
16443.7    85.00  0.26     Sequence
 HLA-DQA10101-DQB10501  630      IHADQLTPTWRVYST  LTPTWRVYS  5        0.1073
15657.2    80.00  0.33     Sequence
 HLA-DQA10101-DQB10501  631      HADQLTPTWRVYSTG  LTPTWRVYS  4        0.0994
17049.6    85.00  0.42     Sequence
 HLA-DQA10101-DQB10501  632      ADQLTPTWRVYSTGS  LTPTWRVYS  3        0.0976
17383.0    85.00  0.44     Sequence
 HLA-DQA10101-DQB10501  633      DQLTPTWRVYSTGSN  LTPTWRVYS  2        0.1156
14318.8    80.00  0.32     Sequence
 HLA-DQA10101-DQB10501  634      QLTPTWRVYSTGSNV  WRVYSTGSN  5        0.1279
12527.1    75.00  0.26     Sequence
```

```
 HLA-DQA10101-DQB10501  635      LTPTWRVYSTGSNVF  WRVYSTGSN  4         0.1316
12036.9    75.00  0.29     Sequence
 HLA-DQA10101-DQB10501  636      TPTWRVYSTGSNVFQ  WRVYSTGSN  3         0.1321
11973.3    75.00  0.26     Sequence
 HLA-DQA10101-DQB10501  637      PTWRVYSTGSNVFQT  WRVYSTGSN  2         0.1301
12241.7    75.00  0.25     Sequence
 HLA-DQA10101-DQB10501  638      TWRVYSTGSNVFQTR  WRVYSTGSN  1         0.1255
12865.5    75.00  0.25     Sequence
 HLA-DQA10101-DQB10501  639      WRVYSTGSNVFQTRA  WRVYSTGSN  0         0.1103
15166.5    80.00  0.18     Sequence
 HLA-DQA10101-DQB10501  640      RVYSTGSNVFQTRAG  YSTGSNVFQ  2         0.0773
21668.7    90.00  0.26     Sequence
 HLA-DQA10101-DQB10501  641      VYSTGSNVFQTRAGC  YSTGSNVFQ  1         0.0706
23290.6    90.00  0.25     Sequence
 HLA-DQA10101-DQB10501  642      YSTGSNVFQTRAGCL  NVFQTRAGC  5         0.0768
21774.3    90.00  0.25     Sequence
 HLA-DQA10101-DQB10501  643      STGSNVFQTRAGCLI  NVFQTRAGC  4         0.1019
16597.3    85.00  0.38     Sequence
 HLA-DQA10101-DQB10501  644      TGSNVFQTRAGCLIG  NVFQTRAGC  3         0.1045
16141.8    80.00  0.35     Sequence
 HLA-DQA10101-DQB10501  645      GSNVFQTRAGCLIGA  TRAGCLIGA  6         0.1628
8585.1    65.00  0.30     Sequence
 HLA-DQA10101-DQB10501  646      SNVFQTRAGCLIGAE  TRAGCLIGA  5         0.1991
5799.3    55.00  0.40     Sequence
 HLA-DQA10101-DQB10501  647      NVFQTRAGCLIGAEY  TRAGCLIGA  4         0.2116
5064.7    49.00  0.50     Sequence
 HLA-DQA10101-DQB10501  648      VFQTRAGCLIGAEYV  TRAGCLIGA  3         0.2376
3825.2    42.00  0.44     Sequence
 HLA-DQA10101-DQB10501  649      FQTRAGCLIGAEYVN  TRAGCLIGA  2         0.2414
3669.3    41.00  0.41     Sequence
 HLA-DQA10101-DQB10501  650      QTRAGCLIGAEYVNN  TRAGCLIGA  1         0.2265
4313.8    45.00  0.33     Sequence
 HLA-DQA10101-DQB10501  651      TRAGCLIGAEYVNNS  TRAGCLIGA  0         0.2144
4916.7    48.00  0.22     Sequence
 HLA-DQA10101-DQB10501  652      RAGCLIGAEYVNNSY  LIGAEYVNN  4         0.1954
6034.6    55.00  0.22     Sequence
 HLA-DQA10101-DQB10501  653      AGCLIGAEYVNNSYE  IGAEYVNNS  4         0.2375
3829.6    42.00  0.50     Sequence
 HLA-DQA10101-DQB10501  654      GCLIGAEYVNNSYEC  IGAEYVNNS  3         0.2446
3543.3    40.00  0.48     Sequence
 HLA-DQA10101-DQB10501  655      CLIGAEYVNNSYECD  IGAEYVNNS  2         0.2850
2290.5    31.00  0.35     Sequence
 HLA-DQA10101-DQB10501  656      LIGAEYVNNSYECDI  IGAEYVNNS  1         0.3392
1273.8    22.00  0.28     Sequence
 HLA-DQA10101-DQB10501  657      IGAEYVNNSYECDIP  YVNNSYECD  4         0.3620
995.3    18.00  0.33     Sequence
 HLA-DQA10101-DQB10501  658      GAEYVNNSYECDIPI  VNNSYECDI  4         0.4893
251.2     6.00  0.33     Sequence         WB
 HLA-DQA10101-DQB10501  659      AEYVNNSYECDIPIG  NNSYECDIP  4         0.5042
213.7     5.50  0.36     Sequence         WB
 HLA-DQA10101-DQB10501  660      EYVNNSYECDIPIGA  NNSYECDIP  3         0.4911
246.1     6.00  0.38     Sequence         WB
 HLA-DQA10101-DQB10501  661      YVNNSYECDIPIGAG  NNSYECDIP  2         0.4539
368.2     8.50  0.38     Sequence         WB
 HLA-DQA10101-DQB10501  662      VNNSYECDIPIGAGI  NNSYECDIP  1         0.4049
625.3    13.00  0.41     Sequence
 HLA-DQA10101-DQB10501  663      NNSYECDIPIGAGIC  NNSYECDIP  0         0.3509
1122.6    20.00  0.43     Sequence
 HLA-DQA10101-DQB10501  664      NSYECDIPIGAGICA  XNSYECDIP -1         0.2927
2107.1    30.00  0.34     Sequence
 HLA-DQA10101-DQB10501  665      SYECDIPIGAGICAS  YECDIPIGA  1         0.1702
7931.3    60.00  0.32     Sequence
 HLA-DQA10101-DQB10501  666      YECDIPIGAGICASY  PIGAGICAS  5         0.1373
11313.4    70.00  0.24     Sequence
 HLA-DQA10101-DQB10501  667      ECDIPIGAGICASYQ  PIGAGICAS  4         0.1337
11768.5    75.00  0.34     Sequence
```

```
 HLA-DQA10101-DQB10501  668      CDIPIGAGICASYQT  PIGAGICAS  3        0.1346
11648.4    75.00  0.34     Sequence
 HLA-DQA10101-DQB10501  669      DIPIGAGICASYQTQ  PIGAGICAS  2        0.1399
11000.6    70.00  0.31     Sequence
 HLA-DQA10101-DQB10501  670      IPIGAGICASYQTQT  PIGAGICAS  1        0.1509
9769.6    70.00  0.26     Sequence
 HLA-DQA10101-DQB10501  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.1500
9861.7    70.00  0.32     Sequence
 HLA-DQA10101-DQB10501  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.1457
10331.4    70.00  0.42     Sequence
 HLA-DQA10101-DQB10501  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.1289
12400.7    75.00  0.56     Sequence
 HLA-DQA10101-DQB10501  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.1159
14260.5    80.00  0.61     Sequence
 HLA-DQA10101-DQB10501  675      GICASYQTQTNSPRR  ICASYQTQT  1        0.0954
17818.7    85.00  0.65     Sequence
 HLA-DQA10101-DQB10501  676      ICASYQTQTNSPRRA  ICASYQTQT  0        0.0611
25817.8    95.00  0.56     Sequence
 HLA-DQA10101-DQB10501  677      CASYQTQTNSPRRAR  XCASYQTQT -1        0.0256
37909.8    100.00  0.28     Sequence
 HLA-DQA10101-DQB10501  678      ASYQTQTNSPRRARS  YQTQTNSPR  2        0.0167
41737.9    100.00  0.31     Sequence
 HLA-DQA10101-DQB10501  679      SYQTQTNSPRRARSV  TNSPRRARS  5        0.0236
38735.3    100.00  0.28     Sequence
 HLA-DQA10101-DQB10501  680      YQTQTNSPRRARSVA  TNSPRRARS  4        0.0259
37762.8    100.00  0.38     Sequence
 HLA-DQA10101-DQB10501  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.0364
33709.2    100.00  0.34     Sequence
 HLA-DQA10101-DQB10501  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.0665
24355.2    95.00  0.52     Sequence
 HLA-DQA10101-DQB10501  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.0780
21509.9    90.00  0.52     Sequence
 HLA-DQA10101-DQB10501  684      TNSPRRARSVASQSI  PRRARSVAS  3        0.0927
18332.3    85.00  0.41     Sequence
 HLA-DQA10101-DQB10501  685      NSPRRARSVASQSII  PRRARSVAS  2        0.1124
14826.1    80.00  0.31     Sequence
 HLA-DQA10101-DQB10501  686      SPRRARSVASQSIIA  RARSVASQS  3        0.1100
15208.6    80.00  0.37     Sequence
 HLA-DQA10101-DQB10501  687      PRRARSVASQSIIAY  VASQSIIAY  6        0.1469
10202.6    70.00  0.23     Sequence
 HLA-DQA10101-DQB10501  688      RRARSVASQSIIAYT  VASQSIIAY  5        0.1675
8168.1    65.00  0.37     Sequence
 HLA-DQA10101-DQB10501  689      RARSVASQSIIAYTM  VASQSIIAY  4        0.1896
6425.7    55.00  0.46     Sequence
 HLA-DQA10101-DQB10501  690      ARSVASQSIIAYTMS  VASQSIIAY  3        0.2134
4966.8    48.00  0.40     Sequence
 HLA-DQA10101-DQB10501  691      RSVASQSIIAYTMSL  ASQSIIAYT  3        0.2342
3965.5    43.00  0.31     Sequence
 HLA-DQA10101-DQB10501  692      SVASQSIIAYTMSLG  SIIAYTMSL  5        0.2400
3724.7    41.00  0.34     Sequence
 HLA-DQA10101-DQB10501  693      VASQSIIAYTMSLGA  SIIAYTMSL  4        0.2455
3510.2    40.00  0.46     Sequence
 HLA-DQA10101-DQB10501  694      ASQSIIAYTMSLGAE  SIIAYTMSL  3        0.2396
3741.5    42.00  0.56     Sequence
 HLA-DQA10101-DQB10501  695      SQSIIAYTMSLGAEN  SIIAYTMSL  2        0.2320
4061.9    43.00  0.55     Sequence
 HLA-DQA10101-DQB10501  696      QSIIAYTMSLGAENS  SIIAYTMSL  1        0.2176
4745.2    47.00  0.52     Sequence
 HLA-DQA10101-DQB10501  697      SIIAYTMSLGAENSV  SIIAYTMSL  0        0.2351
3929.2    43.00  0.31     Sequence
 HLA-DQA10101-DQB10501  698      IIAYTMSLGAENSVA  TMSLGAENS  4        0.2239
4433.5    45.00  0.20     Sequence
 HLA-DQA10101-DQB10501  699      IAYTMSLGAENSVAY  MSLGAENSV  4        0.2134
4968.0    48.00  0.34     Sequence
 HLA-DQA10101-DQB10501  700      AYTMSLGAENSVAYS  MSLGAENSV  3        0.1971
5927.0    55.00  0.38     Sequence
```

```
 HLA-DQA10101-DQB10501  701      YTMSLGAENSVAYSN  MSLGAENSV  2        0.1791
7198.3    60.00  0.43     Sequence
 HLA-DQA10101-DQB10501  702      TMSLGAENSVAYSNN  MSLGAENSV  1        0.1530
9550.5    65.00  0.41     Sequence
 HLA-DQA10101-DQB10501  703      MSLGAENSVAYSNNS  MSLGAENSV  0        0.1207
13541.5    75.00  0.40     Sequence
 HLA-DQA10101-DQB10501  704      SLGAENSVAYSNNSI  NSVAYSNNS  5        0.1365
11419.8    70.00  0.47     Sequence
 HLA-DQA10101-DQB10501  705      LGAENSVAYSNNSIA  NSVAYSNNS  4        0.2102
5142.1    49.00  0.58     Sequence
 HLA-DQA10101-DQB10501  706      GAENSVAYSNNSIAI  NSVAYSNNS  3        0.2538
3207.3    38.00  0.52     Sequence
 HLA-DQA10101-DQB10501  707      AENSVAYSNNSIAIP  NSVAYSNNS  2        0.3107
1732.9    26.00  0.43     Sequence
 HLA-DQA10101-DQB10501  708      ENSVAYSNNSIAIPT  NSVAYSNNS  1        0.3154
1647.4    25.00  0.38     Sequence
 HLA-DQA10101-DQB10501  709      NSVAYSNNSIAIPTN  NSVAYSNNS  0        0.2971
2008.5    29.00  0.34     Sequence
 HLA-DQA10101-DQB10501  710      SVAYSNNSIAIPTNF  SNNSIAIPT  4        0.2751
2549.6    33.00  0.19     Sequence
 HLA-DQA10101-DQB10501  711      VAYSNNSIAIPTNFT  SNNSIAIPT  3        0.2200
4624.9    46.00  0.26     Sequence
 HLA-DQA10101-DQB10501  712      AYSNNSIAIPTNFTI  SNNSIAIPT  2        0.1917
6283.2    55.00  0.29     Sequence
 HLA-DQA10101-DQB10501  713      YSNNSIAIPTNFTIS  SNNSIAIPT  1        0.1611
8753.8    65.00  0.37     Sequence
 HLA-DQA10101-DQB10501  714      SNNSIAIPTNFTISV  IPTNFTISV  6        0.1633
8544.0    65.00  0.25     Sequence
 HLA-DQA10101-DQB10501  715      NNSIAIPTNFTISVT  IPTNFTISV  5        0.1770
7364.5    60.00  0.45     Sequence
 HLA-DQA10101-DQB10501  716      NSIAIPTNFTISVTT  IPTNFTISV  4        0.1802
7114.5    60.00  0.56     Sequence
 HLA-DQA10101-DQB10501  717      SIAIPTNFTISVTTE  IPTNFTISV  3        0.1766
7402.1    60.00  0.54     Sequence
 HLA-DQA10101-DQB10501  718      IAIPTNFTISVTTEI  IPTNFTISV  2        0.1762
7426.4    60.00  0.46     Sequence
 HLA-DQA10101-DQB10501  719      AIPTNFTISVTTEIL  IPTNFTISV  1        0.1678
8139.7    65.00  0.32     Sequence
 HLA-DQA10101-DQB10501  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.1640
8481.3    65.00  0.38     Sequence
 HLA-DQA10101-DQB10501  721      PTNFTISVTTEILPV  FTISVTTEI  3        0.2115
5069.6    49.00  0.23     Sequence
 HLA-DQA10101-DQB10501  722      TNFTISVTTEILPVS  SVTTEILPV  5        0.2407
3698.2    41.00  0.35     Sequence
 HLA-DQA10101-DQB10501  723      NFTISVTTEILPVSM  SVTTEILPV  4        0.2565
3117.4    38.00  0.44     Sequence
 HLA-DQA10101-DQB10501  724      FTISVTTEILPVSMT  SVTTEILPV  3        0.2473
3442.7    40.00  0.45     Sequence
 HLA-DQA10101-DQB10501  725      TISVTTEILPVSMTK  SVTTEILPV  2        0.2237
4442.5    45.00  0.47     Sequence
 HLA-DQA10101-DQB10501  726      ISVTTEILPVSMTKT  SVTTEILPV  1        0.2033
5539.1    55.00  0.48     Sequence
 HLA-DQA10101-DQB10501  727      SVTTEILPVSMTKTS  SVTTEILPV  0        0.1560
9241.1    65.00  0.44     Sequence
 HLA-DQA10101-DQB10501  728      VTTEILPVSMTKTSV  TTEILPVSM  1        0.0761
21955.5    90.00  0.22     Sequence
 HLA-DQA10101-DQB10501  729      TTEILPVSMTKTSVD  PVSMTKTSV  5        0.0667
24301.8    95.00  0.17     Sequence
 HLA-DQA10101-DQB10501  730      TEILPVSMTKTSVDC  PVSMTKTSV  4        0.0679
23990.6    95.00  0.28     Sequence
 HLA-DQA10101-DQB10501  731      EILPVSMTKTSVDCT  PVSMTKTSV  3        0.0705
23312.3    90.00  0.28     Sequence
 HLA-DQA10101-DQB10501  732      ILPVSMTKTSVDCTM  MTKTSVDCT  5        0.0989
17142.3    85.00  0.35     Sequence
 HLA-DQA10101-DQB10501  733      LPVSMTKTSVDCTMY  MTKTSVDCT  4        0.1058
15917.3    80.00  0.38     Sequence
```

```
 HLA-DQA10101-DQB10501  734      PVSMTKTSVDCTMYI  MTKTSVDCT  3        0.1285
12444.3    75.00  0.31     Sequence
 HLA-DQA10101-DQB10501  735      VSMTKTSVDCTMYIC  MTKTSVDCT  2        0.1459
10311.8    70.00  0.28     Sequence
 HLA-DQA10101-DQB10501  736      SMTKTSVDCTMYICG  TSVDCTMYI  4        0.1410
10869.5    70.00  0.22     Sequence
 HLA-DQA10101-DQB10501  737      MTKTSVDCTMYICGD  TSVDCTMYI  3        0.1449
10423.2    70.00  0.19     Sequence
 HLA-DQA10101-DQB10501  738      TKTSVDCTMYICGDS  DCTMYICGD  5        0.1471
10183.3    70.00  0.22     Sequence
 HLA-DQA10101-DQB10501  739      KTSVDCTMYICGDST  DCTMYICGD  4        0.1635
8525.2    65.00  0.29     Sequence
 HLA-DQA10101-DQB10501  740      TSVDCTMYICGDSTE  DCTMYICGD  3        0.1746
7557.9    60.00  0.29     Sequence
 HLA-DQA10101-DQB10501  741      SVDCTMYICGDSTEC  DCTMYICGD  2        0.1747
7549.2    60.00  0.29     Sequence
 HLA-DQA10101-DQB10501  742      VDCTMYICGDSTECS  DCTMYICGD  1        0.1652
8373.0    65.00  0.26     Sequence
 HLA-DQA10101-DQB10501  743      DCTMYICGDSTECSN  CTMYICGDS  1        0.1485
10024.9    70.00  0.27     Sequence
 HLA-DQA10101-DQB10501  744      CTMYICGDSTECSNL  TMYICGDST  1        0.1302
12220.2    75.00  0.26     Sequence
 HLA-DQA10101-DQB10501  745      TMYICGDSTECSNLL  YICGDSTEC  2        0.1047
16110.9    80.00  0.23     Sequence
 HLA-DQA10101-DQB10501  746      MYICGDSTECSNLLL  YICGDSTEC  1        0.0833
20305.6    90.00  0.28     Sequence
 HLA-DQA10101-DQB10501  747      YICGDSTECSNLLLQ  TECSNLLLQ  6        0.1088
15412.8    80.00  0.19     Sequence
 HLA-DQA10101-DQB10501  748      ICGDSTECSNLLLQY  ECSNLLLQY  6        0.2225
4504.4    46.00  0.35     Sequence
 HLA-DQA10101-DQB10501  749      CGDSTECSNLLLQYG  ECSNLLLQY  5        0.2576
3078.8    37.00  0.54     Sequence
 HLA-DQA10101-DQB10501  750      GDSTECSNLLLQYGS  ECSNLLLQY  4        0.2586
3048.2    37.00  0.59     Sequence
 HLA-DQA10101-DQB10501  751      DSTECSNLLLQYGSF  ECSNLLLQY  3        0.2743
2569.6    34.00  0.54     Sequence
 HLA-DQA10101-DQB10501  752      STECSNLLLQYGSFC  ECSNLLLQY  2        0.2913
2139.0    30.00  0.46     Sequence
 HLA-DQA10101-DQB10501  753      TECSNLLLQYGSFCT  ECSNLLLQY  1        0.2925
2110.2    30.00  0.38     Sequence
 HLA-DQA10101-DQB10501  754      ECSNLLLQYGSFCTQ  LLLQYGSFC  4        0.2964
2023.2    29.00  0.33     Sequence
 HLA-DQA10101-DQB10501  755      CSNLLLQYGSFCTQL  LLLQYGSFC  3        0.2933
2093.5    30.00  0.34     Sequence
 HLA-DQA10101-DQB10501  756      SNLLLQYGSFCTQLN  LLLQYGSFC  2        0.3038
1869.0    28.00  0.28     Sequence
 HLA-DQA10101-DQB10501  757      NLLLQYGSFCTQLNR  LLLQYGSFC  1        0.2860
2264.5    31.00  0.27     Sequence
 HLA-DQA10101-DQB10501  758      LLLQYGSFCTQLNRA  QYGSFCTQL  3        0.2615
2953.0    36.00  0.31     Sequence
 HLA-DQA10101-DQB10501  759      LLQYGSFCTQLNRAL  QYGSFCTQL  2        0.2268
4297.4    45.00  0.41     Sequence
 HLA-DQA10101-DQB10501  760      LQYGSFCTQLNRALT  QYGSFCTQL  1        0.1889
6473.6    55.00  0.43     Sequence
 HLA-DQA10101-DQB10501  761      QYGSFCTQLNRALTG  QYGSFCTQL  0        0.1434
10601.3    70.00  0.34     Sequence
 HLA-DQA10101-DQB10501  762      YGSFCTQLNRALTGI  TQLNRALTG  5        0.1202
13613.2    75.00  0.32     Sequence
 HLA-DQA10101-DQB10501  763      GSFCTQLNRALTGIA  TQLNRALTG  4        0.1144
14503.5    80.00  0.45     Sequence
 HLA-DQA10101-DQB10501  764      SFCTQLNRALTGIAV  TQLNRALTG  3        0.1394
11063.0    70.00  0.33     Sequence
 HLA-DQA10101-DQB10501  765      FCTQLNRALTGIAVE  LNRALTGIA  4        0.2403
3713.9    41.00  0.22     Sequence
 HLA-DQA10101-DQB10501  766      CTQLNRALTGIAVEQ  ALTGIAVEQ  6        0.2847
2298.0    31.00  0.25     Sequence
```

```
 HLA-DQA10101-DQB10501  767      TQLNRALTGIAVEQD  ALTGIAVEQ  5        0.3437
1213.5    21.00  0.49     Sequence
 HLA-DQA10101-DQB10501  768      QLNRALTGIAVEQDK  ALTGIAVEQ  4        0.3424
1230.6    21.00  0.55     Sequence
 HLA-DQA10101-DQB10501  769      LNRALTGIAVEQDKN  ALTGIAVEQ  3        0.3304
1400.2    23.00  0.55     Sequence
 HLA-DQA10101-DQB10501  770      NRALTGIAVEQDKNT  ALTGIAVEQ  2        0.3075
1795.5    27.00  0.57     Sequence
 HLA-DQA10101-DQB10501  771      RALTGIAVEQDKNTQ  ALTGIAVEQ  1        0.2749
2552.6    33.00  0.62     Sequence
 HLA-DQA10101-DQB10501  772      ALTGIAVEQDKNTQE  ALTGIAVEQ  0        0.1887
6489.7    55.00  0.60     Sequence
 HLA-DQA10101-DQB10501  773      LTGIAVEQDKNTQEV  XLTGIAVEQ -1        0.1164
14194.1    80.00  0.27     Sequence
 HLA-DQA10101-DQB10501  774      TGIAVEQDKNTQEVF  AVEQDKNTQ  3        0.0782
21458.8    90.00  0.28     Sequence
 HLA-DQA10101-DQB10501  775      GIAVEQDKNTQEVFA  AVEQDKNTQ  2        0.0764
21873.7    90.00  0.30     Sequence
 HLA-DQA10101-DQB10501  776      IAVEQDKNTQEVFAQ  QDKNTQEVF  4        0.0867
19573.9    85.00  0.26     Sequence
 HLA-DQA10101-DQB10501  777      AVEQDKNTQEVFAQV  QDKNTQEVF  3        0.1026
16474.0    85.00  0.22     Sequence
 HLA-DQA10101-DQB10501  778      VEQDKNTQEVFAQVK  NTQEVFAQV  5        0.0976
17398.8    85.00  0.25     Sequence
 HLA-DQA10101-DQB10501  779      EQDKNTQEVFAQVKQ  TQEVFAQVK  5        0.1145
14483.8    80.00  0.33     Sequence
 HLA-DQA10101-DQB10501  780      QDKNTQEVFAQVKQI  TQEVFAQVK  4        0.1810
7057.7    60.00  0.35     Sequence
 HLA-DQA10101-DQB10501  781      DKNTQEVFAQVKQIY  QEVFAQVKQ  4        0.2042
5490.7    55.00  0.34     Sequence
 HLA-DQA10101-DQB10501  782      KNTQEVFAQVKQIYK  QEVFAQVKQ  3        0.1973
5910.6    55.00  0.34     Sequence
 HLA-DQA10101-DQB10501  783      NTQEVFAQVKQIYKT  QEVFAQVKQ  2        0.1895
6431.9    55.00  0.35     Sequence
 HLA-DQA10101-DQB10501  784      TQEVFAQVKQIYKTP  QEVFAQVKQ  1        0.1847
6778.2    60.00  0.36     Sequence
 HLA-DQA10101-DQB10501  785      QEVFAQVKQIYKTPP  QEVFAQVKQ  0        0.1885
6502.8    55.00  0.29     Sequence
 HLA-DQA10101-DQB10501  786      EVFAQVKQIYKTPPI  VKQIYKTPP  5        0.2297
4162.9    44.00  0.47     Sequence
 HLA-DQA10101-DQB10501  787      VFAQVKQIYKTPPIK  VKQIYKTPP  4        0.2536
3216.0    38.00  0.67     Sequence
 HLA-DQA10101-DQB10501  788      FAQVKQIYKTPPIKD  VKQIYKTPP  3        0.2554
3154.5    38.00  0.69     Sequence
 HLA-DQA10101-DQB10501  789      AQVKQIYKTPPIKDF  VKQIYKTPP  2        0.2840
2313.5    32.00  0.64     Sequence
 HLA-DQA10101-DQB10501  790      QVKQIYKTPPIKDFG  VKQIYKTPP  1        0.2694
2711.0    35.00  0.64     Sequence
 HLA-DQA10101-DQB10501  791      VKQIYKTPPIKDFGG  VKQIYKTPP  0        0.2427
3616.8    41.00  0.59     Sequence
 HLA-DQA10101-DQB10501  792      KQIYKTPPIKDFGGF  XKQIYKTPP -1        0.1787
7228.6    60.00  0.37     Sequence
 HLA-DQA10101-DQB10501  793      QIYKTPPIKDFGGFN  YKTPPIKDF  2        0.1163
14206.1    80.00  0.26     Sequence
 HLA-DQA10101-DQB10501  794      IYKTPPIKDFGGFNF  PIKDFGGFN  5        0.1562
9224.0    65.00  0.42     Sequence
 HLA-DQA10101-DQB10501  795      YKTPPIKDFGGFNFS  PIKDFGGFN  4        0.1655
8345.1    65.00  0.48     Sequence
 HLA-DQA10101-DQB10501  796      KTPPIKDFGGFNFSQ  PIKDFGGFN  3        0.1962
5987.5    55.00  0.35     Sequence
 HLA-DQA10101-DQB10501  797      TPPIKDFGGFNFSQI  DFGGFNFSQ  5        0.3041
1862.6    28.00  0.36     Sequence
 HLA-DQA10101-DQB10501  798      PPIKDFGGFNFSQIL  DFGGFNFSQ  4        0.3663
950.4    18.00  0.43     Sequence
 HLA-DQA10101-DQB10501  799      PIKDFGGFNFSQILP  DFGGFNFSQ  3        0.3903
732.9    15.00  0.41     Sequence
```

```
 HLA-DQA10101-DQB10501  800      IKDFGGFNFSQILPD  DFGGFNFSQ  2        0.4105
589.0    13.00  0.41     Sequence
 HLA-DQA10101-DQB10501  801      KDFGGFNFSQILPDP  DFGGFNFSQ  1        0.4033
636.4    13.00  0.37     Sequence
 HLA-DQA10101-DQB10501  802      DFGGFNFSQILPDPS  DFGGFNFSQ  0        0.3849
776.4    15.00  0.35     Sequence
 HLA-DQA10101-DQB10501  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.3316
1382.3    23.00  0.25     Sequence
 HLA-DQA10101-DQB10501  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.2687
2729.9    35.00  0.34     Sequence
 HLA-DQA10101-DQB10501  805      GFNFSQILPDPSKPS  FNFSQILPD  1        0.2358
3898.9    42.00  0.34     Sequence
 HLA-DQA10101-DQB10501  806      FNFSQILPDPSKPSK  FSQILPDPS  2        0.1957
6017.3    55.00  0.31     Sequence
 HLA-DQA10101-DQB10501  807      NFSQILPDPSKPSKR  FSQILPDPS  1        0.1148
14435.4    80.00  0.56     Sequence
 HLA-DQA10101-DQB10501  808      FSQILPDPSKPSKRS  FSQILPDPS  0        0.0656
24584.5    95.00  0.57     Sequence
 HLA-DQA10101-DQB10501  809      SQILPDPSKPSKRSF  XSQILPDPS -1        0.0263
37601.0   100.00  0.38     Sequence
 HLA-DQA10101-DQB10501  810      QILPDPSKPSKRSFI  XXQILPDPS -2        0.0162
41957.0   100.00  0.12     Sequence
 HLA-DQA10101-DQB10501  811      ILPDPSKPSKRSFIE  PSKPSKRSF  4        0.0165
41805.2   100.00  0.40     Sequence
 HLA-DQA10101-DQB10501  812      LPDPSKPSKRSFIED  PSKRSFIED  6        0.0302
36080.5   100.00  0.31     Sequence
 HLA-DQA10101-DQB10501  813      PDPSKPSKRSFIEDL  SKRSFIEDL  6        0.1746
7557.4    60.00  0.35     Sequence
 HLA-DQA10101-DQB10501  814      DPSKPSKRSFIEDLL  SKRSFIEDL  5        0.3734
879.4    17.00  0.56     Sequence
 HLA-DQA10101-DQB10501  815      PSKPSKRSFIEDLLF  SKRSFIEDL  4        0.5241
172.2     4.50  0.55     Sequence         WB
 HLA-DQA10101-DQB10501  816      SKPSKRSFIEDLLFN  SKRSFIEDL  3        0.5437
139.3     3.50  0.50     Sequence         WB
 HLA-DQA10101-DQB10501  817      KPSKRSFIEDLLFNK  SKRSFIEDL  2        0.5464
135.4     3.50  0.41     Sequence         WB
 HLA-DQA10101-DQB10501  818      PSKRSFIEDLLFNKV  SKRSFIEDL  1        0.5566
121.2     3.00  0.35     Sequence         WB
 HLA-DQA10101-DQB10501  819      SKRSFIEDLLFNKVT  SKRSFIEDL  0        0.5488
131.9     3.50  0.34     Sequence         WB
 HLA-DQA10101-DQB10501  820      KRSFIEDLLFNKVTL  FIEDLLFNK  3        0.4971
230.7     5.50  0.38     Sequence         WB
 HLA-DQA10101-DQB10501  821      RSFIEDLLFNKVTLA  FIEDLLFNK  2        0.4528
372.6     8.50  0.35     Sequence         WB
 HLA-DQA10101-DQB10501  822      SFIEDLLFNKVTLAD  FIEDLLFNK  1        0.3684
928.5    17.00  0.34     Sequence
 HLA-DQA10101-DQB10501  823      FIEDLLFNKVTLADA  DLLFNKVTL  3        0.3292
1419.3    23.00  0.37     Sequence
 HLA-DQA10101-DQB10501  824      IEDLLFNKVTLADAG  DLLFNKVTL  2        0.2762
2519.2    33.00  0.41     Sequence
 HLA-DQA10101-DQB10501  825      EDLLFNKVTLADAGF  DLLFNKVTL  1        0.2523
3262.6    38.00  0.42     Sequence
 HLA-DQA10101-DQB10501  826      DLLFNKVTLADAGFI  DLLFNKVTL  0        0.2548
3173.6    38.00  0.30     Sequence
 HLA-DQA10101-DQB10501  827      LLFNKVTLADAGFIK  NKVTLADAG  3        0.2159
4833.7    47.00  0.18     Sequence
 HLA-DQA10101-DQB10501  828      LFNKVTLADAGFIKQ  NKVTLADAG  2        0.1914
6306.8    55.00  0.20     Sequence
 HLA-DQA10101-DQB10501  829      FNKVTLADAGFIKQY  ADAGFIKQY  6        0.2192
4663.9    47.00  0.26     Sequence
 HLA-DQA10101-DQB10501  830      NKVTLADAGFIKQYG  ADAGFIKQY  5        0.2395
3744.9    42.00  0.45     Sequence
 HLA-DQA10101-DQB10501  831      KVTLADAGFIKQYGD  ADAGFIKQY  4        0.2871
2237.3    31.00  0.58     Sequence
 HLA-DQA10101-DQB10501  832      VTLADAGFIKQYGDC  ADAGFIKQY  3        0.3109
1729.9    26.00  0.56     Sequence
```

```
 HLA-DQA10101-DQB10501  833      TLADAGFIKQYGDCL  ADAGFIKQY  2        0.3647
967.0    18.00  0.46     Sequence
 HLA-DQA10101-DQB10501  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.4044
629.1    13.00  0.41     Sequence
 HLA-DQA10101-DQB10501  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4        0.4086
600.9    13.00  0.54     Sequence
 HLA-DQA10101-DQB10501  836      DAGFIKQYGDCLGDI  FIKQYGDCL  3        0.4086
601.0    13.00  0.61     Sequence
 HLA-DQA10101-DQB10501  837      AGFIKQYGDCLGDIA  FIKQYGDCL  2        0.3892
741.4    15.00  0.63     Sequence
 HLA-DQA10101-DQB10501  838      GFIKQYGDCLGDIAA  FIKQYGDCL  1        0.3540
1085.1    19.00  0.62     Sequence
 HLA-DQA10101-DQB10501  839      FIKQYGDCLGDIAAR  FIKQYGDCL  0        0.3074
1795.9    27.00  0.52     Sequence
 HLA-DQA10101-DQB10501  840      IKQYGDCLGDIAARD  XIKQYGDCL -1        0.2326
4034.2    43.00  0.23     Sequence
 HLA-DQA10101-DQB10501  841      KQYGDCLGDIAARDL  DCLGDIAAR  4        0.2075
5295.7    50.00  0.31     Sequence
 HLA-DQA10101-DQB10501  842      QYGDCLGDIAARDLI  DCLGDIAAR  3        0.2138
4948.8    48.00  0.31     Sequence
 HLA-DQA10101-DQB10501  843      YGDCLGDIAARDLIC  GDIAARDLI  5        0.2456
3505.9    40.00  0.35     Sequence
 HLA-DQA10101-DQB10501  844      GDCLGDIAARDLICA  GDIAARDLI  4        0.2603
2992.3    37.00  0.41     Sequence
 HLA-DQA10101-DQB10501  845      DCLGDIAARDLICAQ  GDIAARDLI  3        0.2688
2728.6    35.00  0.34     Sequence
 HLA-DQA10101-DQB10501  846      CLGDIAARDLICAQK  GDIAARDLI  2        0.2425
3627.3    41.00  0.37     Sequence
 HLA-DQA10101-DQB10501  847      LGDIAARDLICAQKF  GDIAARDLI  1        0.2379
3812.4    42.00  0.33     Sequence
 HLA-DQA10101-DQB10501  848      GDIAARDLICAQKFN  DIAARDLIC  1        0.2060
5382.9    50.00  0.25     Sequence
 HLA-DQA10101-DQB10501  849      DIAARDLICAQKFNG  DIAARDLIC  0        0.1770
7368.3    60.00  0.28     Sequence
 HLA-DQA10101-DQB10501  850      IAARDLICAQKFNGL  AARDLICAQ  1        0.1496
9905.0    70.00  0.22     Sequence
 HLA-DQA10101-DQB10501  851      AARDLICAQKFNGLT  ARDLICAQK  1        0.1168
14122.3    80.00  0.24     Sequence
 HLA-DQA10101-DQB10501  852      ARDLICAQKFNGLTV  ICAQKFNGL  4        0.1217
13403.8    75.00  0.25     Sequence
 HLA-DQA10101-DQB10501  853      RDLICAQKFNGLTVL  AQKFNGLTV  5        0.1894
6444.8    55.00  0.28     Sequence
 HLA-DQA10101-DQB10501  854      DLICAQKFNGLTVLP  AQKFNGLTV  4        0.2138
4944.9    48.00  0.34     Sequence
 HLA-DQA10101-DQB10501  855      LICAQKFNGLTVLPP  AQKFNGLTV  3        0.3022
1901.6    28.00  0.20     Sequence
 HLA-DQA10101-DQB10501  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.3751
863.6    17.00  0.37     Sequence
 HLA-DQA10101-DQB10501  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.3957
691.3    14.00  0.41     Sequence
 HLA-DQA10101-DQB10501  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.3855
771.5    15.00  0.43     Sequence
 HLA-DQA10101-DQB10501  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.3626
988.7    18.00  0.47     Sequence
 HLA-DQA10101-DQB10501  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1        0.3250
1484.9    24.00  0.49     Sequence
 HLA-DQA10101-DQB10501  861      FNGLTVLPPLLTDEM  FNGLTVLPP  0        0.2933
2093.5    30.00  0.46     Sequence
 HLA-DQA10101-DQB10501  862      NGLTVLPPLLTDEMI  TVLPPLLTD  3        0.1968
5948.7    55.00  0.21     Sequence
 HLA-DQA10101-DQB10501  863      GLTVLPPLLTDEMIA  LPPLLTDEM  4        0.1967
5949.2    55.00  0.28     Sequence
 HLA-DQA10101-DQB10501  864      LTVLPPLLTDEMIAQ  LLTDEMIAQ  6        0.2280
4244.0    44.00  0.26     Sequence
 HLA-DQA10101-DQB10501  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.2753
2544.1    33.00  0.44     Sequence
```

```
 HLA-DQA10101-DQB10501  866      VLPPLLTDEMIAQYT  LLTDEMIAQ  4        0.2794
2432.5    32.00  0.47     Sequence
 HLA-DQA10101-DQB10501  867      LPPLLTDEMIAQYTS  LLTDEMIAQ  3        0.2653
2833.1    36.00  0.48     Sequence
 HLA-DQA10101-DQB10501  868      PPLLTDEMIAQYTSA  LLTDEMIAQ  2        0.2423
3632.5    41.00  0.52     Sequence
 HLA-DQA10101-DQB10501  869      PLLTDEMIAQYTSAL  LLTDEMIAQ  1        0.2401
3722.2    41.00  0.47     Sequence
 HLA-DQA10101-DQB10501  870      LLTDEMIAQYTSALL  MIAQYTSAL  5        0.2905
2158.3    30.00  0.29     Sequence
 HLA-DQA10101-DQB10501  871      LTDEMIAQYTSALLA  MIAQYTSAL  4        0.3045
1855.0    27.00  0.43     Sequence
 HLA-DQA10101-DQB10501  872      TDEMIAQYTSALLAG  MIAQYTSAL  3        0.2803
2408.5    32.00  0.47     Sequence
 HLA-DQA10101-DQB10501  873      DEMIAQYTSALLAGT  MIAQYTSAL  2        0.2740
2578.1    34.00  0.47     Sequence
 HLA-DQA10101-DQB10501  874      EMIAQYTSALLAGTI  MIAQYTSAL  1        0.2704
2682.3    34.00  0.42     Sequence
 HLA-DQA10101-DQB10501  875      MIAQYTSALLAGTIT  MIAQYTSAL  0        0.2463
3481.6    40.00  0.35     Sequence
 HLA-DQA10101-DQB10501  876      IAQYTSALLAGTITS  YTSALLAGT  3        0.2035
5529.5    55.00  0.30     Sequence
 HLA-DQA10101-DQB10501  877      AQYTSALLAGTITSG  YTSALLAGT  2        0.1523
9618.9    65.00  0.37     Sequence
 HLA-DQA10101-DQB10501  878      QYTSALLAGTITSGW  YTSALLAGT  1        0.1595
8900.4    65.00  0.29     Sequence
 HLA-DQA10101-DQB10501  879      YTSALLAGTITSGWT  LLAGTITSG  4        0.1549
9352.7    65.00  0.41     Sequence
 HLA-DQA10101-DQB10501  880      TSALLAGTITSGWTF  LLAGTITSG  3        0.1528
9575.5    65.00  0.43     Sequence
 HLA-DQA10101-DQB10501  881      SALLAGTITSGWTFG  LLAGTITSG  2        0.1401
10983.2    70.00  0.38     Sequence
 HLA-DQA10101-DQB10501  882      ALLAGTITSGWTFGA  LLAGTITSG  1        0.1469
10197.2    70.00  0.31     Sequence
 HLA-DQA10101-DQB10501  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.1442
10508.1    70.00  0.36     Sequence
 HLA-DQA10101-DQB10501  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.1536
9493.8    65.00  0.57     Sequence
 HLA-DQA10101-DQB10501  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.1645
8434.6    65.00  0.56     Sequence
 HLA-DQA10101-DQB10501  886      GTITSGWTFGAGAAL  ITSGWTFGA  2        0.2365
3871.3    42.00  0.34     Sequence
 HLA-DQA10101-DQB10501  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.2471
3451.1    40.00  0.29     Sequence
 HLA-DQA10101-DQB10501  888      ITSGWTFGAGAALQI  WTFGAGAAL  4        0.3097
1752.2    26.00  0.25     Sequence
 HLA-DQA10101-DQB10501  889      TSGWTFGAGAALQIP  WTFGAGAAL  3        0.3124
1702.8    26.00  0.28     Sequence
 HLA-DQA10101-DQB10501  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.3113
1723.2    26.00  0.29     Sequence
 HLA-DQA10101-DQB10501  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.3067
1811.4    27.00  0.28     Sequence
 HLA-DQA10101-DQB10501  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.3148
1657.7    26.00  0.29     Sequence
 HLA-DQA10101-DQB10501  893      TFGAGAALQIPFAMQ  AGAALQIPF  3        0.2892
2188.9    30.00  0.28     Sequence
 HLA-DQA10101-DQB10501  894      FGAGAALQIPFAMQM  AGAALQIPF  2        0.3141
1671.2    26.00  0.25     Sequence
 HLA-DQA10101-DQB10501  895      GAGAALQIPFAMQMA  LQIPFAMQM  5        0.3459
1185.0    21.00  0.51     Sequence
 HLA-DQA10101-DQB10501  896      AGAALQIPFAMQMAY  LQIPFAMQM  4        0.3722
891.4    17.00  0.58     Sequence
 HLA-DQA10101-DQB10501  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.3466
1175.5    20.00  0.60     Sequence
 HLA-DQA10101-DQB10501  898      AALQIPFAMQMAYRF  LQIPFAMQM  2        0.3520
1109.3    20.00  0.56     Sequence
```

```
 HLA-DQA10101-DQB10501  899      ALQIPFAMQMAYRFN  LQIPFAMQM  1         0.3211
1549.6    24.00  0.54     Sequence
 HLA-DQA10101-DQB10501  900      LQIPFAMQMAYRFNG  LQIPFAMQM  0         0.2822
2359.1    32.00  0.43     Sequence
 HLA-DQA10101-DQB10501  901      QIPFAMQMAYRFNGI  MQMAYRFNG  5         0.2930
2099.2    30.00  0.32     Sequence
 HLA-DQA10101-DQB10501  902      IPFAMQMAYRFNGIG  MQMAYRFNG  4         0.2931
2098.2    30.00  0.46     Sequence
 HLA-DQA10101-DQB10501  903      PFAMQMAYRFNGIGV  MQMAYRFNG  3         0.3183
1597.6    25.00  0.44     Sequence
 HLA-DQA10101-DQB10501  904      FAMQMAYRFNGIGVT  MQMAYRFNG  2         0.3256
1475.3    24.00  0.44     Sequence
 HLA-DQA10101-DQB10501  905      AMQMAYRFNGIGVTQ  MQMAYRFNG  1         0.3040
1863.3    28.00  0.41     Sequence
 HLA-DQA10101-DQB10501  906      MQMAYRFNGIGVTQN  MQMAYRFNG  0         0.2930
2100.3    30.00  0.38     Sequence
 HLA-DQA10101-DQB10501  907      QMAYRFNGIGVTQNV  RFNGIGVTQ  4         0.2606
2981.2    37.00  0.22     Sequence
 HLA-DQA10101-DQB10501  908      MAYRFNGIGVTQNVL  RFNGIGVTQ  3         0.2158
4838.8    47.00  0.43     Sequence
 HLA-DQA10101-DQB10501  909      AYRFNGIGVTQNVLY  RFNGIGVTQ  2         0.2077
5282.8    50.00  0.42     Sequence
 HLA-DQA10101-DQB10501  910      YRFNGIGVTQNVLYE  RFNGIGVTQ  1         0.1747
7548.4    60.00  0.41     Sequence
 HLA-DQA10101-DQB10501  911      RFNGIGVTQNVLYEN  RFNGIGVTQ  0         0.1428
10659.8    70.00  0.29     Sequence
 HLA-DQA10101-DQB10501  912      FNGIGVTQNVLYENQ  GVTQNVLYE  4         0.1361
11468.7    70.00  0.25     Sequence
 HLA-DQA10101-DQB10501  913      NGIGVTQNVLYENQK  GVTQNVLYE  3         0.1310
12116.8    75.00  0.28     Sequence
 HLA-DQA10101-DQB10501  914      GIGVTQNVLYENQKL  QNVLYENQK  5         0.2342
3968.8    43.00  0.44     Sequence
 HLA-DQA10101-DQB10501  915      IGVTQNVLYENQKLI  QNVLYENQK  4         0.2971
2008.7    29.00  0.52     Sequence
 HLA-DQA10101-DQB10501  916      GVTQNVLYENQKLIA  QNVLYENQK  3         0.3132
1687.0    26.00  0.47     Sequence
 HLA-DQA10101-DQB10501  917      VTQNVLYENQKLIAN  QNVLYENQK  2         0.3110
1728.7    26.00  0.45     Sequence
 HLA-DQA10101-DQB10501  918      TQNVLYENQKLIANQ  QNVLYENQK  1         0.2942
2073.3    29.00  0.43     Sequence
 HLA-DQA10101-DQB10501  919      QNVLYENQKLIANQF  QNVLYENQK  0         0.2774
2486.4    33.00  0.37     Sequence
 HLA-DQA10101-DQB10501  920      NVLYENQKLIANQFN  XNVLYENQK -1         0.2425
3624.8    41.00  0.25     Sequence
 HLA-DQA10101-DQB10501  921      VLYENQKLIANQFNS  ENQKLIANQ  3         0.1889
6474.2    55.00  0.25     Sequence
 HLA-DQA10101-DQB10501  922      LYENQKLIANQFNSA  ENQKLIANQ  2         0.1713
7837.7    60.00  0.25     Sequence
 HLA-DQA10101-DQB10501  923      YENQKLIANQFNSAI  LIANQFNSA  5         0.2165
4805.5    47.00  0.41     Sequence
 HLA-DQA10101-DQB10501  924      ENQKLIANQFNSAIG  LIANQFNSA  4         0.2143
4919.9    48.00  0.47     Sequence
 HLA-DQA10101-DQB10501  925      NQKLIANQFNSAIGK  LIANQFNSA  3         0.2046
5465.1    50.00  0.46     Sequence
 HLA-DQA10101-DQB10501  926      QKLIANQFNSAIGKI  LIANQFNSA  2         0.2087
5228.5    49.00  0.46     Sequence
 HLA-DQA10101-DQB10501  927      KLIANQFNSAIGKIQ  LIANQFNSA  1         0.1947
6081.5    55.00  0.43     Sequence
 HLA-DQA10101-DQB10501  928      LIANQFNSAIGKIQD  LIANQFNSA  0         0.1732
7675.9    60.00  0.34     Sequence
 HLA-DQA10101-DQB10501  929      IANQFNSAIGKIQDS  NQFNSAIGK  2         0.1354
11548.7    70.00  0.28     Sequence
 HLA-DQA10101-DQB10501  930      ANQFNSAIGKIQDSL  SAIGKIQDS  5         0.1401
10983.0    70.00  0.28     Sequence
 HLA-DQA10101-DQB10501  931      NQFNSAIGKIQDSLS  SAIGKIQDS  4         0.1567
9174.9    65.00  0.38     Sequence
```

```
 HLA-DQA10101-DQB10501  932      QFNSAIGKIQDSLSS  SAIGKIQDS  3        0.1499
9876.8    70.00  0.46     Sequence
 HLA-DQA10101-DQB10501  933      FNSAIGKIQDSLSST  SAIGKIQDS  2        0.1405
10929.7    70.00  0.46     Sequence
 HLA-DQA10101-DQB10501  934      NSAIGKIQDSLSSTA  SAIGKIQDS  1        0.1289
12398.4    75.00  0.47     Sequence
 HLA-DQA10101-DQB10501  935      SAIGKIQDSLSSTAS  SAIGKIQDS  0        0.1148
14439.3    80.00  0.38     Sequence
 HLA-DQA10101-DQB10501  936      AIGKIQDSLSSTASA  AIGKIQDSL  0        0.0769
21760.6    90.00  0.28     Sequence
 HLA-DQA10101-DQB10501  937      IGKIQDSLSSTASAL  KIQDSLSST  2        0.0561
27246.5    95.00  0.30     Sequence
 HLA-DQA10101-DQB10501  938      GKIQDSLSSTASALG  KIQDSLSST  1        0.0500
29107.4    95.00  0.28     Sequence
 HLA-DQA10101-DQB10501  939      KIQDSLSSTASALGK  SLSSTASAL  4        0.0444
30931.9   100.00  0.31     Sequence
 HLA-DQA10101-DQB10501  940      IQDSLSSTASALGKL  SLSSTASAL  3        0.0476
29872.8   100.00  0.38     Sequence
 HLA-DQA10101-DQB10501  941      QDSLSSTASALGKLQ  SSTASALGK  4        0.0506
28911.2    95.00  0.32     Sequence
 HLA-DQA10101-DQB10501  942      DSLSSTASALGKLQD  SSTASALGK  3        0.0529
28207.3    95.00  0.25     Sequence
 HLA-DQA10101-DQB10501  943      SLSSTASALGKLQDV  SALGKLQDV  6        0.1242
13039.0    75.00  0.28     Sequence
 HLA-DQA10101-DQB10501  944      LSSTASALGKLQDVV  SALGKLQDV  5        0.1868
6622.6    55.00  0.38     Sequence
 HLA-DQA10101-DQB10501  945      SSTASALGKLQDVVN  SALGKLQDV  4        0.2030
5562.9    55.00  0.40     Sequence
 HLA-DQA10101-DQB10501  946      STASALGKLQDVVNQ  SALGKLQDV  3        0.2045
5471.9    50.00  0.37     Sequence
 HLA-DQA10101-DQB10501  947      TASALGKLQDVVNQN  SALGKLQDV  2        0.2032
5548.0    55.00  0.35     Sequence
 HLA-DQA10101-DQB10501  948      ASALGKLQDVVNQNA  SALGKLQDV  1        0.2223
4512.4    46.00  0.29     Sequence
 HLA-DQA10101-DQB10501  949      SALGKLQDVVNQNAQ  KLQDVVNQN  4        0.2091
5203.5    49.00  0.31     Sequence
 HLA-DQA10101-DQB10501  950      ALGKLQDVVNQNAQA  KLQDVVNQN  3        0.1467
10221.9    70.00  0.47     Sequence
 HLA-DQA10101-DQB10501  951      LGKLQDVVNQNAQAL  KLQDVVNQN  2        0.1462
10275.8    70.00  0.47     Sequence
 HLA-DQA10101-DQB10501  952      GKLQDVVNQNAQALN  KLQDVVNQN  1        0.1294
12326.6    75.00  0.44     Sequence
 HLA-DQA10101-DQB10501  953      KLQDVVNQNAQALNT  KLQDVVNQN  0        0.1159
14267.7    80.00  0.31     Sequence
 HLA-DQA10101-DQB10501  954      LQDVVNQNAQALNTL  NQNAQALNT  5        0.1224
13294.7    75.00  0.25     Sequence
 HLA-DQA10101-DQB10501  955      QDVVNQNAQALNTLV  NQNAQALNT  4        0.1669
8218.8    65.00  0.41     Sequence
 HLA-DQA10101-DQB10501  956      DVVNQNAQALNTLVK  NQNAQALNT  3        0.1581
9041.5    65.00  0.43     Sequence
 HLA-DQA10101-DQB10501  957      VVNQNAQALNTLVKQ  NQNAQALNT  2        0.1656
8332.0    65.00  0.36     Sequence
 HLA-DQA10101-DQB10501  958      VNQNAQALNTLVKQL  NQNAQALNT  1        0.1750
7531.3    60.00  0.30     Sequence
 HLA-DQA10101-DQB10501  959      NQNAQALNTLVKQLS  QALNTLVKQ  4        0.1662
8278.8    65.00  0.29     Sequence
 HLA-DQA10101-DQB10501  960      QNAQALNTLVKQLSS  QALNTLVKQ  3        0.1484
10040.3    70.00  0.32     Sequence
 HLA-DQA10101-DQB10501  961      NAQALNTLVKQLSSN  QALNTLVKQ  2        0.1197
13692.1    75.00  0.35     Sequence
 HLA-DQA10101-DQB10501  962      AQALNTLVKQLSSNF  QALNTLVKQ  1        0.0997
17004.5    85.00  0.38     Sequence
 HLA-DQA10101-DQB10501  963      QALNTLVKQLSSNFG  QALNTLVKQ  0        0.0841
20131.0    90.00  0.32     Sequence
 HLA-DQA10101-DQB10501  964      ALNTLVKQLSSNFGA  LVKQLSSNF  4        0.0641
25002.7    95.00  0.26     Sequence
```

```
 HLA-DQA10101-DQB10501  965      LNTLVKQLSSNFGAI  LVKQLSSNF  3        0.0927
18338.2    85.00  0.25     Sequence
 HLA-DQA10101-DQB10501  966      NTLVKQLSSNFGAIS  QLSSNFGAI  5        0.1201
13633.4    75.00  0.31     Sequence
 HLA-DQA10101-DQB10501  967      TLVKQLSSNFGAISS  QLSSNFGAI  4        0.1326
11906.3    75.00  0.33     Sequence
 HLA-DQA10101-DQB10501  968      LVKQLSSNFGAISSV  LSSNFGAIS  4        0.1969
5939.4    55.00  0.32     Sequence
 HLA-DQA10101-DQB10501  969      VKQLSSNFGAISSVL  SSNFGAISS  4        0.2352
3925.5    43.00  0.28     Sequence
 HLA-DQA10101-DQB10501  970      KQLSSNFGAISSVLN  SSNFGAISS  3        0.2383
3796.8    42.00  0.28     Sequence
 HLA-DQA10101-DQB10501  971      QLSSNFGAISSVLND  SSNFGAISS  2        0.2341
3973.4    43.00  0.29     Sequence
 HLA-DQA10101-DQB10501  972      LSSNFGAISSVLNDI  SSNFGAISS  1        0.2267
4302.5    45.00  0.26     Sequence
 HLA-DQA10101-DQB10501  973      SSNFGAISSVLNDIL  GAISSVLND  4        0.2834
2329.5    32.00  0.29     Sequence
 HLA-DQA10101-DQB10501  974      SNFGAISSVLNDILS  AISSVLNDI  4        0.2773
2487.6    33.00  0.35     Sequence
 HLA-DQA10101-DQB10501  975      NFGAISSVLNDILSR  AISSVLNDI  3        0.2587
3042.4    37.00  0.41     Sequence
 HLA-DQA10101-DQB10501  976      FGAISSVLNDILSRL  AISSVLNDI  2        0.2778
2475.7    33.00  0.31     Sequence
 HLA-DQA10101-DQB10501  977      GAISSVLNDILSRLD  SVLNDILSR  4        0.2684
2740.6    35.00  0.26     Sequence
 HLA-DQA10101-DQB10501  978      AISSVLNDILSRLDK  SVLNDILSR  3        0.2536
3216.5    38.00  0.28     Sequence
 HLA-DQA10101-DQB10501  979      ISSVLNDILSRLDKV  SVLNDILSR  2        0.2497
3353.4    39.00  0.28     Sequence
 HLA-DQA10101-DQB10501  980      SSVLNDILSRLDKVE  SVLNDILSR  1        0.2553
3156.8    38.00  0.22     Sequence
 HLA-DQA10101-DQB10501  981      SVLNDILSRLDKVEA  DILSRLDKV  4        0.2467
3466.7    40.00  0.27     Sequence
 HLA-DQA10101-DQB10501  982      VLNDILSRLDKVEAE  DILSRLDKV  3        0.2373
3838.2    42.00  0.31     Sequence
 HLA-DQA10101-DQB10501  983      LNDILSRLDKVEAEV  DILSRLDKV  2        0.2432
3597.6    41.00  0.32     Sequence
 HLA-DQA10101-DQB10501  984      NDILSRLDKVEAEVQ  DILSRLDKV  1        0.2338
3982.2    43.00  0.31     Sequence
 HLA-DQA10101-DQB10501  985      DILSRLDKVEAEVQI  LSRLDKVEA  2        0.2271
4281.7    45.00  0.20     Sequence
 HLA-DQA10101-DQB10501  986      ILSRLDKVEAEVQID  LSRLDKVEA  1        0.1958
6008.1    55.00  0.22     Sequence
 HLA-DQA10101-DQB10501  987      LSRLDKVEAEVQIDR  SRLDKVEAE  1        0.1798
7143.9    60.00  0.19     Sequence
 HLA-DQA10101-DQB10501  988      SRLDKVEAEVQIDRL  VEAEVQIDR  5        0.2111
5094.1    49.00  0.34     Sequence
 HLA-DQA10101-DQB10501  989      RLDKVEAEVQIDRLI  VEAEVQIDR  4        0.2932
2096.0    30.00  0.43     Sequence
 HLA-DQA10101-DQB10501  990      LDKVEAEVQIDRLIT  VEAEVQIDR  3        0.2910
2146.7    30.00  0.45     Sequence
 HLA-DQA10101-DQB10501  991      DKVEAEVQIDRLITG  VEAEVQIDR  2        0.2716
2646.6    34.00  0.43     Sequence
 HLA-DQA10101-DQB10501  992      KVEAEVQIDRLITGR  VEAEVQIDR  1        0.2459
3496.6    40.00  0.42     Sequence
 HLA-DQA10101-DQB10501  993      VEAEVQIDRLITGRL  EAEVQIDRL  1        0.2248
4393.7    45.00  0.33     Sequence
 HLA-DQA10101-DQB10501  994      EAEVQIDRLITGRLQ  EAEVQIDRL  0        0.1844
6800.6    60.00  0.31     Sequence
 HLA-DQA10101-DQB10501  995      AEVQIDRLITGRLQS  VQIDRLITG  2        0.1398
11012.0    70.00  0.31     Sequence
 HLA-DQA10101-DQB10501  996      EVQIDRLITGRLQSL  RLITGRLQS  5        0.1451
10399.4    70.00  0.31     Sequence
 HLA-DQA10101-DQB10501  997      VQIDRLITGRLQSLQ  RLITGRLQS  4        0.1607
8786.0    65.00  0.38     Sequence
```

```
 HLA-DQA10101-DQB10501  998      QIDRLITGRLQSLQT  RLITGRLQS  3        0.1628
8589.8    65.00  0.40     Sequence
 HLA-DQA10101-DQB10501  999      IDRLITGRLQSLQTY  LITGRLQSL  3        0.1700
7942.7    60.00  0.34     Sequence
 HLA-DQA10101-DQB10501 1000      DRLITGRLQSLQTYV  LITGRLQSL  2        0.1896
6428.9    55.00  0.22     Sequence
 HLA-DQA10101-DQB10501 1001      RLITGRLQSLQTYVT  LITGRLQSL  1        0.1932
6180.3    55.00  0.20     Sequence
 HLA-DQA10101-DQB10501 1002      LITGRLQSLQTYVTQ  RLQSLQTYV  4        0.1866
6640.8    55.00  0.19     Sequence
 HLA-DQA10101-DQB10501 1003      ITGRLQSLQTYVTQQ  SLQTYVTQQ  6        0.1975
5903.7    55.00  0.24     Sequence
 HLA-DQA10101-DQB10501 1004      TGRLQSLQTYVTQQL  SLQTYVTQQ  5        0.3601
1016.5    18.00  0.56     Sequence
 HLA-DQA10101-DQB10501 1005      GRLQSLQTYVTQQLI  SLQTYVTQQ  4        0.4164
552.6    12.00  0.65     Sequence
 HLA-DQA10101-DQB10501 1006      RLQSLQTYVTQQLIR  SLQTYVTQQ  3        0.4009
653.6    14.00  0.69     Sequence
 HLA-DQA10101-DQB10501 1007      LQSLQTYVTQQLIRA  SLQTYVTQQ  2        0.3869
760.0    15.00  0.69     Sequence
 HLA-DQA10101-DQB10501 1008      QSLQTYVTQQLIRAA  SLQTYVTQQ  1        0.3558
1064.0    19.00  0.64     Sequence
 HLA-DQA10101-DQB10501 1009      SLQTYVTQQLIRAAE  SLQTYVTQQ  0        0.2906
2155.2    30.00  0.51     Sequence
 HLA-DQA10101-DQB10501 1010      LQTYVTQQLIRAAEI  TQQLIRAAE  5        0.2870
2240.2    31.00  0.20     Sequence
 HLA-DQA10101-DQB10501 1011      QTYVTQQLIRAAEIR  TQQLIRAAE  4        0.2776
2480.7    33.00  0.40     Sequence
 HLA-DQA10101-DQB10501 1012      TYVTQQLIRAAEIRA  TQQLIRAAE  3        0.2795
2429.9    32.00  0.41     Sequence
 HLA-DQA10101-DQB10501 1013      YVTQQLIRAAEIRAS  TQQLIRAAE  2        0.2750
2552.3    33.00  0.40     Sequence
 HLA-DQA10101-DQB10501 1014      VTQQLIRAAEIRASA  TQQLIRAAE  1        0.2649
2846.2    36.00  0.35     Sequence
 HLA-DQA10101-DQB10501 1015      TQQLIRAAEIRASAN  TQQLIRAAE  0        0.2427
3617.3    41.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1016      QQLIRAAEIRASANL  LIRAAEIRA  2        0.2119
5047.7    49.00  0.26     Sequence
 HLA-DQA10101-DQB10501 1017      QLIRAAEIRASANLA  LIRAAEIRA  1        0.1478
10103.4    70.00  0.38     Sequence
 HLA-DQA10101-DQB10501 1018      LIRAAEIRASANLAA  EIRASANLA  5        0.1447
10451.9    70.00  0.29     Sequence
 HLA-DQA10101-DQB10501 1019      IRAAEIRASANLAAI  EIRASANLA  4        0.1705
7902.7    60.00  0.41     Sequence
 HLA-DQA10101-DQB10501 1020      RAAEIRASANLAAIK  EIRASANLA  3        0.1588
8967.4    65.00  0.34     Sequence
 HLA-DQA10101-DQB10501 1021      AAEIRASANLAAIKM  EIRASANLA  2        0.1617
8692.4    65.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.1668
8225.4    65.00  0.33     Sequence
 HLA-DQA10101-DQB10501 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.1559
9254.5    65.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1024      IRASANLAAIKMSEC  NLAAIKMSE  5        0.1720
7774.8    60.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1025      RASANLAAIKMSECV  NLAAIKMSE  4        0.1814
7023.7    60.00  0.51     Sequence
 HLA-DQA10101-DQB10501 1026      ASANLAAIKMSECVL  NLAAIKMSE  3        0.1867
6631.1    55.00  0.57     Sequence
 HLA-DQA10101-DQB10501 1027      SANLAAIKMSECVLG  NLAAIKMSE  2        0.1702
7926.5    60.00  0.58     Sequence
 HLA-DQA10101-DQB10501 1028      ANLAAIKMSECVLGQ  NLAAIKMSE  1        0.1574
9101.7    65.00  0.55     Sequence
 HLA-DQA10101-DQB10501 1029      NLAAIKMSECVLGQS  NLAAIKMSE  0        0.1401
10984.6    70.00  0.41     Sequence
 HLA-DQA10101-DQB10501 1030      LAAIKMSECVLGQSK  XLAAIKMSE -1        0.1068
15738.4    80.00  0.20     Sequence
```

```
 HLA-DQA10101-DQB10501 1031      AAIKMSECVLGQSKR  KMSECVLGQ  3        0.0732
22643.8    90.00  0.29     Sequence
 HLA-DQA10101-DQB10501 1032      AIKMSECVLGQSKRV  KMSECVLGQ  2        0.0660
24487.3    95.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1033      IKMSECVLGQSKRVD  KMSECVLGQ  1        0.0593
26315.9    95.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1034      KMSECVLGQSKRVDF  LGQSKRVDF  6        0.0721
22917.6    90.00  0.22     Sequence
 HLA-DQA10101-DQB10501 1035      MSECVLGQSKRVDFC  LGQSKRVDF  5        0.0875
19407.7    85.00  0.39     Sequence
 HLA-DQA10101-DQB10501 1036      SECVLGQSKRVDFCG  LGQSKRVDF  4        0.0975
17417.3    85.00  0.41     Sequence
 HLA-DQA10101-DQB10501 1037      ECVLGQSKRVDFCGK  LGQSKRVDF  3        0.0948
17924.3    85.00  0.40     Sequence
 HLA-DQA10101-DQB10501 1038      CVLGQSKRVDFCGKG  LGQSKRVDF  2        0.0851
19915.3    90.00  0.38     Sequence
 HLA-DQA10101-DQB10501 1039      VLGQSKRVDFCGKGY  LGQSKRVDF  1        0.0850
19940.5    90.00  0.35     Sequence
 HLA-DQA10101-DQB10501 1040      LGQSKRVDFCGKGYH  KRVDFCGKG  4        0.0830
20362.8    90.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1041      GQSKRVDFCGKGYHL  KRVDFCGKG  3        0.0790
21274.7    90.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1042      QSKRVDFCGKGYHLM  KRVDFCGKG  2        0.0964
17625.0    85.00  0.25     Sequence
 HLA-DQA10101-DQB10501 1043      SKRVDFCGKGYHLMS  DFCGKGYHL  4        0.1129
14734.9    80.00  0.23     Sequence
 HLA-DQA10101-DQB10501 1044      KRVDFCGKGYHLMSF  CGKGYHLMS  5        0.1828
6915.5    60.00  0.41     Sequence
 HLA-DQA10101-DQB10501 1045      RVDFCGKGYHLMSFP  CGKGYHLMS  4        0.2863
2257.0    31.00  0.55     Sequence
 HLA-DQA10101-DQB10501 1046      VDFCGKGYHLMSFPQ  CGKGYHLMS  3        0.3096
1754.8    27.00  0.49     Sequence
 HLA-DQA10101-DQB10501 1047      DFCGKGYHLMSFPQS  CGKGYHLMS  2        0.3379
1292.1    22.00  0.39     Sequence
 HLA-DQA10101-DQB10501 1048      FCGKGYHLMSFPQSA  CGKGYHLMS  1        0.3656
957.1    18.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.3824
798.5    16.00  0.37     Sequence
 HLA-DQA10101-DQB10501 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.3767
848.6    16.00  0.43     Sequence
 HLA-DQA10101-DQB10501 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.3422
1232.4    21.00  0.52     Sequence
 HLA-DQA10101-DQB10501 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.2997
1952.7    28.00  0.60     Sequence
 HLA-DQA10101-DQB10501 1053      YHLMSFPQSAPHGVV  HLMSFPQSA  1        0.2644
2860.1    36.00  0.65     Sequence
 HLA-DQA10101-DQB10501 1054      HLMSFPQSAPHGVVF  HLMSFPQSA  0        0.1844
6800.5    60.00  0.62     Sequence
 HLA-DQA10101-DQB10501 1055      LMSFPQSAPHGVVFL  XLMSFPQSA -1        0.0906
18766.3    85.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1056      MSFPQSAPHGVVFLH  QSAPHGVVF  4        0.0585
26549.8    95.00  0.33     Sequence
 HLA-DQA10101-DQB10501 1057      SFPQSAPHGVVFLHV  QSAPHGVVF  3        0.0742
22394.0    90.00  0.30     Sequence
 HLA-DQA10101-DQB10501 1058      FPQSAPHGVVFLHVT  PHGVVFLHV  5        0.0842
20109.3    90.00  0.30     Sequence
 HLA-DQA10101-DQB10501 1059      PQSAPHGVVFLHVTY  PHGVVFLHV  4        0.1220
13359.6    75.00  0.25     Sequence
 HLA-DQA10101-DQB10501 1060      QSAPHGVVFLHVTYV  GVVFLHVTY  5        0.1648
8403.9    65.00  0.47     Sequence
 HLA-DQA10101-DQB10501 1061      SAPHGVVFLHVTYVP  GVVFLHVTY  4        0.2175
4753.2    47.00  0.56     Sequence
 HLA-DQA10101-DQB10501 1062      APHGVVFLHVTYVPA  GVVFLHVTY  3        0.2506
3322.6    39.00  0.44     Sequence
 HLA-DQA10101-DQB10501 1063      PHGVVFLHVTYVPAQ  GVVFLHVTY  2        0.2754
2540.5    33.00  0.37     Sequence
```

```
 HLA-DQA10101-DQB10501 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.3142
1669.2    26.00  0.35     Sequence
 HLA-DQA10101-DQB10501 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.2978
1994.1    29.00  0.34     Sequence
 HLA-DQA10101-DQB10501 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.2791
2441.8    33.00  0.38     Sequence
 HLA-DQA10101-DQB10501 1067      VFLHVTYVPAQEKNF  FLHVTYVPA  1        0.2517
3284.5    39.00  0.43     Sequence
 HLA-DQA10101-DQB10501 1068      FLHVTYVPAQEKNFT  FLHVTYVPA  0        0.2107
5115.4    49.00  0.41     Sequence
 HLA-DQA10101-DQB10501 1069      LHVTYVPAQEKNFTT  LHVTYVPAQ  0        0.1405
10931.6   70.00  0.32      Sequence
 HLA-DQA10101-DQB10501 1070      HVTYVPAQEKNFTTA  HVTYVPAQE  0        0.0895
18985.9   85.00  0.35      Sequence
 HLA-DQA10101-DQB10501 1071      VTYVPAQEKNFTTAP  QEKNFTTAP  6        0.0712
23142.4   90.00  0.25      Sequence
 HLA-DQA10101-DQB10501 1072      TYVPAQEKNFTTAPA  QEKNFTTAP  5        0.1109
15054.7   80.00  0.56      Sequence
 HLA-DQA10101-DQB10501 1073      YVPAQEKNFTTAPAI  QEKNFTTAP  4        0.1761
7435.4    60.00  0.61     Sequence
 HLA-DQA10101-DQB10501 1074      VPAQEKNFTTAPAIC  QEKNFTTAP  3        0.1858
6698.6    60.00  0.56     Sequence
 HLA-DQA10101-DQB10501 1075      PAQEKNFTTAPAICH  QEKNFTTAP  2        0.1882
6523.8    55.00  0.47     Sequence
 HLA-DQA10101-DQB10501 1076      AQEKNFTTAPAICHD  QEKNFTTAP  1        0.1906
6358.5    55.00  0.44     Sequence
 HLA-DQA10101-DQB10501 1077      QEKNFTTAPAICHDG  QEKNFTTAP  0        0.1624
8627.6    65.00  0.38     Sequence
 HLA-DQA10101-DQB10501 1078      EKNFTTAPAICHDGK  XEKNFTTAP -1        0.1290
12381.1   75.00  0.23      Sequence
 HLA-DQA10101-DQB10501 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.0893
19033.2   85.00  0.29      Sequence
 HLA-DQA10101-DQB10501 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.0661
24453.2   95.00  0.34      Sequence
 HLA-DQA10101-DQB10501 1081      FTTAPAICHDGKAHF  ICHDGKAHF  6        0.0720
22932.0   90.00  0.26      Sequence
 HLA-DQA10101-DQB10501 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.0880
19301.6   85.00  0.55      Sequence
 HLA-DQA10101-DQB10501 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.0875
19404.8   85.00  0.60      Sequence
 HLA-DQA10101-DQB10501 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.0918
18517.2   85.00  0.52      Sequence
 HLA-DQA10101-DQB10501 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.0849
19958.4   90.00  0.49      Sequence
 HLA-DQA10101-DQB10501 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.1010
16757.7   85.00  0.31      Sequence
 HLA-DQA10101-DQB10501 1087      ICHDGKAHFPREGVF  GKAHFPREG  4        0.1187
13848.1   80.00  0.34      Sequence
 HLA-DQA10101-DQB10501 1088      CHDGKAHFPREGVFV  GKAHFPREG  3        0.1144
14497.9   80.00  0.38      Sequence
 HLA-DQA10101-DQB10501 1089      HDGKAHFPREGVFVS  GKAHFPREG  2        0.1222
13328.7   75.00  0.31      Sequence
 HLA-DQA10101-DQB10501 1090      DGKAHFPREGVFVSN  PREGVFVSN  6        0.1343
11686.3   75.00  0.31      Sequence
 HLA-DQA10101-DQB10501 1091      GKAHFPREGVFVSNG  PREGVFVSN  5        0.1433
10603.4   70.00  0.45      Sequence
 HLA-DQA10101-DQB10501 1092      KAHFPREGVFVSNGT  PREGVFVSN  4        0.1485
10030.8   70.00  0.48      Sequence
 HLA-DQA10101-DQB10501 1093      AHFPREGVFVSNGTH  PREGVFVSN  3        0.1340
11729.3   75.00  0.51      Sequence
 HLA-DQA10101-DQB10501 1094      HFPREGVFVSNGTHW  PREGVFVSN  2        0.1267
12688.9   75.00  0.49      Sequence
 HLA-DQA10101-DQB10501 1095      FPREGVFVSNGTHWF  PREGVFVSN  1        0.1216
13408.9   75.00  0.40      Sequence
 HLA-DQA10101-DQB10501 1096      PREGVFVSNGTHWFV  VFVSNGTHW  4        0.1443
10488.4   70.00  0.35      Sequence
```

```
 HLA-DQA10101-DQB10501 1097      REGVFVSNGTHWFVT  VFVSNGTHW  3        0.1486
10011.5    70.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1098      EGVFVSNGTHWFVTQ  VFVSNGTHW  2        0.1696
7976.9    60.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1099      GVFVSNGTHWFVTQR  NGTHWFVTQ  5        0.2129
4993.0    48.00  0.38     Sequence
 HLA-DQA10101-DQB10501 1100      VFVSNGTHWFVTQRN  NGTHWFVTQ  4        0.2979
1990.5    29.00  0.43     Sequence
 HLA-DQA10101-DQB10501 1101      FVSNGTHWFVTQRNF  GTHWFVTQR  4        0.3256
1475.5    24.00  0.47     Sequence
 HLA-DQA10101-DQB10501 1102      VSNGTHWFVTQRNFY  GTHWFVTQR  3        0.3516
1114.0    20.00  0.46     Sequence
 HLA-DQA10101-DQB10501 1103      SNGTHWFVTQRNFYE  GTHWFVTQR  2        0.3479
1158.7    20.00  0.44     Sequence
 HLA-DQA10101-DQB10501 1104      NGTHWFVTQRNFYEP  GTHWFVTQR  1        0.3500
1133.4    20.00  0.41     Sequence
 HLA-DQA10101-DQB10501 1105      GTHWFVTQRNFYEPQ  GTHWFVTQR  0        0.4042
630.4    13.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1106      THWFVTQRNFYEPQI  TQRNFYEPQ  5        0.5690
106.0     2.50  0.61     Sequence         WB
 HLA-DQA10101-DQB10501 1107      HWFVTQRNFYEPQII  TQRNFYEPQ  4        0.6860
29.9     0.50  0.69     Sequence         SB
 HLA-DQA10101-DQB10501 1108      WFVTQRNFYEPQIIT  TQRNFYEPQ  3        0.6894
28.8     0.50  0.66     Sequence         SB
 HLA-DQA10101-DQB10501 1109      FVTQRNFYEPQIITT  TQRNFYEPQ  2        0.6830
30.9     0.50  0.62     Sequence         SB
 HLA-DQA10101-DQB10501 1110      VTQRNFYEPQIITTD  TQRNFYEPQ  1        0.6620
38.8     0.70  0.61     Sequence         SB
 HLA-DQA10101-DQB10501 1111      TQRNFYEPQIITTDN  TQRNFYEPQ  0        0.6134
65.6     1.40  0.56     Sequence         SB
 HLA-DQA10101-DQB10501 1112      QRNFYEPQIITTDNT  XQRNFYEPQ -1        0.4905
247.9     6.00  0.34     Sequence         WB
 HLA-DQA10101-DQB10501 1113      RNFYEPQIITTDNTF  XRNFYEPQI -1        0.3143
1667.2    26.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1114      NFYEPQIITTDNTFV  FYEPQIITT  1        0.1662
8280.1    65.00  0.35     Sequence
 HLA-DQA10101-DQB10501 1115      FYEPQIITTDNTFVS  PQIITTDNT  3        0.1431
10628.4    70.00  0.30     Sequence
 HLA-DQA10101-DQB10501 1116      YEPQIITTDNTFVSG  PQIITTDNT  2        0.1236
13125.2    75.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1117      EPQIITTDNTFVSGN  PQIITTDNT  1        0.1194
13738.4    75.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1118      PQIITTDNTFVSGNC  PQIITTDNT  0        0.1190
13793.7    80.00  0.20     Sequence
 HLA-DQA10101-DQB10501 1119      QIITTDNTFVSGNCD  TDNTFVSGN  4        0.1249
12948.8    75.00  0.23     Sequence
 HLA-DQA10101-DQB10501 1120      IITTDNTFVSGNCDV  TDNTFVSGN  3        0.1561
9235.4    65.00  0.24     Sequence
 HLA-DQA10101-DQB10501 1121      ITTDNTFVSGNCDVV  FVSGNCDVV  6        0.2252
4371.7    45.00  0.35     Sequence
 HLA-DQA10101-DQB10501 1122      TTDNTFVSGNCDVVI  FVSGNCDVV  5        0.4019
646.2    13.00  0.62     Sequence
 HLA-DQA10101-DQB10501 1123      TDNTFVSGNCDVVIG  FVSGNCDVV  4        0.4039
632.3    13.00  0.65     Sequence
 HLA-DQA10101-DQB10501 1124      DNTFVSGNCDVVIGI  FVSGNCDVV  3        0.4215
522.6    11.00  0.62     Sequence
 HLA-DQA10101-DQB10501 1125      NTFVSGNCDVVIGIV  FVSGNCDVV  2        0.4193
535.1    12.00  0.60     Sequence
 HLA-DQA10101-DQB10501 1126      TFVSGNCDVVIGIVN  FVSGNCDVV  1        0.3957
691.2    14.00  0.57     Sequence
 HLA-DQA10101-DQB10501 1127      FVSGNCDVVIGIVNN  FVSGNCDVV  0        0.3319
1378.3    23.00  0.54     Sequence
 HLA-DQA10101-DQB10501 1128      VSGNCDVVIGIVNNT  XVSGNCDVV -1        0.2499
3346.5    39.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1129      SGNCDVVIGIVNNTV  VVIGIVNNT  5        0.2414
3668.8    41.00  0.56     Sequence
```

```
 HLA-DQA10101-DQB10501 1130      GNCDVVIGIVNNTVY  VVIGIVNNT  4        0.2811
2388.0    32.00  0.68     Sequence
 HLA-DQA10101-DQB10501 1131      NCDVVIGIVNNTVYD  VVIGIVNNT  3        0.2861
2262.8    31.00  0.70     Sequence
 HLA-DQA10101-DQB10501 1132      CDVVIGIVNNTVYDP  VVIGIVNNT  2        0.3008
1928.9    28.00  0.63     Sequence
 HLA-DQA10101-DQB10501 1133      DVVIGIVNNTVYDPL  VVIGIVNNT  1        0.3268
1456.4    23.00  0.51     Sequence
 HLA-DQA10101-DQB10501 1134      VVIGIVNNTVYDPLQ  VVIGIVNNT  0        0.3349
1334.8    22.00  0.36     Sequence
 HLA-DQA10101-DQB10501 1135      VIGIVNNTVYDPLQP  VNNTVYDPL  4        0.3245
1493.8    24.00  0.48     Sequence
 HLA-DQA10101-DQB10501 1136      IGIVNNTVYDPLQPE  VNNTVYDPL  3        0.3002
1941.7    28.00  0.52     Sequence
 HLA-DQA10101-DQB10501 1137      GIVNNTVYDPLQPEL  VNNTVYDPL  2        0.3032
1879.8    28.00  0.47     Sequence
 HLA-DQA10101-DQB10501 1138      IVNNTVYDPLQPELD  VNNTVYDPL  1        0.3025
1894.7    28.00  0.43     Sequence
 HLA-DQA10101-DQB10501 1139      VNNTVYDPLQPELDS  VNNTVYDPL  0        0.2618
2944.2    36.00  0.34     Sequence
 HLA-DQA10101-DQB10501 1140      NNTVYDPLQPELDSF  TVYDPLQPE  2        0.2246
4402.1    45.00  0.23     Sequence
 HLA-DQA10101-DQB10501 1141      NTVYDPLQPELDSFK  TVYDPLQPE  1        0.1998
5755.4    55.00  0.23     Sequence
 HLA-DQA10101-DQB10501 1142      TVYDPLQPELDSFKE  PLQPELDSF  4        0.1926
6220.0    55.00  0.40     Sequence
 HLA-DQA10101-DQB10501 1143      VYDPLQPELDSFKEE  PLQPELDSF  3        0.2021
5613.7    55.00  0.44     Sequence
 HLA-DQA10101-DQB10501 1144      YDPLQPELDSFKEEL  ELDSFKEEL  6        0.3155
1645.8    25.00  0.34     Sequence
 HLA-DQA10101-DQB10501 1145      DPLQPELDSFKEELD  ELDSFKEEL  5        0.4446
407.1     9.00  0.62     Sequence          WB
 HLA-DQA10101-DQB10501 1146      PLQPELDSFKEELDK  ELDSFKEEL  4        0.4459
401.4     9.00  0.69     Sequence          WB
 HLA-DQA10101-DQB10501 1147      LQPELDSFKEELDKY  ELDSFKEEL  3        0.4517
376.9     8.50  0.69     Sequence          WB
 HLA-DQA10101-DQB10501 1148      QPELDSFKEELDKYF  ELDSFKEEL  2        0.4437
411.1     9.00  0.67     Sequence          WB
 HLA-DQA10101-DQB10501 1149      PELDSFKEELDKYFK  ELDSFKEEL  1        0.4179
543.5    12.00  0.69     Sequence
 HLA-DQA10101-DQB10501 1150      ELDSFKEELDKYFKN  ELDSFKEEL  0        0.3517
1112.5    20.00  0.60     Sequence
 HLA-DQA10101-DQB10501 1151      LDSFKEELDKYFKNH  XLDSFKEEL -1        0.2208
4585.1    46.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1152      DSFKEELDKYFKNHT  LDKYFKNHT  6        0.2032
5550.1    55.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1153      SFKEELDKYFKNHTS  LDKYFKNHT  5        0.2298
4159.2    44.00  0.41     Sequence
 HLA-DQA10101-DQB10501 1154      FKEELDKYFKNHTSP  LDKYFKNHT  4        0.2658
2817.8    35.00  0.55     Sequence
 HLA-DQA10101-DQB10501 1155      KEELDKYFKNHTSPD  LDKYFKNHT  3        0.2594
3021.4    37.00  0.60     Sequence
 HLA-DQA10101-DQB10501 1156      EELDKYFKNHTSPDV  LDKYFKNHT  2        0.2588
3038.7    37.00  0.55     Sequence
 HLA-DQA10101-DQB10501 1157      ELDKYFKNHTSPDVD  LDKYFKNHT  1        0.2345
3956.0    43.00  0.54     Sequence
 HLA-DQA10101-DQB10501 1158      LDKYFKNHTSPDVDL  LDKYFKNHT  0        0.2009
5689.9    55.00  0.35     Sequence
 HLA-DQA10101-DQB10501 1159      DKYFKNHTSPDVDLG  YFKNHTSPD  2        0.1475
10141.0    70.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1160      KYFKNHTSPDVDLGD  YFKNHTSPD  1        0.1481
10072.9    70.00  0.26     Sequence
 HLA-DQA10101-DQB10501 1161      YFKNHTSPDVDLGDI  NHTSPDVDL  3        0.1496
9904.9    70.00  0.24     Sequence
 HLA-DQA10101-DQB10501 1162      FKNHTSPDVDLGDIS  NHTSPDVDL  2        0.1381
11215.8    70.00  0.29     Sequence
```

```
 HLA-DQA10101-DQB10501 1163      KNHTSPDVDLGDISG  HTSPDVDLG  2        0.1237
13114.6    75.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1164      NHTSPDVDLGDISGI  PDVDLGDIS  4        0.1682
8105.9    65.00  0.25     Sequence
 HLA-DQA10101-DQB10501 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.1542
9429.8    65.00  0.25     Sequence
 HLA-DQA10101-DQB10501 1166      TSPDVDLGDISGINA  VDLGDISGI  4        0.1534
9507.3    65.00  0.27     Sequence
 HLA-DQA10101-DQB10501 1167      SPDVDLGDISGINAS  VDLGDISGI  3        0.1468
10216.4    70.00  0.25     Sequence
 HLA-DQA10101-DQB10501 1168      PDVDLGDISGINASF  VDLGDISGI  2        0.1467
10223.1    70.00  0.25     Sequence
 HLA-DQA10101-DQB10501 1169      DVDLGDISGINASFV  DISGINASF  5        0.2011
5672.6    55.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1170      VDLGDISGINASFVN  DISGINASF  4        0.2102
5141.0    49.00  0.41     Sequence
 HLA-DQA10101-DQB10501 1171      DLGDISGINASFVNI  DISGINASF  3        0.2206
4595.7    46.00  0.42     Sequence
 HLA-DQA10101-DQB10501 1172      LGDISGINASFVNIQ  DISGINASF  2        0.2553
3158.2    38.00  0.29     Sequence
 HLA-DQA10101-DQB10501 1173      GDISGINASFVNIQK  GINASFVNI  4        0.2600
2999.8    37.00  0.36     Sequence
 HLA-DQA10101-DQB10501 1174      DISGINASFVNIQKE  INASFVNIQ  4        0.2916
2131.9    30.00  0.40     Sequence
 HLA-DQA10101-DQB10501 1175      ISGINASFVNIQKEI  INASFVNIQ  3        0.2984
1980.0    29.00  0.44     Sequence
 HLA-DQA10101-DQB10501 1176      SGINASFVNIQKEID  INASFVNIQ  2        0.2877
2223.7    31.00  0.41     Sequence
 HLA-DQA10101-DQB10501 1177      GINASFVNIQKEIDR  INASFVNIQ  1        0.2677
2761.9    35.00  0.38     Sequence
 HLA-DQA10101-DQB10501 1178      INASFVNIQKEIDRL  INASFVNIQ  0        0.2546
3179.9    38.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1179      NASFVNIQKEIDRLN  VNIQKEIDR  4        0.2034
5534.1    55.00  0.22     Sequence
 HLA-DQA10101-DQB10501 1180      ASFVNIQKEIDRLNE  VNIQKEIDR  3        0.1812
7041.3    60.00  0.26     Sequence
 HLA-DQA10101-DQB10501 1181      SFVNIQKEIDRLNEV  VNIQKEIDR  2        0.1735
7649.8    60.00  0.27     Sequence
 HLA-DQA10101-DQB10501 1182      FVNIQKEIDRLNEVA  KEIDRLNEV  5        0.1748
7540.3    60.00  0.22     Sequence
 HLA-DQA10101-DQB10501 1183      VNIQKEIDRLNEVAK  KEIDRLNEV  4        0.1524
9614.8    65.00  0.26     Sequence
 HLA-DQA10101-DQB10501 1184      NIQKEIDRLNEVAKN  KEIDRLNEV  3        0.1461
10289.4    70.00  0.27     Sequence
 HLA-DQA10101-DQB10501 1185      IQKEIDRLNEVAKNL  KEIDRLNEV  2        0.1501
9850.5    70.00  0.26     Sequence
 HLA-DQA10101-DQB10501 1186      QKEIDRLNEVAKNLN  IDRLNEVAK  3        0.1352
11584.7    75.00  0.23     Sequence
 HLA-DQA10101-DQB10501 1187      KEIDRLNEVAKNLNE  IDRLNEVAK  2        0.1228
13244.5    75.00  0.27     Sequence
 HLA-DQA10101-DQB10501 1188      EIDRLNEVAKNLNES  IDRLNEVAK  1        0.1034
16326.5    80.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1189      IDRLNEVAKNLNESL  NEVAKNLNE  4        0.1156
14310.2    80.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1190      DRLNEVAKNLNESLI  NEVAKNLNE  3        0.1289
12397.2    75.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.1420
10754.2    70.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1192      LNEVAKNLNESLIDL  VAKNLNESL  3        0.1905
6365.1    55.00  0.27     Sequence
 HLA-DQA10101-DQB10501 1193      NEVAKNLNESLIDLQ  NLNESLIDL  5        0.2514
3294.8    39.00  0.38     Sequence
 HLA-DQA10101-DQB10501 1194      EVAKNLNESLIDLQE  NLNESLIDL  4        0.3033
1878.8    28.00  0.38     Sequence
 HLA-DQA10101-DQB10501 1195      VAKNLNESLIDLQEL  LNESLIDLQ  4        0.3968
682.7    14.00  0.41     Sequence
```

```
 HLA-DQA10101-DQB10501 1196      AKNLNESLIDLQELG  LNESLIDLQ  3        0.3929
712.8    14.00  0.36     Sequence
 HLA-DQA10101-DQB10501 1197      KNLNESLIDLQELGK  LNESLIDLQ  2        0.3753
862.3    17.00  0.35     Sequence
 HLA-DQA10101-DQB10501 1198      NLNESLIDLQELGKY  LNESLIDLQ  1        0.3566
1054.7    19.00  0.34     Sequence
 HLA-DQA10101-DQB10501 1199      LNESLIDLQELGKYE  LNESLIDLQ  0        0.3142
1670.2    26.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1200      NESLIDLQELGKYEQ  NESLIDLQE  0        0.2442
3558.6    40.00  0.34     Sequence
 HLA-DQA10101-DQB10501 1201      ESLIDLQELGKYEQY  QELGKYEQY  6        0.2855
2278.3    31.00  0.27     Sequence
 HLA-DQA10101-DQB10501 1202      SLIDLQELGKYEQYI  QELGKYEQY  5        0.3450
1196.6    21.00  0.56     Sequence
 HLA-DQA10101-DQB10501 1203      LIDLQELGKYEQYIK  QELGKYEQY  4        0.3671
941.8    18.00  0.61     Sequence
 HLA-DQA10101-DQB10501 1204      IDLQELGKYEQYIKW  QELGKYEQY  3        0.3798
821.0    16.00  0.62     Sequence
 HLA-DQA10101-DQB10501 1205      DLQELGKYEQYIKWP  QELGKYEQY  2        0.3774
842.4    16.00  0.61     Sequence
 HLA-DQA10101-DQB10501 1206      LQELGKYEQYIKWPW  QELGKYEQY  1        0.3917
721.5    15.00  0.50     Sequence
 HLA-DQA10101-DQB10501 1207      QELGKYEQYIKWPWY  QELGKYEQY  0        0.3967
683.8    14.00  0.38     Sequence
 HLA-DQA10101-DQB10501 1208      ELGKYEQYIKWPWYI  YEQYIKWPW  4        0.3547
1076.6    19.00  0.41     Sequence
 HLA-DQA10101-DQB10501 1209      LGKYEQYIKWPWYIW  YEQYIKWPW  3        0.3612
1004.3    18.00  0.40     Sequence
 HLA-DQA10101-DQB10501 1210      GKYEQYIKWPWYIWL  YEQYIKWPW  2        0.3813
807.7    16.00  0.34     Sequence
 HLA-DQA10101-DQB10501 1211      KYEQYIKWPWYIWLG  YEQYIKWPW  1        0.3760
855.6    16.00  0.30     Sequence
 HLA-DQA10101-DQB10501 1212      YEQYIKWPWYIWLGF  IKWPWYIWL  4        0.3959
689.7    14.00  0.21     Sequence
 HLA-DQA10101-DQB10501 1213      EQYIKWPWYIWLGFI  IKWPWYIWL  3        0.3720
893.4    17.00  0.23     Sequence
 HLA-DQA10101-DQB10501 1214      QYIKWPWYIWLGFIA  WPWYIWLGF  4        0.3848
777.5    15.00  0.22     Sequence
 HLA-DQA10101-DQB10501 1215      YIKWPWYIWLGFIAG  WPWYIWLGF  3        0.3624
991.0    18.00  0.24     Sequence
 HLA-DQA10101-DQB10501 1216      IKWPWYIWLGFIAGL  WPWYIWLGF  2        0.4045
628.5    13.00  0.17     Sequence
 HLA-DQA10101-DQB10501 1217      KWPWYIWLGFIAGLI  IWLGFIAGL  5        0.5278
165.5     4.00  0.50     Sequence         WB
 HLA-DQA10101-DQB10501 1218      WPWYIWLGFIAGLIA  IWLGFIAGL  4        0.5635
112.4     3.00  0.62     Sequence         WB
 HLA-DQA10101-DQB10501 1219      PWYIWLGFIAGLIAI  IWLGFIAGL  3        0.5755
98.8     2.50  0.66     Sequence         WB
 HLA-DQA10101-DQB10501 1220      WYIWLGFIAGLIAIV  IWLGFIAGL  2        0.5918
82.8     1.90  0.63     Sequence         SB
 HLA-DQA10101-DQB10501 1221      YIWLGFIAGLIAIVM  IWLGFIAGL  1        0.5819
92.2     2.50  0.61     Sequence         WB
 HLA-DQA10101-DQB10501 1222      IWLGFIAGLIAIVMV  IWLGFIAGL  0        0.5569
120.8     3.00  0.56     Sequence         WB
 HLA-DQA10101-DQB10501 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3        0.4692
312.0     7.50  0.31     Sequence         WB
 HLA-DQA10101-DQB10501 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.3749
865.4    17.00  0.49     Sequence
 HLA-DQA10101-DQB10501 1225      GFIAGLIAIVMVTIM  FIAGLIAIV  1        0.3053
1837.7    27.00  0.54     Sequence
 HLA-DQA10101-DQB10501 1226      FIAGLIAIVMVTIML  FIAGLIAIV  0        0.2587
3044.4    37.00  0.47     Sequence
 HLA-DQA10101-DQB10501 1227      IAGLIAIVMVTIMLC  GLIAIVMVT  2        0.2002
5732.8    55.00  0.29     Sequence
 HLA-DQA10101-DQB10501 1228      AGLIAIVMVTIMLCC  GLIAIVMVT  1        0.1784
7259.5    60.00  0.24     Sequence
```

```
 HLA-DQA10101-DQB10501 1229      GLIAIVMVTIMLCCM  IVMVTIMLC  4         0.1927
6216.0    55.00  0.26     Sequence
 HLA-DQA10101-DQB10501 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3         0.1905
6365.4    55.00  0.26     Sequence
 HLA-DQA10101-DQB10501 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2         0.1783
7264.6    60.00  0.27     Sequence
 HLA-DQA10101-DQB10501 1232      AIVMVTIMLCCMTSC  IVMVTIMLC  1         0.1943
6109.3    55.00  0.20     Sequence
 HLA-DQA10101-DQB10501 1233      IVMVTIMLCCMTSCC  TIMLCCMTS  4         0.1977
5887.0    55.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1234      VMVTIMLCCMTSCCS  TIMLCCMTS  3         0.1834
6869.8    60.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1235      MVTIMLCCMTSCCSC  TIMLCCMTS  2         0.1814
7024.6    60.00  0.35     Sequence
 HLA-DQA10101-DQB10501 1236      VTIMLCCMTSCCSCL  TIMLCCMTS  1         0.1793
7182.4    60.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1237      TIMLCCMTSCCSCLK  TIMLCCMTS  0         0.1726
7723.8    60.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1238      IMLCCMTSCCSCLKG  CCMTSCCSC  3         0.1411
10866.7    70.00  0.26     Sequence
 HLA-DQA10101-DQB10501 1239      MLCCMTSCCSCLKGC  CCMTSCCSC  2         0.1021
16573.4    85.00  0.38     Sequence
 HLA-DQA10101-DQB10501 1240      LCCMTSCCSCLKGCC  CCMTSCCSC  1         0.0900
18873.6    85.00  0.40     Sequence
 HLA-DQA10101-DQB10501 1241      CCMTSCCSCLKGCCS  CCMTSCCSC  0         0.0742
22393.1    90.00  0.30     Sequence
 HLA-DQA10101-DQB10501 1242      CMTSCCSCLKGCCSC  SCCSCLKGC  3         0.0658
24544.6    95.00  0.34     Sequence
 HLA-DQA10101-DQB10501 1243      MTSCCSCLKGCCSCG  SCCSCLKGC  2         0.0580
26681.1    95.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1244      TSCCSCLKGCCSCGS  SCLKGCCSC  4         0.0615
25709.4    95.00  0.26     Sequence
 HLA-DQA10101-DQB10501 1245      SCCSCLKGCCSCGSC  CLKGCCSCG  4         0.0628
25351.1    95.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1246      CCSCLKGCCSCGSCC  CLKGCCSCG  3         0.0590
26409.7    95.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1247      CSCLKGCCSCGSCCK  CLKGCCSCG  2         0.0532
28104.6    95.00  0.33     Sequence
 HLA-DQA10101-DQB10501 1248      SCLKGCCSCGSCCKF  CLKGCCSCG  1         0.0505
28960.3    95.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1249      CLKGCCSCGSCCKFD  CSCGSCCKF  5         0.0383
33033.7   100.00  0.17     Sequence
 HLA-DQA10101-DQB10501 1250      LKGCCSCGSCCKFDE  CSCGSCCKF  4         0.0537
27963.0    95.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1251      KGCCSCGSCCKFDED  CSCGSCCKF  3         0.0666
24334.4    95.00  0.28     Sequence
 HLA-DQA10101-DQB10501 1252      GCCSCGSCCKFDEDD  SCCKFDEDD  6         0.1004
16865.7    85.00  0.23     Sequence
 HLA-DQA10101-DQB10501 1253      CCSCGSCCKFDEDDS  SCCKFDEDD  5         0.1252
12906.2    75.00  0.29     Sequence
 HLA-DQA10101-DQB10501 1254      CSCGSCCKFDEDDSE  CCKFDEDDS  5         0.1749
7535.9    60.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1255      SCGSCCKFDEDDSEP  CCKFDEDDS  4         0.1939
6133.4    55.00  0.38     Sequence
 HLA-DQA10101-DQB10501 1256      CGSCCKFDEDDSEPV  CCKFDEDDS  3         0.2204
4607.5    46.00  0.34     Sequence
 HLA-DQA10101-DQB10501 1257      GSCCKFDEDDSEPVL  CCKFDEDDS  2         0.2299
4157.7    44.00  0.33     Sequence
 HLA-DQA10101-DQB10501 1258      SCCKFDEDDSEPVLK  CCKFDEDDS  1         0.2177
4741.4    47.00  0.31     Sequence
 HLA-DQA10101-DQB10501 1259      CCKFDEDDSEPVLKG  CCKFDEDDS  0         0.1906
6357.0    55.00  0.33     Sequence
 HLA-DQA10101-DQB10501 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2         0.1598
8872.6    65.00  0.32     Sequence
 HLA-DQA10101-DQB10501 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1         0.1003
16883.3    85.00  0.41     Sequence
```

```
 HLA-DQA10101-DQB10501 1262      FDEDDSEPVLKGVKL  FDEDDSEPV  0        0.0735
22565.3    90.00  0.30     Sequence
 HLA-DQA10101-DQB10501 1263      DEDDSEPVLKGVKLH  VLKGVKLHX  7        0.0631
25269.0    95.00  0.12     Sequence
 HLA-DQA10101-DQB10501 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.1264
12729.6    75.00  0.39     Sequence
 HLA-DQA10101-DQB10501 1265      DDSEPVLKGVKLHYT  VLKGVKLHY  5        0.1764
7413.6    60.00  0.64     Sequence
 HLA-DQA10102-DQB10602    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.2116
5068.6    75.00  0.50     Sequence
 HLA-DQA10102-DQB10602    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2        0.1889
6476.7    85.00  0.54     Sequence
 HLA-DQA10102-DQB10602    3      PIKEMFVFLVLLPLV  IKEMFVFLV  1        0.1754
7498.3    85.00  0.43     Sequence
 HLA-DQA10102-DQB10602    4      IKEMFVFLVLLPLVS  IKEMFVFLV  0        0.1828
6920.5    85.00  0.26     Sequence
 HLA-DQA10102-DQB10602    5      KEMFVFLVLLPLVSS  LVLLPLVSS  6        0.2323
4047.8    70.00  0.44     Sequence
 HLA-DQA10102-DQB10602    6      EMFVFLVLLPLVSSQ  LVLLPLVSS  5        0.2816
2375.2    55.00  0.58     Sequence
 HLA-DQA10102-DQB10602    7      MFVFLVLLPLVSSQC  LVLLPLVSS  4        0.3198
1571.5    41.00  0.52     Sequence
 HLA-DQA10102-DQB10602    8      FVFLVLLPLVSSQCV  LVLLPLVSS  3        0.3310
1392.5    38.00  0.50     Sequence
 HLA-DQA10102-DQB10602    9      VFLVLLPLVSSQCVN  LVLLPLVSS  2        0.3193
1579.4    41.00  0.46     Sequence
 HLA-DQA10102-DQB10602   10      FLVLLPLVSSQCVNF  LVLLPLVSS  1        0.3051
1841.8    46.00  0.34     Sequence
 HLA-DQA10102-DQB10602   11      LVLLPLVSSQCVNFT  LPLVSSQCV  3        0.2875
2227.9    55.00  0.20     Sequence
 HLA-DQA10102-DQB10602   12      VLLPLVSSQCVNFTN  VSSQCVNFT  5        0.2789
2444.6    55.00  0.29     Sequence
 HLA-DQA10102-DQB10602   13      LLPLVSSQCVNFTNR  VSSQCVNFT  4        0.2684
2740.5    60.00  0.27     Sequence
 HLA-DQA10102-DQB10602   14      LPLVSSQCVNFTNRT  VSSQCVNFT  3        0.2567
3110.9    65.00  0.30     Sequence
 HLA-DQA10102-DQB10602   15      PLVSSQCVNFTNRTQ  SSQCVNFTN  3        0.2430
3607.1    65.00  0.32     Sequence
 HLA-DQA10102-DQB10602   16      LVSSQCVNFTNRTQL  SSQCVNFTN  2        0.2422
3639.5    65.00  0.31     Sequence
 HLA-DQA10102-DQB10602   17      VSSQCVNFTNRTQLP  NFTNRTQLP  6        0.2555
3150.5    65.00  0.31     Sequence
 HLA-DQA10102-DQB10602   18      SSQCVNFTNRTQLPS  NFTNRTQLP  5        0.2893
2186.4    55.00  0.49     Sequence
 HLA-DQA10102-DQB10602   19      SQCVNFTNRTQLPSA  NFTNRTQLP  4        0.3212
1548.4    41.00  0.47     Sequence
 HLA-DQA10102-DQB10602   20      QCVNFTNRTQLPSAY  NFTNRTQLP  3        0.3621
994.4    30.00  0.41     Sequence
 HLA-DQA10102-DQB10602   21      CVNFTNRTQLPSAYT  TNRTQLPSA  4        0.3640
974.2    30.00  0.31     Sequence
 HLA-DQA10102-DQB10602   22      VNFTNRTQLPSAYTN  TNRTQLPSA  3        0.3420
1236.0    35.00  0.34     Sequence
 HLA-DQA10102-DQB10602   23      NFTNRTQLPSAYTNS  TNRTQLPSA  2        0.2918
2126.3    50.00  0.39     Sequence
 HLA-DQA10102-DQB10602   24      FTNRTQLPSAYTNSF  TNRTQLPSA  1        0.2356
3906.4    70.00  0.34     Sequence
 HLA-DQA10102-DQB10602   25      TNRTQLPSAYTNSFT  TQLPSAYTN  3        0.1952
6049.5    80.00  0.25     Sequence
 HLA-DQA10102-DQB10602   26      NRTQLPSAYTNSFTR  TQLPSAYTN  2        0.1811
7044.5    85.00  0.25     Sequence
 HLA-DQA10102-DQB10602   27      RTQLPSAYTNSFTRG  SAYTNSFTR  5        0.1812
7041.7    85.00  0.41     Sequence
 HLA-DQA10102-DQB10602   28      TQLPSAYTNSFTRGV  YTNSFTRGV  6        0.2651
2839.9    60.00  0.43     Sequence
 HLA-DQA10102-DQB10602   29      QLPSAYTNSFTRGVY  YTNSFTRGV  5        0.3343
1343.4    37.00  0.62     Sequence
```

```
 HLA-DQA10102-DQB10602   30      LPSAYTNSFTRGVYY  YTNSFTRGV  4        0.4024
642.9    21.00  0.49     Sequence
 HLA-DQA10102-DQB10602   31      PSAYTNSFTRGVYYP  YTNSFTRGV  3        0.4144
564.5    19.00  0.43     Sequence
 HLA-DQA10102-DQB10602   32      SAYTNSFTRGVYYPD  YTNSFTRGV  2        0.4185
539.9    18.00  0.40     Sequence
 HLA-DQA10102-DQB10602   33      AYTNSFTRGVYYPDK  NSFTRGVYY  3        0.4001
659.0    21.00  0.41     Sequence
 HLA-DQA10102-DQB10602   34      YTNSFTRGVYYPDKV  NSFTRGVYY  2        0.3664
948.5    29.00  0.44     Sequence
 HLA-DQA10102-DQB10602   35      TNSFTRGVYYPDKVF  NSFTRGVYY  1        0.2989
1969.2    48.00  0.44     Sequence
 HLA-DQA10102-DQB10602   36      NSFTRGVYYPDKVFR  NSFTRGVYY  0        0.2136
4956.2    75.00  0.40     Sequence
 HLA-DQA10102-DQB10602   37      SFTRGVYYPDKVFRS  YYPDKVFRS  6        0.1756
7480.4    85.00  0.34     Sequence
 HLA-DQA10102-DQB10602   38      FTRGVYYPDKVFRSS  YYPDKVFRS  5        0.2241
4427.4    75.00  0.58     Sequence
 HLA-DQA10102-DQB10602   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.2334
4001.6    70.00  0.64     Sequence
 HLA-DQA10102-DQB10602   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.2606
2981.4    60.00  0.57     Sequence
 HLA-DQA10102-DQB10602   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.2535
3219.4    65.00  0.50     Sequence
 HLA-DQA10102-DQB10602   42      VYYPDKVFRSSVLHS  VFRSSVLHS  6        0.3514
1116.8    33.00  0.39     Sequence
 HLA-DQA10102-DQB10602   43      YYPDKVFRSSVLHST  VFRSSVLHS  5        0.5199
180.3     5.50  0.47     Sequence         WB
 HLA-DQA10102-DQB10602   44      YPDKVFRSSVLHSTQ  FRSSVLHST  5        0.5908
83.7     1.80  0.53     Sequence         SB
 HLA-DQA10102-DQB10602   45      PDKVFRSSVLHSTQD  FRSSVLHST  4        0.6177
62.6     1.10  0.50     Sequence         SB
 HLA-DQA10102-DQB10602   46      DKVFRSSVLHSTQDL  FRSSVLHST  3        0.6118
66.7     1.30  0.50     Sequence         SB
 HLA-DQA10102-DQB10602   47      KVFRSSVLHSTQDLF  FRSSVLHST  2        0.5827
91.3     2.50  0.51     Sequence         WB
 HLA-DQA10102-DQB10602   48      VFRSSVLHSTQDLFL  FRSSVLHST  1        0.5183
183.5     5.50  0.44     Sequence         WB
 HLA-DQA10102-DQB10602   49      FRSSVLHSTQDLFLP  FRSSVLHST  0        0.3959
689.9    22.00  0.37     Sequence
 HLA-DQA10102-DQB10602   50      RSSVLHSTQDLFLPF  LHSTQDLFL  4        0.3155
1645.2    43.00  0.29     Sequence
 HLA-DQA10102-DQB10602   51      SSVLHSTQDLFLPFF  LHSTQDLFL  3        0.2883
2210.3    55.00  0.32     Sequence
 HLA-DQA10102-DQB10602   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2        0.2784
2458.5    55.00  0.29     Sequence
 HLA-DQA10102-DQB10602   53      VLHSTQDLFLPFFSN  HSTQDLFLP  2        0.2667
2792.2    60.00  0.22     Sequence
 HLA-DQA10102-DQB10602   54      LHSTQDLFLPFFSNV  DLFLPFFSN  5        0.2558
3140.9    65.00  0.26     Sequence
 HLA-DQA10102-DQB10602   55      HSTQDLFLPFFSNVT  DLFLPFFSN  4        0.2319
4068.7    70.00  0.34     Sequence
 HLA-DQA10102-DQB10602   56      STQDLFLPFFSNVTW  DLFLPFFSN  3        0.2177
4741.5    75.00  0.40     Sequence
 HLA-DQA10102-DQB10602   57      TQDLFLPFFSNVTWF  DLFLPFFSN  2        0.2147
4896.5    75.00  0.40     Sequence
 HLA-DQA10102-DQB10602   58      QDLFLPFFSNVTWFH  DLFLPFFSN  1        0.2339
3979.7    70.00  0.26     Sequence
 HLA-DQA10102-DQB10602   59      DLFLPFFSNVTWFHA  FSNVTWFHA  6        0.3553
1070.4    32.00  0.31     Sequence
 HLA-DQA10102-DQB10602   60      LFLPFFSNVTWFHAI  FSNVTWFHA  5        0.4388
433.7    15.00  0.41     Sequence
 HLA-DQA10102-DQB10602   61      FLPFFSNVTWFHAIH  FSNVTWFHA  4        0.4497
385.2    13.00  0.41     Sequence
 HLA-DQA10102-DQB10602   62      LPFFSNVTWFHAIHV  FSNVTWFHA  3        0.4564
358.5    12.00  0.39     Sequence
```

```
 HLA-DQA10102-DQB10602   63      PFFSNVTWFHAIHVS  FSNVTWFHA  2        0.4724
301.5    10.00  0.31     Sequence
 HLA-DQA10102-DQB10602   64      FFSNVTWFHAIHVSG  TWFHAIHVS  5        0.4950
236.1     7.50  0.32     Sequence         WB
 HLA-DQA10102-DQB10602   65      FSNVTWFHAIHVSGT  TWFHAIHVS  4        0.4893
251.0     8.00  0.38     Sequence         WB
 HLA-DQA10102-DQB10602   66      SNVTWFHAIHVSGTN  FHAIHVSGT  5        0.5021
218.6     7.00  0.38     Sequence         WB
 HLA-DQA10102-DQB10602   67      NVTWFHAIHVSGTNG  FHAIHVSGT  4        0.4971
230.8     7.50  0.44     Sequence         WB
 HLA-DQA10102-DQB10602   68      VTWFHAIHVSGTNGT  FHAIHVSGT  3        0.4784
282.6     9.50  0.47     Sequence         WB
 HLA-DQA10102-DQB10602   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.4396
429.8    15.00  0.55     Sequence
 HLA-DQA10102-DQB10602   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1        0.3809
811.0    26.00  0.54     Sequence
 HLA-DQA10102-DQB10602   71      FHAIHVSGTNGTKRF  FHAIHVSGT  0        0.2695
2707.2    60.00  0.43     Sequence
 HLA-DQA10102-DQB10602   72      HAIHVSGTNGTKRFD  IHVSGTNGT  2        0.1795
7167.8    85.00  0.40     Sequence
 HLA-DQA10102-DQB10602   73      AIHVSGTNGTKRFDN  VSGTNGTKR  3        0.1666
8243.3    90.00  0.22     Sequence
 HLA-DQA10102-DQB10602   74      IHVSGTNGTKRFDNP  TNGTKRFDN  5        0.1549
9358.9    90.00  0.41     Sequence
 HLA-DQA10102-DQB10602   75      HVSGTNGTKRFDNPV  TNGTKRFDN  4        0.1469
10202.0    90.00  0.53     Sequence
 HLA-DQA10102-DQB10602   76      VSGTNGTKRFDNPVL  TNGTKRFDN  3        0.1363
11445.9    95.00  0.60     Sequence
 HLA-DQA10102-DQB10602   77      SGTNGTKRFDNPVLP  TNGTKRFDN  2        0.1220
13353.6    95.00  0.58     Sequence
 HLA-DQA10102-DQB10602   78      GTNGTKRFDNPVLPF  TNGTKRFDN  1        0.1366
11400.1    95.00  0.35     Sequence
 HLA-DQA10102-DQB10602   79      TNGTKRFDNPVLPFN  RFDNPVLPF  5        0.1495
9916.7    90.00  0.38     Sequence
 HLA-DQA10102-DQB10602   80      NGTKRFDNPVLPFND  RFDNPVLPF  4        0.1829
6907.8    85.00  0.37     Sequence
 HLA-DQA10102-DQB10602   81      GTKRFDNPVLPFNDG  DNPVLPFND  5        0.2031
5552.3    80.00  0.35     Sequence
 HLA-DQA10102-DQB10602   82      TKRFDNPVLPFNDGV  DNPVLPFND  4        0.2079
5273.5    80.00  0.35     Sequence
 HLA-DQA10102-DQB10602   83      KRFDNPVLPFNDGVY  DNPVLPFND  3        0.2000
5745.2    80.00  0.37     Sequence
 HLA-DQA10102-DQB10602   84      RFDNPVLPFNDGVYF  DNPVLPFND  2        0.1827
6924.8    85.00  0.38     Sequence
 HLA-DQA10102-DQB10602   85      FDNPVLPFNDGVYFA  DNPVLPFND  1        0.1676
8156.3    90.00  0.24     Sequence
 HLA-DQA10102-DQB10602   86      DNPVLPFNDGVYFAS  PFNDGVYFA  5        0.2469
3457.1    65.00  0.43     Sequence
 HLA-DQA10102-DQB10602   87      NPVLPFNDGVYFAST  PFNDGVYFA  4        0.3133
1685.7    43.00  0.37     Sequence
 HLA-DQA10102-DQB10602   88      PVLPFNDGVYFASTE  NDGVYFAST  5        0.3463
1180.1    34.00  0.38     Sequence
 HLA-DQA10102-DQB10602   89      VLPFNDGVYFASTEK  NDGVYFAST  4        0.3440
1209.6    35.00  0.43     Sequence
 HLA-DQA10102-DQB10602   90      LPFNDGVYFASTEKS  NDGVYFAST  3        0.3642
971.6    29.00  0.37     Sequence
 HLA-DQA10102-DQB10602   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.3642
972.1    29.00  0.43     Sequence
 HLA-DQA10102-DQB10602   92      FNDGVYFASTEKSNI  VYFASTEKS  4        0.3596
1021.1    31.00  0.47     Sequence
 HLA-DQA10102-DQB10602   93      NDGVYFASTEKSNII  VYFASTEKS  3        0.3586
1032.9    31.00  0.54     Sequence
 HLA-DQA10102-DQB10602   94      DGVYFASTEKSNIIR  VYFASTEKS  2        0.3318
1380.6    38.00  0.50     Sequence
 HLA-DQA10102-DQB10602   95      GVYFASTEKSNIIRG  VYFASTEKS  1        0.3308
1395.5    38.00  0.35     Sequence
```

```
 HLA-DQA10102-DQB10602   96      VYFASTEKSNIIRGW  TEKSNIIRG  5         0.3547
1077.4    32.00  0.38     Sequence
 HLA-DQA10102-DQB10602   97      YFASTEKSNIIRGWI  EKSNIIRGW  5         0.3912
725.7    23.00  0.38     Sequence
 HLA-DQA10102-DQB10602   98      FASTEKSNIIRGWIF  EKSNIIRGW  4         0.4663
322.0    11.00  0.34     Sequence
 HLA-DQA10102-DQB10602   99      ASTEKSNIIRGWIFG  EKSNIIRGW  3         0.4487
389.5    13.00  0.33     Sequence
 HLA-DQA10102-DQB10602  100      STEKSNIIRGWIFGT  EKSNIIRGW  2         0.4319
467.4    16.00  0.32     Sequence
 HLA-DQA10102-DQB10602  101      TEKSNIIRGWIFGTT  EKSNIIRGW  1         0.3997
662.2    22.00  0.26     Sequence
 HLA-DQA10102-DQB10602  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4         0.3601
1016.3    30.00  0.31     Sequence
 HLA-DQA10102-DQB10602  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3         0.3231
1515.9    40.00  0.38     Sequence
 HLA-DQA10102-DQB10602  104      SNIIRGWIFGTTLDS  IIRGWIFGT  2         0.3196
1574.2    41.00  0.34     Sequence
 HLA-DQA10102-DQB10602  105      NIIRGWIFGTTLDSK  IFGTTLDSK  6         0.3495
1139.9    33.00  0.51     Sequence
 HLA-DQA10102-DQB10602  106      IIRGWIFGTTLDSKT  IFGTTLDSK  5         0.4040
631.9    21.00  0.69     Sequence
 HLA-DQA10102-DQB10602  107      IRGWIFGTTLDSKTQ  IFGTTLDSK  4         0.4144
564.6    19.00  0.72     Sequence
 HLA-DQA10102-DQB10602  108      RGWIFGTTLDSKTQS  IFGTTLDSK  3         0.4071
611.0    20.00  0.71     Sequence
 HLA-DQA10102-DQB10602  109      GWIFGTTLDSKTQSL  IFGTTLDSK  2         0.3861
767.2    24.00  0.63     Sequence
 HLA-DQA10102-DQB10602  110      WIFGTTLDSKTQSLL  IFGTTLDSK  1         0.3457
1187.5    34.00  0.47     Sequence
 HLA-DQA10102-DQB10602  111      IFGTTLDSKTQSLLI  TLDSKTQSL  4         0.2594
3020.2    60.00  0.39     Sequence
 HLA-DQA10102-DQB10602  112      FGTTLDSKTQSLLIV  TLDSKTQSL  3         0.2427
3620.1    65.00  0.50     Sequence
 HLA-DQA10102-DQB10602  113      GTTLDSKTQSLLIVN  TLDSKTQSL  2         0.2521
3267.7    65.00  0.37     Sequence
 HLA-DQA10102-DQB10602  114      TTLDSKTQSLLIVNN  KTQSLLIVN  5         0.3148
1658.5    43.00  0.33     Sequence
 HLA-DQA10102-DQB10602  115      TLDSKTQSLLIVNNA  TQSLLIVNN  5         0.4223
518.2    17.00  0.32     Sequence
 HLA-DQA10102-DQB10602  116      LDSKTQSLLIVNNAT  QSLLIVNNA  5         0.4585
350.4    12.00  0.53     Sequence
 HLA-DQA10102-DQB10602  117      DSKTQSLLIVNNATN  QSLLIVNNA  4         0.4552
363.0    12.00  0.56     Sequence
 HLA-DQA10102-DQB10602  118      SKTQSLLIVNNATNV  QSLLIVNNA  3         0.4423
417.4    14.00  0.59     Sequence
 HLA-DQA10102-DQB10602  119      KTQSLLIVNNATNVV  QSLLIVNNA  2         0.4179
543.8    18.00  0.60     Sequence
 HLA-DQA10102-DQB10602  120      TQSLLIVNNATNVVI  QSLLIVNNA  1         0.3912
725.7    23.00  0.49     Sequence
 HLA-DQA10102-DQB10602  121      QSLLIVNNATNVVIK  NNATNVVIK  6         0.4088
599.7    20.00  0.25     Sequence
 HLA-DQA10102-DQB10602  122      SLLIVNNATNVVIKV  NNATNVVIK  5         0.4670
319.6    11.00  0.43     Sequence
 HLA-DQA10102-DQB10602  123      LLIVNNATNVVIKVC  NATNVVIKV  5         0.5158
188.5     6.00  0.38     Sequence         WB
 HLA-DQA10102-DQB10602  124      LIVNNATNVVIKVCE  NATNVVIKV  4         0.5651
110.5     3.00  0.34     Sequence         WB
 HLA-DQA10102-DQB10602  125      IVNNATNVVIKVCEF  NATNVVIKV  3         0.5918
82.8     1.80  0.28     Sequence         SB
 HLA-DQA10102-DQB10602  126      VNNATNVVIKVCEFQ  ATNVVIKVC  3         0.5737
100.7     2.50  0.29     Sequence         WB
 HLA-DQA10102-DQB10602  127      NNATNVVIKVCEFQF  ATNVVIKVC  2         0.5379
148.3     4.50  0.31     Sequence         WB
 HLA-DQA10102-DQB10602  128      NATNVVIKVCEFQFC  NVVIKVCEF  3         0.4712
305.4    10.00  0.38     Sequence
```

```
 HLA-DQA10102-DQB10602  129      ATNVVIKVCEFQFCN  NVVIKVCEF  2        0.4152
559.7    19.00  0.43     Sequence
 HLA-DQA10102-DQB10602  130      TNVVIKVCEFQFCNY  NVVIKVCEF  1        0.3555
1067.6    32.00  0.41     Sequence
 HLA-DQA10102-DQB10602  131      NVVIKVCEFQFCNYP  NVVIKVCEF  0        0.2433
3595.0    65.00  0.32     Sequence
 HLA-DQA10102-DQB10602  132      VVIKVCEFQFCNYPF  IKVCEFQFC  2        0.1800
7130.6    85.00  0.27     Sequence
 HLA-DQA10102-DQB10602  133      VIKVCEFQFCNYPFL  IKVCEFQFC  1        0.1641
8466.2    90.00  0.20     Sequence
 HLA-DQA10102-DQB10602  134      IKVCEFQFCNYPFLG  QFCNYPFLG  6        0.1906
6360.2    80.00  0.26     Sequence
 HLA-DQA10102-DQB10602  135      KVCEFQFCNYPFLGV  QFCNYPFLG  5        0.2324
4046.6    70.00  0.46     Sequence
 HLA-DQA10102-DQB10602  136      VCEFQFCNYPFLGVY  QFCNYPFLG  4        0.2428
3614.0    65.00  0.45     Sequence
 HLA-DQA10102-DQB10602  137      CEFQFCNYPFLGVYY  QFCNYPFLG  3        0.2610
2966.9    60.00  0.41     Sequence
 HLA-DQA10102-DQB10602  138      EFQFCNYPFLGVYYH  QFCNYPFLG  2        0.2597
3012.2    60.00  0.37     Sequence
 HLA-DQA10102-DQB10602  139      FQFCNYPFLGVYYHK  QFCNYPFLG  1        0.2625
2922.1    60.00  0.28     Sequence
 HLA-DQA10102-DQB10602  140      QFCNYPFLGVYYHKN  YPFLGVYYH  4        0.2465
3472.7    65.00  0.27     Sequence
 HLA-DQA10102-DQB10602  141      FCNYPFLGVYYHKNN  YPFLGVYYH  3        0.2135
4964.0    75.00  0.37     Sequence
 HLA-DQA10102-DQB10602  142      CNYPFLGVYYHKNNK  YPFLGVYYH  2        0.1851
6748.4    85.00  0.37     Sequence
 HLA-DQA10102-DQB10602  143      NYPFLGVYYHKNNKS  FLGVYYHKN  3        0.1607
8786.7    90.00  0.37     Sequence
 HLA-DQA10102-DQB10602  144      YPFLGVYYHKNNKSW  FLGVYYHKN  2        0.1418
10777.9    95.00  0.40     Sequence
 HLA-DQA10102-DQB10602  145      PFLGVYYHKNNKSWM  VYYHKNNKS  4        0.1329
11873.3    95.00  0.31     Sequence
 HLA-DQA10102-DQB10602  146      FLGVYYHKNNKSWME  HKNNKSWME  6        0.1790
7209.9    85.00  0.38     Sequence
 HLA-DQA10102-DQB10602  147      LGVYYHKNNKSWMES  HKNNKSWME  5        0.2402
3718.0    70.00  0.53     Sequence
 HLA-DQA10102-DQB10602  148      GVYYHKNNKSWMESE  HKNNKSWME  4        0.3052
1839.3    46.00  0.38     Sequence
 HLA-DQA10102-DQB10602  149      VYYHKNNKSWMESEF  NNKSWMESE  5        0.3418
1239.0    35.00  0.52     Sequence
 HLA-DQA10102-DQB10602  150      YYHKNNKSWMESEFR  NNKSWMESE  4        0.3327
1365.9    38.00  0.55     Sequence
 HLA-DQA10102-DQB10602  151      YHKNNKSWMESEFRV  NNKSWMESE  3        0.3261
1468.5    40.00  0.51     Sequence
 HLA-DQA10102-DQB10602  152      HKNNKSWMESEFRVY  NNKSWMESE  2        0.2973
2004.0    48.00  0.50     Sequence
 HLA-DQA10102-DQB10602  153      KNNKSWMESEFRVYS  NNKSWMESE  1        0.2707
2672.9    60.00  0.31     Sequence
 HLA-DQA10102-DQB10602  154      NNKSWMESEFRVYSS  ESEFRVYSS  6        0.3142
1668.8    43.00  0.44     Sequence
 HLA-DQA10102-DQB10602  155      NKSWMESEFRVYSSA  ESEFRVYSS  5        0.4421
418.5    14.00  0.68     Sequence
 HLA-DQA10102-DQB10602  156      KSWMESEFRVYSSAN  ESEFRVYSS  4        0.4493
386.9    13.00  0.69     Sequence
 HLA-DQA10102-DQB10602  157      SWMESEFRVYSSANN  ESEFRVYSS  3        0.4375
439.7    15.00  0.70     Sequence
 HLA-DQA10102-DQB10602  158      WMESEFRVYSSANNC  ESEFRVYSS  2        0.4121
579.1    19.00  0.71     Sequence
 HLA-DQA10102-DQB10602  159      MESEFRVYSSANNCT  ESEFRVYSS  1        0.3461
1182.0    34.00  0.56     Sequence
 HLA-DQA10102-DQB10602  160      ESEFRVYSSANNCTF  ESEFRVYSS  0        0.3159
1638.6    42.00  0.27     Sequence
 HLA-DQA10102-DQB10602  161      SEFRVYSSANNCTFE  VYSSANNCT  4        0.3042
1859.8    46.00  0.25     Sequence
```

```
 HLA-DQA10102-DQB10602  162      EFRVYSSANNCTFEY  SANNCTFEY  6        0.3465
1177.3    34.00  0.28     Sequence
 HLA-DQA10102-DQB10602  163      FRVYSSANNCTFEYV  SANNCTFEY  5        0.3915
723.3    23.00  0.41     Sequence
 HLA-DQA10102-DQB10602  164      RVYSSANNCTFEYVS  SANNCTFEY  4        0.4114
583.2    19.00  0.39     Sequence
 HLA-DQA10102-DQB10602  165      VYSSANNCTFEYVSQ  SANNCTFEY  3        0.4326
463.4    16.00  0.35     Sequence
 HLA-DQA10102-DQB10602  166      YSSANNCTFEYVSQP  NNCTFEYVS  4        0.4169
549.2    18.00  0.38     Sequence
 HLA-DQA10102-DQB10602  167      SSANNCTFEYVSQPF  NNCTFEYVS  3        0.3905
731.2    23.00  0.46     Sequence
 HLA-DQA10102-DQB10602  168      SANNCTFEYVSQPFL  NNCTFEYVS  2        0.3439
1211.2    35.00  0.52     Sequence
 HLA-DQA10102-DQB10602  169      ANNCTFEYVSQPFLM  NNCTFEYVS  1        0.2998
1950.9    47.00  0.45     Sequence
 HLA-DQA10102-DQB10602  170      NNCTFEYVSQPFLMD  EYVSQPFLM  5        0.2473
3442.5    65.00  0.22     Sequence
 HLA-DQA10102-DQB10602  171      NCTFEYVSQPFLMDL  EYVSQPFLM  4        0.2503
3332.5    65.00  0.32     Sequence
 HLA-DQA10102-DQB10602  172      CTFEYVSQPFLMDLE  VSQPFLMDL  5        0.2661
2809.8    60.00  0.35     Sequence
 HLA-DQA10102-DQB10602  173      TFEYVSQPFLMDLEG  VSQPFLMDL  4        0.2734
2596.2    60.00  0.38     Sequence
 HLA-DQA10102-DQB10602  174      FEYVSQPFLMDLEGK  VSQPFLMDL  3        0.2605
2983.3    60.00  0.39     Sequence
 HLA-DQA10102-DQB10602  175      EYVSQPFLMDLEGKQ  VSQPFLMDL  2        0.2450
3530.0    65.00  0.35     Sequence
 HLA-DQA10102-DQB10602  176      YVSQPFLMDLEGKQG  VSQPFLMDL  1        0.2156
4852.5    75.00  0.25     Sequence
 HLA-DQA10102-DQB10602  177      VSQPFLMDLEGKQGN  PFLMDLEGK  3        0.1805
7089.5    85.00  0.27     Sequence
 HLA-DQA10102-DQB10602  178      SQPFLMDLEGKQGNF  PFLMDLEGK  2        0.1479
10093.9    90.00  0.32     Sequence
 HLA-DQA10102-DQB10602  179      QPFLMDLEGKQGNFK  PFLMDLEGK  1        0.1315
12053.9    95.00  0.31     Sequence
 HLA-DQA10102-DQB10602  180      PFLMDLEGKQGNFKN  LMDLEGKQG  2        0.1078
15571.0   100.00  0.34     Sequence
 HLA-DQA10102-DQB10602  181      FLMDLEGKQGNFKNL  LMDLEGKQG  1        0.0881
19281.9   100.00  0.34     Sequence
 HLA-DQA10102-DQB10602  182      LMDLEGKQGNFKNLS  KQGNFKNLS  6        0.0916
18559.0   100.00  0.37     Sequence
 HLA-DQA10102-DQB10602  183      MDLEGKQGNFKNLSE  KQGNFKNLS  5        0.1433
10606.3    95.00  0.61     Sequence
 HLA-DQA10102-DQB10602  184      DLEGKQGNFKNLSEF  KQGNFKNLS  4        0.1836
6859.3    85.00  0.57     Sequence
 HLA-DQA10102-DQB10602  185      LEGKQGNFKNLSEFV  KQGNFKNLS  3        0.2055
5410.9    80.00  0.47     Sequence
 HLA-DQA10102-DQB10602  186      EGKQGNFKNLSEFVF  KQGNFKNLS  2        0.2202
4614.1    75.00  0.35     Sequence
 HLA-DQA10102-DQB10602  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5        0.2319
4065.2    70.00  0.19     Sequence
 HLA-DQA10102-DQB10602  188      KQGNFKNLSEFVFKN  NLSEFVFKN  6        0.2532
3228.4    65.00  0.31     Sequence
 HLA-DQA10102-DQB10602  189      QGNFKNLSEFVFKNI  NLSEFVFKN  5        0.2725
2621.2    60.00  0.44     Sequence
 HLA-DQA10102-DQB10602  190      GNFKNLSEFVFKNID  NLSEFVFKN  4        0.2869
2242.0    55.00  0.48     Sequence
 HLA-DQA10102-DQB10602  191      NFKNLSEFVFKNIDG  NLSEFVFKN  3        0.2811
2388.1    55.00  0.44     Sequence
 HLA-DQA10102-DQB10602  192      FKNLSEFVFKNIDGY  NLSEFVFKN  2        0.2594
3021.9    60.00  0.47     Sequence
 HLA-DQA10102-DQB10602  193      KNLSEFVFKNIDGYF  NLSEFVFKN  1        0.2272
4279.2    70.00  0.35     Sequence
 HLA-DQA10102-DQB10602  194      NLSEFVFKNIDGYFK  SEFVFKNID  2        0.2042
5485.6    80.00  0.27     Sequence
```

```
 HLA-DQA10102-DQB10602  195      LSEFVFKNIDGYFKI  FKNIDGYFK  5        0.1858
6699.3    85.00  0.28     Sequence
 HLA-DQA10102-DQB10602  196      SEFVFKNIDGYFKIY  FKNIDGYFK  4        0.1752
7512.5    85.00  0.38     Sequence
 HLA-DQA10102-DQB10602  197      EFVFKNIDGYFKIYS  FKNIDGYFK  3        0.1923
6245.8    80.00  0.32     Sequence
 HLA-DQA10102-DQB10602  198      FVFKNIDGYFKIYSK  DGYFKIYSK  6        0.2233
4463.9    75.00  0.34     Sequence
 HLA-DQA10102-DQB10602  199      VFKNIDGYFKIYSKH  DGYFKIYSK  5        0.2491
3377.6    65.00  0.51     Sequence
 HLA-DQA10102-DQB10602  200      FKNIDGYFKIYSKHT  DGYFKIYSK  4        0.2580
3066.0    60.00  0.52     Sequence
 HLA-DQA10102-DQB10602  201      KNIDGYFKIYSKHTP  DGYFKIYSK  3        0.2454
3516.2    65.00  0.55     Sequence
 HLA-DQA10102-DQB10602  202      NIDGYFKIYSKHTPI  DGYFKIYSK  2        0.2236
4447.3    75.00  0.56     Sequence
 HLA-DQA10102-DQB10602  203      IDGYFKIYSKHTPIN  DGYFKIYSK  1        0.1884
6508.6    85.00  0.47     Sequence
 HLA-DQA10102-DQB10602  204      DGYFKIYSKHTPINL  SKHTPINLX  7        0.1654
8354.5    90.00  0.20     Sequence
 HLA-DQA10102-DQB10602  205      GYFKIYSKHTPINLV  SKHTPINLV  6        0.3261
1467.5    40.00  0.64     Sequence
 HLA-DQA10102-DQB10602  206      YFKIYSKHTPINLVR  SKHTPINLV  5        0.3975
677.7    22.00  0.79     Sequence
 HLA-DQA10102-DQB10602  207      FKIYSKHTPINLVRD  SKHTPINLV  4        0.4316
468.9    16.00  0.74     Sequence
 HLA-DQA10102-DQB10602  208      KIYSKHTPINLVRDL  SKHTPINLV  3        0.4478
393.6    13.00  0.65     Sequence
 HLA-DQA10102-DQB10602  209      IYSKHTPINLVRDLP  SKHTPINLV  2        0.4361
446.4    15.00  0.54     Sequence
 HLA-DQA10102-DQB10602  210      YSKHTPINLVRDLPQ  SKHTPINLV  1        0.4328
462.9    16.00  0.37     Sequence
 HLA-DQA10102-DQB10602  211      SKHTPINLVRDLPQG  INLVRDLPQ  5        0.3894
739.7    24.00  0.29     Sequence
 HLA-DQA10102-DQB10602  212      KHTPINLVRDLPQGF  INLVRDLPQ  4        0.3551
1072.4    32.00  0.38     Sequence
 HLA-DQA10102-DQB10602  213      HTPINLVRDLPQGFS  INLVRDLPQ  3        0.3318
1379.4    38.00  0.44     Sequence
 HLA-DQA10102-DQB10602  214      TPINLVRDLPQGFSA  INLVRDLPQ  2        0.3040
1864.2    46.00  0.46     Sequence
 HLA-DQA10102-DQB10602  215      PINLVRDLPQGFSAL  INLVRDLPQ  1        0.2613
2958.3    60.00  0.38     Sequence
 HLA-DQA10102-DQB10602  216      INLVRDLPQGFSALE  INLVRDLPQ  0        0.2198
4633.8    75.00  0.34     Sequence
 HLA-DQA10102-DQB10602  217      NLVRDLPQGFSALEP  VRDLPQGFS  2        0.1617
8695.4    90.00  0.31     Sequence
 HLA-DQA10102-DQB10602  218      LVRDLPQGFSALEPL  QGFSALEPL  6        0.2102
5145.5    75.00  0.31     Sequence
 HLA-DQA10102-DQB10602  219      VRDLPQGFSALEPLV  QGFSALEPL  5        0.2522
3264.8    65.00  0.49     Sequence
 HLA-DQA10102-DQB10602  220      RDLPQGFSALEPLVD  QGFSALEPL  4        0.3135
1682.6    43.00  0.40     Sequence
 HLA-DQA10102-DQB10602  221      DLPQGFSALEPLVDL  QGFSALEPL  3        0.3616
999.8    30.00  0.29     Sequence
 HLA-DQA10102-DQB10602  222      LPQGFSALEPLVDLP  QGFSALEPL  2        0.3575
1045.0    31.00  0.26     Sequence
 HLA-DQA10102-DQB10602  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.3442
1207.1    35.00  0.27     Sequence
 HLA-DQA10102-DQB10602  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.3320
1377.3    38.00  0.26     Sequence
 HLA-DQA10102-DQB10602  225      GFSALEPLVDLPIGI  SALEPLVDL  2        0.2977
1995.1    48.00  0.29     Sequence
 HLA-DQA10102-DQB10602  226      FSALEPLVDLPIGIN  SALEPLVDL  1        0.2521
3270.0    65.00  0.26     Sequence
 HLA-DQA10102-DQB10602  227      SALEPLVDLPIGINI  LVDLPIGIN  5        0.1986
5830.9    80.00  0.28     Sequence
```

```
 HLA-DQA10102-DQB10602  228      ALEPLVDLPIGINIT  LVDLPIGIN  4        0.1989
5812.9    80.00  0.29     Sequence
 HLA-DQA10102-DQB10602  229      LEPLVDLPIGINITR  DLPIGINIT  5        0.2044
5473.7    80.00  0.32     Sequence
 HLA-DQA10102-DQB10602  230      EPLVDLPIGINITRF  DLPIGINIT  4        0.2058
5394.7    80.00  0.34     Sequence
 HLA-DQA10102-DQB10602  231      PLVDLPIGINITRFQ  PIGINITRF  5        0.2368
3857.0    70.00  0.30     Sequence
 HLA-DQA10102-DQB10602  232      LVDLPIGINITRFQT  PIGINITRF  4        0.2596
3015.4    60.00  0.26     Sequence
 HLA-DQA10102-DQB10602  233      VDLPIGINITRFQTL  IGINITRFQ  4        0.2786
2454.5    55.00  0.28     Sequence
 HLA-DQA10102-DQB10602  234      DLPIGINITRFQTLL  INITRFQTL  5        0.2767
2505.5    55.00  0.25     Sequence
 HLA-DQA10102-DQB10602  235      LPIGINITRFQTLLA  INITRFQTL  4        0.2713
2654.4    60.00  0.29     Sequence
 HLA-DQA10102-DQB10602  236      PIGINITRFQTLLAL  INITRFQTL  3        0.2841
2313.2    55.00  0.29     Sequence
 HLA-DQA10102-DQB10602  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.2922
2117.4    50.00  0.28     Sequence
 HLA-DQA10102-DQB10602  238      GINITRFQTLLALHR  RFQTLLALH  5        0.3171
1617.8    42.00  0.28     Sequence
 HLA-DQA10102-DQB10602  239      INITRFQTLLALHRS  QTLLALHRS  6        0.4275
489.9    16.00  0.52     Sequence
 HLA-DQA10102-DQB10602  240      NITRFQTLLALHRSY  QTLLALHRS  5        0.4964
232.4     7.50  0.69     Sequence         WB
 HLA-DQA10102-DQB10602  241      ITRFQTLLALHRSYL  QTLLALHRS  4        0.5154
189.2     6.00  0.67     Sequence         WB
 HLA-DQA10102-DQB10602  242      TRFQTLLALHRSYLT  QTLLALHRS  3        0.5229
174.5     5.50  0.64     Sequence         WB
 HLA-DQA10102-DQB10602  243      RFQTLLALHRSYLTP  QTLLALHRS  2        0.5065
208.4     6.50  0.62     Sequence         WB
 HLA-DQA10102-DQB10602  244      FQTLLALHRSYLTPG  QTLLALHRS  1        0.4752
292.3     9.50  0.56     Sequence         WB
 HLA-DQA10102-DQB10602  245      QTLLALHRSYLTPGD  LHRSYLTPG  5        0.4066
614.0    20.00  0.27     Sequence
 HLA-DQA10102-DQB10602  246      TLLALHRSYLTPGDS  LHRSYLTPG  4        0.3669
943.7    29.00  0.47     Sequence
 HLA-DQA10102-DQB10602  247      LLALHRSYLTPGDSS  LHRSYLTPG  3        0.3468
1172.8    34.00  0.52     Sequence
 HLA-DQA10102-DQB10602  248      LALHRSYLTPGDSSS  LHRSYLTPG  2        0.3048
1848.1    46.00  0.55     Sequence
 HLA-DQA10102-DQB10602  249      ALHRSYLTPGDSSSG  LHRSYLTPG  1        0.2573
3091.0    65.00  0.47     Sequence
 HLA-DQA10102-DQB10602  250      LHRSYLTPGDSSSGW  LHRSYLTPG  0        0.2036
5524.6    80.00  0.37     Sequence
 HLA-DQA10102-DQB10602  251      HRSYLTPGDSSSGWT  SYLTPGDSS  2        0.1365
11421.9    95.00  0.36     Sequence
 HLA-DQA10102-DQB10602  252      RSYLTPGDSSSGWTA  GDSSSGWTA  6        0.1758
7459.5    85.00  0.43     Sequence
 HLA-DQA10102-DQB10602  253      SYLTPGDSSSGWTAG  GDSSSGWTA  5        0.2218
4538.2    75.00  0.61     Sequence
 HLA-DQA10102-DQB10602  254      YLTPGDSSSGWTAGA  GDSSSGWTA  4        0.2861
2263.7    55.00  0.44     Sequence
 HLA-DQA10102-DQB10602  255      LTPGDSSSGWTAGAA  GDSSSGWTA  3        0.3571
1049.5    31.00  0.28     Sequence
 HLA-DQA10102-DQB10602  256      TPGDSSSGWTAGAAA  SSGWTAGAA  5        0.4105
588.7    19.00  0.41     Sequence
 HLA-DQA10102-DQB10602  257      PGDSSSGWTAGAAAY  SSGWTAGAA  4        0.4720
302.8    10.00  0.36     Sequence
 HLA-DQA10102-DQB10602  258      GDSSSGWTAGAAAYY  SSGWTAGAA  3        0.5001
223.3     7.00  0.32     Sequence         WB
 HLA-DQA10102-DQB10602  259      DSSSGWTAGAAAYYV  TAGAAAYYV  6        0.5559
122.1     3.50  0.41     Sequence         WB
 HLA-DQA10102-DQB10602  260      SSSGWTAGAAAYYVG  TAGAAAYYV  5        0.6038
72.7     1.50  0.62     Sequence         SB
```

```
 HLA-DQA10102-DQB10602  261      SSGWTAGAAAYYVGY  TAGAAAYYV  4        0.6233
58.9     1.00  0.63     Sequence         SB
 HLA-DQA10102-DQB10602  262      SGWTAGAAAYYVGYL  TAGAAAYYV  3        0.6111
67.2     1.30  0.67     Sequence         SB
 HLA-DQA10102-DQB10602  263      GWTAGAAAYYVGYLQ  TAGAAAYYV  2        0.5855
88.7     2.00  0.68     Sequence         WB
 HLA-DQA10102-DQB10602  264      WTAGAAAYYVGYLQP  TAGAAAYYV  1        0.5021
218.5     7.00  0.62     Sequence         WB
 HLA-DQA10102-DQB10602  265      TAGAAAYYVGYLQPR  TAGAAAYYV  0        0.3573
1047.7    31.00  0.35     Sequence
 HLA-DQA10102-DQB10602  266      AGAAAYYVGYLQPRT  GAAAYYVGY  1        0.2625
2921.2    60.00  0.25     Sequence
 HLA-DQA10102-DQB10602  267      GAAAYYVGYLQPRTF  AAYYVGYLQ  2        0.2040
5500.2    80.00  0.26     Sequence
 HLA-DQA10102-DQB10602  268      AAAYYVGYLQPRTFL  AAYYVGYLQ  1        0.1670
8207.6    90.00  0.25     Sequence
 HLA-DQA10102-DQB10602  269      AAYYVGYLQPRTFLL  VGYLQPRTF  4        0.1471
10178.7    90.00  0.28     Sequence
 HLA-DQA10102-DQB10602  270      AYYVGYLQPRTFLLK  VGYLQPRTF  3        0.1388
11141.9    95.00  0.34     Sequence
 HLA-DQA10102-DQB10602  271      YYVGYLQPRTFLLKY  VGYLQPRTF  2        0.1373
11322.0    95.00  0.28     Sequence
 HLA-DQA10102-DQB10602  272      YVGYLQPRTFLLKYN  QPRTFLLKY  5        0.1357
11511.2    95.00  0.38     Sequence
 HLA-DQA10102-DQB10602  273      VGYLQPRTFLLKYNE  PRTFLLKYN  5        0.1708
7881.4    85.00  0.29     Sequence
 HLA-DQA10102-DQB10602  274      GYLQPRTFLLKYNEN  PRTFLLKYN  4        0.1814
7024.3    85.00  0.29     Sequence
 HLA-DQA10102-DQB10602  275      YLQPRTFLLKYNENG  PRTFLLKYN  3        0.1833
6878.0    85.00  0.29     Sequence
 HLA-DQA10102-DQB10602  276      LQPRTFLLKYNENGT  PRTFLLKYN  2        0.1666
8245.6    90.00  0.29     Sequence
 HLA-DQA10102-DQB10602  277      QPRTFLLKYNENGTI  TFLLKYNEN  3        0.1497
9894.3    90.00  0.27     Sequence
 HLA-DQA10102-DQB10602  278      PRTFLLKYNENGTIT  TFLLKYNEN  2        0.1431
10634.8    95.00  0.29     Sequence
 HLA-DQA10102-DQB10602  279      RTFLLKYNENGTITD  LKYNENGTI  4        0.1386
11157.1    95.00  0.28     Sequence
 HLA-DQA10102-DQB10602  280      TFLLKYNENGTITDA  NENGTITDA  6        0.2476
3431.6    65.00  0.46     Sequence
 HLA-DQA10102-DQB10602  281      FLLKYNENGTITDAV  NENGTITDA  5        0.3622
993.5    30.00  0.57     Sequence
 HLA-DQA10102-DQB10602  282      LLKYNENGTITDAVD  NENGTITDA  4        0.4430
414.1    14.00  0.43     Sequence
 HLA-DQA10102-DQB10602  283      LKYNENGTITDAVDC  NENGTITDA  3        0.4749
293.4     9.50  0.35     Sequence         WB
 HLA-DQA10102-DQB10602  284      KYNENGTITDAVDCA  ENGTITDAV  3        0.4657
324.3    11.00  0.29     Sequence
 HLA-DQA10102-DQB10602  285      YNENGTITDAVDCAL  ENGTITDAV  2        0.4598
345.5    12.00  0.22     Sequence
 HLA-DQA10102-DQB10602  286      NENGTITDAVDCALD  GTITDAVDC  3        0.4287
483.6    16.00  0.22     Sequence
 HLA-DQA10102-DQB10602  287      ENGTITDAVDCALDP  GTITDAVDC  2        0.3908
728.8    23.00  0.23     Sequence
 HLA-DQA10102-DQB10602  288      NGTITDAVDCALDPL  ITDAVDCAL  3        0.3435
1216.1    35.00  0.28     Sequence
 HLA-DQA10102-DQB10602  289      GTITDAVDCALDPLS  ITDAVDCAL  2        0.3019
1907.2    47.00  0.31     Sequence
 HLA-DQA10102-DQB10602  290      TITDAVDCALDPLSE  TDAVDCALD  2        0.2742
2573.3    55.00  0.32     Sequence
 HLA-DQA10102-DQB10602  291      ITDAVDCALDPLSET  TDAVDCALD  1        0.2278
4251.0    70.00  0.23     Sequence
 HLA-DQA10102-DQB10602  292      TDAVDCALDPLSETK  DCALDPLSE  4        0.1757
7468.2    85.00  0.27     Sequence
 HLA-DQA10102-DQB10602  293      DAVDCALDPLSETKC  DCALDPLSE  3        0.1529
9563.6    90.00  0.35     Sequence
```

```
 HLA-DQA10102-DQB10602  294      AVDCALDPLSETKCT  DCALDPLSE  2        0.1401
10980.2    95.00  0.33     Sequence
 HLA-DQA10102-DQB10602  295      VDCALDPLSETKCTL  CALDPLSET  2        0.1324
11933.3    95.00  0.22     Sequence
 HLA-DQA10102-DQB10602  296      DCALDPLSETKCTLK  LSETKCTLK  6        0.1588
8971.7    90.00  0.38     Sequence
 HLA-DQA10102-DQB10602  297      CALDPLSETKCTLKS  LSETKCTLK  5        0.1799
7136.7    85.00  0.46     Sequence
 HLA-DQA10102-DQB10602  298      ALDPLSETKCTLKSF  LSETKCTLK  4        0.2077
5281.9    80.00  0.41     Sequence
 HLA-DQA10102-DQB10602  299      LDPLSETKCTLKSFT  LSETKCTLK  3        0.2151
4875.5    75.00  0.36     Sequence
 HLA-DQA10102-DQB10602  300      DPLSETKCTLKSFTV  SETKCTLKS  3        0.2323
4047.5    70.00  0.22     Sequence
 HLA-DQA10102-DQB10602  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.2281
4237.4    70.00  0.25     Sequence
 HLA-DQA10102-DQB10602  302      LSETKCTLKSFTVEK  KCTLKSFTV  4        0.2230
4479.3    75.00  0.33     Sequence
 HLA-DQA10102-DQB10602  303      SETKCTLKSFTVEKG  LKSFTVEKG  6        0.2316
4079.7    70.00  0.41     Sequence
 HLA-DQA10102-DQB10602  304      ETKCTLKSFTVEKGI  LKSFTVEKG  5        0.2956
2041.3    49.00  0.56     Sequence
 HLA-DQA10102-DQB10602  305      TKCTLKSFTVEKGIY  LKSFTVEKG  4        0.3337
1352.4    37.00  0.53     Sequence
 HLA-DQA10102-DQB10602  306      KCTLKSFTVEKGIYQ  LKSFTVEKG  3        0.3417
1240.2    35.00  0.51     Sequence
 HLA-DQA10102-DQB10602  307      CTLKSFTVEKGIYQT  LKSFTVEKG  2        0.3191
1583.5    42.00  0.50     Sequence
 HLA-DQA10102-DQB10602  308      TLKSFTVEKGIYQTS  LKSFTVEKG  1        0.2922
2118.9    50.00  0.43     Sequence
 HLA-DQA10102-DQB10602  309      LKSFTVEKGIYQTSN  KSFTVEKGI  1        0.2523
3261.2    65.00  0.26     Sequence
 HLA-DQA10102-DQB10602  310      KSFTVEKGIYQTSNF  EKGIYQTSN  5        0.2106
5122.3    75.00  0.17     Sequence
 HLA-DQA10102-DQB10602  311      SFTVEKGIYQTSNFR  EKGIYQTSN  4        0.1594
8910.5    90.00  0.21     Sequence
 HLA-DQA10102-DQB10602  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.1778
7302.3    85.00  0.38     Sequence
 HLA-DQA10102-DQB10602  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.2240
4428.3    75.00  0.55     Sequence
 HLA-DQA10102-DQB10602  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.2714
2652.9    60.00  0.52     Sequence
 HLA-DQA10102-DQB10602  315      EKGIYQTSNFRVQPT  TSNFRVQPT  6        0.3817
804.5    25.00  0.40     Sequence
 HLA-DQA10102-DQB10602  316      KGIYQTSNFRVQPTE  TSNFRVQPT  5        0.4508
380.9    13.00  0.61     Sequence
 HLA-DQA10102-DQB10602  317      GIYQTSNFRVQPTES  TSNFRVQPT  4        0.4633
332.8    11.00  0.64     Sequence
 HLA-DQA10102-DQB10602  318      IYQTSNFRVQPTESI  TSNFRVQPT  3        0.4658
323.9    11.00  0.65     Sequence
 HLA-DQA10102-DQB10602  319      YQTSNFRVQPTESIV  TSNFRVQPT  2        0.4445
407.7    14.00  0.66     Sequence
 HLA-DQA10102-DQB10602  320      QTSNFRVQPTESIVR  TSNFRVQPT  1        0.3900
735.4    24.00  0.54     Sequence
 HLA-DQA10102-DQB10602  321      TSNFRVQPTESIVRF  TSNFRVQPT  0        0.3227
1523.2    41.00  0.31     Sequence
 HLA-DQA10102-DQB10602  322      SNFRVQPTESIVRFP  NFRVQPTES  1        0.2661
2810.4    60.00  0.31     Sequence
 HLA-DQA10102-DQB10602  323      NFRVQPTESIVRFPN  PTESIVRFP  5        0.2456
3507.9    65.00  0.36     Sequence
 HLA-DQA10102-DQB10602  324      FRVQPTESIVRFPNI  PTESIVRFP  4        0.2799
2419.9    55.00  0.38     Sequence
 HLA-DQA10102-DQB10602  325      RVQPTESIVRFPNIT  PTESIVRFP  3        0.2624
2925.2    60.00  0.42     Sequence
 HLA-DQA10102-DQB10602  326      VQPTESIVRFPNITN  PTESIVRFP  2        0.2406
3702.3    70.00  0.41     Sequence
```

```
 HLA-DQA10102-DQB10602  327      QPTESIVRFPNITNL  PTESIVRFP  1        0.2199
4628.6    75.00  0.34     Sequence
 HLA-DQA10102-DQB10602  328      PTESIVRFPNITNLC  VRFPNITNL  5        0.2230
4478.0    75.00  0.20     Sequence
 HLA-DQA10102-DQB10602  329      TESIVRFPNITNLCP  VRFPNITNL  4        0.2211
4569.6    75.00  0.22     Sequence
 HLA-DQA10102-DQB10602  330      ESIVRFPNITNLCPF  VRFPNITNL  3        0.2584
3054.7    60.00  0.20     Sequence
 HLA-DQA10102-DQB10602  331      SIVRFPNITNLCPFG  PNITNLCPF  5        0.2791
2440.3    55.00  0.25     Sequence
 HLA-DQA10102-DQB10602  332      IVRFPNITNLCPFGE  ITNLCPFGE  6        0.3178
1605.5    42.00  0.23     Sequence
 HLA-DQA10102-DQB10602  333      VRFPNITNLCPFGEV  ITNLCPFGE  5        0.3478
1160.6    34.00  0.38     Sequence
 HLA-DQA10102-DQB10602  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.3423
1231.8    35.00  0.50     Sequence
 HLA-DQA10102-DQB10602  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.3163
1632.5    42.00  0.55     Sequence
 HLA-DQA10102-DQB10602  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.2836
2325.6    55.00  0.49     Sequence
 HLA-DQA10102-DQB10602  337      NITNLCPFGEVFNAT  ITNLCPFGE  1        0.2739
2582.2    55.00  0.37     Sequence
 HLA-DQA10102-DQB10602  338      ITNLCPFGEVFNATR  CPFGEVFNA  4        0.2531
3233.8    65.00  0.34     Sequence
 HLA-DQA10102-DQB10602  339      TNLCPFGEVFNATRF  CPFGEVFNA  3        0.2643
2863.1    60.00  0.43     Sequence
 HLA-DQA10102-DQB10602  340      NLCPFGEVFNATRFA  CPFGEVFNA  2        0.2780
2468.6    55.00  0.29     Sequence
 HLA-DQA10102-DQB10602  341      LCPFGEVFNATRFAS  VFNATRFAS  6        0.3369
1306.1    36.00  0.34     Sequence
 HLA-DQA10102-DQB10602  342      CPFGEVFNATRFASV  VFNATRFAS  5        0.4169
549.7    18.00  0.50     Sequence
 HLA-DQA10102-DQB10602  343      PFGEVFNATRFASVY  VFNATRFAS  4        0.4667
320.5    11.00  0.45     Sequence
 HLA-DQA10102-DQB10602  344      FGEVFNATRFASVYA  VFNATRFAS  3        0.4799
277.8     9.00  0.40     Sequence         WB
 HLA-DQA10102-DQB10602  345      GEVFNATRFASVYAW  VFNATRFAS  2        0.4809
275.1     9.00  0.30     Sequence         WB
 HLA-DQA10102-DQB10602  346      EVFNATRFASVYAWN  TRFASVYAW  5        0.4770
286.7     9.50  0.32     Sequence         WB
 HLA-DQA10102-DQB10602  347      VFNATRFASVYAWNR  TRFASVYAW  4        0.4644
328.6    11.00  0.38     Sequence
 HLA-DQA10102-DQB10602  348      FNATRFASVYAWNRK  TRFASVYAW  3        0.4444
408.2    14.00  0.45     Sequence
 HLA-DQA10102-DQB10602  349      NATRFASVYAWNRKR  TRFASVYAW  2        0.3944
700.6    23.00  0.44     Sequence
 HLA-DQA10102-DQB10602  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.3298
1410.8    38.00  0.38     Sequence
 HLA-DQA10102-DQB10602  351      TRFASVYAWNRKRIS  FASVYAWNR  2        0.3037
1870.7    46.00  0.41     Sequence
 HLA-DQA10102-DQB10602  352      RFASVYAWNRKRISN  FASVYAWNR  1        0.2703
2684.6    60.00  0.35     Sequence
 HLA-DQA10102-DQB10602  353      FASVYAWNRKRISNC  YAWNRKRIS  4        0.2235
4454.0    75.00  0.43     Sequence
 HLA-DQA10102-DQB10602  354      ASVYAWNRKRISNCV  YAWNRKRIS  3        0.2069
5328.8    80.00  0.49     Sequence
 HLA-DQA10102-DQB10602  355      SVYAWNRKRISNCVA  YAWNRKRIS  2        0.2269
4293.8    70.00  0.38     Sequence
 HLA-DQA10102-DQB10602  356      VYAWNRKRISNCVAD  KRISNCVAD  6        0.2619
2941.0    60.00  0.27     Sequence
 HLA-DQA10102-DQB10602  357      YAWNRKRISNCVADY  KRISNCVAD  5        0.2865
2253.9    55.00  0.34     Sequence
 HLA-DQA10102-DQB10602  358      AWNRKRISNCVADYS  KRISNCVAD  4        0.3120
1710.3    44.00  0.37     Sequence
 HLA-DQA10102-DQB10602  359      WNRKRISNCVADYSV  KRISNCVAD  3        0.3505
1127.0    33.00  0.31     Sequence
```

```
 HLA-DQA10102-DQB10602  360      NRKRISNCVADYSVL  SNCVADYSV  5        0.3424
1230.0    35.00 0.20      Sequence
 HLA-DQA10102-DQB10602  361      RKRISNCVADYSVLY  SNCVADYSV  4        0.3210
1551.6    41.00 0.27      Sequence
 HLA-DQA10102-DQB10602  362      KRISNCVADYSVLYN  SNCVADYSV  3        0.2955
2043.0    49.00 0.26      Sequence
 HLA-DQA10102-DQB10602  363      RISNCVADYSVLYNS  ADYSVLYNS  6        0.4054
622.6    20.00  0.46     Sequence
 HLA-DQA10102-DQB10602  364      ISNCVADYSVLYNSA  ADYSVLYNS  5        0.4686
314.0    11.00  0.68     Sequence
 HLA-DQA10102-DQB10602  365      SNCVADYSVLYNSAS  ADYSVLYNS  4        0.4945
237.3     7.50  0.68     Sequence         WB
 HLA-DQA10102-DQB10602  366      NCVADYSVLYNSASF  ADYSVLYNS  3        0.5020
218.8     7.00  0.68     Sequence         WB
 HLA-DQA10102-DQB10602  367      CVADYSVLYNSASFS  ADYSVLYNS  2        0.4788
281.2     9.00  0.63     Sequence         WB
 HLA-DQA10102-DQB10602  368      VADYSVLYNSASFST  ADYSVLYNS  1        0.4593
347.2    12.00  0.55     Sequence
 HLA-DQA10102-DQB10602  369      ADYSVLYNSASFSTF  LYNSASFST  5        0.4040
631.9    21.00  0.32     Sequence
 HLA-DQA10102-DQB10602  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.3949
697.5    23.00  0.44     Sequence
 HLA-DQA10102-DQB10602  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.4059
618.7    20.00  0.37     Sequence
 HLA-DQA10102-DQB10602  372      SVLYNSASFSTFKCY  SASFSTFKC  5        0.4059
618.9    20.00  0.27     Sequence
 HLA-DQA10102-DQB10602  373      VLYNSASFSTFKCYG  SASFSTFKC  4        0.4218
521.0    17.00  0.30     Sequence
 HLA-DQA10102-DQB10602  374      LYNSASFSTFKCYGV  SASFSTFKC  3        0.4577
353.3    12.00  0.23     Sequence
 HLA-DQA10102-DQB10602  375      YNSASFSTFKCYGVS  FSTFKCYGV  5        0.4532
370.9    13.00  0.34     Sequence
 HLA-DQA10102-DQB10602  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.4361
446.5    15.00  0.41     Sequence
 HLA-DQA10102-DQB10602  377      SASFSTFKCYGVSPT  FSTFKCYGV  3        0.3906
730.4    23.00  0.48     Sequence
 HLA-DQA10102-DQB10602  378      ASFSTFKCYGVSPTK  FSTFKCYGV  2        0.3537
1089.2    32.00 0.56      Sequence
 HLA-DQA10102-DQB10602  379      SFSTFKCYGVSPTKL  FSTFKCYGV  1        0.2968
2015.5    48.00 0.53      Sequence
 HLA-DQA10102-DQB10602  380      FSTFKCYGVSPTKLN  FSTFKCYGV  0        0.2183
4710.5    75.00 0.34      Sequence
 HLA-DQA10102-DQB10602  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.1541
9440.0    90.00 0.33      Sequence
 HLA-DQA10102-DQB10602  382      TFKCYGVSPTKLNDL  VSPTKLNDL  6        0.1839
6835.7    85.00 0.37      Sequence
 HLA-DQA10102-DQB10602  383      FKCYGVSPTKLNDLC  VSPTKLNDL  5        0.2134
4970.5    75.00 0.59      Sequence
 HLA-DQA10102-DQB10602  384      KCYGVSPTKLNDLCF  VSPTKLNDL  4        0.2159
4835.7    75.00 0.66      Sequence
 HLA-DQA10102-DQB10602  385      CYGVSPTKLNDLCFT  VSPTKLNDL  3        0.2274
4271.0    70.00 0.61      Sequence
 HLA-DQA10102-DQB10602  386      YGVSPTKLNDLCFTN  VSPTKLNDL  2        0.2246
4399.2    75.00 0.50      Sequence
 HLA-DQA10102-DQB10602  387      GVSPTKLNDLCFTNV  VSPTKLNDL  1        0.2267
4303.0    70.00 0.31      Sequence
 HLA-DQA10102-DQB10602  388      VSPTKLNDLCFTNVY  TKLNDLCFT  3        0.2571
3096.7    65.00 0.29      Sequence
 HLA-DQA10102-DQB10602  389      SPTKLNDLCFTNVYA  LCFTNVYAX  7        0.2892
2188.4    55.00 0.19      Sequence
 HLA-DQA10102-DQB10602  390      PTKLNDLCFTNVYAD  LCFTNVYAD  6        0.4305
474.3    16.00  0.60     Sequence
 HLA-DQA10102-DQB10602  391      TKLNDLCFTNVYADS  LCFTNVYAD  5        0.5150
190.2     6.00  0.74     Sequence         WB
 HLA-DQA10102-DQB10602  392      KLNDLCFTNVYADSF  LCFTNVYAD  4        0.5379
148.4     4.50  0.75     Sequence         WB
```

```
 HLA-DQA10102-DQB10602  393      LNDLCFTNVYADSFV  LCFTNVYAD  3        0.5326
157.1     4.50  0.74     Sequence         WB
 HLA-DQA10102-DQB10602  394      NDLCFTNVYADSFVI  LCFTNVYAD  2        0.5016
219.7     7.00  0.72     Sequence         WB
 HLA-DQA10102-DQB10602  395      DLCFTNVYADSFVIR  LCFTNVYAD  1        0.4214
523.3    18.00  0.62     Sequence
 HLA-DQA10102-DQB10602  396      LCFTNVYADSFVIRG  LCFTNVYAD  0        0.3630
984.5    30.00  0.33     Sequence
 HLA-DQA10102-DQB10602  397      CFTNVYADSFVIRGD  YADSFVIRG  5        0.4025
642.1    21.00  0.43     Sequence
 HLA-DQA10102-DQB10602  398      FTNVYADSFVIRGDE  ADSFVIRGD  5        0.4281
486.9    16.00  0.39     Sequence
 HLA-DQA10102-DQB10602  399      TNVYADSFVIRGDEV  ADSFVIRGD  4        0.4429
414.8    14.00  0.38     Sequence
 HLA-DQA10102-DQB10602  400      NVYADSFVIRGDEVR  ADSFVIRGD  3        0.4189
537.8    18.00  0.40     Sequence
 HLA-DQA10102-DQB10602  401      VYADSFVIRGDEVRQ  ADSFVIRGD  2        0.3907
729.8    23.00  0.43     Sequence
 HLA-DQA10102-DQB10602  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.3876
754.8    24.00  0.31     Sequence
 HLA-DQA10102-DQB10602  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.4049
625.9    21.00  0.69     Sequence
 HLA-DQA10102-DQB10602  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.4138
568.1    19.00  0.74     Sequence
 HLA-DQA10102-DQB10602  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.4080
605.2    20.00  0.71     Sequence
 HLA-DQA10102-DQB10602  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.3903
732.6    23.00  0.68     Sequence
 HLA-DQA10102-DQB10602  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.3432
1219.5    35.00  0.54     Sequence
 HLA-DQA10102-DQB10602  408      IRGDEVRQIAPGQTG  IRGDEVRQI  0        0.2937
2083.6    49.00  0.31     Sequence
 HLA-DQA10102-DQB10602  409      RGDEVRQIAPGQTGT  RQIAPGQTG  5        0.2389
3771.7    70.00  0.26     Sequence
 HLA-DQA10102-DQB10602  410      GDEVRQIAPGQTGTI  RQIAPGQTG  4        0.2081
5263.6    80.00  0.34     Sequence
 HLA-DQA10102-DQB10602  411      DEVRQIAPGQTGTIA  RQIAPGQTG  3        0.1814
7024.3    85.00  0.38     Sequence
 HLA-DQA10102-DQB10602  412      EVRQIAPGQTGTIAD  RQIAPGQTG  2        0.1709
7868.9    85.00  0.41     Sequence
 HLA-DQA10102-DQB10602  413      VRQIAPGQTGTIADY  RQIAPGQTG  1        0.1707
7885.0    85.00  0.21     Sequence
 HLA-DQA10102-DQB10602  414      RQIAPGQTGTIADYN  QTGTIADYN  6        0.1946
6090.2    80.00  0.38     Sequence
 HLA-DQA10102-DQB10602  415      QIAPGQTGTIADYNY  QTGTIADYN  5        0.2287
4212.5    70.00  0.56     Sequence
 HLA-DQA10102-DQB10602  416      IAPGQTGTIADYNYK  QTGTIADYN  4        0.2297
4165.6    70.00  0.57     Sequence
 HLA-DQA10102-DQB10602  417      APGQTGTIADYNYKL  QTGTIADYN  3        0.2177
4743.6    75.00  0.59     Sequence
 HLA-DQA10102-DQB10602  418      PGQTGTIADYNYKLP  QTGTIADYN  2        0.2049
5449.9    80.00  0.55     Sequence
 HLA-DQA10102-DQB10602  419      GQTGTIADYNYKLPD  QTGTIADYN  1        0.1847
6778.2    85.00  0.49     Sequence
 HLA-DQA10102-DQB10602  420      QTGTIADYNYKLPDD  QTGTIADYN  0        0.1435
10584.2    95.00  0.32     Sequence
 HLA-DQA10102-DQB10602  421      TGTIADYNYKLPDDF  TIADYNYKL  2        0.1071
15697.4   100.00  0.28     Sequence
 HLA-DQA10102-DQB10602  422      GTIADYNYKLPDDFT  DYNYKLPDD  4        0.0951
17874.3   100.00  0.21     Sequence
 HLA-DQA10102-DQB10602  423      TIADYNYKLPDDFTG  DYNYKLPDD  3        0.0903
18825.5   100.00  0.22     Sequence
 HLA-DQA10102-DQB10602  424      IADYNYKLPDDFTGC  DYNYKLPDD  2        0.0870
19505.6   100.00  0.22     Sequence
 HLA-DQA10102-DQB10602  425      ADYNYKLPDDFTGCV  YKLPDDFTG  4        0.0835
20260.0   100.00  0.23     Sequence
```

```
 HLA-DQA10102-DQB10602  426      DYNYKLPDDFTGCVI  YKLPDDFTG  3        0.0939
18096.5   100.00  0.19     Sequence
 HLA-DQA10102-DQB10602  427      YNYKLPDDFTGCVIA  DDFTGCVIA  6        0.1474
10146.4    90.00  0.31     Sequence
 HLA-DQA10102-DQB10602  428      NYKLPDDFTGCVIAW  DDFTGCVIA  5        0.2197
4643.0    75.00  0.44     Sequence
 HLA-DQA10102-DQB10602  429      YKLPDDFTGCVIAWN  FTGCVIAWN  6        0.3364
1312.3    37.00  0.47     Sequence
 HLA-DQA10102-DQB10602  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.4708
306.7    10.00  0.55     Sequence
 HLA-DQA10102-DQB10602  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.4813
273.7     9.00  0.47     Sequence         WB
 HLA-DQA10102-DQB10602  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.4758
290.5     9.50  0.45     Sequence         WB
 HLA-DQA10102-DQB10602  433      DDFTGCVIAWNSNNL  FTGCVIAWN  2        0.4586
349.9    12.00  0.49     Sequence
 HLA-DQA10102-DQB10602  434      DFTGCVIAWNSNNLD  FTGCVIAWN  1        0.4185
540.3    18.00  0.43     Sequence
 HLA-DQA10102-DQB10602  435      FTGCVIAWNSNNLDS  TGCVIAWNS  1        0.3544
1080.3    32.00  0.28     Sequence
 HLA-DQA10102-DQB10602  436      TGCVIAWNSNNLDSK  AWNSNNLDS  5        0.2785
2457.6    55.00  0.34     Sequence
 HLA-DQA10102-DQB10602  437      GCVIAWNSNNLDSKV  AWNSNNLDS  4        0.2695
2706.8    60.00  0.39     Sequence
 HLA-DQA10102-DQB10602  438      CVIAWNSNNLDSKVG  AWNSNNLDS  3        0.2730
2608.3    60.00  0.36     Sequence
 HLA-DQA10102-DQB10602  439      VIAWNSNNLDSKVGG  AWNSNNLDS  2        0.2721
2632.1    60.00  0.31     Sequence
 HLA-DQA10102-DQB10602  440      IAWNSNNLDSKVGGN  NLDSKVGGN  6        0.2710
2664.6    60.00  0.30     Sequence
 HLA-DQA10102-DQB10602  441      AWNSNNLDSKVGGNY  NLDSKVGGN  5        0.2913
2138.7    50.00  0.50     Sequence
 HLA-DQA10102-DQB10602  442      WNSNNLDSKVGGNYN  NLDSKVGGN  4        0.2902
2164.3    50.00  0.56     Sequence
 HLA-DQA10102-DQB10602  443      NSNNLDSKVGGNYNY  NLDSKVGGN  3        0.2748
2555.7    55.00  0.66     Sequence
 HLA-DQA10102-DQB10602  444      SNNLDSKVGGNYNYL  NLDSKVGGN  2        0.2468
3461.8    65.00  0.70     Sequence
 HLA-DQA10102-DQB10602  445      NNLDSKVGGNYNYLY  NLDSKVGGN  1        0.2426
3623.1    65.00  0.47     Sequence
 HLA-DQA10102-DQB10602  446      NLDSKVGGNYNYLYR  VGGNYNYLY  5        0.2248
4393.4    75.00  0.45     Sequence
 HLA-DQA10102-DQB10602  447      LDSKVGGNYNYLYRL  VGGNYNYLY  4        0.2549
3170.9    65.00  0.46     Sequence
 HLA-DQA10102-DQB10602  448      DSKVGGNYNYLYRLF  GNYNYLYRL  5        0.3086
1774.4    45.00  0.49     Sequence
 HLA-DQA10102-DQB10602  449      SKVGGNYNYLYRLFR  GNYNYLYRL  4        0.3103
1742.1    44.00  0.53     Sequence
 HLA-DQA10102-DQB10602  450      KVGGNYNYLYRLFRK  GNYNYLYRL  3        0.3205
1558.9    41.00  0.43     Sequence
 HLA-DQA10102-DQB10602  451      VGGNYNYLYRLFRKS  GNYNYLYRL  2        0.3074
1797.5    45.00  0.40     Sequence
 HLA-DQA10102-DQB10602  452      GGNYNYLYRLFRKSN  NYLYRLFRK  4        0.2967
2017.9    48.00  0.43     Sequence
 HLA-DQA10102-DQB10602  453      GNYNYLYRLFRKSNL  NYLYRLFRK  3        0.2766
2506.8    55.00  0.47     Sequence
 HLA-DQA10102-DQB10602  454      NYNYLYRLFRKSNLK  NYLYRLFRK  2        0.2387
3779.9    70.00  0.56     Sequence
 HLA-DQA10102-DQB10602  455      YNYLYRLFRKSNLKP  NYLYRLFRK  1        0.2048
5452.7    80.00  0.51     Sequence
 HLA-DQA10102-DQB10602  456      NYLYRLFRKSNLKPF  NYLYRLFRK  0        0.1649
8393.8    90.00  0.32     Sequence
 HLA-DQA10102-DQB10602  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.1459
10316.6    90.00  0.44     Sequence
 HLA-DQA10102-DQB10602  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.1463
10268.5    90.00  0.46     Sequence
```

```
 HLA-DQA10102-DQB10602  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.1596
8892.2    90.00  0.44     Sequence
 HLA-DQA10102-DQB10602  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.1537
9481.8    90.00  0.41     Sequence
 HLA-DQA10102-DQB10602  461      LFRKSNLKPFERDIS  KSNLKPFER  3        0.1396
11036.6    95.00  0.31     Sequence
 HLA-DQA10102-DQB10602  462      FRKSNLKPFERDIST  KSNLKPFER  2        0.1200
13646.6    95.00  0.29     Sequence
 HLA-DQA10102-DQB10602  463      RKSNLKPFERDISTE  KSNLKPFER  1        0.1010
16761.0   100.00  0.23     Sequence
 HLA-DQA10102-DQB10602  464      KSNLKPFERDISTEI  NLKPFERDI  2        0.1004
16866.1   100.00  0.18     Sequence
 HLA-DQA10102-DQB10602  465      SNLKPFERDISTEIY  ERDISTEIY  6        0.1382
11214.4    95.00  0.37     Sequence
 HLA-DQA10102-DQB10602  466      NLKPFERDISTEIYQ  ERDISTEIY  5        0.2194
4656.8    75.00  0.50     Sequence
 HLA-DQA10102-DQB10602  467      LKPFERDISTEIYQA  DISTEIYQA  6        0.3514
1116.3    33.00  0.54     Sequence
 HLA-DQA10102-DQB10602  468      KPFERDISTEIYQAG  DISTEIYQA  5        0.4544
366.4    12.00  0.64     Sequence
 HLA-DQA10102-DQB10602  469      PFERDISTEIYQAGS  DISTEIYQA  4        0.5050
211.9     6.50  0.61     Sequence         WB
 HLA-DQA10102-DQB10602  470      FERDISTEIYQAGST  DISTEIYQA  3        0.5069
207.5     6.50  0.56     Sequence         WB
 HLA-DQA10102-DQB10602  471      ERDISTEIYQAGSTP  DISTEIYQA  2        0.4756
291.2     9.50  0.55     Sequence         WB
 HLA-DQA10102-DQB10602  472      RDISTEIYQAGSTPC  DISTEIYQA  1        0.4101
591.3    20.00  0.47     Sequence
 HLA-DQA10102-DQB10602  473      DISTEIYQAGSTPCN  STEIYQAGS  2        0.3260
1470.0    40.00  0.37     Sequence
 HLA-DQA10102-DQB10602  474      ISTEIYQAGSTPCNG  QAGSTPCNG  6        0.3329
1363.2    38.00  0.34     Sequence
 HLA-DQA10102-DQB10602  475      STEIYQAGSTPCNGV  QAGSTPCNG  5        0.3756
859.2    27.00  0.53     Sequence
 HLA-DQA10102-DQB10602  476      TEIYQAGSTPCNGVK  QAGSTPCNG  4        0.3772
844.3    26.00  0.57     Sequence
 HLA-DQA10102-DQB10602  477      EIYQAGSTPCNGVKG  QAGSTPCNG  3        0.3761
854.0    27.00  0.56     Sequence
 HLA-DQA10102-DQB10602  478      IYQAGSTPCNGVKGF  QAGSTPCNG  2        0.3613
1002.4    30.00  0.51     Sequence
 HLA-DQA10102-DQB10602  479      YQAGSTPCNGVKGFN  QAGSTPCNG  1        0.3187
1589.2    42.00  0.44     Sequence
 HLA-DQA10102-DQB10602  480      QAGSTPCNGVKGFNC  QAGSTPCNG  0        0.2662
2806.5    60.00  0.28     Sequence
 HLA-DQA10102-DQB10602  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.2238
4441.3    75.00  0.41     Sequence
 HLA-DQA10102-DQB10602  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.2343
3960.8    70.00  0.44     Sequence
 HLA-DQA10102-DQB10602  483      STPCNGVKGFNCYFP  CNGVKGFNC  3        0.2518
3279.5    65.00  0.42     Sequence
 HLA-DQA10102-DQB10602  484      TPCNGVKGFNCYFPL  VKGFNCYFP  5        0.2739
2581.0    55.00  0.44     Sequence
 HLA-DQA10102-DQB10602  485      PCNGVKGFNCYFPLQ  VKGFNCYFP  4        0.2978
1994.0    48.00  0.38     Sequence
 HLA-DQA10102-DQB10602  486      CNGVKGFNCYFPLQS  VKGFNCYFP  3        0.3275
1445.9    39.00  0.34     Sequence
 HLA-DQA10102-DQB10602  487      NGVKGFNCYFPLQSY  NCYFPLQSY  6        0.4123
577.3    19.00  0.50     Sequence
 HLA-DQA10102-DQB10602  488      GVKGFNCYFPLQSYG  NCYFPLQSY  5        0.4522
374.9    13.00  0.65     Sequence
 HLA-DQA10102-DQB10602  489      VKGFNCYFPLQSYGF  NCYFPLQSY  4        0.4664
321.8    11.00  0.69     Sequence
 HLA-DQA10102-DQB10602  490      KGFNCYFPLQSYGFQ  NCYFPLQSY  3        0.4594
346.9    12.00  0.74     Sequence
 HLA-DQA10102-DQB10602  491      GFNCYFPLQSYGFQP  NCYFPLQSY  2        0.4240
508.6    17.00  0.73     Sequence
```

```
 HLA-DQA10102-DQB10602  492      FNCYFPLQSYGFQPT  NCYFPLQSY  1        0.3545
1079.1    32.00 0.64      Sequence
 HLA-DQA10102-DQB10602  493      NCYFPLQSYGFQPTY  NCYFPLQSY  0        0.2340
3977.5    70.00 0.41      Sequence
 HLA-DQA10102-DQB10602  494      CYFPLQSYGFQPTYG  SYGFQPTYG  6        0.1632
8552.7    90.00 0.22      Sequence
 HLA-DQA10102-DQB10602  495      YFPLQSYGFQPTYGV  SYGFQPTYG  5        0.1802
7115.7    85.00 0.37      Sequence
 HLA-DQA10102-DQB10602  496      FPLQSYGFQPTYGVG  SYGFQPTYG  4        0.1831
6894.3    85.00 0.40      Sequence
 HLA-DQA10102-DQB10602  497      PLQSYGFQPTYGVGY  SYGFQPTYG  3        0.2009
5688.4    80.00 0.35      Sequence
 HLA-DQA10102-DQB10602  498      LQSYGFQPTYGVGYQ  SYGFQPTYG  2        0.1942
6117.7    80.00 0.33      Sequence
 HLA-DQA10102-DQB10602  499      QSYGFQPTYGVGYQP  SYGFQPTYG  1        0.1750
7524.9    85.00 0.26      Sequence
 HLA-DQA10102-DQB10602  500      SYGFQPTYGVGYQPY  TYGVGYQPY  6        0.1848
6767.5    85.00 0.26      Sequence
 HLA-DQA10102-DQB10602  501      YGFQPTYGVGYQPYR  TYGVGYQPY  5        0.1843
6807.4    85.00 0.41      Sequence
 HLA-DQA10102-DQB10602  502      GFQPTYGVGYQPYRV  TYGVGYQPY  4        0.1879
6544.7    85.00 0.48      Sequence
 HLA-DQA10102-DQB10602  503      FQPTYGVGYQPYRVV  TYGVGYQPY  3        0.1989
5811.4    80.00 0.45      Sequence
 HLA-DQA10102-DQB10602  504      QPTYGVGYQPYRVVV  GVGYQPYRV  4        0.1927
6214.2    80.00 0.37      Sequence
 HLA-DQA10102-DQB10602  505      PTYGVGYQPYRVVVL  GVGYQPYRV  3        0.1768
7378.9    85.00 0.40      Sequence
 HLA-DQA10102-DQB10602  506      TYGVGYQPYRVVVLS  GVGYQPYRV  2        0.1727
7715.3    85.00 0.38      Sequence
 HLA-DQA10102-DQB10602  507      YGVGYQPYRVVVLSF  QPYRVVVLS  5        0.1750
7525.3    85.00 0.28      Sequence
 HLA-DQA10102-DQB10602  508      GVGYQPYRVVVLSFE  QPYRVVVLS  4        0.1893
6446.8    85.00 0.28      Sequence
 HLA-DQA10102-DQB10602  509      VGYQPYRVVVLSFEL  YRVVVLSFE  5        0.1928
6207.9    80.00 0.32      Sequence
 HLA-DQA10102-DQB10602  510      GYQPYRVVVLSFELL  YRVVVLSFE  4        0.1863
6663.3    85.00 0.34      Sequence
 HLA-DQA10102-DQB10602  511      YQPYRVVVLSFELLH  YRVVVLSFE  3        0.1788
7222.5    85.00 0.32      Sequence
 HLA-DQA10102-DQB10602  512      QPYRVVVLSFELLHA  VLSFELLHA  6        0.2069
5333.0    80.00 0.29      Sequence
 HLA-DQA10102-DQB10602  513      PYRVVVLSFELLHAP  VLSFELLHA  5        0.2998
1951.8    47.00 0.47      Sequence
 HLA-DQA10102-DQB10602  514      YRVVVLSFELLHAPA  VLSFELLHA  4        0.3482
1156.1    33.00 0.43      Sequence
 HLA-DQA10102-DQB10602  515      RVVVLSFELLHAPAT  VLSFELLHA  3        0.3654
959.4    29.00 0.40      Sequence
 HLA-DQA10102-DQB10602  516      VVVLSFELLHAPATV  VLSFELLHA  2        0.3626
988.8    30.00 0.37      Sequence
 HLA-DQA10102-DQB10602  517      VVLSFELLHAPATVC  LSFELLHAP  2        0.3672
940.9    29.00 0.27      Sequence
 HLA-DQA10102-DQB10602  518      VLSFELLHAPATVCG  LLHAPATVC  5        0.3670
942.7    29.00 0.17      Sequence
 HLA-DQA10102-DQB10602  519      LSFELLHAPATVCGP  HAPATVCGP  6        0.3875
755.0    24.00 0.29      Sequence
 HLA-DQA10102-DQB10602  520      SFELLHAPATVCGPK  HAPATVCGP  5        0.4044
629.2    21.00 0.44      Sequence
 HLA-DQA10102-DQB10602  521      FELLHAPATVCGPKK  HAPATVCGP  4        0.4014
649.8    21.00 0.49      Sequence
 HLA-DQA10102-DQB10602  522      ELLHAPATVCGPKKS  HAPATVCGP  3        0.3797
821.7    26.00 0.50      Sequence
 HLA-DQA10102-DQB10602  523      LLHAPATVCGPKKST  HAPATVCGP  2        0.3430
1222.4    35.00 0.53      Sequence
 HLA-DQA10102-DQB10602  524      LHAPATVCGPKKSTN  HAPATVCGP  1        0.2486
3393.5    65.00 0.46      Sequence
```

```
 HLA-DQA10102-DQB10602  525      HAPATVCGPKKSTNL  HAPATVCGP  0        0.1394
11063.0    95.00  0.37     Sequence
 HLA-DQA10102-DQB10602  526      APATVCGPKKSTNLV  ATVCGPKKS  2        0.0703
23369.3   100.00  0.30     Sequence
 HLA-DQA10102-DQB10602  527      PATVCGPKKSTNLVK  ATVCGPKKS  1        0.0606
25944.4   100.00  0.26     Sequence
 HLA-DQA10102-DQB10602  528      ATVCGPKKSTNLVKN  KKSTNLVKN  6        0.0926
18365.4   100.00  0.44     Sequence
 HLA-DQA10102-DQB10602  529      TVCGPKKSTNLVKNK  KKSTNLVKN  5        0.1938
6140.4    80.00  0.59     Sequence
 HLA-DQA10102-DQB10602  530      VCGPKKSTNLVKNKC  KKSTNLVKN  4        0.2493
3367.3    65.00  0.47     Sequence
 HLA-DQA10102-DQB10602  531      CGPKKSTNLVKNKCV  KKSTNLVKN  3        0.2815
2378.9    55.00  0.29     Sequence
 HLA-DQA10102-DQB10602  532      GPKKSTNLVKNKCVN  STNLVKNKC  4        0.2832
2334.6    55.00  0.23     Sequence
 HLA-DQA10102-DQB10602  533      PKKSTNLVKNKCVNF  STNLVKNKC  3        0.2827
2348.6    55.00  0.25     Sequence
 HLA-DQA10102-DQB10602  534      KKSTNLVKNKCVNFN  STNLVKNKC  2        0.2780
2468.6    55.00  0.22     Sequence
 HLA-DQA10102-DQB10602  535      KSTNLVKNKCVNFNF  TNLVKNKCV  2        0.2575
3083.0    65.00  0.28     Sequence
 HLA-DQA10102-DQB10602  536      STNLVKNKCVNFNFN  VKNKCVNFN  4        0.2404
3710.6    70.00  0.25     Sequence
 HLA-DQA10102-DQB10602  537      TNLVKNKCVNFNFNG  NKCVNFNFN  5        0.2411
3683.5    70.00  0.26     Sequence
 HLA-DQA10102-DQB10602  538      NLVKNKCVNFNFNGL  NKCVNFNFN  4        0.2097
5170.8    75.00  0.31     Sequence
 HLA-DQA10102-DQB10602  539      LVKNKCVNFNFNGLT  NKCVNFNFN  3        0.2113
5084.8    75.00  0.31     Sequence
 HLA-DQA10102-DQB10602  540      VKNKCVNFNFNGLTG  NKCVNFNFN  2        0.2187
4692.6    75.00  0.20     Sequence
 HLA-DQA10102-DQB10602  541      KNKCVNFNFNGLTGT  NFNFNGLTG  5        0.2491
3377.8    65.00  0.32     Sequence
 HLA-DQA10102-DQB10602  542      NKCVNFNFNGLTGTG  NFNFNGLTG  4        0.2693
2714.8    60.00  0.32     Sequence
 HLA-DQA10102-DQB10602  543      KCVNFNFNGLTGTGV  FNFNGLTGT  4        0.2867
2247.3    55.00  0.28     Sequence
 HLA-DQA10102-DQB10602  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5        0.3001
1943.8    47.00  0.27     Sequence
 HLA-DQA10102-DQB10602  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.3128
1694.2    43.00  0.27     Sequence
 HLA-DQA10102-DQB10602  546      NFNFNGLTGTGVLTE  LTGTGVLTE  6        0.3987
669.0    22.00  0.52     Sequence
 HLA-DQA10102-DQB10602  547      FNFNGLTGTGVLTES  LTGTGVLTE  5        0.5085
204.0     6.50  0.75     Sequence          WB
 HLA-DQA10102-DQB10602  548      NFNGLTGTGVLTESN  LTGTGVLTE  4        0.5270
166.9     5.00  0.74     Sequence          WB
 HLA-DQA10102-DQB10602  549      FNGLTGTGVLTESNK  LTGTGVLTE  3        0.5228
174.7     5.50  0.68     Sequence          WB
 HLA-DQA10102-DQB10602  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.4919
244.2     8.00  0.62     Sequence          WB
 HLA-DQA10102-DQB10602  551      GLTGTGVLTESNKKF  LTGTGVLTE  1        0.4350
451.7    15.00  0.50     Sequence
 HLA-DQA10102-DQB10602  552      LTGTGVLTESNKKFL  GTGVLTESN  2        0.3578
1042.0    31.00  0.56     Sequence
 HLA-DQA10102-DQB10602  553      TGTGVLTESNKKFLP  GTGVLTESN  1        0.2476
3431.9    65.00  0.56     Sequence
 HLA-DQA10102-DQB10602  554      GTGVLTESNKKFLPF  GTGVLTESN  0        0.1950
6061.3    80.00  0.30     Sequence
 HLA-DQA10102-DQB10602  555      TGVLTESNKKFLPFQ  TESNKKFLP  4        0.1783
7262.0    85.00  0.35     Sequence
 HLA-DQA10102-DQB10602  556      GVLTESNKKFLPFQQ  TESNKKFLP  3        0.1931
6186.8    80.00  0.31     Sequence
 HLA-DQA10102-DQB10602  557      VLTESNKKFLPFQQF  NKKFLPFQQ  5        0.2306
4123.2    70.00  0.31     Sequence
```

```
 HLA-DQA10102-DQB10602  558      LTESNKKFLPFQQFG  NKKFLPFQQ  4        0.2392
3757.5    70.00  0.32     Sequence
 HLA-DQA10102-DQB10602  559      TESNKKFLPFQQFGR  KKFLPFQQF  4        0.2337
3987.4    70.00  0.34     Sequence
 HLA-DQA10102-DQB10602  560      ESNKKFLPFQQFGRD  KKFLPFQQF  3        0.2264
4318.5    70.00  0.36     Sequence
 HLA-DQA10102-DQB10602  561      SNKKFLPFQQFGRDI  KKFLPFQQF  2        0.2077
5282.1    80.00  0.37     Sequence
 HLA-DQA10102-DQB10602  562      NKKFLPFQQFGRDIA  KKFLPFQQF  1        0.1647
8417.8    90.00  0.28     Sequence
 HLA-DQA10102-DQB10602  563      KKFLPFQQFGRDIAD  KFLPFQQFG  1        0.1357
11519.2    95.00  0.19     Sequence
 HLA-DQA10102-DQB10602  564      KFLPFQQFGRDIADT  QFGRDIADT  6        0.1445
10465.4    95.00  0.35     Sequence
 HLA-DQA10102-DQB10602  565      FLPFQQFGRDIADTT  QFGRDIADT  5        0.1596
8896.2    90.00  0.56     Sequence
 HLA-DQA10102-DQB10602  566      LPFQQFGRDIADTTD  QFGRDIADT  4        0.1733
7665.9    85.00  0.58     Sequence
 HLA-DQA10102-DQB10602  567      PFQQFGRDIADTTDA  QFGRDIADT  3        0.1836
6861.6    85.00  0.55     Sequence
 HLA-DQA10102-DQB10602  568      FQQFGRDIADTTDAV  QFGRDIADT  2        0.1820
6981.2    85.00  0.49     Sequence
 HLA-DQA10102-DQB10602  569      QQFGRDIADTTDAVR  QFGRDIADT  1        0.1717
7803.9    85.00  0.31     Sequence
 HLA-DQA10102-DQB10602  570      QFGRDIADTTDAVRD  IADTTDAVR  5        0.1843
6804.9    85.00  0.29     Sequence
 HLA-DQA10102-DQB10602  571      FGRDIADTTDAVRDP  ADTTDAVRD  5        0.1783
7260.9    85.00  0.27     Sequence
 HLA-DQA10102-DQB10602  572      GRDIADTTDAVRDPQ  ADTTDAVRD  4        0.1801
7125.6    85.00  0.33     Sequence
 HLA-DQA10102-DQB10602  573      RDIADTTDAVRDPQT  ADTTDAVRD  3        0.1796
7161.9    85.00  0.31     Sequence
 HLA-DQA10102-DQB10602  574      DIADTTDAVRDPQTL  ADTTDAVRD  2        0.1633
8542.5    90.00  0.27     Sequence
 HLA-DQA10102-DQB10602  575      IADTTDAVRDPQTLE  DTTDAVRDP  2        0.1389
11124.6    95.00  0.24     Sequence
 HLA-DQA10102-DQB10602  576      ADTTDAVRDPQTLEI  TDAVRDPQT  3        0.1058
15923.0   100.00  0.25     Sequence
 HLA-DQA10102-DQB10602  577      DTTDAVRDPQTLEIL  TDAVRDPQT  2        0.0984
17250.9   100.00  0.23     Sequence
 HLA-DQA10102-DQB10602  578      TTDAVRDPQTLEILD  VRDPQTLEI  4        0.0944
18011.2   100.00  0.23     Sequence
 HLA-DQA10102-DQB10602  579      TDAVRDPQTLEILDI  PQTLEILDI  6        0.1518
9673.5    90.00  0.38     Sequence
 HLA-DQA10102-DQB10602  580      DAVRDPQTLEILDIT  PQTLEILDI  5        0.2015
5653.4    80.00  0.56     Sequence
 HLA-DQA10102-DQB10602  581      AVRDPQTLEILDITP  PQTLEILDI  4        0.2198
4633.7    75.00  0.53     Sequence
 HLA-DQA10102-DQB10602  582      VRDPQTLEILDITPC  PQTLEILDI  3        0.2568
3106.6    65.00  0.42     Sequence
 HLA-DQA10102-DQB10602  583      RDPQTLEILDITPCS  LEILDITPC  5        0.2758
2530.4    55.00  0.38     Sequence
 HLA-DQA10102-DQB10602  584      DPQTLEILDITPCSF  LEILDITPC  4        0.2826
2350.5    55.00  0.41     Sequence
 HLA-DQA10102-DQB10602  585      PQTLEILDITPCSFG  LEILDITPC  3        0.2911
2143.2    50.00  0.43     Sequence
 HLA-DQA10102-DQB10602  586      QTLEILDITPCSFGG  LEILDITPC  2        0.2753
2543.0    55.00  0.43     Sequence
 HLA-DQA10102-DQB10602  587      TLEILDITPCSFGGV  LEILDITPC  1        0.2554
3155.0    65.00  0.37     Sequence
 HLA-DQA10102-DQB10602  588      LEILDITPCSFGGVS  LDITPCSFG  3        0.2300
4149.3    70.00  0.27     Sequence
 HLA-DQA10102-DQB10602  589      EILDITPCSFGGVSV  LDITPCSFG  2        0.1948
6074.7    80.00  0.31     Sequence
 HLA-DQA10102-DQB10602  590      ILDITPCSFGGVSVI  LDITPCSFG  1        0.1772
7349.9    85.00  0.25     Sequence
```

```
 HLA-DQA10102-DQB10602  591      LDITPCSFGGVSVIT  SFGGVSVIT  6        0.1998
5757.9    80.00  0.22     Sequence
 HLA-DQA10102-DQB10602  592      DITPCSFGGVSVITP  FGGVSVITP  6        0.2487
3392.1    65.00  0.40     Sequence
 HLA-DQA10102-DQB10602  593      ITPCSFGGVSVITPG  FGGVSVITP  5        0.3517
1112.9    33.00  0.50     Sequence
 HLA-DQA10102-DQB10602  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.3784
833.3    26.00  0.50     Sequence
 HLA-DQA10102-DQB10602  595      PCSFGGVSVITPGTN  FGGVSVITP  3        0.3816
805.4    25.00  0.41     Sequence
 HLA-DQA10102-DQB10602  596      CSFGGVSVITPGTNT  FGGVSVITP  2        0.3782
835.7    26.00  0.36     Sequence
 HLA-DQA10102-DQB10602  597      SFGGVSVITPGTNTS  GGVSVITPG  2        0.3279
1438.6    39.00  0.34     Sequence
 HLA-DQA10102-DQB10602  598      FGGVSVITPGTNTSN  GGVSVITPG  1        0.2769
2498.3    55.00  0.35     Sequence
 HLA-DQA10102-DQB10602  599      GGVSVITPGTNTSNQ  GGVSVITPG  0        0.2190
4677.5    75.00  0.28     Sequence
 HLA-DQA10102-DQB10602  600      GVSVITPGTNTSNQV  TPGTNTSNQ  5        0.1842
6814.1    85.00  0.21     Sequence
 HLA-DQA10102-DQB10602  601      VSVITPGTNTSNQVA  GTNTSNQVA  6        0.2374
3830.5    70.00  0.42     Sequence
 HLA-DQA10102-DQB10602  602      SVITPGTNTSNQVAV  GTNTSNQVA  5        0.3787
830.9    26.00  0.62     Sequence
 HLA-DQA10102-DQB10602  603      VITPGTNTSNQVAVL  GTNTSNQVA  4        0.4576
353.9    12.00  0.41     Sequence
 HLA-DQA10102-DQB10602  604      ITPGTNTSNQVAVLY  NTSNQVAVL  5        0.5121
196.1     6.00  0.46     Sequence         WB
 HLA-DQA10102-DQB10602  605      TPGTNTSNQVAVLYQ  NTSNQVAVL  4        0.5558
122.2     3.50  0.34     Sequence         WB
 HLA-DQA10102-DQB10602  606      PGTNTSNQVAVLYQG  SNQVAVLYQ  5        0.6239
58.5     1.00  0.34     Sequence         SB
 HLA-DQA10102-DQB10602  607      GTNTSNQVAVLYQGV  NQVAVLYQG  5        0.6345
52.2     0.90  0.36     Sequence         SB
 HLA-DQA10102-DQB10602  608      TNTSNQVAVLYQGVN  NQVAVLYQG  4        0.6285
55.7     1.00  0.40     Sequence         SB
 HLA-DQA10102-DQB10602  609      NTSNQVAVLYQGVNC  NQVAVLYQG  3        0.6012
74.8     1.50  0.44     Sequence         SB
 HLA-DQA10102-DQB10602  610      TSNQVAVLYQGVNCT  NQVAVLYQG  2        0.5491
131.4     4.00  0.47     Sequence         WB
 HLA-DQA10102-DQB10602  611      SNQVAVLYQGVNCTE  NQVAVLYQG  1        0.4817
272.4     9.00  0.44     Sequence         WB
 HLA-DQA10102-DQB10602  612      NQVAVLYQGVNCTEV  NQVAVLYQG  0        0.3938
705.5    23.00  0.31     Sequence
 HLA-DQA10102-DQB10602  613      QVAVLYQGVNCTEVP  YQGVNCTEV  5        0.3168
1623.5    42.00  0.37     Sequence
 HLA-DQA10102-DQB10602  614      VAVLYQGVNCTEVPV  YQGVNCTEV  4        0.2902
2164.9    50.00  0.52     Sequence
 HLA-DQA10102-DQB10602  615      AVLYQGVNCTEVPVA  YQGVNCTEV  3        0.2962
2027.7    48.00  0.49     Sequence
 HLA-DQA10102-DQB10602  616      VLYQGVNCTEVPVAI  YQGVNCTEV  2        0.3175
1610.6    42.00  0.37     Sequence
 HLA-DQA10102-DQB10602  617      LYQGVNCTEVPVAIH  VNCTEVPVA  4        0.3066
1812.8    45.00  0.38     Sequence
 HLA-DQA10102-DQB10602  618      YQGVNCTEVPVAIHA  VNCTEVPVA  3        0.3136
1679.7    43.00  0.37     Sequence
 HLA-DQA10102-DQB10602  619      QGVNCTEVPVAIHAD  CTEVPVAIH  4        0.3314
1386.4    38.00  0.28     Sequence
 HLA-DQA10102-DQB10602  620      GVNCTEVPVAIHADQ  EVPVAIHAD  5        0.3636
978.7    30.00  0.34     Sequence
 HLA-DQA10102-DQB10602  621      VNCTEVPVAIHADQL  EVPVAIHAD  4        0.3510
1120.9    33.00  0.37     Sequence
 HLA-DQA10102-DQB10602  622      NCTEVPVAIHADQLT  EVPVAIHAD  3        0.3242
1498.2    40.00  0.45     Sequence
 HLA-DQA10102-DQB10602  623      CTEVPVAIHADQLTP  EVPVAIHAD  2        0.2983
1983.2    48.00  0.44     Sequence
```

```
 HLA-DQA10102-DQB10602  624      TEVPVAIHADQLTPT  EVPVAIHAD  1        0.2846
2298.9    55.00  0.28     Sequence
 HLA-DQA10102-DQB10602  625      EVPVAIHADQLTPTW  IHADQLTPT  5        0.2788
2449.4    55.00  0.40     Sequence
 HLA-DQA10102-DQB10602  626      VPVAIHADQLTPTWR  IHADQLTPT  4        0.2631
2901.4    60.00  0.47     Sequence
 HLA-DQA10102-DQB10602  627      PVAIHADQLTPTWRV  IHADQLTPT  3        0.2791
2441.7    55.00  0.43     Sequence
 HLA-DQA10102-DQB10602  628      VAIHADQLTPTWRVY  DQLTPTWRV  5        0.2987
1974.4    48.00  0.44     Sequence
 HLA-DQA10102-DQB10602  629      AIHADQLTPTWRVYS  DQLTPTWRV  4        0.3142
1669.8    43.00  0.48     Sequence
 HLA-DQA10102-DQB10602  630      IHADQLTPTWRVYST  DQLTPTWRV  3        0.3279
1439.1    39.00  0.46     Sequence
 HLA-DQA10102-DQB10602  631      HADQLTPTWRVYSTG  DQLTPTWRV  2        0.3242
1497.5    40.00  0.38     Sequence
 HLA-DQA10102-DQB10602  632      ADQLTPTWRVYSTGS  TPTWRVYST  4        0.3180
1601.8    42.00  0.26     Sequence
 HLA-DQA10102-DQB10602  633      DQLTPTWRVYSTGSN  TPTWRVYST  3        0.2930
2100.7    49.00  0.29     Sequence
 HLA-DQA10102-DQB10602  634      QLTPTWRVYSTGSNV  TPTWRVYST  2        0.2479
3421.8    65.00  0.31     Sequence
 HLA-DQA10102-DQB10602  635      LTPTWRVYSTGSNVF  TPTWRVYST  1        0.2386
3781.0    70.00  0.25     Sequence
 HLA-DQA10102-DQB10602  636      TPTWRVYSTGSNVFQ  STGSNVFQX  7        0.2515
3289.3    65.00  0.23     Sequence
 HLA-DQA10102-DQB10602  637      PTWRVYSTGSNVFQT  STGSNVFQT  6        0.4329
462.0    16.00  0.66     Sequence
 HLA-DQA10102-DQB10602  638      TWRVYSTGSNVFQTR  STGSNVFQT  5        0.5333
155.9     4.50  0.86     Sequence         WB
 HLA-DQA10102-DQB10602  639      WRVYSTGSNVFQTRA  STGSNVFQT  4        0.5688
106.3     3.00  0.82     Sequence         WB
 HLA-DQA10102-DQB10602  640      RVYSTGSNVFQTRAG  STGSNVFQT  3        0.5686
106.4     3.00  0.78     Sequence         WB
 HLA-DQA10102-DQB10602  641      VYSTGSNVFQTRAGC  STGSNVFQT  2        0.5433
139.9     4.00  0.74     Sequence         WB
 HLA-DQA10102-DQB10602  642      YSTGSNVFQTRAGCL  STGSNVFQT  1        0.4758
290.4     9.50  0.57     Sequence         WB
 HLA-DQA10102-DQB10602  643      STGSNVFQTRAGCLI  STGSNVFQT  0        0.3824
798.4    25.00  0.37     Sequence
 HLA-DQA10102-DQB10602  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.3343
1343.1    37.00  0.29     Sequence
 HLA-DQA10102-DQB10602  645      GSNVFQTRAGCLIGA  TRAGCLIGA  6        0.4066
614.2    20.00  0.37     Sequence
 HLA-DQA10102-DQB10602  646      SNVFQTRAGCLIGAE  TRAGCLIGA  5        0.4904
248.0     8.00  0.51     Sequence         WB
 HLA-DQA10102-DQB10602  647      NVFQTRAGCLIGAEY  TRAGCLIGA  4        0.5273
166.4     5.00  0.50     Sequence         WB
 HLA-DQA10102-DQB10602  648      VFQTRAGCLIGAEYV  TRAGCLIGA  3        0.5184
183.3     5.50  0.50     Sequence         WB
 HLA-DQA10102-DQB10602  649      FQTRAGCLIGAEYVN  TRAGCLIGA  2        0.4896
250.3     8.00  0.49     Sequence         WB
 HLA-DQA10102-DQB10602  650      QTRAGCLIGAEYVNN  TRAGCLIGA  1        0.4269
493.4    17.00  0.41     Sequence
 HLA-DQA10102-DQB10602  651      TRAGCLIGAEYVNNS  TRAGCLIGA  0        0.3580
1039.7    31.00  0.32     Sequence
 HLA-DQA10102-DQB10602  652      RAGCLIGAEYVNNSY  GCLIGAEYV  2        0.2842
2309.1    55.00  0.24     Sequence
 HLA-DQA10102-DQB10602  653      AGCLIGAEYVNNSYE  IGAEYVNNS  4        0.2324
4046.1    70.00  0.34     Sequence
 HLA-DQA10102-DQB10602  654      GCLIGAEYVNNSYEC  IGAEYVNNS  3        0.2128
5001.4    75.00  0.37     Sequence
 HLA-DQA10102-DQB10602  655      CLIGAEYVNNSYECD  IGAEYVNNS  2        0.1912
6315.7    80.00  0.40     Sequence
 HLA-DQA10102-DQB10602  656      LIGAEYVNNSYECDI  VNNSYECDI  6        0.2402
3719.4    70.00  0.22     Sequence
```

```
 HLA-DQA10102-DQB10602  657      IGAEYVNNSYECDIP  VNNSYECDI  5        0.2346
3949.7    70.00  0.31     Sequence
 HLA-DQA10102-DQB10602  658      GAEYVNNSYECDIPI  VNNSYECDI  4        0.2369
3852.9    70.00  0.33     Sequence
 HLA-DQA10102-DQB10602  659      AEYVNNSYECDIPIG  VNNSYECDI  3        0.2481
3411.5    65.00  0.29     Sequence
 HLA-DQA10102-DQB10602  660      EYVNNSYECDIPIGA  VNNSYECDI  2        0.2829
2342.0    55.00  0.22     Sequence
 HLA-DQA10102-DQB10602  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.3105
1736.6    44.00  0.28     Sequence
 HLA-DQA10102-DQB10602  662      VNNSYECDIPIGAGI  ECDIPIGAG  5        0.3293
1417.7    39.00  0.35     Sequence
 HLA-DQA10102-DQB10602  663      NNSYECDIPIGAGIC  ECDIPIGAG  4        0.3286
1428.4    39.00  0.38     Sequence
 HLA-DQA10102-DQB10602  664      NSYECDIPIGAGICA  ECDIPIGAG  3        0.3233
1512.2    40.00  0.38     Sequence
 HLA-DQA10102-DQB10602  665      SYECDIPIGAGICAS  ECDIPIGAG  2        0.3304
1401.5    38.00  0.28     Sequence
 HLA-DQA10102-DQB10602  666      YECDIPIGAGICASY  PIGAGICAS  5        0.3603
1014.1    30.00  0.41     Sequence
 HLA-DQA10102-DQB10602  667      ECDIPIGAGICASYQ  PIGAGICAS  4        0.4035
635.1    21.00  0.38     Sequence
 HLA-DQA10102-DQB10602  668      CDIPIGAGICASYQT  GAGICASYQ  5        0.4443
408.4    14.00  0.44     Sequence
 HLA-DQA10102-DQB10602  669      DIPIGAGICASYQTQ  GAGICASYQ  4        0.4384
435.6    15.00  0.45     Sequence
 HLA-DQA10102-DQB10602  670      IPIGAGICASYQTQT  GAGICASYQ  3        0.4290
482.3    16.00  0.44     Sequence
 HLA-DQA10102-DQB10602  671      PIGAGICASYQTQTN  GAGICASYQ  2        0.3893
740.5    24.00  0.45     Sequence
 HLA-DQA10102-DQB10602  672      IGAGICASYQTQTNS  GAGICASYQ  1        0.3625
989.5    30.00  0.44     Sequence
 HLA-DQA10102-DQB10602  673      GAGICASYQTQTNSP  GAGICASYQ  0        0.2888
2197.8    55.00  0.28     Sequence
 HLA-DQA10102-DQB10602  674      AGICASYQTQTNSPR  CASYQTQTN  3        0.2226
4495.4    75.00  0.25     Sequence
 HLA-DQA10102-DQB10602  675      GICASYQTQTNSPRR  CASYQTQTN  2        0.1949
6068.6    80.00  0.28     Sequence
 HLA-DQA10102-DQB10602  676      ICASYQTQTNSPRRA  SYQTQTNSP  3        0.1772
7352.7    85.00  0.25     Sequence
 HLA-DQA10102-DQB10602  677      CASYQTQTNSPRRAR  TQTNSPRRA  5        0.1776
7318.0    85.00  0.42     Sequence
 HLA-DQA10102-DQB10602  678      ASYQTQTNSPRRARS  TQTNSPRRA  4        0.1871
6605.8    85.00  0.47     Sequence
 HLA-DQA10102-DQB10602  679      SYQTQTNSPRRARSV  TQTNSPRRA  3        0.2293
4181.0    70.00  0.34     Sequence
 HLA-DQA10102-DQB10602  680      YQTQTNSPRRARSVA  NSPRRARSV  5        0.2390
3766.1    70.00  0.34     Sequence
 HLA-DQA10102-DQB10602  681      QTQTNSPRRARSVAS  NSPRRARSV  4        0.2431
3601.1    65.00  0.35     Sequence
 HLA-DQA10102-DQB10602  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.2695
2708.9    60.00  0.33     Sequence
 HLA-DQA10102-DQB10602  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.3022
1900.1    47.00  0.30     Sequence
 HLA-DQA10102-DQB10602  684      TNSPRRARSVASQSI  RARSVASQS  5        0.3782
835.4    26.00  0.20     Sequence
 HLA-DQA10102-DQB10602  685      NSPRRARSVASQSII  ARSVASQSI  5        0.4093
596.9    20.00  0.47     Sequence
 HLA-DQA10102-DQB10602  686      SPRRARSVASQSIIA  ARSVASQSI  4        0.4184
540.6    18.00  0.47     Sequence
 HLA-DQA10102-DQB10602  687      PRRARSVASQSIIAY  ARSVASQSI  3        0.4307
473.0    16.00  0.40     Sequence
 HLA-DQA10102-DQB10602  688      RRARSVASQSIIAYT  ARSVASQSI  2        0.4924
242.7     8.00  0.20     Sequence         WB
 HLA-DQA10102-DQB10602  689      RARSVASQSIIAYTM  ASQSIIAYT  5        0.5246
171.3     5.00  0.40     Sequence         WB
```

```
 HLA-DQA10102-DQB10602  690      ARSVASQSIIAYTMS  ASQSIIAYT  4        0.5465
135.2     4.00  0.38     Sequence         WB
 HLA-DQA10102-DQB10602  691      RSVASQSIIAYTMSL  ASQSIIAYT  3        0.5460
135.9     4.00  0.36     Sequence         WB
 HLA-DQA10102-DQB10602  692      SVASQSIIAYTMSLG  SQSIIAYTM  3        0.5105
199.5     6.00  0.32     Sequence         WB
 HLA-DQA10102-DQB10602  693      VASQSIIAYTMSLGA  SQSIIAYTM  2        0.5084
204.2     6.50  0.25     Sequence         WB
 HLA-DQA10102-DQB10602  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.5226
175.1     5.50  0.45     Sequence         WB
 HLA-DQA10102-DQB10602  695      SQSIIAYTMSLGAEN  IAYTMSLGA  4        0.5333
156.0     4.50  0.52     Sequence         WB
 HLA-DQA10102-DQB10602  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.5137
192.9     6.00  0.56     Sequence         WB
 HLA-DQA10102-DQB10602  697      SIIAYTMSLGAENSV  IAYTMSLGA  2        0.5038
214.6     7.00  0.50     Sequence         WB
 HLA-DQA10102-DQB10602  698      IIAYTMSLGAENSVA  IAYTMSLGA  1        0.4956
234.6     7.50  0.38     Sequence         WB
 HLA-DQA10102-DQB10602  699      IAYTMSLGAENSVAY  SLGAENSVA  5        0.4668
320.3    11.00  0.30     Sequence
 HLA-DQA10102-DQB10602  700      AYTMSLGAENSVAYS  SLGAENSVA  4        0.4772
286.2     9.50  0.38     Sequence         WB
 HLA-DQA10102-DQB10602  701      YTMSLGAENSVAYSN  SLGAENSVA  3        0.5496
130.8     3.50  0.25     Sequence         WB
 HLA-DQA10102-DQB10602  702      TMSLGAENSVAYSNN  AENSVAYSN  5        0.5471
134.3     4.00  0.37     Sequence         WB
 HLA-DQA10102-DQB10602  703      MSLGAENSVAYSNNS  AENSVAYSN  4        0.5327
156.9     4.50  0.41     Sequence         WB
 HLA-DQA10102-DQB10602  704      SLGAENSVAYSNNSI  AENSVAYSN  3        0.5015
220.1     7.00  0.43     Sequence         WB
 HLA-DQA10102-DQB10602  705      LGAENSVAYSNNSIA  AENSVAYSN  2        0.4576
353.9    12.00  0.45     Sequence
 HLA-DQA10102-DQB10602  706      GAENSVAYSNNSIAI  AENSVAYSN  1        0.3798
820.8    26.00  0.37     Sequence
 HLA-DQA10102-DQB10602  707      AENSVAYSNNSIAIP  NSVAYSNNS  2        0.3203
1562.5    41.00  0.25     Sequence
 HLA-DQA10102-DQB10602  708      ENSVAYSNNSIAIPT  YSNNSIAIP  5        0.3623
991.6    30.00  0.31     Sequence
 HLA-DQA10102-DQB10602  709      NSVAYSNNSIAIPTN  SNNSIAIPT  5        0.3940
704.0    23.00  0.26     Sequence
 HLA-DQA10102-DQB10602  710      SVAYSNNSIAIPTNF  NNSIAIPTN  5        0.4356
449.0    15.00  0.38     Sequence
 HLA-DQA10102-DQB10602  711      VAYSNNSIAIPTNFT  NNSIAIPTN  4        0.4356
448.6    15.00  0.38     Sequence
 HLA-DQA10102-DQB10602  712      AYSNNSIAIPTNFTI  NNSIAIPTN  3        0.4232
513.3    17.00  0.39     Sequence
 HLA-DQA10102-DQB10602  713      YSNNSIAIPTNFTIS  NNSIAIPTN  2        0.3952
694.8    22.00  0.43     Sequence
 HLA-DQA10102-DQB10602  714      SNNSIAIPTNFTISV  NNSIAIPTN  1        0.3174
1611.8    42.00  0.39     Sequence
 HLA-DQA10102-DQB10602  715      NNSIAIPTNFTISVT  SIAIPTNFT  2        0.2610
2969.5    60.00  0.28     Sequence
 HLA-DQA10102-DQB10602  716      NSIAIPTNFTISVTT  PTNFTISVT  5        0.2468
3461.3    65.00  0.31     Sequence
 HLA-DQA10102-DQB10602  717      SIAIPTNFTISVTTE  PTNFTISVT  4        0.2902
2164.5    50.00  0.26     Sequence
 HLA-DQA10102-DQB10602  718      IAIPTNFTISVTTEI  NFTISVTTE  5        0.3283
1433.5    39.00  0.35     Sequence
 HLA-DQA10102-DQB10602  719      AIPTNFTISVTTEIL  NFTISVTTE  4        0.3302
1403.4    38.00  0.37     Sequence
 HLA-DQA10102-DQB10602  720      IPTNFTISVTTEILP  NFTISVTTE  3        0.3339
1348.9    37.00  0.37     Sequence
 HLA-DQA10102-DQB10602  721      PTNFTISVTTEILPV  NFTISVTTE  2        0.3297
1412.0    38.00  0.31     Sequence
 HLA-DQA10102-DQB10602  722      TNFTISVTTEILPVS  SVTTEILPV  5        0.3290
1422.7    39.00  0.25     Sequence
```

```
 HLA-DQA10102-DQB10602  723      NFTISVTTEILPVSM  SVTTEILPV  4        0.3030
1884.3    46.00  0.35     Sequence
 HLA-DQA10102-DQB10602  724      FTISVTTEILPVSMT  SVTTEILPV  3        0.3365
1311.9    37.00  0.28     Sequence
 HLA-DQA10102-DQB10602  725      TISVTTEILPVSMTK  TEILPVSMT  5        0.3252
1481.8    40.00  0.28     Sequence
 HLA-DQA10102-DQB10602  726      ISVTTEILPVSMTKT  TEILPVSMT  4        0.3254
1478.7    40.00  0.34     Sequence
 HLA-DQA10102-DQB10602  727      SVTTEILPVSMTKTS  TEILPVSMT  3        0.3149
1656.0    43.00  0.34     Sequence
 HLA-DQA10102-DQB10602  728      VTTEILPVSMTKTSV  TEILPVSMT  2        0.3183
1596.2    42.00  0.31     Sequence
 HLA-DQA10102-DQB10602  729      TTEILPVSMTKTSVD  ILPVSMTKT  3        0.3239
1503.4    40.00  0.33     Sequence
 HLA-DQA10102-DQB10602  730      TEILPVSMTKTSVDC  VSMTKTSVD  5        0.3288
1425.7    39.00  0.41     Sequence
 HLA-DQA10102-DQB10602  731      EILPVSMTKTSVDCT  VSMTKTSVD  4        0.3210
1550.2    41.00  0.47     Sequence
 HLA-DQA10102-DQB10602  732      ILPVSMTKTSVDCTM  VSMTKTSVD  3        0.3267
1457.5    39.00  0.47     Sequence
 HLA-DQA10102-DQB10602  733      LPVSMTKTSVDCTMY  VSMTKTSVD  2        0.3341
1346.5    37.00  0.37     Sequence
 HLA-DQA10102-DQB10602  734      PVSMTKTSVDCTMYI  MTKTSVDCT  3        0.3298
1410.5    38.00  0.25     Sequence
 HLA-DQA10102-DQB10602  735      VSMTKTSVDCTMYIC  TKTSVDCTM  3        0.3278
1441.6    39.00  0.18     Sequence
 HLA-DQA10102-DQB10602  736      SMTKTSVDCTMYICG  SVDCTMYIC  5        0.3350
1332.2    37.00  0.20     Sequence
 HLA-DQA10102-DQB10602  737      MTKTSVDCTMYICGD  DCTMYICGD  6        0.3943
701.8    23.00  0.29     Sequence
 HLA-DQA10102-DQB10602  738      TKTSVDCTMYICGDS  DCTMYICGD  5        0.4026
641.7    21.00  0.36     Sequence
 HLA-DQA10102-DQB10602  739      KTSVDCTMYICGDST  DCTMYICGD  4        0.3957
691.3    22.00  0.41     Sequence
 HLA-DQA10102-DQB10602  740      TSVDCTMYICGDSTE  DCTMYICGD  3        0.3762
853.7    27.00  0.41     Sequence
 HLA-DQA10102-DQB10602  741      SVDCTMYICGDSTEC  DCTMYICGD  2        0.3413
1244.4    35.00  0.44     Sequence
 HLA-DQA10102-DQB10602  742      VDCTMYICGDSTECS  DCTMYICGD  1        0.2890
2192.7    55.00  0.37     Sequence
 HLA-DQA10102-DQB10602  743      DCTMYICGDSTECSN  ICGDSTECS  5        0.2378
3815.3    70.00  0.38     Sequence
 HLA-DQA10102-DQB10602  744      CTMYICGDSTECSNL  ICGDSTECS  4        0.2149
4889.3    75.00  0.44     Sequence
 HLA-DQA10102-DQB10602  745      TMYICGDSTECSNLL  ICGDSTECS  3        0.2184
4708.2    75.00  0.45     Sequence
 HLA-DQA10102-DQB10602  746      MYICGDSTECSNLLL  ICGDSTECS  2        0.2214
4558.4    75.00  0.32     Sequence
 HLA-DQA10102-DQB10602  747      YICGDSTECSNLLLQ  TECSNLLLQ  6        0.2544
3186.8    65.00  0.31     Sequence
 HLA-DQA10102-DQB10602  748      ICGDSTECSNLLLQY  TECSNLLLQ  5        0.3706
907.1    28.00  0.54     Sequence
 HLA-DQA10102-DQB10602  749      CGDSTECSNLLLQYG  TECSNLLLQ  4        0.4683
315.2    11.00  0.37     Sequence
 HLA-DQA10102-DQB10602  750      GDSTECSNLLLQYGS  CSNLLLQYG  5        0.5504
129.7     3.50  0.37     Sequence         WB
 HLA-DQA10102-DQB10602  751      DSTECSNLLLQYGSF  CSNLLLQYG  4        0.5639
112.0     3.00  0.38     Sequence         WB
 HLA-DQA10102-DQB10602  752      STECSNLLLQYGSFC  CSNLLLQYG  3        0.5500
130.2     3.50  0.40     Sequence         WB
 HLA-DQA10102-DQB10602  753      TECSNLLLQYGSFCT  CSNLLLQYG  2        0.5230
174.3     5.50  0.44     Sequence         WB
 HLA-DQA10102-DQB10602  754      ECSNLLLQYGSFCTQ  SNLLLQYGS  2        0.4759
290.1     9.50  0.39     Sequence         WB
 HLA-DQA10102-DQB10602  755      CSNLLLQYGSFCTQL  SNLLLQYGS  1        0.4048
626.4    21.00  0.35     Sequence
```

```
 HLA-DQA10102-DQB10602  756       SNLLLQYGSFCTQLN  QYGSFCTQL  5         0.3389
1278.2    36.00  0.32     Sequence
 HLA-DQA10102-DQB10602  757       NLLLQYGSFCTQLNR  QYGSFCTQL  4         0.3379
1291.2    36.00  0.38     Sequence
 HLA-DQA10102-DQB10602  758       LLLQYGSFCTQLNRA  SFCTQLNRA  6         0.4390
432.5    15.00  0.40    Sequence
 HLA-DQA10102-DQB10602  759       LLQYGSFCTQLNRAL  SFCTQLNRA  5         0.5321
157.9     4.50  0.60    Sequence         WB
 HLA-DQA10102-DQB10602  760       LQYGSFCTQLNRALT  SFCTQLNRA  4         0.5429
140.5     4.00  0.65    Sequence         WB
 HLA-DQA10102-DQB10602  761       QYGSFCTQLNRALTG  SFCTQLNRA  3         0.5561
121.9     3.50  0.57    Sequence         WB
 HLA-DQA10102-DQB10602  762       YGSFCTQLNRALTGI  SFCTQLNRA  2         0.5410
143.5     4.00  0.55    Sequence         WB
 HLA-DQA10102-DQB10602  763       GSFCTQLNRALTGIA  SFCTQLNRA  1         0.5053
211.1     6.50  0.51    Sequence         WB
 HLA-DQA10102-DQB10602  764       SFCTQLNRALTGIAV  TQLNRALTG  3         0.4904
248.0     8.00  0.23    Sequence         WB
 HLA-DQA10102-DQB10602  765       FCTQLNRALTGIAVE  NRALTGIAV  5         0.4812
273.9     9.00  0.39    Sequence         WB
 HLA-DQA10102-DQB10602  766       CTQLNRALTGIAVEQ  NRALTGIAV  4         0.5005
222.5     7.00  0.41    Sequence         WB
 HLA-DQA10102-DQB10602  767       TQLNRALTGIAVEQD  NRALTGIAV  3         0.5361
151.2     4.50  0.28    Sequence         WB
 HLA-DQA10102-DQB10602  768       QLNRALTGIAVEQDK  LTGIAVEQD  5         0.5755
98.8     2.50  0.47    Sequence         WB
 HLA-DQA10102-DQB10602  769       LNRALTGIAVEQDKN  LTGIAVEQD  4         0.5640
111.9     3.00  0.52    Sequence         WB
 HLA-DQA10102-DQB10602  770       NRALTGIAVEQDKNT  LTGIAVEQD  3         0.5303
161.2     5.00  0.61    Sequence         WB
 HLA-DQA10102-DQB10602  771       RALTGIAVEQDKNTQ  LTGIAVEQD  2         0.4750
293.0     9.50  0.73    Sequence         WB
 HLA-DQA10102-DQB10602  772       ALTGIAVEQDKNTQE  LTGIAVEQD  1         0.3774
842.5    26.00  0.68    Sequence
 HLA-DQA10102-DQB10602  773       LTGIAVEQDKNTQEV  LTGIAVEQD  0         0.2407
3696.1    70.00  0.56     Sequence
 HLA-DQA10102-DQB10602  774       TGIAVEQDKNTQEVF  EQDKNTQEV  5         0.1130
14725.4   100.00  0.22     Sequence
 HLA-DQA10102-DQB10602  775       GIAVEQDKNTQEVFA  DKNTQEVFA  6         0.1091
15364.7   100.00  0.32     Sequence
 HLA-DQA10102-DQB10602  776       IAVEQDKNTQEVFAQ  DKNTQEVFA  5         0.2162
4819.1    75.00  0.43     Sequence
 HLA-DQA10102-DQB10602  777       AVEQDKNTQEVFAQV  KNTQEVFAQ  5         0.3191
1583.6    42.00  0.33     Sequence
 HLA-DQA10102-DQB10602  778       VEQDKNTQEVFAQVK  KNTQEVFAQ  4         0.3524
1104.2    32.00  0.29     Sequence
 HLA-DQA10102-DQB10602  779       EQDKNTQEVFAQVKQ  TQEVFAQVK  5         0.3591
1027.0    31.00  0.31     Sequence
 HLA-DQA10102-DQB10602  780       QDKNTQEVFAQVKQI  TQEVFAQVK  4         0.3613
1002.5    30.00  0.33     Sequence
 HLA-DQA10102-DQB10602  781       DKNTQEVFAQVKQIY  TQEVFAQVK  3         0.3561
1060.5    31.00  0.34     Sequence
 HLA-DQA10102-DQB10602  782       KNTQEVFAQVKQIYK  EVFAQVKQI  4         0.3561
1061.4    31.00  0.26     Sequence
 HLA-DQA10102-DQB10602  783       NTQEVFAQVKQIYKT  EVFAQVKQI  3         0.3476
1162.7    34.00  0.28     Sequence
 HLA-DQA10102-DQB10602  784       TQEVFAQVKQIYKTP  EVFAQVKQI  2         0.3310
1391.3    38.00  0.25     Sequence
 HLA-DQA10102-DQB10602  785       QEVFAQVKQIYKTPP  AQVKQIYKT  4         0.3119
1711.7    44.00  0.34     Sequence
 HLA-DQA10102-DQB10602  786       EVFAQVKQIYKTPPI  AQVKQIYKT  3         0.2850
2289.5    55.00  0.41     Sequence
 HLA-DQA10102-DQB10602  787       VFAQVKQIYKTPPIK  AQVKQIYKT  2         0.2361
3888.4    70.00  0.46     Sequence
 HLA-DQA10102-DQB10602  788       FAQVKQIYKTPPIKD  AQVKQIYKT  1         0.1809
7061.3    85.00  0.41     Sequence
```

```
 HLA-DQA10102-DQB10602  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.1494
9934.3    90.00  0.42     Sequence
 HLA-DQA10102-DQB10602  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.1502
9846.0    90.00  0.49     Sequence
 HLA-DQA10102-DQB10602  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.1509
9771.7    90.00  0.45     Sequence
 HLA-DQA10102-DQB10602  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.1471
10182.3    90.00  0.38     Sequence
 HLA-DQA10102-DQB10602  793      QIYKTPPIKDFGGFN  TPPIKDFGG  4        0.1257
12833.4    95.00  0.33     Sequence
 HLA-DQA10102-DQB10602  794      IYKTPPIKDFGGFNF  TPPIKDFGG  3        0.1134
14657.0    100.00  0.42     Sequence
 HLA-DQA10102-DQB10602  795      YKTPPIKDFGGFNFS  TPPIKDFGG  2        0.1017
16629.3    100.00  0.35     Sequence
 HLA-DQA10102-DQB10602  796      KTPPIKDFGGFNFSQ  DFGGFNFSQ  6        0.1140
14566.0    100.00  0.29     Sequence
 HLA-DQA10102-DQB10602  797      TPPIKDFGGFNFSQI  DFGGFNFSQ  5        0.1434
10594.1    95.00  0.47     Sequence
 HLA-DQA10102-DQB10602  798      PPIKDFGGFNFSQIL  DFGGFNFSQ  4        0.1883
6521.0    85.00  0.37     Sequence
 HLA-DQA10102-DQB10602  799      PIKDFGGFNFSQILP  GGFNFSQIL  5        0.2102
5142.3    75.00  0.34     Sequence
 HLA-DQA10102-DQB10602  800      IKDFGGFNFSQILPD  FNFSQILPD  6        0.2908
2150.5    50.00  0.40     Sequence
 HLA-DQA10102-DQB10602  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.3607
1009.3    30.00  0.61     Sequence
 HLA-DQA10102-DQB10602  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.3763
852.3    27.00  0.66     Sequence
 HLA-DQA10102-DQB10602  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.3788
830.1    26.00  0.64     Sequence
 HLA-DQA10102-DQB10602  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.3458
1185.7    34.00  0.61     Sequence
 HLA-DQA10102-DQB10602  805      GFNFSQILPDPSKPS  FNFSQILPD  1        0.3047
1850.4    46.00  0.55     Sequence
 HLA-DQA10102-DQB10602  806      FNFSQILPDPSKPSK  FNFSQILPD  0        0.2381
3801.3    70.00  0.44     Sequence
 HLA-DQA10102-DQB10602  807      NFSQILPDPSKPSKR  SQILPDPSK  2        0.1282
12491.9    95.00  0.25     Sequence
 HLA-DQA10102-DQB10602  808      FSQILPDPSKPSKRS  ILPDPSKPS  3        0.0775
21615.1    100.00  0.29     Sequence
 HLA-DQA10102-DQB10602  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.0495
29271.3    100.00  0.36     Sequence
 HLA-DQA10102-DQB10602  810      QILPDPSKPSKRSFI  SKPSKRSFI  6        0.0609
25884.1    100.00  0.35     Sequence
 HLA-DQA10102-DQB10602  811      ILPDPSKPSKRSFIE  SKPSKRSFI  5        0.0751
22180.4    100.00  0.51     Sequence
 HLA-DQA10102-DQB10602  812      LPDPSKPSKRSFIED  SKPSKRSFI  4        0.0899
18902.3    100.00  0.46     Sequence
 HLA-DQA10102-DQB10602  813      PDPSKPSKRSFIEDL  SKRSFIEDL  6        0.1600
8849.2    90.00  0.52     Sequence
 HLA-DQA10102-DQB10602  814      DPSKPSKRSFIEDLL  SKRSFIEDL  5        0.2047
5458.8    80.00  0.70     Sequence
 HLA-DQA10102-DQB10602  815      PSKPSKRSFIEDLLF  SKRSFIEDL  4        0.2373
3836.9    70.00  0.67     Sequence
 HLA-DQA10102-DQB10602  816      SKPSKRSFIEDLLFN  SKRSFIEDL  3        0.2469
3456.1    65.00  0.64     Sequence
 HLA-DQA10102-DQB10602  817      KPSKRSFIEDLLFNK  SKRSFIEDL  2        0.2461
3489.5    65.00  0.56     Sequence
 HLA-DQA10102-DQB10602  818      PSKRSFIEDLLFNKV  SKRSFIEDL  1        0.2430
3608.6    65.00  0.38     Sequence
 HLA-DQA10102-DQB10602  819      SKRSFIEDLLFNKVT  IEDLLFNKV  5        0.2357
3902.7    70.00  0.29     Sequence
 HLA-DQA10102-DQB10602  820      KRSFIEDLLFNKVTL  IEDLLFNKV  4        0.2197
4639.8    75.00  0.38     Sequence
 HLA-DQA10102-DQB10602  821      RSFIEDLLFNKVTLA  LLFNKVTLA  6        0.2689
2725.8    60.00  0.29     Sequence
```

```
 HLA-DQA10102-DQB10602  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5         0.3440
1209.2    35.00  0.50     Sequence
 HLA-DQA10102-DQB10602  823      FIEDLLFNKVTLADA  LLFNKVTLA  4         0.4236
510.9    17.00  0.43     Sequence
 HLA-DQA10102-DQB10602  824      IEDLLFNKVTLADAG  FNKVTLADA  5         0.4826
270.0     9.00  0.42     Sequence         WB
 HLA-DQA10102-DQB10602  825      EDLLFNKVTLADAGF  FNKVTLADA  4         0.4968
231.5     7.50  0.46     Sequence         WB
 HLA-DQA10102-DQB10602  826      DLLFNKVTLADAGFI  FNKVTLADA  3         0.4889
252.1     8.00  0.45     Sequence         WB
 HLA-DQA10102-DQB10602  827      LLFNKVTLADAGFIK  FNKVTLADA  2         0.4574
354.7    12.00  0.48     Sequence
 HLA-DQA10102-DQB10602  828      LFNKVTLADAGFIKQ  FNKVTLADA  1         0.3803
816.7    26.00  0.45     Sequence
 HLA-DQA10102-DQB10602  829      FNKVTLADAGFIKQY  FNKVTLADA  0         0.3119
1711.9    44.00  0.30     Sequence
 HLA-DQA10102-DQB10602  830      NKVTLADAGFIKQYG  ADAGFIKQY  5         0.2766
2507.1    55.00  0.22     Sequence
 HLA-DQA10102-DQB10602  831      KVTLADAGFIKQYGD  DAGFIKQYG  5         0.3343
1342.6    37.00  0.33     Sequence
 HLA-DQA10102-DQB10602  832      VTLADAGFIKQYGDC  AGFIKQYGD  5         0.3520
1109.2    32.00  0.43     Sequence
 HLA-DQA10102-DQB10602  833      TLADAGFIKQYGDCL  AGFIKQYGD  4         0.3427
1225.8    35.00  0.46     Sequence
 HLA-DQA10102-DQB10602  834      LADAGFIKQYGDCLG  AGFIKQYGD  3         0.3302
1404.4    38.00  0.47     Sequence
 HLA-DQA10102-DQB10602  835      ADAGFIKQYGDCLGD  AGFIKQYGD  2         0.2960
2032.7    48.00  0.51     Sequence
 HLA-DQA10102-DQB10602  836      DAGFIKQYGDCLGDI  AGFIKQYGD  1         0.2702
2687.0    60.00  0.38     Sequence
 HLA-DQA10102-DQB10602  837      AGFIKQYGDCLGDIA  QYGDCLGDI  5         0.2435
3587.9    65.00  0.42     Sequence
 HLA-DQA10102-DQB10602  838      GFIKQYGDCLGDIAA  QYGDCLGDI  4         0.2327
4031.7    70.00  0.47     Sequence
 HLA-DQA10102-DQB10602  839      FIKQYGDCLGDIAAR  QYGDCLGDI  3         0.2435
3586.8    65.00  0.40     Sequence
 HLA-DQA10102-DQB10602  840      IKQYGDCLGDIAARD  QYGDCLGDI  2         0.2521
3270.0    65.00  0.28     Sequence
 HLA-DQA10102-DQB10602  841      KQYGDCLGDIAARDL  CLGDIAARD  5         0.2811
2387.5    55.00  0.25     Sequence
 HLA-DQA10102-DQB10602  842      QYGDCLGDIAARDLI  LGDIAARDL  5         0.2939
2080.5    49.00  0.40     Sequence
 HLA-DQA10102-DQB10602  843      YGDCLGDIAARDLIC  LGDIAARDL  4         0.3105
1736.6    44.00  0.37     Sequence
 HLA-DQA10102-DQB10602  844      GDCLGDIAARDLICA  LGDIAARDL  3         0.3366
1309.5    37.00  0.31     Sequence
 HLA-DQA10102-DQB10602  845      DCLGDIAARDLICAQ  IAARDLICA  5         0.4270
492.4    17.00  0.29     Sequence
 HLA-DQA10102-DQB10602  846      CLGDIAARDLICAQK  AARDLICAQ  5         0.4398
429.0    15.00  0.34     Sequence
 HLA-DQA10102-DQB10602  847      LGDIAARDLICAQKF  AARDLICAQ  4         0.4499
384.7    13.00  0.37     Sequence
 HLA-DQA10102-DQB10602  848      GDIAARDLICAQKFN  AARDLICAQ  3         0.4255
500.9    17.00  0.39     Sequence
 HLA-DQA10102-DQB10602  849      DIAARDLICAQKFNG  AARDLICAQ  2         0.4003
657.8    21.00  0.41     Sequence
 HLA-DQA10102-DQB10602  850      IAARDLICAQKFNGL  AARDLICAQ  1         0.3572
1048.0    31.00  0.38     Sequence
 HLA-DQA10102-DQB10602  851      AARDLICAQKFNGLT  RDLICAQKF  2         0.2833
2333.0    55.00  0.22     Sequence
 HLA-DQA10102-DQB10602  852      ARDLICAQKFNGLTV  LICAQKFNG  3         0.2361
3887.2    70.00  0.28     Sequence
 HLA-DQA10102-DQB10602  853      RDLICAQKFNGLTVL  LICAQKFNG  2         0.2271
4284.3    70.00  0.27     Sequence
 HLA-DQA10102-DQB10602  854      DLICAQKFNGLTVLP  QKFNGLTVL  5         0.2373
3838.2    70.00  0.19     Sequence
```

```
 HLA-DQA10102-DQB10602  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.3310
1391.8    38.00  0.57      Sequence
 HLA-DQA10102-DQB10602  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.4334
459.7    15.00  0.69     Sequence
 HLA-DQA10102-DQB10602  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.4383
436.0    15.00  0.69     Sequence
 HLA-DQA10102-DQB10602  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.4388
433.5    15.00  0.66     Sequence
 HLA-DQA10102-DQB10602  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.4300
476.8    16.00  0.63     Sequence
 HLA-DQA10102-DQB10602  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1        0.3793
825.8    26.00  0.47     Sequence
 HLA-DQA10102-DQB10602  861      FNGLTVLPPLLTDEM  NGLTVLPPL  1        0.3062
1821.3    45.00  0.23      Sequence
 HLA-DQA10102-DQB10602  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.2183
4713.4    75.00  0.35      Sequence
 HLA-DQA10102-DQB10602  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.1793
7186.6    85.00  0.34      Sequence
 HLA-DQA10102-DQB10602  864      LTVLPPLLTDEMIAQ  PLLTDEMIA  5        0.1949
6068.1    80.00  0.25      Sequence
 HLA-DQA10102-DQB10602  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.2432
3598.1    65.00  0.26      Sequence
 HLA-DQA10102-DQB10602  866      VLPPLLTDEMIAQYT  LTDEMIAQY  5        0.2874
2231.2    55.00  0.31      Sequence
 HLA-DQA10102-DQB10602  867      LPPLLTDEMIAQYTS  TDEMIAQYT  5        0.3571
1049.0    31.00  0.34      Sequence
 HLA-DQA10102-DQB10602  868      PPLLTDEMIAQYTSA  DEMIAQYTS  5        0.4250
503.3    17.00  0.47     Sequence
 HLA-DQA10102-DQB10602  869      PLLTDEMIAQYTSAL  DEMIAQYTS  4        0.4270
492.9    17.00  0.51     Sequence
 HLA-DQA10102-DQB10602  870      LLTDEMIAQYTSALL  DEMIAQYTS  3        0.4179
543.4    18.00  0.54     Sequence
 HLA-DQA10102-DQB10602  871      LTDEMIAQYTSALLA  DEMIAQYTS  2        0.4143
565.4    19.00  0.44     Sequence
 HLA-DQA10102-DQB10602  872      TDEMIAQYTSALLAG  AQYTSALLA  5        0.4437
411.0    14.00  0.44     Sequence
 HLA-DQA10102-DQB10602  873      DEMIAQYTSALLAGT  AQYTSALLA  4        0.5182
183.6     5.50  0.34     Sequence         WB
 HLA-DQA10102-DQB10602  874      EMIAQYTSALLAGTI  YTSALLAGT  5        0.5511
128.7     3.50  0.39     Sequence         WB
 HLA-DQA10102-DQB10602  875      MIAQYTSALLAGTIT  YTSALLAGT  4        0.5434
139.8     4.00  0.43     Sequence         WB
 HLA-DQA10102-DQB10602  876      IAQYTSALLAGTITS  YTSALLAGT  3        0.5258
169.1     5.00  0.49     Sequence         WB
 HLA-DQA10102-DQB10602  877      AQYTSALLAGTITSG  YTSALLAGT  2        0.4968
231.5     7.50  0.46     Sequence         WB
 HLA-DQA10102-DQB10602  878      QYTSALLAGTITSGW  YTSALLAGT  1        0.4733
298.4    10.00  0.35     Sequence
 HLA-DQA10102-DQB10602  879      YTSALLAGTITSGWT  LAGTITSGW  5        0.4462
400.1    14.00  0.35     Sequence
 HLA-DQA10102-DQB10602  880      TSALLAGTITSGWTF  LAGTITSGW  4        0.4410
423.6    14.00  0.41     Sequence
 HLA-DQA10102-DQB10602  881      SALLAGTITSGWTFG  LAGTITSGW  3        0.4034
635.7    21.00  0.47     Sequence
 HLA-DQA10102-DQB10602  882      ALLAGTITSGWTFGA  LAGTITSGW  2        0.3957
691.0    22.00  0.41     Sequence
 HLA-DQA10102-DQB10602  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.3915
723.6    23.00  0.37     Sequence
 HLA-DQA10102-DQB10602  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.3960
688.6    22.00  0.41     Sequence
 HLA-DQA10102-DQB10602  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.4069
612.0    20.00  0.36     Sequence
 HLA-DQA10102-DQB10602  886      GTITSGWTFGAGAAL  ITSGWTFGA  2        0.4149
561.6    19.00  0.31     Sequence
 HLA-DQA10102-DQB10602  887      TITSGWTFGAGAALQ  TFGAGAALQ  6        0.4521
375.5    13.00  0.28     Sequence
```

```
 HLA-DQA10102-DQB10602  888      ITSGWTFGAGAALQI  TFGAGAALQ  5        0.4991
225.8     7.00  0.49     Sequence         WB
 HLA-DQA10102-DQB10602  889      TSGWTFGAGAALQIP  TFGAGAALQ  4        0.5334
155.8     4.50  0.47     Sequence         WB
 HLA-DQA10102-DQB10602  890      SGWTFGAGAALQIPF  GAGAALQIP  5        0.5895
84.9     1.90  0.44     Sequence         SB
 HLA-DQA10102-DQB10602  891      GWTFGAGAALQIPFA  GAGAALQIP  4        0.6023
73.9     1.50  0.46     Sequence         SB
 HLA-DQA10102-DQB10602  892      WTFGAGAALQIPFAM  GAGAALQIP  3        0.6116
66.8     1.30  0.42     Sequence         SB
 HLA-DQA10102-DQB10602  893      TFGAGAALQIPFAMQ  GAGAALQIP  2        0.5880
86.3     1.90  0.34     Sequence         SB
 HLA-DQA10102-DQB10602  894      FGAGAALQIPFAMQM  GAALQIPFA  3        0.5391
146.5     4.50  0.34     Sequence         WB
 HLA-DQA10102-DQB10602  895      GAGAALQIPFAMQMA  GAALQIPFA  2        0.4875
256.0     8.50  0.35     Sequence         WB
 HLA-DQA10102-DQB10602  896      AGAALQIPFAMQMAY  GAALQIPFA  1        0.4808
275.2     9.00  0.31     Sequence         WB
 HLA-DQA10102-DQB10602  897      GAALQIPFAMQMAYR  QIPFAMQMA  4        0.4546
365.5    12.00  0.26     Sequence
 HLA-DQA10102-DQB10602  898      AALQIPFAMQMAYRF  QIPFAMQMA  3        0.4467
398.0    13.00  0.31     Sequence
 HLA-DQA10102-DQB10602  899      ALQIPFAMQMAYRFN  QIPFAMQMA  2        0.4405
425.6    14.00  0.31     Sequence
 HLA-DQA10102-DQB10602  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.4441
409.6    14.00  0.22     Sequence
 HLA-DQA10102-DQB10602  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.4039
632.5    21.00  0.28     Sequence
 HLA-DQA10102-DQB10602  902      IPFAMQMAYRFNGIG  MQMAYRFNG  4        0.3676
936.3    29.00  0.26     Sequence
 HLA-DQA10102-DQB10602  903      PFAMQMAYRFNGIGV  MQMAYRFNG  3        0.3380
1290.3    36.00  0.32     Sequence
 HLA-DQA10102-DQB10602  904      FAMQMAYRFNGIGVT  MQMAYRFNG  2        0.2962
2027.7    48.00  0.38     Sequence
 HLA-DQA10102-DQB10602  905      AMQMAYRFNGIGVTQ  MQMAYRFNG  1        0.2520
3271.2    65.00  0.29     Sequence
 HLA-DQA10102-DQB10602  906      MQMAYRFNGIGVTQN  FNGIGVTQN  6        0.2506
3321.2    65.00  0.28     Sequence
 HLA-DQA10102-DQB10602  907      QMAYRFNGIGVTQNV  FNGIGVTQN  5        0.3155
1646.1    43.00  0.49     Sequence
 HLA-DQA10102-DQB10602  908      MAYRFNGIGVTQNVL  FNGIGVTQN  4        0.3429
1223.9    35.00  0.43     Sequence
 HLA-DQA10102-DQB10602  909      AYRFNGIGVTQNVLY  FNGIGVTQN  3        0.3585
1034.0    31.00  0.38     Sequence
 HLA-DQA10102-DQB10602  910      YRFNGIGVTQNVLYE  FNGIGVTQN  2        0.3658
954.7    29.00  0.34     Sequence
 HLA-DQA10102-DQB10602  911      RFNGIGVTQNVLYEN  VTQNVLYEN  6        0.4394
430.6    15.00  0.42     Sequence
 HLA-DQA10102-DQB10602  912      FNGIGVTQNVLYENQ  VTQNVLYEN  5        0.4863
259.3     8.50  0.63     Sequence         WB
 HLA-DQA10102-DQB10602  913      NGIGVTQNVLYENQK  VTQNVLYEN  4        0.4720
302.8    10.00  0.70     Sequence
 HLA-DQA10102-DQB10602  914      GIGVTQNVLYENQKL  VTQNVLYEN  3        0.4532
371.2    13.00  0.77     Sequence
 HLA-DQA10102-DQB10602  915      IGVTQNVLYENQKLI  VTQNVLYEN  2        0.4323
465.3    16.00  0.78     Sequence
 HLA-DQA10102-DQB10602  916      GVTQNVLYENQKLIA  VTQNVLYEN  1        0.3770
846.2    26.00  0.65     Sequence
 HLA-DQA10102-DQB10602  917      VTQNVLYENQKLIAN  VTQNVLYEN  0        0.3293
1418.3    39.00  0.41     Sequence
 HLA-DQA10102-DQB10602  918      TQNVLYENQKLIANQ  YENQKLIAN  5        0.3128
1695.6    43.00  0.41     Sequence
 HLA-DQA10102-DQB10602  919      QNVLYENQKLIANQF  YENQKLIAN  4        0.3661
952.0    29.00  0.36     Sequence
 HLA-DQA10102-DQB10602  920      NVLYENQKLIANQFN  YENQKLIAN  3        0.3683
930.0    28.00  0.32     Sequence
```

```
 HLA-DQA10102-DQB10602  921      VLYENQKLIANQFNS  YENQKLIAN  2        0.3721
891.8    28.00  0.26     Sequence
 HLA-DQA10102-DQB10602  922      LYENQKLIANQFNSA  QKLIANQFN  4        0.3626
988.4    30.00  0.22     Sequence
 HLA-DQA10102-DQB10602  923      YENQKLIANQFNSAI  QKLIANQFN  3        0.3552
1070.8    32.00  0.25     Sequence
 HLA-DQA10102-DQB10602  924      ENQKLIANQFNSAIG  LIANQFNSA  4        0.3432
1219.8    35.00  0.21     Sequence
 HLA-DQA10102-DQB10602  925      NQKLIANQFNSAIGK  LIANQFNSA  3        0.3313
1387.7    38.00  0.19     Sequence
 HLA-DQA10102-DQB10602  926      QKLIANQFNSAIGKI  NQFNSAIGK  5        0.3524
1103.7    32.00  0.26     Sequence
 HLA-DQA10102-DQB10602  927      KLIANQFNSAIGKIQ  QFNSAIGKI  5        0.3784
833.8    26.00  0.34     Sequence
 HLA-DQA10102-DQB10602  928      LIANQFNSAIGKIQD  QFNSAIGKI  4        0.4039
632.8    21.00  0.36     Sequence
 HLA-DQA10102-DQB10602  929      IANQFNSAIGKIQDS  QFNSAIGKI  3        0.4300
477.0    16.00  0.31     Sequence
 HLA-DQA10102-DQB10602  930      ANQFNSAIGKIQDSL  SAIGKIQDS  5        0.4264
495.7    17.00  0.32     Sequence
 HLA-DQA10102-DQB10602  931      NQFNSAIGKIQDSLS  SAIGKIQDS  4        0.4254
501.2    17.00  0.37     Sequence
 HLA-DQA10102-DQB10602  932      QFNSAIGKIQDSLSS  SAIGKIQDS  3        0.4010
652.5    21.00  0.50     Sequence
 HLA-DQA10102-DQB10602  933      FNSAIGKIQDSLSST  SAIGKIQDS  2        0.3573
1046.9    31.00  0.56     Sequence
 HLA-DQA10102-DQB10602  934      NSAIGKIQDSLSSTA  SAIGKIQDS  1        0.2922
2118.9    50.00  0.43     Sequence
 HLA-DQA10102-DQB10602  935      SAIGKIQDSLSSTAS  IQDSLSSTA  5        0.2402
3717.4    70.00  0.25     Sequence
 HLA-DQA10102-DQB10602  936      AIGKIQDSLSSTASA  DSLSSTASA  6        0.2686
2734.2    60.00  0.25     Sequence
 HLA-DQA10102-DQB10602  937      IGKIQDSLSSTASAL  DSLSSTASA  5        0.3479
1159.1    34.00  0.46     Sequence
 HLA-DQA10102-DQB10602  938      GKIQDSLSSTASALG  DSLSSTASA  4        0.3873
756.6    24.00  0.40     Sequence
 HLA-DQA10102-DQB10602  939      KIQDSLSSTASALGK  DSLSSTASA  3        0.4353
450.5    15.00  0.28     Sequence
 HLA-DQA10102-DQB10602  940      IQDSLSSTASALGKL  SSTASALGK  5        0.4651
326.3    11.00  0.29     Sequence
 HLA-DQA10102-DQB10602  941      QDSLSSTASALGKLQ  SSTASALGK  4        0.4814
273.4     9.00  0.30     Sequence         WB
 HLA-DQA10102-DQB10602  942      DSLSSTASALGKLQD  STASALGKL  4        0.4784
282.4     9.50  0.32     Sequence         WB
 HLA-DQA10102-DQB10602  943      SLSSTASALGKLQDV  STASALGKL  3        0.4819
272.1     9.00  0.34     Sequence         WB
 HLA-DQA10102-DQB10602  944      LSSTASALGKLQDVV  STASALGKL  2        0.4461
400.8    14.00  0.35     Sequence
 HLA-DQA10102-DQB10602  945      SSTASALGKLQDVVN  SALGKLQDV  4        0.3934
708.5    23.00  0.34     Sequence
 HLA-DQA10102-DQB10602  946      STASALGKLQDVVNQ  SALGKLQDV  3        0.3539
1086.0    32.00  0.44     Sequence
 HLA-DQA10102-DQB10602  947      TASALGKLQDVVNQN  SALGKLQDV  2        0.3125
1701.2    44.00  0.54     Sequence
 HLA-DQA10102-DQB10602  948      ASALGKLQDVVNQNA  SALGKLQDV  1        0.3034
1876.9    46.00  0.32     Sequence
 HLA-DQA10102-DQB10602  949      SALGKLQDVVNQNAQ  LQDVVNQNA  5        0.3075
1794.6    45.00  0.43     Sequence
 HLA-DQA10102-DQB10602  950      ALGKLQDVVNQNAQA  LQDVVNQNA  4        0.3139
1675.3    43.00  0.56     Sequence
 HLA-DQA10102-DQB10602  951      LGKLQDVVNQNAQAL  LQDVVNQNA  3        0.3209
1552.1    41.00  0.52     Sequence
 HLA-DQA10102-DQB10602  952      GKLQDVVNQNAQALN  LQDVVNQNA  2        0.3244
1494.8    40.00  0.43     Sequence
 HLA-DQA10102-DQB10602  953      KLQDVVNQNAQALNT  NQNAQALNT  6        0.3671
941.8    29.00  0.31     Sequence
```

```
 HLA-DQA10102-DQB10602  954      LQDVVNQNAQALNTL  NQNAQALNT  5         0.3948
697.7    23.00  0.50     Sequence
 HLA-DQA10102-DQB10602  955      QDVVNQNAQALNTLV  NQNAQALNT  4         0.4198
532.7    18.00  0.51     Sequence
 HLA-DQA10102-DQB10602  956      DVVNQNAQALNTLVK  NQNAQALNT  3         0.4185
539.8    18.00  0.47     Sequence
 HLA-DQA10102-DQB10602  957      VVNQNAQALNTLVKQ  NQNAQALNT  2         0.4390
432.6    15.00  0.38     Sequence
 HLA-DQA10102-DQB10602  958      VNQNAQALNTLVKQL  QALNTLVKQ  5         0.4499
384.4    13.00  0.32     Sequence
 HLA-DQA10102-DQB10602  959      NQNAQALNTLVKQLS  QALNTLVKQ  4         0.4334
459.4    15.00  0.40     Sequence
 HLA-DQA10102-DQB10602  960      QNAQALNTLVKQLSS  QALNTLVKQ  3         0.4816
272.7     9.00  0.29     Sequence         WB
 HLA-DQA10102-DQB10602  961      NAQALNTLVKQLSSN  NTLVKQLSS  5         0.4861
259.9     8.50  0.44     Sequence         WB
 HLA-DQA10102-DQB10602  962      AQALNTLVKQLSSNF  NTLVKQLSS  4         0.4764
288.5     9.50  0.50     Sequence         WB
 HLA-DQA10102-DQB10602  963      QALNTLVKQLSSNFG  NTLVKQLSS  3         0.4515
378.1    13.00  0.56     Sequence
 HLA-DQA10102-DQB10602  964      ALNTLVKQLSSNFGA  NTLVKQLSS  2         0.4140
567.2    19.00  0.58     Sequence
 HLA-DQA10102-DQB10602  965      LNTLVKQLSSNFGAI  NTLVKQLSS  1         0.4007
655.1    21.00  0.43     Sequence
 HLA-DQA10102-DQB10602  966      NTLVKQLSSNFGAIS  KQLSSNFGA  4         0.3689
924.0    28.00  0.38     Sequence
 HLA-DQA10102-DQB10602  967      TLVKQLSSNFGAISS  KQLSSNFGA  3         0.4141
566.4    19.00  0.35     Sequence
 HLA-DQA10102-DQB10602  968      LVKQLSSNFGAISSV  SSNFGAISS  5         0.4593
347.3    12.00  0.34     Sequence
 HLA-DQA10102-DQB10602  969      VKQLSSNFGAISSVL  SSNFGAISS  4         0.4757
290.8     9.50  0.33     Sequence         WB
 HLA-DQA10102-DQB10602  970      KQLSSNFGAISSVLN  SSNFGAISS  3         0.4721
302.3    10.00  0.30     Sequence
 HLA-DQA10102-DQB10602  971      QLSSNFGAISSVLND  NFGAISSVL  4         0.4815
273.2     9.00  0.32     Sequence         WB
 HLA-DQA10102-DQB10602  972      LSSNFGAISSVLNDI  NFGAISSVL  3         0.4850
262.9     8.50  0.31     Sequence         WB
 HLA-DQA10102-DQB10602  973      SSNFGAISSVLNDIL  GAISSVLND  4         0.4581
352.0    12.00  0.28     Sequence
 HLA-DQA10102-DQB10602  974      SNFGAISSVLNDILS  GAISSVLND  3         0.4401
427.6    14.00  0.31     Sequence
 HLA-DQA10102-DQB10602  975      NFGAISSVLNDILSR  GAISSVLND  2         0.4041
631.3    21.00  0.31     Sequence
 HLA-DQA10102-DQB10602  976      FGAISSVLNDILSRL  AISSVLNDI  2         0.3641
972.8    29.00  0.31     Sequence
 HLA-DQA10102-DQB10602  977      GAISSVLNDILSRLD  AISSVLNDI  1         0.3221
1532.5    41.00  0.28     Sequence
 HLA-DQA10102-DQB10602  978      AISSVLNDILSRLDK  SSVLNDILS  2         0.3024
1896.0    47.00  0.26     Sequence
 HLA-DQA10102-DQB10602  979      ISSVLNDILSRLDKV  SVLNDILSR  2         0.2798
2423.0    55.00  0.22     Sequence
 HLA-DQA10102-DQB10602  980      SSVLNDILSRLDKVE  LNDILSRLD  3         0.2370
3850.7    70.00  0.26     Sequence
 HLA-DQA10102-DQB10602  981      SVLNDILSRLDKVEA  LNDILSRLD  2         0.2257
4350.7    70.00  0.25     Sequence
 HLA-DQA10102-DQB10602  982      VLNDILSRLDKVEAE  SRLDKVEAE  6         0.2443
3556.8    65.00  0.26     Sequence
 HLA-DQA10102-DQB10602  983      LNDILSRLDKVEAEV  SRLDKVEAE  5         0.2649
2846.3    60.00  0.42     Sequence
 HLA-DQA10102-DQB10602  984      NDILSRLDKVEAEVQ  SRLDKVEAE  4         0.2664
2800.9    60.00  0.47     Sequence
 HLA-DQA10102-DQB10602  985      DILSRLDKVEAEVQI  SRLDKVEAE  3         0.2627
2915.7    60.00  0.45     Sequence
 HLA-DQA10102-DQB10602  986      ILSRLDKVEAEVQID  SRLDKVEAE  2         0.2588
3038.7    60.00  0.43     Sequence
```

```
 HLA-DQA10102-DQB10602  987      LSRLDKVEAEVQIDR  KVEAEVQID  5        0.2963
2026.2    48.00  0.38     Sequence
 HLA-DQA10102-DQB10602  988      SRLDKVEAEVQIDRL  KVEAEVQID  4        0.2931
2098.0    49.00  0.47     Sequence
 HLA-DQA10102-DQB10602  989      RLDKVEAEVQIDRLI  KVEAEVQID  3        0.3087
1772.1    45.00  0.41     Sequence
 HLA-DQA10102-DQB10602  990      LDKVEAEVQIDRLIT  KVEAEVQID  2        0.3000
1946.0    47.00  0.43     Sequence
 HLA-DQA10102-DQB10602  991      DKVEAEVQIDRLITG  KVEAEVQID  1        0.2870
2241.8    55.00  0.34     Sequence
 HLA-DQA10102-DQB10602  992      KVEAEVQIDRLITGR  EAEVQIDRL  2        0.2605
2984.7    60.00  0.22     Sequence
 HLA-DQA10102-DQB10602  993      VEAEVQIDRLITGRL  VQIDRLITG  4        0.2341
3972.7    70.00  0.32     Sequence
 HLA-DQA10102-DQB10602  994      EAEVQIDRLITGRLQ  VQIDRLITG  3        0.2399
3728.3    70.00  0.28     Sequence
 HLA-DQA10102-DQB10602  995      AEVQIDRLITGRLQS  DRLITGRLQ  5        0.2768
2502.5    55.00  0.40     Sequence
 HLA-DQA10102-DQB10602  996      EVQIDRLITGRLQSL  DRLITGRLQ  4        0.2964
2024.4    48.00  0.40     Sequence
 HLA-DQA10102-DQB10602  997      VQIDRLITGRLQSLQ  DRLITGRLQ  3        0.3294
1416.7    39.00  0.34     Sequence
 HLA-DQA10102-DQB10602  998      QIDRLITGRLQSLQT  LITGRLQSL  4        0.3421
1234.1    35.00  0.28     Sequence
 HLA-DQA10102-DQB10602  999      IDRLITGRLQSLQTY  ITGRLQSLQ  4        0.3439
1210.0    35.00  0.28     Sequence
 HLA-DQA10102-DQB10602 1000      DRLITGRLQSLQTYV  ITGRLQSLQ  3        0.3315
1384.5    38.00  0.32     Sequence
 HLA-DQA10102-DQB10602 1001      RLITGRLQSLQTYVT  ITGRLQSLQ  2        0.3051
1842.3    46.00  0.26     Sequence
 HLA-DQA10102-DQB10602 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.3130
1691.6    43.00  0.36     Sequence
 HLA-DQA10102-DQB10602 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.3386
1282.0    36.00  0.35     Sequence
 HLA-DQA10102-DQB10602 1004      TGRLQSLQTYVTQQL  SLQTYVTQQ  5        0.3521
1107.5    32.00  0.41     Sequence
 HLA-DQA10102-DQB10602 1005      GRLQSLQTYVTQQLI  SLQTYVTQQ  4        0.3773
843.1    26.00  0.41     Sequence
 HLA-DQA10102-DQB10602 1006      RLQSLQTYVTQQLIR  SLQTYVTQQ  3        0.3794
824.5    26.00  0.39     Sequence
 HLA-DQA10102-DQB10602 1007      LQSLQTYVTQQLIRA  QTYVTQQLI  4        0.3796
822.6    26.00  0.38     Sequence
 HLA-DQA10102-DQB10602 1008      QSLQTYVTQQLIRAA  VTQQLIRAA  6        0.4339
457.3    15.00  0.38     Sequence
 HLA-DQA10102-DQB10602 1009      SLQTYVTQQLIRAAE  VTQQLIRAA  5        0.4866
258.5     8.50  0.58     Sequence         WB
 HLA-DQA10102-DQB10602 1010      LQTYVTQQLIRAAEI  VTQQLIRAA  4        0.5380
148.3     4.50  0.58     Sequence         WB
 HLA-DQA10102-DQB10602 1011      QTYVTQQLIRAAEIR  VTQQLIRAA  3        0.5279
165.3     5.00  0.56     Sequence         WB
 HLA-DQA10102-DQB10602 1012      TYVTQQLIRAAEIRA  VTQQLIRAA  2        0.5374
149.2     4.50  0.49     Sequence         WB
 HLA-DQA10102-DQB10602 1013      YVTQQLIRAAEIRAS  IRAAEIRAS  6        0.6608
39.2     0.50  0.57     Sequence         SB
 HLA-DQA10102-DQB10602 1014      VTQQLIRAAEIRASA  IRAAEIRAS  5        0.7664
12.5     0.03  0.81     Sequence         SB
 HLA-DQA10102-DQB10602 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.7799
10.8     0.01  0.81     Sequence         SB
 HLA-DQA10102-DQB10602 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.7742
11.5     0.02  0.79     Sequence         SB
 HLA-DQA10102-DQB10602 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.7515
14.7     0.04  0.77     Sequence         SB
 HLA-DQA10102-DQB10602 1018      LIRAAEIRASANLAA  IRAAEIRAS  1        0.7229
20.1     0.10  0.67     Sequence         SB
 HLA-DQA10102-DQB10602 1019      IRAAEIRASANLAAI  IRAAEIRAS  0        0.6488
44.7     0.70  0.48     Sequence         SB
```

```
 HLA-DQA10102-DQB10602 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.5884
85.9     1.90  0.49     Sequence         SB
 HLA-DQA10102-DQB10602 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.5711
103.6     2.50  0.46     Sequence         WB
 HLA-DQA10102-DQB10602 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.5755
98.8     2.50  0.35     Sequence         WB
 HLA-DQA10102-DQB10602 1023      EIRASANLAAIKMSE  ANLAAIKMS  5        0.5852
89.0     2.00  0.28     Sequence         WB
 HLA-DQA10102-DQB10602 1024      IRASANLAAIKMSEC  ANLAAIKMS  4        0.5839
90.3     2.50  0.28     Sequence         WB
 HLA-DQA10102-DQB10602 1025      RASANLAAIKMSECV  LAAIKMSEC  5        0.6118
66.7     1.30  0.43     Sequence         SB
 HLA-DQA10102-DQB10602 1026      ASANLAAIKMSECVL  LAAIKMSEC  4        0.6070
70.2     1.40  0.53     Sequence         SB
 HLA-DQA10102-DQB10602 1027      SANLAAIKMSECVLG  LAAIKMSEC  3        0.5978
77.6     1.60  0.55     Sequence         SB
 HLA-DQA10102-DQB10602 1028      ANLAAIKMSECVLGQ  LAAIKMSEC  2        0.5808
93.3     2.50  0.54     Sequence         WB
 HLA-DQA10102-DQB10602 1029      NLAAIKMSECVLGQS  LAAIKMSEC  1        0.5622
114.1     3.00  0.44     Sequence         WB
 HLA-DQA10102-DQB10602 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.5268
167.4     5.00  0.39     Sequence         WB
 HLA-DQA10102-DQB10602 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.4594
346.9    12.00  0.41     Sequence
 HLA-DQA10102-DQB10602 1032      AIKMSECVLGQSKRV  IKMSECVLG  1        0.3950
696.3    23.00  0.34     Sequence
 HLA-DQA10102-DQB10602 1033      IKMSECVLGQSKRVD  MSECVLGQS  2        0.3422
1232.6    35.00  0.35     Sequence
 HLA-DQA10102-DQB10602 1034      KMSECVLGQSKRVDF  MSECVLGQS  1        0.2659
2814.8    60.00  0.37     Sequence
 HLA-DQA10102-DQB10602 1035      MSECVLGQSKRVDFC  MSECVLGQS  0        0.2062
5369.2    80.00  0.26     Sequence
 HLA-DQA10102-DQB10602 1036      SECVLGQSKRVDFCG  GQSKRVDFC  5        0.1650
8390.0    90.00  0.25     Sequence
 HLA-DQA10102-DQB10602 1037      ECVLGQSKRVDFCGK  GQSKRVDFC  4        0.1628
8589.3    90.00  0.28     Sequence
 HLA-DQA10102-DQB10602 1038      CVLGQSKRVDFCGKG  GQSKRVDFC  3        0.1582
9025.4    90.00  0.26     Sequence
 HLA-DQA10102-DQB10602 1039      VLGQSKRVDFCGKGY  GQSKRVDFC  2        0.1484
10040.8    90.00  0.23     Sequence
 HLA-DQA10102-DQB10602 1040      LGQSKRVDFCGKGYH  SKRVDFCGK  3        0.1341
11721.5    95.00  0.22     Sequence
 HLA-DQA10102-DQB10602 1041      GQSKRVDFCGKGYHL  SKRVDFCGK  2        0.1229
13221.7    95.00  0.22     Sequence
 HLA-DQA10102-DQB10602 1042      QSKRVDFCGKGYHLM  DFCGKGYHL  5        0.1442
10506.6    95.00  0.22     Sequence
 HLA-DQA10102-DQB10602 1043      SKRVDFCGKGYHLMS  FCGKGYHLM  5        0.1747
7553.9    85.00  0.26     Sequence
 HLA-DQA10102-DQB10602 1044      KRVDFCGKGYHLMSF  GKGYHLMSF  6        0.2369
3854.0    70.00  0.48     Sequence
 HLA-DQA10102-DQB10602 1045      RVDFCGKGYHLMSFP  GKGYHLMSF  5        0.2767
2504.4    55.00  0.61     Sequence
 HLA-DQA10102-DQB10602 1046      VDFCGKGYHLMSFPQ  GKGYHLMSF  4        0.3163
1631.9    42.00  0.56     Sequence
 HLA-DQA10102-DQB10602 1047      DFCGKGYHLMSFPQS  GKGYHLMSF  3        0.3302
1404.6    38.00  0.47     Sequence
 HLA-DQA10102-DQB10602 1048      FCGKGYHLMSFPQSA  GKGYHLMSF  2        0.3917
721.8    23.00  0.26     Sequence
 HLA-DQA10102-DQB10602 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.4172
547.6    18.00  0.49     Sequence
 HLA-DQA10102-DQB10602 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.4118
580.5    19.00  0.51     Sequence
 HLA-DQA10102-DQB10602 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.4067
613.7    20.00  0.54     Sequence
 HLA-DQA10102-DQB10602 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.3812
808.9    25.00  0.57     Sequence
```

```
 HLA-DQA10102-DQB10602 1053      YHLMSFPQSAPHGVV  HLMSFPQSA  1         0.3511
1119.5    33.00  0.54     Sequence
 HLA-DQA10102-DQB10602 1054      HLMSFPQSAPHGVVF  HLMSFPQSA  0         0.2711
2660.8    60.00  0.38     Sequence
 HLA-DQA10102-DQB10602 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3         0.1861
6674.4    85.00  0.26     Sequence
 HLA-DQA10102-DQB10602 1056      MSFPQSAPHGVVFLH  SAPHGVVFL  5         0.1737
7637.8    85.00  0.25     Sequence
 HLA-DQA10102-DQB10602 1057      SFPQSAPHGVVFLHV  APHGVVFLH  5         0.2360
3890.8    70.00  0.19     Sequence
 HLA-DQA10102-DQB10602 1058      FPQSAPHGVVFLHVT  PHGVVFLHV  5         0.3297
1411.2    38.00  0.38     Sequence
 HLA-DQA10102-DQB10602 1059      PQSAPHGVVFLHVTY  HGVVFLHVT  5         0.3508
1124.0    33.00  0.36     Sequence
 HLA-DQA10102-DQB10602 1060      QSAPHGVVFLHVTYV  HGVVFLHVT  4         0.3546
1078.3    32.00  0.41     Sequence
 HLA-DQA10102-DQB10602 1061      SAPHGVVFLHVTYVP  HGVVFLHVT  3         0.3415
1242.8    35.00  0.44     Sequence
 HLA-DQA10102-DQB10602 1062      APHGVVFLHVTYVPA  HGVVFLHVT  2         0.3350
1332.7    37.00  0.41     Sequence
 HLA-DQA10102-DQB10602 1063      PHGVVFLHVTYVPAQ  HGVVFLHVT  1         0.3540
1084.8    32.00  0.27     Sequence
 HLA-DQA10102-DQB10602 1064      HGVVFLHVTYVPAQE  LHVTYVPAQ  5         0.3715
898.5    28.00  0.44     Sequence
 HLA-DQA10102-DQB10602 1065      GVVFLHVTYVPAQEK  LHVTYVPAQ  4         0.4162
553.8    18.00  0.38     Sequence
 HLA-DQA10102-DQB10602 1066      VVFLHVTYVPAQEKN  VTYVPAQEK  5         0.4286
483.9    16.00  0.41     Sequence
 HLA-DQA10102-DQB10602 1067      VFLHVTYVPAQEKNF  VTYVPAQEK  4         0.4272
491.6    17.00  0.48     Sequence
 HLA-DQA10102-DQB10602 1068      FLHVTYVPAQEKNFT  VTYVPAQEK  3         0.4020
645.7    21.00  0.50     Sequence
 HLA-DQA10102-DQB10602 1069      LHVTYVPAQEKNFTT  VTYVPAQEK  2         0.3302
1404.1    38.00  0.60     Sequence
 HLA-DQA10102-DQB10602 1070      HVTYVPAQEKNFTTA  VTYVPAQEK  1         0.2381
3803.9    70.00  0.60     Sequence
 HLA-DQA10102-DQB10602 1071      VTYVPAQEKNFTTAP  VTYVPAQEK  0         0.1383
11194.7    95.00  0.41     Sequence
 HLA-DQA10102-DQB10602 1072      TYVPAQEKNFTTAPA  EKNFTTAPA  6         0.1068
15746.7   100.00  0.25     Sequence
 HLA-DQA10102-DQB10602 1073      YVPAQEKNFTTAPAI  EKNFTTAPA  5         0.2299
4157.1    70.00  0.41     Sequence
 HLA-DQA10102-DQB10602 1074      VPAQEKNFTTAPAIC  KNFTTAPAI  5         0.3431
1220.4    35.00  0.28     Sequence
 HLA-DQA10102-DQB10602 1075      PAQEKNFTTAPAICH  FTTAPAICH  6         0.4146
563.4    19.00  0.32     Sequence
 HLA-DQA10102-DQB10602 1076      AQEKNFTTAPAICHD  FTTAPAICH  5         0.4773
286.0     9.50  0.35     Sequence        WB
 HLA-DQA10102-DQB10602 1077      QEKNFTTAPAICHDG  FTTAPAICH  4         0.5226
175.2     5.50  0.34     Sequence        WB
 HLA-DQA10102-DQB10602 1078      EKNFTTAPAICHDGK  FTTAPAICH  3         0.5139
192.5     6.00  0.34     Sequence        WB
 HLA-DQA10102-DQB10602 1079      KNFTTAPAICHDGKA  FTTAPAICH  2         0.4927
241.9     8.00  0.31     Sequence        WB
 HLA-DQA10102-DQB10602 1080      NFTTAPAICHDGKAH  TAPAICHDG  3         0.4231
514.1    17.00  0.31     Sequence
 HLA-DQA10102-DQB10602 1081      FTTAPAICHDGKAHF  TAPAICHDG  2         0.3128
1694.4    43.00  0.49     Sequence
 HLA-DQA10102-DQB10602 1082      TTAPAICHDGKAHFP  TAPAICHDG  1         0.2027
5577.6    80.00  0.50     Sequence
 HLA-DQA10102-DQB10602 1083      TAPAICHDGKAHFPR  TAPAICHDG  0         0.1413
10838.7    95.00  0.34     Sequence
 HLA-DQA10102-DQB10602 1084      APAICHDGKAHFPRE  CHDGKAHFP  4         0.1097
15264.4   100.00  0.35     Sequence
 HLA-DQA10102-DQB10602 1085      PAICHDGKAHFPREG  GKAHFPREG  6         0.1437
10556.2    95.00  0.34     Sequence
```

```
 HLA-DQA10102-DQB10602 1086      AICHDGKAHFPREGV  GKAHFPREG  5        0.1791
7197.4    85.00  0.51      Sequence
 HLA-DQA10102-DQB10602 1087      ICHDGKAHFPREGVF  GKAHFPREG  4        0.2058
5391.6    80.00  0.47      Sequence
 HLA-DQA10102-DQB10602 1088      CHDGKAHFPREGVFV  GKAHFPREG  3        0.1967
5952.0    80.00  0.50      Sequence
 HLA-DQA10102-DQB10602 1089      HDGKAHFPREGVFVS  GKAHFPREG  2        0.1903
6379.9    80.00  0.44      Sequence
 HLA-DQA10102-DQB10602 1090      DGKAHFPREGVFVSN  GKAHFPREG  1        0.1861
6674.9    85.00  0.34      Sequence
 HLA-DQA10102-DQB10602 1091      GKAHFPREGVFVSNG  REGVFVSNG  6        0.2100
5154.6    75.00  0.43      Sequence
 HLA-DQA10102-DQB10602 1092      KAHFPREGVFVSNGT  REGVFVSNG  5        0.2714
2652.5    60.00  0.69      Sequence
 HLA-DQA10102-DQB10602 1093      AHFPREGVFVSNGTH  REGVFVSNG  4        0.2813
2382.4    55.00  0.73      Sequence
 HLA-DQA10102-DQB10602 1094      HFPREGVFVSNGTHW  REGVFVSNG  3        0.2795
2430.2    55.00  0.69      Sequence
 HLA-DQA10102-DQB10602 1095      FPREGVFVSNGTHWF  REGVFVSNG  2        0.2643
2863.6    60.00  0.68      Sequence
 HLA-DQA10102-DQB10602 1096      PREGVFVSNGTHWFV  REGVFVSNG  1        0.2597
3010.1    60.00  0.42      Sequence
 HLA-DQA10102-DQB10602 1097      REGVFVSNGTHWFVT  SNGTHWFVT  6        0.3024
1897.4    47.00  0.35      Sequence
 HLA-DQA10102-DQB10602 1098      EGVFVSNGTHWFVTQ  SNGTHWFVT  5        0.3234
1511.3    40.00  0.51      Sequence
 HLA-DQA10102-DQB10602 1099      GVFVSNGTHWFVTQR  SNGTHWFVT  4        0.3219
1535.6    41.00  0.50      Sequence
 HLA-DQA10102-DQB10602 1100      VFVSNGTHWFVTQRN  SNGTHWFVT  3        0.3234
1511.3    40.00  0.41      Sequence
 HLA-DQA10102-DQB10602 1101      FVSNGTHWFVTQRNF  SNGTHWFVT  2        0.3493
1142.3    33.00  0.28      Sequence
 HLA-DQA10102-DQB10602 1102      VSNGTHWFVTQRNFY  THWFVTQRN  4        0.3356
1324.7    37.00  0.32      Sequence
 HLA-DQA10102-DQB10602 1103      SNGTHWFVTQRNFYE  THWFVTQRN  3        0.3178
1606.1    42.00  0.38      Sequence
 HLA-DQA10102-DQB10602 1104      NGTHWFVTQRNFYEP  THWFVTQRN  2        0.2877
2223.3    55.00  0.39      Sequence
 HLA-DQA10102-DQB10602 1105      GTHWFVTQRNFYEPQ  HWFVTQRNF  2        0.2445
3547.5    65.00  0.39      Sequence
 HLA-DQA10102-DQB10602 1106      THWFVTQRNFYEPQI  HWFVTQRNF  1        0.1960
5999.8    80.00  0.37      Sequence
 HLA-DQA10102-DQB10602 1107      HWFVTQRNFYEPQII  HWFVTQRNF  0        0.1437
10561.8    95.00  0.25      Sequence
 HLA-DQA10102-DQB10602 1108      WFVTQRNFYEPQIIT  RNFYEPQII  5        0.1309
12134.5    95.00  0.25      Sequence
 HLA-DQA10102-DQB10602 1109      FVTQRNFYEPQIITT  RNFYEPQII  4        0.1349
11613.1    95.00  0.25      Sequence
 HLA-DQA10102-DQB10602 1110      VTQRNFYEPQIITTD  NFYEPQIIT  4        0.1515
9710.6    90.00  0.24      Sequence
 HLA-DQA10102-DQB10602 1111      TQRNFYEPQIITTDN  YEPQIITTD  5        0.1538
9467.6    90.00  0.22      Sequence
 HLA-DQA10102-DQB10602 1112      QRNFYEPQIITTDNT  YEPQIITTD  4        0.1516
9699.4    90.00  0.26      Sequence
 HLA-DQA10102-DQB10602 1113      RNFYEPQIITTDNTF  YEPQIITTD  3        0.1426
10691.0    95.00  0.28      Sequence
 HLA-DQA10102-DQB10602 1114      NFYEPQIITTDNTFV  YEPQIITTD  2        0.1197
13696.7    95.00  0.31      Sequence
 HLA-DQA10102-DQB10602 1115      FYEPQIITTDNTFVS  ITTDNTFVS  6        0.1292
12358.4    95.00  0.29      Sequence
 HLA-DQA10102-DQB10602 1116      YEPQIITTDNTFVSG  ITTDNTFVS  5        0.1862
6669.0    85.00  0.44      Sequence
 HLA-DQA10102-DQB10602 1117      EPQIITTDNTFVSGN  ITTDNTFVS  4        0.2338
3983.0    70.00  0.35      Sequence
 HLA-DQA10102-DQB10602 1118      PQIITTDNTFVSGNC  TDNTFVSGN  5        0.2757
2533.3    55.00  0.49      Sequence
```

```
 HLA-DQA10102-DQB10602 1119      QIITTDNTFVSGNCD  TDNTFVSGN  4        0.2944
2067.4    49.00  0.46     Sequence
 HLA-DQA10102-DQB10602 1120      IITTDNTFVSGNCDV  TDNTFVSGN  3        0.3397
1267.5    36.00  0.38     Sequence
 HLA-DQA10102-DQB10602 1121      ITTDNTFVSGNCDVV  TDNTFVSGN  2        0.3302
1404.6    38.00  0.32     Sequence
 HLA-DQA10102-DQB10602 1122      TTDNTFVSGNCDVVI  NTFVSGNCD  3        0.3281
1436.7    39.00  0.30     Sequence
 HLA-DQA10102-DQB10602 1123      TDNTFVSGNCDVVIG  VSGNCDVVI  5        0.3420
1236.0    35.00  0.29     Sequence
 HLA-DQA10102-DQB10602 1124      DNTFVSGNCDVVIGI  VSGNCDVVI  4        0.3650
963.2    29.00  0.26     Sequence
 HLA-DQA10102-DQB10602 1125      NTFVSGNCDVVIGIV  VSGNCDVVI  3        0.4040
631.9    21.00  0.22     Sequence
 HLA-DQA10102-DQB10602 1126      TFVSGNCDVVIGIVN  NCDVVIGIV  5        0.4073
609.9    20.00  0.29     Sequence
 HLA-DQA10102-DQB10602 1127      FVSGNCDVVIGIVNN  NCDVVIGIV  4        0.3914
723.9    23.00  0.31     Sequence
 HLA-DQA10102-DQB10602 1128      VSGNCDVVIGIVNNT  NCDVVIGIV  3        0.3676
936.7    29.00  0.32     Sequence
 HLA-DQA10102-DQB10602 1129      SGNCDVVIGIVNNTV  NCDVVIGIV  2        0.3610
1006.5    30.00  0.31     Sequence
 HLA-DQA10102-DQB10602 1130      GNCDVVIGIVNNTVY  VIGIVNNTV  5        0.3610
1006.5    30.00  0.25     Sequence
 HLA-DQA10102-DQB10602 1131      NCDVVIGIVNNTVYD  VIGIVNNTV  4        0.3405
1255.8    36.00  0.31     Sequence
 HLA-DQA10102-DQB10602 1132      CDVVIGIVNNTVYDP  VIGIVNNTV  3        0.3345
1339.6    37.00  0.31     Sequence
 HLA-DQA10102-DQB10602 1133      DVVIGIVNNTVYDPL  IVNNTVYDP  5        0.3608
1008.2    30.00  0.46     Sequence
 HLA-DQA10102-DQB10602 1134      VVIGIVNNTVYDPLQ  IVNNTVYDP  4        0.3628
986.4    30.00  0.52     Sequence
 HLA-DQA10102-DQB10602 1135      VIGIVNNTVYDPLQP  IVNNTVYDP  3        0.3427
1226.8    35.00  0.56     Sequence
 HLA-DQA10102-DQB10602 1136      IGIVNNTVYDPLQPE  IVNNTVYDP  2        0.3173
1615.0    42.00  0.63     Sequence
 HLA-DQA10102-DQB10602 1137      GIVNNTVYDPLQPEL  IVNNTVYDP  1        0.2867
2247.1    55.00  0.47     Sequence
 HLA-DQA10102-DQB10602 1138      IVNNTVYDPLQPELD  TVYDPLQPE  4        0.2434
3591.6    65.00  0.26     Sequence
 HLA-DQA10102-DQB10602 1139      VNNTVYDPLQPELDS  TVYDPLQPE  3        0.1952
6052.9    80.00  0.35     Sequence
 HLA-DQA10102-DQB10602 1140      NNTVYDPLQPELDSF  TVYDPLQPE  2        0.1608
8773.0    90.00  0.46     Sequence
 HLA-DQA10102-DQB10602 1141      NTVYDPLQPELDSFK  TVYDPLQPE  1        0.1248
12958.0    95.00  0.38     Sequence
 HLA-DQA10102-DQB10602 1142      TVYDPLQPELDSFKE  YDPLQPELD  2        0.1023
16524.4   100.00  0.28     Sequence
 HLA-DQA10102-DQB10602 1143      VYDPLQPELDSFKEE  YDPLQPELD  1        0.0840
20158.5   100.00  0.25     Sequence
 HLA-DQA10102-DQB10602 1144      YDPLQPELDSFKEEL  QPELDSFKE  4        0.0685
23840.5   100.00  0.17     Sequence
 HLA-DQA10102-DQB10602 1145      DPLQPELDSFKEELD  ELDSFKEEL  5        0.0753
22132.5   100.00  0.32     Sequence
 HLA-DQA10102-DQB10602 1146      PLQPELDSFKEELDK  LDSFKEELD  5        0.1023
16521.3   100.00  0.34     Sequence
 HLA-DQA10102-DQB10602 1147      LQPELDSFKEELDKY  LDSFKEELD  4        0.1082
15509.3   100.00  0.37     Sequence
 HLA-DQA10102-DQB10602 1148      QPELDSFKEELDKYF  LDSFKEELD  3        0.1115
14960.3   100.00  0.37     Sequence
 HLA-DQA10102-DQB10602 1149      PELDSFKEELDKYFK  LDSFKEELD  2        0.1069
15726.3   100.00  0.32     Sequence
 HLA-DQA10102-DQB10602 1150      ELDSFKEELDKYFKN  LDSFKEELD  1        0.1037
16279.6   100.00  0.27     Sequence
 HLA-DQA10102-DQB10602 1151      LDSFKEELDKYFKNH  SFKEELDKY  2        0.0860
19725.7   100.00  0.23     Sequence
```

```
 HLA-DQA10102-DQB10602 1152      DSFKEELDKYFKNHT  KEELDKYFK  3         0.0673
24143.2   100.00  0.22     Sequence
 HLA-DQA10102-DQB10602 1153      SFKEELDKYFKNHTS  DKYFKNHTS  6         0.0645
24887.2   100.00  0.34     Sequence
 HLA-DQA10102-DQB10602 1154      FKEELDKYFKNHTSP  DKYFKNHTS  5         0.0932
18236.7   100.00  0.62     Sequence
 HLA-DQA10102-DQB10602 1155      KEELDKYFKNHTSPD  DKYFKNHTS  4         0.1085
15465.4   100.00  0.67     Sequence
 HLA-DQA10102-DQB10602 1156      EELDKYFKNHTSPDV  DKYFKNHTS  3         0.1265
12726.4    95.00  0.56     Sequence
 HLA-DQA10102-DQB10602 1157      ELDKYFKNHTSPDVD  DKYFKNHTS  2         0.1392
11084.3    95.00  0.44     Sequence
 HLA-DQA10102-DQB10602 1158      LDKYFKNHTSPDVDL  NHTSPDVDL  6         0.1915
6295.5    80.00  0.40     Sequence
 HLA-DQA10102-DQB10602 1159      DKYFKNHTSPDVDLG  NHTSPDVDL  5         0.2072
5314.0    80.00  0.50     Sequence
 HLA-DQA10102-DQB10602 1160      KYFKNHTSPDVDLGD  NHTSPDVDL  4         0.2211
4569.1    75.00  0.46     Sequence
 HLA-DQA10102-DQB10602 1161      YFKNHTSPDVDLGDI  NHTSPDVDL  3         0.2272
4279.9    70.00  0.41     Sequence
 HLA-DQA10102-DQB10602 1162      FKNHTSPDVDLGDIS  NHTSPDVDL  2         0.2110
5100.0    75.00  0.39     Sequence
 HLA-DQA10102-DQB10602 1163      KNHTSPDVDLGDISG  NHTSPDVDL  1         0.1700
7945.2    85.00  0.31     Sequence
 HLA-DQA10102-DQB10602 1164      NHTSPDVDLGDISGI  SPDVDLGDI  3         0.1413
10840.2    95.00  0.20     Sequence
 HLA-DQA10102-DQB10602 1165      HTSPDVDLGDISGIN  VDLGDISGI  5         0.1258
12820.0    95.00  0.32     Sequence
 HLA-DQA10102-DQB10602 1166      TSPDVDLGDISGINA  VDLGDISGI  4         0.1418
10779.3    95.00  0.28     Sequence
 HLA-DQA10102-DQB10602 1167      SPDVDLGDISGINAS  GDISGINAS  6         0.2068
5337.8    80.00  0.37     Sequence
 HLA-DQA10102-DQB10602 1168      PDVDLGDISGINASF  GDISGINAS  5         0.2590
3032.0    60.00  0.55     Sequence
 HLA-DQA10102-DQB10602 1169      DVDLGDISGINASFV  ISGINASFV  6         0.3468
1172.9    34.00  0.40     Sequence
 HLA-DQA10102-DQB10602 1170      VDLGDISGINASFVN  ISGINASFV  5         0.3910
727.1    23.00  0.51     Sequence
 HLA-DQA10102-DQB10602 1171      DLGDISGINASFVNI  ISGINASFV  4         0.4017
647.5    21.00  0.54     Sequence
 HLA-DQA10102-DQB10602 1172      LGDISGINASFVNIQ  ISGINASFV  3         0.4351
451.2    15.00  0.41     Sequence
 HLA-DQA10102-DQB10602 1173      GDISGINASFVNIQK  INASFVNIQ  5         0.4977
229.3     7.50  0.50     Sequence         WB
 HLA-DQA10102-DQB10602 1174      DISGINASFVNIQKE  INASFVNIQ  4         0.5613
115.2     3.00  0.49     Sequence         WB
 HLA-DQA10102-DQB10602 1175      ISGINASFVNIQKEI  ASFVNIQKE  5         0.5729
101.6     2.50  0.40     Sequence         WB
 HLA-DQA10102-DQB10602 1176      SGINASFVNIQKEID  ASFVNIQKE  4         0.5681
107.1     3.00  0.50     Sequence         WB
 HLA-DQA10102-DQB10602 1177      GINASFVNIQKEIDR  ASFVNIQKE  3         0.5437
139.4     4.00  0.53     Sequence         WB
 HLA-DQA10102-DQB10602 1178      INASFVNIQKEIDRL  ASFVNIQKE  2         0.5071
207.1     6.50  0.63     Sequence         WB
 HLA-DQA10102-DQB10602 1179      NASFVNIQKEIDRLN  ASFVNIQKE  1         0.4157
556.8    19.00  0.62     Sequence
 HLA-DQA10102-DQB10602 1180      ASFVNIQKEIDRLNE  ASFVNIQKE  0         0.2901
2165.7    50.00  0.50     Sequence
 HLA-DQA10102-DQB10602 1181      SFVNIQKEIDRLNEV  KEIDRLNEV  6         0.2120
5042.7    75.00  0.21     Sequence
 HLA-DQA10102-DQB10602 1182      FVNIQKEIDRLNEVA  KEIDRLNEV  5         0.2000
5745.7    80.00  0.38     Sequence
 HLA-DQA10102-DQB10602 1183      VNIQKEIDRLNEVAK  KEIDRLNEV  4         0.2012
5667.1    80.00  0.40     Sequence
 HLA-DQA10102-DQB10602 1184      NIQKEIDRLNEVAKN  KEIDRLNEV  3         0.2128
5002.1    75.00  0.34     Sequence
```

```
 HLA-DQA10102-DQB10602 1185      IQKEIDRLNEVAKNL  DRLNEVAKN  5        0.2332
4009.5    70.00  0.37     Sequence
 HLA-DQA10102-DQB10602 1186      QKEIDRLNEVAKNLN  DRLNEVAKN  4        0.2455
3510.9    65.00  0.40     Sequence
 HLA-DQA10102-DQB10602 1187      KEIDRLNEVAKNLNE  DRLNEVAKN  3        0.2637
2882.4    60.00  0.38     Sequence
 HLA-DQA10102-DQB10602 1188      EIDRLNEVAKNLNES  DRLNEVAKN  2        0.2576
3079.7    65.00  0.31     Sequence
 HLA-DQA10102-DQB10602 1189      IDRLNEVAKNLNESL  NEVAKNLNE  4        0.2519
3275.7    65.00  0.32     Sequence
 HLA-DQA10102-DQB10602 1190      DRLNEVAKNLNESLI  NEVAKNLNE  3        0.2471
3450.2    65.00  0.31     Sequence
 HLA-DQA10102-DQB10602 1191      RLNEVAKNLNESLID  NEVAKNLNE  2        0.2360
3890.4    70.00  0.28     Sequence
 HLA-DQA10102-DQB10602 1192      LNEVAKNLNESLIDL  EVAKNLNES  2        0.2174
4758.6    75.00  0.22     Sequence
 HLA-DQA10102-DQB10602 1193      NEVAKNLNESLIDLQ  LNESLIDLQ  6        0.2327
4032.4    70.00  0.30     Sequence
 HLA-DQA10102-DQB10602 1194      EVAKNLNESLIDLQE  LNESLIDLQ  5        0.3054
1836.5    46.00  0.46     Sequence
 HLA-DQA10102-DQB10602 1195      VAKNLNESLIDLQEL  ESLIDLQEL  6        0.4042
630.1    21.00  0.34     Sequence
 HLA-DQA10102-DQB10602 1196      AKNLNESLIDLQELG  ESLIDLQEL  5        0.4260
498.1    17.00  0.46     Sequence
 HLA-DQA10102-DQB10602 1197      KNLNESLIDLQELGK  ESLIDLQEL  4        0.4230
514.6    17.00  0.49     Sequence
 HLA-DQA10102-DQB10602 1198      NLNESLIDLQELGKY  ESLIDLQEL  3        0.4115
582.5    19.00  0.56     Sequence
 HLA-DQA10102-DQB10602 1199      LNESLIDLQELGKYE  ESLIDLQEL  2        0.3710
902.6    28.00  0.58     Sequence
 HLA-DQA10102-DQB10602 1200      NESLIDLQELGKYEQ  ESLIDLQEL  1        0.2800
2416.4    55.00  0.61     Sequence
 HLA-DQA10102-DQB10602 1201      ESLIDLQELGKYEQY  ESLIDLQEL  0        0.1993
5785.3    80.00  0.40     Sequence
 HLA-DQA10102-DQB10602 1202      SLIDLQELGKYEQYI  LQELGKYEQ  4        0.1423
10724.4    95.00  0.31     Sequence
 HLA-DQA10102-DQB10602 1203      LIDLQELGKYEQYIK  ELGKYEQYI  5        0.1475
10134.0    90.00  0.36     Sequence
 HLA-DQA10102-DQB10602 1204      IDLQELGKYEQYIKW  ELGKYEQYI  4        0.1385
11174.5    95.00  0.41     Sequence
 HLA-DQA10102-DQB10602 1205      DLQELGKYEQYIKWP  ELGKYEQYI  3        0.1272
12623.3    95.00  0.43     Sequence
 HLA-DQA10102-DQB10602 1206      LQELGKYEQYIKWPW  ELGKYEQYI  2        0.1176
14003.7    95.00  0.43     Sequence
 HLA-DQA10102-DQB10602 1207      QELGKYEQYIKWPWY  ELGKYEQYI  1        0.1093
15321.4    100.00  0.31     Sequence
 HLA-DQA10102-DQB10602 1208      ELGKYEQYIKWPWYI  QYIKWPWYI  6        0.1227
13253.1    95.00  0.25     Sequence
 HLA-DQA10102-DQB10602 1209      LGKYEQYIKWPWYIW  QYIKWPWYI  5        0.1276
12573.2    95.00  0.37     Sequence
 HLA-DQA10102-DQB10602 1210      GKYEQYIKWPWYIWL  QYIKWPWYI  4        0.1413
10836.8    95.00  0.36     Sequence
 HLA-DQA10102-DQB10602 1211      KYEQYIKWPWYIWLG  KWPWYIWLG  6        0.1757
7470.9    85.00  0.35     Sequence
 HLA-DQA10102-DQB10602 1212      YEQYIKWPWYIWLGF  KWPWYIWLG  5        0.2091
5206.4    75.00  0.50     Sequence
 HLA-DQA10102-DQB10602 1213      EQYIKWPWYIWLGFI  KWPWYIWLG  4        0.2284
4223.5    70.00  0.51     Sequence
 HLA-DQA10102-DQB10602 1214      QYIKWPWYIWLGFIA  KWPWYIWLG  3        0.2601
2998.6    60.00  0.39     Sequence
 HLA-DQA10102-DQB10602 1215      YIKWPWYIWLGFIAG  KWPWYIWLG  2        0.2858
2269.0    55.00  0.31     Sequence
 HLA-DQA10102-DQB10602 1216      IKWPWYIWLGFIAGL  IWLGFIAGL  6        0.3079
1787.0    45.00  0.30     Sequence
 HLA-DQA10102-DQB10602 1217      KWPWYIWLGFIAGLI  IWLGFIAGL  5        0.3218
1537.8    41.00  0.46     Sequence
```

```
 HLA-DQA10102-DQB10602 1218      WPWYIWLGFIAGLIA  IWLGFIAGL  4         0.3450
1196.5    34.00  0.45      Sequence
 HLA-DQA10102-DQB10602 1219      PWYIWLGFIAGLIAI  IWLGFIAGL  3         0.3446
1201.6    34.00  0.44      Sequence
 HLA-DQA10102-DQB10602 1220      WYIWLGFIAGLIAIV  IWLGFIAGL  2         0.3340
1347.8    37.00  0.44      Sequence
 HLA-DQA10102-DQB10602 1221      YIWLGFIAGLIAIVM  IWLGFIAGL  1         0.3305
1399.9    38.00  0.29      Sequence
 HLA-DQA10102-DQB10602 1222      IWLGFIAGLIAIVMV  IAGLIAIVM  5         0.3468
1173.2    34.00  0.41      Sequence
 HLA-DQA10102-DQB10602 1223      WLGFIAGLIAIVMVT  IAGLIAIVM  4         0.3342
1344.0    37.00  0.45      Sequence
 HLA-DQA10102-DQB10602 1224      LGFIAGLIAIVMVTI  IAGLIAIVM  3         0.3166
1626.2    42.00  0.49      Sequence
 HLA-DQA10102-DQB10602 1225      GFIAGLIAIVMVTIM  IAGLIAIVM  2         0.3034
1875.4    46.00  0.49      Sequence
 HLA-DQA10102-DQB10602 1226      FIAGLIAIVMVTIML  IAGLIAIVM  1         0.2798
2423.1    55.00  0.43      Sequence
 HLA-DQA10102-DQB10602 1227      IAGLIAIVMVTIMLC  AGLIAIVMV  1         0.2239
4434.4    75.00  0.22      Sequence
 HLA-DQA10102-DQB10602 1228      AGLIAIVMVTIMLCC  IVMVTIMLC  5         0.2424
3631.8    65.00  0.43      Sequence
 HLA-DQA10102-DQB10602 1229      GLIAIVMVTIMLCCM  IVMVTIMLC  4         0.2578
3073.1    65.00  0.47      Sequence
 HLA-DQA10102-DQB10602 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3         0.2951
2053.3    49.00  0.37      Sequence
 HLA-DQA10102-DQB10602 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2         0.3385
1283.4    36.00  0.26      Sequence
 HLA-DQA10102-DQB10602 1232      AIVMVTIMLCCMTSC  TIMLCCMTS  5         0.3580
1039.0    31.00  0.34      Sequence
 HLA-DQA10102-DQB10602 1233      IVMVTIMLCCMTSCC  TIMLCCMTS  4         0.3583
1035.7    31.00  0.34      Sequence
 HLA-DQA10102-DQB10602 1234      VMVTIMLCCMTSCCS  TIMLCCMTS  3         0.3561
1061.3    31.00  0.38      Sequence
 HLA-DQA10102-DQB10602 1235      MVTIMLCCMTSCCSC  TIMLCCMTS  2         0.3606
1010.2    30.00  0.34      Sequence
 HLA-DQA10102-DQB10602 1236      VTIMLCCMTSCCSCL  TIMLCCMTS  1         0.3504
1127.9    33.00  0.25      Sequence
 HLA-DQA10102-DQB10602 1237      TIMLCCMTSCCSCLK  CCMTSCCSC  4         0.3275
1445.9    39.00  0.23      Sequence
 HLA-DQA10102-DQB10602 1238      IMLCCMTSCCSCLKG  CCMTSCCSC  3         0.3273
1448.0    39.00  0.26      Sequence
 HLA-DQA10102-DQB10602 1239      MLCCMTSCCSCLKGC  TSCCSCLKG  5         0.3509
1121.7    33.00  0.26      Sequence
 HLA-DQA10102-DQB10602 1240      LCCMTSCCSCLKGCC  SCCSCLKGC  5         0.3663
950.3    29.00  0.38      Sequence
 HLA-DQA10102-DQB10602 1241      CCMTSCCSCLKGCCS  SCCSCLKGC  4         0.3726
887.6    27.00  0.41      Sequence
 HLA-DQA10102-DQB10602 1242      CMTSCCSCLKGCCSC  SCCSCLKGC  3         0.3777
839.5    26.00  0.40      Sequence
 HLA-DQA10102-DQB10602 1243      MTSCCSCLKGCCSCG  SCCSCLKGC  2         0.3665
947.5    29.00  0.41      Sequence
 HLA-DQA10102-DQB10602 1244      TSCCSCLKGCCSCGS  SCCSCLKGC  1         0.3479
1159.0    34.00  0.31      Sequence
 HLA-DQA10102-DQB10602 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5         0.3236
1507.3    40.00  0.31      Sequence
 HLA-DQA10102-DQB10602 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4         0.2999
1948.4    47.00  0.38      Sequence
 HLA-DQA10102-DQB10602 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3         0.2691
2719.3    60.00  0.45      Sequence
 HLA-DQA10102-DQB10602 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2         0.2467
3463.8    65.00  0.46      Sequence
 HLA-DQA10102-DQB10602 1249      CLKGCCSCGSCCKFD  SCGSCCKFD  6         0.2575
3083.6    65.00  0.36      Sequence
 HLA-DQA10102-DQB10602 1250      LKGCCSCGSCCKFDE  SCGSCCKFD  5         0.2660
2811.9    60.00  0.52      Sequence
```

```
 HLA-DQA10102-DQB10602 1251      KGCCSCGSCCKFDED  SCGSCCKFD  4        0.2656
2824.7    60.00  0.61     Sequence
 HLA-DQA10102-DQB10602 1252      GCCSCGSCCKFDEDD  SCGSCCKFD  3        0.2553
3157.8    65.00  0.61     Sequence
 HLA-DQA10102-DQB10602 1253      CCSCGSCCKFDEDDS  SCGSCCKFD  2        0.2364
3873.8    70.00  0.63     Sequence
 HLA-DQA10102-DQB10602 1254      CSCGSCCKFDEDDSE  SCGSCCKFD  1        0.1955
6028.0    80.00  0.58     Sequence
 HLA-DQA10102-DQB10602 1255      SCGSCCKFDEDDSEP  SCGSCCKFD  0        0.1218
13380.2    95.00  0.40     Sequence
 HLA-DQA10102-DQB10602 1256      CGSCCKFDEDDSEPV  GSCCKFDED  1        0.0613
25757.0   100.00  0.25     Sequence
 HLA-DQA10102-DQB10602 1257      GSCCKFDEDDSEPVL  SCCKFDEDD  1        0.0429
31417.6   100.00  0.17     Sequence
 HLA-DQA10102-DQB10602 1258      SCCKFDEDDSEPVLK  EDDSEPVLK  6        0.0472
30014.3   100.00  0.22     Sequence
 HLA-DQA10102-DQB10602 1259      CCKFDEDDSEPVLKG  DDSEPVLKG  6        0.0779
21520.1   100.00  0.38     Sequence
 HLA-DQA10102-DQB10602 1260      CKFDEDDSEPVLKGV  DDSEPVLKG  5        0.1319
11993.5    95.00  0.37     Sequence
 HLA-DQA10102-DQB10602 1261      KFDEDDSEPVLKGVK  DSEPVLKGV  5        0.1764
7414.5    85.00  0.41     Sequence
 HLA-DQA10102-DQB10602 1262      FDEDDSEPVLKGVKL  DSEPVLKGV  4        0.1826
6936.6    85.00  0.38     Sequence
 HLA-DQA10102-DQB10602 1263      DEDDSEPVLKGVKLH  DSEPVLKGV  3        0.1840
6826.2    85.00  0.40     Sequence
 HLA-DQA10102-DQB10602 1264      EDDSEPVLKGVKLHY  DSEPVLKGV  2        0.2299
4155.8    70.00  0.34     Sequence
 HLA-DQA10102-DQB10602 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.3686
926.2    28.00  0.65     Sequence
 HLA-DPA10201-DPB10101    1      PSPIKEMFVFLVLLP  MFVFLVLLP  6        0.3933
709.6    29.00  0.25     Sequence
 HLA-DPA10201-DPB10101    2      SPIKEMFVFLVLLPL  MFVFLVLLP  5        0.4500
384.0    17.00  0.47     Sequence
 HLA-DPA10201-DPB10101    3      PIKEMFVFLVLLPLV  MFVFLVLLP  4        0.4422
418.0    18.00  0.50     Sequence
 HLA-DPA10201-DPB10101    4      IKEMFVFLVLLPLVS  MFVFLVLLP  3        0.4516
377.6    16.00  0.43     Sequence
 HLA-DPA10201-DPB10101    5      KEMFVFLVLLPLVSS  MFVFLVLLP  2        0.4424
417.0    18.00  0.44     Sequence
 HLA-DPA10201-DPB10101    6      EMFVFLVLLPLVSSQ  FLVLLPLVS  4        0.4218
520.9    22.00  0.37     Sequence
 HLA-DPA10201-DPB10101    7      MFVFLVLLPLVSSQC  FLVLLPLVS  3        0.4070
611.9    25.00  0.41     Sequence
 HLA-DPA10201-DPB10101    8      FVFLVLLPLVSSQCV  FLVLLPLVS  2        0.3921
718.7    29.00  0.41     Sequence
 HLA-DPA10201-DPB10101    9      VFLVLLPLVSSQCVN  FLVLLPLVS  1        0.3605
1011.9    37.00  0.35     Sequence
 HLA-DPA10201-DPB10101   10      FLVLLPLVSSQCVNF  PLVSSQCVN  5        0.3539
1085.9    39.00  0.20     Sequence
 HLA-DPA10201-DPB10101   11      LVLLPLVSSQCVNFT  PLVSSQCVN  4        0.3114
1720.9    55.00  0.28     Sequence
 HLA-DPA10201-DPB10101   12      VLLPLVSSQCVNFTN  PLVSSQCVN  3        0.3066
1812.9    55.00  0.31     Sequence
 HLA-DPA10201-DPB10101   13      LLPLVSSQCVNFTNR  PLVSSQCVN  2        0.2943
2071.5    60.00  0.35     Sequence
 HLA-DPA10201-DPB10101   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.2625
2921.7    65.00  0.39     Sequence
 HLA-DPA10201-DPB10101   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.2259
4338.6    75.00  0.29     Sequence
 HLA-DPA10201-DPB10101   16      LVSSQCVNFTNRTQL  CVNFTNRTQ  5        0.2076
5289.2    80.00  0.25     Sequence
 HLA-DPA10201-DPB10101   17      VSSQCVNFTNRTQLP  CVNFTNRTQ  4        0.2045
5472.8    85.00  0.28     Sequence
 HLA-DPA10201-DPB10101   18      SSQCVNFTNRTQLPS  NFTNRTQLP  5        0.2160
4833.0    80.00  0.29     Sequence
```

```
 HLA-DPA10201-DPB10101   19      SQCVNFTNRTQLPSA  NFTNRTQLP  4        0.2259
4337.9    75.00 0.31      Sequence
 HLA-DPA10201-DPB10101   20      QCVNFTNRTQLPSAY  NFTNRTQLP  3        0.2421
3642.9    75.00 0.28      Sequence
 HLA-DPA10201-DPB10101   21      CVNFTNRTQLPSAYT  NFTNRTQLP  2        0.2613
2957.7    70.00 0.27      Sequence
 HLA-DPA10201-DPB10101   22      VNFTNRTQLPSAYTN  FTNRTQLPS  2        0.2451
3524.9    70.00 0.27      Sequence
 HLA-DPA10201-DPB10101   23      NFTNRTQLPSAYTNS  NRTQLPSAY  3        0.2217
4539.9    80.00 0.25      Sequence
 HLA-DPA10201-DPB10101   24      FTNRTQLPSAYTNSF  QLPSAYTNS  5        0.2158
4843.1    80.00 0.24      Sequence
 HLA-DPA10201-DPB10101   25      TNRTQLPSAYTNSFT  QLPSAYTNS  4        0.2022
5606.3    85.00 0.28      Sequence
 HLA-DPA10201-DPB10101   26      NRTQLPSAYTNSFTR  QLPSAYTNS  3        0.2123
5027.0    80.00 0.23      Sequence
 HLA-DPA10201-DPB10101   27      RTQLPSAYTNSFTRG  QLPSAYTNS  2        0.2037
5517.3    85.00 0.23      Sequence
 HLA-DPA10201-DPB10101   28      TQLPSAYTNSFTRGV  SAYTNSFTR  4        0.2083
5248.0    80.00 0.29      Sequence
 HLA-DPA10201-DPB10101   29      QLPSAYTNSFTRGVY  SAYTNSFTR  3        0.2356
3905.5    75.00 0.23      Sequence
 HLA-DPA10201-DPB10101   30      LPSAYTNSFTRGVYY  SFTRGVYYX  7        0.2748
2556.2    65.00 0.25      Sequence
 HLA-DPA10201-DPB10101   31      PSAYTNSFTRGVYYP  SFTRGVYYP  6        0.3031
1881.6    55.00 0.44      Sequence
 HLA-DPA10201-DPB10101   32      SAYTNSFTRGVYYPD  SFTRGVYYP  5        0.3621
994.0    37.00 0.60      Sequence
 HLA-DPA10201-DPB10101   33      AYTNSFTRGVYYPDK  SFTRGVYYP  4        0.3765
850.8    33.00 0.63      Sequence
 HLA-DPA10201-DPB10101   34      YTNSFTRGVYYPDKV  SFTRGVYYP  3        0.3829
793.7    31.00 0.62      Sequence
 HLA-DPA10201-DPB10101   35      TNSFTRGVYYPDKVF  SFTRGVYYP  2        0.3807
813.2    32.00 0.57      Sequence
 HLA-DPA10201-DPB10101   36      NSFTRGVYYPDKVFR  SFTRGVYYP  1        0.3700
912.3    34.00 0.44      Sequence
 HLA-DPA10201-DPB10101   37      SFTRGVYYPDKVFRS  VYYPDKVFR  5        0.3393
1272.3    43.00 0.38      Sequence
 HLA-DPA10201-DPB10101   38      FTRGVYYPDKVFRSS  VYYPDKVFR  4        0.3166
1627.0    50.00 0.43      Sequence
 HLA-DPA10201-DPB10101   39      TRGVYYPDKVFRSSV  VYYPDKVFR  3        0.2857
2271.5    60.00 0.47      Sequence
 HLA-DPA10201-DPB10101   40      RGVYYPDKVFRSSVL  VYYPDKVFR  2        0.3416
1240.7    42.00 0.29      Sequence
 HLA-DPA10201-DPB10101   41      GVYYPDKVFRSSVLH  VFRSSVLHX  7        0.3916
722.6    29.00 0.35      Sequence
 HLA-DPA10201-DPB10101   42      VYYPDKVFRSSVLHS  VFRSSVLHS  6        0.4919
244.1    10.00 0.56      Sequence
 HLA-DPA10201-DPB10101   43      YYPDKVFRSSVLHST  VFRSSVLHS  5        0.5447
137.8     5.00 0.73      Sequence         WB
 HLA-DPA10201-DPB10101   44      YPDKVFRSSVLHSTQ  VFRSSVLHS  4        0.5593
117.7     4.00 0.73      Sequence         WB
 HLA-DPA10201-DPB10101   45      PDKVFRSSVLHSTQD  VFRSSVLHS  3        0.5522
127.1     4.50 0.72      Sequence         WB
 HLA-DPA10201-DPB10101   46      DKVFRSSVLHSTQDL  VFRSSVLHS  2        0.5508
129.1     4.50 0.72      Sequence         WB
 HLA-DPA10201-DPB10101   47      KVFRSSVLHSTQDLF  VFRSSVLHS  1        0.5337
155.3     5.50 0.56      Sequence         WB
 HLA-DPA10201-DPB10101   48      VFRSSVLHSTQDLFL  VLHSTQDLF  5        0.4754
291.8    13.00 0.34      Sequence
 HLA-DPA10201-DPB10101   49      FRSSVLHSTQDLFLP  VLHSTQDLF  4        0.4448
406.4    18.00 0.41      Sequence
 HLA-DPA10201-DPB10101   50      RSSVLHSTQDLFLPF  VLHSTQDLF  3        0.4713
304.9    13.00 0.32      Sequence
 HLA-DPA10201-DPB10101   51      SSVLHSTQDLFLPFF  VLHSTQDLF  2        0.4954
235.1     9.50 0.25      Sequence         WB
```

```
 HLA-DPA10201-DPB10101   52      SVLHSTQDLFLPFFS  HSTQDLFLP  3         0.5392
146.2     5.50  0.30     Sequence         WB
 HLA-DPA10201-DPB10101   53      VLHSTQDLFLPFFSN  HSTQDLFLP  2         0.5501
130.1     4.50  0.24     Sequence         WB
 HLA-DPA10201-DPB10101   54      LHSTQDLFLPFFSNV  DLFLPFFSN  5         0.5868
87.5     2.50  0.32     Sequence         WB
 HLA-DPA10201-DPB10101   55      HSTQDLFLPFFSNVT  LFLPFFSNV  5         0.5844
89.7     2.50  0.31     Sequence         WB
 HLA-DPA10201-DPB10101   56      STQDLFLPFFSNVTW  LFLPFFSNV  4         0.5897
84.7     2.50  0.34     Sequence         WB
 HLA-DPA10201-DPB10101   57      TQDLFLPFFSNVTWF  LFLPFFSNV  3         0.5949
80.1     2.50  0.29     Sequence         WB
 HLA-DPA10201-DPB10101   58      QDLFLPFFSNVTWFH  LFLPFFSNV  2         0.6084
69.2     1.60  0.21     Sequence         SB
 HLA-DPA10201-DPB10101   59      DLFLPFFSNVTWFHA  FFSNVTWFH  5         0.6080
69.5     1.60  0.51     Sequence         SB
 HLA-DPA10201-DPB10101   60      LFLPFFSNVTWFHAI  FFSNVTWFH  4         0.6106
67.6     1.60  0.58     Sequence         SB
 HLA-DPA10201-DPB10101   61      FLPFFSNVTWFHAIH  FFSNVTWFH  3         0.6163
63.6     1.40  0.58     Sequence         SB
 HLA-DPA10201-DPB10101   62      LPFFSNVTWFHAIHV  FFSNVTWFH  2         0.6026
73.7     1.80  0.57     Sequence         SB
 HLA-DPA10201-DPB10101   63      PFFSNVTWFHAIHVS  FFSNVTWFH  1         0.5573
120.3     4.00  0.44     Sequence         WB
 HLA-DPA10201-DPB10101   64      FFSNVTWFHAIHVSG  FFSNVTWFH  0         0.4932
240.7    10.00  0.28     Sequence
 HLA-DPA10201-DPB10101   65      FSNVTWFHAIHVSGT  WFHAIHVSG  5         0.4098
593.7    25.00  0.21     Sequence
 HLA-DPA10201-DPB10101   66      SNVTWFHAIHVSGTN  WFHAIHVSG  4         0.3303
1402.2    46.00  0.28     Sequence
 HLA-DPA10201-DPB10101   67      NVTWFHAIHVSGTNG  WFHAIHVSG  3         0.2975
1999.9    55.00  0.35     Sequence
 HLA-DPA10201-DPB10101   68      VTWFHAIHVSGTNGT  WFHAIHVSG  2         0.2581
3063.8    70.00  0.44     Sequence
 HLA-DPA10201-DPB10101   69      TWFHAIHVSGTNGTK  WFHAIHVSG  1         0.2070
5323.9    80.00  0.35     Sequence
 HLA-DPA10201-DPB10101   70      WFHAIHVSGTNGTKR  HVSGTNGTK  5         0.1637
8507.3    90.00  0.24     Sequence
 HLA-DPA10201-DPB10101   71      FHAIHVSGTNGTKRF  HVSGTNGTK  4         0.1391
11101.1    95.00  0.36     Sequence
 HLA-DPA10201-DPB10101   72      HAIHVSGTNGTKRFD  HVSGTNGTK  3         0.1170
14092.4   100.00  0.47     Sequence
 HLA-DPA10201-DPB10101   73      AIHVSGTNGTKRFDN  HVSGTNGTK  2         0.1069
15733.3   100.00  0.46     Sequence
 HLA-DPA10201-DPB10101   74      IHVSGTNGTKRFDNP  HVSGTNGTK  1         0.0848
19980.0   100.00  0.41     Sequence
 HLA-DPA10201-DPB10101   75      HVSGTNGTKRFDNPV  TNGTKRFDN  4         0.0674
24100.9   100.00  0.28     Sequence
 HLA-DPA10201-DPB10101   76      VSGTNGTKRFDNPVL  RFDNPVLXX  8         0.1192
13769.4   100.00  0.19     Sequence
 HLA-DPA10201-DPB10101   77      SGTNGTKRFDNPVLP  RFDNPVLPX  7         0.1583
9014.3    90.00  0.29     Sequence
 HLA-DPA10201-DPB10101   78      GTNGTKRFDNPVLPF  KRFDNPVLP  5         0.3157
1642.7    50.00  0.39     Sequence
 HLA-DPA10201-DPB10101   79      TNGTKRFDNPVLPFN  KRFDNPVLP  4         0.3428
1225.6    42.00  0.32     Sequence
 HLA-DPA10201-DPB10101   80      NGTKRFDNPVLPFND  KRFDNPVLP  3         0.3523
1105.1    39.00  0.30     Sequence
 HLA-DPA10201-DPB10101   81      GTKRFDNPVLPFNDG  RFDNPVLPF  3         0.3455
1189.2    41.00  0.36     Sequence
 HLA-DPA10201-DPB10101   82      TKRFDNPVLPFNDGV  RFDNPVLPF  2         0.3500
1133.8    40.00  0.34     Sequence
 HLA-DPA10201-DPB10101   83      KRFDNPVLPFNDGVY  RFDNPVLPF  1         0.3263
1463.9    47.00  0.25     Sequence
 HLA-DPA10201-DPB10101   84      RFDNPVLPFNDGVYF  PFNDGVYFX  7         0.3118
1712.6    55.00  0.22     Sequence
```

```
 HLA-DPA10201-DPB10101   85      FDNPVLPFNDGVYFA  PFNDGVYFA  6        0.3178
1605.2    49.00  0.43     Sequence
 HLA-DPA10201-DPB10101   86      DNPVLPFNDGVYFAS  PFNDGVYFA  5        0.3592
1025.4    37.00  0.58     Sequence
 HLA-DPA10201-DPB10101   87      NPVLPFNDGVYFAST  PFNDGVYFA  4        0.3780
837.0    32.00  0.58     Sequence
 HLA-DPA10201-DPB10101   88      PVLPFNDGVYFASTE  PFNDGVYFA  3        0.4029
639.5    26.00  0.57     Sequence
 HLA-DPA10201-DPB10101   89      VLPFNDGVYFASTEK  PFNDGVYFA  2        0.4055
621.3    26.00  0.55     Sequence
 HLA-DPA10201-DPB10101   90      LPFNDGVYFASTEKS  PFNDGVYFA  1        0.3889
743.9    30.00  0.47     Sequence
 HLA-DPA10201-DPB10101   91      PFNDGVYFASTEKSN  YFASTEKSN  6        0.3551
1072.7    39.00  0.31     Sequence
 HLA-DPA10201-DPB10101   92      FNDGVYFASTEKSNI  YFASTEKSN  5        0.3621
994.3    37.00  0.51     Sequence
 HLA-DPA10201-DPB10101   93      NDGVYFASTEKSNII  YFASTEKSN  4        0.3650
963.9    36.00  0.60     Sequence
 HLA-DPA10201-DPB10101   94      DGVYFASTEKSNIIR  YFASTEKSN  3        0.3786
831.7    32.00  0.60     Sequence
 HLA-DPA10201-DPB10101   95      GVYFASTEKSNIIRG  YFASTEKSN  2        0.3578
1041.0    38.00  0.67     Sequence
 HLA-DPA10201-DPB10101   96      VYFASTEKSNIIRGW  YFASTEKSN  1        0.3247
1490.5    47.00  0.54     Sequence
 HLA-DPA10201-DPB10101   97      YFASTEKSNIIRGWI  YFASTEKSN  0        0.2548
3175.7    70.00  0.36     Sequence
 HLA-DPA10201-DPB10101   98      FASTEKSNIIRGWIF  KSNIIRGWI  5        0.2244
4410.7    80.00  0.20     Sequence
 HLA-DPA10201-DPB10101   99      ASTEKSNIIRGWIFG  IIRGWIFGX  7        0.2418
3655.9    75.00  0.33     Sequence
 HLA-DPA10201-DPB10101  100      STEKSNIIRGWIFGT  IIRGWIFGT  6        0.3120
1709.0    55.00  0.56     Sequence
 HLA-DPA10201-DPB10101  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5        0.3582
1037.3    38.00  0.62     Sequence
 HLA-DPA10201-DPB10101  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.4322
465.6    20.00  0.52     Sequence
 HLA-DPA10201-DPB10101  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3        0.4413
421.9    18.00  0.46     Sequence
 HLA-DPA10201-DPB10101  104      SNIIRGWIFGTTLDS  IIRGWIFGT  2        0.4544
366.3    16.00  0.35     Sequence
 HLA-DPA10201-DPB10101  105      NIIRGWIFGTTLDSK  WIFGTTLDS  5        0.4648
327.2    14.00  0.37     Sequence
 HLA-DPA10201-DPB10101  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.4445
407.5    18.00  0.44     Sequence
 HLA-DPA10201-DPB10101  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3        0.4215
522.8    22.00  0.49     Sequence
 HLA-DPA10201-DPB10101  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2        0.4054
622.2    26.00  0.51     Sequence
 HLA-DPA10201-DPB10101  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1        0.3241
1499.2    47.00  0.37     Sequence
 HLA-DPA10201-DPB10101  110      WIFGTTLDSKTQSLL  IFGTTLDSK  1        0.3352
1330.0    44.00  0.23     Sequence
 HLA-DPA10201-DPB10101  111      IFGTTLDSKTQSLLI  LDSKTQSLL  5        0.3234
1511.3    48.00  0.19     Sequence
 HLA-DPA10201-DPB10101  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5        0.3655
958.3    36.00  0.22     Sequence
 HLA-DPA10201-DPB10101  113      GTTLDSKTQSLLIVN  SKTQSLLIV  5        0.3901
734.5    29.00  0.20     Sequence
 HLA-DPA10201-DPB10101  114      TTLDSKTQSLLIVNN  SKTQSLLIV  4        0.3976
677.0    28.00  0.19     Sequence
 HLA-DPA10201-DPB10101  115      TLDSKTQSLLIVNNA  SKTQSLLIV  3        0.3887
745.9    30.00  0.19     Sequence
 HLA-DPA10201-DPB10101  116      LDSKTQSLLIVNNAT  SKTQSLLIV  2        0.3713
900.2    34.00  0.20     Sequence
 HLA-DPA10201-DPB10101  117      DSKTQSLLIVNNATN  KTQSLLIVN  2        0.3161
1635.5    50.00  0.28     Sequence
```

```
 HLA-DPA10201-DPB10101  118      SKTQSLLIVNNATNV  SLLIVNNAT  4        0.3007
1932.4    55.00  0.23     Sequence
 HLA-DPA10201-DPB10101  119      KTQSLLIVNNATNVV  SLLIVNNAT  3        0.2692
2715.2    65.00  0.31     Sequence
 HLA-DPA10201-DPB10101  120      TQSLLIVNNATNVVI  SLLIVNNAT  2        0.2694
2710.6    65.00  0.29     Sequence
 HLA-DPA10201-DPB10101  121      QSLLIVNNATNVVIK  IVNNATNVV  4        0.2682
2745.9    65.00  0.17     Sequence
 HLA-DPA10201-DPB10101  122      SLLIVNNATNVVIKV  IVNNATNVV  3        0.2676
2763.4    65.00  0.21     Sequence
 HLA-DPA10201-DPB10101  123      LLIVNNATNVVIKVC  IVNNATNVV  2        0.2629
2909.5    65.00  0.25     Sequence
 HLA-DPA10201-DPB10101  124      LIVNNATNVVIKVCE  VNNATNVVI  2        0.2501
3339.0    70.00  0.21     Sequence
 HLA-DPA10201-DPB10101  125      IVNNATNVVIKVCEF  TNVVIKVCE  5        0.2716
2648.0    65.00  0.15     Sequence
 HLA-DPA10201-DPB10101  126      VNNATNVVIKVCEFQ  VIKVCEFQX  7        0.2805
2402.8    60.00  0.19     Sequence
 HLA-DPA10201-DPB10101  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.3425
1229.1    42.00  0.43     Sequence
 HLA-DPA10201-DPB10101  128      NATNVVIKVCEFQFC  VIKVCEFQF  5        0.4030
639.0    26.00  0.55     Sequence
 HLA-DPA10201-DPB10101  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.4169
549.7    23.00  0.53     Sequence
 HLA-DPA10201-DPB10101  130      TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.4647
327.7    14.00  0.45     Sequence
 HLA-DPA10201-DPB10101  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.4572
355.5    15.00  0.46     Sequence
 HLA-DPA10201-DPB10101  132      VVIKVCEFQFCNYPF  VIKVCEFQF  1        0.4817
272.6    12.00  0.30     Sequence
 HLA-DPA10201-DPB10101  133      VIKVCEFQFCNYPFL  EFQFCNYPF  5        0.5287
164.0     6.00  0.46     Sequence         WB
 HLA-DPA10201-DPB10101  134      IKVCEFQFCNYPFLG  EFQFCNYPF  4        0.5150
190.0     7.50  0.49     Sequence         WB
 HLA-DPA10201-DPB10101  135      KVCEFQFCNYPFLGV  EFQFCNYPF  3        0.5333
156.0     6.00  0.45     Sequence         WB
 HLA-DPA10201-DPB10101  136      VCEFQFCNYPFLGVY  EFQFCNYPF  2        0.5294
162.7     6.00  0.44     Sequence         WB
 HLA-DPA10201-DPB10101  137      CEFQFCNYPFLGVYY  EFQFCNYPF  1        0.5366
150.5     5.50  0.35     Sequence         WB
 HLA-DPA10201-DPB10101  138      EFQFCNYPFLGVYYH  QFCNYPFLG  2        0.5384
147.6     5.50  0.25     Sequence         WB
 HLA-DPA10201-DPB10101  139      FQFCNYPFLGVYYHK  PFLGVYYHK  6        0.5549
123.4     4.00  0.37     Sequence         WB
 HLA-DPA10201-DPB10101  140      QFCNYPFLGVYYHKN  PFLGVYYHK  5        0.5839
90.2     2.50  0.65     Sequence         WB
 HLA-DPA10201-DPB10101  141      FCNYPFLGVYYHKNN  PFLGVYYHK  4        0.5826
91.4     3.00  0.68     Sequence         WB
 HLA-DPA10201-DPB10101  142      CNYPFLGVYYHKNNK  PFLGVYYHK  3        0.5740
100.4     3.00  0.69     Sequence         WB
 HLA-DPA10201-DPB10101  143      NYPFLGVYYHKNNKS  PFLGVYYHK  2        0.5663
109.1     3.50  0.69     Sequence         WB
 HLA-DPA10201-DPB10101  144      YPFLGVYYHKNNKSW  PFLGVYYHK  1        0.5024
217.9     9.00  0.57     Sequence         WB
 HLA-DPA10201-DPB10101  145      PFLGVYYHKNNKSWM  PFLGVYYHK  0        0.3904
732.0    29.00  0.43     Sequence
 HLA-DPA10201-DPB10101  146      FLGVYYHKNNKSWME  XFLGVYYHK -1        0.2817
2373.8    60.00  0.22     Sequence
 HLA-DPA10201-DPB10101  147      LGVYYHKNNKSWMES  YHKNNKSWM  4        0.1486
10019.2    95.00  0.19     Sequence
 HLA-DPA10201-DPB10101  148      GVYYHKNNKSWMESE  KNNKSWMES  5        0.1563
9220.4    90.00  0.19     Sequence
 HLA-DPA10201-DPB10101  149      VYYHKNNKSWMESEF  KNNKSWMES  4        0.1894
6443.8    85.00  0.14     Sequence
 HLA-DPA10201-DPB10101  150      YYHKNNKSWMESEFR  SWMESEFRX  7        0.2526
3250.1    70.00  0.25     Sequence
```

```
 HLA-DPA10201-DPB10101  151       YHKNNKSWMESEFRV  SWMESEFRV  6         0.3487
1149.1    40.00  0.41     Sequence
 HLA-DPA10201-DPB10101  152       HKNNKSWMESEFRVY  SWMESEFRV  5         0.4479
393.0    17.00  0.56     Sequence
 HLA-DPA10201-DPB10101  153       KNNKSWMESEFRVYS  SWMESEFRV  4         0.4649
327.0    14.00  0.55     Sequence
 HLA-DPA10201-DPB10101  154       NNKSWMESEFRVYSS  SWMESEFRV  3         0.4724
301.4    13.00  0.52     Sequence
 HLA-DPA10201-DPB10101  155       NKSWMESEFRVYSSA  SWMESEFRV  2         0.4695
311.1    13.00  0.51     Sequence
 HLA-DPA10201-DPB10101  156       KSWMESEFRVYSSAN  SWMESEFRV  1         0.4423
417.4    18.00  0.38     Sequence
 HLA-DPA10201-DPB10101  157       SWMESEFRVYSSANN  EFRVYSSAN  5         0.3832
791.7    31.00  0.16     Sequence
 HLA-DPA10201-DPB10101  158       WMESEFRVYSSANNC  EFRVYSSAN  4         0.3304
1401.2    46.00  0.23     Sequence
 HLA-DPA10201-DPB10101  159       MESEFRVYSSANNCT  EFRVYSSAN  3         0.2735
2594.3    65.00  0.33     Sequence
 HLA-DPA10201-DPB10101  160       ESEFRVYSSANNCTF  EFRVYSSAN  2         0.2759
2526.7    65.00  0.33     Sequence
 HLA-DPA10201-DPB10101  161       SEFRVYSSANNCTFE  VYSSANNCT  4         0.2570
3098.8    70.00  0.22     Sequence
 HLA-DPA10201-DPB10101  162       EFRVYSSANNCTFEY  VYSSANNCT  3         0.2519
3275.5    70.00  0.25     Sequence
 HLA-DPA10201-DPB10101  163       FRVYSSANNCTFEYV  SANNCTFEY  5         0.3011
1924.6    55.00  0.43     Sequence
 HLA-DPA10201-DPB10101  164       RVYSSANNCTFEYVS  SANNCTFEY  4         0.2753
2543.6    65.00  0.52     Sequence
 HLA-DPA10201-DPB10101  165       VYSSANNCTFEYVSQ  SANNCTFEY  3         0.2863
2258.0    60.00  0.50     Sequence
 HLA-DPA10201-DPB10101  166       YSSANNCTFEYVSQP  SANNCTFEY  2         0.2918
2127.1    60.00  0.44     Sequence
 HLA-DPA10201-DPB10101  167       SSANNCTFEYVSQPF  TFEYVSQPF  6         0.3466
1175.9    41.00  0.30     Sequence
 HLA-DPA10201-DPB10101  168       SANNCTFEYVSQPFL  TFEYVSQPF  5         0.4590
348.5    15.00  0.32     Sequence
 HLA-DPA10201-DPB10101  169       ANNCTFEYVSQPFLM  EYVSQPFLM  6         0.5179
184.1     7.00  0.38     Sequence         WB
 HLA-DPA10201-DPB10101  170       NNCTFEYVSQPFLMD  EYVSQPFLM  5         0.5781
96.1     3.00  0.47     Sequence         WB
 HLA-DPA10201-DPB10101  171       NCTFEYVSQPFLMDL  EYVSQPFLM  4         0.6147
64.7     1.40  0.44     Sequence         SB
 HLA-DPA10201-DPB10101  172       CTFEYVSQPFLMDLE  EYVSQPFLM  3         0.6196
61.3     1.30  0.47     Sequence         SB
 HLA-DPA10201-DPB10101  173       TFEYVSQPFLMDLEG  EYVSQPFLM  2         0.6053
71.6     1.70  0.48     Sequence         SB
 HLA-DPA10201-DPB10101  174       FEYVSQPFLMDLEGK  YVSQPFLMD  2         0.5699
105.0     3.50  0.35     Sequence         WB
 HLA-DPA10201-DPB10101  175       EYVSQPFLMDLEGKQ  YVSQPFLMD  1         0.4763
289.0    12.00  0.34     Sequence
 HLA-DPA10201-DPB10101  176       YVSQPFLMDLEGKQG  FLMDLEGKQ  5         0.3925
715.3    29.00  0.17     Sequence
 HLA-DPA10201-DPB10101  177       VSQPFLMDLEGKQGN  FLMDLEGKQ  4         0.3142
1669.4    50.00  0.31     Sequence
 HLA-DPA10201-DPB10101  178       SQPFLMDLEGKQGNF  FLMDLEGKQ  3         0.3039
1865.8    55.00  0.35     Sequence
 HLA-DPA10201-DPB10101  179       QPFLMDLEGKQGNFK  FLMDLEGKQ  2         0.2805
2402.9    60.00  0.40     Sequence
 HLA-DPA10201-DPB10101  180       PFLMDLEGKQGNFKN  FLMDLEGKQ  1         0.2460
3493.0    70.00  0.27     Sequence
 HLA-DPA10201-DPB10101  181       FLMDLEGKQGNFKNL  DLEGKQGNF  3         0.2326
4036.1    75.00  0.22     Sequence
 HLA-DPA10201-DPB10101  182       LMDLEGKQGNFKNLS  EGKQGNFKN  4         0.1766
7401.8    90.00  0.26     Sequence
 HLA-DPA10201-DPB10101  183       MDLEGKQGNFKNLSE  EGKQGNFKN  3         0.1797
7155.5    90.00  0.25     Sequence
```

```
 HLA-DPA10201-DPB10101  184      DLEGKQGNFKNLSEF  EGKQGNFKN  2        0.1955
6028.6    85.00  0.19     Sequence
 HLA-DPA10201-DPB10101  185      LEGKQGNFKNLSEFV  NFKNLSEFV  6        0.2601
2997.7    70.00  0.24     Sequence
 HLA-DPA10201-DPB10101  186      EGKQGNFKNLSEFVF  NFKNLSEFV  5        0.4188
538.5    23.00  0.35     Sequence
 HLA-DPA10201-DPB10101  187      GKQGNFKNLSEFVFK  NFKNLSEFV  4        0.4946
237.0    10.00  0.31     Sequence
 HLA-DPA10201-DPB10101  188      KQGNFKNLSEFVFKN  NLSEFVFKN  6        0.5511
128.7     4.50  0.44     Sequence         WB
 HLA-DPA10201-DPB10101  189      QGNFKNLSEFVFKNI  NLSEFVFKN  5        0.6069
70.3     1.70  0.52     Sequence         SB
 HLA-DPA10201-DPB10101  190      GNFKNLSEFVFKNID  NLSEFVFKN  4        0.5917
82.9     2.50  0.55     Sequence         WB
 HLA-DPA10201-DPB10101  191      NFKNLSEFVFKNIDG  NLSEFVFKN  3        0.5825
91.5     3.00  0.56     Sequence         WB
 HLA-DPA10201-DPB10101  192      FKNLSEFVFKNIDGY  NLSEFVFKN  2        0.5653
110.3     3.50  0.60     Sequence         WB
 HLA-DPA10201-DPB10101  193      KNLSEFVFKNIDGYF  NLSEFVFKN  1        0.4915
245.1    10.00  0.43     Sequence
 HLA-DPA10201-DPB10101  194      NLSEFVFKNIDGYFK  VFKNIDGYF  5        0.4308
472.9    20.00  0.26     Sequence
 HLA-DPA10201-DPB10101  195      LSEFVFKNIDGYFKI  VFKNIDGYF  4        0.4270
492.7    21.00  0.35     Sequence
 HLA-DPA10201-DPB10101  196      SEFVFKNIDGYFKIY  VFKNIDGYF  3        0.4380
437.3    19.00  0.34     Sequence
 HLA-DPA10201-DPB10101  197      EFVFKNIDGYFKIYS  VFKNIDGYF  2        0.4386
434.3    19.00  0.32     Sequence
 HLA-DPA10201-DPB10101  198      FVFKNIDGYFKIYSK  VFKNIDGYF  1        0.4361
446.5    19.00  0.30     Sequence
 HLA-DPA10201-DPB10101  199      VFKNIDGYFKIYSKH  NIDGYFKIY  3        0.4031
637.7    26.00  0.19     Sequence
 HLA-DPA10201-DPB10101  200      FKNIDGYFKIYSKHT  YFKIYSKHT  6        0.3861
766.7    30.00  0.21     Sequence
 HLA-DPA10201-DPB10101  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.3637
977.1    36.00  0.26     Sequence
 HLA-DPA10201-DPB10101  202      NIDGYFKIYSKHTPI  YFKIYSKHT  4        0.3624
990.8    37.00  0.34     Sequence
 HLA-DPA10201-DPB10101  203      IDGYFKIYSKHTPIN  YFKIYSKHT  3        0.3582
1036.9    38.00  0.36     Sequence
 HLA-DPA10201-DPB10101  204      DGYFKIYSKHTPINL  YFKIYSKHT  2        0.3829
794.1    31.00  0.28     Sequence
 HLA-DPA10201-DPB10101  205      GYFKIYSKHTPINLV  YSKHTPINL  5        0.4123
577.2    24.00  0.31     Sequence
 HLA-DPA10201-DPB10101  206      YFKIYSKHTPINLVR  YSKHTPINL  4        0.4436
411.6    18.00  0.34     Sequence
 HLA-DPA10201-DPB10101  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.4301
476.4    20.00  0.38     Sequence
 HLA-DPA10201-DPB10101  208      KIYSKHTPINLVRDL  KHTPINLVR  4        0.4265
495.6    21.00  0.37     Sequence
 HLA-DPA10201-DPB10101  209      IYSKHTPINLVRDLP  KHTPINLVR  3        0.4040
631.8    26.00  0.39     Sequence
 HLA-DPA10201-DPB10101  210      YSKHTPINLVRDLPQ  KHTPINLVR  2        0.3798
821.1    32.00  0.41     Sequence
 HLA-DPA10201-DPB10101  211      SKHTPINLVRDLPQG  PINLVRDLP  4        0.3207
1555.9    48.00  0.23     Sequence
 HLA-DPA10201-DPB10101  212      KHTPINLVRDLPQGF  PINLVRDLP  3        0.2971
2008.1    55.00  0.35     Sequence
 HLA-DPA10201-DPB10101  213      HTPINLVRDLPQGFS  PINLVRDLP  2        0.2569
3104.0    70.00  0.36     Sequence
 HLA-DPA10201-DPB10101  214      TPINLVRDLPQGFSA  LVRDLPQGF  4        0.2518
3279.3    70.00  0.31     Sequence
 HLA-DPA10201-DPB10101  215      PINLVRDLPQGFSAL  LVRDLPQGF  3        0.2826
2349.4    60.00  0.25     Sequence
 HLA-DPA10201-DPB10101  216      INLVRDLPQGFSALE  LVRDLPQGF  2        0.3152
1650.9    50.00  0.20     Sequence
```

```
 HLA-DPA10201-DPB10101  217      NLVRDLPQGFSALEP  LPQGFSALE  5        0.3027
1889.8    55.00  0.29     Sequence
 HLA-DPA10201-DPB10101  218      LVRDLPQGFSALEPL  LPQGFSALE  4        0.3272
1450.9    46.00  0.31     Sequence
 HLA-DPA10201-DPB10101  219      VRDLPQGFSALEPLV  LPQGFSALE  3        0.3540
1085.1    39.00  0.25     Sequence
 HLA-DPA10201-DPB10101  220      RDLPQGFSALEPLVD  GFSALEPLV  5        0.3939
705.1    29.00  0.25     Sequence
 HLA-DPA10201-DPB10101  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.4180
543.1    23.00  0.37     Sequence
 HLA-DPA10201-DPB10101  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.4232
513.0    22.00  0.38     Sequence
 HLA-DPA10201-DPB10101  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.4298
478.1    21.00  0.37     Sequence
 HLA-DPA10201-DPB10101  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.4168
550.3    23.00  0.36     Sequence
 HLA-DPA10201-DPB10101  225      GFSALEPLVDLPIGI  ALEPLVDLP  3        0.4094
595.6    25.00  0.25     Sequence
 HLA-DPA10201-DPB10101  226      FSALEPLVDLPIGIN  PLVDLPIGI  5        0.4198
532.5    23.00  0.46     Sequence
 HLA-DPA10201-DPB10101  227      SALEPLVDLPIGINI  PLVDLPIGI  4        0.4076
608.0    25.00  0.58     Sequence
 HLA-DPA10201-DPB10101  228      ALEPLVDLPIGINIT  PLVDLPIGI  3        0.4050
625.1    26.00  0.58     Sequence
 HLA-DPA10201-DPB10101  229      LEPLVDLPIGINITR  PLVDLPIGI  2        0.3985
670.4    27.00  0.54     Sequence
 HLA-DPA10201-DPB10101  230      EPLVDLPIGINITRF  PLVDLPIGI  1        0.3797
821.8    32.00  0.40     Sequence
 HLA-DPA10201-DPB10101  231      PLVDLPIGINITRFQ  LPIGINITR  4        0.3707
905.9    34.00  0.19     Sequence
 HLA-DPA10201-DPB10101  232      LVDLPIGINITRFQT  GINITRFQT  6        0.3647
966.8    36.00  0.38     Sequence
 HLA-DPA10201-DPB10101  233      VDLPIGINITRFQTL  GINITRFQT  5        0.4593
347.2    15.00  0.63     Sequence
 HLA-DPA10201-DPB10101  234      DLPIGINITRFQTLL  GINITRFQT  4        0.5038
214.7     8.50  0.63     Sequence         WB
 HLA-DPA10201-DPB10101  235      LPIGINITRFQTLLA  GINITRFQT  3        0.5561
121.8     4.00  0.62     Sequence         WB
 HLA-DPA10201-DPB10101  236      PIGINITRFQTLLAL  GINITRFQT  2        0.5518
127.7     4.50  0.56     Sequence         WB
 HLA-DPA10201-DPB10101  237      IGINITRFQTLLALH  GINITRFQT  1        0.5501
130.1     4.50  0.45     Sequence         WB
 HLA-DPA10201-DPB10101  238      GINITRFQTLLALHR  RFQTLLALH  5        0.5202
179.7     7.00  0.25     Sequence         WB
 HLA-DPA10201-DPB10101  239      INITRFQTLLALHRS  RFQTLLALH  4        0.4937
239.3    10.00  0.30     Sequence
 HLA-DPA10201-DPB10101  240      NITRFQTLLALHRSY  RFQTLLALH  3        0.4582
351.4    15.00  0.38     Sequence
 HLA-DPA10201-DPB10101  241      ITRFQTLLALHRSYL  RFQTLLALH  2        0.4504
382.6    17.00  0.34     Sequence
 HLA-DPA10201-DPB10101  242      TRFQTLLALHRSYLT  TLLALHRSY  4        0.4265
495.3    21.00  0.22     Sequence
 HLA-DPA10201-DPB10101  243      RFQTLLALHRSYLTP  TLLALHRSY  3        0.4098
593.5    25.00  0.22     Sequence
 HLA-DPA10201-DPB10101  244      FQTLLALHRSYLTPG  TLLALHRSY  2        0.3611
1004.6    37.00  0.29     Sequence
 HLA-DPA10201-DPB10101  245      QTLLALHRSYLTPGD  ALHRSYLTP  4        0.3276
1444.1    46.00  0.31     Sequence
 HLA-DPA10201-DPB10101  246      TLLALHRSYLTPGDS  ALHRSYLTP  3        0.2967
2016.5    55.00  0.37     Sequence
 HLA-DPA10201-DPB10101  247      LLALHRSYLTPGDSS  ALHRSYLTP  2        0.2646
2856.6    65.00  0.47     Sequence
 HLA-DPA10201-DPB10101  248      LALHRSYLTPGDSSS  ALHRSYLTP  1        0.2142
4924.1    80.00  0.44     Sequence
 HLA-DPA10201-DPB10101  249      ALHRSYLTPGDSSSG  ALHRSYLTP  0        0.1533
9515.0    95.00  0.25     Sequence
```

```
 HLA-DPA10201-DPB10101  250      LHRSYLTPGDSSSGW  RSYLTPGDS  2        0.1254
12877.6    95.00  0.26     Sequence
 HLA-DPA10201-DPB10101  251      HRSYLTPGDSSSGWT  YLTPGDSSS  3        0.1112
15004.6   100.00  0.28     Sequence
 HLA-DPA10201-DPB10101  252      RSYLTPGDSSSGWTA  YLTPGDSSS  2        0.0943
18028.5   100.00  0.40     Sequence
 HLA-DPA10201-DPB10101  253      SYLTPGDSSSGWTAG  YLTPGDSSS  1        0.0693
23630.2   100.00  0.31     Sequence
 HLA-DPA10201-DPB10101  254      YLTPGDSSSGWTAGA  TPGDSSSGW  2        0.0568
27029.5   100.00  0.20     Sequence
 HLA-DPA10201-DPB10101  255      LTPGDSSSGWTAGAA  PGDSSSGWT  2        0.0420
31743.2   100.00  0.22     Sequence
 HLA-DPA10201-DPB10101  256      TPGDSSSGWTAGAAA  SSGWTAGAA  5        0.0467
30169.3   100.00  0.25     Sequence
 HLA-DPA10201-DPB10101  257      PGDSSSGWTAGAAAY  SGWTAGAAA  5        0.0612
25799.9   100.00  0.29     Sequence
 HLA-DPA10201-DPB10101  258      GDSSSGWTAGAAAYY  GWTAGAAAY  5        0.1286
12440.2    95.00  0.22     Sequence
 HLA-DPA10201-DPB10101  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.1650
8384.3    90.00  0.24    Sequence
 HLA-DPA10201-DPB10101  260      SSSGWTAGAAAYYVG  AGAAAYYVG  6        0.1647
8412.2    90.00  0.29    Sequence
 HLA-DPA10201-DPB10101  261      SSGWTAGAAAYYVGY  AGAAAYYVG  5        0.1786
7241.7    90.00  0.31    Sequence
 HLA-DPA10201-DPB10101  262      SGWTAGAAAYYVGYL  AGAAAYYVG  4        0.2548
3175.5    70.00  0.19    Sequence
 HLA-DPA10201-DPB10101  263      GWTAGAAAYYVGYLQ  AAYYVGYLQ  6        0.3058
1829.2    55.00  0.23    Sequence
 HLA-DPA10201-DPB10101  264      WTAGAAAYYVGYLQP  AYYVGYLQP  6        0.3480
1158.1    41.00  0.31    Sequence
 HLA-DPA10201-DPB10101  265      TAGAAAYYVGYLQPR  AYYVGYLQP  5        0.3791
827.1    32.00  0.50    Sequence
 HLA-DPA10201-DPB10101  266      AGAAAYYVGYLQPRT  AYYVGYLQP  4        0.4080
605.0    25.00  0.46    Sequence
 HLA-DPA10201-DPB10101  267      GAAAYYVGYLQPRTF  AYYVGYLQP  3        0.4420
418.8    18.00  0.41    Sequence
 HLA-DPA10201-DPB10101  268      AAAYYVGYLQPRTFL  AYYVGYLQP  2        0.4675
317.9    14.00  0.35    Sequence
 HLA-DPA10201-DPB10101  269      AAYYVGYLQPRTFLL  YLQPRTFLL  6        0.5175
185.1     7.00  0.34    Sequence         WB
 HLA-DPA10201-DPB10101  270      AYYVGYLQPRTFLLK  YLQPRTFLL  5        0.5187
182.7     7.00  0.40    Sequence         WB
 HLA-DPA10201-DPB10101  271      YYVGYLQPRTFLLKY  YLQPRTFLL  4        0.5088
203.3     8.00  0.44    Sequence         WB
 HLA-DPA10201-DPB10101  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.4920
243.8    10.00  0.46    Sequence
 HLA-DPA10201-DPB10101  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.4701
309.1    13.00  0.47    Sequence
 HLA-DPA10201-DPB10101  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.4485
390.3    17.00  0.38    Sequence
 HLA-DPA10201-DPB10101  275      YLQPRTFLLKYNENG  QPRTFLLKY  2        0.3908
728.7    29.00  0.15    Sequence
 HLA-DPA10201-DPB10101  276      LQPRTFLLKYNENGT  RTFLLKYNE  3        0.3346
1338.5    44.00  0.22    Sequence
 HLA-DPA10201-DPB10101  277      QPRTFLLKYNENGTI  LLKYNENGT  5        0.3469
1172.2    41.00  0.23    Sequence
 HLA-DPA10201-DPB10101  278      PRTFLLKYNENGTIT  LLKYNENGT  4        0.3481
1157.0    40.00  0.27    Sequence
 HLA-DPA10201-DPB10101  279      RTFLLKYNENGTITD  LLKYNENGT  3        0.3386
1282.0    43.00  0.30    Sequence
 HLA-DPA10201-DPB10101  280      TFLLKYNENGTITDA  LLKYNENGT  2        0.2738
2586.0    65.00  0.36    Sequence
 HLA-DPA10201-DPB10101  281      FLLKYNENGTITDAV  LLKYNENGT  1        0.2436
3583.2    75.00  0.39    Sequence
 HLA-DPA10201-DPB10101  282      LLKYNENGTITDAVD  LLKYNENGT  0        0.1848
6767.4    85.00  0.30    Sequence
```

```
 HLA-DPA10201-DPB10101  283      LKYNENGTITDAVDC  YNENGTITD  2        0.1479
10089.3    95.00  0.25     Sequence
 HLA-DPA10201-DPB10101  284      KYNENGTITDAVDCA  NENGTITDA  2        0.1137
14614.3   100.00  0.17     Sequence
 HLA-DPA10201-DPB10101  285      YNENGTITDAVDCAL  TITDAVDCA  5        0.1262
12766.4    95.00  0.24     Sequence
 HLA-DPA10201-DPB10101  286      NENGTITDAVDCALD  TITDAVDCA  4        0.1255
12856.8    95.00  0.29     Sequence
 HLA-DPA10201-DPB10101  287      ENGTITDAVDCALDP  TITDAVDCA  3        0.1270
12649.5    95.00  0.27     Sequence
 HLA-DPA10201-DPB10101  288      NGTITDAVDCALDPL  DAVDCALDP  5        0.1611
8747.8    90.00  0.33     Sequence
 HLA-DPA10201-DPB10101  289      GTITDAVDCALDPLS  DAVDCALDP  4        0.1654
8354.0    90.00  0.34     Sequence
 HLA-DPA10201-DPB10101  290      TITDAVDCALDPLSE  DAVDCALDP  3        0.1809
7064.4    90.00  0.31     Sequence
 HLA-DPA10201-DPB10101  291      ITDAVDCALDPLSET  DCALDPLSE  5        0.2023
5603.9    85.00  0.34     Sequence
 HLA-DPA10201-DPB10101  292      TDAVDCALDPLSETK  DCALDPLSE  4        0.2164
4808.0    80.00  0.35     Sequence
 HLA-DPA10201-DPB10101  293      DAVDCALDPLSETKC  DCALDPLSE  3        0.2254
4364.4    75.00  0.33     Sequence
 HLA-DPA10201-DPB10101  294      AVDCALDPLSETKCT  DCALDPLSE  2        0.2301
4145.3    75.00  0.35     Sequence
 HLA-DPA10201-DPB10101  295      VDCALDPLSETKCTL  ALDPLSETK  3        0.2359
3894.1    75.00  0.31     Sequence
 HLA-DPA10201-DPB10101  296      DCALDPLSETKCTLK  ALDPLSETK  2        0.2453
3519.8    70.00  0.28     Sequence
 HLA-DPA10201-DPB10101  297      CALDPLSETKCTLKS  PLSETKCTL  4        0.2324
4047.1    75.00  0.31     Sequence
 HLA-DPA10201-DPB10101  298      ALDPLSETKCTLKSF  PLSETKCTL  3        0.2355
3912.1    75.00  0.34     Sequence
 HLA-DPA10201-DPB10101  299      LDPLSETKCTLKSFT  PLSETKCTL  2        0.2298
4162.3    75.00  0.34     Sequence
 HLA-DPA10201-DPB10101  300      DPLSETKCTLKSFTV  KCTLKSFTV  6        0.2303
4137.8    75.00  0.17     Sequence
 HLA-DPA10201-DPB10101  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.3009
1926.9    55.00  0.26     Sequence
 HLA-DPA10201-DPB10101  302      LSETKCTLKSFTVEK  TLKSFTVEK  6        0.3864
764.2    30.00  0.46     Sequence
 HLA-DPA10201-DPB10101  303      SETKCTLKSFTVEKG  TLKSFTVEK  5        0.4136
569.6    24.00  0.54     Sequence
 HLA-DPA10201-DPB10101  304      ETKCTLKSFTVEKGI  TLKSFTVEK  4        0.4399
428.2    19.00  0.51     Sequence
 HLA-DPA10201-DPB10101  305      TKCTLKSFTVEKGIY  TLKSFTVEK  3        0.4486
390.0    17.00  0.53     Sequence
 HLA-DPA10201-DPB10101  306      KCTLKSFTVEKGIYQ  TLKSFTVEK  2        0.4493
387.0    17.00  0.51     Sequence
 HLA-DPA10201-DPB10101  307      CTLKSFTVEKGIYQT  TLKSFTVEK  1        0.4242
507.7    22.00  0.47     Sequence
 HLA-DPA10201-DPB10101  308      TLKSFTVEKGIYQTS  SFTVEKGIY  3        0.3665
948.5    35.00  0.26     Sequence
 HLA-DPA10201-DPB10101  309      LKSFTVEKGIYQTSN  SFTVEKGIY  2        0.3030
1884.9    55.00  0.35     Sequence
 HLA-DPA10201-DPB10101  310      KSFTVEKGIYQTSNF  TVEKGIYQT  3        0.2907
2152.4    60.00  0.33     Sequence
 HLA-DPA10201-DPB10101  311      SFTVEKGIYQTSNFR  TVEKGIYQT  2        0.2722
2630.8    65.00  0.33     Sequence
 HLA-DPA10201-DPB10101  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.3640
973.5    36.00  0.47     Sequence
 HLA-DPA10201-DPB10101  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.3930
711.6    29.00  0.60     Sequence
 HLA-DPA10201-DPB10101  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.3930
711.6    29.00  0.63     Sequence
 HLA-DPA10201-DPB10101  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.3932
710.1    29.00  0.63     Sequence
```

```
 HLA-DPA10201-DPB10101  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.3844
781.0    31.00   0.64    Sequence
 HLA-DPA10201-DPB10101  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.3308
1395.4    45.00  0.47     Sequence
 HLA-DPA10201-DPB10101  318      IYQTSNFRVQPTESI  NFRVQPTES  5        0.3381
1289.1    43.00  0.29     Sequence
 HLA-DPA10201-DPB10101  319      YQTSNFRVQPTESIV  NFRVQPTES  4        0.3401
1261.1    43.00  0.35     Sequence
 HLA-DPA10201-DPB10101  320      QTSNFRVQPTESIVR  NFRVQPTES  3        0.3384
1284.4    43.00  0.34     Sequence
 HLA-DPA10201-DPB10101  321      TSNFRVQPTESIVRF  NFRVQPTES  2        0.3536
1089.9    39.00  0.31     Sequence
 HLA-DPA10201-DPB10101  322      SNFRVQPTESIVRFP  NFRVQPTES  1        0.3503
1129.4    40.00  0.28     Sequence
 HLA-DPA10201-DPB10101  323      NFRVQPTESIVRFPN  RVQPTESIV  2        0.3341
1346.2    44.00  0.29     Sequence
 HLA-DPA10201-DPB10101  324      FRVQPTESIVRFPNI  TESIVRFPN  5        0.3191
1583.7    49.00  0.20     Sequence
 HLA-DPA10201-DPB10101  325      RVQPTESIVRFPNIT  TESIVRFPN  4        0.2614
2955.7    70.00  0.34     Sequence
 HLA-DPA10201-DPB10101  326      VQPTESIVRFPNITN  TESIVRFPN  3        0.2471
3448.8    70.00  0.34     Sequence
 HLA-DPA10201-DPB10101  327      QPTESIVRFPNITNL  TESIVRFPN  2        0.2617
2946.8    70.00  0.28     Sequence
 HLA-DPA10201-DPB10101  328      PTESIVRFPNITNLC  IVRFPNITN  4        0.2585
3051.3    70.00  0.27     Sequence
 HLA-DPA10201-DPB10101  329      TESIVRFPNITNLCP  IVRFPNITN  3        0.2550
3168.3    70.00  0.25     Sequence
 HLA-DPA10201-DPB10101  330      ESIVRFPNITNLCPF  FPNITNLCP  5        0.2621
2933.2    70.00  0.28     Sequence
 HLA-DPA10201-DPB10101  331      SIVRFPNITNLCPFG  FPNITNLCP  4        0.2449
3533.0    70.00  0.34     Sequence
 HLA-DPA10201-DPB10101  332      IVRFPNITNLCPFGE  FPNITNLCP  3        0.2504
3328.8    70.00  0.34     Sequence
 HLA-DPA10201-DPB10101  333      VRFPNITNLCPFGEV  ITNLCPFGE  5        0.2581
3063.0    70.00  0.35     Sequence
 HLA-DPA10201-DPB10101  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.2551
3162.5    70.00  0.42     Sequence
 HLA-DPA10201-DPB10101  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.2492
3373.2    70.00  0.41     Sequence
 HLA-DPA10201-DPB10101  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.2612
2962.8    70.00  0.31     Sequence
 HLA-DPA10201-DPB10101  337      NITNLCPFGEVFNAT  CPFGEVFNA  5        0.3059
1826.7    55.00  0.36     Sequence
 HLA-DPA10201-DPB10101  338      ITNLCPFGEVFNATR  CPFGEVFNA  4        0.3346
1338.4    44.00  0.34     Sequence
 HLA-DPA10201-DPB10101  339      TNLCPFGEVFNATRF  CPFGEVFNA  3        0.4037
633.9    26.00   0.32    Sequence
 HLA-DPA10201-DPB10101  340      NLCPFGEVFNATRFA  VFNATRFAX  7        0.4710
305.9    13.00   0.35    Sequence
 HLA-DPA10201-DPB10101  341      LCPFGEVFNATRFAS  VFNATRFAS  6        0.5977
77.7     2.00  0.62     Sequence         WB
 HLA-DPA10201-DPB10101  342      CPFGEVFNATRFASV  VFNATRFAS  5        0.7189
20.9     0.12  0.86     Sequence         SB
 HLA-DPA10201-DPB10101  343      PFGEVFNATRFASVY  VFNATRFAS  4        0.7329
18.0     0.08  0.87     Sequence         SB
 HLA-DPA10201-DPB10101  344      FGEVFNATRFASVYA  VFNATRFAS  3        0.7732
11.6     0.02  0.79     Sequence         SB
 HLA-DPA10201-DPB10101  345      GEVFNATRFASVYAW  VFNATRFAS  2        0.7478
15.3     0.05  0.79     Sequence         SB
 HLA-DPA10201-DPB10101  346      EVFNATRFASVYAWN  VFNATRFAS  1        0.7054
24.2     0.15  0.65     Sequence         SB
 HLA-DPA10201-DPB10101  347      VFNATRFASVYAWNR  VFNATRFAS  0        0.6004
75.4     1.80  0.45     Sequence         SB
 HLA-DPA10201-DPB10101  348      FNATRFASVYAWNRK  RFASVYAWN  4        0.4669
319.8    14.00   0.28    Sequence
```

```
 HLA-DPA10201-DPB10101  349      NATRFASVYAWNRKR  RFASVYAWN  3        0.3581
1038.0    38.00  0.41     Sequence
 HLA-DPA10201-DPB10101  350      ATRFASVYAWNRKRI  RFASVYAWN  2        0.3574
1045.8    38.00  0.44     Sequence
 HLA-DPA10201-DPB10101  351      TRFASVYAWNRKRIS  VYAWNRKRI  5        0.3095
1755.9    55.00  0.22     Sequence
 HLA-DPA10201-DPB10101  352      RFASVYAWNRKRISN  VYAWNRKRI  4        0.2932
2095.5    60.00  0.29     Sequence
 HLA-DPA10201-DPB10101  353      FASVYAWNRKRISNC  VYAWNRKRI  3        0.2606
2980.6    70.00  0.38     Sequence
 HLA-DPA10201-DPB10101  354      ASVYAWNRKRISNCV  VYAWNRKRI  2        0.2091
5204.8    80.00  0.46     Sequence
 HLA-DPA10201-DPB10101  355      SVYAWNRKRISNCVA  VYAWNRKRI  1        0.2390
3768.3    75.00  0.28     Sequence
 HLA-DPA10201-DPB10101  356      VYAWNRKRISNCVAD  RISNCVADX  7        0.2402
3715.9    75.00  0.19     Sequence
 HLA-DPA10201-DPB10101  357      YAWNRKRISNCVADY  RISNCVADY  6        0.2676
2763.0    65.00  0.38     Sequence
 HLA-DPA10201-DPB10101  358      AWNRKRISNCVADYS  RISNCVADY  5        0.2745
2563.8    65.00  0.43     Sequence
 HLA-DPA10201-DPB10101  359      WNRKRISNCVADYSV  RISNCVADY  4        0.2869
2242.6    60.00  0.44     Sequence
 HLA-DPA10201-DPB10101  360      NRKRISNCVADYSVL  RISNCVADY  3        0.2976
1997.0    55.00  0.35     Sequence
 HLA-DPA10201-DPB10101  361      RKRISNCVADYSVLY  RISNCVADY  2        0.3341
1345.3    44.00  0.25     Sequence
 HLA-DPA10201-DPB10101  362      KRISNCVADYSVLYN  CVADYSVLY  5        0.3526
1101.7    39.00  0.36     Sequence
 HLA-DPA10201-DPB10101  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.3467
1174.1    41.00  0.38     Sequence
 HLA-DPA10201-DPB10101  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.3433
1218.4    42.00  0.41     Sequence
 HLA-DPA10201-DPB10101  365      SNCVADYSVLYNSAS  CVADYSVLY  2        0.3433
1217.9    42.00  0.38     Sequence
 HLA-DPA10201-DPB10101  366      NCVADYSVLYNSASF  CVADYSVLY  1        0.3525
1102.6    39.00  0.32     Sequence
 HLA-DPA10201-DPB10101  367      CVADYSVLYNSASFS  ADYSVLYNS  2        0.3372
1301.1    44.00  0.18     Sequence
 HLA-DPA10201-DPB10101  368      VADYSVLYNSASFST  LYNSASFST  6        0.3648
965.2    36.00  0.39    Sequence
 HLA-DPA10201-DPB10101  369      ADYSVLYNSASFSTF  LYNSASFST  5        0.4627
334.6    14.00  0.64    Sequence
 HLA-DPA10201-DPB10101  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.4942
238.0    10.00  0.63    Sequence
 HLA-DPA10201-DPB10101  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.5172
185.6     7.00  0.61    Sequence         WB
 HLA-DPA10201-DPB10101  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.5093
202.1     8.00  0.57    Sequence         WB
 HLA-DPA10201-DPB10101  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.4725
301.1    13.00  0.47    Sequence
 HLA-DPA10201-DPB10101  374      LYNSASFSTFKCYGV  SASFSTFKC  3        0.4531
371.5    16.00  0.23    Sequence
 HLA-DPA10201-DPB10101  375      YNSASFSTFKCYGVS  SASFSTFKC  2        0.4024
643.2    26.00  0.33    Sequence
 HLA-DPA10201-DPB10101  376      NSASFSTFKCYGVSP  SFSTFKCYG  3        0.3024
1895.9    55.00  0.36     Sequence
 HLA-DPA10201-DPB10101  377      SASFSTFKCYGVSPT  SFSTFKCYG  2        0.2837
2321.0    60.00  0.47     Sequence
 HLA-DPA10201-DPB10101  378      ASFSTFKCYGVSPTK  SFSTFKCYG  1        0.2542
3196.6    70.00  0.46     Sequence
 HLA-DPA10201-DPB10101  379      SFSTFKCYGVSPTKL  KCYGVSPTK  5        0.2808
2395.5    60.00  0.25     Sequence
 HLA-DPA10201-DPB10101  380      FSTFKCYGVSPTKLN  KCYGVSPTK  4        0.2849
2292.8    60.00  0.27     Sequence
 HLA-DPA10201-DPB10101  381      STFKCYGVSPTKLND  GVSPTKLND  6        0.3023
1899.4    55.00  0.34     Sequence
```

```
 HLA-DPA10201-DPB10101  382      TFKCYGVSPTKLNDL  GVSPTKLND  5        0.3396
1268.0    43.00  0.46     Sequence
 HLA-DPA10201-DPB10101  383      FKCYGVSPTKLNDLC  GVSPTKLND  4        0.3281
1435.6    46.00  0.50     Sequence
 HLA-DPA10201-DPB10101  384      KCYGVSPTKLNDLCF  GVSPTKLND  3        0.3172
1615.5    49.00  0.52     Sequence
 HLA-DPA10201-DPB10101  385      CYGVSPTKLNDLCFT  GVSPTKLND  2        0.3088
1769.8    55.00  0.50     Sequence
 HLA-DPA10201-DPB10101  386      YGVSPTKLNDLCFTN  KLNDLCFTN  6        0.3119
1711.2    55.00  0.43     Sequence
 HLA-DPA10201-DPB10101  387      GVSPTKLNDLCFTNV  KLNDLCFTN  5        0.3667
945.5    35.00  0.70     Sequence
 HLA-DPA10201-DPB10101  388      VSPTKLNDLCFTNVY  KLNDLCFTN  4        0.3933
709.4    29.00  0.61     Sequence
 HLA-DPA10201-DPB10101  389      SPTKLNDLCFTNVYA  KLNDLCFTN  3        0.4138
568.4    24.00  0.58     Sequence
 HLA-DPA10201-DPB10101  390      PTKLNDLCFTNVYAD  KLNDLCFTN  2        0.4062
616.9    26.00  0.56     Sequence
 HLA-DPA10201-DPB10101  391      TKLNDLCFTNVYADS  KLNDLCFTN  1        0.3964
686.2    28.00  0.47     Sequence
 HLA-DPA10201-DPB10101  392      KLNDLCFTNVYADSF  CFTNVYADS  5        0.3725
888.5    34.00  0.26     Sequence
 HLA-DPA10201-DPB10101  393      LNDLCFTNVYADSFV  CFTNVYADS  4        0.3617
998.3    37.00  0.34     Sequence
 HLA-DPA10201-DPB10101  394      NDLCFTNVYADSFVI  CFTNVYADS  3        0.3875
755.2    30.00  0.31     Sequence
 HLA-DPA10201-DPB10101  395      DLCFTNVYADSFVIR  NVYADSFVI  5        0.4239
509.2    22.00  0.28     Sequence
 HLA-DPA10201-DPB10101  396      LCFTNVYADSFVIRG  VYADSFVIR  5        0.4139
567.8    24.00  0.35     Sequence
 HLA-DPA10201-DPB10101  397      CFTNVYADSFVIRGD  VYADSFVIR  4        0.3978
675.7    28.00  0.38     Sequence
 HLA-DPA10201-DPB10101  398      FTNVYADSFVIRGDE  VYADSFVIR  3        0.3786
831.4    32.00  0.44     Sequence
 HLA-DPA10201-DPB10101  399      TNVYADSFVIRGDEV  VYADSFVIR  2        0.3402
1260.7    43.00  0.47     Sequence
 HLA-DPA10201-DPB10101  400      NVYADSFVIRGDEVR  VYADSFVIR  1        0.2894
2184.0    60.00  0.26     Sequence
 HLA-DPA10201-DPB10101  401      VYADSFVIRGDEVRQ  VIRGDEVRQ  6        0.2545
3185.6    70.00  0.26     Sequence
 HLA-DPA10201-DPB10101  402      YADSFVIRGDEVRQI  VIRGDEVRQ  5        0.2607
2979.2    70.00  0.40     Sequence
 HLA-DPA10201-DPB10101  403      ADSFVIRGDEVRQIA  VIRGDEVRQ  4        0.2628
2910.7    65.00  0.43     Sequence
 HLA-DPA10201-DPB10101  404      DSFVIRGDEVRQIAP  VIRGDEVRQ  3        0.2574
3086.8    70.00  0.46     Sequence
 HLA-DPA10201-DPB10101  405      SFVIRGDEVRQIAPG  VIRGDEVRQ  2        0.2473
3442.6    70.00  0.49     Sequence
 HLA-DPA10201-DPB10101  406      FVIRGDEVRQIAPGQ  VIRGDEVRQ  1        0.2079
5273.1    80.00  0.37     Sequence
 HLA-DPA10201-DPB10101  407      VIRGDEVRQIAPGQT  VRQIAPGQT  6        0.1899
6405.0    85.00  0.23     Sequence
 HLA-DPA10201-DPB10101  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.1771
7359.8    90.00  0.34     Sequence
 HLA-DPA10201-DPB10101  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.1673
8183.0    90.00  0.43     Sequence
 HLA-DPA10201-DPB10101  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.1800
7133.1    90.00  0.42     Sequence
 HLA-DPA10201-DPB10101  411      DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.1864
6657.2    85.00  0.41     Sequence
 HLA-DPA10201-DPB10101  412      EVRQIAPGQTGTIAD  VRQIAPGQT  1        0.1851
6747.7    85.00  0.35     Sequence
 HLA-DPA10201-DPB10101  413      VRQIAPGQTGTIADY  QIAPGQTGT  2        0.1578
9070.3    90.00  0.38     Sequence
 HLA-DPA10201-DPB10101  414      RQIAPGQTGTIADYN  QIAPGQTGT  1        0.1014
16685.1   100.00  0.25     Sequence
```

```
 HLA-DPA10201-DPB10101  415      QIAPGQTGTIADYNY  PGQTGTIAD  3        0.1131
14701.3   100.00  0.23      Sequence
 HLA-DPA10201-DPB10101  416      IAPGQTGTIADYNYK  TIADYNYKX  7        0.1276
12577.1    95.00  0.31      Sequence
 HLA-DPA10201-DPB10101  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.1680
8119.2    90.00  0.43     Sequence
 HLA-DPA10201-DPB10101  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.1968
5942.7    85.00  0.44     Sequence
 HLA-DPA10201-DPB10101  419      GQTGTIADYNYKLPD  TIADYNYKL  4        0.2026
5586.7    85.00  0.43     Sequence
 HLA-DPA10201-DPB10101  420      QTGTIADYNYKLPDD  TIADYNYKL  3        0.2056
5404.9    80.00  0.44     Sequence
 HLA-DPA10201-DPB10101  421      TGTIADYNYKLPDDF  TIADYNYKL  2        0.2083
5251.0    80.00  0.38     Sequence
 HLA-DPA10201-DPB10101  422      GTIADYNYKLPDDFT  TIADYNYKL  1        0.2015
5654.0    85.00  0.25     Sequence
 HLA-DPA10201-DPB10101  423      TIADYNYKLPDDFTG  ADYNYKLPD  2        0.1862
6671.6    85.00  0.20     Sequence
 HLA-DPA10201-DPB10101  424      IADYNYKLPDDFTGC  YKLPDDFTG  5        0.1663
8270.9    90.00  0.25     Sequence
 HLA-DPA10201-DPB10101  425      ADYNYKLPDDFTGCV  YKLPDDFTG  4        0.1750
7526.9    90.00  0.29     Sequence
 HLA-DPA10201-DPB10101  426      DYNYKLPDDFTGCVI  LPDDFTGCV  5        0.2251
4378.7    80.00  0.21     Sequence
 HLA-DPA10201-DPB10101  427      YNYKLPDDFTGCVIA  DFTGCVIAX  7        0.2614
2955.4    70.00  0.23     Sequence
 HLA-DPA10201-DPB10101  428      NYKLPDDFTGCVIAW  DFTGCVIAW  6        0.2913
2139.8    60.00  0.44     Sequence
 HLA-DPA10201-DPB10101  429      YKLPDDFTGCVIAWN  DFTGCVIAW  5        0.3190
1584.0    49.00  0.56     Sequence
 HLA-DPA10201-DPB10101  430      KLPDDFTGCVIAWNS  DFTGCVIAW  4        0.3192
1582.3    49.00  0.60     Sequence
 HLA-DPA10201-DPB10101  431      LPDDFTGCVIAWNSN  DFTGCVIAW  3        0.3096
1754.0    55.00  0.63     Sequence
 HLA-DPA10201-DPB10101  432      PDDFTGCVIAWNSNN  DFTGCVIAW  2        0.3012
1920.8    55.00  0.60     Sequence
 HLA-DPA10201-DPB10101  433      DDFTGCVIAWNSNNL  DFTGCVIAW  1        0.2808
2397.3    60.00  0.42     Sequence
 HLA-DPA10201-DPB10101  434      DFTGCVIAWNSNNLD  VIAWNSNNL  5        0.2592
3028.2    70.00  0.25     Sequence
 HLA-DPA10201-DPB10101  435      FTGCVIAWNSNNLDS  VIAWNSNNL  4        0.2447
3541.1    70.00  0.29     Sequence
 HLA-DPA10201-DPB10101  436      TGCVIAWNSNNLDSK  AWNSNNLDS  5        0.2344
3957.1    75.00  0.31     Sequence
 HLA-DPA10201-DPB10101  437      GCVIAWNSNNLDSKV  AWNSNNLDS  4        0.2326
4036.1    75.00  0.32     Sequence
 HLA-DPA10201-DPB10101  438      CVIAWNSNNLDSKVG  AWNSNNLDS  3        0.2298
4161.5    75.00  0.32     Sequence
 HLA-DPA10201-DPB10101  439      VIAWNSNNLDSKVGG  AWNSNNLDS  2        0.1998
5755.6    85.00  0.44     Sequence
 HLA-DPA10201-DPB10101  440      IAWNSNNLDSKVGGN  AWNSNNLDS  1        0.1287
12424.9    95.00  0.38      Sequence
 HLA-DPA10201-DPB10101  441      AWNSNNLDSKVGGNY  AWNSNNLDS  0        0.0842
20110.6   100.00  0.25      Sequence
 HLA-DPA10201-DPB10101  442      WNSNNLDSKVGGNYN  NLDSKVGGN  4        0.0734
22608.3   100.00  0.28      Sequence
 HLA-DPA10201-DPB10101  443      NSNNLDSKVGGNYNY  NLDSKVGGN  3        0.0946
17965.4   100.00  0.22      Sequence
 HLA-DPA10201-DPB10101  444      SNNLDSKVGGNYNYL  SKVGGNYNY  5        0.2241
4423.6    80.00  0.32     Sequence
 HLA-DPA10201-DPB10101  445      NNLDSKVGGNYNYLY  SKVGGNYNY  4        0.2651
2839.8    65.00  0.28     Sequence
 HLA-DPA10201-DPB10101  446      NLDSKVGGNYNYLYR  SKVGGNYNY  3        0.2924
2112.9    60.00  0.27     Sequence
 HLA-DPA10201-DPB10101  447      LDSKVGGNYNYLYRL  GGNYNYLYR  5        0.3218
1537.9    48.00  0.14     Sequence
```

```
 HLA-DPA10201-DPB10101  448      DSKVGGNYNYLYRLF  GGNYNYLYR  4        0.3557
1065.8    38.00  0.12     Sequence
 HLA-DPA10201-DPB10101  449      SKVGGNYNYLYRLFR  NYNYLYRLF  5        0.3789
829.4    32.00  0.12    Sequence
 HLA-DPA10201-DPB10101  450      KVGGNYNYLYRLFRK  NYLYRLFRK  6        0.4046
627.8    26.00  0.29    Sequence
 HLA-DPA10201-DPB10101  451      VGGNYNYLYRLFRKS  NYLYRLFRK  5        0.4016
648.6    27.00  0.39    Sequence
 HLA-DPA10201-DPB10101  452      GGNYNYLYRLFRKSN  NYLYRLFRK  4        0.4009
653.2    27.00  0.38    Sequence
 HLA-DPA10201-DPB10101  453      GNYNYLYRLFRKSNL  NYLYRLFRK  3        0.4595
346.7    15.00  0.31    Sequence
 HLA-DPA10201-DPB10101  454      NYNYLYRLFRKSNLK  NYLYRLFRK  2        0.4816
272.8    12.00  0.31    Sequence
 HLA-DPA10201-DPB10101  455      YNYLYRLFRKSNLKP  LFRKSNLKP  6        0.4842
265.2    11.00  0.38    Sequence
 HLA-DPA10201-DPB10101  456      NYLYRLFRKSNLKPF  LFRKSNLKP  5        0.4995
224.8     9.00  0.60    Sequence         WB
 HLA-DPA10201-DPB10101  457      YLYRLFRKSNLKPFE  LFRKSNLKP  4        0.4905
247.7    11.00  0.68    Sequence
 HLA-DPA10201-DPB10101  458      LYRLFRKSNLKPFER  LFRKSNLKP  3        0.4944
237.6    10.00  0.64    Sequence
 HLA-DPA10201-DPB10101  459      YRLFRKSNLKPFERD  LFRKSNLKP  2        0.4880
254.6    11.00  0.63    Sequence
 HLA-DPA10201-DPB10101  460      RLFRKSNLKPFERDI  LFRKSNLKP  1        0.4079
605.9    25.00  0.47    Sequence
 HLA-DPA10201-DPB10101  461      LFRKSNLKPFERDIS  KSNLKPFER  3        0.3391
1275.4    43.00  0.28     Sequence
 HLA-DPA10201-DPB10101  462      FRKSNLKPFERDIST  KSNLKPFER  2        0.2746
2563.1    65.00  0.36     Sequence
 HLA-DPA10201-DPB10101  463      RKSNLKPFERDISTE  KSNLKPFER  1        0.2084
5245.5    80.00  0.32     Sequence
 HLA-DPA10201-DPB10101  464      KSNLKPFERDISTEI  PFERDISTE  5        0.2649
2846.6    65.00  0.36     Sequence
 HLA-DPA10201-DPB10101  465      SNLKPFERDISTEIY  PFERDISTE  4        0.3214
1544.8    48.00  0.28     Sequence
 HLA-DPA10201-DPB10101  466      NLKPFERDISTEIYQ  PFERDISTE  3        0.3804
815.8    32.00  0.23    Sequence
 HLA-DPA10201-DPB10101  467      LKPFERDISTEIYQA  DISTEIYQA  6        0.4318
467.8    20.00  0.41    Sequence
 HLA-DPA10201-DPB10101  468      KPFERDISTEIYQAG  DISTEIYQA  5        0.4307
473.5    20.00  0.45    Sequence
 HLA-DPA10201-DPB10101  469      PFERDISTEIYQAGS  DISTEIYQA  4        0.4227
515.9    22.00  0.52    Sequence
 HLA-DPA10201-DPB10101  470      FERDISTEIYQAGST  DISTEIYQA  3        0.4091
598.0    25.00  0.56    Sequence
 HLA-DPA10201-DPB10101  471      ERDISTEIYQAGSTP  DISTEIYQA  2        0.3519
1110.1    39.00  0.66     Sequence
 HLA-DPA10201-DPB10101  472      RDISTEIYQAGSTPC  DISTEIYQA  1        0.2969
2012.2    55.00  0.59     Sequence
 HLA-DPA10201-DPB10101  473      DISTEIYQAGSTPCN  DISTEIYQA  0        0.1867
6629.6    85.00  0.34     Sequence
 HLA-DPA10201-DPB10101  474      ISTEIYQAGSTPCNG  EIYQAGSTP  3        0.1383
11192.2    95.00  0.28     Sequence
 HLA-DPA10201-DPB10101  475      STEIYQAGSTPCNGV  EIYQAGSTP  2        0.1329
11875.9    95.00  0.34     Sequence
 HLA-DPA10201-DPB10101  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.1281
12506.5    95.00  0.22     Sequence
 HLA-DPA10201-DPB10101  477      EIYQAGSTPCNGVKG  YQAGSTPCN  2        0.1130
14717.2   100.00  0.25     Sequence
 HLA-DPA10201-DPB10101  478      IYQAGSTPCNGVKGF  QAGSTPCNG  2        0.0949
17913.6   100.00  0.25     Sequence
 HLA-DPA10201-DPB10101  479      YQAGSTPCNGVKGFN  PCNGVKGFN  6        0.0680
23968.3   100.00  0.25     Sequence
 HLA-DPA10201-DPB10101  480      QAGSTPCNGVKGFNC  PCNGVKGFN  5        0.0794
21186.5   100.00  0.53     Sequence
```

```
 HLA-DPA10201-DPB10101  481      AGSTPCNGVKGFNCY  PCNGVKGFN  4        0.0959
17716.2   100.00  0.45      Sequence
 HLA-DPA10201-DPB10101  482      GSTPCNGVKGFNCYF  PCNGVKGFN  3        0.1602
8838.9    90.00  0.28     Sequence
 HLA-DPA10201-DPB10101  483      STPCNGVKGFNCYFP  GVKGFNCYF  5        0.1774
7336.3    90.00  0.25     Sequence
 HLA-DPA10201-DPB10101  484      TPCNGVKGFNCYFPL  VKGFNCYFP  5        0.2392
3756.7    75.00  0.32     Sequence
 HLA-DPA10201-DPB10101  485      PCNGVKGFNCYFPLQ  VKGFNCYFP  4        0.2779
2472.0    65.00  0.26     Sequence
 HLA-DPA10201-DPB10101  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.3294
1416.4    46.00  0.22     Sequence
 HLA-DPA10201-DPB10101  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.3445
1202.2    41.00  0.25     Sequence
 HLA-DPA10201-DPB10101  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.3523
1105.7    39.00  0.23     Sequence
 HLA-DPA10201-DPB10101  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3        0.3805
814.6    32.00  0.22     Sequence
 HLA-DPA10201-DPB10101  490      KGFNCYFPLQSYGFQ  YFPLQSYGF  5        0.3864
764.6    30.00  0.26     Sequence
 HLA-DPA10201-DPB10101  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4        0.3618
997.1    37.00  0.29     Sequence
 HLA-DPA10201-DPB10101  492      FNCYFPLQSYGFQPT  PLQSYGFQP  5        0.3838
786.3    31.00  0.37     Sequence
 HLA-DPA10201-DPB10101  493      NCYFPLQSYGFQPTY  PLQSYGFQP  4        0.3664
948.7    35.00  0.46     Sequence
 HLA-DPA10201-DPB10101  494      CYFPLQSYGFQPTYG  PLQSYGFQP  3        0.3619
996.3    37.00  0.48     Sequence
 HLA-DPA10201-DPB10101  495      YFPLQSYGFQPTYGV  PLQSYGFQP  2        0.3373
1299.6    44.00  0.52     Sequence
 HLA-DPA10201-DPB10101  496      FPLQSYGFQPTYGVG  PLQSYGFQP  1        0.2971
2009.3    55.00  0.44     Sequence
 HLA-DPA10201-DPB10101  497      PLQSYGFQPTYGVGY  GFQPTYGVG  5        0.2569
3104.1    70.00  0.28     Sequence
 HLA-DPA10201-DPB10101  498      LQSYGFQPTYGVGYQ  GFQPTYGVG  4        0.2350
3931.2    75.00  0.38     Sequence
 HLA-DPA10201-DPB10101  499      QSYGFQPTYGVGYQP  GFQPTYGVG  3        0.2037
5515.5    85.00  0.45     Sequence
 HLA-DPA10201-DPB10101  500      SYGFQPTYGVGYQPY  GFQPTYGVG  2        0.2087
5226.8    80.00  0.39     Sequence
 HLA-DPA10201-DPB10101  501      YGFQPTYGVGYQPYR  PTYGVGYQP  4        0.2112
5088.2    80.00  0.26     Sequence
 HLA-DPA10201-DPB10101  502      GFQPTYGVGYQPYRV  PTYGVGYQP  3        0.2204
4607.3    80.00  0.22     Sequence
 HLA-DPA10201-DPB10101  503      FQPTYGVGYQPYRVV  GVGYQPYRV  5        0.2535
3219.6    70.00  0.32     Sequence
 HLA-DPA10201-DPB10101  504      QPTYGVGYQPYRVVV  GVGYQPYRV  4        0.2705
2677.4    65.00  0.34     Sequence
 HLA-DPA10201-DPB10101  505      PTYGVGYQPYRVVVL  GYQPYRVVV  5        0.3277
1441.8    46.00  0.36     Sequence
 HLA-DPA10201-DPB10101  506      TYGVGYQPYRVVVLS  GYQPYRVVV  4        0.3324
1371.4    45.00  0.38     Sequence
 HLA-DPA10201-DPB10101  507      YGVGYQPYRVVVLSF  GYQPYRVVV  3        0.3539
1086.7    39.00  0.35     Sequence
 HLA-DPA10201-DPB10101  508      GVGYQPYRVVVLSFE  PYRVVVLSF  5        0.3835
788.7    31.00  0.37     Sequence
 HLA-DPA10201-DPB10101  509      VGYQPYRVVVLSFEL  PYRVVVLSF  4        0.4506
381.6    17.00  0.25     Sequence
 HLA-DPA10201-DPB10101  510      GYQPYRVVVLSFELL  RVVVLSFEL  5        0.5251
170.4     6.50  0.44     Sequence          WB
 HLA-DPA10201-DPB10101  511      YQPYRVVVLSFELLH  RVVVLSFEL  4        0.5756
98.7      3.00  0.35     Sequence          WB
 HLA-DPA10201-DPB10101  512      QPYRVVVLSFELLHA  VVLSFELLH  5        0.6159
63.8      1.40  0.34     Sequence          SB
 HLA-DPA10201-DPB10101  513      PYRVVVLSFELLHAP  VVLSFELLH  4        0.6064
70.7      1.70  0.35     Sequence          SB
```

```
 HLA-DPA10201-DPB10101  514      YRVVVLSFELLHAPA  VVLSFELLH  3        0.6063
70.8     1.70  0.35     Sequence         SB
 HLA-DPA10201-DPB10101  515      RVVVLSFELLHAPAT  VVLSFELLH  2        0.5763
97.9     3.00  0.40     Sequence         WB
 HLA-DPA10201-DPB10101  516      VVVLSFELLHAPATV  VLSFELLHA  2        0.5239
172.7     6.50  0.35     Sequence         WB
 HLA-DPA10201-DPB10101  517      VVLSFELLHAPATVC  VLSFELLHA  1        0.4919
244.2    10.00  0.31     Sequence
 HLA-DPA10201-DPB10101  518      VLSFELLHAPATVCG  ELLHAPATV  4        0.3989
667.4    27.00  0.25     Sequence
 HLA-DPA10201-DPB10101  519      LSFELLHAPATVCGP  ELLHAPATV  3        0.2962
2028.6    60.00  0.39     Sequence
 HLA-DPA10201-DPB10101  520      SFELLHAPATVCGPK  ELLHAPATV  2        0.2791
2440.9    65.00  0.46     Sequence
 HLA-DPA10201-DPB10101  521      FELLHAPATVCGPKK  ELLHAPATV  1        0.2318
4070.8    75.00  0.41     Sequence
 HLA-DPA10201-DPB10101  522      ELLHAPATVCGPKKS  LHAPATVCG  2        0.1497
9900.1    95.00  0.24     Sequence
 HLA-DPA10201-DPB10101  523      LLHAPATVCGPKKST  XLLHAPATV -1        0.0855
19823.9   100.00  0.22     Sequence
 HLA-DPA10201-DPB10101  524      LHAPATVCGPKKSTN  APATVCGPK  2        0.0536
27999.3   100.00  0.25     Sequence
 HLA-DPA10201-DPB10101  525      HAPATVCGPKKSTNL  VCGPKKSTN  5        0.0589
26438.3   100.00  0.26     Sequence
 HLA-DPA10201-DPB10101  526      APATVCGPKKSTNLV  PKKSTNLVX  7        0.0786
21359.4   100.00  0.21     Sequence
 HLA-DPA10201-DPB10101  527      PATVCGPKKSTNLVK  PKKSTNLVK  6        0.1220
13361.2    95.00  0.38     Sequence
 HLA-DPA10201-DPB10101  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5        0.1625
8622.0    90.00  0.53     Sequence
 HLA-DPA10201-DPB10101  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4        0.1791
7202.5    90.00  0.49     Sequence
 HLA-DPA10201-DPB10101  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3        0.1821
6970.4    85.00  0.48     Sequence
 HLA-DPA10201-DPB10101  531      CGPKKSTNLVKNKCV  PKKSTNLVK  2        0.1959
6006.8    85.00  0.46     Sequence
 HLA-DPA10201-DPB10101  532      GPKKSTNLVKNKCVN  PKKSTNLVK  1        0.1976
5894.6    85.00  0.34     Sequence
 HLA-DPA10201-DPB10101  533      PKKSTNLVKNKCVNF  NLVKNKCVN  5        0.2023
5602.8    85.00  0.19     Sequence
 HLA-DPA10201-DPB10101  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.1920
6260.8    85.00  0.28     Sequence
 HLA-DPA10201-DPB10101  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.2003
5726.2    85.00  0.31     Sequence
 HLA-DPA10201-DPB10101  536      STNLVKNKCVNFNFN  LVKNKCVNF  3        0.2185
4700.8    80.00  0.26     Sequence
 HLA-DPA10201-DPB10101  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2        0.2151
4877.5    80.00  0.25     Sequence
 HLA-DPA10201-DPB10101  538      NLVKNKCVNFNFNGL  KCVNFNFNG  5        0.2663
2803.4    65.00  0.37     Sequence
 HLA-DPA10201-DPB10101  539      LVKNKCVNFNFNGLT  KCVNFNFNG  4        0.2638
2880.2    65.00  0.39     Sequence
 HLA-DPA10201-DPB10101  540      VKNKCVNFNFNGLTG  KCVNFNFNG  3        0.2468
3462.2    70.00  0.41     Sequence
 HLA-DPA10201-DPB10101  541      KNKCVNFNFNGLTGT  KCVNFNFNG  2        0.2405
3705.0    75.00  0.38     Sequence
 HLA-DPA10201-DPB10101  542      NKCVNFNFNGLTGTG  KCVNFNFNG  1        0.2144
4916.7    80.00  0.30     Sequence
 HLA-DPA10201-DPB10101  543      KCVNFNFNGLTGTGV  NFNGLTGTG  5        0.2100
5153.8    80.00  0.23     Sequence
 HLA-DPA10201-DPB10101  544      CVNFNFNGLTGTGVL  NFNGLTGTG  4        0.2196
4646.2    80.00  0.28     Sequence
 HLA-DPA10201-DPB10101  545      VNFNFNGLTGTGVLT  NFNGLTGTG  3        0.2142
4924.0    80.00  0.35     Sequence
 HLA-DPA10201-DPB10101  546      NFNFNGLTGTGVLTE  GLTGTGVLT  5        0.2553
3156.1    70.00  0.50     Sequence
```

```
 HLA-DPA10201-DPB10101  547      FNFNGLTGTGVLTES  GLTGTGVLT  4         0.2554
3155.5    70.00  0.51     Sequence
 HLA-DPA10201-DPB10101  548      NFNGLTGTGVLTESN  GLTGTGVLT  3         0.2509
3310.6    70.00  0.50     Sequence
 HLA-DPA10201-DPB10101  549      FNGLTGTGVLTESNK  GLTGTGVLT  2         0.2529
3239.9    70.00  0.49     Sequence
 HLA-DPA10201-DPB10101  550      NGLTGTGVLTESNKK  GLTGTGVLT  1         0.2184
4704.7    80.00  0.46     Sequence
 HLA-DPA10201-DPB10101  551      GLTGTGVLTESNKKF  VLTESNKKF  6         0.2288
4206.4    75.00  0.28     Sequence
 HLA-DPA10201-DPB10101  552      LTGTGVLTESNKKFL  VLTESNKKF  5         0.2595
3018.6    70.00  0.34     Sequence
 HLA-DPA10201-DPB10101  553      TGTGVLTESNKKFLP  VLTESNKKF  4         0.2659
2816.0    65.00  0.38     Sequence
 HLA-DPA10201-DPB10101  554      GTGVLTESNKKFLPF  TESNKKFLP  5         0.3100
1747.2    55.00  0.39     Sequence
 HLA-DPA10201-DPB10101  555      TGVLTESNKKFLPFQ  TESNKKFLP  4         0.3499
1134.1    40.00  0.33     Sequence
 HLA-DPA10201-DPB10101  556      GVLTESNKKFLPFQQ  NKKFLPFQQ  6         0.4305
474.3    20.00  0.29     Sequence
 HLA-DPA10201-DPB10101  557      VLTESNKKFLPFQQF  NKKFLPFQQ  5         0.5058
210.0     8.50  0.40     Sequence          WB
 HLA-DPA10201-DPB10101  558      LTESNKKFLPFQQFG  NKKFLPFQQ  4         0.5170
186.0     7.00  0.41     Sequence          WB
 HLA-DPA10201-DPB10101  559      TESNKKFLPFQQFGR  NKKFLPFQQ  3         0.5571
120.5     4.00  0.35     Sequence          WB
 HLA-DPA10201-DPB10101  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5         0.5708
104.0     3.50  0.35     Sequence          WB
 HLA-DPA10201-DPB10101  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4         0.5681
107.1     3.50  0.41     Sequence          WB
 HLA-DPA10201-DPB10101  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3         0.5566
121.3     4.00  0.41     Sequence          WB
 HLA-DPA10201-DPB10101  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2         0.5172
185.5     7.00  0.48     Sequence          WB
 HLA-DPA10201-DPB10101  564      KFLPFQQFGRDIADT  FLPFQQFGR  1         0.4454
403.5    18.00  0.43     Sequence
 HLA-DPA10201-DPB10101  565      FLPFQQFGRDIADTT  PFQQFGRDI  2         0.3454
1190.9    41.00  0.27     Sequence
 HLA-DPA10201-DPB10101  566      LPFQQFGRDIADTTD  QFGRDIADT  4         0.2536
3217.3    70.00  0.27     Sequence
 HLA-DPA10201-DPB10101  567      PFQQFGRDIADTTDA  QFGRDIADT  3         0.2325
4038.7    75.00  0.31     Sequence
 HLA-DPA10201-DPB10101  568      FQQFGRDIADTTDAV  QFGRDIADT  2         0.2044
5478.8    85.00  0.29     Sequence
 HLA-DPA10201-DPB10101  569      QQFGRDIADTTDAVR  DIADTTDAV  5         0.1509
9774.6    95.00  0.39     Sequence
 HLA-DPA10201-DPB10101  570      QFGRDIADTTDAVRD  DIADTTDAV  4         0.1436
10574.2    95.00  0.49     Sequence
 HLA-DPA10201-DPB10101  571      FGRDIADTTDAVRDP  DIADTTDAV  3         0.1356
11523.7    95.00  0.50     Sequence
 HLA-DPA10201-DPB10101  572      GRDIADTTDAVRDPQ  DIADTTDAV  2         0.1090
15372.5   100.00  0.59     Sequence
 HLA-DPA10201-DPB10101  573      RDIADTTDAVRDPQT  DIADTTDAV  1         0.1040
16228.6   100.00  0.49     Sequence
 HLA-DPA10201-DPB10101  574      DIADTTDAVRDPQTL  DIADTTDAV  0         0.0793
21195.7   100.00  0.34     Sequence
 HLA-DPA10201-DPB10101  575      IADTTDAVRDPQTLE  AVRDPQTLE  6         0.0762
21932.2   100.00  0.28     Sequence
 HLA-DPA10201-DPB10101  576      ADTTDAVRDPQTLEI  AVRDPQTLE  5         0.1331
11840.1    95.00  0.34     Sequence
 HLA-DPA10201-DPB10101  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5         0.2779
2472.0    65.00  0.35     Sequence
 HLA-DPA10201-DPB10101  578      TTDAVRDPQTLEILD  DPQTLEILD  6         0.3284
1431.1    46.00  0.37     Sequence
 HLA-DPA10201-DPB10101  579      TDAVRDPQTLEILDI  DPQTLEILD  5         0.4276
489.6    21.00  0.46     Sequence
```

```
 HLA-DPA10201-DPB10101  580      DAVRDPQTLEILDIT  DPQTLEILD  4        0.4457
402.5    18.00  0.44     Sequence
 HLA-DPA10201-DPB10101  581      AVRDPQTLEILDITP  DPQTLEILD  3        0.5089
203.1     8.00  0.41     Sequence         WB
 HLA-DPA10201-DPB10101  582      VRDPQTLEILDITPC  DPQTLEILD  2        0.5011
220.9     9.00  0.40     Sequence         WB
 HLA-DPA10201-DPB10101  583      RDPQTLEILDITPCS  DPQTLEILD  1        0.4847
263.8    11.00  0.34     Sequence
 HLA-DPA10201-DPB10101  584      DPQTLEILDITPCSF  TLEILDITP  3        0.4527
373.2    16.00  0.36     Sequence
 HLA-DPA10201-DPB10101  585      PQTLEILDITPCSFG  TLEILDITP  2        0.4423
417.4    18.00  0.37     Sequence
 HLA-DPA10201-DPB10101  586      QTLEILDITPCSFGG  TLEILDITP  1        0.3906
730.7    29.00  0.37     Sequence
 HLA-DPA10201-DPB10101  587      TLEILDITPCSFGGV  ILDITPCSF  3        0.3802
817.3    32.00  0.34     Sequence
 HLA-DPA10201-DPB10101  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.3112
1723.7    55.00  0.43     Sequence
 HLA-DPA10201-DPB10101  589      EILDITPCSFGGVSV  DITPCSFGG  3        0.2794
2431.8    65.00  0.46     Sequence
 HLA-DPA10201-DPB10101  590      ILDITPCSFGGVSVI  DITPCSFGG  2        0.2831
2336.6    60.00  0.40     Sequence
 HLA-DPA10201-DPB10101  591      LDITPCSFGGVSVIT  SFGGVSVIT  6        0.2749
2553.7    65.00  0.39     Sequence
 HLA-DPA10201-DPB10101  592      DITPCSFGGVSVITP  SFGGVSVIT  5        0.2735
2592.1    65.00  0.49     Sequence
 HLA-DPA10201-DPB10101  593      ITPCSFGGVSVITPG  SFGGVSVIT  4        0.2650
2842.0    65.00  0.47     Sequence
 HLA-DPA10201-DPB10101  594      TPCSFGGVSVITPGT  SFGGVSVIT  3        0.2569
3104.0    70.00  0.52     Sequence
 HLA-DPA10201-DPB10101  595      PCSFGGVSVITPGTN  SFGGVSVIT  2        0.2559
3136.0    70.00  0.52     Sequence
 HLA-DPA10201-DPB10101  596      CSFGGVSVITPGTNT  SFGGVSVIT  1        0.2366
3864.3    75.00  0.47     Sequence
 HLA-DPA10201-DPB10101  597      SFGGVSVITPGTNTS  SFGGVSVIT  0        0.1504
9826.0    95.00  0.31     Sequence
 HLA-DPA10201-DPB10101  598      FGGVSVITPGTNTSN  GVSVITPGT  2        0.1135
14648.6   100.00  0.28     Sequence
 HLA-DPA10201-DPB10101  599      GGVSVITPGTNTSNQ  VITPGTNTS  4        0.0864
19643.1   100.00  0.28     Sequence
 HLA-DPA10201-DPB10101  600      GVSVITPGTNTSNQV  VITPGTNTS  3        0.0905
18785.0   100.00  0.30     Sequence
 HLA-DPA10201-DPB10101  601      VSVITPGTNTSNQVA  VITPGTNTS  2        0.0870
19513.6   100.00  0.32     Sequence
 HLA-DPA10201-DPB10101  602      SVITPGTNTSNQVAV  VITPGTNTS  1        0.0709
23213.1   100.00  0.22     Sequence
 HLA-DPA10201-DPB10101  603      VITPGTNTSNQVAVL  TNTSNQVAV  5        0.1317
12020.4    95.00  0.28     Sequence
 HLA-DPA10201-DPB10101  604      ITPGTNTSNQVAVLY  TNTSNQVAV  4        0.1569
9154.1    90.00  0.31     Sequence
 HLA-DPA10201-DPB10101  605      TPGTNTSNQVAVLYQ  SNQVAVLYQ  6        0.2333
4006.0    75.00  0.31     Sequence
 HLA-DPA10201-DPB10101  606      PGTNTSNQVAVLYQG  SNQVAVLYQ  5        0.2268
4299.2    75.00  0.31     Sequence
 HLA-DPA10201-DPB10101  607      GTNTSNQVAVLYQGV  SNQVAVLYQ  4        0.2626
2918.8    65.00  0.28     Sequence
 HLA-DPA10201-DPB10101  608      TNTSNQVAVLYQGVN  QVAVLYQGV  5        0.2683
2743.4    65.00  0.22     Sequence
 HLA-DPA10201-DPB10101  609      NTSNQVAVLYQGVNC  QVAVLYQGV  4        0.2695
2706.5    65.00  0.19     Sequence
 HLA-DPA10201-DPB10101  610      TSNQVAVLYQGVNCT  QVAVLYQGV  3        0.2625
2921.7    65.00  0.20     Sequence
 HLA-DPA10201-DPB10101  611      SNQVAVLYQGVNCTE  LYQGVNCTE  6        0.2871
2237.2    60.00  0.21     Sequence
 HLA-DPA10201-DPB10101  612      NQVAVLYQGVNCTEV  LYQGVNCTE  5        0.2747
2559.9    65.00  0.40     Sequence
```

```
 HLA-DPA10201-DPB10101  613      QVAVLYQGVNCTEVP  LYQGVNCTE  4        0.2717
2645.2    65.00  0.39     Sequence
 HLA-DPA10201-DPB10101  614      VAVLYQGVNCTEVPV  LYQGVNCTE  3        0.2652
2835.6    65.00  0.41     Sequence
 HLA-DPA10201-DPB10101  615      AVLYQGVNCTEVPVA  LYQGVNCTE  2        0.2577
3075.6    70.00  0.46     Sequence
 HLA-DPA10201-DPB10101  616      VLYQGVNCTEVPVAI  LYQGVNCTE  1        0.2294
4176.9    75.00  0.34     Sequence
 HLA-DPA10201-DPB10101  617      LYQGVNCTEVPVAIH  NCTEVPVAI  5        0.2080
5267.7    80.00  0.20     Sequence
 HLA-DPA10201-DPB10101  618      YQGVNCTEVPVAIHA  NCTEVPVAI  4        0.1720
7777.9    90.00  0.31     Sequence
 HLA-DPA10201-DPB10101  619      QGVNCTEVPVAIHAD  TEVPVAIHA  5        0.1960
5998.7    85.00  0.21     Sequence
 HLA-DPA10201-DPB10101  620      GVNCTEVPVAIHADQ  EVPVAIHAD  5        0.2071
5317.0    80.00  0.28     Sequence
 HLA-DPA10201-DPB10101  621      VNCTEVPVAIHADQL  EVPVAIHAD  4        0.2304
4131.9    75.00  0.28     Sequence
 HLA-DPA10201-DPB10101  622      NCTEVPVAIHADQLT  EVPVAIHAD  3        0.2495
3362.9    70.00  0.26     Sequence
 HLA-DPA10201-DPB10101  623      CTEVPVAIHADQLTP  AIHADQLTP  6        0.2721
2633.3    65.00  0.29     Sequence
 HLA-DPA10201-DPB10101  624      TEVPVAIHADQLTPT  AIHADQLTP  5        0.2816
2376.2    60.00  0.47     Sequence
 HLA-DPA10201-DPB10101  625      EVPVAIHADQLTPTW  AIHADQLTP  4        0.2858
2270.4    60.00  0.56     Sequence
 HLA-DPA10201-DPB10101  626      VPVAIHADQLTPTWR  AIHADQLTP  3        0.2977
1996.2    55.00  0.63     Sequence
 HLA-DPA10201-DPB10101  627      PVAIHADQLTPTWRV  AIHADQLTP  2        0.2949
2057.8    60.00  0.57     Sequence
 HLA-DPA10201-DPB10101  628      VAIHADQLTPTWRVY  AIHADQLTP  1        0.2819
2367.6    60.00  0.43     Sequence
 HLA-DPA10201-DPB10101  629      AIHADQLTPTWRVYS  QLTPTWRVY  5        0.2502
3337.3    70.00  0.26     Sequence
 HLA-DPA10201-DPB10101  630      IHADQLTPTWRVYST  QLTPTWRVY  4        0.2208
4586.9    80.00  0.31     Sequence
 HLA-DPA10201-DPB10101  631      HADQLTPTWRVYSTG  QLTPTWRVY  3        0.1886
6497.8    85.00  0.34     Sequence
 HLA-DPA10201-DPB10101  632      ADQLTPTWRVYSTGS  QLTPTWRVY  2        0.1770
7366.2    90.00  0.35     Sequence
 HLA-DPA10201-DPB10101  633      DQLTPTWRVYSTGSN  QLTPTWRVY  1        0.1535
9501.5    95.00  0.20     Sequence
 HLA-DPA10201-DPB10101  634      QLTPTWRVYSTGSNV  WRVYSTGSN  5        0.1758
7466.7    90.00  0.20     Sequence
 HLA-DPA10201-DPB10101  635      LTPTWRVYSTGSNVF  RVYSTGSNV  5        0.2240
4430.4    80.00  0.31     Sequence
 HLA-DPA10201-DPB10101  636      TPTWRVYSTGSNVFQ  RVYSTGSNV  4        0.2611
2964.8    70.00  0.27     Sequence
 HLA-DPA10201-DPB10101  637      PTWRVYSTGSNVFQT  RVYSTGSNV  3        0.2812
2386.6    60.00  0.23     Sequence
 HLA-DPA10201-DPB10101  638      TWRVYSTGSNVFQTR  YSTGSNVFQ  4        0.2887
2200.4    60.00  0.23     Sequence
 HLA-DPA10201-DPB10101  639      WRVYSTGSNVFQTRA  YSTGSNVFQ  3        0.2853
2281.5    60.00  0.24     Sequence
 HLA-DPA10201-DPB10101  640      RVYSTGSNVFQTRAG  YSTGSNVFQ  2        0.2650
2842.3    65.00  0.27     Sequence
 HLA-DPA10201-DPB10101  641      VYSTGSNVFQTRAGC  STGSNVFQT  2        0.2180
4726.3    80.00  0.27     Sequence
 HLA-DPA10201-DPB10101  642      YSTGSNVFQTRAGCL  NVFQTRAGC  5        0.1970
5929.8    85.00  0.25     Sequence
 HLA-DPA10201-DPB10101  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.2350
3931.1    75.00  0.31     Sequence
 HLA-DPA10201-DPB10101  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.2534
3224.6    70.00  0.34     Sequence
 HLA-DPA10201-DPB10101  645      GSNVFQTRAGCLIGA  VFQTRAGCL  3        0.2709
2667.8    65.00  0.31     Sequence
```

```
 HLA-DPA10201-DPB10101  646      SNVFQTRAGCLIGAE  TRAGCLIGA  5        0.3008
1930.6    55.00  0.35     Sequence
 HLA-DPA10201-DPB10101  647      NVFQTRAGCLIGAEY  TRAGCLIGA  4        0.3107
1734.0    55.00  0.38     Sequence
 HLA-DPA10201-DPB10101  648      VFQTRAGCLIGAEYV  TRAGCLIGA  3        0.3320
1377.1    45.00  0.35     Sequence
 HLA-DPA10201-DPB10101  649      FQTRAGCLIGAEYVN  TRAGCLIGA  2        0.3625
990.3    37.00  0.31     Sequence
 HLA-DPA10201-DPB10101  650      QTRAGCLIGAEYVNN  CLIGAEYVN  5        0.3615
1000.9    37.00  0.38     Sequence
 HLA-DPA10201-DPB10101  651      TRAGCLIGAEYVNNS  CLIGAEYVN  4        0.3659
954.5    36.00  0.38     Sequence
 HLA-DPA10201-DPB10101  652      RAGCLIGAEYVNNSY  CLIGAEYVN  3        0.3764
851.5    33.00  0.37     Sequence
 HLA-DPA10201-DPB10101  653      AGCLIGAEYVNNSYE  CLIGAEYVN  2        0.3564
1057.2    38.00  0.41     Sequence
 HLA-DPA10201-DPB10101  654      GCLIGAEYVNNSYEC  LIGAEYVNN  2        0.3322
1373.3    45.00  0.34     Sequence
 HLA-DPA10201-DPB10101  655      CLIGAEYVNNSYECD  LIGAEYVNN  1        0.3118
1714.1    55.00  0.28     Sequence
 HLA-DPA10201-DPB10101  656      LIGAEYVNNSYECDI  EYVNNSYEC  4        0.2551
3165.8    70.00  0.41     Sequence
 HLA-DPA10201-DPB10101  657      IGAEYVNNSYECDIP  EYVNNSYEC  3        0.2243
4414.9    80.00  0.50     Sequence
 HLA-DPA10201-DPB10101  658      GAEYVNNSYECDIPI  EYVNNSYEC  2        0.2241
4424.2    80.00  0.49     Sequence
 HLA-DPA10201-DPB10101  659      AEYVNNSYECDIPIG  EYVNNSYEC  1        0.2069
5328.4    80.00  0.38     Sequence
 HLA-DPA10201-DPB10101  660      EYVNNSYECDIPIGA  YVNNSYECD  1        0.1843
6807.6    85.00  0.22     Sequence
 HLA-DPA10201-DPB10101  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.1489
9981.0    95.00  0.18     Sequence
 HLA-DPA10201-DPB10101  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.1201
13634.2   100.00  0.28     Sequence
 HLA-DPA10201-DPB10101  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.1150
14403.4   100.00  0.26     Sequence
 HLA-DPA10201-DPB10101  664      NSYECDIPIGAGICA  YECDIPIGA  2        0.1271
12636.9    95.00  0.23     Sequence
 HLA-DPA10201-DPB10101  665      SYECDIPIGAGICAS  PIGAGICAS  6        0.1435
10584.0    95.00  0.22     Sequence
 HLA-DPA10201-DPB10101  666      YECDIPIGAGICASY  PIGAGICAS  5        0.1468
10210.2    95.00  0.26     Sequence
 HLA-DPA10201-DPB10101  667      ECDIPIGAGICASYQ  PIGAGICAS  4        0.1420
10755.4    95.00  0.30     Sequence
 HLA-DPA10201-DPB10101  668      CDIPIGAGICASYQT  PIGAGICAS  3        0.1425
10702.9    95.00  0.28     Sequence
 HLA-DPA10201-DPB10101  669      DIPIGAGICASYQTQ  PIGAGICAS  2        0.1397
11031.9    95.00  0.26     Sequence
 HLA-DPA10201-DPB10101  670      IPIGAGICASYQTQT  ICASYQTQT  6        0.1459
10312.2    95.00  0.23     Sequence
 HLA-DPA10201-DPB10101  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.1678
8134.4    90.00  0.41     Sequence
 HLA-DPA10201-DPB10101  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.1618
8684.7    90.00  0.44     Sequence
 HLA-DPA10201-DPB10101  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.1621
8651.5    90.00  0.42     Sequence
 HLA-DPA10201-DPB10101  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.1708
7873.3    90.00  0.39     Sequence
 HLA-DPA10201-DPB10101  675      GICASYQTQTNSPRR  ICASYQTQT  1        0.1605
8808.2    90.00  0.31     Sequence
 HLA-DPA10201-DPB10101  676      ICASYQTQTNSPRRA  SYQTQTNSP  3        0.1430
10637.0    95.00  0.28     Sequence
 HLA-DPA10201-DPB10101  677      CASYQTQTNSPRRAR  SYQTQTNSP  2        0.1195
13728.0   100.00  0.35     Sequence
 HLA-DPA10201-DPB10101  678      ASYQTQTNSPRRARS  SYQTQTNSP  1        0.0893
19022.7   100.00  0.31     Sequence
```

```
 HLA-DPA10201-DPB10101  679      SYQTQTNSPRRARSV  SYQTQTNSP  0        0.0808
20851.3   100.00  0.21      Sequence
 HLA-DPA10201-DPB10101  680      YQTQTNSPRRARSVA  TQTNSPRRA  2        0.0690
23691.7   100.00  0.25      Sequence
 HLA-DPA10201-DPB10101  681      QTQTNSPRRARSVAS  QTNSPRRAR  2        0.0505
28963.1   100.00  0.20      Sequence
 HLA-DPA10201-DPB10101  682      TQTNSPRRARSVASQ  SPRRARSVA  4        0.0580
26685.5   100.00  0.15      Sequence
 HLA-DPA10201-DPB10101  683      QTNSPRRARSVASQS  RRARSVASQ  5        0.0731
22664.6   100.00  0.23      Sequence
 HLA-DPA10201-DPB10101  684      TNSPRRARSVASQSI  RARSVASQS  5        0.1311
12108.0    95.00  0.35     Sequence
 HLA-DPA10201-DPB10101  685      NSPRRARSVASQSII  SVASQSIIX  7        0.2056
5407.5    80.00  0.28     Sequence
 HLA-DPA10201-DPB10101  686      SPRRARSVASQSIIA  SVASQSIIA  6        0.2360
3890.0    75.00  0.33     Sequence
 HLA-DPA10201-DPB10101  687      PRRARSVASQSIIAY  SVASQSIIA  5        0.2868
2244.5    60.00  0.34     Sequence
 HLA-DPA10201-DPB10101  688      RRARSVASQSIIAYT  SVASQSIIA  4        0.3098
1750.0    55.00  0.32     Sequence
 HLA-DPA10201-DPB10101  689      RARSVASQSIIAYTM  SVASQSIIA  3        0.3338
1349.9    45.00  0.29     Sequence
 HLA-DPA10201-DPB10101  690      ARSVASQSIIAYTMS  VASQSIIAY  3        0.3457
1186.9    41.00  0.27     Sequence
 HLA-DPA10201-DPB10101  691      RSVASQSIIAYTMSL  VASQSIIAY  2        0.3511
1119.9    40.00  0.24     Sequence
 HLA-DPA10201-DPB10101  692      SVASQSIIAYTMSLG  SIIAYTMSL  5        0.3249
1486.6    47.00  0.26     Sequence
 HLA-DPA10201-DPB10101  693      VASQSIIAYTMSLGA  SIIAYTMSL  4        0.3164
1630.8    50.00  0.30     Sequence
 HLA-DPA10201-DPB10101  694      ASQSIIAYTMSLGAE  SIIAYTMSL  3        0.3162
1633.6    50.00  0.28     Sequence
 HLA-DPA10201-DPB10101  695      SQSIIAYTMSLGAEN  SIIAYTMSL  2        0.3270
1452.9    46.00  0.22     Sequence
 HLA-DPA10201-DPB10101  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.3140
1673.3    50.00  0.25     Sequence
 HLA-DPA10201-DPB10101  697      SIIAYTMSLGAENSV  IAYTMSLGA  2        0.3033
1879.1    55.00  0.29     Sequence
 HLA-DPA10201-DPB10101  698      IIAYTMSLGAENSVA  AYTMSLGAE  2        0.2619
2940.0    70.00  0.33     Sequence
 HLA-DPA10201-DPB10101  699      IAYTMSLGAENSVAY  AYTMSLGAE  1        0.2441
3565.0    75.00  0.32     Sequence
 HLA-DPA10201-DPB10101  700      AYTMSLGAENSVAYS  SLGAENSVA  4        0.2186
4696.8    80.00  0.18     Sequence
 HLA-DPA10201-DPB10101  701      YTMSLGAENSVAYSN  SLGAENSVA  3        0.1760
7443.6    90.00  0.23     Sequence
 HLA-DPA10201-DPB10101  702      TMSLGAENSVAYSNN  SLGAENSVA  2        0.1525
9607.0    95.00  0.27     Sequence
 HLA-DPA10201-DPB10101  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.1445
10468.3    95.00  0.26     Sequence
 HLA-DPA10201-DPB10101  704      SLGAENSVAYSNNSI  SVAYSNNSI  6        0.1333
11824.3    95.00  0.29     Sequence
 HLA-DPA10201-DPB10101  705      LGAENSVAYSNNSIA  SVAYSNNSI  5        0.1542
9430.1    95.00  0.34     Sequence
 HLA-DPA10201-DPB10101  706      GAENSVAYSNNSIAI  AYSNNSIAI  6        0.1994
5779.6    85.00  0.36     Sequence
 HLA-DPA10201-DPB10101  707      AENSVAYSNNSIAIP  AYSNNSIAI  5        0.2171
4775.8    80.00  0.41     Sequence
 HLA-DPA10201-DPB10101  708      ENSVAYSNNSIAIPT  AYSNNSIAI  4        0.2280
4244.2    75.00  0.43     Sequence
 HLA-DPA10201-DPB10101  709      NSVAYSNNSIAIPTN  AYSNNSIAI  3        0.2234
4457.5    80.00  0.47     Sequence
 HLA-DPA10201-DPB10101  710      SVAYSNNSIAIPTNF  AYSNNSIAI  2        0.2247
4397.2    80.00  0.47     Sequence
 HLA-DPA10201-DPB10101  711      VAYSNNSIAIPTNFT  AYSNNSIAI  1        0.2091
5204.9    80.00  0.34     Sequence
```

```
 HLA-DPA10201-DPB10101  712      AYSNNSIAIPTNFTI  SIAIPTNFT  5        0.1964
5970.3    85.00  0.18     Sequence
 HLA-DPA10201-DPB10101  713      YSNNSIAIPTNFTIS  IAIPTNFTI  5        0.1857
6706.2    85.00  0.34     Sequence
 HLA-DPA10201-DPB10101  714      SNNSIAIPTNFTISV  IAIPTNFTI  4        0.2082
5255.9    80.00  0.29     Sequence
 HLA-DPA10201-DPB10101  715      NNSIAIPTNFTISVT  IPTNFTISV  5        0.2500
3342.5    70.00  0.22     Sequence
 HLA-DPA10201-DPB10101  716      NSIAIPTNFTISVTT  IPTNFTISV  4        0.2579
3070.3    70.00  0.22     Sequence
 HLA-DPA10201-DPB10101  717      SIAIPTNFTISVTTE  IPTNFTISV  3        0.2882
2210.5    60.00  0.17     Sequence
 HLA-DPA10201-DPB10101  718      IAIPTNFTISVTTEI  NFTISVTTE  5        0.3442
1207.0    42.00  0.35     Sequence
 HLA-DPA10201-DPB10101  719      AIPTNFTISVTTEIL  NFTISVTTE  4        0.4032
637.0    26.00  0.31     Sequence
 HLA-DPA10201-DPB10101  720      IPTNFTISVTTEILP  NFTISVTTE  3        0.4019
646.1    27.00  0.29     Sequence
 HLA-DPA10201-DPB10101  721      PTNFTISVTTEILPV  ISVTTEILP  5        0.4513
378.7    16.00  0.28     Sequence
 HLA-DPA10201-DPB10101  722      TNFTISVTTEILPVS  ISVTTEILP  4        0.4525
373.7    16.00  0.31     Sequence
 HLA-DPA10201-DPB10101  723      NFTISVTTEILPVSM  ISVTTEILP  3        0.4781
283.3    12.00  0.31     Sequence
 HLA-DPA10201-DPB10101  724      FTISVTTEILPVSMT  ISVTTEILP  2        0.4548
364.6    16.00  0.37     Sequence
 HLA-DPA10201-DPB10101  725      TISVTTEILPVSMTK  EILPVSMTK  6        0.4636
331.6    14.00  0.25     Sequence
 HLA-DPA10201-DPB10101  726      ISVTTEILPVSMTKT  EILPVSMTK  5        0.4716
304.0    13.00  0.44     Sequence
 HLA-DPA10201-DPB10101  727      SVTTEILPVSMTKTS  EILPVSMTK  4        0.4492
387.3    17.00  0.51     Sequence
 HLA-DPA10201-DPB10101  728      VTTEILPVSMTKTSV  EILPVSMTK  3        0.4334
459.7    20.00  0.60     Sequence
 HLA-DPA10201-DPB10101  729      TTEILPVSMTKTSVD  EILPVSMTK  2        0.4038
633.2    26.00  0.60     Sequence
 HLA-DPA10201-DPB10101  730      TEILPVSMTKTSVDC  EILPVSMTK  1        0.3588
1030.2    38.00  0.47     Sequence
 HLA-DPA10201-DPB10101  731      EILPVSMTKTSVDCT  EILPVSMTK  0        0.3227
1522.1    48.00  0.40     Sequence
 HLA-DPA10201-DPB10101  732      ILPVSMTKTSVDCTM  PVSMTKTSV  2        0.2187
4693.1    80.00  0.25     Sequence
 HLA-DPA10201-DPB10101  733      LPVSMTKTSVDCTMY  SMTKTSVDC  3        0.1567
9177.0    90.00  0.23     Sequence
 HLA-DPA10201-DPB10101  734      PVSMTKTSVDCTMYI  SMTKTSVDC  2        0.1706
7890.9    90.00  0.17     Sequence
 HLA-DPA10201-DPB10101  735      VSMTKTSVDCTMYIC  TSVDCTMYI  5        0.1982
5858.3    85.00  0.31     Sequence
 HLA-DPA10201-DPB10101  736      SMTKTSVDCTMYICG  TSVDCTMYI  4        0.1875
6576.3    85.00  0.34     Sequence
 HLA-DPA10201-DPB10101  737      MTKTSVDCTMYICGD  TSVDCTMYI  3        0.1854
6724.4    85.00  0.34     Sequence
 HLA-DPA10201-DPB10101  738      TKTSVDCTMYICGDS  SVDCTMYIC  3        0.1780
7289.2    90.00  0.34     Sequence
 HLA-DPA10201-DPB10101  739      KTSVDCTMYICGDST  SVDCTMYIC  2        0.1665
8250.2    90.00  0.35     Sequence
 HLA-DPA10201-DPB10101  740      TSVDCTMYICGDSTE  SVDCTMYIC  1        0.1493
9936.8    95.00  0.25     Sequence
 HLA-DPA10201-DPB10101  741      SVDCTMYICGDSTEC  TMYICGDST  4        0.1319
12003.1    95.00  0.14     Sequence
 HLA-DPA10201-DPB10101  742      VDCTMYICGDSTECS  YICGDSTEC  5        0.1121
14872.4   100.00  0.23     Sequence
 HLA-DPA10201-DPB10101  743      DCTMYICGDSTECSN  YICGDSTEC  4        0.1174
14042.9   100.00  0.25     Sequence
 HLA-DPA10201-DPB10101  744      CTMYICGDSTECSNL  YICGDSTEC  3        0.1248
12960.3    95.00  0.25     Sequence
```

```
 HLA-DPA10201-DPB10101  745       TMYICGDSTECSNLL  YICGDSTEC  2         0.1333
11813.2    95.00  0.20      Sequence
 HLA-DPA10201-DPB10101  746       MYICGDSTECSNLLL  DSTECSNLL  5         0.1932
6183.4    85.00  0.20     Sequence
 HLA-DPA10201-DPB10101  747       YICGDSTECSNLLLQ  ECSNLLLQX  7         0.2252
4370.9    80.00  0.29     Sequence
 HLA-DPA10201-DPB10101  748       ICGDSTECSNLLLQY  ECSNLLLQY  6         0.2713
2656.4    65.00  0.46     Sequence
 HLA-DPA10201-DPB10101  749       CGDSTECSNLLLQYG  ECSNLLLQY  5         0.2871
2237.5    60.00  0.52     Sequence
 HLA-DPA10201-DPB10101  750       GDSTECSNLLLQYGS  ECSNLLLQY  4         0.2921
2121.5    60.00  0.47     Sequence
 HLA-DPA10201-DPB10101  751       DSTECSNLLLQYGSF  ECSNLLLQY  3         0.3263
1464.7    47.00  0.37     Sequence
 HLA-DPA10201-DPB10101  752       STECSNLLLQYGSFC  ECSNLLLQY  2         0.3401
1262.0    43.00  0.32     Sequence
 HLA-DPA10201-DPB10101  753       TECSNLLLQYGSFCT  LLQYGSFCT  6         0.3754
860.8    33.00  0.40    Sequence
 HLA-DPA10201-DPB10101  754       ECSNLLLQYGSFCTQ  LLQYGSFCT  5         0.4141
566.4    24.00  0.55    Sequence
 HLA-DPA10201-DPB10101  755       CSNLLLQYGSFCTQL  LLQYGSFCT  4         0.4369
442.6    19.00  0.56    Sequence
 HLA-DPA10201-DPB10101  756       SNLLLQYGSFCTQLN  LLQYGSFCT  3         0.4631
333.4    14.00  0.53    Sequence
 HLA-DPA10201-DPB10101  757       NLLLQYGSFCTQLNR  LLQYGSFCT  2         0.4638
330.8    14.00  0.54    Sequence
 HLA-DPA10201-DPB10101  758       LLLQYGSFCTQLNRA  LLQYGSFCT  1         0.4468
397.4    17.00  0.49    Sequence
 HLA-DPA10201-DPB10101  759       LLQYGSFCTQLNRAL  LLQYGSFCT  0         0.4068
613.2    25.00  0.29    Sequence
 HLA-DPA10201-DPB10101  760       LQYGSFCTQLNRALT  SFCTQLNRA  4         0.3587
1032.0    38.00  0.22     Sequence
 HLA-DPA10201-DPB10101  761       QYGSFCTQLNRALTG  SFCTQLNRA  3         0.3300
1406.4    46.00  0.25     Sequence
 HLA-DPA10201-DPB10101  762       YGSFCTQLNRALTGI  SFCTQLNRA  2         0.3223
1529.0    48.00  0.28     Sequence
 HLA-DPA10201-DPB10101  763       GSFCTQLNRALTGIA  FCTQLNRAL  2         0.2904
2160.1    60.00  0.20     Sequence
 HLA-DPA10201-DPB10101  764       SFCTQLNRALTGIAV  CTQLNRALT  2         0.2807
2398.5    60.00  0.25     Sequence
 HLA-DPA10201-DPB10101  765       FCTQLNRALTGIAVE  ALTGIAVEX  7         0.3027
1890.6    55.00  0.23     Sequence
 HLA-DPA10201-DPB10101  766       CTQLNRALTGIAVEQ  ALTGIAVEQ  6         0.3081
1783.7    55.00  0.37     Sequence
 HLA-DPA10201-DPB10101  767       TQLNRALTGIAVEQD  ALTGIAVEQ  5         0.3301
1405.7    46.00  0.59     Sequence
 HLA-DPA10201-DPB10101  768       QLNRALTGIAVEQDK  ALTGIAVEQ  4         0.3437
1213.7    42.00  0.61     Sequence
 HLA-DPA10201-DPB10101  769       LNRALTGIAVEQDKN  ALTGIAVEQ  3         0.3366
1310.5    44.00  0.61     Sequence
 HLA-DPA10201-DPB10101  770       NRALTGIAVEQDKNT  ALTGIAVEQ  2         0.3237
1506.6    47.00  0.60     Sequence
 HLA-DPA10201-DPB10101  771       RALTGIAVEQDKNTQ  ALTGIAVEQ  1         0.3064
1817.2    55.00  0.54     Sequence
 HLA-DPA10201-DPB10101  772       ALTGIAVEQDKNTQE  ALTGIAVEQ  0         0.2189
4683.6    80.00  0.36     Sequence
 HLA-DPA10201-DPB10101  773       LTGIAVEQDKNTQEV  GIAVEQDKN  2         0.1540
9452.8    95.00  0.35     Sequence
 HLA-DPA10201-DPB10101  774       TGIAVEQDKNTQEVF  GIAVEQDKN  1         0.1323
11953.8    95.00  0.22      Sequence
 HLA-DPA10201-DPB10101  775       GIAVEQDKNTQEVFA  KNTQEVFAX  7         0.1373
11318.1    95.00  0.17      Sequence
 HLA-DPA10201-DPB10101  776       IAVEQDKNTQEVFAQ  KNTQEVFAQ  6         0.1670
8210.0    90.00  0.32     Sequence
 HLA-DPA10201-DPB10101  777       AVEQDKNTQEVFAQV  KNTQEVFAQ  5         0.2402
3718.2    75.00  0.45     Sequence
```

```
 HLA-DPA10201-DPB10101  778      VEQDKNTQEVFAQVK  KNTQEVFAQ  4        0.2754
2539.5    65.00  0.38     Sequence
 HLA-DPA10201-DPB10101  779      EQDKNTQEVFAQVKQ  KNTQEVFAQ  3        0.3136
1679.7    50.00  0.32     Sequence
 HLA-DPA10201-DPB10101  780      QDKNTQEVFAQVKQI  VFAQVKQIX  7        0.3647
966.2    36.00  0.29     Sequence
 HLA-DPA10201-DPB10101  781      DKNTQEVFAQVKQIY  VFAQVKQIY  6        0.4034
635.9    26.00  0.50     Sequence
 HLA-DPA10201-DPB10101  782      KNTQEVFAQVKQIYK  VFAQVKQIY  5        0.4411
422.9    18.00  0.56     Sequence
 HLA-DPA10201-DPB10101  783      NTQEVFAQVKQIYKT  VFAQVKQIY  4        0.4346
453.6    20.00  0.60     Sequence
 HLA-DPA10201-DPB10101  784      TQEVFAQVKQIYKTP  VFAQVKQIY  3        0.4244
506.6    22.00  0.61     Sequence
 HLA-DPA10201-DPB10101  785      QEVFAQVKQIYKTPP  VFAQVKQIY  2        0.4085
601.9    25.00  0.63     Sequence
 HLA-DPA10201-DPB10101  786      EVFAQVKQIYKTPPI  VFAQVKQIY  1        0.3602
1014.3    37.00  0.40     Sequence
 HLA-DPA10201-DPB10101  787      VFAQVKQIYKTPPIK  VFAQVKQIY  0        0.3015
1916.2    55.00  0.23     Sequence
 HLA-DPA10201-DPB10101  788      FAQVKQIYKTPPIKD  QIYKTPPIK  5        0.2746
2561.2    65.00  0.29     Sequence
 HLA-DPA10201-DPB10101  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.2731
2604.2    65.00  0.36     Sequence
 HLA-DPA10201-DPB10101  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.2729
2609.6    65.00  0.35     Sequence
 HLA-DPA10201-DPB10101  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.2626
2917.4    65.00  0.38     Sequence
 HLA-DPA10201-DPB10101  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.2434
3592.9    75.00  0.41     Sequence
 HLA-DPA10201-DPB10101  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.1618
8687.8    90.00  0.30     Sequence
 HLA-DPA10201-DPB10101  794      IYKTPPIKDFGGFNF  PIKDFGGFN  5        0.2331
4014.8    75.00  0.22     Sequence
 HLA-DPA10201-DPB10101  795      YKTPPIKDFGGFNFS  DFGGFNFSX  7        0.3191
1583.9    49.00  0.40     Sequence
 HLA-DPA10201-DPB10101  796      KTPPIKDFGGFNFSQ  DFGGFNFSQ  6        0.3972
680.3    28.00  0.58     Sequence
 HLA-DPA10201-DPB10101  797      TPPIKDFGGFNFSQI  DFGGFNFSQ  5        0.5293
162.8     6.00  0.80     Sequence         WB
 HLA-DPA10201-DPB10101  798      PPIKDFGGFNFSQIL  DFGGFNFSQ  4        0.5592
117.8     4.00  0.75     Sequence         WB
 HLA-DPA10201-DPB10101  799      PIKDFGGFNFSQILP  DFGGFNFSQ  3        0.5704
104.4     3.50  0.68     Sequence         WB
 HLA-DPA10201-DPB10101  800      IKDFGGFNFSQILPD  DFGGFNFSQ  2        0.5771
97.1     3.00  0.56     Sequence         WB
 HLA-DPA10201-DPB10101  801      KDFGGFNFSQILPDP  GFNFSQILP  4        0.5488
131.9     4.50  0.37     Sequence         WB
 HLA-DPA10201-DPB10101  802      DFGGFNFSQILPDPS  GFNFSQILP  3        0.4868
257.9    11.00  0.50     Sequence
 HLA-DPA10201-DPB10101  803      FGGFNFSQILPDPSK  GFNFSQILP  2        0.4664
321.6    14.00  0.60     Sequence
 HLA-DPA10201-DPB10101  804      GGFNFSQILPDPSKP  GFNFSQILP  1        0.4059
618.8    26.00  0.54     Sequence
 HLA-DPA10201-DPB10101  805      GFNFSQILPDPSKPS  GFNFSQILP  0        0.3525
1103.5    39.00  0.34     Sequence
 HLA-DPA10201-DPB10101  806      FNFSQILPDPSKPSK  XFNFSQILP -1        0.2902
2165.2    60.00  0.22     Sequence
 HLA-DPA10201-DPB10101  807      NFSQILPDPSKPSKR  QILPDPSKP  3        0.1835
6865.9    85.00  0.31     Sequence
 HLA-DPA10201-DPB10101  808      FSQILPDPSKPSKRS  QILPDPSKP  2        0.1483
10044.1    95.00  0.40     Sequence
 HLA-DPA10201-DPB10101  809      SQILPDPSKPSKRSF  QILPDPSKP  1        0.0790
21265.5   100.00  0.32     Sequence
 HLA-DPA10201-DPB10101  810      QILPDPSKPSKRSFI  PSKPSKRSF  5        0.0735
22562.1   100.00  0.20     Sequence
```

```
 HLA-DPA10201-DPB10101  811      ILPDPSKPSKRSFIE  KPSKRSFIE  6        0.1060
15873.1   100.00  0.26     Sequence
 HLA-DPA10201-DPB10101  812      LPDPSKPSKRSFIED  PSKRSFIED  6        0.1275
12582.5    95.00  0.32     Sequence
 HLA-DPA10201-DPB10101  813      PDPSKPSKRSFIEDL  PSKRSFIED  5        0.2386
3784.3    75.00  0.37     Sequence
 HLA-DPA10201-DPB10101  814      DPSKPSKRSFIEDLL  PSKRSFIED  4        0.3913
724.8    29.00  0.22     Sequence
 HLA-DPA10201-DPB10101  815      PSKPSKRSFIEDLLF  SFIEDLLFX  7        0.4747
293.9    13.00  0.23     Sequence
 HLA-DPA10201-DPB10101  816      SKPSKRSFIEDLLFN  SFIEDLLFN  6        0.5296
162.3     6.00  0.35     Sequence         WB
 HLA-DPA10201-DPB10101  817      KPSKRSFIEDLLFNK  SFIEDLLFN  5        0.5961
79.0     2.00  0.31     Sequence         WB
 HLA-DPA10201-DPB10101  818      PSKRSFIEDLLFNKV  FIEDLLFNK  5        0.6527
42.9     0.70  0.55     Sequence         SB
 HLA-DPA10201-DPB10101  819      SKRSFIEDLLFNKVT  FIEDLLFNK  4        0.6480
45.1     0.70  0.55     Sequence         SB
 HLA-DPA10201-DPB10101  820      KRSFIEDLLFNKVTL  FIEDLLFNK  3        0.6440
47.1     0.80  0.54     Sequence         SB
 HLA-DPA10201-DPB10101  821      RSFIEDLLFNKVTLA  FIEDLLFNK  2        0.6123
66.4     1.50  0.56     Sequence         SB
 HLA-DPA10201-DPB10101  822      SFIEDLLFNKVTLAD  FIEDLLFNK  1        0.5901
84.3     2.50  0.37     Sequence         WB
 HLA-DPA10201-DPB10101  823      FIEDLLFNKVTLADA  LFNKVTLAD  5        0.5720
102.6     3.00  0.45     Sequence         WB
 HLA-DPA10201-DPB10101  824      IEDLLFNKVTLADAG  LFNKVTLAD  4        0.5275
166.1     6.50  0.58     Sequence         WB
 HLA-DPA10201-DPB10101  825      EDLLFNKVTLADAGF  LFNKVTLAD  3        0.5040
214.1     8.50  0.67     Sequence         WB
 HLA-DPA10201-DPB10101  826      DLLFNKVTLADAGFI  LFNKVTLAD  2        0.4839
266.1    11.00  0.73     Sequence
 HLA-DPA10201-DPB10101  827      LLFNKVTLADAGFIK  LFNKVTLAD  1        0.4498
384.8    17.00  0.64     Sequence
 HLA-DPA10201-DPB10101  828      LFNKVTLADAGFIKQ  LFNKVTLAD  0        0.3897
737.2    30.00  0.40     Sequence
 HLA-DPA10201-DPB10101  829      FNKVTLADAGFIKQY  TLADAGFIK  4        0.3111
1726.0    55.00  0.51     Sequence
 HLA-DPA10201-DPB10101  830      NKVTLADAGFIKQYG  TLADAGFIK  3        0.2872
2235.1    60.00  0.57     Sequence
 HLA-DPA10201-DPB10101  831      KVTLADAGFIKQYGD  TLADAGFIK  2        0.2864
2256.3    60.00  0.58     Sequence
 HLA-DPA10201-DPB10101  832      VTLADAGFIKQYGDC  TLADAGFIK  1        0.2489
3384.6    70.00  0.38     Sequence
 HLA-DPA10201-DPB10101  833      TLADAGFIKQYGDCL  GFIKQYGDC  5        0.2918
2127.0    60.00  0.23     Sequence
 HLA-DPA10201-DPB10101  834      LADAGFIKQYGDCLG  GFIKQYGDC  4        0.3037
1869.4    55.00  0.25     Sequence
 HLA-DPA10201-DPB10101  835      ADAGFIKQYGDCLGD  GFIKQYGDC  3        0.2992
1962.5    55.00  0.26     Sequence
 HLA-DPA10201-DPB10101  836      DAGFIKQYGDCLGDI  KQYGDCLGD  5        0.3313
1387.3    45.00  0.31     Sequence
 HLA-DPA10201-DPB10101  837      AGFIKQYGDCLGDIA  KQYGDCLGD  4        0.3391
1275.3    43.00  0.32     Sequence
 HLA-DPA10201-DPB10101  838      GFIKQYGDCLGDIAA  KQYGDCLGD  3        0.3358
1321.5    44.00  0.34     Sequence
 HLA-DPA10201-DPB10101  839      FIKQYGDCLGDIAAR  KQYGDCLGD  2        0.3402
1259.4    43.00  0.32     Sequence
 HLA-DPA10201-DPB10101  840      IKQYGDCLGDIAARD  QYGDCLGDI  2        0.2601
2998.6    70.00  0.33     Sequence
 HLA-DPA10201-DPB10101  841      KQYGDCLGDIAARDL  CLGDIAARD  5        0.2664
2800.3    65.00  0.30     Sequence
 HLA-DPA10201-DPB10101  842      QYGDCLGDIAARDLI  CLGDIAARD  4        0.2605
2986.1    70.00  0.34     Sequence
 HLA-DPA10201-DPB10101  843      YGDCLGDIAARDLIC  CLGDIAARD  3        0.2476
3433.1    70.00  0.38     Sequence
```

```
 HLA-DPA10201-DPB10101  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.2314
4089.2    75.00  0.40     Sequence
 HLA-DPA10201-DPB10101  845      DCLGDIAARDLICAQ  CLGDIAARD  1        0.2325
4040.6    75.00  0.37     Sequence
 HLA-DPA10201-DPB10101  846      CLGDIAARDLICAQK  DIAARDLIC  3        0.2171
4774.4    80.00  0.28     Sequence
 HLA-DPA10201-DPB10101  847      LGDIAARDLICAQKF  ARDLICAQK  5        0.2231
4473.0    80.00  0.25     Sequence
 HLA-DPA10201-DPB10101  848      GDIAARDLICAQKFN  ARDLICAQK  4        0.2209
4580.6    80.00  0.31     Sequence
 HLA-DPA10201-DPB10101  849      DIAARDLICAQKFNG  LICAQKFNG  6        0.2280
4241.6    75.00  0.33     Sequence
 HLA-DPA10201-DPB10101  850      IAARDLICAQKFNGL  LICAQKFNG  5        0.2764
2511.8    65.00  0.46     Sequence
 HLA-DPA10201-DPB10101  851      AARDLICAQKFNGLT  LICAQKFNG  4        0.2936
2087.0    60.00  0.41     Sequence
 HLA-DPA10201-DPB10101  852      ARDLICAQKFNGLTV  LICAQKFNG  3        0.3429
1223.7    42.00  0.31     Sequence
 HLA-DPA10201-DPB10101  853      RDLICAQKFNGLTVL  LICAQKFNG  2        0.3915
723.3    29.00  0.17     Sequence
 HLA-DPA10201-DPB10101  854      DLICAQKFNGLTVLP  KFNGLTVLP  6        0.4671
319.3    14.00  0.53     Sequence
 HLA-DPA10201-DPB10101  855      LICAQKFNGLTVLPP  KFNGLTVLP  5        0.5074
206.5     8.50  0.71     Sequence         WB
 HLA-DPA10201-DPB10101  856      ICAQKFNGLTVLPPL  KFNGLTVLP  4        0.5311
159.8     6.00  0.69     Sequence         WB
 HLA-DPA10201-DPB10101  857      CAQKFNGLTVLPPLL  KFNGLTVLP  3        0.5532
125.7     4.50  0.68     Sequence         WB
 HLA-DPA10201-DPB10101  858      AQKFNGLTVLPPLLT  KFNGLTVLP  2        0.5585
118.7     4.00  0.62     Sequence         WB
 HLA-DPA10201-DPB10101  859      QKFNGLTVLPPLLTD  KFNGLTVLP  1        0.5293
162.8     6.00  0.56     Sequence         WB
 HLA-DPA10201-DPB10101  860      KFNGLTVLPPLLTDE  KFNGLTVLP  0        0.4622
336.5    15.00  0.35     Sequence
 HLA-DPA10201-DPB10101  861      FNGLTVLPPLLTDEM  VLPPLLTDE  5        0.3840
784.8    31.00  0.22     Sequence
 HLA-DPA10201-DPB10101  862      NGLTVLPPLLTDEMI  VLPPLLTDE  4        0.3567
1053.6    38.00  0.28     Sequence
 HLA-DPA10201-DPB10101  863      GLTVLPPLLTDEMIA  VLPPLLTDE  3        0.3628
986.6    36.00  0.28     Sequence
 HLA-DPA10201-DPB10101  864      LTVLPPLLTDEMIAQ  LLTDEMIAQ  6        0.3758
857.5    33.00  0.26     Sequence
 HLA-DPA10201-DPB10101  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.3682
930.3    35.00  0.37     Sequence
 HLA-DPA10201-DPB10101  866      VLPPLLTDEMIAQYT  LLTDEMIAQ  4        0.3549
1074.4    39.00  0.44     Sequence
 HLA-DPA10201-DPB10101  867      LPPLLTDEMIAQYTS  LLTDEMIAQ  3        0.3474
1165.5    41.00  0.46     Sequence
 HLA-DPA10201-DPB10101  868      PPLLTDEMIAQYTSA  LLTDEMIAQ  2        0.3333
1358.1    45.00  0.46     Sequence
 HLA-DPA10201-DPB10101  869      PLLTDEMIAQYTSAL  LLTDEMIAQ  1        0.3284
1431.6    46.00  0.31     Sequence
 HLA-DPA10201-DPB10101  870      LLTDEMIAQYTSALL  MIAQYTSAL  5        0.3684
928.9    35.00  0.21     Sequence
 HLA-DPA10201-DPB10101  871      LTDEMIAQYTSALLA  IAQYTSALL  5        0.3776
841.1    33.00  0.32     Sequence
 HLA-DPA10201-DPB10101  872      TDEMIAQYTSALLAG  IAQYTSALL  4        0.3718
895.3    34.00  0.33     Sequence
 HLA-DPA10201-DPB10101  873      DEMIAQYTSALLAGT  IAQYTSALL  3        0.3730
883.3    34.00  0.31     Sequence
 HLA-DPA10201-DPB10101  874      EMIAQYTSALLAGTI  QYTSALLAG  4        0.3922
718.0    29.00  0.27     Sequence
 HLA-DPA10201-DPB10101  875      MIAQYTSALLAGTIT  QYTSALLAG  3        0.3723
890.7    34.00  0.29     Sequence
 HLA-DPA10201-DPB10101  876      IAQYTSALLAGTITS  QYTSALLAG  2        0.3391
1275.3    43.00  0.35     Sequence
```

```
 HLA-DPA10201-DPB10101  877      AQYTSALLAGTITSG  ALLAGTITS  5        0.2814
2381.4    60.00  0.22     Sequence
 HLA-DPA10201-DPB10101  878      QYTSALLAGTITSGW  ALLAGTITS  4        0.2576
3078.4    70.00  0.37     Sequence
 HLA-DPA10201-DPB10101  879      YTSALLAGTITSGWT  ALLAGTITS  3        0.2528
3242.3    70.00  0.39     Sequence
 HLA-DPA10201-DPB10101  880      TSALLAGTITSGWTF  LLAGTITSG  3        0.2362
3883.0    75.00  0.35     Sequence
 HLA-DPA10201-DPB10101  881      SALLAGTITSGWTFG  LLAGTITSG  2        0.2209
4580.5    80.00  0.40     Sequence
 HLA-DPA10201-DPB10101  882      ALLAGTITSGWTFGA  LLAGTITSG  1        0.2014
5657.6    85.00  0.24     Sequence
 HLA-DPA10201-DPB10101  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.1710
7861.6    90.00  0.34     Sequence
 HLA-DPA10201-DPB10101  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.1607
8790.8    90.00  0.37     Sequence
 HLA-DPA10201-DPB10101  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.1527
9577.0    95.00  0.38     Sequence
 HLA-DPA10201-DPB10101  886      GTITSGWTFGAGAAL  ITSGWTFGA  2        0.1960
5997.2    85.00  0.26     Sequence
 HLA-DPA10201-DPB10101  887      TITSGWTFGAGAALQ  FGAGAALQX  7        0.2180
4725.1    80.00  0.20     Sequence
 HLA-DPA10201-DPB10101  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.2878
2221.8    60.00  0.34     Sequence
 HLA-DPA10201-DPB10101  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.2967
2017.7    55.00  0.35     Sequence
 HLA-DPA10201-DPB10101  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.3154
1647.8    50.00  0.34     Sequence
 HLA-DPA10201-DPB10101  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.3222
1530.5    48.00  0.32     Sequence
 HLA-DPA10201-DPB10101  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.3503
1129.5    40.00  0.28     Sequence
 HLA-DPA10201-DPB10101  893      TFGAGAALQIPFAMQ  AALQIPFAM  5        0.3819
802.2    31.00  0.28     Sequence
 HLA-DPA10201-DPB10101  894      FGAGAALQIPFAMQM  AALQIPFAM  4        0.3708
905.1    34.00  0.36     Sequence
 HLA-DPA10201-DPB10101  895      GAGAALQIPFAMQMA  AALQIPFAM  3        0.3784
833.3    32.00  0.30     Sequence
 HLA-DPA10201-DPB10101  896      AGAALQIPFAMQMAY  AALQIPFAM  2        0.3892
741.1    30.00  0.28     Sequence
 HLA-DPA10201-DPB10101  897      GAALQIPFAMQMAYR  ALQIPFAMQ  2        0.3811
809.2    32.00  0.25     Sequence
 HLA-DPA10201-DPB10101  898      AALQIPFAMQMAYRF  IPFAMQMAY  4        0.3718
895.0    34.00  0.22     Sequence
 HLA-DPA10201-DPB10101  899      ALQIPFAMQMAYRFN  IPFAMQMAY  3        0.3692
920.6    35.00  0.22     Sequence
 HLA-DPA10201-DPB10101  900      LQIPFAMQMAYRFNG  IPFAMQMAY  2        0.3303
1402.6    46.00  0.23     Sequence
 HLA-DPA10201-DPB10101  901      QIPFAMQMAYRFNGI  MQMAYRFNG  5        0.3376
1295.7    43.00  0.27     Sequence
 HLA-DPA10201-DPB10101  902      IPFAMQMAYRFNGIG  MQMAYRFNG  4        0.2959
2035.1    60.00  0.35     Sequence
 HLA-DPA10201-DPB10101  903      PFAMQMAYRFNGIGV  MQMAYRFNG  3        0.2969
2012.3    55.00  0.38     Sequence
 HLA-DPA10201-DPB10101  904      FAMQMAYRFNGIGVT  MQMAYRFNG  2        0.3016
1912.5    55.00  0.31     Sequence
 HLA-DPA10201-DPB10101  905      AMQMAYRFNGIGVTQ  RFNGIGVTQ  6        0.2791
2439.8    65.00  0.29     Sequence
 HLA-DPA10201-DPB10101  906      MQMAYRFNGIGVTQN  RFNGIGVTQ  5        0.2709
2665.9    65.00  0.43     Sequence
 HLA-DPA10201-DPB10101  907      QMAYRFNGIGVTQNV  RFNGIGVTQ  4        0.2875
2228.7    60.00  0.43     Sequence
 HLA-DPA10201-DPB10101  908      MAYRFNGIGVTQNVL  RFNGIGVTQ  3        0.3045
1853.2    55.00  0.43     Sequence
 HLA-DPA10201-DPB10101  909      AYRFNGIGVTQNVLY  RFNGIGVTQ  2        0.3112
1724.5    55.00  0.38     Sequence
```

```
 HLA-DPA10201-DPB10101  910      YRFNGIGVTQNVLYE  RFNGIGVTQ  1        0.2989
1969.7    55.00  0.25     Sequence
 HLA-DPA10201-DPB10101  911      RFNGIGVTQNVLYEN  GVTQNVLYE  5        0.2866
2250.1    60.00  0.22     Sequence
 HLA-DPA10201-DPB10101  912      FNGIGVTQNVLYENQ  VTQNVLYEN  5        0.2797
2424.9    60.00  0.22     Sequence
 HLA-DPA10201-DPB10101  913      NGIGVTQNVLYENQK  VTQNVLYEN  4        0.2735
2592.0    65.00  0.27     Sequence
 HLA-DPA10201-DPB10101  914      GIGVTQNVLYENQKL  VTQNVLYEN  3        0.3207
1555.9    48.00  0.18     Sequence
 HLA-DPA10201-DPB10101  915      IGVTQNVLYENQKLI  VLYENQKLI  6        0.3911
726.4    29.00  0.27     Sequence
 HLA-DPA10201-DPB10101  916      GVTQNVLYENQKLIA  VLYENQKLI  5        0.4247
505.2    22.00  0.31     Sequence
 HLA-DPA10201-DPB10101  917      VTQNVLYENQKLIAN  LYENQKLIA  5        0.4282
486.5    21.00  0.33     Sequence
 HLA-DPA10201-DPB10101  918      TQNVLYENQKLIANQ  LYENQKLIA  4        0.4320
466.7    20.00  0.33     Sequence
 HLA-DPA10201-DPB10101  919      QNVLYENQKLIANQF  LYENQKLIA  3        0.4296
479.0    21.00  0.34     Sequence
 HLA-DPA10201-DPB10101  920      NVLYENQKLIANQFN  LYENQKLIA  2        0.4228
515.6    22.00  0.37     Sequence
 HLA-DPA10201-DPB10101  921      VLYENQKLIANQFNS  KLIANQFNS  6        0.4255
500.5    21.00  0.31     Sequence
 HLA-DPA10201-DPB10101  922      LYENQKLIANQFNSA  KLIANQFNS  5        0.4673
318.6    14.00  0.60     Sequence
 HLA-DPA10201-DPB10101  923      YENQKLIANQFNSAI  KLIANQFNS  4        0.4766
288.1    12.00  0.62     Sequence
 HLA-DPA10201-DPB10101  924      ENQKLIANQFNSAIG  KLIANQFNS  3        0.4829
269.1    12.00  0.57     Sequence
 HLA-DPA10201-DPB10101  925      NQKLIANQFNSAIGK  KLIANQFNS  2        0.4712
305.4    13.00  0.56     Sequence
 HLA-DPA10201-DPB10101  926      QKLIANQFNSAIGKI  KLIANQFNS  1        0.4585
350.4    15.00  0.49     Sequence
 HLA-DPA10201-DPB10101  927      KLIANQFNSAIGKIQ  KLIANQFNS  0        0.3912
726.0    29.00  0.34     Sequence
 HLA-DPA10201-DPB10101  928      LIANQFNSAIGKIQD  QFNSAIGKI  4        0.3114
1719.9    55.00  0.36     Sequence
 HLA-DPA10201-DPB10101  929      IANQFNSAIGKIQDS  QFNSAIGKI  3        0.2501
3341.5    70.00  0.47     Sequence
 HLA-DPA10201-DPB10101  930      ANQFNSAIGKIQDSL  QFNSAIGKI  2        0.2559
3136.8    70.00  0.41     Sequence
 HLA-DPA10201-DPB10101  931      NQFNSAIGKIQDSLS  QFNSAIGKI  1        0.2502
3338.1    70.00  0.32     Sequence
 HLA-DPA10201-DPB10101  932      QFNSAIGKIQDSLSS  AIGKIQDSL  4        0.2577
3075.4    70.00  0.16     Sequence
 HLA-DPA10201-DPB10101  933      FNSAIGKIQDSLSST  KIQDSLSST  6        0.2930
2100.6    60.00  0.38     Sequence
 HLA-DPA10201-DPB10101  934      NSAIGKIQDSLSSTA  KIQDSLSST  5        0.2981
1987.8    55.00  0.47     Sequence
 HLA-DPA10201-DPB10101  935      SAIGKIQDSLSSTAS  KIQDSLSST  4        0.3054
1836.9    55.00  0.49     Sequence
 HLA-DPA10201-DPB10101  936      AIGKIQDSLSSTASA  KIQDSLSST  3        0.3049
1845.3    55.00  0.50     Sequence
 HLA-DPA10201-DPB10101  937      IGKIQDSLSSTASAL  KIQDSLSST  2        0.2887
2199.9    60.00  0.47     Sequence
 HLA-DPA10201-DPB10101  938      GKIQDSLSSTASALG  KIQDSLSST  1        0.2581
3062.3    70.00  0.35     Sequence
 HLA-DPA10201-DPB10101  939      KIQDSLSSTASALGK  SLSSTASAL  4        0.2270
4288.1    75.00  0.28     Sequence
 HLA-DPA10201-DPB10101  940      IQDSLSSTASALGKL  SLSSTASAL  3        0.1929
6203.0    85.00  0.38     Sequence
 HLA-DPA10201-DPB10101  941      QDSLSSTASALGKLQ  SLSSTASAL  2        0.2013
5665.8    85.00  0.36     Sequence
 HLA-DPA10201-DPB10101  942      DSLSSTASALGKLQD  SLSSTASAL  1        0.1983
5852.9    85.00  0.28     Sequence
```

```
 HLA-DPA10201-DPB10101  943      SLSSTASALGKLQDV  ASALGKLQD  5        0.2078
5276.0    80.00  0.27     Sequence
 HLA-DPA10201-DPB10101  944      LSSTASALGKLQDVV  ASALGKLQD  4        0.2294
4177.7    75.00  0.35     Sequence
 HLA-DPA10201-DPB10101  945      SSTASALGKLQDVVN  ASALGKLQD  3        0.2319
4067.0    75.00  0.32     Sequence
 HLA-DPA10201-DPB10101  946      STASALGKLQDVVNQ  ASALGKLQD  2        0.2399
3731.1    75.00  0.28     Sequence
 HLA-DPA10201-DPB10101  947      TASALGKLQDVVNQN  ALGKLQDVV  3        0.2372
3838.8    75.00  0.23     Sequence
 HLA-DPA10201-DPB10101  948      ASALGKLQDVVNQNA  KLQDVVNQN  5        0.2350
3933.6    75.00  0.38     Sequence
 HLA-DPA10201-DPB10101  949      SALGKLQDVVNQNAQ  KLQDVVNQN  4        0.2279
4245.1    75.00  0.43     Sequence
 HLA-DPA10201-DPB10101  950      ALGKLQDVVNQNAQA  KLQDVVNQN  3        0.2103
5137.6    80.00  0.46     Sequence
 HLA-DPA10201-DPB10101  951      LGKLQDVVNQNAQAL  KLQDVVNQN  2        0.1943
6105.7    85.00  0.49     Sequence
 HLA-DPA10201-DPB10101  952      GKLQDVVNQNAQALN  KLQDVVNQN  1        0.1862
6671.1    85.00  0.36     Sequence
 HLA-DPA10201-DPB10101  953      KLQDVVNQNAQALNT  DVVNQNAQA  3        0.1792
7192.2    90.00  0.15     Sequence
 HLA-DPA10201-DPB10101  954      LQDVVNQNAQALNTL  VNQNAQALN  4        0.1871
6602.7    85.00  0.26     Sequence
 HLA-DPA10201-DPB10101  955      QDVVNQNAQALNTLV  NQNAQALNT  4        0.2292
4189.7    75.00  0.17     Sequence
 HLA-DPA10201-DPB10101  956      DVVNQNAQALNTLVK  NAQALNTLV  5        0.2491
3376.7    70.00  0.19     Sequence
 HLA-DPA10201-DPB10101  957      VVNQNAQALNTLVKQ  AQALNTLVK  5        0.2658
2818.1    65.00  0.23     Sequence
 HLA-DPA10201-DPB10101  958      VNQNAQALNTLVKQL  AQALNTLVK  4        0.2872
2236.6    60.00  0.22     Sequence
 HLA-DPA10201-DPB10101  959      NQNAQALNTLVKQLS  ALNTLVKQL  5        0.2941
2074.8    60.00  0.34     Sequence
 HLA-DPA10201-DPB10101  960      QNAQALNTLVKQLSS  ALNTLVKQL  4        0.2983
1983.4    55.00  0.31     Sequence
 HLA-DPA10201-DPB10101  961      NAQALNTLVKQLSSN  ALNTLVKQL  3        0.2655
2827.9    65.00  0.35     Sequence
 HLA-DPA10201-DPB10101  962      AQALNTLVKQLSSNF  ALNTLVKQL  2        0.2945
2066.5    60.00  0.26     Sequence
 HLA-DPA10201-DPB10101  963      QALNTLVKQLSSNFG  LVKQLSSNF  5        0.2919
2125.5    60.00  0.19     Sequence
 HLA-DPA10201-DPB10101  964      ALNTLVKQLSSNFGA  LVKQLSSNF  4        0.2908
2150.1    60.00  0.25     Sequence
 HLA-DPA10201-DPB10101  965      LNTLVKQLSSNFGAI  KQLSSNFGA  5        0.3411
1247.5    42.00  0.28     Sequence
 HLA-DPA10201-DPB10101  966      NTLVKQLSSNFGAIS  QLSSNFGAI  5        0.3487
1149.7    40.00  0.34     Sequence
 HLA-DPA10201-DPB10101  967      TLVKQLSSNFGAISS  QLSSNFGAI  4        0.3456
1188.5    41.00  0.34     Sequence
 HLA-DPA10201-DPB10101  968      LVKQLSSNFGAISSV  QLSSNFGAI  3        0.3398
1265.7    43.00  0.43     Sequence
 HLA-DPA10201-DPB10101  969      VKQLSSNFGAISSVL  QLSSNFGAI  2        0.3071
1802.0    55.00  0.46     Sequence
 HLA-DPA10201-DPB10101  970      KQLSSNFGAISSVLN  QLSSNFGAI  1        0.2979
1991.2    55.00  0.30     Sequence
 HLA-DPA10201-DPB10101  971      QLSSNFGAISSVLND  NFGAISSVL  4        0.2837
2321.6    60.00  0.23     Sequence
 HLA-DPA10201-DPB10101  972      LSSNFGAISSVLNDI  AISSVLNDI  6        0.2904
2160.7    60.00  0.25     Sequence
 HLA-DPA10201-DPB10101  973      SSNFGAISSVLNDIL  AISSVLNDI  5        0.3409
1250.0    42.00  0.31     Sequence
 HLA-DPA10201-DPB10101  974      SNFGAISSVLNDILS  AISSVLNDI  4        0.3342
1344.2    44.00  0.29     Sequence
 HLA-DPA10201-DPB10101  975      NFGAISSVLNDILSR  AISSVLNDI  3        0.3398
1265.7    43.00  0.31     Sequence
```

```
 HLA-DPA10201-DPB10101  976      FGAISSVLNDILSRL  AISSVLNDI  2        0.3656
957.0    36.00  0.25     Sequence
 HLA-DPA10201-DPB10101  977      GAISSVLNDILSRLD  SVLNDILSR  4        0.3478
1160.3    41.00  0.24     Sequence
 HLA-DPA10201-DPB10101  978      AISSVLNDILSRLDK  SVLNDILSR  3        0.3422
1233.1    42.00  0.28     Sequence
 HLA-DPA10201-DPB10101  979      ISSVLNDILSRLDKV  VLNDILSRL  3        0.3580
1039.7    38.00  0.23     Sequence
 HLA-DPA10201-DPB10101  980      SSVLNDILSRLDKVE  VLNDILSRL  2        0.3645
969.0    36.00  0.20     Sequence
 HLA-DPA10201-DPB10101  981      SVLNDILSRLDKVEA  ILSRLDKVE  5        0.3655
958.8    36.00  0.23     Sequence
 HLA-DPA10201-DPB10101  982      VLNDILSRLDKVEAE  ILSRLDKVE  4        0.3468
1173.0    41.00  0.25     Sequence
 HLA-DPA10201-DPB10101  983      LNDILSRLDKVEAEV  ILSRLDKVE  3        0.3347
1337.4    44.00  0.28     Sequence
 HLA-DPA10201-DPB10101  984      NDILSRLDKVEAEVQ  RLDKVEAEV  5        0.3351
1331.5    44.00  0.23     Sequence
 HLA-DPA10201-DPB10101  985      DILSRLDKVEAEVQI  RLDKVEAEV  4        0.3416
1241.5    42.00  0.29     Sequence
 HLA-DPA10201-DPB10101  986      ILSRLDKVEAEVQID  RLDKVEAEV  3        0.3437
1212.6    42.00  0.29     Sequence
 HLA-DPA10201-DPB10101  987      LSRLDKVEAEVQIDR  RLDKVEAEV  2        0.3358
1322.2    44.00  0.29     Sequence
 HLA-DPA10201-DPB10101  988      SRLDKVEAEVQIDRL  VEAEVQIDR  5        0.3525
1103.0    39.00  0.25     Sequence
 HLA-DPA10201-DPB10101  989      RLDKVEAEVQIDRLI  VEAEVQIDR  4        0.3733
880.7    34.00  0.25     Sequence
 HLA-DPA10201-DPB10101  990      LDKVEAEVQIDRLIT  EVQIDRLIT  6        0.4026
641.5    26.00  0.35     Sequence
 HLA-DPA10201-DPB10101  991      DKVEAEVQIDRLITG  EVQIDRLIT  5        0.3785
832.8    32.00  0.43     Sequence
 HLA-DPA10201-DPB10101  992      KVEAEVQIDRLITGR  EVQIDRLIT  4        0.3712
900.8    34.00  0.52     Sequence
 HLA-DPA10201-DPB10101  993      VEAEVQIDRLITGRL  EVQIDRLIT  3        0.3865
763.4    30.00  0.55     Sequence
 HLA-DPA10201-DPB10101  994      EAEVQIDRLITGRLQ  EVQIDRLIT  2        0.3998
661.3    27.00  0.47     Sequence
 HLA-DPA10201-DPB10101  995      AEVQIDRLITGRLQS  RLITGRLQS  6        0.3945
700.4    28.00  0.28     Sequence
 HLA-DPA10201-DPB10101  996      EVQIDRLITGRLQSL  RLITGRLQS  5        0.4395
430.4    19.00  0.57     Sequence
 HLA-DPA10201-DPB10101  997      VQIDRLITGRLQSLQ  RLITGRLQS  4        0.4229
515.1    22.00  0.62     Sequence
 HLA-DPA10201-DPB10101  998      QIDRLITGRLQSLQT  RLITGRLQS  3        0.4258
498.9    21.00  0.58     Sequence
 HLA-DPA10201-DPB10101  999      IDRLITGRLQSLQTY  RLITGRLQS  2        0.4194
535.1    23.00  0.52     Sequence
 HLA-DPA10201-DPB10101 1000      DRLITGRLQSLQTYV  RLITGRLQS  1        0.4297
478.3    21.00  0.32     Sequence
 HLA-DPA10201-DPB10101 1001      RLITGRLQSLQTYVT  RLQSLQTYV  5        0.4253
501.7    21.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1002      LITGRLQSLQTYVTQ  RLQSLQTYV  4        0.3901
734.3    29.00  0.52     Sequence
 HLA-DPA10201-DPB10101 1003      ITGRLQSLQTYVTQQ  RLQSLQTYV  3        0.3813
807.6    32.00  0.54     Sequence
 HLA-DPA10201-DPB10101 1004      TGRLQSLQTYVTQQL  RLQSLQTYV  2        0.3994
663.9    27.00  0.45     Sequence
 HLA-DPA10201-DPB10101 1005      GRLQSLQTYVTQQLI  RLQSLQTYV  1        0.4192
536.1    23.00  0.38     Sequence
 HLA-DPA10201-DPB10101 1006      RLQSLQTYVTQQLIR  TYVTQQLIR  6        0.4275
489.9    21.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1007      LQSLQTYVTQQLIRA  TYVTQQLIR  5        0.4049
625.7    26.00  0.37     Sequence
 HLA-DPA10201-DPB10101 1008      QSLQTYVTQQLIRAA  TYVTQQLIR  4        0.4028
639.9    26.00  0.38     Sequence
```

```
 HLA-DPA10201-DPB10101 1009      SLQTYVTQQLIRAAE  TYVTQQLIR  3        0.3966
684.1    28.00  0.41     Sequence
 HLA-DPA10201-DPB10101 1010      LQTYVTQQLIRAAEI  TYVTQQLIR  2        0.4008
654.4    27.00  0.37     Sequence
 HLA-DPA10201-DPB10101 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.3814
806.9    32.00  0.23     Sequence
 HLA-DPA10201-DPB10101 1012      TYVTQQLIRAAEIRA  TQQLIRAAE  3        0.3646
967.2    36.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1013      YVTQQLIRAAEIRAS  LIRAAEIRA  5        0.3491
1144.5    40.00  0.37     Sequence
 HLA-DPA10201-DPB10101 1014      VTQQLIRAAEIRASA  LIRAAEIRA  4        0.3326
1368.2    45.00  0.44     Sequence
 HLA-DPA10201-DPB10101 1015      TQQLIRAAEIRASAN  LIRAAEIRA  3        0.3229
1520.0    48.00  0.46     Sequence
 HLA-DPA10201-DPB10101 1016      QQLIRAAEIRASANL  LIRAAEIRA  2        0.3185
1592.7    49.00  0.50     Sequence
 HLA-DPA10201-DPB10101 1017      QLIRAAEIRASANLA  LIRAAEIRA  1        0.2839
2317.3    60.00  0.33     Sequence
 HLA-DPA10201-DPB10101 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.2560
3134.3    70.00  0.26     Sequence
 HLA-DPA10201-DPB10101 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.3027
1890.4    55.00  0.54     Sequence
 HLA-DPA10201-DPB10101 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.3166
1626.2    50.00  0.54     Sequence
 HLA-DPA10201-DPB10101 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.3208
1554.9    48.00  0.53     Sequence
 HLA-DPA10201-DPB10101 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.3249
1486.6    47.00  0.50     Sequence
 HLA-DPA10201-DPB10101 1023      EIRASANLAAIKMSE  NLAAIKMSE  6        0.3359
1319.4    44.00  0.36     Sequence
 HLA-DPA10201-DPB10101 1024      IRASANLAAIKMSEC  NLAAIKMSE  5        0.3649
964.6    36.00  0.60     Sequence
 HLA-DPA10201-DPB10101 1025      RASANLAAIKMSECV  NLAAIKMSE  4        0.3753
861.7    33.00  0.64     Sequence
 HLA-DPA10201-DPB10101 1026      ASANLAAIKMSECVL  NLAAIKMSE  3        0.4235
511.6    22.00  0.54     Sequence
 HLA-DPA10201-DPB10101 1027      SANLAAIKMSECVLG  NLAAIKMSE  2        0.4130
572.9    24.00  0.54     Sequence
 HLA-DPA10201-DPB10101 1028      ANLAAIKMSECVLGQ  NLAAIKMSE  1        0.4060
618.4    26.00  0.42     Sequence
 HLA-DPA10201-DPB10101 1029      NLAAIKMSECVLGQS  KMSECVLGQ  5        0.3755
859.8    33.00  0.20     Sequence
 HLA-DPA10201-DPB10101 1030      LAAIKMSECVLGQSK  KMSECVLGQ  4        0.3436
1214.9    42.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1031      AAIKMSECVLGQSKR  KMSECVLGQ  3        0.3166
1627.3    50.00  0.38     Sequence
 HLA-DPA10201-DPB10101 1032      AIKMSECVLGQSKRV  KMSECVLGQ  2        0.3121
1707.9    55.00  0.38     Sequence
 HLA-DPA10201-DPB10101 1033      IKMSECVLGQSKRVD  KMSECVLGQ  1        0.2617
2945.5    70.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1034      KMSECVLGQSKRVDF  VLGQSKRVD  5        0.2550
3166.3    70.00  0.30     Sequence
 HLA-DPA10201-DPB10101 1035      MSECVLGQSKRVDFC  VLGQSKRVD  4        0.2322
4053.8    75.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1036      SECVLGQSKRVDFCG  VLGQSKRVD  3        0.2260
4333.0    75.00  0.35     Sequence
 HLA-DPA10201-DPB10101 1037      ECVLGQSKRVDFCGK  VLGQSKRVD  2        0.2118
5056.1    80.00  0.41     Sequence
 HLA-DPA10201-DPB10101 1038      CVLGQSKRVDFCGKG  VLGQSKRVD  1        0.1834
6876.1    85.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1039      VLGQSKRVDFCGKGY  LGQSKRVDF  1        0.1185
13873.0   100.00  0.19     Sequence
 HLA-DPA10201-DPB10101 1040      LGQSKRVDFCGKGYH  RVDFCGKGY  5        0.1193
13750.6   100.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1041      GQSKRVDFCGKGYHL  DFCGKGYHL  6        0.1414
10826.9    95.00  0.25     Sequence
```

```
 HLA-DPA10201-DPB10101 1042      QSKRVDFCGKGYHLM  DFCGKGYHL  5         0.2288
4206.0    75.00  0.32     Sequence
 HLA-DPA10201-DPB10101 1043      SKRVDFCGKGYHLMS  DFCGKGYHL  4         0.2579
3071.0    70.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1044      KRVDFCGKGYHLMSF  CGKGYHLMS  5         0.2830
2339.8    60.00  0.32     Sequence
 HLA-DPA10201-DPB10101 1045      RVDFCGKGYHLMSFP  CGKGYHLMS  4         0.2951
2053.5    60.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1046      VDFCGKGYHLMSFPQ  CGKGYHLMS  3         0.3063
1817.4    55.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1047      DFCGKGYHLMSFPQS  GYHLMSFPQ  5         0.3157
1642.6    50.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1048      FCGKGYHLMSFPQSA  GYHLMSFPQ  4         0.3251
1483.1    47.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5         0.3150
1655.7    50.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4         0.3133
1685.3    50.00  0.29     Sequence
 HLA-DPA10201-DPB10101 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3         0.3006
1933.3    55.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2         0.2751
2547.5    65.00  0.36     Sequence
 HLA-DPA10201-DPB10101 1053      YHLMSFPQSAPHGVV  LMSFPQSAP  2         0.2580
3067.4    70.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1054      HLMSFPQSAPHGVVF  FPQSAPHGV  4         0.2111
5095.3    80.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3         0.2269
4295.3    75.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1056      MSFPQSAPHGVVFLH  APHGVVFLH  6         0.2680
2753.2    65.00  0.42     Sequence
 HLA-DPA10201-DPB10101 1057      SFPQSAPHGVVFLHV  APHGVVFLH  5         0.3855
771.5    31.00  0.56     Sequence
 HLA-DPA10201-DPB10101 1058      FPQSAPHGVVFLHVT  APHGVVFLH  4         0.4040
631.7    26.00  0.54     Sequence
 HLA-DPA10201-DPB10101 1059      PQSAPHGVVFLHVTY  APHGVVFLH  3         0.4584
350.6    15.00  0.46     Sequence
 HLA-DPA10201-DPB10101 1060      QSAPHGVVFLHVTYV  APHGVVFLH  2         0.4732
298.9    13.00  0.41     Sequence
 HLA-DPA10201-DPB10101 1061      SAPHGVVFLHVTYVP  VFLHVTYVP  6         0.4793
279.7    12.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1062      APHGVVFLHVTYVPA  VFLHVTYVP  5         0.5113
197.9     8.00  0.50     Sequence        WB
 HLA-DPA10201-DPB10101 1063      PHGVVFLHVTYVPAQ  VFLHVTYVP  4         0.5097
201.3     8.00  0.56     Sequence        WB
 HLA-DPA10201-DPB10101 1064      HGVVFLHVTYVPAQE  VFLHVTYVP  3         0.5098
201.1     8.00  0.56     Sequence        WB
 HLA-DPA10201-DPB10101 1065      GVVFLHVTYVPAQEK  VFLHVTYVP  2         0.5073
206.6     8.50  0.57     Sequence        WB
 HLA-DPA10201-DPB10101 1066      VVFLHVTYVPAQEKN  VFLHVTYVP  1         0.4605
342.7    15.00  0.40     Sequence
 HLA-DPA10201-DPB10101 1067      VFLHVTYVPAQEKNF  HVTYVPAQE  3         0.4279
487.6    21.00  0.33     Sequence
 HLA-DPA10201-DPB10101 1068      FLHVTYVPAQEKNFT  HVTYVPAQE  2         0.3660
953.0    36.00  0.44     Sequence
 HLA-DPA10201-DPB10101 1069      LHVTYVPAQEKNFTT  HVTYVPAQE  1         0.2723
2628.0    65.00  0.49     Sequence
 HLA-DPA10201-DPB10101 1070      HVTYVPAQEKNFTTA  TYVPAQEKN  2         0.2330
4018.8    75.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1071      VTYVPAQEKNFTTAP  YVPAQEKNF  2         0.1853
6735.5    85.00  0.20     Sequence
 HLA-DPA10201-DPB10101 1072      TYVPAQEKNFTTAPA  PAQEKNFTT  3         0.1758
7465.0    90.00  0.16     Sequence
 HLA-DPA10201-DPB10101 1073      YVPAQEKNFTTAPAI  NFTTAPAIX  7         0.2273
4275.8    75.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1074      VPAQEKNFTTAPAIC  NFTTAPAIC  6         0.2391
3760.4    75.00  0.30     Sequence
```

```
 HLA-DPA10201-DPB10101 1075      PAQEKNFTTAPAICH  NFTTAPAIC  5         0.2601
2998.7    70.00  0.37     Sequence
 HLA-DPA10201-DPB10101 1076      AQEKNFTTAPAICHD  NFTTAPAIC  4         0.2707
2673.7    65.00  0.38     Sequence
 HLA-DPA10201-DPB10101 1077      QEKNFTTAPAICHDG  NFTTAPAIC  3         0.2678
2757.9    65.00  0.38     Sequence
 HLA-DPA10201-DPB10101 1078      EKNFTTAPAICHDGK  NFTTAPAIC  2         0.2534
3221.4    70.00  0.43     Sequence
 HLA-DPA10201-DPB10101 1079      KNFTTAPAICHDGKA  NFTTAPAIC  1         0.2217
4540.3    80.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1080      NFTTAPAICHDGKAH  TTAPAICHD  2         0.1163
14211.5   100.00  0.26     Sequence
 HLA-DPA10201-DPB10101 1081      FTTAPAICHDGKAHF  TTAPAICHD  1         0.1089
15395.5   100.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5         0.0897
18944.2   100.00  0.21     Sequence
 HLA-DPA10201-DPB10101 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4         0.0954
17811.2   100.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1084      APAICHDGKAHFPRE  ICHDGKAHF  3         0.1039
16241.3   100.00  0.23     Sequence
 HLA-DPA10201-DPB10101 1085      PAICHDGKAHFPREG  ICHDGKAHF  2         0.1086
15441.4   100.00  0.23     Sequence
 HLA-DPA10201-DPB10101 1086      AICHDGKAHFPREGV  GKAHFPREG  5         0.1147
14451.5   100.00  0.21     Sequence
 HLA-DPA10201-DPB10101 1087      ICHDGKAHFPREGVF  GKAHFPREG  4         0.1189
13817.7   100.00  0.20     Sequence
 HLA-DPA10201-DPB10101 1088      CHDGKAHFPREGVFV  HFPREGVFV  6         0.1362
11448.3    95.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1089      HDGKAHFPREGVFVS  FPREGVFVS  6         0.1855
6719.5    85.00  0.31     Sequence
 HLA-DPA10201-DPB10101 1090      DGKAHFPREGVFVSN  FPREGVFVS  5         0.2059
5387.1    80.00  0.33     Sequence
 HLA-DPA10201-DPB10101 1091      GKAHFPREGVFVSNG  FPREGVFVS  4         0.2150
4883.2    80.00  0.32     Sequence
 HLA-DPA10201-DPB10101 1092      KAHFPREGVFVSNGT  FPREGVFVS  3         0.2271
4281.8    75.00  0.32     Sequence
 HLA-DPA10201-DPB10101 1093      AHFPREGVFVSNGTH  FPREGVFVS  2         0.2209
4582.1    80.00  0.31     Sequence
 HLA-DPA10201-DPB10101 1094      HFPREGVFVSNGTHW  PREGVFVSN  2         0.2195
4649.4    80.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1095      FPREGVFVSNGTHWF  VFVSNGTHW  5         0.2578
3072.0    70.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5         0.2842
2308.5    60.00  0.32     Sequence
 HLA-DPA10201-DPB10101 1097      REGVFVSNGTHWFVT  VSNGTHWFV  5         0.3009
1926.9    55.00  0.27     Sequence
 HLA-DPA10201-DPB10101 1098      EGVFVSNGTHWFVTQ  VSNGTHWFV  4         0.3110
1728.1    55.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1099      GVFVSNGTHWFVTQR  VSNGTHWFV  3         0.3215
1542.6    48.00  0.27     Sequence
 HLA-DPA10201-DPB10101 1100      VFVSNGTHWFVTQRN  VSNGTHWFV  2         0.3234
1512.0    48.00  0.29     Sequence
 HLA-DPA10201-DPB10101 1101      FVSNGTHWFVTQRNF  THWFVTQRN  5         0.3420
1235.3    42.00  0.18     Sequence
 HLA-DPA10201-DPB10101 1102      VSNGTHWFVTQRNFY  HWFVTQRNF  5         0.3457
1187.0    41.00  0.24     Sequence
 HLA-DPA10201-DPB10101 1103      SNGTHWFVTQRNFYE  WFVTQRNFY  5         0.3593
1024.7    37.00  0.27     Sequence
 HLA-DPA10201-DPB10101 1104      NGTHWFVTQRNFYEP  WFVTQRNFY  4         0.3697
915.4    35.00  0.27     Sequence
 HLA-DPA10201-DPB10101 1105      GTHWFVTQRNFYEPQ  WFVTQRNFY  3         0.3715
898.3    34.00  0.27     Sequence
 HLA-DPA10201-DPB10101 1106      THWFVTQRNFYEPQI  WFVTQRNFY  2         0.3811
809.2    32.00  0.29     Sequence
 HLA-DPA10201-DPB10101 1107      HWFVTQRNFYEPQII  VTQRNFYEP  3         0.4084
602.5    25.00  0.14     Sequence
```

```
 HLA-DPA10201-DPB10101 1108      WFVTQRNFYEPQIIT  NFYEPQIIT  6        0.4209
526.0    22.00  0.26     Sequence
 HLA-DPA10201-DPB10101 1109      FVTQRNFYEPQIITT  NFYEPQIIT  5        0.4370
442.1    19.00  0.45     Sequence
 HLA-DPA10201-DPB10101 1110      VTQRNFYEPQIITTD  NFYEPQIIT  4        0.4267
494.1    21.00  0.48     Sequence
 HLA-DPA10201-DPB10101 1111      TQRNFYEPQIITTDN  NFYEPQIIT  3        0.4232
513.5    22.00  0.49     Sequence
 HLA-DPA10201-DPB10101 1112      QRNFYEPQIITTDNT  NFYEPQIIT  2        0.4118
580.9    24.00  0.48     Sequence
 HLA-DPA10201-DPB10101 1113      RNFYEPQIITTDNTF  FYEPQIITT  2        0.3684
928.3    35.00  0.41     Sequence
 HLA-DPA10201-DPB10101 1114      NFYEPQIITTDNTFV  FYEPQIITT  1        0.2794
2431.6    65.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.2519
3276.0    70.00  0.19     Sequence
 HLA-DPA10201-DPB10101 1116      YEPQIITTDNTFVSG  IITTDNTFV  4        0.2209
4578.7    80.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1117      EPQIITTDNTFVSGN  ITTDNTFVS  4        0.2063
5365.4    80.00  0.30     Sequence
 HLA-DPA10201-DPB10101 1118      PQIITTDNTFVSGNC  ITTDNTFVS  3        0.2077
5283.1    80.00  0.31     Sequence
 HLA-DPA10201-DPB10101 1119      QIITTDNTFVSGNCD  ITTDNTFVS  2        0.1942
6113.0    85.00  0.31     Sequence
 HLA-DPA10201-DPB10101 1120      IITTDNTFVSGNCDV  TFVSGNCDV  6        0.1806
7087.0    90.00  0.33     Sequence
 HLA-DPA10201-DPB10101 1121      ITTDNTFVSGNCDVV  TFVSGNCDV  5        0.2003
5723.5    85.00  0.50     Sequence
 HLA-DPA10201-DPB10101 1122      TTDNTFVSGNCDVVI  TFVSGNCDV  4        0.2197
4641.9    80.00  0.45     Sequence
 HLA-DPA10201-DPB10101 1123      TDNTFVSGNCDVVIG  TFVSGNCDV  3        0.2211
4572.3    80.00  0.45     Sequence
 HLA-DPA10201-DPB10101 1124      DNTFVSGNCDVVIGI  TFVSGNCDV  2        0.2339
3978.3    75.00  0.40     Sequence
 HLA-DPA10201-DPB10101 1125      NTFVSGNCDVVIGIV  FVSGNCDVV  2        0.2290
4195.0    75.00  0.29     Sequence
 HLA-DPA10201-DPB10101 1126      TFVSGNCDVVIGIVN  FVSGNCDVV  1        0.2181
4720.7    80.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1127      FVSGNCDVVIGIVNN  NCDVVIGIV  4        0.2026
5584.5    85.00  0.12     Sequence
 HLA-DPA10201-DPB10101 1128      VSGNCDVVIGIVNNT  DVVIGIVNN  5        0.1794
7178.4    90.00  0.21     Sequence
 HLA-DPA10201-DPB10101 1129      SGNCDVVIGIVNNTV  VVIGIVNNT  5        0.2216
4544.8    80.00  0.31     Sequence
 HLA-DPA10201-DPB10101 1130      GNCDVVIGIVNNTVY  VVIGIVNNT  4        0.2382
3799.4    75.00  0.31     Sequence
 HLA-DPA10201-DPB10101 1131      NCDVVIGIVNNTVYD  VVIGIVNNT  3        0.2497
3353.2    70.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1132      CDVVIGIVNNTVYDP  VVIGIVNNT  2        0.2551
3164.7    70.00  0.26     Sequence
 HLA-DPA10201-DPB10101 1133      DVVIGIVNNTVYDPL  IVNNTVYDP  5        0.2829
2342.7    60.00  0.54     Sequence
 HLA-DPA10201-DPB10101 1134      VVIGIVNNTVYDPLQ  IVNNTVYDP  4        0.3057
1829.5    55.00  0.58     Sequence
 HLA-DPA10201-DPB10101 1135      VIGIVNNTVYDPLQP  IVNNTVYDP  3        0.3330
1362.6    45.00  0.55     Sequence
 HLA-DPA10201-DPB10101 1136      IGIVNNTVYDPLQPE  IVNNTVYDP  2        0.3349
1334.3    44.00  0.54     Sequence
 HLA-DPA10201-DPB10101 1137      GIVNNTVYDPLQPEL  NTVYDPLQP  4        0.3531
1095.4    39.00  0.24     Sequence
 HLA-DPA10201-DPB10101 1138      IVNNTVYDPLQPELD  NTVYDPLQP  3        0.3502
1131.0    40.00  0.30     Sequence
 HLA-DPA10201-DPB10101 1139      VNNTVYDPLQPELDS  NTVYDPLQP  2        0.3411
1247.8    42.00  0.29     Sequence
 HLA-DPA10201-DPB10101 1140      NNTVYDPLQPELDSF  VYDPLQPEL  3        0.3305
1399.9    45.00  0.35     Sequence
```

```
 HLA-DPA10201-DPB10101 1141      NTVYDPLQPELDSFK  VYDPLQPEL  2        0.2945
2066.3    60.00  0.39     Sequence
 HLA-DPA10201-DPB10101 1142      TVYDPLQPELDSFKE  VYDPLQPEL  1        0.2684
2739.9    65.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1143      VYDPLQPELDSFKEE  PLQPELDSF  3        0.2773
2489.8    65.00  0.18     Sequence
 HLA-DPA10201-DPB10101 1144      YDPLQPELDSFKEEL  ELDSFKEEL  6        0.2958
2037.8    60.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1145      DPLQPELDSFKEELD  ELDSFKEEL  5        0.3207
1556.0    48.00  0.44     Sequence
 HLA-DPA10201-DPB10101 1146      PLQPELDSFKEELDK  ELDSFKEEL  4        0.3358
1320.8    44.00  0.46     Sequence
 HLA-DPA10201-DPB10101 1147      LQPELDSFKEELDKY  ELDSFKEEL  3        0.3464
1178.1    41.00  0.45     Sequence
 HLA-DPA10201-DPB10101 1148      QPELDSFKEELDKYF  ELDSFKEEL  2        0.3746
868.3    33.00  0.35     Sequence
 HLA-DPA10201-DPB10101 1149      PELDSFKEELDKYFK  SFKEELDKY  4        0.3796
823.0    32.00  0.29     Sequence
 HLA-DPA10201-DPB10101 1150      ELDSFKEELDKYFKN  SFKEELDKY  3        0.3638
976.1    36.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1151      LDSFKEELDKYFKNH  SFKEELDKY  2        0.3523
1105.0    39.00  0.31     Sequence
 HLA-DPA10201-DPB10101 1152      DSFKEELDKYFKNHT  SFKEELDKY  1        0.3302
1403.3    46.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1153      SFKEELDKYFKNHTS  EELDKYFKN  3        0.3259
1471.0    47.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1154      FKEELDKYFKNHTSP  EELDKYFKN  2        0.2954
2045.4    60.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1155      KEELDKYFKNHTSPD  ELDKYFKNH  2        0.2155
4854.9    80.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1156      EELDKYFKNHTSPDV  YFKNHTSPD  5        0.2243
4413.4    80.00  0.29     Sequence
 HLA-DPA10201-DPB10101 1157      ELDKYFKNHTSPDVD  YFKNHTSPD  4        0.2174
4756.3    80.00  0.32     Sequence
 HLA-DPA10201-DPB10101 1158      LDKYFKNHTSPDVDL  YFKNHTSPD  3        0.2192
4668.2    80.00  0.36     Sequence
 HLA-DPA10201-DPB10101 1159      DKYFKNHTSPDVDLG  YFKNHTSPD  2        0.2085
5238.6    80.00  0.41     Sequence
 HLA-DPA10201-DPB10101 1160      KYFKNHTSPDVDLGD  YFKNHTSPD  1        0.2031
5551.4    85.00  0.37     Sequence
 HLA-DPA10201-DPB10101 1161      YFKNHTSPDVDLGDI  KNHTSPDVD  2        0.1601
8843.2    90.00  0.17     Sequence
 HLA-DPA10201-DPB10101 1162      FKNHTSPDVDLGDIS  TSPDVDLGD  4        0.1179
13963.8   100.00  0.15     Sequence
 HLA-DPA10201-DPB10101 1163      KNHTSPDVDLGDISG  TSPDVDLGD  3        0.0721
22912.4   100.00  0.32     Sequence
 HLA-DPA10201-DPB10101 1164      NHTSPDVDLGDISGI  DVDLGDISG  5        0.0923
18425.7   100.00  0.31     Sequence
 HLA-DPA10201-DPB10101 1165      HTSPDVDLGDISGIN  DLGDISGIN  6        0.1107
15096.4   100.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1166      TSPDVDLGDISGINA  DLGDISGIN  5        0.1387
11145.0    95.00  0.42     Sequence
 HLA-DPA10201-DPB10101 1167      SPDVDLGDISGINAS  DLGDISGIN  4        0.1482
10061.4    95.00  0.38     Sequence
 HLA-DPA10201-DPB10101 1168      PDVDLGDISGINASF  DLGDISGIN  3        0.1636
8516.5    90.00  0.33     Sequence
 HLA-DPA10201-DPB10101 1169      DVDLGDISGINASFV  DISGINASF  5        0.1989
5811.3    85.00  0.42     Sequence
 HLA-DPA10201-DPB10101 1170      VDLGDISGINASFVN  DISGINASF  4        0.2097
5172.4    80.00  0.39     Sequence
 HLA-DPA10201-DPB10101 1171      DLGDISGINASFVNI  GINASFVNI  6        0.2547
3179.4    70.00  0.35     Sequence
 HLA-DPA10201-DPB10101 1172      LGDISGINASFVNIQ  GINASFVNI  5        0.2786
2453.0    65.00  0.42     Sequence
 HLA-DPA10201-DPB10101 1173      GDISGINASFVNIQK  GINASFVNI  4        0.3315
1384.5    45.00  0.40     Sequence
```

```
 HLA-DPA10201-DPB10101 1174      DISGINASFVNIQKE  GINASFVNI  3         0.3648
965.9    36.00  0.33     Sequence
 HLA-DPA10201-DPB10101 1175      ISGINASFVNIQKEI  SFVNIQKEI  6         0.3928
713.0    29.00  0.31     Sequence
 HLA-DPA10201-DPB10101 1176      SGINASFVNIQKEID  SFVNIQKEI  5         0.4342
455.5    20.00  0.47     Sequence
 HLA-DPA10201-DPB10101 1177      GINASFVNIQKEIDR  SFVNIQKEI  4         0.4366
444.2    19.00  0.53     Sequence
 HLA-DPA10201-DPB10101 1178      INASFVNIQKEIDRL  SFVNIQKEI  3         0.4483
391.1    17.00  0.52     Sequence
 HLA-DPA10201-DPB10101 1179      NASFVNIQKEIDRLN  SFVNIQKEI  2         0.4369
442.6    19.00  0.53     Sequence
 HLA-DPA10201-DPB10101 1180      ASFVNIQKEIDRLNE  SFVNIQKEI  1         0.3967
683.9    28.00  0.38     Sequence
 HLA-DPA10201-DPB10101 1181      SFVNIQKEIDRLNEV  SFVNIQKEI  0         0.3600
1017.4    37.00  0.26     Sequence
 HLA-DPA10201-DPB10101 1182      FVNIQKEIDRLNEVA  QKEIDRLNE  4         0.3086
1774.2    55.00  0.23     Sequence
 HLA-DPA10201-DPB10101 1183      VNIQKEIDRLNEVAK  QKEIDRLNE  3         0.2556
3147.0    70.00  0.32     Sequence
 HLA-DPA10201-DPB10101 1184      NIQKEIDRLNEVAKN  QKEIDRLNE  2         0.2519
3275.1    70.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1185      IQKEIDRLNEVAKNL  EIDRLNEVA  3         0.2597
3010.9    70.00  0.26     Sequence
 HLA-DPA10201-DPB10101 1186      QKEIDRLNEVAKNLN  EIDRLNEVA  2         0.2553
3155.7    70.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1187      KEIDRLNEVAKNLNE  RLNEVAKNL  4         0.2507
3318.8    70.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1188      EIDRLNEVAKNLNES  RLNEVAKNL  3         0.2162
4820.5    80.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1189      IDRLNEVAKNLNESL  EVAKNLNES  5         0.2463
3481.2    70.00  0.29     Sequence
 HLA-DPA10201-DPB10101 1190      DRLNEVAKNLNESLI  EVAKNLNES  4         0.2902
2163.6    60.00  0.32     Sequence
 HLA-DPA10201-DPB10101 1191      RLNEVAKNLNESLID  EVAKNLNES  3         0.3269
1455.6    47.00  0.27     Sequence
 HLA-DPA10201-DPB10101 1192      LNEVAKNLNESLIDL  NLNESLIDL  6         0.3936
707.2    29.00  0.39     Sequence
 HLA-DPA10201-DPB10101 1193      NEVAKNLNESLIDLQ  NLNESLIDL  5         0.4097
594.2    25.00  0.44     Sequence
 HLA-DPA10201-DPB10101 1194      EVAKNLNESLIDLQE  NLNESLIDL  4         0.4367
443.7    19.00  0.44     Sequence
 HLA-DPA10201-DPB10101 1195      VAKNLNESLIDLQEL  NLNESLIDL  3         0.4631
333.4    14.00  0.36     Sequence
 HLA-DPA10201-DPB10101 1196      AKNLNESLIDLQELG  NLNESLIDL  2         0.4474
395.1    17.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1197      KNLNESLIDLQELGK  NLNESLIDL  1         0.4301
476.6    20.00  0.27     Sequence
 HLA-DPA10201-DPB10101 1198      NLNESLIDLQELGKY  LIDLQELGK  5         0.3846
779.6    31.00  0.31     Sequence
 HLA-DPA10201-DPB10101 1199      LNESLIDLQELGKYE  LIDLQELGK  4         0.3758
857.6    33.00  0.37     Sequence
 HLA-DPA10201-DPB10101 1200      NESLIDLQELGKYEQ  LIDLQELGK  3         0.3629
985.9    36.00  0.40     Sequence
 HLA-DPA10201-DPB10101 1201      ESLIDLQELGKYEQY  LIDLQELGK  2         0.3453
1192.3    41.00  0.43     Sequence
 HLA-DPA10201-DPB10101 1202      SLIDLQELGKYEQYI  LIDLQELGK  1         0.3044
1856.9    55.00  0.31     Sequence
 HLA-DPA10201-DPB10101 1203      LIDLQELGKYEQYIK  DLQELGKYE  2         0.2840
2313.5    60.00  0.23     Sequence
 HLA-DPA10201-DPB10101 1204      IDLQELGKYEQYIKW  LGKYEQYIK  5         0.2794
2433.7    65.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1205      DLQELGKYEQYIKWP  LGKYEQYIK  4         0.2641
2871.2    65.00  0.27     Sequence
 HLA-DPA10201-DPB10101 1206      LQELGKYEQYIKWPW  LGKYEQYIK  3         0.3050
1844.8    55.00  0.28     Sequence
```

```
 HLA-DPA10201-DPB10101 1207      QELGKYEQYIKWPWY  LGKYEQYIK  2        0.3197
1573.3    49.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1208      ELGKYEQYIKWPWYI  YEQYIKWPW  4        0.3549
1074.2    39.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1209      LGKYEQYIKWPWYIW  QYIKWPWYI  5        0.4212
524.6    22.00  0.26     Sequence
 HLA-DPA10201-DPB10101 1210      GKYEQYIKWPWYIWL  YIKWPWYIW  5        0.4653
325.3    14.00  0.23     Sequence
 HLA-DPA10201-DPB10101 1211      KYEQYIKWPWYIWLG  YIKWPWYIW  4        0.4702
308.5    13.00  0.21     Sequence
 HLA-DPA10201-DPB10101 1212      YEQYIKWPWYIWLGF  YIKWPWYIW  3        0.4789
281.1    12.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1213      EQYIKWPWYIWLGFI  WPWYIWLGF  5        0.4914
245.4    10.00  0.19     Sequence
 HLA-DPA10201-DPB10101 1214      QYIKWPWYIWLGFIA  WPWYIWLGF  4        0.5213
177.6     7.00  0.17     Sequence         WB
 HLA-DPA10201-DPB10101 1215      YIKWPWYIWLGFIAG  WYIWLGFIA  5        0.4999
223.8     9.00  0.20     Sequence         WB
 HLA-DPA10201-DPB10101 1216      IKWPWYIWLGFIAGL  YIWLGFIAG  5        0.4724
301.3    13.00  0.25     Sequence
 HLA-DPA10201-DPB10101 1217      KWPWYIWLGFIAGLI  YIWLGFIAG  4        0.4873
256.4    11.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1218      WPWYIWLGFIAGLIA  YIWLGFIAG  3        0.4695
311.1    13.00  0.30     Sequence
 HLA-DPA10201-DPB10101 1219      PWYIWLGFIAGLIAI  YIWLGFIAG  2        0.4590
348.5    15.00  0.30     Sequence
 HLA-DPA10201-DPB10101 1220      WYIWLGFIAGLIAIV  GFIAGLIAI  5        0.4700
309.3    13.00  0.29     Sequence
 HLA-DPA10201-DPB10101 1221      YIWLGFIAGLIAIVM  GFIAGLIAI  4        0.4152
559.5    24.00  0.41     Sequence
 HLA-DPA10201-DPB10101 1222      IWLGFIAGLIAIVMV  GFIAGLIAI  3        0.3961
688.3    28.00  0.44     Sequence
 HLA-DPA10201-DPB10101 1223      WLGFIAGLIAIVMVT  GFIAGLIAI  2        0.3736
877.8    34.00  0.47     Sequence
 HLA-DPA10201-DPB10101 1224      LGFIAGLIAIVMVTI  GFIAGLIAI  1        0.3432
1220.3    42.00  0.36     Sequence
 HLA-DPA10201-DPB10101 1225      GFIAGLIAIVMVTIM  GFIAGLIAI  0        0.3036
1871.3    55.00  0.26     Sequence
 HLA-DPA10201-DPB10101 1226      FIAGLIAIVMVTIML  GLIAIVMVT  3        0.2592
3026.7    70.00  0.20     Sequence
 HLA-DPA10201-DPB10101 1227      IAGLIAIVMVTIMLC  GLIAIVMVT  2        0.2101
5149.6    80.00  0.35     Sequence
 HLA-DPA10201-DPB10101 1228      AGLIAIVMVTIMLCC  LIAIVMVTI  2        0.1977
5889.0    85.00  0.26     Sequence
 HLA-DPA10201-DPB10101 1229      GLIAIVMVTIMLCCM  AIVMVTIML  3        0.1930
6193.1    85.00  0.20     Sequence
 HLA-DPA10201-DPB10101 1230      LIAIVMVTIMLCCMT  AIVMVTIML  2        0.1745
7567.1    90.00  0.23     Sequence
 HLA-DPA10201-DPB10101 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2        0.1667
8231.9    90.00  0.21     Sequence
 HLA-DPA10201-DPB10101 1232      AIVMVTIMLCCMTSC  TIMLCCMTS  5        0.1755
7486.6    90.00  0.38     Sequence
 HLA-DPA10201-DPB10101 1233      IVMVTIMLCCMTSCC  TIMLCCMTS  4        0.1581
9040.5    90.00  0.48     Sequence
 HLA-DPA10201-DPB10101 1234      VMVTIMLCCMTSCCS  TIMLCCMTS  3        0.1533
9521.5    95.00  0.50     Sequence
 HLA-DPA10201-DPB10101 1235      MVTIMLCCMTSCCSC  TIMLCCMTS  2        0.1455
10360.5    95.00  0.50     Sequence
 HLA-DPA10201-DPB10101 1236      VTIMLCCMTSCCSCL  TIMLCCMTS  1        0.1470
10193.3    95.00  0.30     Sequence
 HLA-DPA10201-DPB10101 1237      TIMLCCMTSCCSCLK  CCMTSCCSC  4        0.1562
9229.9    90.00  0.19     Sequence
 HLA-DPA10201-DPB10101 1238      IMLCCMTSCCSCLKG  CCMTSCCSC  3        0.1411
10864.4    95.00  0.22     Sequence
 HLA-DPA10201-DPB10101 1239      MLCCMTSCCSCLKGC  CCMTSCCSC  2        0.1267
12696.3    95.00  0.25     Sequence
```

```
 HLA-DPA10201-DPB10101 1240      LCCMTSCCSCLKGCC  CMTSCCSCL  2        0.1212
13476.9    95.00  0.26     Sequence
 HLA-DPA10201-DPB10101 1241      CCMTSCCSCLKGCCS  CMTSCCSCL  1        0.1107
15098.0   100.00  0.23     Sequence
 HLA-DPA10201-DPB10101 1242      CMTSCCSCLKGCCSC  SCCSCLKGC  3        0.1020
16578.6   100.00  0.13     Sequence
 HLA-DPA10201-DPB10101 1243      MTSCCSCLKGCCSCG  CLKGCCSCG  6        0.0767
21795.7   100.00  0.31     Sequence
 HLA-DPA10201-DPB10101 1244      TSCCSCLKGCCSCGS  CLKGCCSCG  5        0.0644
24916.3   100.00  0.41     Sequence
 HLA-DPA10201-DPB10101 1245      SCCSCLKGCCSCGSC  CLKGCCSCG  4        0.0649
24771.9   100.00  0.44     Sequence
 HLA-DPA10201-DPB10101 1246      CCSCLKGCCSCGSCC  CLKGCCSCG  3        0.0640
25020.0   100.00  0.50     Sequence
 HLA-DPA10201-DPB10101 1247      CSCLKGCCSCGSCCK  CLKGCCSCG  2        0.0625
25414.8   100.00  0.46     Sequence
 HLA-DPA10201-DPB10101 1248      SCLKGCCSCGSCCKF  CLKGCCSCG  1        0.0564
27155.0   100.00  0.28     Sequence
 HLA-DPA10201-DPB10101 1249      CLKGCCSCGSCCKFD  SCGSCCKFD  6        0.0528
28237.5   100.00  0.21     Sequence
 HLA-DPA10201-DPB10101 1250      LKGCCSCGSCCKFDE  SCGSCCKFD  5        0.0669
24237.7   100.00  0.35     Sequence
 HLA-DPA10201-DPB10101 1251      KGCCSCGSCCKFDED  CGSCCKFDE  5        0.0745
22321.0   100.00  0.40     Sequence
 HLA-DPA10201-DPB10101 1252      GCCSCGSCCKFDEDD  CGSCCKFDE  4        0.0767
21798.5   100.00  0.40     Sequence
 HLA-DPA10201-DPB10101 1253      CCSCGSCCKFDEDDS  CGSCCKFDE  3        0.0827
20423.7   100.00  0.37     Sequence
 HLA-DPA10201-DPB10101 1254      CSCGSCCKFDEDDSE  CGSCCKFDE  2        0.0944
17998.9   100.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1255      SCGSCCKFDEDDSEP  KFDEDDSEP  6        0.1151
14391.1   100.00  0.37     Sequence
 HLA-DPA10201-DPB10101 1256      CGSCCKFDEDDSEPV  KFDEDDSEP  5        0.1428
10663.4    95.00  0.50     Sequence
 HLA-DPA10201-DPB10101 1257      GSCCKFDEDDSEPVL  KFDEDDSEP  4        0.1653
8362.9    90.00  0.54     Sequence
 HLA-DPA10201-DPB10101 1258      SCCKFDEDDSEPVLK  KFDEDDSEP  3        0.1885
6506.1    85.00  0.50     Sequence
 HLA-DPA10201-DPB10101 1259      CCKFDEDDSEPVLKG  KFDEDDSEP  2        0.1842
6813.1    85.00  0.47     Sequence
 HLA-DPA10201-DPB10101 1260      CKFDEDDSEPVLKGV  KFDEDDSEP  1        0.1823
6953.6    85.00  0.42     Sequence
 HLA-DPA10201-DPB10101 1261      KFDEDDSEPVLKGVK  EDDSEPVLK  3        0.1692
8011.9    90.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1262      FDEDDSEPVLKGVKL  EDDSEPVLK  2        0.1902
6388.2    85.00  0.34     Sequence
 HLA-DPA10201-DPB10101 1263      DEDDSEPVLKGVKLH  VLKGVKLHX  7        0.2695
2706.5    65.00  0.38     Sequence
 HLA-DPA10201-DPB10101 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.4332
460.7    20.00  0.62     Sequence
 HLA-DPA10201-DPB10101 1265      DDSEPVLKGVKLHYT  VLKGVKLHY  5        0.5435
139.6     5.00  0.81     Sequence         WB
 HLA-DPA10103-DPB10201    1      PSPIKEMFVFLVLLP  KEMFVFLVL  4        0.5608
115.8     7.50  0.25     Sequence         WB
 HLA-DPA10103-DPB10201    2      SPIKEMFVFLVLLPL  FVFLVLLPL  6        0.6172
62.9     4.00  0.40     Sequence         WB
 HLA-DPA10103-DPB10201    3      PIKEMFVFLVLLPLV  FVFLVLLPL  5        0.6487
44.8     2.50  0.31     Sequence         WB
 HLA-DPA10103-DPB10201    4      IKEMFVFLVLLPLVS  FVFLVLLPL  4        0.6384
50.0     3.00  0.33     Sequence         WB
 HLA-DPA10103-DPB10201    5      KEMFVFLVLLPLVSS  FVFLVLLPL  3        0.6231
59.0     4.00  0.34     Sequence         WB
 HLA-DPA10103-DPB10201    6      EMFVFLVLLPLVSSQ  VFLVLLPLV  3        0.5856
88.6     6.00  0.38     Sequence         WB
 HLA-DPA10103-DPB10201    7      MFVFLVLLPLVSSQC  VFLVLLPLV  2        0.5595
117.4     7.50  0.43     Sequence         WB
```

```
 HLA-DPA10103-DPB10201    8       FVFLVLLPLVSSQCV  VFLVLLPLV  1         0.5047
212.5    13.00  0.37     Sequence
 HLA-DPA10103-DPB10201    9       VFLVLLPLVSSQCVN  LVLLPLVSS  2         0.4265
495.3    23.00  0.17     Sequence
 HLA-DPA10103-DPB10201    10      FLVLLPLVSSQCVNF  LVSSQCVNF  6         0.3943
701.7    28.00  0.47     Sequence
 HLA-DPA10103-DPB10201    11      LVLLPLVSSQCVNFT  LVSSQCVNF  5         0.3734
879.7    31.00  0.54     Sequence
 HLA-DPA10103-DPB10201    12      VLLPLVSSQCVNFTN  LVSSQCVNF  4         0.3703
910.0    32.00  0.54     Sequence
 HLA-DPA10103-DPB10201    13      LLPLVSSQCVNFTNR  LVSSQCVNF  3         0.3554
1068.5    34.00  0.55     Sequence
 HLA-DPA10103-DPB10201    14      LPLVSSQCVNFTNRT  LVSSQCVNF  2         0.3410
1248.5    37.00  0.46     Sequence
 HLA-DPA10103-DPB10201    15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1         0.2968
2015.8    46.00  0.38     Sequence
 HLA-DPA10103-DPB10201    16      LVSSQCVNFTNRTQL  VNFTNRTQL  6         0.2965
2022.3    46.00  0.28     Sequence
 HLA-DPA10103-DPB10201    17      VSSQCVNFTNRTQLP  VNFTNRTQL  5         0.2611
2965.4    55.00  0.44     Sequence
 HLA-DPA10103-DPB10201    18      SSQCVNFTNRTQLPS  VNFTNRTQL  4         0.2596
3014.8    55.00  0.35     Sequence
 HLA-DPA10103-DPB10201    19      SQCVNFTNRTQLPSA  VNFTNRTQL  3         0.2414
3670.3    60.00  0.38     Sequence
 HLA-DPA10103-DPB10201    20      QCVNFTNRTQLPSAY  VNFTNRTQL  2         0.2386
3781.8    60.00  0.35     Sequence
 HLA-DPA10103-DPB10201    21      CVNFTNRTQLPSAYT  FTNRTQLPS  3         0.2161
4824.3    70.00  0.33     Sequence
 HLA-DPA10103-DPB10201    22      VNFTNRTQLPSAYTN  FTNRTQLPS  2         0.1881
6532.4    75.00  0.29     Sequence
 HLA-DPA10103-DPB10201    23      NFTNRTQLPSAYTNS  QLPSAYTNS  6         0.1447
10444.6    85.00  0.22     Sequence
 HLA-DPA10103-DPB10201    24      FTNRTQLPSAYTNSF  LPSAYTNSF  6         0.2242
4420.7    65.00  0.41     Sequence
 HLA-DPA10103-DPB10201    25      TNRTQLPSAYTNSFT  LPSAYTNSF  5         0.2196
4643.9    65.00  0.44     Sequence
 HLA-DPA10103-DPB10201    26      NRTQLPSAYTNSFTR  LPSAYTNSF  4         0.2930
2099.6    47.00  0.38     Sequence
 HLA-DPA10103-DPB10201    27      RTQLPSAYTNSFTRG  AYTNSFTRG  6         0.3249
1487.5    40.00  0.44     Sequence
 HLA-DPA10103-DPB10201    28      TQLPSAYTNSFTRGV  AYTNSFTRG  5         0.3547
1077.2    35.00  0.44     Sequence
 HLA-DPA10103-DPB10201    29      QLPSAYTNSFTRGVY  AYTNSFTRG  4         0.3810
810.4    30.00  0.37     Sequence
 HLA-DPA10103-DPB10201    30      LPSAYTNSFTRGVYY  AYTNSFTRG  3         0.3940
703.8    28.00  0.34     Sequence
 HLA-DPA10103-DPB10201    31      PSAYTNSFTRGVYYP  AYTNSFTRG  2         0.3919
720.3    28.00  0.29     Sequence
 HLA-DPA10103-DPB10201    32      SAYTNSFTRGVYYPD  FTRGVYYPD  6         0.4153
559.3    24.00  0.34     Sequence
 HLA-DPA10103-DPB10201    33      AYTNSFTRGVYYPDK  FTRGVYYPD  5         0.3858
769.1    29.00  0.43     Sequence
 HLA-DPA10103-DPB10201    34      YTNSFTRGVYYPDKV  FTRGVYYPD  4         0.3853
773.8    29.00  0.44     Sequence
 HLA-DPA10103-DPB10201    35      TNSFTRGVYYPDKVF  FTRGVYYPD  3         0.4131
572.9    25.00  0.35     Sequence
 HLA-DPA10103-DPB10201    36      NSFTRGVYYPDKVFR  TRGVYYPDK  3         0.4162
553.8    24.00  0.19     Sequence
 HLA-DPA10103-DPB10201    37      SFTRGVYYPDKVFRS  YYPDKVFRS  6         0.4216
522.4    23.00  0.25     Sequence
 HLA-DPA10103-DPB10201    38      FTRGVYYPDKVFRSS  YYPDKVFRS  5         0.4029
639.2    26.00  0.28     Sequence
 HLA-DPA10103-DPB10201    39      TRGVYYPDKVFRSSV  YYPDKVFRS  4         0.3931
711.2    28.00  0.28     Sequence
 HLA-DPA10103-DPB10201    40      RGVYYPDKVFRSSVL  YYPDKVFRS  3         0.4160
554.7    24.00  0.25     Sequence
```

```
 HLA-DPA10103-DPB10201   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.3904
732.0    28.00  0.23     Sequence
 HLA-DPA10103-DPB10201   42      VYYPDKVFRSSVLHS  VFRSSVLHS  6        0.3812
809.0    30.00  0.33     Sequence
 HLA-DPA10103-DPB10201   43      YYPDKVFRSSVLHST  FRSSVLHST  6        0.3840
784.8    29.00  0.41     Sequence
 HLA-DPA10103-DPB10201   44      YPDKVFRSSVLHSTQ  FRSSVLHST  5        0.3466
1175.5    36.00  0.46     Sequence
 HLA-DPA10103-DPB10201   45      PDKVFRSSVLHSTQD  FRSSVLHST  4        0.3354
1327.8    38.00  0.49     Sequence
 HLA-DPA10103-DPB10201   46      DKVFRSSVLHSTQDL  FRSSVLHST  3        0.3445
1203.0    37.00  0.45     Sequence
 HLA-DPA10103-DPB10201   47      KVFRSSVLHSTQDLF  VLHSTQDLF  6        0.3735
878.7    31.00  0.34     Sequence
 HLA-DPA10103-DPB10201   48      VFRSSVLHSTQDLFL  LHSTQDLFL  6        0.4376
439.1    21.00  0.33     Sequence
 HLA-DPA10103-DPB10201   49      FRSSVLHSTQDLFLP  LHSTQDLFL  5        0.4387
434.0    21.00  0.34     Sequence
 HLA-DPA10103-DPB10201   50      RSSVLHSTQDLFLPF  LHSTQDLFL  4        0.4962
233.1    14.00  0.23     Sequence
 HLA-DPA10103-DPB10201   51      SSVLHSTQDLFLPFF  TQDLFLPFF  6        0.5898
84.6     5.50  0.28     Sequence         WB
 HLA-DPA10103-DPB10201   52      SVLHSTQDLFLPFFS  TQDLFLPFF  5        0.6192
61.6     4.00  0.26     Sequence         WB
 HLA-DPA10103-DPB10201   53      VLHSTQDLFLPFFSN  TQDLFLPFF  4        0.6259
57.2     3.50  0.25     Sequence         WB
 HLA-DPA10103-DPB10201   54      LHSTQDLFLPFFSNV  LFLPFFSNV  6        0.6777
32.7     1.60  0.49     Sequence         SB
 HLA-DPA10103-DPB10201   55      HSTQDLFLPFFSNVT  LFLPFFSNV  5        0.6665
36.9     1.90  0.49     Sequence         SB
 HLA-DPA10103-DPB10201   56      STQDLFLPFFSNVTW  LFLPFFSNV  4        0.6588
40.1     2.50  0.46     Sequence         WB
 HLA-DPA10103-DPB10201   57      TQDLFLPFFSNVTWF  LFLPFFSNV  3        0.6628
38.4     2.00  0.43     Sequence         WB
 HLA-DPA10103-DPB10201   58      QDLFLPFFSNVTWFH  LFLPFFSNV  2        0.6630
38.3     2.00  0.34     Sequence         WB
 HLA-DPA10103-DPB10201   59      DLFLPFFSNVTWFHA  FSNVTWFHA  6        0.6763
33.2     1.60  0.40     Sequence         SB
 HLA-DPA10103-DPB10201   60      LFLPFFSNVTWFHAI  FSNVTWFHA  5        0.6715
35.0     1.80  0.43     Sequence         SB
 HLA-DPA10103-DPB10201   61      FLPFFSNVTWFHAIH  FSNVTWFHA  4        0.6382
50.1     3.00  0.49     Sequence         WB
 HLA-DPA10103-DPB10201   62      LPFFSNVTWFHAIHV  FSNVTWFHA  3        0.6256
57.5     3.50  0.50     Sequence         WB
 HLA-DPA10103-DPB10201   63      PFFSNVTWFHAIHVS  FSNVTWFHA  2        0.5828
91.3     6.00  0.50     Sequence         WB
 HLA-DPA10103-DPB10201   64      FFSNVTWFHAIHVSG  FSNVTWFHA  1        0.5142
191.8    12.00  0.43     Sequence
 HLA-DPA10103-DPB10201   65      FSNVTWFHAIHVSGT  VTWFHAIHV  3        0.3968
683.0    27.00  0.19     Sequence
 HLA-DPA10103-DPB10201   66      SNVTWFHAIHVSGTN  VTWFHAIHV  2        0.3083
1779.2    44.00  0.27     Sequence
 HLA-DPA10103-DPB10201   67      NVTWFHAIHVSGTNG  FHAIHVSGT  4        0.2645
2858.3    55.00  0.26     Sequence
 HLA-DPA10103-DPB10201   68      VTWFHAIHVSGTNGT  FHAIHVSGT  3        0.2455
3511.8    60.00  0.31     Sequence
 HLA-DPA10103-DPB10201   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.1907
6351.3    75.00  0.37     Sequence
 HLA-DPA10103-DPB10201   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1        0.1696
7981.3    80.00  0.32     Sequence
 HLA-DPA10103-DPB10201   71      FHAIHVSGTNGTKRF  VSGTNGTKR  5        0.1520
9659.7    85.00  0.24     Sequence
 HLA-DPA10103-DPB10201   72      HAIHVSGTNGTKRFD  VSGTNGTKR  4        0.1038
16255.0    95.00  0.31     Sequence
 HLA-DPA10103-DPB10201   73      AIHVSGTNGTKRFDN  VSGTNGTKR  3        0.0988
17164.9    95.00  0.34     Sequence
```

```
 HLA-DPA10103-DPB10201   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.0923
18411.0    95.00  0.33      Sequence
 HLA-DPA10103-DPB10201   75      HVSGTNGTKRFDNPV  NGTKRFDNP  5        0.0703
23376.2   100.00  0.19      Sequence
 HLA-DPA10103-DPB10201   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.0955
17791.3    95.00  0.30      Sequence
 HLA-DPA10103-DPB10201   77      SGTNGTKRFDNPVLP  TKRFDNPVL  5        0.1089
15398.3    95.00  0.30      Sequence
 HLA-DPA10103-DPB10201   78      GTNGTKRFDNPVLPF  RFDNPVLPF  6        0.2150
4882.1    70.00  0.42      Sequence
 HLA-DPA10103-DPB10201   79      TNGTKRFDNPVLPFN  FDNPVLPFN  6        0.2774
2484.8    55.00  0.44     Sequence
 HLA-DPA10103-DPB10201   80      NGTKRFDNPVLPFND  FDNPVLPFN  5        0.2739
2580.8    55.00  0.41     Sequence
 HLA-DPA10103-DPB10201   81      GTKRFDNPVLPFNDG  FDNPVLPFN  4        0.2654
2831.7    55.00  0.40     Sequence
 HLA-DPA10103-DPB10201   82      TKRFDNPVLPFNDGV  FDNPVLPFN  3        0.2822
2360.7    50.00  0.34     Sequence
 HLA-DPA10103-DPB10201   83      KRFDNPVLPFNDGVY  FDNPVLPFN  2        0.3090
1766.5    44.00  0.22     Sequence
 HLA-DPA10103-DPB10201   84      RFDNPVLPFNDGVYF  LPFNDGVYF  6        0.3574
1045.8    34.00  0.35     Sequence
 HLA-DPA10103-DPB10201   85      FDNPVLPFNDGVYFA  LPFNDGVYF  5        0.3665
947.9     32.00  0.32    Sequence
 HLA-DPA10103-DPB10201   86      DNPVLPFNDGVYFAS  FNDGVYFAS  6        0.4113
584.0     25.00  0.46    Sequence
 HLA-DPA10103-DPB10201   87      NPVLPFNDGVYFAST  FNDGVYFAS  5        0.4566
357.8     19.00  0.35    Sequence
 HLA-DPA10103-DPB10201   88      PVLPFNDGVYFASTE  FNDGVYFAS  4        0.4865
258.7     15.00  0.34    Sequence
 HLA-DPA10103-DPB10201   89      VLPFNDGVYFASTEK  FNDGVYFAS  3        0.4826
269.8     15.00  0.34    Sequence
 HLA-DPA10103-DPB10201   90      LPFNDGVYFASTEKS  NDGVYFAST  3        0.4500
384.3     19.00  0.29    Sequence
 HLA-DPA10103-DPB10201   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.4158
556.1     24.00  0.24    Sequence
 HLA-DPA10103-DPB10201   92      FNDGVYFASTEKSNI  VYFASTEKS  4        0.3889
744.2     29.00  0.28    Sequence
 HLA-DPA10103-DPB10201   93      NDGVYFASTEKSNII  VYFASTEKS  3        0.3322
1374.2    39.00  0.35     Sequence
 HLA-DPA10103-DPB10201   94      DGVYFASTEKSNIIR  VYFASTEKS  2        0.2985
1979.4    46.00  0.41     Sequence
 HLA-DPA10103-DPB10201   95      GVYFASTEKSNIIRG  YFASTEKSN  2        0.2541
3200.1    60.00  0.26     Sequence
 HLA-DPA10103-DPB10201   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.2025
5591.7    70.00  0.22     Sequence
 HLA-DPA10103-DPB10201   97      YFASTEKSNIIRGWI  EKSNIIRGW  5        0.2022
5609.1    70.00  0.18     Sequence
 HLA-DPA10103-DPB10201   98      FASTEKSNIIRGWIF  SNIIRGWIF  6        0.2631
2902.7    55.00  0.25     Sequence
 HLA-DPA10103-DPB10201   99      ASTEKSNIIRGWIFG  NIIRGWIFG  6        0.2940
2077.5    47.00  0.29     Sequence
 HLA-DPA10103-DPB10201  100      STEKSNIIRGWIFGT  IIRGWIFGT  6        0.3888
744.5     29.00  0.44    Sequence
 HLA-DPA10103-DPB10201  101      TEKSNIIRGWIFGTT  IRGWIFGTT  6        0.4518
376.7     19.00  0.44    Sequence
 HLA-DPA10103-DPB10201  102      EKSNIIRGWIFGTTL  IRGWIFGTT  5        0.4887
252.8     15.00  0.42    Sequence
 HLA-DPA10103-DPB10201  103      KSNIIRGWIFGTTLD  IRGWIFGTT  4        0.4927
241.9     14.00  0.38    Sequence
 HLA-DPA10103-DPB10201  104      SNIIRGWIFGTTLDS  IRGWIFGTT  3        0.4903
248.4     14.00  0.33    Sequence
 HLA-DPA10103-DPB10201  105      NIIRGWIFGTTLDSK  IFGTTLDSK  6        0.4868
258.1     15.00  0.26    Sequence
 HLA-DPA10103-DPB10201  106      IIRGWIFGTTLDSKT  IFGTTLDSK  5        0.4634
332.2     18.00  0.30    Sequence
```

```
 HLA-DPA10103-DPB10201  107      IRGWIFGTTLDSKTQ  IFGTTLDSK  4        0.4269
492.9    23.00  0.38     Sequence
 HLA-DPA10103-DPB10201  108      RGWIFGTTLDSKTQS  IFGTTLDSK  3        0.3740
874.0    31.00  0.45     Sequence
 HLA-DPA10103-DPB10201  109      GWIFGTTLDSKTQSL  IFGTTLDSK  2        0.2931
2097.1    47.00  0.47     Sequence
 HLA-DPA10103-DPB10201  110      WIFGTTLDSKTQSLL  IFGTTLDSK  1        0.2448
3537.6    60.00  0.30     Sequence
 HLA-DPA10103-DPB10201  111      IFGTTLDSKTQSLLI  LDSKTQSLL  5        0.2152
4871.9    70.00  0.20     Sequence
 HLA-DPA10103-DPB10201  112      FGTTLDSKTQSLLIV  SKTQSLLIV  6        0.2694
2709.2    55.00  0.37     Sequence
 HLA-DPA10103-DPB10201  113      GTTLDSKTQSLLIVN  SKTQSLLIV  5        0.2650
2843.1    55.00  0.35     Sequence
 HLA-DPA10103-DPB10201  114      TTLDSKTQSLLIVNN  SKTQSLLIV  4        0.2590
3034.3    55.00  0.37     Sequence
 HLA-DPA10103-DPB10201  115      TLDSKTQSLLIVNNA  SKTQSLLIV  3        0.2495
3362.8    60.00  0.38     Sequence
 HLA-DPA10103-DPB10201  116      LDSKTQSLLIVNNAT  SKTQSLLIV  2        0.2409
3691.2    60.00  0.43     Sequence
 HLA-DPA10103-DPB10201  117      DSKTQSLLIVNNATN  SKTQSLLIV  1        0.2032
5547.6    70.00  0.43     Sequence
 HLA-DPA10103-DPB10201  118      SKTQSLLIVNNATNV  LIVNNATNV  6        0.2033
5541.9    70.00  0.32     Sequence
 HLA-DPA10103-DPB10201  119      KTQSLLIVNNATNVV  LIVNNATNV  5        0.2133
4976.0    70.00  0.31     Sequence
 HLA-DPA10103-DPB10201  120      TQSLLIVNNATNVVI  LIVNNATNV  4        0.2188
4687.6    65.00  0.31     Sequence
 HLA-DPA10103-DPB10201  121      QSLLIVNNATNVVIK  LIVNNATNV  3        0.2092
5196.8    70.00  0.31     Sequence
 HLA-DPA10103-DPB10201  122      SLLIVNNATNVVIKV  LIVNNATNV  2        0.2064
5358.7    70.00  0.28     Sequence
 HLA-DPA10103-DPB10201  123      LLIVNNATNVVIKVC  IVNNATNVV  2        0.1998
5757.2    70.00  0.22     Sequence
 HLA-DPA10103-DPB10201  124      LIVNNATNVVIKVCE  ATNVVIKVC  5        0.1765
7408.5    80.00  0.22     Sequence
 HLA-DPA10103-DPB10201  125      IVNNATNVVIKVCEF  NVVIKVCEF  6        0.2169
4784.8    65.00  0.25     Sequence
 HLA-DPA10103-DPB10201  126      VNNATNVVIKVCEFQ  VVIKVCEFQ  6        0.2699
2694.6    55.00  0.29     Sequence
 HLA-DPA10103-DPB10201  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.4257
499.5    23.00  0.35     Sequence
 HLA-DPA10103-DPB10201  128      NATNVVIKVCEFQFC  IKVCEFQFC  6        0.4799
277.8    16.00  0.40     Sequence
 HLA-DPA10103-DPB10201  129      ATNVVIKVCEFQFCN  IKVCEFQFC  5        0.4927
242.0    14.00  0.34     Sequence
 HLA-DPA10103-DPB10201  130      TNVVIKVCEFQFCNY  VCEFQFCNY  6        0.5869
87.4     6.00  0.44     Sequence         WB
 HLA-DPA10103-DPB10201  131      NVVIKVCEFQFCNYP  VCEFQFCNY  5        0.6095
68.4     4.50  0.41     Sequence         WB
 HLA-DPA10103-DPB10201  132      VVIKVCEFQFCNYPF  VCEFQFCNY  4        0.6656
37.3     1.90  0.38     Sequence         SB
 HLA-DPA10103-DPB10201  133      VIKVCEFQFCNYPFL  FQFCNYPFL  6        0.7556
14.1     0.25  0.47     Sequence         SB
 HLA-DPA10103-DPB10201  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.7433
16.1     0.40  0.49     Sequence         SB
 HLA-DPA10103-DPB10201  135      KVCEFQFCNYPFLGV  FQFCNYPFL  4        0.7787
11.0     0.12  0.38     Sequence         SB
 HLA-DPA10103-DPB10201  136      VCEFQFCNYPFLGVY  FQFCNYPFL  3        0.8017
8.5     0.04  0.34     Sequence         SB
 HLA-DPA10103-DPB10201  137      CEFQFCNYPFLGVYY  FCNYPFLGV  4        0.7993
8.8     0.05  0.42     Sequence         SB
 HLA-DPA10103-DPB10201  138      EFQFCNYPFLGVYYH  FCNYPFLGV  3        0.7863
10.1     0.08  0.41     Sequence         SB
 HLA-DPA10103-DPB10201  139      FQFCNYPFLGVYYHK  FCNYPFLGV  2        0.7514
14.7     0.30  0.41     Sequence         SB
```

```
 HLA-DPA10103-DPB10201  140      QFCNYPFLGVYYHKN  FLGVYYHKN  6        0.6996
25.8     1.10  0.19     Sequence        SB
 HLA-DPA10103-DPB10201  141      FCNYPFLGVYYHKNN  FLGVYYHKN  5        0.6560
41.3     2.50  0.26     Sequence        WB
 HLA-DPA10103-DPB10201  142      CNYPFLGVYYHKNNK  FLGVYYHKN  4        0.5328
156.8    10.00  0.56     Sequence
 HLA-DPA10103-DPB10201  143      NYPFLGVYYHKNNKS  FLGVYYHKN  3        0.4406
425.1    21.00  0.70     Sequence
 HLA-DPA10103-DPB10201  144      YPFLGVYYHKNNKSW  FLGVYYHKN  2        0.3675
937.3    32.00  0.69     Sequence
 HLA-DPA10103-DPB10201  145      PFLGVYYHKNNKSWM  FLGVYYHKN  1        0.2939
2079.4    47.00  0.51     Sequence
 HLA-DPA10103-DPB10201  146      FLGVYYHKNNKSWME  FLGVYYHKN  0        0.2271
4286.0    65.00  0.35     Sequence
 HLA-DPA10103-DPB10201  147      LGVYYHKNNKSWMES  YYHKNNKSW  3        0.1666
8247.0    80.00  0.28     Sequence
 HLA-DPA10103-DPB10201  148      GVYYHKNNKSWMESE  YYHKNNKSW  2        0.1654
8351.8    80.00  0.26     Sequence
 HLA-DPA10103-DPB10201  149      VYYHKNNKSWMESEF  KNNKSWMES  4        0.2030
5557.3    70.00  0.17     Sequence
 HLA-DPA10103-DPB10201  150      YYHKNNKSWMESEFR  KNNKSWMES  3        0.2196
4648.3    65.00  0.17     Sequence
 HLA-DPA10103-DPB10201  151      YHKNNKSWMESEFRV  WMESEFRVX  7        0.3639
974.7    33.00  0.31     Sequence
 HLA-DPA10103-DPB10201  152      HKNNKSWMESEFRVY  WMESEFRVY  6        0.4815
273.2    15.00  0.61     Sequence
 HLA-DPA10103-DPB10201  153      KNNKSWMESEFRVYS  WMESEFRVY  5        0.4789
280.9    16.00  0.60     Sequence
 HLA-DPA10103-DPB10201  154      NNKSWMESEFRVYSS  WMESEFRVY  4        0.4702
308.7    17.00  0.58     Sequence
 HLA-DPA10103-DPB10201  155      NKSWMESEFRVYSSA  WMESEFRVY  3        0.4695
310.9    17.00  0.56     Sequence
 HLA-DPA10103-DPB10201  156      KSWMESEFRVYSSAN  WMESEFRVY  2        0.4522
375.2    19.00  0.51     Sequence
 HLA-DPA10103-DPB10201  157      SWMESEFRVYSSANN  WMESEFRVY  1        0.4086
600.9    25.00  0.44     Sequence
 HLA-DPA10103-DPB10201  158      WMESEFRVYSSANNC  WMESEFRVY  0        0.2939
2079.6    47.00  0.29     Sequence
 HLA-DPA10103-DPB10201  159      MESEFRVYSSANNCT  RVYSSANNC  5        0.2168
4789.6    65.00  0.19     Sequence
 HLA-DPA10103-DPB10201  160      ESEFRVYSSANNCTF  YSSANNCTF  6        0.2360
3891.5    65.00  0.22     Sequence
 HLA-DPA10103-DPB10201  161      SEFRVYSSANNCTFE  YSSANNCTF  5        0.2321
4056.8    65.00  0.29     Sequence
 HLA-DPA10103-DPB10201  162      EFRVYSSANNCTFEY  YSSANNCTF  4        0.2665
2795.7    55.00  0.25     Sequence
 HLA-DPA10103-DPB10201  163      FRVYSSANNCTFEYV  ANNCTFEYV  6        0.3685
927.2    32.00  0.57     Sequence
 HLA-DPA10103-DPB10201  164      RVYSSANNCTFEYVS  ANNCTFEYV  5        0.3855
771.7    29.00  0.52     Sequence
 HLA-DPA10103-DPB10201  165      VYSSANNCTFEYVSQ  ANNCTFEYV  4        0.4163
553.1    24.00  0.44     Sequence
 HLA-DPA10103-DPB10201  166      YSSANNCTFEYVSQP  ANNCTFEYV  3        0.4601
344.2    18.00  0.40     Sequence
 HLA-DPA10103-DPB10201  167      SSANNCTFEYVSQPF  ANNCTFEYV  2        0.5225
175.4    11.00  0.25     Sequence
 HLA-DPA10103-DPB10201  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.6197
61.3     4.00  0.43     Sequence        WB
 HLA-DPA10103-DPB10201  169      ANNCTFEYVSQPFLM  FEYVSQPFL  5        0.6513
43.5     2.50  0.38     Sequence        WB
 HLA-DPA10103-DPB10201  170      NNCTFEYVSQPFLMD  YVSQPFLMD  6        0.6639
38.0     2.00  0.34     Sequence        WB
 HLA-DPA10103-DPB10201  171      NCTFEYVSQPFLMDL  YVSQPFLMD  5        0.6873
29.5     1.30  0.35     Sequence        SB
 HLA-DPA10103-DPB10201  172      CTFEYVSQPFLMDLE  YVSQPFLMD  4        0.6787
32.3     1.60  0.37     Sequence        SB
```

```
 HLA-DPA10103-DPB10201  173       TFEYVSQPFLMDLEG  YVSQPFLMD  3         0.6486
44.8     2.50  0.41     Sequence         WB
 HLA-DPA10103-DPB10201  174       FEYVSQPFLMDLEGK  YVSQPFLMD  2         0.5978
77.7     5.00  0.41     Sequence         WB
 HLA-DPA10103-DPB10201  175       EYVSQPFLMDLEGKQ  YVSQPFLMD  1         0.4634
332.4    18.00  0.35     Sequence
 HLA-DPA10103-DPB10201  176       YVSQPFLMDLEGKQG  VSQPFLMDL  1         0.3405
1256.1    37.00  0.28     Sequence
 HLA-DPA10103-DPB10201  177       VSQPFLMDLEGKQGN  FLMDLEGKQ  4         0.2714
2653.0    55.00  0.28     Sequence
 HLA-DPA10103-DPB10201  178       SQPFLMDLEGKQGNF  FLMDLEGKQ  3         0.2134
4971.0    70.00  0.44     Sequence
 HLA-DPA10103-DPB10201  179       QPFLMDLEGKQGNFK  FLMDLEGKQ  2         0.2003
5722.3    70.00  0.37     Sequence
 HLA-DPA10103-DPB10201  180       PFLMDLEGKQGNFKN  DLEGKQGNF  4         0.1813
7028.1    75.00  0.22     Sequence
 HLA-DPA10103-DPB10201  181       FLMDLEGKQGNFKNL  GKQGNFKNL  6         0.1761
7440.7    80.00  0.23     Sequence
 HLA-DPA10103-DPB10201  182       LMDLEGKQGNFKNLS  GKQGNFKNL  5         0.1362
11457.3    85.00  0.34     Sequence
 HLA-DPA10103-DPB10201  183       MDLEGKQGNFKNLSE  GKQGNFKNL  4         0.1286
12441.4    90.00  0.38     Sequence
 HLA-DPA10103-DPB10201  184       DLEGKQGNFKNLSEF  GNFKNLSEF  6         0.1513
9733.0    85.00  0.27     Sequence
 HLA-DPA10103-DPB10201  185       LEGKQGNFKNLSEFV  NFKNLSEFV  6         0.2440
3567.2    60.00  0.32     Sequence
 HLA-DPA10103-DPB10201  186       EGKQGNFKNLSEFVF  FKNLSEFVF  6         0.4443
408.7    20.00  0.43     Sequence
 HLA-DPA10103-DPB10201  187       GKQGNFKNLSEFVFK  FKNLSEFVF  5         0.4882
254.2    15.00  0.37     Sequence
 HLA-DPA10103-DPB10201  188       KQGNFKNLSEFVFKN  FKNLSEFVF  4         0.5019
219.1    13.00  0.31     Sequence
 HLA-DPA10103-DPB10201  189       QGNFKNLSEFVFKNI  LSEFVFKNI  6         0.6049
71.9     4.50  0.50     Sequence         WB
 HLA-DPA10103-DPB10201  190       GNFKNLSEFVFKNID  LSEFVFKNI  5         0.6084
69.2     4.50  0.50     Sequence         WB
 HLA-DPA10103-DPB10201  191       NFKNLSEFVFKNIDG  LSEFVFKNI  4         0.5987
76.9     5.00  0.47     Sequence         WB
 HLA-DPA10103-DPB10201  192       FKNLSEFVFKNIDGY  LSEFVFKNI  3         0.5939
81.0     5.50  0.47     Sequence         WB
 HLA-DPA10103-DPB10201  193       KNLSEFVFKNIDGYF  LSEFVFKNI  2         0.5476
133.5     8.50  0.39     Sequence         WB
 HLA-DPA10103-DPB10201  194       NLSEFVFKNIDGYFK  FVFKNIDGY  4         0.5260
168.8    11.00  0.35     Sequence
 HLA-DPA10103-DPB10201  195       LSEFVFKNIDGYFKI  FVFKNIDGY  3         0.5502
129.9     8.50  0.33     Sequence         WB
 HLA-DPA10103-DPB10201  196       SEFVFKNIDGYFKIY  NIDGYFKIY  6         0.5289
163.5    11.00  0.29     Sequence
 HLA-DPA10103-DPB10201  197       EFVFKNIDGYFKIYS  NIDGYFKIY  5         0.4870
257.3    15.00  0.32     Sequence
 HLA-DPA10103-DPB10201  198       FVFKNIDGYFKIYSK  NIDGYFKIY  4         0.4715
304.4    17.00  0.35     Sequence
 HLA-DPA10103-DPB10201  199       VFKNIDGYFKIYSKH  NIDGYFKIY  3         0.4426
416.0    20.00  0.40     Sequence
 HLA-DPA10103-DPB10201  200       FKNIDGYFKIYSKHT  NIDGYFKIY  2         0.4229
515.0    23.00  0.30     Sequence
 HLA-DPA10103-DPB10201  201       KNIDGYFKIYSKHTP  NIDGYFKIY  1         0.3879
751.9    29.00  0.25     Sequence
 HLA-DPA10103-DPB10201  202       NIDGYFKIYSKHTPI  YFKIYSKHT  4         0.3221
1532.2    41.00  0.31     Sequence
 HLA-DPA10103-DPB10201  203       IDGYFKIYSKHTPIN  YFKIYSKHT  3         0.3113
1723.1    43.00  0.31     Sequence
 HLA-DPA10103-DPB10201  204       DGYFKIYSKHTPINL  YFKIYSKHT  2         0.3045
1853.9    45.00  0.25     Sequence
 HLA-DPA10103-DPB10201  205       GYFKIYSKHTPINLV  KIYSKHTPI  3         0.3005
1936.9    46.00  0.20     Sequence
```

```
 HLA-DPA10103-DPB10201  206      YFKIYSKHTPINLVR  IYSKHTPIN  3        0.2994
1959.1    46.00  0.19     Sequence
 HLA-DPA10103-DPB10201  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.2562
3127.0    60.00  0.22     Sequence
 HLA-DPA10103-DPB10201  208      KIYSKHTPINLVRDL  YSKHTPINL  2        0.2455
3509.4    60.00  0.17     Sequence
 HLA-DPA10103-DPB10201  209      IYSKHTPINLVRDLP  HTPINLVRD  4        0.2186
4694.0    65.00  0.20     Sequence
 HLA-DPA10103-DPB10201  210      YSKHTPINLVRDLPQ  HTPINLVRD  3        0.1926
6223.2    75.00  0.18     Sequence
 HLA-DPA10103-DPB10201  211      SKHTPINLVRDLPQG  TPINLVRDL  3        0.1680
8119.5    80.00  0.19     Sequence
 HLA-DPA10103-DPB10201  212      KHTPINLVRDLPQGF  LVRDLPQGF  6        0.2175
4754.1    65.00  0.44     Sequence
 HLA-DPA10103-DPB10201  213      HTPINLVRDLPQGFS  LVRDLPQGF  5        0.2195
4650.5    65.00  0.41     Sequence
 HLA-DPA10103-DPB10201  214      TPINLVRDLPQGFSA  LVRDLPQGF  4        0.2379
3810.2    60.00  0.40     Sequence
 HLA-DPA10103-DPB10201  215      PINLVRDLPQGFSAL  DLPQGFSAL  6        0.3139
1675.1    43.00  0.52     Sequence
 HLA-DPA10103-DPB10201  216      INLVRDLPQGFSALE  DLPQGFSAL  5        0.3131
1688.5    43.00  0.51     Sequence
 HLA-DPA10103-DPB10201  217      NLVRDLPQGFSALEP  DLPQGFSAL  4        0.3049
1846.3    45.00  0.48     Sequence
 HLA-DPA10103-DPB10201  218      LVRDLPQGFSALEPL  DLPQGFSAL  3        0.3347
1336.9    38.00  0.39     Sequence
 HLA-DPA10103-DPB10201  219      VRDLPQGFSALEPLV  GFSALEPLV  6        0.3594
1023.4    34.00  0.25     Sequence
 HLA-DPA10103-DPB10201  220      RDLPQGFSALEPLVD  GFSALEPLV  5        0.3455
1189.9    36.00  0.27     Sequence
 HLA-DPA10103-DPB10201  221      DLPQGFSALEPLVDL  GFSALEPLV  4        0.3618
997.4    33.00  0.23     Sequence
 HLA-DPA10103-DPB10201  222      LPQGFSALEPLVDLP  GFSALEPLV  3        0.3650
963.4    33.00  0.25     Sequence
 HLA-DPA10103-DPB10201  223      PQGFSALEPLVDLPI  SALEPLVDL  4        0.3745
869.3    31.00  0.18     Sequence
 HLA-DPA10103-DPB10201  224      QGFSALEPLVDLPIG  SALEPLVDL  3        0.3568
1052.9    34.00  0.19     Sequence
 HLA-DPA10103-DPB10201  225      GFSALEPLVDLPIGI  SALEPLVDL  2        0.3226
1524.9    41.00  0.22     Sequence
 HLA-DPA10103-DPB10201  226      FSALEPLVDLPIGIN  LVDLPIGIN  6        0.3064
1815.5    44.00  0.17     Sequence
 HLA-DPA10103-DPB10201  227      SALEPLVDLPIGINI  LVDLPIGIN  5        0.2964
2024.1    46.00  0.20     Sequence
 HLA-DPA10103-DPB10201  228      ALEPLVDLPIGINIT  LVDLPIGIN  4        0.2803
2408.5    50.00  0.20     Sequence
 HLA-DPA10103-DPB10201  229      LEPLVDLPIGINITR  LVDLPIGIN  3        0.2610
2967.7    55.00  0.23     Sequence
 HLA-DPA10103-DPB10201  230      EPLVDLPIGINITRF  DLPIGINIT  4        0.2464
3476.2    60.00  0.22     Sequence
 HLA-DPA10103-DPB10201  231      PLVDLPIGINITRFQ  DLPIGINIT  3        0.2661
2810.5    55.00  0.19     Sequence
 HLA-DPA10103-DPB10201  232      LVDLPIGINITRFQT  INITRFQTX  7        0.2574
3087.5    55.00  0.28     Sequence
 HLA-DPA10103-DPB10201  233      VDLPIGINITRFQTL  INITRFQTL  6        0.3954
693.7    28.00  0.61     Sequence
 HLA-DPA10103-DPB10201  234      DLPIGINITRFQTLL  INITRFQTL  5        0.4161
554.2    24.00  0.51     Sequence
 HLA-DPA10103-DPB10201  235      LPIGINITRFQTLLA  INITRFQTL  4        0.4158
555.8    24.00  0.50     Sequence
 HLA-DPA10103-DPB10201  236      PIGINITRFQTLLAL  TRFQTLLAL  6        0.4754
291.8    16.00  0.38     Sequence
 HLA-DPA10103-DPB10201  237      IGINITRFQTLLALH  TRFQTLLAL  5        0.4877
255.4    15.00  0.37     Sequence
 HLA-DPA10103-DPB10201  238      GINITRFQTLLALHR  TRFQTLLAL  4        0.4783
282.7    16.00  0.39     Sequence
```

```
 HLA-DPA10103-DPB10201  239      INITRFQTLLALHRS  TRFQTLLAL  3        0.4678
316.7    17.00  0.44     Sequence
 HLA-DPA10103-DPB10201  240      NITRFQTLLALHRSY  TRFQTLLAL  2        0.4431
414.0    20.00  0.47     Sequence
 HLA-DPA10103-DPB10201  241      ITRFQTLLALHRSYL  TRFQTLLAL  1        0.4564
358.4    19.00  0.38     Sequence
 HLA-DPA10103-DPB10201  242      TRFQTLLALHRSYLT  LLALHRSYL  5        0.4135
569.8    25.00  0.19     Sequence
 HLA-DPA10103-DPB10201  243      RFQTLLALHRSYLTP  ALHRSYLTP  6        0.4035
635.5    26.00  0.32     Sequence
 HLA-DPA10103-DPB10201  244      FQTLLALHRSYLTPG  ALHRSYLTP  5        0.4036
634.9    26.00  0.32     Sequence
 HLA-DPA10103-DPB10201  245      QTLLALHRSYLTPGD  ALHRSYLTP  4        0.3848
777.8    29.00  0.34     Sequence
 HLA-DPA10103-DPB10201  246      TLLALHRSYLTPGDS  ALHRSYLTP  3        0.3733
880.5    31.00  0.34     Sequence
 HLA-DPA10103-DPB10201  247      LLALHRSYLTPGDSS  LHRSYLTPG  3        0.3504
1128.8    35.00  0.34     Sequence
 HLA-DPA10103-DPB10201  248      LALHRSYLTPGDSSS  LHRSYLTPG  2        0.2864
2255.0    49.00  0.34     Sequence
 HLA-DPA10103-DPB10201  249      ALHRSYLTPGDSSSG  LHRSYLTPG  1        0.2152
4872.4    70.00  0.29     Sequence
 HLA-DPA10103-DPB10201  250      LHRSYLTPGDSSSGW  LHRSYLTPG  0        0.1322
11963.3    90.00  0.22     Sequence
 HLA-DPA10103-DPB10201  251      HRSYLTPGDSSSGWT  YLTPGDSSS  3        0.0980
17317.7    95.00  0.25     Sequence
 HLA-DPA10103-DPB10201  252      RSYLTPGDSSSGWTA  GDSSSGWTA  6        0.1033
16345.6    95.00  0.28     Sequence
 HLA-DPA10103-DPB10201  253      SYLTPGDSSSGWTAG  DSSSGWTAG  6        0.1188
13832.1    90.00  0.44     Sequence
 HLA-DPA10103-DPB10201  254      YLTPGDSSSGWTAGA  DSSSGWTAG  5        0.1164
14186.5    90.00  0.46     Sequence
 HLA-DPA10103-DPB10201  255      LTPGDSSSGWTAGAA  DSSSGWTAG  4        0.1158
14282.2    90.00  0.44     Sequence
 HLA-DPA10103-DPB10201  256      TPGDSSSGWTAGAAA  DSSSGWTAG  3        0.1115
14970.0    95.00  0.42     Sequence
 HLA-DPA10103-DPB10201  257      PGDSSSGWTAGAAAY  DSSSGWTAG  2        0.1225
13287.3    90.00  0.26     Sequence
 HLA-DPA10103-DPB10201  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.1555
9300.3    85.00  0.25     Sequence
 HLA-DPA10103-DPB10201  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.1741
7602.5    80.00  0.22     Sequence
 HLA-DPA10103-DPB10201  260      SSSGWTAGAAAYYVG  AGAAAYYVG  6        0.1731
7682.7    80.00  0.30     Sequence
 HLA-DPA10103-DPB10201  261      SSGWTAGAAAYYVGY  GAAAYYVGY  6        0.2233
4464.6    65.00  0.42     Sequence
 HLA-DPA10103-DPB10201  262      SGWTAGAAAYYVGYL  AAAYYVGYL  6        0.3497
1136.4    36.00  0.24     Sequence
 HLA-DPA10103-DPB10201  263      GWTAGAAAYYVGYLQ  AYYVGYLQX  7        0.4046
627.4    26.00  0.26     Sequence
 HLA-DPA10103-DPB10201  264      WTAGAAAYYVGYLQP  AYYVGYLQP  6        0.4827
269.7    15.00  0.44     Sequence
 HLA-DPA10103-DPB10201  265      TAGAAAYYVGYLQPR  AYYVGYLQP  5        0.5134
193.3    12.00  0.35     Sequence
 HLA-DPA10103-DPB10201  266      AGAAAYYVGYLQPRT  AYYVGYLQP  4        0.5345
153.9    10.00  0.31     Sequence
 HLA-DPA10103-DPB10201  267      GAAAYYVGYLQPRTF  AYYVGYLQP  3        0.5473
134.0     8.50  0.28     Sequence         WB
 HLA-DPA10103-DPB10201  268      AAAYYVGYLQPRTFL  AYYVGYLQP  2        0.5638
112.1     7.50  0.26     Sequence         WB
 HLA-DPA10103-DPB10201  269      AAYYVGYLQPRTFLL  YLQPRTFLL  6        0.6122
66.4     4.50  0.20     Sequence         WB
 HLA-DPA10103-DPB10201  270      AYYVGYLQPRTFLLK  LQPRTFLLK  6        0.6063
70.8     4.50  0.34     Sequence         WB
 HLA-DPA10103-DPB10201  271      YYVGYLQPRTFLLKY  LQPRTFLLK  5        0.5782
95.9     6.50  0.41     Sequence         WB
```

```
 HLA-DPA10103-DPB10201  272      YVGYLQPRTFLLKYN  LQPRTFLLK  4        0.5545
123.9     8.00  0.44     Sequence          WB
 HLA-DPA10103-DPB10201  273      VGYLQPRTFLLKYNE  LQPRTFLLK  3        0.5337
155.2    10.00  0.45     Sequence
 HLA-DPA10103-DPB10201  274      GYLQPRTFLLKYNEN  LQPRTFLLK  2        0.4846
264.0    15.00  0.41     Sequence
 HLA-DPA10103-DPB10201  275      YLQPRTFLLKYNENG  LQPRTFLLK  1        0.4357
448.3    21.00  0.33     Sequence
 HLA-DPA10103-DPB10201  276      LQPRTFLLKYNENGT  FLLKYNENG  5        0.3024
1897.0    45.00  0.29     Sequence
 HLA-DPA10103-DPB10201  277      QPRTFLLKYNENGTI  FLLKYNENG  4        0.2896
2177.3    48.00  0.29     Sequence
 HLA-DPA10103-DPB10201  278      PRTFLLKYNENGTIT  FLLKYNENG  3        0.2877
2223.9    48.00  0.31     Sequence
 HLA-DPA10103-DPB10201  279      RTFLLKYNENGTITD  FLLKYNENG  2        0.2694
2710.6    55.00  0.26     Sequence
 HLA-DPA10103-DPB10201  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.2297
4166.7    65.00  0.25     Sequence
 HLA-DPA10103-DPB10201  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.1920
6263.7    75.00  0.26     Sequence
 HLA-DPA10103-DPB10201  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.1407
10910.0    85.00  0.27     Sequence
 HLA-DPA10103-DPB10201  283      LKYNENGTITDAVDC  YNENGTITD  2        0.1057
15931.1    95.00  0.22     Sequence
 HLA-DPA10103-DPB10201  284      KYNENGTITDAVDCA  TITDAVDCA  6        0.0780
21508.7   100.00  0.29     Sequence
 HLA-DPA10103-DPB10201  285      YNENGTITDAVDCAL  ITDAVDCAL  6        0.1277
12558.7    90.00  0.38     Sequence
 HLA-DPA10103-DPB10201  286      NENGTITDAVDCALD  ITDAVDCAL  5        0.1263
12755.6    90.00  0.38     Sequence
 HLA-DPA10103-DPB10201  287      ENGTITDAVDCALDP  ITDAVDCAL  4        0.1419
10764.6    85.00  0.34     Sequence
 HLA-DPA10103-DPB10201  288      NGTITDAVDCALDPL  AVDCALDPL  6        0.1956
6023.5    75.00  0.40     Sequence
 HLA-DPA10103-DPB10201  289      GTITDAVDCALDPLS  AVDCALDPL  5        0.1884
6510.8    75.00  0.35     Sequence
 HLA-DPA10103-DPB10201  290      TITDAVDCALDPLSE  AVDCALDPL  4        0.1879
6548.6    75.00  0.34     Sequence
 HLA-DPA10103-DPB10201  291      ITDAVDCALDPLSET  AVDCALDPL  3        0.2025
5591.1    70.00  0.28     Sequence
 HLA-DPA10103-DPB10201  292      TDAVDCALDPLSETK  CALDPLSET  5        0.1893
6451.7    75.00  0.22     Sequence
 HLA-DPA10103-DPB10201  293      DAVDCALDPLSETKC  CALDPLSET  4        0.1834
6873.8    75.00  0.23     Sequence
 HLA-DPA10103-DPB10201  294      AVDCALDPLSETKCT  CALDPLSET  3        0.1755
7488.1    80.00  0.28     Sequence
 HLA-DPA10103-DPB10201  295      VDCALDPLSETKCTL  LDPLSETKC  4        0.2034
5534.2    70.00  0.18     Sequence
 HLA-DPA10103-DPB10201  296      DCALDPLSETKCTLK  LSETKCTLK  6        0.2006
5706.8    70.00  0.20     Sequence
 HLA-DPA10103-DPB10201  297      CALDPLSETKCTLKS  LSETKCTLK  5        0.1901
6390.9    75.00  0.21     Sequence
 HLA-DPA10103-DPB10201  298      ALDPLSETKCTLKSF  ETKCTLKSF  6        0.2260
4335.9    65.00  0.46     Sequence
 HLA-DPA10103-DPB10201  299      LDPLSETKCTLKSFT  ETKCTLKSF  5        0.2479
3419.0    60.00  0.45     Sequence
 HLA-DPA10103-DPB10201  300      DPLSETKCTLKSFTV  ETKCTLKSF  4        0.3428
1225.6    37.00  0.32     Sequence
 HLA-DPA10103-DPB10201  301      PLSETKCTLKSFTVE  CTLKSFTVE  6        0.4258
499.3    23.00  0.41     Sequence
 HLA-DPA10103-DPB10201  302      LSETKCTLKSFTVEK  CTLKSFTVE  5        0.4413
422.0    21.00  0.42     Sequence
 HLA-DPA10103-DPB10201  303      SETKCTLKSFTVEKG  CTLKSFTVE  4        0.4439
410.3    20.00  0.39     Sequence
 HLA-DPA10103-DPB10201  304      ETKCTLKSFTVEKGI  CTLKSFTVE  3        0.4589
349.0    18.00  0.40     Sequence
```

```
 HLA-DPA10103-DPB10201  305      TKCTLKSFTVEKGIY  CTLKSFTVE  2        0.4685
314.3    17.00  0.34     Sequence
 HLA-DPA10103-DPB10201  306      KCTLKSFTVEKGIYQ  LKSFTVEKG  3        0.4631
333.2    18.00  0.25     Sequence
 HLA-DPA10103-DPB10201  307      CTLKSFTVEKGIYQT  FTVEKGIYQ  5        0.3904
731.9    28.00  0.31     Sequence
 HLA-DPA10103-DPB10201  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4        0.3562
1059.2    34.00  0.37     Sequence
 HLA-DPA10103-DPB10201  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3        0.3431
1220.6    37.00  0.40     Sequence
 HLA-DPA10103-DPB10201  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2        0.3184
1595.4    42.00  0.38     Sequence
 HLA-DPA10103-DPB10201  311      SFTVEKGIYQTSNFR  VEKGIYQTS  3        0.2948
2059.8    47.00  0.22     Sequence
 HLA-DPA10103-DPB10201  312      FTVEKGIYQTSNFRV  YQTSNFRVX  7        0.3971
680.7    27.00  0.33     Sequence
 HLA-DPA10103-DPB10201  313      TVEKGIYQTSNFRVQ  YQTSNFRVQ  6        0.4450
405.5    20.00  0.50     Sequence
 HLA-DPA10103-DPB10201  314      VEKGIYQTSNFRVQP  YQTSNFRVQ  5        0.4365
444.7    21.00  0.52     Sequence
 HLA-DPA10103-DPB10201  315      EKGIYQTSNFRVQPT  YQTSNFRVQ  4        0.4304
474.9    22.00  0.51     Sequence
 HLA-DPA10103-DPB10201  316      KGIYQTSNFRVQPTE  YQTSNFRVQ  3        0.4191
536.4    24.00  0.51     Sequence
 HLA-DPA10103-DPB10201  317      GIYQTSNFRVQPTES  YQTSNFRVQ  2        0.3727
886.3    31.00  0.47     Sequence
 HLA-DPA10103-DPB10201  318      IYQTSNFRVQPTESI  YQTSNFRVQ  1        0.3701
912.0    32.00  0.29     Sequence
 HLA-DPA10103-DPB10201  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.2543
3192.4    60.00  0.45     Sequence
 HLA-DPA10103-DPB10201  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.2339
3978.6    65.00  0.50     Sequence
 HLA-DPA10103-DPB10201  321      TSNFRVQPTESIVRF  FRVQPTESI  3        0.2468
3461.9    60.00  0.43     Sequence
 HLA-DPA10103-DPB10201  322      SNFRVQPTESIVRFP  FRVQPTESI  2        0.2481
3414.3    60.00  0.36     Sequence
 HLA-DPA10103-DPB10201  323      NFRVQPTESIVRFPN  FRVQPTESI  1        0.2449
3532.5    60.00  0.32     Sequence
 HLA-DPA10103-DPB10201  324      FRVQPTESIVRFPNI  ESIVRFPNI  6        0.3155
1645.2    42.00  0.56     Sequence
 HLA-DPA10103-DPB10201  325      RVQPTESIVRFPNIT  ESIVRFPNI  5        0.2957
2040.2    47.00  0.65     Sequence
 HLA-DPA10103-DPB10201  326      VQPTESIVRFPNITN  ESIVRFPNI  4        0.2876
2226.2    48.00  0.64     Sequence
 HLA-DPA10103-DPB10201  327      QPTESIVRFPNITNL  ESIVRFPNI  3        0.3224
1527.7    41.00  0.39     Sequence
 HLA-DPA10103-DPB10201  328      PTESIVRFPNITNLC  VRFPNITNL  5        0.3087
1772.2    44.00  0.37     Sequence
 HLA-DPA10103-DPB10201  329      TESIVRFPNITNLCP  VRFPNITNL  4        0.3012
1921.6    45.00  0.41     Sequence
 HLA-DPA10103-DPB10201  330      ESIVRFPNITNLCPF  VRFPNITNL  3        0.2916
2131.8    48.00  0.47     Sequence
 HLA-DPA10103-DPB10201  331      SIVRFPNITNLCPFG  VRFPNITNL  2        0.2568
3107.4    60.00  0.50     Sequence
 HLA-DPA10103-DPB10201  332      IVRFPNITNLCPFGE  VRFPNITNL  1        0.2463
3481.3    60.00  0.41     Sequence
 HLA-DPA10103-DPB10201  333      VRFPNITNLCPFGEV  TNLCPFGEV  6        0.2826
2348.8    50.00  0.34     Sequence
 HLA-DPA10103-DPB10201  334      RFPNITNLCPFGEVF  TNLCPFGEV  5        0.3273
1448.2    40.00  0.32     Sequence
 HLA-DPA10103-DPB10201  335      FPNITNLCPFGEVFN  TNLCPFGEV  4        0.3405
1256.1    37.00  0.29     Sequence
 HLA-DPA10103-DPB10201  336      PNITNLCPFGEVFNA  TNLCPFGEV  3        0.3443
1205.8    37.00  0.26     Sequence
 HLA-DPA10103-DPB10201  337      NITNLCPFGEVFNAT  PFGEVFNAT  6        0.3612
1003.4    33.00  0.28     Sequence
```

```
 HLA-DPA10103-DPB10201  338      ITNLCPFGEVFNATR  PFGEVFNAT  5        0.3605
1012.0    34.00  0.28     Sequence
 HLA-DPA10103-DPB10201  339      TNLCPFGEVFNATRF  PFGEVFNAT  4        0.3686
927.1    32.00  0.26     Sequence
 HLA-DPA10103-DPB10201  340      NLCPFGEVFNATRFA  PFGEVFNAT  3        0.3631
983.1    33.00  0.24     Sequence
 HLA-DPA10103-DPB10201  341      LCPFGEVFNATRFAS  VFNATRFAS  6        0.3907
729.7    28.00  0.25     Sequence
 HLA-DPA10103-DPB10201  342      CPFGEVFNATRFASV  FNATRFASV  6        0.5032
216.0    13.00  0.64     Sequence
 HLA-DPA10103-DPB10201  343      PFGEVFNATRFASVY  FNATRFASV  5        0.4933
240.5    14.00  0.62     Sequence
 HLA-DPA10103-DPB10201  344      FGEVFNATRFASVYA  FNATRFASV  4        0.4808
275.2    16.00  0.64     Sequence
 HLA-DPA10103-DPB10201  345      GEVFNATRFASVYAW  FNATRFASV  3        0.4927
242.0    14.00  0.52     Sequence
 HLA-DPA10103-DPB10201  346      EVFNATRFASVYAWN  FNATRFASV  2        0.4576
353.9    18.00  0.44     Sequence
 HLA-DPA10103-DPB10201  347      VFNATRFASVYAWNR  FNATRFASV  1        0.4409
423.6    21.00  0.28     Sequence
 HLA-DPA10103-DPB10201  348      FNATRFASVYAWNRK  TRFASVYAW  3        0.4109
586.1    25.00  0.26     Sequence
 HLA-DPA10103-DPB10201  349      NATRFASVYAWNRKR  TRFASVYAW  2        0.3741
873.4    31.00  0.30     Sequence
 HLA-DPA10103-DPB10201  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.3942
702.6    28.00  0.20     Sequence
 HLA-DPA10103-DPB10201  351      TRFASVYAWNRKRIS  VYAWNRKRI  5        0.3693
919.5    32.00  0.17     Sequence
 HLA-DPA10103-DPB10201  352      RFASVYAWNRKRISN  VYAWNRKRI  4        0.3046
1852.6    45.00  0.26     Sequence
 HLA-DPA10103-DPB10201  353      FASVYAWNRKRISNC  VYAWNRKRI  3        0.2665
2795.6    55.00  0.31     Sequence
 HLA-DPA10103-DPB10201  354      ASVYAWNRKRISNCV  VYAWNRKRI  2        0.2218
4536.2    65.00  0.38     Sequence
 HLA-DPA10103-DPB10201  355      SVYAWNRKRISNCVA  YAWNRKRIS  2        0.1966
5960.6    70.00  0.37     Sequence
 HLA-DPA10103-DPB10201  356      VYAWNRKRISNCVAD  YAWNRKRIS  1        0.1634
8533.4    80.00  0.23     Sequence
 HLA-DPA10103-DPB10201  357      YAWNRKRISNCVADY  RISNCVADY  6        0.0992
17091.7    95.00  0.32     Sequence
 HLA-DPA10103-DPB10201  358      AWNRKRISNCVADYS  RISNCVADY  5        0.1165
14182.6    90.00  0.32     Sequence
 HLA-DPA10103-DPB10201  359      WNRKRISNCVADYSV  RISNCVADY  4        0.1292
12356.2    90.00  0.31     Sequence
 HLA-DPA10103-DPB10201  360      NRKRISNCVADYSVL  NCVADYSVL  6        0.3190
1584.5    42.00  0.60     Sequence
 HLA-DPA10103-DPB10201  361      RKRISNCVADYSVLY  NCVADYSVL  5        0.3691
921.7    32.00  0.44     Sequence
 HLA-DPA10103-DPB10201  362      KRISNCVADYSVLYN  NCVADYSVL  4        0.3726
887.4    31.00  0.38     Sequence
 HLA-DPA10103-DPB10201  363      RISNCVADYSVLYNS  NCVADYSVL  3        0.3982
672.7    27.00  0.31     Sequence
 HLA-DPA10103-DPB10201  364      ISNCVADYSVLYNSA  DYSVLYNSA  6        0.4199
532.0    24.00  0.28     Sequence
 HLA-DPA10103-DPB10201  365      SNCVADYSVLYNSAS  DYSVLYNSA  5        0.4205
528.3    24.00  0.28     Sequence
 HLA-DPA10103-DPB10201  366      NCVADYSVLYNSASF  DYSVLYNSA  4        0.4402
427.1    21.00  0.25     Sequence
 HLA-DPA10103-DPB10201  367      CVADYSVLYNSASFS  VLYNSASFS  6        0.4523
374.8    19.00  0.26     Sequence
 HLA-DPA10103-DPB10201  368      VADYSVLYNSASFST  VLYNSASFS  5        0.4813
273.6    15.00  0.21     Sequence
 HLA-DPA10103-DPB10201  369      ADYSVLYNSASFSTF  YNSASFSTF  6        0.5952
79.8     5.50  0.63     Sequence         WB
 HLA-DPA10103-DPB10201  370      DYSVLYNSASFSTFK  YNSASFSTF  5        0.5956
79.5     5.50  0.62     Sequence         WB
```

```
 HLA-DPA10103-DPB10201  371      YSVLYNSASFSTFKC  YNSASFSTF  4        0.5941
80.8     5.50  0.57      Sequence         WB
 HLA-DPA10103-DPB10201  372      SVLYNSASFSTFKCY  YNSASFSTF  3        0.6171
63.0     4.00  0.45      Sequence         WB
 HLA-DPA10103-DPB10201  373      VLYNSASFSTFKCYG  ASFSTFKCY  5        0.5812
92.9     6.00  0.40      Sequence         WB
 HLA-DPA10103-DPB10201  374      LYNSASFSTFKCYGV  ASFSTFKCY  4        0.5648
111.0     7.50  0.41      Sequence        WB
 HLA-DPA10103-DPB10201  375      YNSASFSTFKCYGVS  ASFSTFKCY  3        0.5302
161.3    10.00  0.47      Sequence
 HLA-DPA10103-DPB10201  376      NSASFSTFKCYGVSP  ASFSTFKCY  2        0.4931
240.9    14.00  0.47      Sequence
 HLA-DPA10103-DPB10201  377      SASFSTFKCYGVSPT  ASFSTFKCY  1        0.4694
311.4    17.00  0.36      Sequence
 HLA-DPA10103-DPB10201  378      ASFSTFKCYGVSPTK  FSTFKCYGV  2        0.4317
468.2    22.00  0.28      Sequence
 HLA-DPA10103-DPB10201  379      SFSTFKCYGVSPTKL  CYGVSPTKL  6        0.3821
800.9    30.00  0.19      Sequence
 HLA-DPA10103-DPB10201  380      FSTFKCYGVSPTKLN  CYGVSPTKL  5        0.3533
1093.7    35.00  0.23      Sequence
 HLA-DPA10103-DPB10201  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.2977
1995.5    46.00  0.38      Sequence
 HLA-DPA10103-DPB10201  382      TFKCYGVSPTKLNDL  CYGVSPTKL  3        0.3129
1692.4    43.00  0.31      Sequence
 HLA-DPA10103-DPB10201  383      FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.2739
2581.2    55.00  0.31      Sequence
 HLA-DPA10103-DPB10201  384      KCYGVSPTKLNDLCF  VSPTKLNDL  4        0.2542
3194.3    60.00  0.40      Sequence
 HLA-DPA10103-DPB10201  385      CYGVSPTKLNDLCFT  VSPTKLNDL  3        0.2870
2241.0    49.00  0.31      Sequence
 HLA-DPA10103-DPB10201  386      YGVSPTKLNDLCFTN  LNDLCFTNX  7        0.2676
2763.1    55.00  0.28      Sequence
 HLA-DPA10103-DPB10201  387      GVSPTKLNDLCFTNV  LNDLCFTNV  6        0.3606
1010.9    34.00  0.61      Sequence
 HLA-DPA10103-DPB10201  388      VSPTKLNDLCFTNVY  LNDLCFTNV  5        0.4155
557.6    24.00  0.53      Sequence
 HLA-DPA10103-DPB10201  389      SPTKLNDLCFTNVYA  LNDLCFTNV  4        0.4224
517.9    23.00  0.49      Sequence
 HLA-DPA10103-DPB10201  390      PTKLNDLCFTNVYAD  LNDLCFTNV  3        0.4454
403.6    20.00  0.39      Sequence
 HLA-DPA10103-DPB10201  391      TKLNDLCFTNVYADS  LCFTNVYAD  5        0.4486
390.0    20.00  0.31      Sequence
 HLA-DPA10103-DPB10201  392      KLNDLCFTNVYADSF  FTNVYADSF  6        0.5257
169.3    11.00  0.31      Sequence
 HLA-DPA10103-DPB10201  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.5122
196.0    12.00  0.35      Sequence
 HLA-DPA10103-DPB10201  394      NDLCFTNVYADSFVI  FTNVYADSF  4        0.5609
115.7     7.50  0.31      Sequence        WB
 HLA-DPA10103-DPB10201  395      DLCFTNVYADSFVIR  VYADSFVIR  6        0.5815
92.6     6.00  0.44      Sequence         WB
 HLA-DPA10103-DPB10201  396      LCFTNVYADSFVIRG  VYADSFVIR  5        0.5628
113.4     7.50  0.44      Sequence        WB
 HLA-DPA10103-DPB10201  397      CFTNVYADSFVIRGD  VYADSFVIR  4        0.5414
142.9     9.00  0.46      Sequence        WB
 HLA-DPA10103-DPB10201  398      FTNVYADSFVIRGDE  VYADSFVIR  3        0.5165
187.1    12.00  0.48      Sequence
 HLA-DPA10103-DPB10201  399      TNVYADSFVIRGDEV  VYADSFVIR  2        0.4468
397.4    20.00  0.49      Sequence
 HLA-DPA10103-DPB10201  400      NVYADSFVIRGDEVR  VYADSFVIR  1        0.4130
572.9    25.00  0.39      Sequence
 HLA-DPA10103-DPB10201  401      VYADSFVIRGDEVRQ  FVIRGDEVR  5        0.3196
1573.8    42.00  0.24      Sequence
 HLA-DPA10103-DPB10201  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.3140
1672.4    43.00  0.38      Sequence
 HLA-DPA10103-DPB10201  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.3055
1833.9    45.00  0.39      Sequence
```

```
 HLA-DPA10103-DPB10201  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.2895
2180.6    48.00  0.44     Sequence
 HLA-DPA10103-DPB10201  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.2545
3183.2    60.00  0.49     Sequence
 HLA-DPA10103-DPB10201  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.1782
7272.2    75.00  0.57     Sequence
 HLA-DPA10103-DPB10201  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.1325
11920.7    90.00  0.50     Sequence
 HLA-DPA10103-DPB10201  408      IRGDEVRQIAPGQTG  IRGDEVRQI  0        0.1065
15792.8    95.00  0.34     Sequence
 HLA-DPA10103-DPB10201  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.0773
21659.1  100.00  0.26     Sequence
 HLA-DPA10103-DPB10201  410      GDEVRQIAPGQTGTI  IAPGQTGTI  6        0.1029
16427.4    95.00  0.35     Sequence
 HLA-DPA10103-DPB10201  411      DEVRQIAPGQTGTIA  IAPGQTGTI  5        0.1016
16658.6    95.00  0.38     Sequence
 HLA-DPA10103-DPB10201  412      EVRQIAPGQTGTIAD  IAPGQTGTI  4        0.1016
16658.1    95.00  0.36     Sequence
 HLA-DPA10103-DPB10201  413      VRQIAPGQTGTIADY  IAPGQTGTI  3        0.1167
14138.2    90.00  0.25     Sequence
 HLA-DPA10103-DPB10201  414      RQIAPGQTGTIADYN  GQTGTIADY  5        0.1163
14200.4    90.00  0.34     Sequence
 HLA-DPA10103-DPB10201  415      QIAPGQTGTIADYNY  GQTGTIADY  4        0.1207
13548.4    90.00  0.33     Sequence
 HLA-DPA10103-DPB10201  416      IAPGQTGTIADYNYK  GQTGTIADY  3        0.1289
12391.6    90.00  0.29     Sequence
 HLA-DPA10103-DPB10201  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.2350
3932.6    65.00  0.32     Sequence
 HLA-DPA10103-DPB10201  418      PGQTGTIADYNYKLP  IADYNYKLP  6        0.2806
2400.4    50.00  0.37     Sequence
 HLA-DPA10103-DPB10201  419      GQTGTIADYNYKLPD  IADYNYKLP  5        0.2967
2017.4    46.00  0.34     Sequence
 HLA-DPA10103-DPB10201  420      QTGTIADYNYKLPDD  IADYNYKLP  4        0.3097
1752.7    44.00  0.27     Sequence
 HLA-DPA10103-DPB10201  421      TGTIADYNYKLPDDF  IADYNYKLP  3        0.3192
1580.6    42.00  0.24     Sequence
 HLA-DPA10103-DPB10201  422      GTIADYNYKLPDDFT  DYNYKLPDD  4        0.3049
1845.3    45.00  0.25     Sequence
 HLA-DPA10103-DPB10201  423      TIADYNYKLPDDFTG  DYNYKLPDD  3        0.2864
2254.9    49.00  0.25     Sequence
 HLA-DPA10103-DPB10201  424      IADYNYKLPDDFTGC  YNYKLPDDF  3        0.2459
3496.1    60.00  0.25     Sequence
 HLA-DPA10103-DPB10201  425      ADYNYKLPDDFTGCV  KLPDDFTGC  5        0.2641
2869.9    55.00  0.29     Sequence
 HLA-DPA10103-DPB10201  426      DYNYKLPDDFTGCVI  KLPDDFTGC  4        0.2626
2917.1    55.00  0.28     Sequence
 HLA-DPA10103-DPB10201  427      YNYKLPDDFTGCVIA  KLPDDFTGC  3        0.2952
2049.7    47.00  0.27     Sequence
 HLA-DPA10103-DPB10201  428      NYKLPDDFTGCVIAW  DFTGCVIAW  6        0.3581
1038.1    34.00  0.32     Sequence
 HLA-DPA10103-DPB10201  429      YKLPDDFTGCVIAWN  FTGCVIAWN  6        0.3841
783.6    29.00  0.39     Sequence
 HLA-DPA10103-DPB10201  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.3737
876.5    31.00  0.40     Sequence
 HLA-DPA10103-DPB10201  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.3621
994.7    33.00  0.40     Sequence
 HLA-DPA10103-DPB10201  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.3382
1287.8    38.00  0.42     Sequence
 HLA-DPA10103-DPB10201  433      DDFTGCVIAWNSNNL  FTGCVIAWN  2        0.3208
1553.6    41.00  0.37     Sequence
 HLA-DPA10103-DPB10201  434      DFTGCVIAWNSNNLD  FTGCVIAWN  1        0.2609
2970.8    55.00  0.25     Sequence
 HLA-DPA10103-DPB10201  435      FTGCVIAWNSNNLDS  VIAWNSNNL  4        0.2010
5681.2    70.00  0.26     Sequence
 HLA-DPA10103-DPB10201  436      TGCVIAWNSNNLDSK  VIAWNSNNL  3        0.1857
6703.4    75.00  0.28     Sequence
```

```
 HLA-DPA10103-DPB10201  437      GCVIAWNSNNLDSKV  VIAWNSNNL  2        0.1769
7371.2    75.00  0.27     Sequence
 HLA-DPA10103-DPB10201  438      CVIAWNSNNLDSKVG  WNSNNLDSK  4        0.1619
8677.6    80.00  0.23     Sequence
 HLA-DPA10103-DPB10201  439      VIAWNSNNLDSKVGG  WNSNNLDSK  3        0.1447
10442.9    85.00  0.25     Sequence
 HLA-DPA10103-DPB10201  440      IAWNSNNLDSKVGGN  WNSNNLDSK  2        0.0908
18727.6    95.00  0.26     Sequence
 HLA-DPA10103-DPB10201  441      AWNSNNLDSKVGGNY  LDSKVGGNY  6        0.0814
20726.7   100.00  0.32     Sequence
 HLA-DPA10103-DPB10201  442      WNSNNLDSKVGGNYN  LDSKVGGNY  5        0.0732
22658.2   100.00  0.41     Sequence
 HLA-DPA10103-DPB10201  443      NSNNLDSKVGGNYNY  LDSKVGGNY  4        0.0859
19728.7    95.00  0.35     Sequence
 HLA-DPA10103-DPB10201  444      SNNLDSKVGGNYNYL  KVGGNYNYL  6        0.1699
7954.4    80.00  0.52     Sequence
 HLA-DPA10103-DPB10201  445      NNLDSKVGGNYNYLY  KVGGNYNYL  5        0.2220
4524.7    65.00  0.35     Sequence
 HLA-DPA10103-DPB10201  446      NLDSKVGGNYNYLYR  KVGGNYNYL  4        0.2335
3995.8    65.00  0.34     Sequence
 HLA-DPA10103-DPB10201  447      LDSKVGGNYNYLYRL  GNYNYLYRL  6        0.3463
1179.8    36.00  0.31     Sequence
 HLA-DPA10103-DPB10201  448      DSKVGGNYNYLYRLF  NYNYLYRLF  6        0.5528
126.3     8.50  0.43     Sequence          WB
 HLA-DPA10103-DPB10201  449      SKVGGNYNYLYRLFR  NYNYLYRLF  5        0.5930
81.7     5.50  0.38     Sequence          WB
 HLA-DPA10103-DPB10201  450      KVGGNYNYLYRLFRK  NYNYLYRLF  4        0.6331
53.0     3.50  0.34     Sequence          WB
 HLA-DPA10103-DPB10201  451      VGGNYNYLYRLFRKS  YLYRLFRKS  6        0.6564
41.2     2.50  0.49     Sequence          WB
 HLA-DPA10103-DPB10201  452      GGNYNYLYRLFRKSN  YLYRLFRKS  5        0.6425
47.9     3.00  0.52     Sequence          WB
 HLA-DPA10103-DPB10201  453      GNYNYLYRLFRKSNL  YLYRLFRKS  4        0.6417
48.3     3.00  0.52     Sequence          WB
 HLA-DPA10103-DPB10201  454      NYNYLYRLFRKSNLK  YLYRLFRKS  3        0.6116
66.8     4.50  0.59     Sequence          WB
 HLA-DPA10103-DPB10201  455      YNYLYRLFRKSNLKP  YLYRLFRKS  2        0.5451
137.2     9.00  0.61     Sequence          WB
 HLA-DPA10103-DPB10201  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6        0.4941
238.3    14.00  0.28     Sequence
 HLA-DPA10103-DPB10201  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.4049
625.9    26.00  0.44     Sequence
 HLA-DPA10103-DPB10201  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.3667
946.3    32.00  0.56     Sequence
 HLA-DPA10103-DPB10201  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.3451
1194.7    36.00  0.56     Sequence
 HLA-DPA10103-DPB10201  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.2663
2804.0    55.00  0.54     Sequence
 HLA-DPA10103-DPB10201  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.2282
4231.7    65.00  0.43     Sequence
 HLA-DPA10103-DPB10201  462      FRKSNLKPFERDIST  FRKSNLKPF  0        0.1860
6681.3    75.00  0.28     Sequence
 HLA-DPA10103-DPB10201  463      RKSNLKPFERDISTE  KPFERDIST  5        0.1342
11707.4    90.00  0.20     Sequence
 HLA-DPA10103-DPB10201  464      KSNLKPFERDISTEI  FERDISTEI  6        0.1778
7305.7    75.00  0.34     Sequence
 HLA-DPA10103-DPB10201  465      SNLKPFERDISTEIY  FERDISTEI  5        0.1905
6362.4    75.00  0.31     Sequence
 HLA-DPA10103-DPB10201  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.1992
5796.4    70.00  0.34     Sequence
 HLA-DPA10103-DPB10201  467      LKPFERDISTEIYQA  FERDISTEI  3        0.2264
4316.4    65.00  0.28     Sequence
 HLA-DPA10103-DPB10201  468      KPFERDISTEIYQAG  ISTEIYQAG  6        0.2853
2282.4    49.00  0.50     Sequence
 HLA-DPA10103-DPB10201  469      PFERDISTEIYQAGS  ISTEIYQAG  5        0.2907
2153.7    48.00  0.51     Sequence
```

```
 HLA-DPA10103-DPB10201  470      FERDISTEIYQAGST  ISTEIYQAG  4         0.2843
2306.9    49.00  0.52     Sequence
 HLA-DPA10103-DPB10201  471      ERDISTEIYQAGSTP  ISTEIYQAG  3         0.2599
3005.1    55.00  0.52     Sequence
 HLA-DPA10103-DPB10201  472      RDISTEIYQAGSTPC  ISTEIYQAG  2         0.2542
3196.3    60.00  0.50     Sequence
 HLA-DPA10103-DPB10201  473      DISTEIYQAGSTPCN  ISTEIYQAG  1         0.2318
4069.6    65.00  0.38     Sequence
 HLA-DPA10103-DPB10201  474      ISTEIYQAGSTPCNG  ISTEIYQAG  0         0.1914
6304.0    75.00  0.25     Sequence
 HLA-DPA10103-DPB10201  475      STEIYQAGSTPCNGV  YQAGSTPCN  4         0.1471
10180.6    85.00  0.34     Sequence
 HLA-DPA10103-DPB10201  476      TEIYQAGSTPCNGVK  YQAGSTPCN  3         0.1334
11810.2    90.00  0.38     Sequence
 HLA-DPA10103-DPB10201  477      EIYQAGSTPCNGVKG  YQAGSTPCN  2         0.1104
15139.3    95.00  0.36     Sequence
 HLA-DPA10103-DPB10201  478      IYQAGSTPCNGVKGF  YQAGSTPCN  1         0.1099
15223.5    95.00  0.24     Sequence
 HLA-DPA10103-DPB10201  479      YQAGSTPCNGVKGFN  TPCNGVKGF  5         0.1010
16764.8    95.00  0.29     Sequence
 HLA-DPA10103-DPB10201  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6         0.0996
17021.8    95.00  0.38     Sequence
 HLA-DPA10103-DPB10201  481      AGSTPCNGVKGFNCY  NGVKGFNCY  6         0.1329
11866.1    90.00  0.31     Sequence
 HLA-DPA10103-DPB10201  482      GSTPCNGVKGFNCYF  NGVKGFNCY  5         0.1529
9565.6    85.00  0.22     Sequence
 HLA-DPA10103-DPB10201  483      STPCNGVKGFNCYFP  VKGFNCYFP  6         0.1902
6382.5    75.00  0.17     Sequence
 HLA-DPA10103-DPB10201  484      TPCNGVKGFNCYFPL  KGFNCYFPL  6         0.3625
989.9    33.00  0.44     Sequence
 HLA-DPA10103-DPB10201  485      PCNGVKGFNCYFPLQ  GFNCYFPLQ  6         0.4902
248.6    15.00  0.44     Sequence
 HLA-DPA10103-DPB10201  486      CNGVKGFNCYFPLQS  GFNCYFPLQ  5         0.5014
220.3    13.00  0.43     Sequence
 HLA-DPA10103-DPB10201  487      NGVKGFNCYFPLQSY  NCYFPLQSY  6         0.5839
90.2     6.00  0.32     Sequence         WB
 HLA-DPA10103-DPB10201  488      GVKGFNCYFPLQSYG  NCYFPLQSY  5         0.6056
71.3     4.50  0.29     Sequence         WB
 HLA-DPA10103-DPB10201  489      VKGFNCYFPLQSYGF  NCYFPLQSY  4         0.6601
39.6     2.50  0.23     Sequence         WB
 HLA-DPA10103-DPB10201  490      KGFNCYFPLQSYGFQ  NCYFPLQSY  3         0.6570
40.9     2.50  0.23     Sequence         WB
 HLA-DPA10103-DPB10201  491      GFNCYFPLQSYGFQP  YFPLQSYGF  4         0.6366
51.0     3.00  0.22     Sequence         WB
 HLA-DPA10103-DPB10201  492      FNCYFPLQSYGFQPT  LQSYGFQPT  6         0.6413
48.5     3.00  0.29     Sequence         WB
 HLA-DPA10103-DPB10201  493      NCYFPLQSYGFQPTY  LQSYGFQPT  5         0.6252
57.7     3.50  0.33     Sequence         WB
 HLA-DPA10103-DPB10201  494      CYFPLQSYGFQPTYG  LQSYGFQPT  4         0.5820
92.0     6.00  0.41     Sequence         WB
 HLA-DPA10103-DPB10201  495      YFPLQSYGFQPTYGV  LQSYGFQPT  3         0.5276
166.0    11.00  0.46     Sequence
 HLA-DPA10103-DPB10201  496      FPLQSYGFQPTYGVG  LQSYGFQPT  2         0.4200
531.6    24.00  0.47     Sequence
 HLA-DPA10103-DPB10201  497      PLQSYGFQPTYGVGY  FQPTYGVGY  6         0.4068
612.9    26.00  0.25     Sequence
 HLA-DPA10103-DPB10201  498      LQSYGFQPTYGVGYQ  FQPTYGVGY  5         0.3772
844.4    31.00  0.28     Sequence
 HLA-DPA10103-DPB10201  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4         0.3365
1311.8    38.00  0.35     Sequence
 HLA-DPA10103-DPB10201  500      SYGFQPTYGVGYQPY  TYGVGYQPY  6         0.3846
779.1    29.00  0.41     Sequence
 HLA-DPA10103-DPB10201  501      YGFQPTYGVGYQPYR  TYGVGYQPY  5         0.3952
694.8    28.00  0.42     Sequence
 HLA-DPA10103-DPB10201  502      GFQPTYGVGYQPYRV  TYGVGYQPY  4         0.4012
651.2    27.00  0.42     Sequence
```

```
 HLA-DPA10103-DPB10201  503      FQPTYGVGYQPYRVV  VGYQPYRVV  6        0.4572
355.3    18.00  0.37     Sequence
 HLA-DPA10103-DPB10201  504      QPTYGVGYQPYRVVV  VGYQPYRVV  5        0.4583
351.2    18.00  0.39     Sequence
 HLA-DPA10103-DPB10201  505      PTYGVGYQPYRVVVL  VGYQPYRVV  4        0.4713
305.1    17.00  0.40     Sequence
 HLA-DPA10103-DPB10201  506      TYGVGYQPYRVVVLS  VGYQPYRVV  3        0.4631
333.4    18.00  0.39     Sequence
 HLA-DPA10103-DPB10201  507      YGVGYQPYRVVVLSF  VGYQPYRVV  2        0.4727
300.4    17.00  0.34     Sequence
 HLA-DPA10103-DPB10201  508      GVGYQPYRVVVLSFE  YQPYRVVVL  3        0.4872
256.7    15.00  0.21     Sequence
 HLA-DPA10103-DPB10201  509      VGYQPYRVVVLSFEL  VVVLSFELX  7        0.5539
124.8     8.00  0.27     Sequence         WB
 HLA-DPA10103-DPB10201  510      GYQPYRVVVLSFELL  VVVLSFELL  6        0.6549
41.8     2.50  0.63     Sequence         WB
 HLA-DPA10103-DPB10201  511      YQPYRVVVLSFELLH  VVVLSFELL  5        0.6462
46.0     3.00  0.60     Sequence         WB
 HLA-DPA10103-DPB10201  512      QPYRVVVLSFELLHA  VVVLSFELL  4        0.6606
39.3     2.50  0.50     Sequence         WB
 HLA-DPA10103-DPB10201  513      PYRVVVLSFELLHAP  VVVLSFELL  3        0.6669
36.8     1.90  0.47     Sequence         SB
 HLA-DPA10103-DPB10201  514      YRVVVLSFELLHAPA  VVVLSFELL  2        0.6542
42.2     2.50  0.44     Sequence         WB
 HLA-DPA10103-DPB10201  515      RVVVLSFELLHAPAT  VLSFELLHA  3        0.6097
68.3     4.50  0.31     Sequence         WB
 HLA-DPA10103-DPB10201  516      VVVLSFELLHAPATV  VLSFELLHA  2        0.5251
170.5    11.00  0.28     Sequence
 HLA-DPA10103-DPB10201  517      VVLSFELLHAPATVC  LSFELLHAP  2        0.4661
322.6    17.00  0.25     Sequence
 HLA-DPA10103-DPB10201  518      VLSFELLHAPATVCG  FELLHAPAT  3        0.4116
581.9    25.00  0.23     Sequence
 HLA-DPA10103-DPB10201  519      LSFELLHAPATVCGP  FELLHAPAT  2        0.3182
1599.4    42.00  0.34     Sequence
 HLA-DPA10103-DPB10201  520      SFELLHAPATVCGPK  LLHAPATVC  3        0.2637
2882.4    55.00  0.28     Sequence
 HLA-DPA10103-DPB10201  521      FELLHAPATVCGPKK  LLHAPATVC  2        0.2246
4403.1    65.00  0.32     Sequence
 HLA-DPA10103-DPB10201  522      ELLHAPATVCGPKKS  LLHAPATVC  1        0.1263
12746.0    90.00  0.32     Sequence
 HLA-DPA10103-DPB10201  523      LLHAPATVCGPKKST  LLHAPATVC  0        0.0780
21511.5   100.00  0.31     Sequence
 HLA-DPA10103-DPB10201  524      LHAPATVCGPKKSTN  VCGPKKSTN  6        0.0527
28280.0   100.00  0.26     Sequence
 HLA-DPA10103-DPB10201  525      HAPATVCGPKKSTNL  CGPKKSTNL  6        0.0563
27177.3   100.00  0.22     Sequence
 HLA-DPA10103-DPB10201  526      APATVCGPKKSTNLV  CGPKKSTNL  5        0.0588
26472.9   100.00  0.17     Sequence
 HLA-DPA10103-DPB10201  527      PATVCGPKKSTNLVK  CGPKKSTNL  4        0.0584
26581.1   100.00  0.20     Sequence
 HLA-DPA10103-DPB10201  528      ATVCGPKKSTNLVKN  KKSTNLVKN  6        0.0637
25087.3   100.00  0.32     Sequence
 HLA-DPA10103-DPB10201  529      TVCGPKKSTNLVKNK  KKSTNLVKN  5        0.0633
25199.3   100.00  0.34     Sequence
 HLA-DPA10103-DPB10201  530      VCGPKKSTNLVKNKC  KKSTNLVKN  4        0.0622
25517.9   100.00  0.34     Sequence
 HLA-DPA10103-DPB10201  531      CGPKKSTNLVKNKCV  TNLVKNKCV  6        0.0769
21752.4   100.00  0.25     Sequence
 HLA-DPA10103-DPB10201  532      GPKKSTNLVKNKCVN  LVKNKCVNX  7        0.0841
20117.6   100.00  0.24     Sequence
 HLA-DPA10103-DPB10201  533      PKKSTNLVKNKCVNF  LVKNKCVNF  6        0.1572
9130.1    80.00  0.63     Sequence
 HLA-DPA10103-DPB10201  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.1606
8800.5    80.00  0.63     Sequence
 HLA-DPA10103-DPB10201  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.2036
5521.7    70.00  0.51     Sequence
```

```
 HLA-DPA10103-DPB10201  536      STNLVKNKCVNFNFN  LVKNKCVNF  3         0.2317
4076.7    65.00  0.44     Sequence
 HLA-DPA10103-DPB10201  537      TNLVKNKCVNFNFNG  LVKNKCVNF  2         0.2497
3356.0    60.00  0.37     Sequence
 HLA-DPA10103-DPB10201  538      NLVKNKCVNFNFNGL  CVNFNFNGL  6         0.4032
637.3    26.00  0.58     Sequence
 HLA-DPA10103-DPB10201  539      LVKNKCVNFNFNGLT  CVNFNFNGL  5         0.4414
421.4    21.00  0.52     Sequence
 HLA-DPA10103-DPB10201  540      VKNKCVNFNFNGLTG  CVNFNFNGL  4         0.4394
430.6    21.00  0.46     Sequence
 HLA-DPA10103-DPB10201  541      KNKCVNFNFNGLTGT  CVNFNFNGL  3         0.4462
400.1    20.00  0.40     Sequence
 HLA-DPA10103-DPB10201  542      NKCVNFNFNGLTGTG  FNFNGLTGT  5         0.4292
480.9    22.00  0.37     Sequence
 HLA-DPA10103-DPB10201  543      KCVNFNFNGLTGTGV  FNFNGLTGT  4         0.4214
523.4    24.00  0.43     Sequence
 HLA-DPA10103-DPB10201  544      CVNFNFNGLTGTGVL  FNFNGLTGT  3         0.4120
579.4    25.00  0.40     Sequence
 HLA-DPA10103-DPB10201  545      VNFNFNGLTGTGVLT  FNFNGLTGT  2         0.3343
1343.7    39.00  0.46     Sequence
 HLA-DPA10103-DPB10201  546      NFNFNGLTGTGVLTE  LTGTGVLTE  6         0.3081
1782.4    44.00  0.31     Sequence
 HLA-DPA10103-DPB10201  547      FNFNGLTGTGVLTES  LTGTGVLTE  5         0.2602
2994.9    55.00  0.49     Sequence
 HLA-DPA10103-DPB10201  548      NFNGLTGTGVLTESN  LTGTGVLTE  4         0.2306
4123.4    65.00  0.56     Sequence
 HLA-DPA10103-DPB10201  549      FNGLTGTGVLTESNK  LTGTGVLTE  3         0.2270
4286.7    65.00  0.58     Sequence
 HLA-DPA10103-DPB10201  550      NGLTGTGVLTESNKK  LTGTGVLTE  2         0.1895
6436.6    75.00  0.56     Sequence
 HLA-DPA10103-DPB10201  551      GLTGTGVLTESNKKF  VLTESNKKF  6         0.2508
3315.9    60.00  0.46     Sequence
 HLA-DPA10103-DPB10201  552      LTGTGVLTESNKKFL  VLTESNKKF  5         0.2981
1987.4    46.00  0.40     Sequence
 HLA-DPA10103-DPB10201  553      TGTGVLTESNKKFLP  VLTESNKKF  4         0.3089
1768.4    44.00  0.40     Sequence
 HLA-DPA10103-DPB10201  554      GTGVLTESNKKFLPF  ESNKKFLPF  6         0.3653
960.3    33.00  0.47     Sequence
 HLA-DPA10103-DPB10201  555      TGVLTESNKKFLPFQ  ESNKKFLPF  5         0.3777
839.5    31.00  0.45     Sequence
 HLA-DPA10103-DPB10201  556      GVLTESNKKFLPFQQ  ESNKKFLPF  4         0.3706
906.5    32.00  0.41     Sequence
 HLA-DPA10103-DPB10201  557      VLTESNKKFLPFQQF  KKFLPFQQF  6         0.4495
386.4    19.00  0.34     Sequence
 HLA-DPA10103-DPB10201  558      LTESNKKFLPFQQFG  KKFLPFQQF  5         0.4965
232.3    14.00  0.34     Sequence
 HLA-DPA10103-DPB10201  559      TESNKKFLPFQQFGR  LPFQQFGRX  7         0.5821
92.0     6.00  0.31    Sequence         WB
 HLA-DPA10103-DPB10201  560      ESNKKFLPFQQFGRD  LPFQQFGRD  6         0.5837
90.4     6.00  0.36    Sequence         WB
 HLA-DPA10103-DPB10201  561      SNKKFLPFQQFGRDI  LPFQQFGRD  5         0.5847
89.4     6.00  0.37    Sequence         WB
 HLA-DPA10103-DPB10201  562      NKKFLPFQQFGRDIA  LPFQQFGRD  4         0.5731
101.4     6.50  0.37     Sequence         WB
 HLA-DPA10103-DPB10201  563      KKFLPFQQFGRDIAD  LPFQQFGRD  3         0.5510
128.7     8.50  0.40     Sequence         WB
 HLA-DPA10103-DPB10201  564      KFLPFQQFGRDIADT  LPFQQFGRD  2         0.4670
319.4    17.00  0.47     Sequence
 HLA-DPA10103-DPB10201  565      FLPFQQFGRDIADTT  LPFQQFGRD  1         0.3543
1081.7    35.00  0.34     Sequence
 HLA-DPA10103-DPB10201  566      LPFQQFGRDIADTTD  FQQFGRDIA  2         0.1787
7232.1    75.00  0.28     Sequence
 HLA-DPA10103-DPB10201  567      PFQQFGRDIADTTDA  FGRDIADTT  4         0.1363
11440.1    85.00  0.15     Sequence
 HLA-DPA10103-DPB10201  568      FQQFGRDIADTTDAV  FGRDIADTT  3         0.1355
11540.8    90.00  0.18     Sequence
```

```
 HLA-DPA10103-DPB10201  569      QQFGRDIADTTDAVR  DIADTTDAV  5        0.0920
18482.0    95.00  0.36     Sequence
 HLA-DPA10103-DPB10201  570      QFGRDIADTTDAVRD  DIADTTDAV  4        0.0839
20172.3   100.00  0.38     Sequence
 HLA-DPA10103-DPB10201  571      FGRDIADTTDAVRDP  DIADTTDAV  3        0.0830
20377.1   100.00  0.40     Sequence
 HLA-DPA10103-DPB10201  572      GRDIADTTDAVRDPQ  DIADTTDAV  2        0.0735
22570.4   100.00  0.34     Sequence
 HLA-DPA10103-DPB10201  573      RDIADTTDAVRDPQT  DIADTTDAV  1        0.0734
22597.0   100.00  0.28     Sequence
 HLA-DPA10103-DPB10201  574      DIADTTDAVRDPQTL  DAVRDPQTL  6        0.0683
23892.7   100.00  0.16     Sequence
 HLA-DPA10103-DPB10201  575      IADTTDAVRDPQTLE  DAVRDPQTL  5        0.0649
24762.6   100.00  0.17     Sequence
 HLA-DPA10103-DPB10201  576      ADTTDAVRDPQTLEI  VRDPQTLEI  6        0.1355
11546.4    90.00  0.45     Sequence
 HLA-DPA10103-DPB10201  577      DTTDAVRDPQTLEIL  RDPQTLEIL  6        0.1912
6318.1    75.00  0.47     Sequence
 HLA-DPA10103-DPB10201  578      TTDAVRDPQTLEILD  RDPQTLEIL  5        0.2006
5706.3    70.00  0.44     Sequence
 HLA-DPA10103-DPB10201  579      TDAVRDPQTLEILDI  RDPQTLEIL  4        0.2512
3301.4    60.00  0.29     Sequence
 HLA-DPA10103-DPB10201  580      DAVRDPQTLEILDIT  QTLEILDIT  6        0.3098
1751.3    44.00  0.20     Sequence
 HLA-DPA10103-DPB10201  581      AVRDPQTLEILDITP  QTLEILDIT  5        0.3241
1499.2    41.00  0.18     Sequence
 HLA-DPA10103-DPB10201  582      VRDPQTLEILDITPC  LEILDITPC  6        0.3134
1683.7    43.00  0.30     Sequence
 HLA-DPA10103-DPB10201  583      RDPQTLEILDITPCS  LEILDITPC  5        0.2929
2102.8    47.00  0.32     Sequence
 HLA-DPA10103-DPB10201  584      DPQTLEILDITPCSF  ILDITPCSF  6        0.3536
1090.5    35.00  0.29     Sequence
 HLA-DPA10103-DPB10201  585      PQTLEILDITPCSFG  ILDITPCSF  5        0.3593
1024.4    34.00  0.33     Sequence
 HLA-DPA10103-DPB10201  586      QTLEILDITPCSFGG  ILDITPCSF  4        0.3690
922.2    32.00  0.34     Sequence
 HLA-DPA10103-DPB10201  587      TLEILDITPCSFGGV  ITPCSFGGV  6        0.4182
541.6    24.00  0.56     Sequence
 HLA-DPA10103-DPB10201  588      LEILDITPCSFGGVS  ITPCSFGGV  5        0.4016
648.5    27.00  0.61     Sequence
 HLA-DPA10103-DPB10201  589      EILDITPCSFGGVSV  ITPCSFGGV  4        0.4071
610.7    26.00  0.55     Sequence
 HLA-DPA10103-DPB10201  590      ILDITPCSFGGVSVI  ITPCSFGGV  3        0.4536
369.6    19.00  0.44     Sequence
 HLA-DPA10103-DPB10201  591      LDITPCSFGGVSVIT  ITPCSFGGV  2        0.4306
473.6    22.00  0.35     Sequence
 HLA-DPA10103-DPB10201  592      DITPCSFGGVSVITP  FGGVSVITP  6        0.4119
579.9    25.00  0.32     Sequence
 HLA-DPA10103-DPB10201  593      ITPCSFGGVSVITPG  FGGVSVITP  5        0.3807
812.9    30.00  0.34     Sequence
 HLA-DPA10103-DPB10201  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.3471
1169.9    36.00  0.38     Sequence
 HLA-DPA10103-DPB10201  595      PCSFGGVSVITPGTN  FGGVSVITP  3        0.3263
1464.3    40.00  0.40     Sequence
 HLA-DPA10103-DPB10201  596      CSFGGVSVITPGTNT  FGGVSVITP  2        0.2467
3465.8    60.00  0.44     Sequence
 HLA-DPA10103-DPB10201  597      SFGGVSVITPGTNTS  FGGVSVITP  1        0.1333
11821.5    90.00  0.37     Sequence
 HLA-DPA10103-DPB10201  598      FGGVSVITPGTNTSN  GVSVITPGT  2        0.0892
19040.0    95.00  0.22     Sequence
 HLA-DPA10103-DPB10201  599      GGVSVITPGTNTSNQ  VITPGTNTS  4        0.0712
23139.1   100.00  0.22     Sequence
 HLA-DPA10103-DPB10201  600      GVSVITPGTNTSNQV  VITPGTNTS  3        0.0670
24215.7   100.00  0.25     Sequence
 HLA-DPA10103-DPB10201  601      VSVITPGTNTSNQVA  VITPGTNTS  2        0.0646
24868.3   100.00  0.25     Sequence
```

```
 HLA-DPA10103-DPB10201  602      SVITPGTNTSNQVAV  TNTSNQVAV  6        0.0622
25516.2   100.00  0.25     Sequence
 HLA-DPA10103-DPB10201  603      VITPGTNTSNQVAVL  NTSNQVAVL  6        0.1308
12139.6    90.00  0.56     Sequence
 HLA-DPA10103-DPB10201  604      ITPGTNTSNQVAVLY  NTSNQVAVL  5        0.1439
10533.4    85.00  0.51     Sequence
 HLA-DPA10103-DPB10201  605      TPGTNTSNQVAVLYQ  NTSNQVAVL  4        0.1501
9853.6    85.00  0.42     Sequence
 HLA-DPA10103-DPB10201  606      PGTNTSNQVAVLYQG  NTSNQVAVL  3        0.1543
9414.2    85.00  0.34     Sequence
 HLA-DPA10103-DPB10201  607      GTNTSNQVAVLYQGV  QVAVLYQGV  6        0.2407
3698.7    60.00  0.50     Sequence
 HLA-DPA10103-DPB10201  608      TNTSNQVAVLYQGVN  QVAVLYQGV  5        0.2871
2238.5    49.00  0.46     Sequence
 HLA-DPA10103-DPB10201  609      NTSNQVAVLYQGVNC  QVAVLYQGV  4        0.2803
2408.0    50.00  0.41     Sequence
 HLA-DPA10103-DPB10201  610      TSNQVAVLYQGVNCT  VLYQGVNCT  6        0.3039
1866.2    45.00  0.36     Sequence
 HLA-DPA10103-DPB10201  611      SNQVAVLYQGVNCTE  VLYQGVNCT  5        0.3116
1717.4    43.00  0.36     Sequence
 HLA-DPA10103-DPB10201  612      NQVAVLYQGVNCTEV  VLYQGVNCT  4        0.3319
1378.0    39.00  0.32     Sequence
 HLA-DPA10103-DPB10201  613      QVAVLYQGVNCTEVP  VLYQGVNCT  3        0.3192
1581.6    42.00  0.36     Sequence
 HLA-DPA10103-DPB10201  614      VAVLYQGVNCTEVPV  YQGVNCTEV  4        0.3031
1883.1    45.00  0.35     Sequence
 HLA-DPA10103-DPB10201  615      AVLYQGVNCTEVPVA  YQGVNCTEV  3        0.2555
3149.2    60.00  0.41     Sequence
 HLA-DPA10103-DPB10201  616      VLYQGVNCTEVPVAI  YQGVNCTEV  2        0.2777
2478.5    55.00  0.28     Sequence
 HLA-DPA10103-DPB10201  617      LYQGVNCTEVPVAIH  NCTEVPVAI  5        0.2681
2749.3    55.00  0.25     Sequence
 HLA-DPA10103-DPB10201  618      YQGVNCTEVPVAIHA  NCTEVPVAI  4        0.2579
3068.3    55.00  0.26     Sequence
 HLA-DPA10103-DPB10201  619      QGVNCTEVPVAIHAD  NCTEVPVAI  3        0.2434
3591.1    60.00  0.28     Sequence
 HLA-DPA10103-DPB10201  620      GVNCTEVPVAIHADQ  NCTEVPVAI  2        0.2325
4042.6    65.00  0.28     Sequence
 HLA-DPA10103-DPB10201  621      VNCTEVPVAIHADQL  NCTEVPVAI  1        0.2259
4341.1    65.00  0.27     Sequence
 HLA-DPA10103-DPB10201  622      NCTEVPVAIHADQLT  EVPVAIHAD  3        0.1955
6031.6    75.00  0.20     Sequence
 HLA-DPA10103-DPB10201  623      CTEVPVAIHADQLTP  IHADQLTPX  7        0.1649
8401.2    80.00  0.19     Sequence
 HLA-DPA10103-DPB10201  624      TEVPVAIHADQLTPT  IHADQLTPT  6        0.2007
5701.8    70.00  0.55     Sequence
 HLA-DPA10103-DPB10201  625      EVPVAIHADQLTPTW  IHADQLTPT  5        0.1976
5895.4    70.00  0.52     Sequence
 HLA-DPA10103-DPB10201  626      VPVAIHADQLTPTWR  IHADQLTPT  4        0.1965
5968.1    75.00  0.52     Sequence
 HLA-DPA10103-DPB10201  627      PVAIHADQLTPTWRV  IHADQLTPT  3        0.2222
4515.4    65.00  0.43     Sequence
 HLA-DPA10103-DPB10201  628      VAIHADQLTPTWRVY  QLTPTWRVY  6        0.2650
2842.2    55.00  0.32     Sequence
 HLA-DPA10103-DPB10201  629      AIHADQLTPTWRVYS  QLTPTWRVY  5        0.2569
3103.7    55.00  0.28     Sequence
 HLA-DPA10103-DPB10201  630      IHADQLTPTWRVYST  QLTPTWRVY  4        0.2350
3934.5    65.00  0.34     Sequence
 HLA-DPA10103-DPB10201  631      HADQLTPTWRVYSTG  QLTPTWRVY  3        0.2120
5043.8    70.00  0.35     Sequence
 HLA-DPA10103-DPB10201  632      ADQLTPTWRVYSTGS  QLTPTWRVY  2        0.2179
4734.2    65.00  0.32     Sequence
 HLA-DPA10103-DPB10201  633      DQLTPTWRVYSTGSN  QLTPTWRVY  1        0.2073
5304.7    70.00  0.30     Sequence
 HLA-DPA10103-DPB10201  634      QLTPTWRVYSTGSNV  RVYSTGSNV  6        0.1904
6368.9    75.00  0.26     Sequence
```

```
 HLA-DPA10103-DPB10201  635      LTPTWRVYSTGSNVF  VYSTGSNVF  6        0.2658
2819.1    55.00  0.40     Sequence
 HLA-DPA10103-DPB10201  636      TPTWRVYSTGSNVFQ  VYSTGSNVF  5        0.2705
2678.3    55.00  0.38     Sequence
 HLA-DPA10103-DPB10201  637      PTWRVYSTGSNVFQT  VYSTGSNVF  4        0.2830
2339.4    49.00  0.36     Sequence
 HLA-DPA10103-DPB10201  638      TWRVYSTGSNVFQTR  VYSTGSNVF  3        0.2855
2276.5    49.00  0.36     Sequence
 HLA-DPA10103-DPB10201  639      WRVYSTGSNVFQTRA  VYSTGSNVF  2        0.2709
2666.1    55.00  0.36     Sequence
 HLA-DPA10103-DPB10201  640      RVYSTGSNVFQTRAG  TGSNVFQTR  4        0.2438
3575.6    60.00  0.25     Sequence
 HLA-DPA10103-DPB10201  641      VYSTGSNVFQTRAGC  TGSNVFQTR  3        0.2174
4758.7    65.00  0.27     Sequence
 HLA-DPA10103-DPB10201  642      YSTGSNVFQTRAGCL  VFQTRAGCL  6        0.2841
2311.5    49.00  0.43     Sequence
 HLA-DPA10103-DPB10201  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.3412
1247.1    37.00  0.34     Sequence
 HLA-DPA10103-DPB10201  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.3339
1348.4    39.00  0.34     Sequence
 HLA-DPA10103-DPB10201  645      GSNVFQTRAGCLIGA  VFQTRAGCL  3        0.3319
1378.9    39.00  0.32     Sequence
 HLA-DPA10103-DPB10201  646      SNVFQTRAGCLIGAE  VFQTRAGCL  2        0.3250
1485.3    40.00  0.31     Sequence
 HLA-DPA10103-DPB10201  647      NVFQTRAGCLIGAEY  VFQTRAGCL  1        0.3134
1683.2    43.00  0.29     Sequence
 HLA-DPA10103-DPB10201  648      VFQTRAGCLIGAEYV  VFQTRAGCL  0        0.3566
1055.0    34.00  0.19     Sequence
 HLA-DPA10103-DPB10201  649      FQTRAGCLIGAEYVN  LIGAEYVNX  7        0.3475
1164.6    36.00  0.23     Sequence
 HLA-DPA10103-DPB10201  650      QTRAGCLIGAEYVNN  LIGAEYVNN  6        0.3676
936.5    32.00  0.56     Sequence
 HLA-DPA10103-DPB10201  651      TRAGCLIGAEYVNNS  LIGAEYVNN  5        0.3681
931.8    32.00  0.57     Sequence
 HLA-DPA10103-DPB10201  652      RAGCLIGAEYVNNSY  LIGAEYVNN  4        0.3664
948.8    32.00  0.56     Sequence
 HLA-DPA10103-DPB10201  653      AGCLIGAEYVNNSYE  LIGAEYVNN  3        0.3610
1005.8    33.00  0.57     Sequence
 HLA-DPA10103-DPB10201  654      GCLIGAEYVNNSYEC  LIGAEYVNN  2        0.3475
1164.5    36.00  0.49     Sequence
 HLA-DPA10103-DPB10201  655      CLIGAEYVNNSYECD  YVNNSYECD  6        0.3294
1416.6    40.00  0.52     Sequence
 HLA-DPA10103-DPB10201  656      LIGAEYVNNSYECDI  YVNNSYECD  5        0.3321
1375.9    39.00  0.59     Sequence
 HLA-DPA10103-DPB10201  657      IGAEYVNNSYECDIP  YVNNSYECD  4        0.3129
1693.4    43.00  0.64     Sequence
 HLA-DPA10103-DPB10201  658      GAEYVNNSYECDIPI  YVNNSYECD  3        0.3225
1526.7    41.00  0.59     Sequence
 HLA-DPA10103-DPB10201  659      AEYVNNSYECDIPIG  YVNNSYECD  2        0.3194
1578.5    42.00  0.50     Sequence
 HLA-DPA10103-DPB10201  660      EYVNNSYECDIPIGA  YVNNSYECD  1        0.2782
2463.6    55.00  0.34     Sequence
 HLA-DPA10103-DPB10201  661      YVNNSYECDIPIGAG  YVNNSYECD  0        0.2316
4080.7    65.00  0.20     Sequence
 HLA-DPA10103-DPB10201  662      VNNSYECDIPIGAGI  SYECDIPIG  3        0.2068
5334.4    70.00  0.25     Sequence
 HLA-DPA10103-DPB10201  663      NNSYECDIPIGAGIC  SYECDIPIG  2        0.1910
6333.5    75.00  0.22     Sequence
 HLA-DPA10103-DPB10201  664      NSYECDIPIGAGICA  IPIGAGICA  6        0.1839
6838.2    75.00  0.16     Sequence
 HLA-DPA10103-DPB10201  665      SYECDIPIGAGICAS  IPIGAGICA  5        0.1656
8332.1    80.00  0.22     Sequence
 HLA-DPA10103-DPB10201  666      YECDIPIGAGICASY  IPIGAGICA  4        0.1565
9193.6    80.00  0.23     Sequence
 HLA-DPA10103-DPB10201  667      ECDIPIGAGICASYQ  IPIGAGICA  3        0.1522
9631.8    85.00  0.23     Sequence
```

```
 HLA-DPA10103-DPB10201  668      CDIPIGAGICASYQT  IGAGICASY  4        0.1617
8688.2    80.00  0.33     Sequence
 HLA-DPA10103-DPB10201  669      DIPIGAGICASYQTQ  GICASYQTQ  6        0.1641
8469.0    80.00  0.37     Sequence
 HLA-DPA10103-DPB10201  670      IPIGAGICASYQTQT  ICASYQTQT  6        0.2251
4375.9    65.00  0.38     Sequence
 HLA-DPA10103-DPB10201  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.2168
4790.9    65.00  0.38     Sequence
 HLA-DPA10103-DPB10201  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.2125
5017.0    70.00  0.38     Sequence
 HLA-DPA10103-DPB10201  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.2028
5569.5    70.00  0.41     Sequence
 HLA-DPA10103-DPB10201  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.1936
6153.0    75.00  0.42     Sequence
 HLA-DPA10103-DPB10201  675      GICASYQTQTNSPRR  ICASYQTQT  1        0.1507
9795.1    85.00  0.37     Sequence
 HLA-DPA10103-DPB10201  676      ICASYQTQTNSPRRA  ICASYQTQT  0        0.1257
12827.4    90.00  0.34     Sequence
 HLA-DPA10103-DPB10201  677      CASYQTQTNSPRRAR  YQTQTNSPR  3        0.0589
26424.6   100.00  0.20     Sequence
 HLA-DPA10103-DPB10201  678      ASYQTQTNSPRRARS  TQTNSPRRA  4        0.0523
28385.2   100.00  0.25     Sequence
 HLA-DPA10103-DPB10201  679      SYQTQTNSPRRARSV  TQTNSPRRA  3        0.0542
27807.3   100.00  0.25     Sequence
 HLA-DPA10103-DPB10201  680      YQTQTNSPRRARSVA  NSPRRARSV  5        0.0447
30817.6   100.00  0.30     Sequence
 HLA-DPA10103-DPB10201  681      QTQTNSPRRARSVAS  NSPRRARSV  4        0.0414
31953.1   100.00  0.28     Sequence
 HLA-DPA10103-DPB10201  682      TQTNSPRRARSVASQ  NSPRRARSV  3        0.0389
32837.7   100.00  0.25     Sequence
 HLA-DPA10103-DPB10201  683      QTNSPRRARSVASQS  RRARSVASQ  5        0.0356
34007.1   100.00  0.31     Sequence
 HLA-DPA10103-DPB10201  684      TNSPRRARSVASQSI  ARSVASQSI  6        0.0805
20925.2   100.00  0.49     Sequence
 HLA-DPA10103-DPB10201  685      NSPRRARSVASQSII  ARSVASQSI  5        0.1337
11768.2    90.00  0.35     Sequence
 HLA-DPA10103-DPB10201  686      SPRRARSVASQSIIA  VASQSIIAX  7        0.1518
9679.4    85.00  0.37     Sequence
 HLA-DPA10103-DPB10201  687      PRRARSVASQSIIAY  VASQSIIAY  6        0.2326
4037.3    65.00  0.75     Sequence
 HLA-DPA10103-DPB10201  688      RRARSVASQSIIAYT  VASQSIIAY  5        0.2457
3502.8    60.00  0.68     Sequence
 HLA-DPA10103-DPB10201  689      RARSVASQSIIAYTM  VASQSIIAY  4        0.2979
1991.4    46.00  0.57     Sequence
 HLA-DPA10103-DPB10201  690      ARSVASQSIIAYTMS  VASQSIIAY  3        0.3185
1593.4    42.00  0.51     Sequence
 HLA-DPA10103-DPB10201  691      RSVASQSIIAYTMSL  VASQSIIAY  2        0.4120
579.5    25.00  0.27     Sequence
 HLA-DPA10103-DPB10201  692      SVASQSIIAYTMSLG  IIAYTMSLG  6        0.4009
653.1    27.00  0.28     Sequence
 HLA-DPA10103-DPB10201  693      VASQSIIAYTMSLGA  IIAYTMSLG  5        0.4169
549.5    24.00  0.26     Sequence
 HLA-DPA10103-DPB10201  694      ASQSIIAYTMSLGAE  IIAYTMSLG  4        0.4183
541.2    24.00  0.26     Sequence
 HLA-DPA10103-DPB10201  695      SQSIIAYTMSLGAEN  IIAYTMSLG  3        0.4068
613.0    26.00  0.27     Sequence
 HLA-DPA10103-DPB10201  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.3780
837.2    30.00  0.22     Sequence
 HLA-DPA10103-DPB10201  697      SIIAYTMSLGAENSV  IAYTMSLGA  2        0.3502
1130.8    35.00  0.25     Sequence
 HLA-DPA10103-DPB10201  698      IIAYTMSLGAENSVA  YTMSLGAEN  3        0.2638
2881.1    55.00  0.26     Sequence
 HLA-DPA10103-DPB10201  699      IAYTMSLGAENSVAY  YTMSLGAEN  2        0.2183
4712.3    65.00  0.25     Sequence
 HLA-DPA10103-DPB10201  700      AYTMSLGAENSVAYS  LGAENSVAY  5        0.1655
8338.1    80.00  0.31     Sequence
```

```
 HLA-DPA10103-DPB10201  701      YTMSLGAENSVAYSN  LGAENSVAY  4        0.1406
10926.5    85.00  0.44     Sequence
 HLA-DPA10103-DPB10201  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.1335
11787.9    90.00  0.46     Sequence
 HLA-DPA10103-DPB10201  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.1361
11465.4    85.00  0.46     Sequence
 HLA-DPA10103-DPB10201  704      SLGAENSVAYSNNSI  ENSVAYSNN  4        0.1453
10376.8    85.00  0.16     Sequence
 HLA-DPA10103-DPB10201  705      LGAENSVAYSNNSIA  VAYSNNSIA  6        0.1615
8709.8    80.00  0.31     Sequence
 HLA-DPA10103-DPB10201  706      GAENSVAYSNNSIAI  AYSNNSIAI  6        0.2435
3586.8    60.00  0.34     Sequence
 HLA-DPA10103-DPB10201  707      AENSVAYSNNSIAIP  YSNNSIAIP  6        0.2782
2464.4    55.00  0.38     Sequence
 HLA-DPA10103-DPB10201  708      ENSVAYSNNSIAIPT  YSNNSIAIP  5        0.2764
2512.9    55.00  0.40     Sequence
 HLA-DPA10103-DPB10201  709      NSVAYSNNSIAIPTN  YSNNSIAIP  4        0.2687
2731.2    55.00  0.41     Sequence
 HLA-DPA10103-DPB10201  710      SVAYSNNSIAIPTNF  YSNNSIAIP  3        0.2652
2837.7    55.00  0.41     Sequence
 HLA-DPA10103-DPB10201  711      VAYSNNSIAIPTNFT  YSNNSIAIP  2        0.2458
3500.1    60.00  0.40     Sequence
 HLA-DPA10103-DPB10201  712      AYSNNSIAIPTNFTI  IAIPTNFTI  6        0.2774
2486.2    55.00  0.20     Sequence
 HLA-DPA10103-DPB10201  713      YSNNSIAIPTNFTIS  AIPTNFTIS  6        0.2721
2632.6    55.00  0.51     Sequence
 HLA-DPA10103-DPB10201  714      SNNSIAIPTNFTISV  AIPTNFTIS  5        0.3071
1803.2    44.00  0.44     Sequence
 HLA-DPA10103-DPB10201  715      NNSIAIPTNFTISVT  AIPTNFTIS  4        0.3102
1743.1    44.00  0.41     Sequence
 HLA-DPA10103-DPB10201  716      NSIAIPTNFTISVTT  AIPTNFTIS  3        0.3078
1789.0    44.00  0.40     Sequence
 HLA-DPA10103-DPB10201  717      SIAIPTNFTISVTTE  AIPTNFTIS  2        0.2965
2022.1    46.00  0.32     Sequence
 HLA-DPA10103-DPB10201  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.3346
1339.4    38.00  0.37     Sequence
 HLA-DPA10103-DPB10201  719      AIPTNFTISVTTEIL  TISVTTEIL  6        0.3741
872.9    31.00  0.36     Sequence
 HLA-DPA10103-DPB10201  720      IPTNFTISVTTEILP  TISVTTEIL  5        0.3843
781.6    29.00  0.35     Sequence
 HLA-DPA10103-DPB10201  721      PTNFTISVTTEILPV  TISVTTEIL  4        0.4411
422.9    21.00  0.27     Sequence
 HLA-DPA10103-DPB10201  722      TNFTISVTTEILPVS  VTTEILPVS  6        0.4727
300.3    17.00  0.39     Sequence
 HLA-DPA10103-DPB10201  723      NFTISVTTEILPVSM  VTTEILPVS  5        0.4675
317.8    17.00  0.41     Sequence
 HLA-DPA10103-DPB10201  724      FTISVTTEILPVSMT  VTTEILPVS  4        0.4591
348.1    18.00  0.40     Sequence
 HLA-DPA10103-DPB10201  725      TISVTTEILPVSMTK  VTTEILPVS  3        0.4295
479.7    22.00  0.45     Sequence
 HLA-DPA10103-DPB10201  726      ISVTTEILPVSMTKT  VTTEILPVS  2        0.4150
560.7    24.00  0.41     Sequence
 HLA-DPA10103-DPB10201  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.3721
892.0    31.00  0.33     Sequence
 HLA-DPA10103-DPB10201  728      VTTEILPVSMTKTSV  ILPVSMTKT  4        0.3298
1410.5    39.00  0.50     Sequence
 HLA-DPA10103-DPB10201  729      TTEILPVSMTKTSVD  ILPVSMTKT  3        0.2814
2381.2    50.00  0.62     Sequence
 HLA-DPA10103-DPB10201  730      TEILPVSMTKTSVDC  ILPVSMTKT  2        0.2456
3508.4    60.00  0.56     Sequence
 HLA-DPA10103-DPB10201  731      EILPVSMTKTSVDCT  ILPVSMTKT  1        0.2167
4796.5    70.00  0.46     Sequence
 HLA-DPA10103-DPB10201  732      ILPVSMTKTSVDCTM  ILPVSMTKT  0        0.1704
7910.9    80.00  0.35     Sequence
 HLA-DPA10103-DPB10201  733      LPVSMTKTSVDCTMY  MTKTSVDCT  4        0.1277
12558.7    90.00  0.29     Sequence
```

```
 HLA-DPA10103-DPB10201  734      PVSMTKTSVDCTMYI  TSVDCTMYI  6        0.2174
4760.2    65.00  0.26     Sequence
 HLA-DPA10103-DPB10201  735      VSMTKTSVDCTMYIC  VDCTMYICX  7        0.2656
2824.8    55.00  0.28     Sequence
 HLA-DPA10103-DPB10201  736      SMTKTSVDCTMYICG  VDCTMYICG  6        0.2731
2605.4    55.00  0.46     Sequence
 HLA-DPA10103-DPB10201  737      MTKTSVDCTMYICGD  VDCTMYICG  5        0.2762
2518.9    55.00  0.44     Sequence
 HLA-DPA10103-DPB10201  738      TKTSVDCTMYICGDS  VDCTMYICG  4        0.2717
2643.7    55.00  0.47     Sequence
 HLA-DPA10103-DPB10201  739      KTSVDCTMYICGDST  VDCTMYICG  3        0.2629
2907.8    55.00  0.43     Sequence
 HLA-DPA10103-DPB10201  740      TSVDCTMYICGDSTE  VDCTMYICG  2        0.2485
3399.8    60.00  0.41     Sequence
 HLA-DPA10103-DPB10201  741      SVDCTMYICGDSTEC  VDCTMYICG  1        0.2119
5047.2    70.00  0.32     Sequence
 HLA-DPA10103-DPB10201  742      VDCTMYICGDSTECS  ICGDSTECS  6        0.2050
5440.7    70.00  0.35     Sequence
 HLA-DPA10103-DPB10201  743      DCTMYICGDSTECSN  ICGDSTECS  5        0.1926
6219.2    75.00  0.42     Sequence
 HLA-DPA10103-DPB10201  744      CTMYICGDSTECSNL  ICGDSTECS  4        0.1865
6645.2    75.00  0.47     Sequence
 HLA-DPA10103-DPB10201  745      TMYICGDSTECSNLL  ICGDSTECS  3        0.1844
6798.9    75.00  0.45     Sequence
 HLA-DPA10103-DPB10201  746      MYICGDSTECSNLLL  ICGDSTECS  2        0.2355
3912.4    65.00  0.28     Sequence
 HLA-DPA10103-DPB10201  747      YICGDSTECSNLLLQ  TECSNLLLQ  6        0.2584
3051.9    55.00  0.31     Sequence
 HLA-DPA10103-DPB10201  748      ICGDSTECSNLLLQY  ECSNLLLQY  6        0.3377
1294.8    38.00  0.48     Sequence
 HLA-DPA10103-DPB10201  749      CGDSTECSNLLLQYG  ECSNLLLQY  5        0.3622
992.8    33.00  0.46     Sequence
 HLA-DPA10103-DPB10201  750      GDSTECSNLLLQYGS  ECSNLLLQY  4        0.3601
1016.4    34.00  0.44     Sequence
 HLA-DPA10103-DPB10201  751      DSTECSNLLLQYGSF  NLLLQYGSF  6        0.4936
239.6    14.00  0.37     Sequence
 HLA-DPA10103-DPB10201  752      STECSNLLLQYGSFC  NLLLQYGSF  5        0.5163
187.6    12.00  0.36     Sequence
 HLA-DPA10103-DPB10201  753      TECSNLLLQYGSFCT  NLLLQYGSF  4        0.5493
131.2     8.50  0.33     Sequence         WB
 HLA-DPA10103-DPB10201  754      ECSNLLLQYGSFCTQ  LQYGSFCTQ  6        0.5916
83.0      5.50  0.35     Sequence         WB
 HLA-DPA10103-DPB10201  755      CSNLLLQYGSFCTQL  LQYGSFCTQ  5        0.6006
75.3      5.00  0.38     Sequence         WB
 HLA-DPA10103-DPB10201  756      SNLLLQYGSFCTQLN  LQYGSFCTQ  4        0.5820
92.1      6.00  0.38     Sequence         WB
 HLA-DPA10103-DPB10201  757      NLLLQYGSFCTQLNR  LQYGSFCTQ  3        0.5606
116.1     7.50  0.41     Sequence         WB
 HLA-DPA10103-DPB10201  758      LLLQYGSFCTQLNRA  LQYGSFCTQ  2        0.4845
264.3    15.00  0.44     Sequence
 HLA-DPA10103-DPB10201  759      LLQYGSFCTQLNRAL  FCTQLNRAL  6        0.4854
261.8    15.00  0.26     Sequence
 HLA-DPA10103-DPB10201  760      LQYGSFCTQLNRALT  FCTQLNRAL  5        0.4015
648.9    27.00  0.38     Sequence
 HLA-DPA10103-DPB10201  761      QYGSFCTQLNRALTG  FCTQLNRAL  4        0.3295
1415.4    40.00  0.50     Sequence
 HLA-DPA10103-DPB10201  762      YGSFCTQLNRALTGI  FCTQLNRAL  3        0.3294
1416.8    40.00  0.49     Sequence
 HLA-DPA10103-DPB10201  763      GSFCTQLNRALTGIA  FCTQLNRAL  2        0.2959
2035.6    47.00  0.44     Sequence
 HLA-DPA10103-DPB10201  764      SFCTQLNRALTGIAV  FCTQLNRAL  1        0.2649
2846.5    55.00  0.37     Sequence
 HLA-DPA10103-DPB10201  765      FCTQLNRALTGIAVE  FCTQLNRAL  0        0.2478
3424.5    60.00  0.31     Sequence
 HLA-DPA10103-DPB10201  766      CTQLNRALTGIAVEQ  LTGIAVEQX  7        0.1593
8919.8    80.00  0.22     Sequence
```

```
 HLA-DPA10103-DPB10201  767      TQLNRALTGIAVEQD  LTGIAVEQD  6         0.1649
8397.0    80.00  0.44     Sequence
 HLA-DPA10103-DPB10201  768      QLNRALTGIAVEQDK  LTGIAVEQD  5         0.1607
8789.2    80.00  0.47     Sequence
 HLA-DPA10103-DPB10201  769      LNRALTGIAVEQDKN  LTGIAVEQD  4         0.1530
9552.9    85.00  0.50     Sequence
 HLA-DPA10103-DPB10201  770      NRALTGIAVEQDKNT  LTGIAVEQD  3         0.1457
10330.6    85.00  0.52     Sequence
 HLA-DPA10103-DPB10201  771      RALTGIAVEQDKNTQ  LTGIAVEQD  2         0.1355
11541.8    90.00  0.51     Sequence
 HLA-DPA10103-DPB10201  772      ALTGIAVEQDKNTQE  LTGIAVEQD  1         0.1067
15752.7    95.00  0.40     Sequence
 HLA-DPA10103-DPB10201  773      LTGIAVEQDKNTQEV  IAVEQDKNT  3         0.0831
20342.3    100.00  0.32     Sequence
 HLA-DPA10103-DPB10201  774      TGIAVEQDKNTQEVF  IAVEQDKNT  2         0.0833
20295.5    100.00  0.29     Sequence
 HLA-DPA10103-DPB10201  775      GIAVEQDKNTQEVFA  QDKNTQEVF  5         0.0926
18367.8    95.00  0.28     Sequence
 HLA-DPA10103-DPB10201  776      IAVEQDKNTQEVFAQ  NTQEVFAQX  7         0.1110
15040.2    95.00  0.27     Sequence
 HLA-DPA10103-DPB10201  777      AVEQDKNTQEVFAQV  NTQEVFAQV  6         0.2136
4957.2    70.00  0.63     Sequence
 HLA-DPA10103-DPB10201  778      VEQDKNTQEVFAQVK  NTQEVFAQV  5         0.2566
3111.9    60.00  0.55     Sequence
 HLA-DPA10103-DPB10201  779      EQDKNTQEVFAQVKQ  NTQEVFAQV  4         0.2672
2777.4    55.00  0.52     Sequence
 HLA-DPA10103-DPB10201  780      QDKNTQEVFAQVKQI  EVFAQVKQI  6         0.3274
1446.8    40.00  0.45     Sequence
 HLA-DPA10103-DPB10201  781      DKNTQEVFAQVKQIY  EVFAQVKQI  5         0.3401
1261.2    37.00  0.38     Sequence
 HLA-DPA10103-DPB10201  782      KNTQEVFAQVKQIYK  EVFAQVKQI  4         0.3297
1411.5    39.00  0.38     Sequence
 HLA-DPA10103-DPB10201  783      NTQEVFAQVKQIYKT  EVFAQVKQI  3         0.3133
1685.7    43.00  0.41     Sequence
 HLA-DPA10103-DPB10201  784      TQEVFAQVKQIYKTP  EVFAQVKQI  2         0.3019
1906.1    45.00  0.43     Sequence
 HLA-DPA10103-DPB10201  785      QEVFAQVKQIYKTPP  VFAQVKQIY  2         0.2555
3151.9    60.00  0.29     Sequence
 HLA-DPA10103-DPB10201  786      EVFAQVKQIYKTPPI  VFAQVKQIY  1         0.2332
4010.7    65.00  0.18     Sequence
 HLA-DPA10103-DPB10201  787      VFAQVKQIYKTPPIK  KQIYKTPPI  5         0.2089
5217.2    70.00  0.20     Sequence
 HLA-DPA10103-DPB10201  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6         0.2007
5698.9    70.00  0.22     Sequence
 HLA-DPA10103-DPB10201  789      AQVKQIYKTPPIKDF  YKTPPIKDF  6         0.2478
3425.1    60.00  0.44     Sequence
 HLA-DPA10103-DPB10201  790      QVKQIYKTPPIKDFG  YKTPPIKDF  5         0.2381
3802.1    60.00  0.43     Sequence
 HLA-DPA10103-DPB10201  791      VKQIYKTPPIKDFGG  YKTPPIKDF  4         0.2316
4079.8    65.00  0.44     Sequence
 HLA-DPA10103-DPB10201  792      KQIYKTPPIKDFGGF  YKTPPIKDF  3         0.2216
4547.3    65.00  0.43     Sequence
 HLA-DPA10103-DPB10201  793      QIYKTPPIKDFGGFN  YKTPPIKDF  2         0.1869
6617.6    75.00  0.38     Sequence
 HLA-DPA10103-DPB10201  794      IYKTPPIKDFGGFNF  IKDFGGFNF  6         0.3091
1763.4    44.00  0.35     Sequence
 HLA-DPA10103-DPB10201  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5         0.3580
1039.4    34.00  0.34     Sequence
 HLA-DPA10103-DPB10201  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4         0.3942
702.8    28.00  0.34     Sequence
 HLA-DPA10103-DPB10201  797      TPPIKDFGGFNFSQI  FGGFNFSQI  6         0.4971
230.8    14.00  0.56     Sequence
 HLA-DPA10103-DPB10201  798      PPIKDFGGFNFSQIL  FGGFNFSQI  5         0.5212
177.7    11.00  0.51     Sequence
 HLA-DPA10103-DPB10201  799      PIKDFGGFNFSQILP  FGGFNFSQI  4         0.5240
172.4    11.00  0.47     Sequence
```

```
 HLA-DPA10103-DPB10201  800      IKDFGGFNFSQILPD  FGGFNFSQI  3        0.5372
149.5     9.50  0.40     Sequence         WB
 HLA-DPA10103-DPB10201  801      KDFGGFNFSQILPDP  FGGFNFSQI  2        0.4988
226.5    14.00  0.38     Sequence
 HLA-DPA10103-DPB10201  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.4794
279.5    16.00  0.38     Sequence
 HLA-DPA10103-DPB10201  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.4513
378.6    19.00  0.44     Sequence
 HLA-DPA10103-DPB10201  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.3698
914.7    32.00  0.50     Sequence
 HLA-DPA10103-DPB10201  805      GFNFSQILPDPSKPS  FNFSQILPD  1        0.2956
2041.8    47.00  0.46     Sequence
 HLA-DPA10103-DPB10201  806      FNFSQILPDPSKPSK  FNFSQILPD  0        0.1887
6487.4    75.00  0.31     Sequence
 HLA-DPA10103-DPB10201  807      NFSQILPDPSKPSKR  ILPDPSKPS  4        0.0870
19514.5    95.00  0.23     Sequence
 HLA-DPA10103-DPB10201  808      FSQILPDPSKPSKRS  ILPDPSKPS  3        0.0688
23742.5   100.00  0.35     Sequence
 HLA-DPA10103-DPB10201  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.0505
28946.2   100.00  0.37     Sequence
 HLA-DPA10103-DPB10201  810      QILPDPSKPSKRSFI  SKPSKRSFI  6        0.0717
23006.3   100.00  0.27     Sequence
 HLA-DPA10103-DPB10201  811      ILPDPSKPSKRSFIE  SKPSKRSFI  5        0.0793
21208.3   100.00  0.23     Sequence
 HLA-DPA10103-DPB10201  812      LPDPSKPSKRSFIED  PSKRSFIED  6        0.0973
17454.1    95.00  0.38     Sequence
 HLA-DPA10103-DPB10201  813      PDPSKPSKRSFIEDL  SKRSFIEDL  6        0.2097
5171.8    70.00  0.50     Sequence
 HLA-DPA10103-DPB10201  814      DPSKPSKRSFIEDLL  SKRSFIEDL  5        0.3121
1707.3    43.00  0.38     Sequence
 HLA-DPA10103-DPB10201  815      PSKPSKRSFIEDLLF  RSFIEDLLF  6        0.4008
653.8    27.00  0.27     Sequence
 HLA-DPA10103-DPB10201  816      SKPSKRSFIEDLLFN  SFIEDLLFN  6        0.4847
263.9    15.00  0.25     Sequence
 HLA-DPA10103-DPB10201  817      KPSKRSFIEDLLFNK  FIEDLLFNK  6        0.5374
149.2     9.50  0.42     Sequence         WB
 HLA-DPA10103-DPB10201  818      PSKRSFIEDLLFNKV  IEDLLFNKV  6        0.5852
88.9     6.00  0.39     Sequence         WB
 HLA-DPA10103-DPB10201  819      SKRSFIEDLLFNKVT  IEDLLFNKV  5        0.5821
92.0     6.00  0.38     Sequence         WB
 HLA-DPA10103-DPB10201  820      KRSFIEDLLFNKVTL  IEDLLFNKV  4        0.5860
88.2     6.00  0.35     Sequence         WB
 HLA-DPA10103-DPB10201  821      RSFIEDLLFNKVTLA  IEDLLFNKV  3        0.5780
96.2     6.50  0.32     Sequence         WB
 HLA-DPA10103-DPB10201  822      SFIEDLLFNKVTLAD  LLFNKVTLA  5        0.5593
117.7     7.50  0.37     Sequence         WB
 HLA-DPA10103-DPB10201  823      FIEDLLFNKVTLADA  LLFNKVTLA  4        0.5297
162.1    10.00  0.41     Sequence
 HLA-DPA10103-DPB10201  824      IEDLLFNKVTLADAG  LLFNKVTLA  3        0.4874
256.3    15.00  0.47     Sequence
 HLA-DPA10103-DPB10201  825      EDLLFNKVTLADAGF  LLFNKVTLA  2        0.4707
307.0    17.00  0.44     Sequence
 HLA-DPA10103-DPB10201  826      DLLFNKVTLADAGFI  FNKVTLADA  3        0.4696
310.5    17.00  0.28     Sequence
 HLA-DPA10103-DPB10201  827      LLFNKVTLADAGFIK  LADAGFIKX  7        0.4429
415.0    20.00  0.34     Sequence
 HLA-DPA10103-DPB10201  828      LFNKVTLADAGFIKQ  LADAGFIKQ  6        0.4369
442.4    21.00  0.49     Sequence
 HLA-DPA10103-DPB10201  829      FNKVTLADAGFIKQY  LADAGFIKQ  5        0.4374
440.2    21.00  0.50     Sequence
 HLA-DPA10103-DPB10201  830      NKVTLADAGFIKQYG  LADAGFIKQ  4        0.4191
536.3    24.00  0.52     Sequence
 HLA-DPA10103-DPB10201  831      KVTLADAGFIKQYGD  LADAGFIKQ  3        0.4060
618.1    26.00  0.52     Sequence
 HLA-DPA10103-DPB10201  832      VTLADAGFIKQYGDC  LADAGFIKQ  2        0.3607
1009.3    33.00  0.47     Sequence
```

```
 HLA-DPA10103-DPB10201  833      TLADAGFIKQYGDCL  FIKQYGDCL  6        0.3793
825.5    30.00  0.35     Sequence
 HLA-DPA10103-DPB10201  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.3169
1621.0    42.00  0.41     Sequence
 HLA-DPA10103-DPB10201  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4        0.2957
2038.7    47.00  0.44     Sequence
 HLA-DPA10103-DPB10201  836      DAGFIKQYGDCLGDI  FIKQYGDCL  3        0.3274
1447.5    40.00  0.40     Sequence
 HLA-DPA10103-DPB10201  837      AGFIKQYGDCLGDIA  FIKQYGDCL  2        0.3168
1622.6    42.00  0.39     Sequence
 HLA-DPA10103-DPB10201  838      GFIKQYGDCLGDIAA  FIKQYGDCL  1        0.2917
2130.3    48.00  0.32     Sequence
 HLA-DPA10103-DPB10201  839      FIKQYGDCLGDIAAR  QYGDCLGDI  3        0.2699
2697.1    55.00  0.22     Sequence
 HLA-DPA10103-DPB10201  840      IKQYGDCLGDIAARD  QYGDCLGDI  2        0.1871
6600.4    75.00  0.28     Sequence
 HLA-DPA10103-DPB10201  841      KQYGDCLGDIAARDL  LGDIAARDL  6        0.1825
6942.8    75.00  0.17     Sequence
 HLA-DPA10103-DPB10201  842      QYGDCLGDIAARDLI  LGDIAARDL  5        0.1775
7330.0    75.00  0.22     Sequence
 HLA-DPA10103-DPB10201  843      YGDCLGDIAARDLIC  DIAARDLIC  6        0.1687
8060.1    80.00  0.26     Sequence
 HLA-DPA10103-DPB10201  844      GDCLGDIAARDLICA  IAARDLICA  6        0.1759
7454.7    80.00  0.28     Sequence
 HLA-DPA10103-DPB10201  845      DCLGDIAARDLICAQ  IAARDLICA  5        0.1784
7252.6    75.00  0.30     Sequence
 HLA-DPA10103-DPB10201  846      CLGDIAARDLICAQK  IAARDLICA  4        0.1694
7999.9    80.00  0.35     Sequence
 HLA-DPA10103-DPB10201  847      LGDIAARDLICAQKF  IAARDLICA  3        0.1949
6067.6    75.00  0.31     Sequence
 HLA-DPA10103-DPB10201  848      GDIAARDLICAQKFN  ICAQKFNXX  8        0.2449
3533.8    60.00  0.22     Sequence
 HLA-DPA10103-DPB10201  849      DIAARDLICAQKFNG  ICAQKFNGX  7        0.2625
2920.7    55.00  0.28     Sequence
 HLA-DPA10103-DPB10201  850      IAARDLICAQKFNGL  ICAQKFNGL  6        0.4042
630.8    26.00  0.64     Sequence
 HLA-DPA10103-DPB10201  851      AARDLICAQKFNGLT  ICAQKFNGL  5        0.4028
640.2    26.00  0.65     Sequence
 HLA-DPA10103-DPB10201  852      ARDLICAQKFNGLTV  ICAQKFNGL  4        0.4157
556.8    24.00  0.59     Sequence
 HLA-DPA10103-DPB10201  853      RDLICAQKFNGLTVL  ICAQKFNGL  3        0.4611
340.5    18.00  0.42     Sequence
 HLA-DPA10103-DPB10201  854      DLICAQKFNGLTVLP  ICAQKFNGL  2        0.4588
349.0    18.00  0.34     Sequence
 HLA-DPA10103-DPB10201  855      LICAQKFNGLTVLPP  FNGLTVLPP  6        0.4411
422.8    21.00  0.29     Sequence
 HLA-DPA10103-DPB10201  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5        0.4353
450.5    21.00  0.32     Sequence
 HLA-DPA10103-DPB10201  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4        0.4337
458.1    22.00  0.31     Sequence
 HLA-DPA10103-DPB10201  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3        0.4236
510.9    23.00  0.27     Sequence
 HLA-DPA10103-DPB10201  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2        0.4019
646.6    26.00  0.22     Sequence
 HLA-DPA10103-DPB10201  860      KFNGLTVLPPLLTDE  GLTVLPPLL  3        0.3450
1196.4    36.00  0.26     Sequence
 HLA-DPA10103-DPB10201  861      FNGLTVLPPLLTDEM  VLPPLLTDE  5        0.3290
1422.5    40.00  0.21     Sequence
 HLA-DPA10103-DPB10201  862      NGLTVLPPLLTDEMI  VLPPLLTDE  4        0.3139
1674.6    43.00  0.23     Sequence
 HLA-DPA10103-DPB10201  863      GLTVLPPLLTDEMIA  VLPPLLTDE  3        0.3045
1854.0    45.00  0.23     Sequence
 HLA-DPA10103-DPB10201  864      LTVLPPLLTDEMIAQ  LLTDEMIAQ  6        0.2963
2026.8    46.00  0.38     Sequence
 HLA-DPA10103-DPB10201  865      TVLPPLLTDEMIAQY  LTDEMIAQY  6        0.3299
1409.3    39.00  0.49     Sequence
```

```
 HLA-DPA10103-DPB10201  866      VLPPLLTDEMIAQYT  LTDEMIAQY  5        0.3201
1566.0    41.00  0.51     Sequence
 HLA-DPA10103-DPB10201  867      LPPLLTDEMIAQYTS  LTDEMIAQY  4        0.3142
1669.9    43.00  0.50     Sequence
 HLA-DPA10103-DPB10201  868      PPLLTDEMIAQYTSA  LTDEMIAQY  3        0.3127
1697.4    43.00  0.46     Sequence
 HLA-DPA10103-DPB10201  869      PLLTDEMIAQYTSAL  LTDEMIAQY  2        0.3549
1075.0    35.00  0.30     Sequence
 HLA-DPA10103-DPB10201  870      LLTDEMIAQYTSALL  MIAQYTSAL  5        0.3856
770.7     29.00  0.17    Sequence
 HLA-DPA10103-DPB10201  871      LTDEMIAQYTSALLA  AQYTSALLA  6        0.4146
563.2    25.00  0.22     Sequence
 HLA-DPA10103-DPB10201  872      TDEMIAQYTSALLAG  AQYTSALLA  5        0.4186
539.8    24.00  0.21     Sequence
 HLA-DPA10103-DPB10201  873      DEMIAQYTSALLAGT  YTSALLAGT  6        0.4342
455.6    22.00  0.40     Sequence
 HLA-DPA10103-DPB10201  874      EMIAQYTSALLAGTI  YTSALLAGT  5        0.4497
385.3    19.00  0.39     Sequence
 HLA-DPA10103-DPB10201  875      MIAQYTSALLAGTIT  YTSALLAGT  4        0.4338
457.5    22.00  0.40     Sequence
 HLA-DPA10103-DPB10201  876      IAQYTSALLAGTITS  YTSALLAGT  3        0.3925
715.2    28.00  0.45     Sequence
 HLA-DPA10103-DPB10201  877      AQYTSALLAGTITSG  YTSALLAGT  2        0.3249
1487.3    40.00  0.44     Sequence
 HLA-DPA10103-DPB10201  878      QYTSALLAGTITSGW  LLAGTITSG  5        0.2576
3081.2    55.00  0.37     Sequence
 HLA-DPA10103-DPB10201  879      YTSALLAGTITSGWT  LLAGTITSG  4        0.2313
4093.7    65.00  0.48     Sequence
 HLA-DPA10103-DPB10201  880      TSALLAGTITSGWTF  LLAGTITSG  3        0.2666
2794.9    55.00  0.34     Sequence
 HLA-DPA10103-DPB10201  881      SALLAGTITSGWTFG  TITSGWTFG  6        0.2767
2503.5    55.00  0.29     Sequence
 HLA-DPA10103-DPB10201  882      ALLAGTITSGWTFGA  TITSGWTFG  5        0.3045
1854.2    45.00  0.31     Sequence
 HLA-DPA10103-DPB10201  883      LLAGTITSGWTFGAG  ITSGWTFGA  5        0.2960
2033.7    47.00  0.25     Sequence
 HLA-DPA10103-DPB10201  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.2936
2086.7    47.00  0.26     Sequence
 HLA-DPA10103-DPB10201  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.2934
2090.4    47.00  0.26     Sequence
 HLA-DPA10103-DPB10201  886      GTITSGWTFGAGAAL  WTFGAGAAL  6        0.3656
957.4    33.00  0.34     Sequence
 HLA-DPA10103-DPB10201  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.3524
1104.1    35.00  0.37     Sequence
 HLA-DPA10103-DPB10201  888      ITSGWTFGAGAALQI  WTFGAGAAL  4        0.3762
853.8    31.00  0.33     Sequence
 HLA-DPA10103-DPB10201  889      TSGWTFGAGAALQIP  WTFGAGAAL  3        0.3681
932.1    32.00  0.35     Sequence
 HLA-DPA10103-DPB10201  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.3721
892.5    31.00  0.29     Sequence
 HLA-DPA10103-DPB10201  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.3534
1091.8    35.00  0.28     Sequence
 HLA-DPA10103-DPB10201  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.3231
1516.2    41.00  0.26     Sequence
 HLA-DPA10103-DPB10201  893      TFGAGAALQIPFAMQ  ALQIPFAMQ  6        0.2701
2691.1    55.00  0.29     Sequence
 HLA-DPA10103-DPB10201  894      FGAGAALQIPFAMQM  ALQIPFAMQ  5        0.3285
1430.6    40.00  0.31     Sequence
 HLA-DPA10103-DPB10201  895      GAGAALQIPFAMQMA  ALQIPFAMQ  4        0.3278
1440.5    40.00  0.28     Sequence
 HLA-DPA10103-DPB10201  896      AGAALQIPFAMQMAY  IPFAMQMAY  6        0.3585
1033.9    34.00  0.40     Sequence
 HLA-DPA10103-DPB10201  897      GAALQIPFAMQMAYR  IPFAMQMAY  5        0.3502
1131.2    35.00  0.41     Sequence
 HLA-DPA10103-DPB10201  898      AALQIPFAMQMAYRF  IPFAMQMAY  4        0.4005
656.3    27.00  0.34     Sequence
```

```
 HLA-DPA10103-DPB10201  899      ALQIPFAMQMAYRFN  IPFAMQMAY  3        0.3963
686.3    27.00  0.36     Sequence
 HLA-DPA10103-DPB10201  900      LQIPFAMQMAYRFNG  IPFAMQMAY  2        0.3727
886.7    31.00  0.38     Sequence
 HLA-DPA10103-DPB10201  901      QIPFAMQMAYRFNGI  QMAYRFNGI  6        0.3743
871.5    31.00  0.25     Sequence
 HLA-DPA10103-DPB10201  902      IPFAMQMAYRFNGIG  QMAYRFNGI  5        0.3601
1015.9    34.00  0.26     Sequence
 HLA-DPA10103-DPB10201  903      PFAMQMAYRFNGIGV  QMAYRFNGI  4        0.3636
978.6    33.00  0.27     Sequence
 HLA-DPA10103-DPB10201  904      FAMQMAYRFNGIGVT  YRFNGIGVT  6        0.3915
722.9    28.00  0.42     Sequence
 HLA-DPA10103-DPB10201  905      AMQMAYRFNGIGVTQ  YRFNGIGVT  5        0.3586
1032.2    34.00  0.49     Sequence
 HLA-DPA10103-DPB10201  906      MQMAYRFNGIGVTQN  YRFNGIGVT  4        0.3467
1174.6    36.00  0.50     Sequence
 HLA-DPA10103-DPB10201  907      QMAYRFNGIGVTQNV  YRFNGIGVT  3        0.3298
1410.6    39.00  0.53     Sequence
 HLA-DPA10103-DPB10201  908      MAYRFNGIGVTQNVL  YRFNGIGVT  2        0.3044
1856.1    45.00  0.51     Sequence
 HLA-DPA10103-DPB10201  909      AYRFNGIGVTQNVLY  YRFNGIGVT  1        0.2849
2291.5    49.00  0.38     Sequence
 HLA-DPA10103-DPB10201  910      YRFNGIGVTQNVLYE  YRFNGIGVT  0        0.2166
4798.0    70.00  0.21     Sequence
 HLA-DPA10103-DPB10201  911      RFNGIGVTQNVLYEN  VTQNVLYEN  6        0.1927
6212.4    75.00  0.24     Sequence
 HLA-DPA10103-DPB10201  912      FNGIGVTQNVLYENQ  TQNVLYENQ  6        0.2210
4578.4    65.00  0.34     Sequence
 HLA-DPA10103-DPB10201  913      NGIGVTQNVLYENQK  TQNVLYENQ  5        0.2466
3467.6    60.00  0.34     Sequence
 HLA-DPA10103-DPB10201  914      GIGVTQNVLYENQKL  TQNVLYENQ  4        0.3204
1560.9    41.00  0.28     Sequence
 HLA-DPA10103-DPB10201  915      IGVTQNVLYENQKLI  VLYENQKLI  6        0.4715
304.3    17.00  0.47     Sequence
 HLA-DPA10103-DPB10201  916      GVTQNVLYENQKLIA  VLYENQKLI  5        0.4855
261.7    15.00  0.44     Sequence
 HLA-DPA10103-DPB10201  917      VTQNVLYENQKLIAN  VLYENQKLI  4        0.4883
253.8    15.00  0.45     Sequence
 HLA-DPA10103-DPB10201  918      TQNVLYENQKLIANQ  VLYENQKLI  3        0.4792
280.0    16.00  0.46     Sequence
 HLA-DPA10103-DPB10201  919      QNVLYENQKLIANQF  VLYENQKLI  2        0.4731
299.2    16.00  0.43     Sequence
 HLA-DPA10103-DPB10201  920      NVLYENQKLIANQFN  VLYENQKLI  1        0.4433
413.2    20.00  0.36     Sequence
 HLA-DPA10103-DPB10201  921      VLYENQKLIANQFNS  YENQKLIAN  2        0.3920
719.7    28.00  0.20     Sequence
 HLA-DPA10103-DPB10201  922      LYENQKLIANQFNSA  LIANQFNSA  6        0.3499
1134.5    35.00  0.69     Sequence
 HLA-DPA10103-DPB10201  923      YENQKLIANQFNSAI  LIANQFNSA  5        0.3432
1219.3    37.00  0.75     Sequence
 HLA-DPA10103-DPB10201  924      ENQKLIANQFNSAIG  LIANQFNSA  4        0.3284
1431.2    40.00  0.77     Sequence
 HLA-DPA10103-DPB10201  925      NQKLIANQFNSAIGK  LIANQFNSA  3        0.3239
1503.0    41.00  0.75     Sequence
 HLA-DPA10103-DPB10201  926      QKLIANQFNSAIGKI  LIANQFNSA  2        0.3177
1607.1    42.00  0.61     Sequence
 HLA-DPA10103-DPB10201  927      KLIANQFNSAIGKIQ  LIANQFNSA  1        0.2715
2650.2    55.00  0.42     Sequence
 HLA-DPA10103-DPB10201  928      LIANQFNSAIGKIQD  FNSAIGKIQ  5        0.2075
5295.0    70.00  0.32     Sequence
 HLA-DPA10103-DPB10201  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4        0.1630
8571.5    80.00  0.39     Sequence
 HLA-DPA10103-DPB10201  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.1675
8167.4    80.00  0.35     Sequence
 HLA-DPA10103-DPB10201  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.1500
9865.5    85.00  0.32     Sequence
```

```
 HLA-DPA10103-DPB10201  932       QFNSAIGKIQDSLSS  AIGKIQDSL  4         0.1246
12988.8    90.00  0.31     Sequence
 HLA-DPA10103-DPB10201  933       FNSAIGKIQDSLSST  AIGKIQDSL  3         0.1074
15640.3    95.00  0.31     Sequence
 HLA-DPA10103-DPB10201  934       NSAIGKIQDSLSSTA  AIGKIQDSL  2         0.1026
16480.1    95.00  0.25     Sequence
 HLA-DPA10103-DPB10201  935       SAIGKIQDSLSSTAS  KIQDSLSST  4         0.0981
17289.8    95.00  0.24     Sequence
 HLA-DPA10103-DPB10201  936       AIGKIQDSLSSTASA  KIQDSLSST  3         0.0964
17628.3    95.00  0.23     Sequence
 HLA-DPA10103-DPB10201  937       IGKIQDSLSSTASAL  SLSSTASAL  6         0.1463
10268.7    85.00  0.41     Sequence
 HLA-DPA10103-DPB10201  938       GKIQDSLSSTASALG  SLSSTASAL  5         0.1436
10568.2    85.00  0.37     Sequence
 HLA-DPA10103-DPB10201  939       KIQDSLSSTASALGK  SLSSTASAL  4         0.1431
10629.2    85.00  0.38     Sequence
 HLA-DPA10103-DPB10201  940       IQDSLSSTASALGKL  STASALGKL  6         0.1569
9155.0    80.00  0.22     Sequence
 HLA-DPA10103-DPB10201  941       QDSLSSTASALGKLQ  STASALGKL  5         0.1475
10138.3    85.00  0.25     Sequence
 HLA-DPA10103-DPB10201  942       DSLSSTASALGKLQD  STASALGKL  4         0.1386
11158.9    85.00  0.26     Sequence
 HLA-DPA10103-DPB10201  943       SLSSTASALGKLQDV  STASALGKL  3         0.1318
12011.9    90.00  0.25     Sequence
 HLA-DPA10103-DPB10201  944       LSSTASALGKLQDVV  ALGKLQDVV  6         0.1462
10281.0    85.00  0.22     Sequence
 HLA-DPA10103-DPB10201  945       SSTASALGKLQDVVN  ALGKLQDVV  5         0.1315
12048.9    90.00  0.22     Sequence
 HLA-DPA10103-DPB10201  946       STASALGKLQDVVNQ  ALGKLQDVV  4         0.1235
13138.7    90.00  0.24     Sequence
 HLA-DPA10103-DPB10201  947       TASALGKLQDVVNQN  ALGKLQDVV  3         0.1141
14544.4    90.00  0.27     Sequence
 HLA-DPA10103-DPB10201  948       ASALGKLQDVVNQNA  ALGKLQDVV  2         0.1091
15355.7    95.00  0.25     Sequence
 HLA-DPA10103-DPB10201  949       SALGKLQDVVNQNAQ  ALGKLQDVV  1         0.1003
16893.3    95.00  0.24     Sequence
 HLA-DPA10103-DPB10201  950       ALGKLQDVVNQNAQA  LQDVVNQNA  4         0.0820
20583.9   100.00  0.19     Sequence
 HLA-DPA10103-DPB10201  951       LGKLQDVVNQNAQAL  VVNQNAQAL  6         0.1227
13250.8    90.00  0.56     Sequence
 HLA-DPA10103-DPB10201  952       GKLQDVVNQNAQALN  VVNQNAQAL  5         0.1198
13671.2    90.00  0.56     Sequence
 HLA-DPA10103-DPB10201  953       KLQDVVNQNAQALNT  VVNQNAQAL  4         0.1224
13292.9    90.00  0.52     Sequence
 HLA-DPA10103-DPB10201  954       LQDVVNQNAQALNTL  VVNQNAQAL  3         0.1248
12958.4    90.00  0.48     Sequence
 HLA-DPA10103-DPB10201  955       QDVVNQNAQALNTLV  VVNQNAQAL  2         0.1240
13065.9    90.00  0.38     Sequence
 HLA-DPA10103-DPB10201  956       DVVNQNAQALNTLVK  VVNQNAQAL  1         0.1165
14181.4    90.00  0.29     Sequence
 HLA-DPA10103-DPB10201  957       VVNQNAQALNTLVKQ  QALNTLVKQ  6         0.1097
15254.4    95.00  0.17     Sequence
 HLA-DPA10103-DPB10201  958       VNQNAQALNTLVKQL  ALNTLVKQL  6         0.1707
7887.3    80.00  0.49     Sequence
 HLA-DPA10103-DPB10201  959       NQNAQALNTLVKQLS  ALNTLVKQL  5         0.1694
7998.3    80.00  0.44     Sequence
 HLA-DPA10103-DPB10201  960       QNAQALNTLVKQLSS  ALNTLVKQL  4         0.1747
7552.8    80.00  0.43     Sequence
 HLA-DPA10103-DPB10201  961       NAQALNTLVKQLSSN  ALNTLVKQL  3         0.1721
7769.7    80.00  0.41     Sequence
 HLA-DPA10103-DPB10201  962       AQALNTLVKQLSSNF  LVKQLSSNF  6         0.1866
6640.2    75.00  0.34     Sequence
 HLA-DPA10103-DPB10201  963       QALNTLVKQLSSNFG  LVKQLSSNF  5         0.1778
7300.9    75.00  0.34     Sequence
 HLA-DPA10103-DPB10201  964       ALNTLVKQLSSNFGA  LVKQLSSNF  4         0.1988
5816.6    70.00  0.30     Sequence
```

```
 HLA-DPA10103-DPB10201  965      LNTLVKQLSSNFGAI  QLSSNFGAI  6        0.3318
1380.5    39.00  0.59     Sequence
 HLA-DPA10103-DPB10201  966      NTLVKQLSSNFGAIS  QLSSNFGAI  5        0.3240
1501.7    41.00  0.59     Sequence
 HLA-DPA10103-DPB10201  967      TLVKQLSSNFGAISS  QLSSNFGAI  4        0.3099
1748.1    44.00  0.59     Sequence
 HLA-DPA10103-DPB10201  968      LVKQLSSNFGAISSV  QLSSNFGAI  3        0.3083
1778.5    44.00  0.55     Sequence
 HLA-DPA10103-DPB10201  969      VKQLSSNFGAISSVL  QLSSNFGAI  2        0.3217
1538.8    41.00  0.37     Sequence
 HLA-DPA10103-DPB10201  970      KQLSSNFGAISSVLN  QLSSNFGAI  1        0.2957
2039.8    47.00  0.34     Sequence
 HLA-DPA10103-DPB10201  971      QLSSNFGAISSVLND  NFGAISSVL  4        0.2420
3646.5    60.00  0.23     Sequence
 HLA-DPA10103-DPB10201  972      LSSNFGAISSVLNDI  AISSVLNDI  6        0.2260
4335.0    65.00  0.31     Sequence
 HLA-DPA10103-DPB10201  973      SSNFGAISSVLNDIL  AISSVLNDI  5        0.2371
3845.9    60.00  0.25     Sequence
 HLA-DPA10103-DPB10201  974      SNFGAISSVLNDILS  AISSVLNDI  4        0.2254
4365.6    65.00  0.27     Sequence
 HLA-DPA10103-DPB10201  975      NFGAISSVLNDILSR  AISSVLNDI  3        0.2320
4062.9    65.00  0.24     Sequence
 HLA-DPA10103-DPB10201  976      FGAISSVLNDILSRL  VLNDILSRL  6        0.3280
1438.1    40.00  0.49     Sequence
 HLA-DPA10103-DPB10201  977      GAISSVLNDILSRLD  VLNDILSRL  5        0.3227
1522.9    41.00  0.47     Sequence
 HLA-DPA10103-DPB10201  978      AISSVLNDILSRLDK  VLNDILSRL  4        0.3184
1595.6    42.00  0.46     Sequence
 HLA-DPA10103-DPB10201  979      ISSVLNDILSRLDKV  VLNDILSRL  3        0.3453
1192.5    36.00  0.32     Sequence
 HLA-DPA10103-DPB10201  980      SSVLNDILSRLDKVE  VLNDILSRL  2        0.3257
1474.1    40.00  0.32     Sequence
 HLA-DPA10103-DPB10201  981      SVLNDILSRLDKVEA  DILSRLDKV  4        0.3106
1735.4    43.00  0.38     Sequence
 HLA-DPA10103-DPB10201  982      VLNDILSRLDKVEAE  DILSRLDKV  3        0.2737
2588.3    55.00  0.40     Sequence
 HLA-DPA10103-DPB10201  983      LNDILSRLDKVEAEV  DILSRLDKV  2        0.2147
4896.8    70.00  0.45     Sequence
 HLA-DPA10103-DPB10201  984      NDILSRLDKVEAEVQ  DILSRLDKV  1        0.1968
5948.7    70.00  0.34     Sequence
 HLA-DPA10103-DPB10201  985      DILSRLDKVEAEVQI  DILSRLDKV  0        0.1783
7265.1    75.00  0.25     Sequence
 HLA-DPA10103-DPB10201  986      ILSRLDKVEAEVQID  LDKVEAEVQ  4        0.1395
11051.1    85.00  0.19     Sequence
 HLA-DPA10103-DPB10201  987      LSRLDKVEAEVQIDR  VEAEVQIDR  6        0.1375
11292.4    85.00  0.22     Sequence
 HLA-DPA10103-DPB10201  988      SRLDKVEAEVQIDRL  EAEVQIDRL  6        0.1741
7604.4    80.00  0.35     Sequence
 HLA-DPA10103-DPB10201  989      RLDKVEAEVQIDRLI  EAEVQIDRL  5        0.1852
6742.1    75.00  0.34     Sequence
 HLA-DPA10103-DPB10201  990      LDKVEAEVQIDRLIT  EAEVQIDRL  4        0.1913
6313.1    75.00  0.33     Sequence
 HLA-DPA10103-DPB10201  991      DKVEAEVQIDRLITG  VQIDRLITG  6        0.2061
5379.2    70.00  0.41     Sequence
 HLA-DPA10103-DPB10201  992      KVEAEVQIDRLITGR  VQIDRLITG  5        0.2015
5653.5    70.00  0.44     Sequence
 HLA-DPA10103-DPB10201  993      VEAEVQIDRLITGRL  VQIDRLITG  4        0.2242
4421.9    65.00  0.41     Sequence
 HLA-DPA10103-DPB10201  994      EAEVQIDRLITGRLQ  VQIDRLITG  3        0.2267
4304.4    65.00  0.40     Sequence
 HLA-DPA10103-DPB10201  995      AEVQIDRLITGRLQS  VQIDRLITG  2        0.2357
3902.0    65.00  0.34     Sequence
 HLA-DPA10103-DPB10201  996      EVQIDRLITGRLQSL  LITGRLQSL  6        0.4425
416.7    20.00  0.64     Sequence
 HLA-DPA10103-DPB10201  997      VQIDRLITGRLQSLQ  LITGRLQSL  5        0.4324
464.6    22.00  0.68     Sequence
```

```
 HLA-DPA10103-DPB10201  998      QIDRLITGRLQSLQT  LITGRLQSL  4        0.4186
539.6    24.00  0.68     Sequence
 HLA-DPA10103-DPB10201  999      IDRLITGRLQSLQTY  LITGRLQSL  3        0.4138
568.0    25.00  0.67     Sequence
 HLA-DPA10103-DPB10201 1000      DRLITGRLQSLQTYV  LITGRLQSL  2        0.3902
733.2    28.00  0.59     Sequence
 HLA-DPA10103-DPB10201 1001      RLITGRLQSLQTYVT  LITGRLQSL  1        0.3743
871.1    31.00  0.47     Sequence
 HLA-DPA10103-DPB10201 1002      LITGRLQSLQTYVTQ  LITGRLQSL  0        0.3315
1384.3    39.00  0.32     Sequence
 HLA-DPA10103-DPB10201 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.2463
3478.5    60.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1004      TGRLQSLQTYVTQQL  LQTYVTQQL  6        0.3522
1106.7    35.00  0.39     Sequence
 HLA-DPA10103-DPB10201 1005      GRLQSLQTYVTQQLI  LQTYVTQQL  5        0.4325
464.2    22.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1006      RLQSLQTYVTQQLIR  LQTYVTQQL  4        0.4731
299.0    16.00  0.31     Sequence
 HLA-DPA10103-DPB10201 1007      LQSLQTYVTQQLIRA  YVTQQLIRA  6        0.4858
260.6    15.00  0.43     Sequence
 HLA-DPA10103-DPB10201 1008      QSLQTYVTQQLIRAA  YVTQQLIRA  5        0.4797
278.6    16.00  0.44     Sequence
 HLA-DPA10103-DPB10201 1009      SLQTYVTQQLIRAAE  YVTQQLIRA  4        0.4678
317.0    17.00  0.47     Sequence
 HLA-DPA10103-DPB10201 1010      LQTYVTQQLIRAAEI  YVTQQLIRA  3        0.4468
397.5    20.00  0.45     Sequence
 HLA-DPA10103-DPB10201 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.3426
1228.1    37.00  0.41     Sequence
 HLA-DPA10103-DPB10201 1012      TYVTQQLIRAAEIRA  YVTQQLIRA  1        0.2978
1993.0    46.00  0.32     Sequence
 HLA-DPA10103-DPB10201 1013      YVTQQLIRAAEIRAS  IRAAEIRAS  6        0.2648
2848.2    55.00  0.40     Sequence
 HLA-DPA10103-DPB10201 1014      VTQQLIRAAEIRASA  IRAAEIRAS  5        0.2482
3411.2    60.00  0.48     Sequence
 HLA-DPA10103-DPB10201 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.2392
3758.3    60.00  0.49     Sequence
 HLA-DPA10103-DPB10201 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.2308
4113.9    65.00  0.50     Sequence
 HLA-DPA10103-DPB10201 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.1786
7241.9    75.00  0.50     Sequence
 HLA-DPA10103-DPB10201 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.1376
11278.4    85.00  0.28     Sequence
 HLA-DPA10103-DPB10201 1019      IRAAEIRASANLAAI  RASANLAAI  6        0.1765
7405.8    80.00  0.49     Sequence
 HLA-DPA10103-DPB10201 1020      RAAEIRASANLAAIK  RASANLAAI  5        0.1833
6881.3    75.00  0.50     Sequence
 HLA-DPA10103-DPB10201 1021      AAEIRASANLAAIKM  RASANLAAI  4        0.1859
6691.7    75.00  0.48     Sequence
 HLA-DPA10103-DPB10201 1022      AEIRASANLAAIKMS  RASANLAAI  3        0.1774
7337.2    75.00  0.47     Sequence
 HLA-DPA10103-DPB10201 1023      EIRASANLAAIKMSE  RASANLAAI  2        0.1681
8112.0    80.00  0.42     Sequence
 HLA-DPA10103-DPB10201 1024      IRASANLAAIKMSEC  LAAIKMSEC  6        0.1716
7808.4    80.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1025      RASANLAAIKMSECV  LAAIKMSEC  5        0.1748
7545.4    80.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1026      ASANLAAIKMSECVL  LAAIKMSEC  4        0.2030
5560.7    70.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1027      SANLAAIKMSECVLG  LAAIKMSEC  3        0.2073
5307.9    70.00  0.21     Sequence
 HLA-DPA10103-DPB10201 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.2120
5045.0    70.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.2241
4426.1    65.00  0.23     Sequence
 HLA-DPA10103-DPB10201 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.2180
4725.5    65.00  0.25     Sequence
```

```
 HLA-DPA10103-DPB10201 1031      AAIKMSECVLGQSKR  MSECVLGQS  4        0.2101
5148.5    70.00  0.19     Sequence
 HLA-DPA10103-DPB10201 1032      AIKMSECVLGQSKRV  CVLGQSKRV  6        0.2279
4246.3    65.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1033      IKMSECVLGQSKRVD  VLGQSKRVD  6        0.2185
4703.8    65.00  0.22     Sequence
 HLA-DPA10103-DPB10201 1034      KMSECVLGQSKRVDF  LGQSKRVDF  6        0.2220
4527.9    65.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1035      MSECVLGQSKRVDFC  LGQSKRVDF  5        0.2159
4836.2    70.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1036      SECVLGQSKRVDFCG  LGQSKRVDF  4        0.2066
5346.1    70.00  0.30     Sequence
 HLA-DPA10103-DPB10201 1037      ECVLGQSKRVDFCGK  LGQSKRVDF  3        0.2038
5514.5    70.00  0.30     Sequence
 HLA-DPA10103-DPB10201 1038      CVLGQSKRVDFCGKG  LGQSKRVDF  2        0.1584
9012.4    80.00  0.29     Sequence
 HLA-DPA10103-DPB10201 1039      VLGQSKRVDFCGKGY  RVDFCGKGY  6        0.1451
10404.7    85.00  0.17     Sequence
 HLA-DPA10103-DPB10201 1040      LGQSKRVDFCGKGYH  VDFCGKGYH  6        0.1775
7329.5    75.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1041      GQSKRVDFCGKGYHL  FCGKGYHLX  7        0.2199
4630.3    65.00  0.31     Sequence
 HLA-DPA10103-DPB10201 1042      QSKRVDFCGKGYHLM  FCGKGYHLM  6        0.3743
871.4    31.00  0.64     Sequence
 HLA-DPA10103-DPB10201 1043      SKRVDFCGKGYHLMS  FCGKGYHLM  5        0.3681
931.4    32.00  0.64     Sequence
 HLA-DPA10103-DPB10201 1044      KRVDFCGKGYHLMSF  FCGKGYHLM  4        0.4060
618.0    26.00  0.51     Sequence
 HLA-DPA10103-DPB10201 1045      RVDFCGKGYHLMSFP  FCGKGYHLM  3        0.4407
424.7    21.00  0.41     Sequence
 HLA-DPA10103-DPB10201 1046      VDFCGKGYHLMSFPQ  FCGKGYHLM  2        0.4600
344.7    18.00  0.32     Sequence
 HLA-DPA10103-DPB10201 1047      DFCGKGYHLMSFPQS  YHLMSFPQS  6        0.4744
294.9    16.00  0.44     Sequence
 HLA-DPA10103-DPB10201 1048      FCGKGYHLMSFPQSA  YHLMSFPQS  5        0.4590
348.5    18.00  0.50     Sequence
 HLA-DPA10103-DPB10201 1049      CGKGYHLMSFPQSAP  YHLMSFPQS  4        0.4352
450.6    21.00  0.52     Sequence
 HLA-DPA10103-DPB10201 1050      GKGYHLMSFPQSAPH  YHLMSFPQS  3        0.4222
518.9    23.00  0.53     Sequence
 HLA-DPA10103-DPB10201 1051      KGYHLMSFPQSAPHG  YHLMSFPQS  2        0.3951
695.3    28.00  0.60     Sequence
 HLA-DPA10103-DPB10201 1052      GYHLMSFPQSAPHGV  YHLMSFPQS  1        0.3461
1181.7    36.00  0.52     Sequence
 HLA-DPA10103-DPB10201 1053      YHLMSFPQSAPHGVV  YHLMSFPQS  0        0.2728
2613.7    55.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1054      HLMSFPQSAPHGVVF  FPQSAPHGV  4        0.2104
5134.8    70.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.2166
4798.7    70.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1056      MSFPQSAPHGVVFLH  APHGVVFLH  6        0.1994
5781.5    70.00  0.19     Sequence
 HLA-DPA10103-DPB10201 1057      SFPQSAPHGVVFLHV  PHGVVFLHV  6        0.3133
1685.1    43.00  0.50     Sequence
 HLA-DPA10103-DPB10201 1058      FPQSAPHGVVFLHVT  PHGVVFLHV  5        0.3678
935.2    32.00  0.46     Sequence
 HLA-DPA10103-DPB10201 1059      PQSAPHGVVFLHVTY  PHGVVFLHV  4        0.3942
702.2    28.00  0.40     Sequence
 HLA-DPA10103-DPB10201 1060      QSAPHGVVFLHVTYV  VVFLHVTYV  6        0.4497
385.3    19.00  0.37     Sequence
 HLA-DPA10103-DPB10201 1061      SAPHGVVFLHVTYVP  VVFLHVTYV  5        0.4655
324.8    17.00  0.31     Sequence
 HLA-DPA10103-DPB10201 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.5441
138.8     9.00  0.43     Sequence         WB
 HLA-DPA10103-DPB10201 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.5619
114.5     7.50  0.42     Sequence         WB
```

```
 HLA-DPA10103-DPB10201 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.5573
120.3     8.00  0.41     Sequence         WB
 HLA-DPA10103-DPB10201 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.5507
129.2     8.50  0.41     Sequence         WB
 HLA-DPA10103-DPB10201 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.5372
149.6     9.50  0.40     Sequence         WB
 HLA-DPA10103-DPB10201 1067      VFLHVTYVPAQEKNF  FLHVTYVPA  1        0.5205
179.1    11.00  0.37     Sequence
 HLA-DPA10103-DPB10201 1068      FLHVTYVPAQEKNFT  YVPAQEKNF  5        0.4567
357.1    19.00  0.22     Sequence
 HLA-DPA10103-DPB10201 1069      LHVTYVPAQEKNFTT  YVPAQEKNF  4        0.3269
1454.4    40.00  0.37     Sequence
 HLA-DPA10103-DPB10201 1070      HVTYVPAQEKNFTTA  YVPAQEKNF  3        0.2747
2558.5    55.00  0.41     Sequence
 HLA-DPA10103-DPB10201 1071      VTYVPAQEKNFTTAP  YVPAQEKNF  2        0.2459
3496.4    60.00  0.37     Sequence
 HLA-DPA10103-DPB10201 1072      TYVPAQEKNFTTAPA  AQEKNFTTA  4        0.2149
4890.2    70.00  0.43     Sequence
 HLA-DPA10103-DPB10201 1073      YVPAQEKNFTTAPAI  AQEKNFTTA  3        0.2369
3851.0    60.00  0.32     Sequence
 HLA-DPA10103-DPB10201 1074      VPAQEKNFTTAPAIC  AQEKNFTTA  2        0.2111
5092.4    70.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.2138
4945.5    70.00  0.28     Sequence
 HLA-DPA10103-DPB10201 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.1957
6016.6    75.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.1826
6929.5    75.00  0.38     Sequence
 HLA-DPA10103-DPB10201 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.1739
7615.1    80.00  0.42     Sequence
 HLA-DPA10103-DPB10201 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.1535
9499.1    85.00  0.41     Sequence
 HLA-DPA10103-DPB10201 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.0889
19103.6    95.00  0.40     Sequence
 HLA-DPA10103-DPB10201 1081      FTTAPAICHDGKAHF  ICHDGKAHF  6        0.1486
10018.0    85.00  0.44     Sequence
 HLA-DPA10103-DPB10201 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.1685
8077.4    80.00  0.47     Sequence
 HLA-DPA10103-DPB10201 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.1857
6705.4    75.00  0.43     Sequence
 HLA-DPA10103-DPB10201 1084      APAICHDGKAHFPRE  DGKAHFPRE  6        0.2012
5666.5    70.00  0.38     Sequence
 HLA-DPA10103-DPB10201 1085      PAICHDGKAHFPREG  DGKAHFPRE  5        0.1949
6068.6    75.00  0.38     Sequence
 HLA-DPA10103-DPB10201 1086      AICHDGKAHFPREGV  DGKAHFPRE  4        0.1979
5874.0    70.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1087      ICHDGKAHFPREGVF  AHFPREGVF  6        0.2733
2599.4    55.00  0.23     Sequence
 HLA-DPA10103-DPB10201 1088      CHDGKAHFPREGVFV  FPREGVFVX  7        0.2900
2168.6    48.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1089      HDGKAHFPREGVFVS  FPREGVFVS  6        0.3131
1688.4    43.00  0.38     Sequence
 HLA-DPA10103-DPB10201 1090      DGKAHFPREGVFVSN  FPREGVFVS  5        0.3117
1714.6    43.00  0.38     Sequence
 HLA-DPA10103-DPB10201 1091      GKAHFPREGVFVSNG  FPREGVFVS  4        0.3066
1812.0    44.00  0.37     Sequence
 HLA-DPA10103-DPB10201 1092      KAHFPREGVFVSNGT  FPREGVFVS  3        0.3116
1716.1    43.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1093      AHFPREGVFVSNGTH  FPREGVFVS  2        0.2933
2093.8    47.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1094      HFPREGVFVSNGTHW  VFVSNGTHW  6        0.3139
1674.0    43.00  0.40     Sequence
 HLA-DPA10103-DPB10201 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6        0.3794
824.7    30.00  0.40     Sequence
 HLA-DPA10103-DPB10201 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5        0.4009
653.3    27.00  0.34     Sequence
```

```
 HLA-DPA10103-DPB10201 1097      REGVFVSNGTHWFVT  FVSNGTHWF  4        0.4260
498.1    23.00  0.31     Sequence
 HLA-DPA10103-DPB10201 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.4265
495.3    23.00  0.31     Sequence
 HLA-DPA10103-DPB10201 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.4004
656.9    27.00  0.29     Sequence
 HLA-DPA10103-DPB10201 1100      VFVSNGTHWFVTQRN  SNGTHWFVT  3        0.3851
774.9    29.00  0.20     Sequence
 HLA-DPA10103-DPB10201 1101      FVSNGTHWFVTQRNF  HWFVTQRNF  6        0.3867
761.5    29.00  0.30     Sequence
 HLA-DPA10103-DPB10201 1102      VSNGTHWFVTQRNFY  HWFVTQRNF  5        0.4220
519.9    23.00  0.28     Sequence
 HLA-DPA10103-DPB10201 1103      SNGTHWFVTQRNFYE  HWFVTQRNF  4        0.4185
540.2    24.00  0.29     Sequence
 HLA-DPA10103-DPB10201 1104      NGTHWFVTQRNFYEP  VTQRNFYEP  6        0.4177
544.8    24.00  0.24     Sequence
 HLA-DPA10103-DPB10201 1105      GTHWFVTQRNFYEPQ  VTQRNFYEP  5        0.4224
517.6    23.00  0.23     Sequence
 HLA-DPA10103-DPB10201 1106      THWFVTQRNFYEPQI  VTQRNFYEP  4        0.4413
422.1    21.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1107      HWFVTQRNFYEPQII  VTQRNFYEP  3        0.4138
568.5    25.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1108      WFVTQRNFYEPQIIT  VTQRNFYEP  2        0.4046
627.4    26.00  0.20     Sequence
 HLA-DPA10103-DPB10201 1109      FVTQRNFYEPQIITT  FYEPQIITT  6        0.4293
480.5    22.00  0.46     Sequence
 HLA-DPA10103-DPB10201 1110      VTQRNFYEPQIITTD  FYEPQIITT  5        0.4088
600.1    25.00  0.46     Sequence
 HLA-DPA10103-DPB10201 1111      TQRNFYEPQIITTDN  FYEPQIITT  4        0.3920
719.5    28.00  0.48     Sequence
 HLA-DPA10103-DPB10201 1112      QRNFYEPQIITTDNT  FYEPQIITT  3        0.3821
800.6    30.00  0.50     Sequence
 HLA-DPA10103-DPB10201 1113      RNFYEPQIITTDNTF  FYEPQIITT  2        0.3345
1339.8    39.00  0.46     Sequence
 HLA-DPA10103-DPB10201 1114      NFYEPQIITTDNTFV  FYEPQIITT  1        0.3015
1914.9    45.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1115      FYEPQIITTDNTFVS  ITTDNTFVS  6        0.2525
3253.1    60.00  0.17     Sequence
 HLA-DPA10103-DPB10201 1116      YEPQIITTDNTFVSG  TTDNTFVSG  6        0.2268
4299.6    65.00  0.40     Sequence
 HLA-DPA10103-DPB10201 1117      EPQIITTDNTFVSGN  TTDNTFVSG  5        0.2350
3932.7    65.00  0.37     Sequence
 HLA-DPA10103-DPB10201 1118      PQIITTDNTFVSGNC  TTDNTFVSG  4        0.2357
3901.2    65.00  0.37     Sequence
 HLA-DPA10103-DPB10201 1119      QIITTDNTFVSGNCD  TTDNTFVSG  3        0.2361
3888.2    65.00  0.40     Sequence
 HLA-DPA10103-DPB10201 1120      IITTDNTFVSGNCDV  TTDNTFVSG  2        0.2506
3320.9    60.00  0.28     Sequence
 HLA-DPA10103-DPB10201 1121      ITTDNTFVSGNCDVV  FVSGNCDVV  6        0.2916
2132.8    48.00  0.52     Sequence
 HLA-DPA10103-DPB10201 1122      TTDNTFVSGNCDVVI  FVSGNCDVV  5        0.2832
2334.6    49.00  0.57     Sequence
 HLA-DPA10103-DPB10201 1123      TDNTFVSGNCDVVIG  FVSGNCDVV  4        0.2679
2754.8    55.00  0.58     Sequence
 HLA-DPA10103-DPB10201 1124      DNTFVSGNCDVVIGI  FVSGNCDVV  3        0.2619
2941.1    55.00  0.56     Sequence
 HLA-DPA10103-DPB10201 1125      NTFVSGNCDVVIGIV  FVSGNCDVV  2        0.2877
2223.5    48.00  0.40     Sequence
 HLA-DPA10103-DPB10201 1126      TFVSGNCDVVIGIVN  FVSGNCDVV  1        0.2728
2614.1    55.00  0.29     Sequence
 HLA-DPA10103-DPB10201 1127      FVSGNCDVVIGIVNN  NCDVVIGIV  4        0.2162
4819.9    70.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1128      VSGNCDVVIGIVNNT  NCDVVIGIV  3        0.1968
5946.7    70.00  0.30     Sequence
 HLA-DPA10103-DPB10201 1129      SGNCDVVIGIVNNTV  VVIGIVNNT  5        0.1945
6097.3    75.00  0.26     Sequence
```

```
 HLA-DPA10103-DPB10201 1130      GNCDVVIGIVNNTVY  VVIGIVNNT  4        0.1987
5824.8    70.00  0.22     Sequence
 HLA-DPA10103-DPB10201 1131      NCDVVIGIVNNTVYD  VVIGIVNNT  3        0.1951
6056.3    75.00  0.23     Sequence
 HLA-DPA10103-DPB10201 1132      CDVVIGIVNNTVYDP  IVNNTVYDP  6        0.1889
6473.0    75.00  0.23     Sequence
 HLA-DPA10103-DPB10201 1133      DVVIGIVNNTVYDPL  VNNTVYDPL  6        0.2451
3524.6    60.00  0.47     Sequence
 HLA-DPA10103-DPB10201 1134      VVIGIVNNTVYDPLQ  VNNTVYDPL  5        0.2534
3223.1    60.00  0.44     Sequence
 HLA-DPA10103-DPB10201 1135      VIGIVNNTVYDPLQP  VNNTVYDPL  4        0.2492
3370.9    60.00  0.44     Sequence
 HLA-DPA10103-DPB10201 1136      IGIVNNTVYDPLQPE  VNNTVYDPL  3        0.2505
3326.6    60.00  0.40     Sequence
 HLA-DPA10103-DPB10201 1137      GIVNNTVYDPLQPEL  VYDPLQPEL  6        0.3167
1624.6    42.00  0.28     Sequence
 HLA-DPA10103-DPB10201 1138      IVNNTVYDPLQPELD  VYDPLQPEL  5        0.3124
1702.6    43.00  0.29     Sequence
 HLA-DPA10103-DPB10201 1139      VNNTVYDPLQPELDS  VYDPLQPEL  4        0.2988
1972.3    46.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1140      NNTVYDPLQPELDSF  VYDPLQPEL  3        0.3075
1795.7    44.00  0.31     Sequence
 HLA-DPA10103-DPB10201 1141      NTVYDPLQPELDSFK  VYDPLQPEL  2        0.2978
1992.8    46.00  0.29     Sequence
 HLA-DPA10103-DPB10201 1142      TVYDPLQPELDSFKE  VYDPLQPEL  1        0.2833
2331.2    49.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1143      VYDPLQPELDSFKEE  VYDPLQPEL  0        0.2582
3060.5    55.00  0.21     Sequence
 HLA-DPA10103-DPB10201 1144      YDPLQPELDSFKEEL  ELDSFKEEL  6        0.2298
4158.3    65.00  0.35     Sequence
 HLA-DPA10103-DPB10201 1145      DPLQPELDSFKEELD  ELDSFKEEL  5        0.2194
4658.5    65.00  0.31     Sequence
 HLA-DPA10103-DPB10201 1146      PLQPELDSFKEELDK  ELDSFKEEL  4        0.2203
4611.0    65.00  0.31     Sequence
 HLA-DPA10103-DPB10201 1147      LQPELDSFKEELDKY  SFKEELDKY  6        0.2445
3547.8    60.00  0.32     Sequence
 HLA-DPA10103-DPB10201 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.3252
1481.6    40.00  0.36     Sequence
 HLA-DPA10103-DPB10201 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.3310
1391.7    39.00  0.37     Sequence
 HLA-DPA10103-DPB10201 1150      ELDSFKEELDKYFKN  FKEELDKYF  4        0.3465
1176.8    36.00  0.35     Sequence
 HLA-DPA10103-DPB10201 1151      LDSFKEELDKYFKNH  FKEELDKYF  3        0.3435
1216.5    37.00  0.35     Sequence
 HLA-DPA10103-DPB10201 1152      DSFKEELDKYFKNHT  FKEELDKYF  2        0.3239
1503.8    41.00  0.31     Sequence
 HLA-DPA10103-DPB10201 1153      SFKEELDKYFKNHTS  ELDKYFKNH  4        0.3049
1846.0    45.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1154      FKEELDKYFKNHTSP  ELDKYFKNH  3        0.2725
2621.7    55.00  0.38     Sequence
 HLA-DPA10103-DPB10201 1155      KEELDKYFKNHTSPD  ELDKYFKNH  2        0.1736
7645.1    80.00  0.35     Sequence
 HLA-DPA10103-DPB10201 1156      EELDKYFKNHTSPDV  FKNHTSPDV  6        0.1794
7173.9    75.00  0.29     Sequence
 HLA-DPA10103-DPB10201 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.1571
9137.4    80.00  0.38     Sequence
 HLA-DPA10103-DPB10201 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.1698
7967.3    80.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.1575
9100.2    80.00  0.32     Sequence
 HLA-DPA10103-DPB10201 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.1455
10361.2    85.00  0.35     Sequence
 HLA-DPA10103-DPB10201 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.1399
10999.9    85.00  0.30     Sequence
 HLA-DPA10103-DPB10201 1162      FKNHTSPDVDLGDIS  FKNHTSPDV  0        0.1282
12494.4    90.00  0.19     Sequence
```

```
 HLA-DPA10103-DPB10201 1163      KNHTSPDVDLGDISG  SPDVDLGDI  4        0.0886
19169.4    95.00  0.22     Sequence
 HLA-DPA10103-DPB10201 1164      NHTSPDVDLGDISGI  VDLGDISGI  6        0.1296
12298.8    90.00  0.50     Sequence
 HLA-DPA10103-DPB10201 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.1352
11574.3    90.00  0.50     Sequence
 HLA-DPA10103-DPB10201 1166      TSPDVDLGDISGINA  VDLGDISGI  4        0.1353
11568.8    90.00  0.47     Sequence
 HLA-DPA10103-DPB10201 1167      SPDVDLGDISGINAS  VDLGDISGI  3        0.1346
11650.8    90.00  0.46     Sequence
 HLA-DPA10103-DPB10201 1168      PDVDLGDISGINASF  VDLGDISGI  2        0.1493
9940.4    85.00  0.28     Sequence
 HLA-DPA10103-DPB10201 1169      DVDLGDISGINASFV  ISGINASFV  6        0.1832
6886.8    75.00  0.19     Sequence
 HLA-DPA10103-DPB10201 1170      VDLGDISGINASFVN  GINASFVNX  7        0.1995
5773.6    70.00  0.29     Sequence
 HLA-DPA10103-DPB10201 1171      DLGDISGINASFVNI  GINASFVNI  6        0.2939
2079.8    47.00  0.65     Sequence
 HLA-DPA10103-DPB10201 1172      LGDISGINASFVNIQ  GINASFVNI  5        0.3143
1666.9    43.00  0.56     Sequence
 HLA-DPA10103-DPB10201 1173      GDISGINASFVNIQK  GINASFVNI  4        0.3069
1806.4    44.00  0.56     Sequence
 HLA-DPA10103-DPB10201 1174      DISGINASFVNIQKE  GINASFVNI  3        0.3081
1784.2    44.00  0.55     Sequence
 HLA-DPA10103-DPB10201 1175      ISGINASFVNIQKEI  GINASFVNI  2        0.3287
1426.9    40.00  0.41     Sequence
 HLA-DPA10103-DPB10201 1176      SGINASFVNIQKEID  GINASFVNI  1        0.3106
1736.3    43.00  0.29     Sequence
 HLA-DPA10103-DPB10201 1177      GINASFVNIQKEIDR  FVNIQKEID  5        0.2818
2369.2    50.00  0.29     Sequence
 HLA-DPA10103-DPB10201 1178      INASFVNIQKEIDRL  FVNIQKEID  4        0.2671
2778.5    55.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1179      NASFVNIQKEIDRLN  FVNIQKEID  3        0.2401
3721.9    60.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1180      ASFVNIQKEIDRLNE  FVNIQKEID  2        0.2218
4535.0    65.00  0.32     Sequence
 HLA-DPA10103-DPB10201 1181      SFVNIQKEIDRLNEV  FVNIQKEID  1        0.1965
5966.8    75.00  0.24     Sequence
 HLA-DPA10103-DPB10201 1182      FVNIQKEIDRLNEVA  IQKEIDRLN  3        0.1494
9929.7    85.00  0.20     Sequence
 HLA-DPA10103-DPB10201 1183      VNIQKEIDRLNEVAK  KEIDRLNEV  4        0.1200
13643.6    90.00  0.23     Sequence
 HLA-DPA10103-DPB10201 1184      NIQKEIDRLNEVAKN  KEIDRLNEV  3        0.1100
15215.6    95.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1185      IQKEIDRLNEVAKNL  RLNEVAKNL  6        0.1156
14320.1    90.00  0.22     Sequence
 HLA-DPA10103-DPB10201 1186      QKEIDRLNEVAKNLN  RLNEVAKNL  5        0.1105
15123.1    95.00  0.24     Sequence
 HLA-DPA10103-DPB10201 1187      KEIDRLNEVAKNLNE  RLNEVAKNL  4        0.1054
15986.2    95.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1188      EIDRLNEVAKNLNES  RLNEVAKNL  3        0.0842
20099.9   100.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1189      IDRLNEVAKNLNESL  VAKNLNESL  6        0.1288
12406.3    90.00  0.41     Sequence
 HLA-DPA10103-DPB10201 1190      DRLNEVAKNLNESLI  VAKNLNESL  5        0.1524
9607.8    85.00  0.39     Sequence
 HLA-DPA10103-DPB10201 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.1740
7609.3    80.00  0.35     Sequence
 HLA-DPA10103-DPB10201 1192      LNEVAKNLNESLIDL  NLNESLIDL  6        0.2805
2403.0    50.00  0.47     Sequence
 HLA-DPA10103-DPB10201 1193      NEVAKNLNESLIDLQ  NLNESLIDL  5        0.2950
2054.6    47.00  0.44     Sequence
 HLA-DPA10103-DPB10201 1194      EVAKNLNESLIDLQE  NLNESLIDL  4        0.2857
2272.9    49.00  0.44     Sequence
 HLA-DPA10103-DPB10201 1195      VAKNLNESLIDLQEL  NLNESLIDL  3        0.3281
1436.0    40.00  0.32     Sequence
```

```
 HLA-DPA10103-DPB10201 1196      AKNLNESLIDLQELG  NLNESLIDL  2        0.3320
1376.5    39.00  0.28     Sequence
 HLA-DPA10103-DPB10201 1197      KNLNESLIDLQELGK  ESLIDLQEL  4        0.3227
1523.3    41.00  0.20     Sequence
 HLA-DPA10103-DPB10201 1198      NLNESLIDLQELGKY  IDLQELGKY  6        0.3181
1600.9    42.00  0.27     Sequence
 HLA-DPA10103-DPB10201 1199      LNESLIDLQELGKYE  IDLQELGKY  5        0.2961
2031.6    47.00  0.34     Sequence
 HLA-DPA10103-DPB10201 1200      NESLIDLQELGKYEQ  IDLQELGKY  4        0.2831
2336.7    49.00  0.36     Sequence
 HLA-DPA10103-DPB10201 1201      ESLIDLQELGKYEQY  IDLQELGKY  3        0.2864
2254.7    49.00  0.29     Sequence
 HLA-DPA10103-DPB10201 1202      SLIDLQELGKYEQYI  IDLQELGKY  2        0.3011
1922.7    45.00  0.23     Sequence
 HLA-DPA10103-DPB10201 1203      LIDLQELGKYEQYIK  QELGKYEQY  4        0.2788
2448.2    50.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1204      IDLQELGKYEQYIKW  GKYEQYIKW  6        0.3525
1102.7    35.00  0.50     Sequence
 HLA-DPA10103-DPB10201 1205      DLQELGKYEQYIKWP  GKYEQYIKW  5        0.3776
841.1    31.00  0.45     Sequence
 HLA-DPA10103-DPB10201 1206      LQELGKYEQYIKWPW  GKYEQYIKW  4        0.4676
317.4    17.00  0.33     Sequence
 HLA-DPA10103-DPB10201 1207      QELGKYEQYIKWPWY  EQYIKWPWY  6        0.5549
123.5     8.00  0.43     Sequence         WB
 HLA-DPA10103-DPB10201 1208      ELGKYEQYIKWPWYI  EQYIKWPWY  5        0.6173
62.9     4.00  0.35     Sequence         WB
 HLA-DPA10103-DPB10201 1209      LGKYEQYIKWPWYIW  YIKWPWYIW  6        0.6690
35.9     1.80  0.34     Sequence         SB
 HLA-DPA10103-DPB10201 1210      GKYEQYIKWPWYIWL  IKWPWYIWL  6        0.7198
20.7     0.70  0.39     Sequence         SB
 HLA-DPA10103-DPB10201 1211      KYEQYIKWPWYIWLG  IKWPWYIWL  5        0.7137
22.1     0.80  0.37     Sequence         SB
 HLA-DPA10103-DPB10201 1212      YEQYIKWPWYIWLGF  IKWPWYIWL  4        0.7210
20.5     0.70  0.34     Sequence         SB
 HLA-DPA10103-DPB10201 1213      EQYIKWPWYIWLGFI  IKWPWYIWL  3        0.7240
19.8     0.60  0.27     Sequence         SB
 HLA-DPA10103-DPB10201 1214      QYIKWPWYIWLGFIA  WPWYIWLGF  4        0.7183
21.1     0.70  0.22     Sequence         SB
 HLA-DPA10103-DPB10201 1215      YIKWPWYIWLGFIAG  YIWLGFIAG  6        0.6916
28.1     1.20  0.28     Sequence         SB
 HLA-DPA10103-DPB10201 1216      IKWPWYIWLGFIAGL  YIWLGFIAG  5        0.6956
26.9     1.10  0.31     Sequence         SB
 HLA-DPA10103-DPB10201 1217      KWPWYIWLGFIAGLI  YIWLGFIAG  4        0.6745
33.8     1.70  0.34     Sequence         SB
 HLA-DPA10103-DPB10201 1218      WPWYIWLGFIAGLIA  YIWLGFIAG  3        0.6609
39.2     2.50  0.34     Sequence         WB
 HLA-DPA10103-DPB10201 1219      PWYIWLGFIAGLIAI  YIWLGFIAG  2        0.6493
44.4     2.50  0.30     Sequence         WB
 HLA-DPA10103-DPB10201 1220      WYIWLGFIAGLIAIV  FIAGLIAIV  6        0.6170
63.1     4.00  0.19     Sequence         WB
 HLA-DPA10103-DPB10201 1221      YIWLGFIAGLIAIVM  FIAGLIAIV  5        0.5796
94.5     6.50  0.28     Sequence         WB
 HLA-DPA10103-DPB10201 1222      IWLGFIAGLIAIVMV  FIAGLIAIV  4        0.5433
140.0     9.00  0.34     Sequence         WB
 HLA-DPA10103-DPB10201 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3        0.4803
276.9    16.00  0.47     Sequence
 HLA-DPA10103-DPB10201 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.3989
667.4    27.00  0.38     Sequence
 HLA-DPA10103-DPB10201 1225      GFIAGLIAIVMVTIM  LIAIVMVTI  5        0.3534
1092.5    35.00  0.18     Sequence
 HLA-DPA10103-DPB10201 1226      FIAGLIAIVMVTIML  LIAIVMVTI  4        0.3113
1721.7    43.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1227      IAGLIAIVMVTIMLC  IVMVTIMLC  6        0.3142
1668.7    43.00  0.38     Sequence
 HLA-DPA10103-DPB10201 1228      AGLIAIVMVTIMLCC  IVMVTIMLC  5        0.3072
1801.3    44.00  0.35     Sequence
```

```
 HLA-DPA10103-DPB10201 1229      GLIAIVMVTIMLCCM  IVMVTIMLC  4        0.3061
1822.6    44.00  0.35     Sequence
 HLA-DPA10103-DPB10201 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3        0.2869
2243.6    49.00  0.41     Sequence
 HLA-DPA10103-DPB10201 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2        0.2589
3037.2    55.00  0.43     Sequence
 HLA-DPA10103-DPB10201 1232      AIVMVTIMLCCMTSC  IMLCCMTSC  6        0.2549
3171.6    60.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1233      IVMVTIMLCCMTSCC  IMLCCMTSC  5        0.2161
4827.1    70.00  0.38     Sequence
 HLA-DPA10103-DPB10201 1234      VMVTIMLCCMTSCCS  IMLCCMTSC  4        0.1947
6083.0    75.00  0.41     Sequence
 HLA-DPA10103-DPB10201 1235      MVTIMLCCMTSCCSC  IMLCCMTSC  3        0.1907
6353.2    75.00  0.40     Sequence
 HLA-DPA10103-DPB10201 1236      VTIMLCCMTSCCSCL  IMLCCMTSC  2        0.2078
5280.6    70.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1237      TIMLCCMTSCCSCLK  CMTSCCSCL  5        0.2026
5584.0    70.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1238      IMLCCMTSCCSCLKG  CMTSCCSCL  4        0.1856
6710.3    75.00  0.26     Sequence
 HLA-DPA10103-DPB10201 1239      MLCCMTSCCSCLKGC  CMTSCCSCL  3        0.1662
8276.8    80.00  0.31     Sequence
 HLA-DPA10103-DPB10201 1240      LCCMTSCCSCLKGCC  CMTSCCSCL  2        0.1643
8449.1    80.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1241      CCMTSCCSCLKGCCS  CMTSCCSCL  1        0.1513
9722.8    85.00  0.22     Sequence
 HLA-DPA10103-DPB10201 1242      CMTSCCSCLKGCCSC  CCSCLKGCC  4        0.1338
11755.6    90.00  0.19     Sequence
 HLA-DPA10103-DPB10201 1243      MTSCCSCLKGCCSCG  CLKGCCSCG  6        0.1087
15425.2    95.00  0.20     Sequence
 HLA-DPA10103-DPB10201 1244      TSCCSCLKGCCSCGS  CLKGCCSCG  5        0.0995
17039.6    95.00  0.20     Sequence
 HLA-DPA10103-DPB10201 1245      SCCSCLKGCCSCGSC  CLKGCCSCG  4        0.0949
17902.8    95.00  0.22     Sequence
 HLA-DPA10103-DPB10201 1246      CCSCLKGCCSCGSCC  CLKGCCSCG  3        0.0897
18945.1    95.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1247      CSCLKGCCSCGSCCK  CLKGCCSCG  2        0.0829
20384.4   100.00  0.20     Sequence
 HLA-DPA10103-DPB10201 1248      SCLKGCCSCGSCCKF  CSCGSCCKF  6        0.1002
16904.3    95.00  0.30     Sequence
 HLA-DPA10103-DPB10201 1249      CLKGCCSCGSCCKFD  CSCGSCCKF  5        0.1008
16808.9    95.00  0.29     Sequence
 HLA-DPA10103-DPB10201 1250      LKGCCSCGSCCKFDE  CSCGSCCKF  4        0.1114
14972.1    95.00  0.27     Sequence
 HLA-DPA10103-DPB10201 1251      KGCCSCGSCCKFDED  GSCCKFDED  6        0.1153
14357.1    90.00  0.23     Sequence
 HLA-DPA10103-DPB10201 1252      GCCSCGSCCKFDEDD  GSCCKFDED  5        0.1139
14587.7    90.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1253      CCSCGSCCKFDEDDS  GSCCKFDED  4        0.1166
14165.3    90.00  0.25     Sequence
 HLA-DPA10103-DPB10201 1254      CSCGSCCKFDEDDSE  GSCCKFDED  3        0.1055
15973.6    95.00  0.24     Sequence
 HLA-DPA10103-DPB10201 1255      SCGSCCKFDEDDSEP  GSCCKFDED  2        0.0967
17558.2    95.00  0.24     Sequence
 HLA-DPA10103-DPB10201 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.1374
11306.0    85.00  0.47     Sequence
 HLA-DPA10103-DPB10201 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.1568
9169.7    80.00  0.44     Sequence
 HLA-DPA10103-DPB10201 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.1594
8910.4    80.00  0.43     Sequence
 HLA-DPA10103-DPB10201 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.1609
8772.2    80.00  0.38     Sequence
 HLA-DPA10103-DPB10201 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.1699
7957.2    80.00  0.31     Sequence
 HLA-DPA10103-DPB10201 1261      KFDEDDSEPVLKGVK  DDSEPVLKG  4        0.1550
9345.9    85.00  0.22     Sequence
```

```
 HLA-DPA10103-DPB10201 1262      FDEDDSEPVLKGVKL  DDSEPVLKG  3        0.1580
9049.0    80.00  0.22     Sequence
 HLA-DPA10103-DPB10201 1263      DEDDSEPVLKGVKLH  DDSEPVLKG  2        0.1531
9543.2    85.00  0.20     Sequence
 HLA-DPA10103-DPB10201 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.2326
4036.8    65.00  0.41     Sequence
 HLA-DPA10103-DPB10201 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.2794
2432.5    50.00  0.38     Sequence
 HLA-DPA10103-DPB10401    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.3549
1075.0    26.00  0.28     Sequence
 HLA-DPA10103-DPB10401    2      SPIKEMFVFLVLLPL  FVFLVLLPL  6        0.3950
696.8    21.00  0.35     Sequence
 HLA-DPA10103-DPB10401    3      PIKEMFVFLVLLPLV  FVFLVLLPL  5        0.3719
894.2    24.00  0.41     Sequence
 HLA-DPA10103-DPB10401    4      IKEMFVFLVLLPLVS  FVFLVLLPL  4        0.3515
1114.9    27.00  0.48     Sequence
 HLA-DPA10103-DPB10401    5      KEMFVFLVLLPLVSS  FVFLVLLPL  3        0.3436
1214.1    28.00  0.49     Sequence
 HLA-DPA10103-DPB10401    6      EMFVFLVLLPLVSSQ  FVFLVLLPL  2        0.3257
1474.3    31.00  0.37     Sequence
 HLA-DPA10103-DPB10401    7      MFVFLVLLPLVSSQC  LVLLPLVSS  4        0.3419
1236.6    28.00  0.22     Sequence
 HLA-DPA10103-DPB10401    8      FVFLVLLPLVSSQCV  LVLLPLVSS  3        0.3557
1065.1    26.00  0.24     Sequence
 HLA-DPA10103-DPB10401    9      VFLVLLPLVSSQCVN  LVSSQCVNX  7        0.3573
1046.7    26.00  0.32     Sequence
 HLA-DPA10103-DPB10401   10      FLVLLPLVSSQCVNF  LVSSQCVNF  6        0.4724
301.4    12.00  0.62     Sequence
 HLA-DPA10103-DPB10401   11      LVLLPLVSSQCVNFT  LVSSQCVNF  5        0.4622
336.5    13.00  0.70     Sequence
 HLA-DPA10103-DPB10401   12      VLLPLVSSQCVNFTN  LVSSQCVNF  4        0.4562
359.3    13.00  0.70     Sequence
 HLA-DPA10103-DPB10401   13      LLPLVSSQCVNFTNR  LVSSQCVNF  3        0.4443
408.5    15.00  0.71     Sequence
 HLA-DPA10103-DPB10401   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.4037
634.0    19.00  0.64     Sequence
 HLA-DPA10103-DPB10401   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.3178
1605.7    33.00  0.39     Sequence
 HLA-DPA10103-DPB10401   16      LVSSQCVNFTNRTQL  SQCVNFTNR  3        0.2732
2602.0    42.00  0.29     Sequence
 HLA-DPA10103-DPB10401   17      VSSQCVNFTNRTQLP  VNFTNRTQL  5        0.2151
4875.3    55.00  0.18     Sequence
 HLA-DPA10103-DPB10401   18      SSQCVNFTNRTQLPS  VNFTNRTQL  4        0.2116
5065.3    60.00  0.19     Sequence
 HLA-DPA10103-DPB10401   19      SQCVNFTNRTQLPSA  VNFTNRTQL  3        0.2037
5517.2    60.00  0.19     Sequence
 HLA-DPA10103-DPB10401   20      QCVNFTNRTQLPSAY  VNFTNRTQL  2        0.2000
5746.2    60.00  0.25     Sequence
 HLA-DPA10103-DPB10401   21      CVNFTNRTQLPSAYT  FTNRTQLPS  3        0.1860
6682.6    65.00  0.28     Sequence
 HLA-DPA10103-DPB10401   22      VNFTNRTQLPSAYTN  TNRTQLPSA  3        0.1400
10990.9    75.00  0.25     Sequence
 HLA-DPA10103-DPB10401   23      NFTNRTQLPSAYTNS  QLPSAYTNS  6        0.1026
16467.6    90.00  0.17     Sequence
 HLA-DPA10103-DPB10401   24      FTNRTQLPSAYTNSF  LPSAYTNSF  6        0.1231
13203.9    80.00  0.40     Sequence
 HLA-DPA10103-DPB10401   25      TNRTQLPSAYTNSFT  LPSAYTNSF  5        0.1281
12508.9    80.00  0.41     Sequence
 HLA-DPA10103-DPB10401   26      NRTQLPSAYTNSFTR  LPSAYTNSF  4        0.1379
11250.6    80.00  0.37     Sequence
 HLA-DPA10103-DPB10401   27      RTQLPSAYTNSFTRG  AYTNSFTRG  6        0.1497
9893.8    75.00  0.34     Sequence
 HLA-DPA10103-DPB10401   28      TQLPSAYTNSFTRGV  AYTNSFTRG  5        0.1863
6663.0    65.00  0.34     Sequence
 HLA-DPA10103-DPB10401   29      QLPSAYTNSFTRGVY  AYTNSFTRG  4        0.2333
4005.6    55.00  0.32     Sequence
```

```
 HLA-DPA10103-DPB10401   30      LPSAYTNSFTRGVYY  AYTNSFTRG  3        0.2768
2501.9    41.00  0.26     Sequence
 HLA-DPA10103-DPB10401   31      PSAYTNSFTRGVYYP  FTRGVYYPX  7        0.3369
1306.5    29.00  0.38     Sequence
 HLA-DPA10103-DPB10401   32      SAYTNSFTRGVYYPD  FTRGVYYPD  6        0.3699
913.7    24.00  0.50     Sequence
 HLA-DPA10103-DPB10401   33      AYTNSFTRGVYYPDK  FTRGVYYPD  5        0.3892
741.4    21.00  0.56     Sequence
 HLA-DPA10103-DPB10401   34      YTNSFTRGVYYPDKV  FTRGVYYPD  4        0.4047
626.8    19.00  0.56     Sequence
 HLA-DPA10103-DPB10401   35      TNSFTRGVYYPDKVF  FTRGVYYPD  3        0.3980
674.1    20.00  0.55     Sequence
 HLA-DPA10103-DPB10401   36      NSFTRGVYYPDKVFR  FTRGVYYPD  2        0.3539
1086.2    26.00  0.41     Sequence
 HLA-DPA10103-DPB10401   37      SFTRGVYYPDKVFRS  TRGVYYPDK  2        0.3004
1939.3    36.00  0.23     Sequence
 HLA-DPA10103-DPB10401   38      FTRGVYYPDKVFRSS  YYPDKVFRS  5        0.2465
3472.2    48.00  0.36     Sequence
 HLA-DPA10103-DPB10401   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.2269
4294.2    55.00  0.41     Sequence
 HLA-DPA10103-DPB10401   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.2973
2003.3    37.00  0.28     Sequence
 HLA-DPA10103-DPB10401   41      GVYYPDKVFRSSVLH  FRSSVLHXX  8        0.3526
1102.2    27.00  0.32     Sequence
 HLA-DPA10103-DPB10401   42      VYYPDKVFRSSVLHS  FRSSVLHSX  7        0.4159
555.3    18.00  0.50     Sequence
 HLA-DPA10103-DPB10401   43      YYPDKVFRSSVLHST  FRSSVLHST  6        0.5804
93.6     4.50  0.82     Sequence         WB
 HLA-DPA10103-DPB10401   44      YPDKVFRSSVLHSTQ  FRSSVLHST  5        0.6017
74.4     3.50  0.83     Sequence         WB
 HLA-DPA10103-DPB10401   45      PDKVFRSSVLHSTQD  FRSSVLHST  4        0.5849
89.3     4.50  0.84     Sequence         WB
 HLA-DPA10103-DPB10401   46      DKVFRSSVLHSTQDL  FRSSVLHST  3        0.5941
80.8     4.00  0.83     Sequence         WB
 HLA-DPA10103-DPB10401   47      KVFRSSVLHSTQDLF  FRSSVLHST  2        0.5699
105.0     5.00  0.69     Sequence         WB
 HLA-DPA10103-DPB10401   48      VFRSSVLHSTQDLFL  FRSSVLHST  1        0.4876
255.7    10.00  0.37     Sequence
 HLA-DPA10103-DPB10401   49      FRSSVLHSTQDLFLP  LHSTQDLFL  5        0.4709
306.4    12.00  0.44     Sequence
 HLA-DPA10103-DPB10401   50      RSSVLHSTQDLFLPF  STQDLFLPF  6        0.5178
184.5     8.00  0.38     Sequence         WB
 HLA-DPA10103-DPB10401   51      SSVLHSTQDLFLPFF  STQDLFLPF  5        0.5888
85.5     4.00  0.41     Sequence         WB
 HLA-DPA10103-DPB10401   52      SVLHSTQDLFLPFFS  STQDLFLPF  4        0.5968
78.5     4.00  0.38     Sequence         WB
 HLA-DPA10103-DPB10401   53      VLHSTQDLFLPFFSN  STQDLFLPF  3        0.5997
76.1     3.50  0.37     Sequence         WB
 HLA-DPA10103-DPB10401   54      LHSTQDLFLPFFSNV  LFLPFFSNV  6        0.6583
40.3     1.80  0.55     Sequence         SB
 HLA-DPA10103-DPB10401   55      HSTQDLFLPFFSNVT  LFLPFFSNV  5        0.6530
42.7     1.90  0.62     Sequence         SB
 HLA-DPA10103-DPB10401   56      STQDLFLPFFSNVTW  LFLPFFSNV  4        0.6520
43.2     2.00  0.61     Sequence         WB
 HLA-DPA10103-DPB10401   57      TQDLFLPFFSNVTWF  LFLPFFSNV  3        0.6616
38.9     1.70  0.59     Sequence         SB
 HLA-DPA10103-DPB10401   58      QDLFLPFFSNVTWFH  LFLPFFSNV  2        0.6950
27.1     1.10  0.47     Sequence         SB
 HLA-DPA10103-DPB10401   59      DLFLPFFSNVTWFHA  FSNVTWFHA  6        0.6884
29.1     1.20  0.40     Sequence         SB
 HLA-DPA10103-DPB10401   60      LFLPFFSNVTWFHAI  FSNVTWFHA  5        0.6917
28.1     1.20  0.48     Sequence         SB
 HLA-DPA10103-DPB10401   61      FLPFFSNVTWFHAIH  FSNVTWFHA  4        0.6895
28.8     1.20  0.54     Sequence         SB
 HLA-DPA10103-DPB10401   62      LPFFSNVTWFHAIHV  FSNVTWFHA  3        0.6672
36.6     1.60  0.55     Sequence         SB
```

```
 HLA-DPA10103-DPB10401   63      PFFSNVTWFHAIHVS  FSNVTWFHA  2        0.6219
59.8     3.00  0.49     Sequence         WB
 HLA-DPA10103-DPB10401   64      FFSNVTWFHAIHVSG  FSNVTWFHA  1        0.5388
146.9     6.50  0.35     Sequence         WB
 HLA-DPA10103-DPB10401   65      FSNVTWFHAIHVSGT  FHAIHVSGT  6        0.3865
763.7    22.00  0.28     Sequence
 HLA-DPA10103-DPB10401   66      SNVTWFHAIHVSGTN  FHAIHVSGT  5        0.2969
2012.4    37.00  0.39     Sequence
 HLA-DPA10103-DPB10401   67      NVTWFHAIHVSGTNG  FHAIHVSGT  4        0.2760
2522.9    41.00  0.47     Sequence
 HLA-DPA10103-DPB10401   68      VTWFHAIHVSGTNGT  FHAIHVSGT  3        0.2342
3966.1    50.00  0.56     Sequence
 HLA-DPA10103-DPB10401   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.1698
7964.2    70.00  0.52     Sequence
 HLA-DPA10103-DPB10401   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1        0.1251
12916.9    80.00  0.25     Sequence
 HLA-DPA10103-DPB10401   71      FHAIHVSGTNGTKRF  VSGTNGTKR  5        0.1006
16830.0    90.00  0.54     Sequence
 HLA-DPA10103-DPB10401   72      HAIHVSGTNGTKRFD  VSGTNGTKR  4        0.0871
19487.9    90.00  0.63     Sequence
 HLA-DPA10103-DPB10401   73      AIHVSGTNGTKRFDN  VSGTNGTKR  3        0.0877
19360.3    90.00  0.62     Sequence
 HLA-DPA10103-DPB10401   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.0824
20495.0    95.00  0.52     Sequence
 HLA-DPA10103-DPB10401   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.0673
24150.3    95.00  0.38     Sequence
 HLA-DPA10103-DPB10401   76      VSGTNGTKRFDNPVL  NGTKRFDNP  4        0.0656
24579.7    95.00  0.28     Sequence
 HLA-DPA10103-DPB10401   77      SGTNGTKRFDNPVLP  NGTKRFDNP  3        0.0808
20858.8    95.00  0.19     Sequence
 HLA-DPA10103-DPB10401   78      GTNGTKRFDNPVLPF  RFDNPVLPF  6        0.1779
7294.4    65.00  0.34     Sequence
 HLA-DPA10103-DPB10401   79      TNGTKRFDNPVLPFN  FDNPVLPFN  6        0.1974
5905.7    60.00  0.41     Sequence
 HLA-DPA10103-DPB10401   80      NGTKRFDNPVLPFND  FDNPVLPFN  5        0.1936
6156.8    65.00  0.42     Sequence
 HLA-DPA10103-DPB10401   81      GTKRFDNPVLPFNDG  FDNPVLPFN  4        0.1876
6568.2    65.00  0.43     Sequence
 HLA-DPA10103-DPB10401   82      TKRFDNPVLPFNDGV  FDNPVLPFN  3        0.1984
5845.8    60.00  0.41     Sequence
 HLA-DPA10103-DPB10401   83      KRFDNPVLPFNDGVY  FDNPVLPFN  2        0.2201
4620.5    55.00  0.31     Sequence
 HLA-DPA10103-DPB10401   84      RFDNPVLPFNDGVYF  FNDGVYFXX  8        0.2325
4042.1    55.00  0.29     Sequence
 HLA-DPA10103-DPB10401   85      FDNPVLPFNDGVYFA  FNDGVYFAX  7        0.2732
2602.3    42.00  0.47     Sequence
 HLA-DPA10103-DPB10401   86      DNPVLPFNDGVYFAS  FNDGVYFAS  6        0.3425
1228.5    28.00  0.62     Sequence
 HLA-DPA10103-DPB10401   87      NPVLPFNDGVYFAST  FNDGVYFAS  5        0.3811
809.8    22.00  0.55     Sequence
 HLA-DPA10103-DPB10401   88      PVLPFNDGVYFASTE  FNDGVYFAS  4        0.4022
644.4    20.00  0.50     Sequence
 HLA-DPA10103-DPB10401   89      VLPFNDGVYFASTEK  FNDGVYFAS  3        0.4053
623.1    19.00  0.50     Sequence
 HLA-DPA10103-DPB10401   90      LPFNDGVYFASTEKS  NDGVYFAST  3        0.3553
1069.7    26.00  0.35     Sequence
 HLA-DPA10103-DPB10401   91      PFNDGVYFASTEKSN  NDGVYFAST  2        0.2519
3276.8    46.00  0.35     Sequence
 HLA-DPA10103-DPB10401   92      FNDGVYFASTEKSNI  FASTEKSNI  6        0.2471
3451.6    47.00  0.44     Sequence
 HLA-DPA10103-DPB10401   93      NDGVYFASTEKSNII  FASTEKSNI  5        0.2413
3674.2    49.00  0.56     Sequence
 HLA-DPA10103-DPB10401   94      DGVYFASTEKSNIIR  FASTEKSNI  4        0.2436
3583.1    48.00  0.59     Sequence
 HLA-DPA10103-DPB10401   95      GVYFASTEKSNIIRG  FASTEKSNI  3        0.2196
4647.1    55.00  0.64     Sequence
```

```
 HLA-DPA10103-DPB10401   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.1971
5926.4    60.00  0.57     Sequence
 HLA-DPA10103-DPB10401   97      YFASTEKSNIIRGWI  FASTEKSNI  1        0.1771
7356.9    65.00  0.38     Sequence
 HLA-DPA10103-DPB10401   98      FASTEKSNIIRGWIF  SNIIRGWIF  6        0.1871
6606.7    65.00  0.19     Sequence
 HLA-DPA10103-DPB10401   99      ASTEKSNIIRGWIFG  IRGWIFGXX  8        0.1991
5799.3    60.00  0.26     Sequence
 HLA-DPA10103-DPB10401  100      STEKSNIIRGWIFGT  IRGWIFGTX  7        0.2455
3511.0    48.00  0.38     Sequence
 HLA-DPA10103-DPB10401  101      TEKSNIIRGWIFGTT  IRGWIFGTT  6        0.3672
940.9    24.00  0.68     Sequence
 HLA-DPA10103-DPB10401  102      EKSNIIRGWIFGTTL  IRGWIFGTT  5        0.4227
515.9    17.00  0.62     Sequence
 HLA-DPA10103-DPB10401  103      KSNIIRGWIFGTTLD  IRGWIFGTT  4        0.4172
547.6    18.00  0.58     Sequence
 HLA-DPA10103-DPB10401  104      SNIIRGWIFGTTLDS  IRGWIFGTT  3        0.4301
476.3    16.00  0.53     Sequence
 HLA-DPA10103-DPB10401  105      NIIRGWIFGTTLDSK  IRGWIFGTT  2        0.4228
515.4    17.00  0.46     Sequence
 HLA-DPA10103-DPB10401  106      IIRGWIFGTTLDSKT  IFGTTLDSK  5        0.3902
733.3    21.00  0.47     Sequence
 HLA-DPA10103-DPB10401  107      IRGWIFGTTLDSKTQ  IFGTTLDSK  4        0.3696
916.7    24.00  0.49     Sequence
 HLA-DPA10103-DPB10401  108      RGWIFGTTLDSKTQS  IFGTTLDSK  3        0.3343
1343.6    30.00  0.56     Sequence
 HLA-DPA10103-DPB10401  109      GWIFGTTLDSKTQSL  IFGTTLDSK  2        0.2205
4602.1    55.00  0.41     Sequence
 HLA-DPA10103-DPB10401  110      WIFGTTLDSKTQSLL  FGTTLDSKT  2        0.1961
5990.3    60.00  0.34     Sequence
 HLA-DPA10103-DPB10401  111      IFGTTLDSKTQSLLI  DSKTQSLLI  6        0.1645
8434.8    70.00  0.28     Sequence
 HLA-DPA10103-DPB10401  112      FGTTLDSKTQSLLIV  SKTQSLLIV  6        0.2444
3553.8    48.00  0.40     Sequence
 HLA-DPA10103-DPB10401  113      GTTLDSKTQSLLIVN  SKTQSLLIV  5        0.2770
2496.4    41.00  0.38     Sequence
 HLA-DPA10103-DPB10401  114      TTLDSKTQSLLIVNN  SKTQSLLIV  4        0.2744
2567.3    41.00  0.35     Sequence
 HLA-DPA10103-DPB10401  115      TLDSKTQSLLIVNNA  SKTQSLLIV  3        0.2651
2840.4    43.00  0.36     Sequence
 HLA-DPA10103-DPB10401  116      LDSKTQSLLIVNNAT  SKTQSLLIV  2        0.2516
3286.1    46.00  0.38     Sequence
 HLA-DPA10103-DPB10401  117      DSKTQSLLIVNNATN  SKTQSLLIV  1        0.2108
5109.3    60.00  0.24     Sequence
 HLA-DPA10103-DPB10401  118      SKTQSLLIVNNATNV  LIVNNATNV  6        0.2314
4091.1    55.00  0.31     Sequence
 HLA-DPA10103-DPB10401  119      KTQSLLIVNNATNVV  LIVNNATNV  5        0.2285
4217.8    55.00  0.41     Sequence
 HLA-DPA10103-DPB10401  120      TQSLLIVNNATNVVI  LIVNNATNV  4        0.2170
4776.3    55.00  0.44     Sequence
 HLA-DPA10103-DPB10401  121      QSLLIVNNATNVVIK  LIVNNATNV  3        0.2120
5044.7    60.00  0.45     Sequence
 HLA-DPA10103-DPB10401  122      SLLIVNNATNVVIKV  LIVNNATNV  2        0.2023
5601.7    60.00  0.39     Sequence
 HLA-DPA10103-DPB10401  123      LLIVNNATNVVIKVC  LIVNNATNV  1        0.1886
6498.1    65.00  0.29     Sequence
 HLA-DPA10103-DPB10401  124      LIVNNATNVVIKVCE  NATNVVIKV  4        0.1607
8789.5    70.00  0.17     Sequence
 HLA-DPA10103-DPB10401  125      IVNNATNVVIKVCEF  NATNVVIKV  3        0.1689
8045.0    70.00  0.22     Sequence
 HLA-DPA10103-DPB10401  126      VNNATNVVIKVCEFQ  IKVCEFQXX  8        0.1987
5823.7    60.00  0.25     Sequence
 HLA-DPA10103-DPB10401  127      NNATNVVIKVCEFQF  IKVCEFQFX  7        0.2779
2472.3    41.00  0.44     Sequence
 HLA-DPA10103-DPB10401  128      NATNVVIKVCEFQFC  IKVCEFQFC  6        0.3766
849.8    23.00  0.66     Sequence
```

```
 HLA-DPA10103-DPB10401  129      ATNVVIKVCEFQFCN  IKVCEFQFC  5        0.3873
756.8    22.00  0.64     Sequence
 HLA-DPA10103-DPB10401  130      TNVVIKVCEFQFCNY  IKVCEFQFC  4        0.4727
300.6    12.00  0.51     Sequence
 HLA-DPA10103-DPB10401  131      NVVIKVCEFQFCNYP  IKVCEFQFC  3        0.5030
216.5     9.00  0.43     Sequence         WB
 HLA-DPA10103-DPB10401  132      VVIKVCEFQFCNYPF  IKVCEFQFC  2        0.5333
156.0     7.00  0.28     Sequence         WB
 HLA-DPA10103-DPB10401  133      VIKVCEFQFCNYPFL  FQFCNYPFL  6        0.6205
60.7     3.00  0.54    Sequence         WB
 HLA-DPA10103-DPB10401  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.6169
63.1     3.00  0.57    Sequence         WB
 HLA-DPA10103-DPB10401  135      KVCEFQFCNYPFLGV  FQFCNYPFL  4        0.6814
31.4     1.30  0.43    Sequence         SB
 HLA-DPA10103-DPB10401  136      VCEFQFCNYPFLGVY  FQFCNYPFL  3        0.6995
25.8     1.00  0.38    Sequence         SB
 HLA-DPA10103-DPB10401  137      CEFQFCNYPFLGVYY  FCNYPFLGV  4        0.7017
25.2     1.00  0.33    Sequence         SB
 HLA-DPA10103-DPB10401  138      EFQFCNYPFLGVYYH  FCNYPFLGV  3        0.6898
28.7     1.20  0.34    Sequence         SB
 HLA-DPA10103-DPB10401  139      FQFCNYPFLGVYYHK  FCNYPFLGV  2        0.7037
24.7     1.00  0.25    Sequence         SB
 HLA-DPA10103-DPB10401  140      QFCNYPFLGVYYHKN  FLGVYYHKN  6        0.7058
24.1     1.00  0.68    Sequence         SB
 HLA-DPA10103-DPB10401  141      FCNYPFLGVYYHKNN  FLGVYYHKN  5        0.6880
29.2     1.20  0.76    Sequence         SB
 HLA-DPA10103-DPB10401  142      CNYPFLGVYYHKNNK  FLGVYYHKN  4        0.6723
34.7     1.50  0.81    Sequence         SB
 HLA-DPA10103-DPB10401  143      NYPFLGVYYHKNNKS  FLGVYYHKN  3        0.6745
33.9     1.50  0.85    Sequence         SB
 HLA-DPA10103-DPB10401  144      YPFLGVYYHKNNKSW  FLGVYYHKN  2        0.5712
103.5     5.00  0.73     Sequence         WB
 HLA-DPA10103-DPB10401  145      PFLGVYYHKNNKSWM  FLGVYYHKN  1        0.4067
613.7    19.00  0.52     Sequence
 HLA-DPA10103-DPB10401  146      FLGVYYHKNNKSWME  FLGVYYHKN  0        0.2443
3556.3    48.00  0.34     Sequence
 HLA-DPA10103-DPB10401  147      LGVYYHKNNKSWMES  HKNNKSWME  5        0.0892
19045.1    90.00  0.40     Sequence
 HLA-DPA10103-DPB10401  148      GVYYHKNNKSWMESE  HKNNKSWME  4        0.0926
18367.2    90.00  0.31     Sequence
 HLA-DPA10103-DPB10401  149      VYYHKNNKSWMESEF  HKNNKSWME  3        0.1451
10399.4    75.00  0.25     Sequence
 HLA-DPA10103-DPB10401  150      YYHKNNKSWMESEFR  WMESEFRXX  8        0.1819
6988.2    65.00  0.31     Sequence
 HLA-DPA10103-DPB10401  151      YHKNNKSWMESEFRV  WMESEFRVX  7        0.3133
1685.7    34.00  0.53     Sequence
 HLA-DPA10103-DPB10401  152      HKNNKSWMESEFRVY  WMESEFRVY  6        0.5070
207.3     8.50  0.75     Sequence         WB
 HLA-DPA10103-DPB10401  153      KNNKSWMESEFRVYS  WMESEFRVY  5        0.5119
196.6     8.50  0.73     Sequence         WB
 HLA-DPA10103-DPB10401  154      NNKSWMESEFRVYSS  WMESEFRVY  4        0.5142
191.7     8.00  0.73     Sequence         WB
 HLA-DPA10103-DPB10401  155      NKSWMESEFRVYSSA  WMESEFRVY  3        0.5273
166.4     7.00  0.70     Sequence         WB
 HLA-DPA10103-DPB10401  156      KSWMESEFRVYSSAN  WMESEFRVY  2        0.4919
244.1    10.00  0.56     Sequence
 HLA-DPA10103-DPB10401  157      SWMESEFRVYSSANN  WMESEFRVY  1        0.4102
590.7    18.00  0.38     Sequence
 HLA-DPA10103-DPB10401  158      WMESEFRVYSSANNC  WMESEFRVY  0        0.3036
1871.2    35.00  0.24     Sequence
 HLA-DPA10103-DPB10401  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.1851
6751.6    65.00  0.38     Sequence
 HLA-DPA10103-DPB10401  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.1890
6466.0    65.00  0.37     Sequence
 HLA-DPA10103-DPB10401  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.1849
6765.3    65.00  0.35     Sequence
```

```
 HLA-DPA10103-DPB10401  162       EFRVYSSANNCTFEY  YSSANNCTF  4         0.1748
7543.7    70.00  0.23     Sequence
 HLA-DPA10103-DPB10401  163       FRVYSSANNCTFEYV  ANNCTFEYV  6         0.2715
2650.6    42.00  0.54     Sequence
 HLA-DPA10103-DPB10401  164       RVYSSANNCTFEYVS  ANNCTFEYV  5         0.2719
2638.7    42.00  0.54     Sequence
 HLA-DPA10103-DPB10401  165       VYSSANNCTFEYVSQ  ANNCTFEYV  4         0.2821
2363.5    40.00  0.46     Sequence
 HLA-DPA10103-DPB10401  166       YSSANNCTFEYVSQP  ANNCTFEYV  3         0.2971
2009.1    37.00  0.43     Sequence
 HLA-DPA10103-DPB10401  167       SSANNCTFEYVSQPF  CTFEYVSQP  5         0.3488
1148.3    27.00  0.34     Sequence
 HLA-DPA10103-DPB10401  168       SANNCTFEYVSQPFL  YVSQPFLXX  8         0.4701
309.1    12.00  0.28     Sequence
 HLA-DPA10103-DPB10401  169       ANNCTFEYVSQPFLM  YVSQPFLMX  7         0.5479
133.2     6.00  0.44     Sequence         WB
 HLA-DPA10103-DPB10401  170       NNCTFEYVSQPFLMD  YVSQPFLMD  6         0.6697
35.7     1.60  0.73     Sequence         SB
 HLA-DPA10103-DPB10401  171       NCTFEYVSQPFLMDL  YVSQPFLMD  5         0.7070
23.8     0.90  0.75     Sequence         SB
 HLA-DPA10103-DPB10401  172       CTFEYVSQPFLMDLE  YVSQPFLMD  4         0.7205
20.6     0.80  0.70     Sequence         SB
 HLA-DPA10103-DPB10401  173       TFEYVSQPFLMDLEG  YVSQPFLMD  3         0.7115
22.7     0.90  0.74     Sequence         SB
 HLA-DPA10103-DPB10401  174       FEYVSQPFLMDLEGK  YVSQPFLMD  2         0.6473
45.4     2.50  0.63     Sequence         WB
 HLA-DPA10103-DPB10401  175       EYVSQPFLMDLEGKQ  YVSQPFLMD  1         0.4652
325.8    12.00  0.43     Sequence
 HLA-DPA10103-DPB10401  176       YVSQPFLMDLEGKQG  YVSQPFLMD  0         0.3677
935.5    24.00  0.28     Sequence
 HLA-DPA10103-DPB10401  177       VSQPFLMDLEGKQGN  FLMDLEGKQ  4         0.2434
3591.7    48.00  0.56     Sequence
 HLA-DPA10103-DPB10401  178       SQPFLMDLEGKQGNF  FLMDLEGKQ  3         0.2155
4856.0    55.00  0.67     Sequence
 HLA-DPA10103-DPB10401  179       QPFLMDLEGKQGNFK  FLMDLEGKQ  2         0.1650
8383.9    70.00  0.56     Sequence
 HLA-DPA10103-DPB10401  180       PFLMDLEGKQGNFKN  FLMDLEGKQ  1         0.1355
11542.3    80.00  0.40     Sequence
 HLA-DPA10103-DPB10401  181       FLMDLEGKQGNFKNL  GKQGNFKNL  6         0.1443
10491.9    75.00  0.31     Sequence
 HLA-DPA10103-DPB10401  182       LMDLEGKQGNFKNLS  GKQGNFKNL  5         0.1230
13212.7    80.00  0.46     Sequence
 HLA-DPA10103-DPB10401  183       MDLEGKQGNFKNLSE  GKQGNFKNL  4         0.1277
12558.6    80.00  0.43     Sequence
 HLA-DPA10103-DPB10401  184       DLEGKQGNFKNLSEF  GKQGNFKNL  3         0.1436
10574.5    75.00  0.32     Sequence
 HLA-DPA10103-DPB10401  185       LEGKQGNFKNLSEFV  FKNLSEFVX  7         0.2150
4882.7    55.00  0.25     Sequence
 HLA-DPA10103-DPB10401  186       EGKQGNFKNLSEFVF  FKNLSEFVF  6         0.3841
784.0    22.00  0.38     Sequence
 HLA-DPA10103-DPB10401  187       GKQGNFKNLSEFVFK  FKNLSEFVF  5         0.4449
405.8    14.00  0.33     Sequence
 HLA-DPA10103-DPB10401  188       KQGNFKNLSEFVFKN  LSEFVFKNX  7         0.4820
271.7    11.00  0.31     Sequence
 HLA-DPA10103-DPB10401  189       QGNFKNLSEFVFKNI  LSEFVFKNI  6         0.6161
63.7     3.00  0.60     Sequence         WB
 HLA-DPA10103-DPB10401  190       GNFKNLSEFVFKNID  LSEFVFKNI  5         0.5965
78.7     4.00  0.58     Sequence         WB
 HLA-DPA10103-DPB10401  191       NFKNLSEFVFKNIDG  LSEFVFKNI  4         0.5877
86.6     4.00  0.58     Sequence         WB
 HLA-DPA10103-DPB10401  192       FKNLSEFVFKNIDGY  LSEFVFKNI  3         0.5787
95.4     4.50  0.62     Sequence         WB
 HLA-DPA10103-DPB10401  193       KNLSEFVFKNIDGYF  LSEFVFKNI  2         0.5112
198.2     8.50  0.50     Sequence         WB
 HLA-DPA10103-DPB10401  194       NLSEFVFKNIDGYFK  FVFKNIDGY  4         0.4499
384.5    14.00  0.20     Sequence
```

```
 HLA-DPA10103-DPB10401  195      LSEFVFKNIDGYFKI  FKNIDGYFK  5        0.4564
358.3    13.00  0.30     Sequence
 HLA-DPA10103-DPB10401  196      SEFVFKNIDGYFKIY  FKNIDGYFK  4        0.4273
491.0    16.00  0.31     Sequence
 HLA-DPA10103-DPB10401  197      EFVFKNIDGYFKIYS  FKNIDGYFK  3        0.4135
570.3    18.00  0.34     Sequence
 HLA-DPA10103-DPB10401  198      FVFKNIDGYFKIYSK  FKNIDGYFK  2        0.4057
620.2    19.00  0.31     Sequence
 HLA-DPA10103-DPB10401  199      VFKNIDGYFKIYSKH  NIDGYFKIY  3        0.3556
1066.5    26.00  0.21     Sequence
 HLA-DPA10103-DPB10401  200      FKNIDGYFKIYSKHT  GYFKIYSKH  5        0.2704
2680.1    42.00  0.14     Sequence
 HLA-DPA10103-DPB10401  201      KNIDGYFKIYSKHTP  YFKIYSKHT  5        0.2316
4082.3    55.00  0.20     Sequence
 HLA-DPA10103-DPB10401  202      NIDGYFKIYSKHTPI  YFKIYSKHT  4        0.2192
4665.1    55.00  0.25     Sequence
 HLA-DPA10103-DPB10401  203      IDGYFKIYSKHTPIN  YFKIYSKHT  3        0.2164
4811.7    55.00  0.28     Sequence
 HLA-DPA10103-DPB10401  204      DGYFKIYSKHTPINL  KIYSKHTPI  4        0.2232
4469.2    55.00  0.19     Sequence
 HLA-DPA10103-DPB10401  205      GYFKIYSKHTPINLV  SKHTPINLV  6        0.2687
2729.9    43.00  0.31     Sequence
 HLA-DPA10103-DPB10401  206      YFKIYSKHTPINLVR  SKHTPINLV  5        0.2891
2189.7    38.00  0.37     Sequence
 HLA-DPA10103-DPB10401  207      FKIYSKHTPINLVRD  SKHTPINLV  4        0.2547
3178.1    46.00  0.42     Sequence
 HLA-DPA10103-DPB10401  208      KIYSKHTPINLVRDL  SKHTPINLV  3        0.2401
3719.8    49.00  0.47     Sequence
 HLA-DPA10103-DPB10401  209      IYSKHTPINLVRDLP  SKHTPINLV  2        0.2201
4622.6    55.00  0.35     Sequence
 HLA-DPA10103-DPB10401  210      YSKHTPINLVRDLPQ  SKHTPINLV  1        0.2097
5170.8    60.00  0.26     Sequence
 HLA-DPA10103-DPB10401  211      SKHTPINLVRDLPQG  INLVRDLPQ  5        0.1701
7933.7    70.00  0.28     Sequence
 HLA-DPA10103-DPB10401  212      KHTPINLVRDLPQGF  INLVRDLPQ  4        0.1702
7932.3    70.00  0.25     Sequence
 HLA-DPA10103-DPB10401  213      HTPINLVRDLPQGFS  INLVRDLPQ  3        0.1614
8721.8    70.00  0.25     Sequence
 HLA-DPA10103-DPB10401  214      TPINLVRDLPQGFSA  LVRDLPQGF  4        0.1650
8388.8    70.00  0.28     Sequence
 HLA-DPA10103-DPB10401  215      PINLVRDLPQGFSAL  DLPQGFSAL  6        0.2431
3602.5    48.00  0.40     Sequence
 HLA-DPA10103-DPB10401  216      INLVRDLPQGFSALE  DLPQGFSAL  5        0.2789
2445.2    40.00  0.40     Sequence
 HLA-DPA10103-DPB10401  217      NLVRDLPQGFSALEP  DLPQGFSAL  4        0.2873
2233.2    39.00  0.37     Sequence
 HLA-DPA10103-DPB10401  218      LVRDLPQGFSALEPL  DLPQGFSAL  3        0.3059
1825.4    35.00  0.26     Sequence
 HLA-DPA10103-DPB10401  219      VRDLPQGFSALEPLV  DLPQGFSAL  2        0.3228
1521.1    32.00  0.26     Sequence
 HLA-DPA10103-DPB10401  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.3242
1498.1    32.00  0.28     Sequence
 HLA-DPA10103-DPB10401  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.3492
1142.9    27.00  0.28     Sequence
 HLA-DPA10103-DPB10401  222      LPQGFSALEPLVDLP  SALEPLVDL  5        0.3803
816.9    23.00  0.30     Sequence
 HLA-DPA10103-DPB10401  223      PQGFSALEPLVDLPI  SALEPLVDL  4        0.3957
691.2    20.00  0.28     Sequence
 HLA-DPA10103-DPB10401  224      QGFSALEPLVDLPIG  SALEPLVDL  3        0.3823
799.4    22.00  0.28     Sequence
 HLA-DPA10103-DPB10401  225      GFSALEPLVDLPIGI  LEPLVDLPI  4        0.3639
974.8    25.00  0.27     Sequence
 HLA-DPA10103-DPB10401  226      FSALEPLVDLPIGIN  LEPLVDLPI  3        0.3514
1115.9    27.00  0.31     Sequence
 HLA-DPA10103-DPB10401  227      SALEPLVDLPIGINI  LVDLPIGIN  5        0.3164
1630.5    33.00  0.23     Sequence
```

```
 HLA-DPA10103-DPB10401  228      ALEPLVDLPIGINIT  LVDLPIGIN  4        0.2753
2543.4    41.00  0.35     Sequence
 HLA-DPA10103-DPB10401  229      LEPLVDLPIGINITR  LVDLPIGIN  3        0.2362
3880.5    50.00  0.46     Sequence
 HLA-DPA10103-DPB10401  230      EPLVDLPIGINITRF  LVDLPIGIN  2        0.2143
4920.3    55.00  0.30     Sequence
 HLA-DPA10103-DPB10401  231      PLVDLPIGINITRFQ  PIGINITRF  5        0.2226
4498.9    55.00  0.31     Sequence
 HLA-DPA10103-DPB10401  232      LVDLPIGINITRFQT  INITRFQTX  7        0.2536
3214.9    46.00  0.39     Sequence
 HLA-DPA10103-DPB10401  233      VDLPIGINITRFQTL  INITRFQTL  6        0.4485
390.4    14.00  0.74     Sequence
 HLA-DPA10103-DPB10401  234      DLPIGINITRFQTLL  INITRFQTL  5        0.4983
227.8     9.50  0.76     Sequence         WB
 HLA-DPA10103-DPB10401  235      LPIGINITRFQTLLA  INITRFQTL  4        0.5228
174.7     7.50  0.69     Sequence         WB
 HLA-DPA10103-DPB10401  236      PIGINITRFQTLLAL  INITRFQTL  3        0.5328
156.8     7.00  0.64     Sequence         WB
 HLA-DPA10103-DPB10401  237      IGINITRFQTLLALH  INITRFQTL  2        0.5901
84.3     4.00  0.40     Sequence         WB
 HLA-DPA10103-DPB10401  238      GINITRFQTLLALHR  FQTLLALHR  6        0.5876
86.7     4.00  0.46     Sequence         WB
 HLA-DPA10103-DPB10401  239      INITRFQTLLALHRS  FQTLLALHR  5        0.5802
93.9     4.50  0.51     Sequence         WB
 HLA-DPA10103-DPB10401  240      NITRFQTLLALHRSY  FQTLLALHR  4        0.5743
100.0     5.00  0.56     Sequence         WB
 HLA-DPA10103-DPB10401  241      ITRFQTLLALHRSYL  FQTLLALHR  3        0.5931
81.6     4.00  0.52     Sequence         WB
 HLA-DPA10103-DPB10401  242      TRFQTLLALHRSYLT  FQTLLALHR  2        0.5781
96.0     4.50  0.49     Sequence         WB
 HLA-DPA10103-DPB10401  243      RFQTLLALHRSYLTP  LLALHRSYL  4        0.5449
137.6     6.00  0.25     Sequence         WB
 HLA-DPA10103-DPB10401  244      FQTLLALHRSYLTPG  LLALHRSYL  3        0.4614
339.5    13.00  0.34     Sequence
 HLA-DPA10103-DPB10401  245      QTLLALHRSYLTPGD  LLALHRSYL  2        0.3481
1156.5    27.00  0.34     Sequence
 HLA-DPA10103-DPB10401  246      TLLALHRSYLTPGDS  LHRSYLTPG  4        0.3246
1491.0    31.00  0.29     Sequence
 HLA-DPA10103-DPB10401  247      LLALHRSYLTPGDSS  LHRSYLTPG  3        0.3009
1927.4    36.00  0.37     Sequence
 HLA-DPA10103-DPB10401  248      LALHRSYLTPGDSSS  LHRSYLTPG  2        0.1816
7007.3    65.00  0.34     Sequence
 HLA-DPA10103-DPB10401  249      ALHRSYLTPGDSSSG  LHRSYLTPG  1        0.1142
14530.9    85.00  0.33     Sequence
 HLA-DPA10103-DPB10401  250      LHRSYLTPGDSSSGW  LTPGDSSSG  5        0.0665
24355.0    95.00  0.25     Sequence
 HLA-DPA10103-DPB10401  251      HRSYLTPGDSSSGWT  LTPGDSSSG  4        0.0522
28432.5   100.00  0.34     Sequence
 HLA-DPA10103-DPB10401  252      RSYLTPGDSSSGWTA  LTPGDSSSG  3        0.0565
27140.6   100.00  0.33     Sequence
 HLA-DPA10103-DPB10401  253      SYLTPGDSSSGWTAG  DSSSGWTAG  6        0.0590
26420.0   100.00  0.34     Sequence
 HLA-DPA10103-DPB10401  254      YLTPGDSSSGWTAGA  DSSSGWTAG  5        0.0600
26132.9   100.00  0.41     Sequence
 HLA-DPA10103-DPB10401  255      LTPGDSSSGWTAGAA  DSSSGWTAG  4        0.0573
26893.0   100.00  0.45     Sequence
 HLA-DPA10103-DPB10401  256      TPGDSSSGWTAGAAA  DSSSGWTAG  3        0.0575
26830.8   100.00  0.41     Sequence
 HLA-DPA10103-DPB10401  257      PGDSSSGWTAGAAAY  DSSSGWTAG  2        0.0632
25223.9   100.00  0.25     Sequence
 HLA-DPA10103-DPB10401  258      GDSSSGWTAGAAAYY  WTAGAAAYY  6        0.0991
17112.1    90.00  0.28     Sequence
 HLA-DPA10103-DPB10401  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5        0.1182
13922.9    85.00  0.23     Sequence
 HLA-DPA10103-DPB10401  260      SSSGWTAGAAAYYVG  GAAAYYVGX  7        0.1195
13720.3    85.00  0.25     Sequence
```

```
 HLA-DPA10103-DPB10401  261      SSGWTAGAAAYYVGY  GAAAYYVGY  6        0.1665
8256.9    70.00  0.44     Sequence
 HLA-DPA10103-DPB10401  262      SGWTAGAAAYYVGYL  GAAAYYVGY  5        0.2432
3597.4    48.00  0.34     Sequence
 HLA-DPA10103-DPB10401  263      GWTAGAAAYYVGYLQ  GAAAYYVGY  4        0.2645
2856.9    43.00  0.26     Sequence
 HLA-DPA10103-DPB10401  264      WTAGAAAYYVGYLQP  YYVGYLQPX  7        0.3171
1617.5    33.00  0.31     Sequence
 HLA-DPA10103-DPB10401  265      TAGAAAYYVGYLQPR  YYVGYLQPR  6        0.3505
1127.6    27.00  0.47     Sequence
 HLA-DPA10103-DPB10401  266      AGAAAYYVGYLQPRT  YYVGYLQPR  5        0.3638
976.5    25.00    0.43   Sequence
 HLA-DPA10103-DPB10401  267      GAAAYYVGYLQPRTF  YYVGYLQPR  4        0.3838
786.2    22.00    0.41   Sequence
 HLA-DPA10103-DPB10401  268      AAAYYVGYLQPRTFL  YYVGYLQPR  3        0.4162
553.9    18.00    0.40   Sequence
 HLA-DPA10103-DPB10401  269      AAYYVGYLQPRTFLL  LQPRTFLLX  7        0.4972
230.5     9.50    0.35   Sequence         WB
 HLA-DPA10103-DPB10401  270      AYYVGYLQPRTFLLK  LQPRTFLLK  6        0.5420
141.9     6.50    0.59   Sequence         WB
 HLA-DPA10103-DPB10401  271      YYVGYLQPRTFLLKY  LQPRTFLLK  5        0.5577
119.7     5.50    0.66   Sequence         WB
 HLA-DPA10103-DPB10401  272      YVGYLQPRTFLLKYN  LQPRTFLLK  4        0.5514
128.2     6.00    0.68   Sequence         WB
 HLA-DPA10103-DPB10401  273      VGYLQPRTFLLKYNE  LQPRTFLLK  3        0.5323
157.7     7.00    0.69   Sequence         WB
 HLA-DPA10103-DPB10401  274      GYLQPRTFLLKYNEN  LQPRTFLLK  2        0.4868
257.9    11.00    0.59   Sequence
 HLA-DPA10103-DPB10401  275      YLQPRTFLLKYNENG  LQPRTFLLK  1        0.3663
950.3    25.00    0.39   Sequence
 HLA-DPA10103-DPB10401  276      LQPRTFLLKYNENGT  FLLKYNENG  5        0.2233
4462.4    55.00  0.26     Sequence
 HLA-DPA10103-DPB10401  277      QPRTFLLKYNENGTI  FLLKYNENG  4        0.1894
6442.2    65.00  0.32     Sequence
 HLA-DPA10103-DPB10401  278      PRTFLLKYNENGTIT  FLLKYNENG  3        0.1845
6789.7    65.00  0.36     Sequence
 HLA-DPA10103-DPB10401  279      RTFLLKYNENGTITD  FLLKYNENG  2        0.1772
7352.3    65.00  0.32     Sequence
 HLA-DPA10103-DPB10401  280      TFLLKYNENGTITDA  LKYNENGTI  3        0.1323
11946.0    80.00  0.34     Sequence
 HLA-DPA10103-DPB10401  281      FLLKYNENGTITDAV  LKYNENGTI  2        0.1153
14360.3    85.00  0.37     Sequence
 HLA-DPA10103-DPB10401  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.0710
23180.2    95.00  0.27     Sequence
 HLA-DPA10103-DPB10401  283      LKYNENGTITDAVDC  ENGTITDAV  4        0.0589
26424.9   100.00  0.18     Sequence
 HLA-DPA10103-DPB10401  284      KYNENGTITDAVDCA  ENGTITDAV  3        0.0423
31645.5   100.00  0.29     Sequence
 HLA-DPA10103-DPB10401  285      YNENGTITDAVDCAL  ITDAVDCAL  6        0.0576
26814.0   100.00  0.17     Sequence
 HLA-DPA10103-DPB10401  286      NENGTITDAVDCALD  ITDAVDCAL  5        0.0588
26462.1   100.00  0.18     Sequence
 HLA-DPA10103-DPB10401  287      ENGTITDAVDCALDP  DAVDCALDP  6        0.0659
24507.7    95.00  0.29     Sequence
 HLA-DPA10103-DPB10401  288      NGTITDAVDCALDPL  AVDCALDPL  6        0.1185
13875.1    85.00  0.28     Sequence
 HLA-DPA10103-DPB10401  289      GTITDAVDCALDPLS  AVDCALDPL  5        0.1212
13470.8    80.00  0.28     Sequence
 HLA-DPA10103-DPB10401  290      TITDAVDCALDPLSE  CALDPLSEX  7        0.1304
12192.0    80.00  0.29     Sequence
 HLA-DPA10103-DPB10401  291      ITDAVDCALDPLSET  CALDPLSET  6        0.1493
9937.7    75.00  0.54     Sequence
 HLA-DPA10103-DPB10401  292      TDAVDCALDPLSETK  CALDPLSET  5        0.1452
10389.6    75.00  0.62     Sequence
 HLA-DPA10103-DPB10401  293      DAVDCALDPLSETKC  CALDPLSET  4        0.1412
10845.3    75.00  0.61     Sequence
```

```
 HLA-DPA10103-DPB10401  294      AVDCALDPLSETKCT  CALDPLSET  3         0.1397
11023.6    75.00  0.62     Sequence
 HLA-DPA10103-DPB10401  295      VDCALDPLSETKCTL  CALDPLSET  2         0.1247
12970.4    80.00  0.46     Sequence
 HLA-DPA10103-DPB10401  296      DCALDPLSETKCTLK  LSETKCTLK  6         0.1227
13259.3    80.00  0.37     Sequence
 HLA-DPA10103-DPB10401  297      CALDPLSETKCTLKS  LSETKCTLK  5         0.1204
13586.2    85.00  0.49     Sequence
 HLA-DPA10103-DPB10401  298      ALDPLSETKCTLKSF  LSETKCTLK  4         0.1397
11025.5    75.00  0.47     Sequence
 HLA-DPA10103-DPB10401  299      LDPLSETKCTLKSFT  LSETKCTLK  3         0.1518
9675.3    75.00  0.41     Sequence
 HLA-DPA10103-DPB10401  300      DPLSETKCTLKSFTV  CTLKSFTVX  7         0.1927
6216.3    65.00  0.31     Sequence
 HLA-DPA10103-DPB10401  301      PLSETKCTLKSFTVE  CTLKSFTVE  6         0.2567
3110.5    45.00  0.50     Sequence
 HLA-DPA10103-DPB10401  302      LSETKCTLKSFTVEK  CTLKSFTVE  5         0.3042
1859.4    35.00  0.49     Sequence
 HLA-DPA10103-DPB10401  303      SETKCTLKSFTVEKG  CTLKSFTVE  4         0.3155
1646.4    33.00  0.40     Sequence
 HLA-DPA10103-DPB10401  304      ETKCTLKSFTVEKGI  LKSFTVEKG  5         0.3428
1225.2    28.00  0.45     Sequence
 HLA-DPA10103-DPB10401  305      TKCTLKSFTVEKGIY  LKSFTVEKG  4         0.3528
1099.6    27.00  0.45     Sequence
 HLA-DPA10103-DPB10401  306      KCTLKSFTVEKGIYQ  LKSFTVEKG  3         0.3656
956.9    25.00  0.44     Sequence
 HLA-DPA10103-DPB10401  307      CTLKSFTVEKGIYQT  FTVEKGIYQ  5         0.3458
1186.3    28.00  0.31     Sequence
 HLA-DPA10103-DPB10401  308      TLKSFTVEKGIYQTS  FTVEKGIYQ  4         0.3085
1776.5    34.00  0.41     Sequence
 HLA-DPA10103-DPB10401  309      LKSFTVEKGIYQTSN  FTVEKGIYQ  3         0.2794
2432.4    40.00  0.51     Sequence
 HLA-DPA10103-DPB10401  310      KSFTVEKGIYQTSNF  FTVEKGIYQ  2         0.2779
2471.7    41.00  0.41     Sequence
 HLA-DPA10103-DPB10401  311      SFTVEKGIYQTSNFR  VEKGIYQTS  3         0.2697
2701.0    42.00  0.23     Sequence
 HLA-DPA10103-DPB10401  312      FTVEKGIYQTSNFRV  YQTSNFRVX  7         0.3737
877.3    23.00  0.46     Sequence
 HLA-DPA10103-DPB10401  313      TVEKGIYQTSNFRVQ  YQTSNFRVQ  6         0.4959
233.9     9.50  0.79     Sequence         WB
 HLA-DPA10103-DPB10401  314      VEKGIYQTSNFRVQP  YQTSNFRVQ  5         0.5209
178.3     7.50  0.81     Sequence         WB
 HLA-DPA10103-DPB10401  315      EKGIYQTSNFRVQPT  YQTSNFRVQ  4         0.5231
174.1     7.50  0.81     Sequence         WB
 HLA-DPA10103-DPB10401  316      KGIYQTSNFRVQPTE  YQTSNFRVQ  3         0.5197
180.7     8.00  0.83     Sequence         WB
 HLA-DPA10103-DPB10401  317      GIYQTSNFRVQPTES  YQTSNFRVQ  2         0.4325
464.1    16.00  0.68     Sequence
 HLA-DPA10103-DPB10401  318      IYQTSNFRVQPTESI  YQTSNFRVQ  1         0.3369
1305.9    29.00  0.43     Sequence
 HLA-DPA10103-DPB10401  319      YQTSNFRVQPTESIV  FRVQPTESI  5         0.2384
3791.3    49.00  0.46     Sequence
 HLA-DPA10103-DPB10401  320      QTSNFRVQPTESIVR  FRVQPTESI  4         0.2054
5418.6    60.00  0.56     Sequence
 HLA-DPA10103-DPB10401  321      TSNFRVQPTESIVRF  FRVQPTESI  3         0.2188
4686.5    55.00  0.52     Sequence
 HLA-DPA10103-DPB10401  322      SNFRVQPTESIVRFP  FRVQPTESI  2         0.2364
3873.0    50.00  0.46     Sequence
 HLA-DPA10103-DPB10401  323      NFRVQPTESIVRFPN  FRVQPTESI  1         0.2110
5097.2    60.00  0.32     Sequence
 HLA-DPA10103-DPB10401  324      FRVQPTESIVRFPNI  ESIVRFPNI  6         0.2437
3580.5    48.00  0.40     Sequence
 HLA-DPA10103-DPB10401  325      RVQPTESIVRFPNIT  ESIVRFPNI  5         0.2281
4239.9    55.00  0.53     Sequence
 HLA-DPA10103-DPB10401  326      VQPTESIVRFPNITN  ESIVRFPNI  4         0.2149
4888.4    55.00  0.56     Sequence
```

```
 HLA-DPA10103-DPB10401  327      QPTESIVRFPNITNL  ESIVRFPNI  3        0.2564
3119.4    45.00  0.39     Sequence
 HLA-DPA10103-DPB10401  328      PTESIVRFPNITNLC  VRFPNITNL  5        0.2671
2779.7    43.00  0.28     Sequence
 HLA-DPA10103-DPB10401  329      TESIVRFPNITNLCP  VRFPNITNL  4        0.2691
2719.3    42.00  0.26     Sequence
 HLA-DPA10103-DPB10401  330      ESIVRFPNITNLCPF  VRFPNITNL  3        0.2800
2418.0    40.00  0.25     Sequence
 HLA-DPA10103-DPB10401  331      SIVRFPNITNLCPFG  PNITNLCPF  5        0.2714
2652.9    42.00  0.28     Sequence
 HLA-DPA10103-DPB10401  332      IVRFPNITNLCPFGE  PNITNLCPF  4        0.2692
2717.0    42.00  0.28     Sequence
 HLA-DPA10103-DPB10401  333      VRFPNITNLCPFGEV  TNLCPFGEV  6        0.2707
2673.9    42.00  0.25     Sequence
 HLA-DPA10103-DPB10401  334      RFPNITNLCPFGEVF  TNLCPFGEV  5        0.2485
3399.4    47.00  0.35     Sequence
 HLA-DPA10103-DPB10401  335      FPNITNLCPFGEVFN  TNLCPFGEV  4        0.2369
3853.6    50.00  0.34     Sequence
 HLA-DPA10103-DPB10401  336      PNITNLCPFGEVFNA  TNLCPFGEV  3        0.2258
4342.7    55.00  0.38     Sequence
 HLA-DPA10103-DPB10401  337      NITNLCPFGEVFNAT  PFGEVFNAT  6        0.2930
2100.3    37.00  0.41     Sequence
 HLA-DPA10103-DPB10401  338      ITNLCPFGEVFNATR  PFGEVFNAT  5        0.3170
1619.9    33.00  0.46     Sequence
 HLA-DPA10103-DPB10401  339      TNLCPFGEVFNATRF  PFGEVFNAT  4        0.4298
478.1    16.00  0.38     Sequence
 HLA-DPA10103-DPB10401  340      NLCPFGEVFNATRFA  FNATRFAXX  8        0.5191
181.9     8.00  0.38     Sequence        WB
 HLA-DPA10103-DPB10401  341      LCPFGEVFNATRFAS  FNATRFASX  7        0.6411
48.6     2.50  0.57     Sequence        WB
 HLA-DPA10103-DPB10401  342      CPFGEVFNATRFASV  FNATRFASV  6        0.8361
5.9     0.07  0.89     Sequence        SB
 HLA-DPA10103-DPB10401  343      PFGEVFNATRFASVY  FNATRFASV  5        0.8541
4.8     0.05  0.89     Sequence        SB
 HLA-DPA10103-DPB10401  344      FGEVFNATRFASVYA  FNATRFASV  4        0.8572
4.7     0.04  0.88     Sequence        SB
 HLA-DPA10103-DPB10401  345      GEVFNATRFASVYAW  FNATRFASV  3        0.8425
5.5     0.06  0.89     Sequence        SB
 HLA-DPA10103-DPB10401  346      EVFNATRFASVYAWN  FNATRFASV  2        0.7806
10.7     0.25  0.75     Sequence        SB
 HLA-DPA10103-DPB10401  347      VFNATRFASVYAWNR  FNATRFASV  1        0.6994
25.8     1.10  0.50     Sequence        SB
 HLA-DPA10103-DPB10401  348      FNATRFASVYAWNRK  FASVYAWNR  5        0.6239
58.5     3.00  0.51     Sequence        WB
 HLA-DPA10103-DPB10401  349      NATRFASVYAWNRKR  FASVYAWNR  4        0.5633
112.8     5.50  0.70     Sequence        WB
 HLA-DPA10103-DPB10401  350      ATRFASVYAWNRKRI  FASVYAWNR  3        0.5617
114.8     5.50  0.71     Sequence        WB
 HLA-DPA10103-DPB10401  351      TRFASVYAWNRKRIS  FASVYAWNR  2        0.5346
153.8     7.00  0.66     Sequence        WB
 HLA-DPA10103-DPB10401  352      RFASVYAWNRKRISN  FASVYAWNR  1        0.4288
483.2    16.00  0.50     Sequence
 HLA-DPA10103-DPB10401  353      FASVYAWNRKRISNC  FASVYAWNR  0        0.3174
1613.2    33.00  0.32     Sequence
 HLA-DPA10103-DPB10401  354      ASVYAWNRKRISNCV  YAWNRKRIS  3        0.1121
14869.0    85.00  0.34     Sequence
 HLA-DPA10103-DPB10401  355      SVYAWNRKRISNCVA  WNRKRISNC  4        0.1115
14964.9    85.00  0.26     Sequence
 HLA-DPA10103-DPB10401  356      VYAWNRKRISNCVAD  WNRKRISNC  3        0.1068
15742.5    85.00  0.28     Sequence
 HLA-DPA10103-DPB10401  357      YAWNRKRISNCVADY  RISNCVADY  6        0.1356
11533.3    80.00  0.44     Sequence
 HLA-DPA10103-DPB10401  358      AWNRKRISNCVADYS  RISNCVADY  5        0.1375
11288.4    80.00  0.41     Sequence
 HLA-DPA10103-DPB10401  359      WNRKRISNCVADYSV  RISNCVADY  4        0.1443
10492.4    75.00  0.37     Sequence
```

```
 HLA-DPA10103-DPB10401  360      NRKRISNCVADYSVL  RISNCVADY  3        0.1853
6733.5    65.00  0.25     Sequence
 HLA-DPA10103-DPB10401  361      RKRISNCVADYSVLY  CVADYSVLY  6        0.2666
2795.3    43.00  0.32     Sequence
 HLA-DPA10103-DPB10401  362      KRISNCVADYSVLYN  CVADYSVLY  5        0.2679
2754.0    43.00  0.31     Sequence
 HLA-DPA10103-DPB10401  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.2694
2710.2    42.00  0.31     Sequence
 HLA-DPA10103-DPB10401  364      ISNCVADYSVLYNSA  DYSVLYNSA  6        0.3029
1885.8    36.00  0.47     Sequence
 HLA-DPA10103-DPB10401  365      SNCVADYSVLYNSAS  DYSVLYNSA  5        0.3006
1933.7    36.00  0.49     Sequence
 HLA-DPA10103-DPB10401  366      NCVADYSVLYNSASF  DYSVLYNSA  4        0.3441
1207.7    28.00  0.44     Sequence
 HLA-DPA10103-DPB10401  367      CVADYSVLYNSASFS  DYSVLYNSA  3        0.3720
892.9    24.00  0.43     Sequence
 HLA-DPA10103-DPB10401  368      VADYSVLYNSASFST  YNSASFSTX  7        0.4016
648.4    20.00  0.39     Sequence
 HLA-DPA10103-DPB10401  369      ADYSVLYNSASFSTF  YNSASFSTF  6        0.5890
85.4     4.00  0.75     Sequence         WB
 HLA-DPA10103-DPB10401  370      DYSVLYNSASFSTFK  YNSASFSTF  5        0.6017
74.4     3.50  0.78     Sequence         WB
 HLA-DPA10103-DPB10401  371      YSVLYNSASFSTFKC  YNSASFSTF  4        0.6149
64.5     3.00  0.76     Sequence         WB
 HLA-DPA10103-DPB10401  372      SVLYNSASFSTFKCY  YNSASFSTF  3        0.6187
61.9     3.00  0.72     Sequence         WB
 HLA-DPA10103-DPB10401  373      VLYNSASFSTFKCYG  YNSASFSTF  2        0.5806
93.5     4.50  0.65     Sequence         WB
 HLA-DPA10103-DPB10401  374      LYNSASFSTFKCYGV  FSTFKCYGV  6        0.5328
156.8     7.00  0.22     Sequence         WB
 HLA-DPA10103-DPB10401  375      YNSASFSTFKCYGVS  FSTFKCYGV  5        0.4823
270.7    11.00  0.37     Sequence
 HLA-DPA10103-DPB10401  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.4581
351.9    13.00  0.47     Sequence
 HLA-DPA10103-DPB10401  377      SASFSTFKCYGVSPT  FSTFKCYGV  3        0.4510
379.9    14.00  0.49     Sequence
 HLA-DPA10103-DPB10401  378      ASFSTFKCYGVSPTK  FSTFKCYGV  2        0.4313
470.3    16.00  0.47     Sequence
 HLA-DPA10103-DPB10401  379      SFSTFKCYGVSPTKL  FKCYGVSPT  4        0.4142
566.1    18.00  0.26     Sequence
 HLA-DPA10103-DPB10401  380      FSTFKCYGVSPTKLN  FKCYGVSPT  3        0.3693
919.6    24.00  0.31     Sequence
 HLA-DPA10103-DPB10401  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.2634
2893.0    44.00  0.32     Sequence
 HLA-DPA10103-DPB10401  382      TFKCYGVSPTKLNDL  CYGVSPTKL  3        0.2731
2603.1    42.00  0.31     Sequence
 HLA-DPA10103-DPB10401  383      FKCYGVSPTKLNDLC  VSPTKLNDL  5        0.2297
4167.1    55.00  0.34     Sequence
 HLA-DPA10103-DPB10401  384      KCYGVSPTKLNDLCF  VSPTKLNDL  4        0.2176
4746.6    55.00  0.41     Sequence
 HLA-DPA10103-DPB10401  385      CYGVSPTKLNDLCFT  VSPTKLNDL  3        0.2130
4988.3    60.00  0.41     Sequence
 HLA-DPA10103-DPB10401  386      YGVSPTKLNDLCFTN  LNDLCFTNX  7        0.2064
5357.0    60.00  0.37     Sequence
 HLA-DPA10103-DPB10401  387      GVSPTKLNDLCFTNV  LNDLCFTNV  6        0.3128
1694.4    34.00  0.66     Sequence
 HLA-DPA10103-DPB10401  388      VSPTKLNDLCFTNVY  LNDLCFTNV  5        0.3408
1252.3    29.00  0.70     Sequence
 HLA-DPA10103-DPB10401  389      SPTKLNDLCFTNVYA  LNDLCFTNV  4        0.3539
1086.4    27.00  0.67     Sequence
 HLA-DPA10103-DPB10401  390      PTKLNDLCFTNVYAD  LNDLCFTNV  3        0.3638
975.6    25.00  0.62     Sequence
 HLA-DPA10103-DPB10401  391      TKLNDLCFTNVYADS  LNDLCFTNV  2        0.3670
942.5    24.00  0.41     Sequence
 HLA-DPA10103-DPB10401  392      KLNDLCFTNVYADSF  FTNVYADSF  6        0.4232
513.1    17.00  0.35     Sequence
```

```
 HLA-DPA10103-DPB10401  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.4468
397.6    14.00  0.39     Sequence
 HLA-DPA10103-DPB10401  394      NDLCFTNVYADSFVI  FTNVYADSF  4        0.4644
328.6    13.00  0.39     Sequence
 HLA-DPA10103-DPB10401  395      DLCFTNVYADSFVIR  VYADSFVIR  6        0.4972
230.5     9.50  0.35     Sequence         WB
 HLA-DPA10103-DPB10401  396      LCFTNVYADSFVIRG  VYADSFVIR  5        0.4905
247.7    10.00  0.37     Sequence
 HLA-DPA10103-DPB10401  397      CFTNVYADSFVIRGD  VYADSFVIR  4        0.4595
346.6    13.00  0.43     Sequence
 HLA-DPA10103-DPB10401  398      FTNVYADSFVIRGDE  VYADSFVIR  3        0.4304
475.0    16.00  0.48     Sequence
 HLA-DPA10103-DPB10401  399      TNVYADSFVIRGDEV  YADSFVIRG  3        0.3255
1477.1    31.00  0.35     Sequence
 HLA-DPA10103-DPB10401  400      NVYADSFVIRGDEVR  YADSFVIRG  2        0.2823
2357.2    40.00  0.32     Sequence
 HLA-DPA10103-DPB10401  401      VYADSFVIRGDEVRQ  YADSFVIRG  1        0.2310
4106.8    55.00  0.22     Sequence
 HLA-DPA10103-DPB10401  402      YADSFVIRGDEVRQI  IRGDEVRQI  6        0.2240
4431.2    55.00  0.53     Sequence
 HLA-DPA10103-DPB10401  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.2192
4665.7    55.00  0.61     Sequence
 HLA-DPA10103-DPB10401  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.2215
4553.9    55.00  0.62     Sequence
 HLA-DPA10103-DPB10401  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.2207
4591.6    55.00  0.68     Sequence
 HLA-DPA10103-DPB10401  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.1905
6367.1    65.00  0.67     Sequence
 HLA-DPA10103-DPB10401  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.1148
14432.5    85.00  0.43     Sequence
 HLA-DPA10103-DPB10401  408      IRGDEVRQIAPGQTG  IRGDEVRQI  0        0.0811
20786.4    95.00  0.27     Sequence
 HLA-DPA10103-DPB10401  409      RGDEVRQIAPGQTGT  RQIAPGQTG  5        0.0619
25584.5   100.00  0.30     Sequence
 HLA-DPA10103-DPB10401  410      GDEVRQIAPGQTGTI  IAPGQTGTI  6        0.0629
25320.4   100.00  0.23     Sequence
 HLA-DPA10103-DPB10401  411      DEVRQIAPGQTGTIA  IAPGQTGTI  5        0.0670
24205.2    95.00  0.23     Sequence
 HLA-DPA10103-DPB10401  412      EVRQIAPGQTGTIAD  IAPGQTGTI  4        0.0662
24430.7    95.00  0.22     Sequence
 HLA-DPA10103-DPB10401  413      VRQIAPGQTGTIADY  GQTGTIADY  6        0.0646
24863.2   100.00  0.35     Sequence
 HLA-DPA10103-DPB10401  414      RQIAPGQTGTIADYN  GQTGTIADY  5        0.0601
26093.9   100.00  0.35     Sequence
 HLA-DPA10103-DPB10401  415      QIAPGQTGTIADYNY  GQTGTIADY  4        0.0582
26647.1   100.00  0.35     Sequence
 HLA-DPA10103-DPB10401  416      IAPGQTGTIADYNYK  GQTGTIADY  3        0.0585
26539.5   100.00  0.32     Sequence
 HLA-DPA10103-DPB10401  417      APGQTGTIADYNYKL  GTIADYNYK  5        0.0822
20539.8    95.00  0.29     Sequence
 HLA-DPA10103-DPB10401  418      PGQTGTIADYNYKLP  IADYNYKLP  6        0.1288
12412.8    80.00  0.25     Sequence
 HLA-DPA10103-DPB10401  419      GQTGTIADYNYKLPD  IADYNYKLP  5        0.1223
13318.9    80.00  0.27     Sequence
 HLA-DPA10103-DPB10401  420      QTGTIADYNYKLPDD  IADYNYKLP  4        0.1195
13728.8    85.00  0.29     Sequence
 HLA-DPA10103-DPB10401  421      TGTIADYNYKLPDDF  IADYNYKLP  3        0.1285
12448.7    80.00  0.32     Sequence
 HLA-DPA10103-DPB10401  422      GTIADYNYKLPDDFT  IADYNYKLP  2        0.1240
13068.3    80.00  0.32     Sequence
 HLA-DPA10103-DPB10401  423      TIADYNYKLPDDFTG  DYNYKLPDD  3        0.1161
14234.3    85.00  0.21     Sequence
 HLA-DPA10103-DPB10401  424      IADYNYKLPDDFTGC  KLPDDFTGC  6        0.1165
14176.2    85.00  0.37     Sequence
 HLA-DPA10103-DPB10401  425      ADYNYKLPDDFTGCV  KLPDDFTGC  5        0.1247
12965.2    80.00  0.50     Sequence
```

```
 HLA-DPA10103-DPB10401  426      DYNYKLPDDFTGCVI  KLPDDFTGC  4        0.1662
8281.0    70.00  0.44     Sequence
 HLA-DPA10103-DPB10401  427      YNYKLPDDFTGCVIA  KLPDDFTGC  3        0.1853
6733.4    65.00  0.38     Sequence
 HLA-DPA10103-DPB10401  428      NYKLPDDFTGCVIAW  FTGCVIAWX  7        0.1996
5765.4    60.00  0.34     Sequence
 HLA-DPA10103-DPB10401  429      YKLPDDFTGCVIAWN  FTGCVIAWN  6        0.2374
3834.1    50.00  0.58     Sequence
 HLA-DPA10103-DPB10401  430      KLPDDFTGCVIAWNS  FTGCVIAWN  5        0.2293
4184.5    55.00  0.63     Sequence
 HLA-DPA10103-DPB10401  431      LPDDFTGCVIAWNSN  FTGCVIAWN  4        0.2250
4380.9    55.00  0.63     Sequence
 HLA-DPA10103-DPB10401  432      PDDFTGCVIAWNSNN  FTGCVIAWN  3        0.2148
4892.1    55.00  0.63     Sequence
 HLA-DPA10103-DPB10401  433      DDFTGCVIAWNSNNL  FTGCVIAWN  2        0.1990
5802.8    60.00  0.40     Sequence
 HLA-DPA10103-DPB10401  434      DFTGCVIAWNSNNLD  FTGCVIAWN  1        0.1645
8432.6    70.00  0.20     Sequence
 HLA-DPA10103-DPB10401  435      FTGCVIAWNSNNLDS  VIAWNSNNL  4        0.1594
8907.2    70.00  0.23     Sequence
 HLA-DPA10103-DPB10401  436      TGCVIAWNSNNLDSK  WNSNNLDSK  6        0.1504
9819.6    75.00  0.43     Sequence
 HLA-DPA10103-DPB10401  437      GCVIAWNSNNLDSKV  WNSNNLDSK  5        0.1544
9403.5    75.00  0.51     Sequence
 HLA-DPA10103-DPB10401  438      CVIAWNSNNLDSKVG  WNSNNLDSK  4        0.1538
9473.2    75.00  0.50     Sequence
 HLA-DPA10103-DPB10401  439      VIAWNSNNLDSKVGG  WNSNNLDSK  3        0.1491
9959.6    75.00  0.56     Sequence
 HLA-DPA10103-DPB10401  440      IAWNSNNLDSKVGGN  WNSNNLDSK  2        0.0922
18432.1    90.00  0.57     Sequence
 HLA-DPA10103-DPB10401  441      AWNSNNLDSKVGGNY  WNSNNLDSK  1        0.0639
25036.5   100.00  0.36     Sequence
 HLA-DPA10103-DPB10401  442      WNSNNLDSKVGGNYN  LDSKVGGNY  5        0.0480
29732.5   100.00  0.29     Sequence
 HLA-DPA10103-DPB10401  443      NSNNLDSKVGGNYNY  LDSKVGGNY  4        0.0423
31627.7   100.00  0.35     Sequence
 HLA-DPA10103-DPB10401  444      SNNLDSKVGGNYNYL  KVGGNYNYL  6        0.1349
11616.7    80.00  0.45     Sequence
 HLA-DPA10103-DPB10401  445      NNLDSKVGGNYNYLY  KVGGNYNYL  5        0.1986
5831.9    60.00  0.38     Sequence
 HLA-DPA10103-DPB10401  446      NLDSKVGGNYNYLYR  KVGGNYNYL  4        0.2104
5131.6    60.00  0.35     Sequence
 HLA-DPA10103-DPB10401  447      LDSKVGGNYNYLYRL  GNYNYLYRL  6        0.2891
2191.1    38.00  0.28     Sequence
 HLA-DPA10103-DPB10401  448      DSKVGGNYNYLYRLF  GNYNYLYRL  5        0.3794
824.1    23.00  0.23     Sequence
 HLA-DPA10103-DPB10401  449      SKVGGNYNYLYRLFR  GNYNYLYRL  4        0.4083
603.0    19.00  0.20     Sequence
 HLA-DPA10103-DPB10401  450      KVGGNYNYLYRLFRK  YLYRLFRKX  7        0.4500
384.2    14.00  0.37     Sequence
 HLA-DPA10103-DPB10401  451      VGGNYNYLYRLFRKS  YLYRLFRKS  6        0.4776
285.0    11.00  0.52     Sequence
 HLA-DPA10103-DPB10401  452      GGNYNYLYRLFRKSN  YLYRLFRKS  5        0.4646
328.0    13.00  0.51     Sequence
 HLA-DPA10103-DPB10401  453      GNYNYLYRLFRKSNL  YLYRLFRKS  4        0.5165
187.1     8.00  0.50     Sequence          WB
 HLA-DPA10103-DPB10401  454      NYNYLYRLFRKSNLK  YLYRLFRKS  3        0.5259
169.0     7.50  0.51     Sequence          WB
 HLA-DPA10103-DPB10401  455      YNYLYRLFRKSNLKP  YLYRLFRKS  2        0.5279
165.4     7.00  0.41     Sequence          WB
 HLA-DPA10103-DPB10401  456      NYLYRLFRKSNLKPF  FRKSNLKPF  6        0.5393
146.2     6.50  0.56     Sequence          WB
 HLA-DPA10103-DPB10401  457      YLYRLFRKSNLKPFE  FRKSNLKPF  5        0.5231
174.1     7.50  0.64     Sequence          WB
 HLA-DPA10103-DPB10401  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.5067
208.0     8.50  0.70     Sequence          WB
```

```
 HLA-DPA10103-DPB10401  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.4963
232.6     9.50  0.73     Sequence          WB
 HLA-DPA10103-DPB10401  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.3340
1347.2    30.00  0.62     Sequence
 HLA-DPA10103-DPB10401  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.2231
4474.6    55.00  0.41     Sequence
 HLA-DPA10103-DPB10401  462      FRKSNLKPFERDIST  SNLKPFERD  3        0.1534
9509.1    75.00  0.36     Sequence
 HLA-DPA10103-DPB10401  463      RKSNLKPFERDISTE  SNLKPFERD  2        0.1051
16033.0    85.00  0.42     Sequence
 HLA-DPA10103-DPB10401  464      KSNLKPFERDISTEI  FERDISTEI  6        0.1276
12572.0    80.00  0.41     Sequence
 HLA-DPA10103-DPB10401  465      SNLKPFERDISTEIY  FERDISTEI  5        0.1580
9042.9    70.00  0.42     Sequence
 HLA-DPA10103-DPB10401  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.2134
4968.3    55.00  0.38     Sequence
 HLA-DPA10103-DPB10401  467      LKPFERDISTEIYQA  ISTEIYQAX  7        0.3123
1704.3    34.00  0.42     Sequence
 HLA-DPA10103-DPB10401  468      KPFERDISTEIYQAG  ISTEIYQAG  6        0.3301
1405.8    30.00  0.59     Sequence
 HLA-DPA10103-DPB10401  469      PFERDISTEIYQAGS  ISTEIYQAG  5        0.3352
1330.4    30.00  0.63     Sequence
 HLA-DPA10103-DPB10401  470      FERDISTEIYQAGST  ISTEIYQAG  4        0.3332
1358.6    30.00  0.62     Sequence
 HLA-DPA10103-DPB10401  471      ERDISTEIYQAGSTP  ISTEIYQAG  3        0.3101
1745.5    34.00  0.71     Sequence
 HLA-DPA10103-DPB10401  472      RDISTEIYQAGSTPC  ISTEIYQAG  2        0.2909
2148.7    38.00  0.67     Sequence
 HLA-DPA10103-DPB10401  473      DISTEIYQAGSTPCN  ISTEIYQAG  1        0.1519
9669.0    75.00  0.44     Sequence
 HLA-DPA10103-DPB10401  474      ISTEIYQAGSTPCNG  ISTEIYQAG  0        0.0946
17956.5    90.00  0.25     Sequence
 HLA-DPA10103-DPB10401  475      STEIYQAGSTPCNGV  AGSTPCNGV  6        0.0864
19641.2    90.00  0.34     Sequence
 HLA-DPA10103-DPB10401  476      TEIYQAGSTPCNGVK  AGSTPCNGV  5        0.0844
20066.7    95.00  0.35     Sequence
 HLA-DPA10103-DPB10401  477      EIYQAGSTPCNGVKG  AGSTPCNGV  4        0.0795
21161.1    95.00  0.37     Sequence
 HLA-DPA10103-DPB10401  478      IYQAGSTPCNGVKGF  AGSTPCNGV  3        0.0719
22959.6    95.00  0.43     Sequence
 HLA-DPA10103-DPB10401  479      YQAGSTPCNGVKGFN  AGSTPCNGV  2        0.0637
25085.6   100.00  0.36     Sequence
 HLA-DPA10103-DPB10401  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.0814
20732.8    95.00  0.50     Sequence
 HLA-DPA10103-DPB10401  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.1067
15759.3    85.00  0.55     Sequence
 HLA-DPA10103-DPB10401  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.1417
10793.8    75.00  0.41     Sequence
 HLA-DPA10103-DPB10401  483      STPCNGVKGFNCYFP  VKGFNCYFP  6        0.2020
5621.8    60.00  0.25     Sequence
 HLA-DPA10103-DPB10401  484      TPCNGVKGFNCYFPL  KGFNCYFPL  6        0.2811
2389.1    40.00  0.34     Sequence
 HLA-DPA10103-DPB10401  485      PCNGVKGFNCYFPLQ  KGFNCYFPL  5        0.3617
998.4    25.00  0.34     Sequence
 HLA-DPA10103-DPB10401  486      CNGVKGFNCYFPLQS  KGFNCYFPL  4        0.4068
612.9    19.00  0.29     Sequence
 HLA-DPA10103-DPB10401  487      NGVKGFNCYFPLQSY  KGFNCYFPL  3        0.4372
440.9    15.00  0.26     Sequence
 HLA-DPA10103-DPB10401  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.4359
447.4    15.00  0.15     Sequence
 HLA-DPA10103-DPB10401  489      VKGFNCYFPLQSYGF  YFPLQSYGF  6        0.4726
300.7    12.00  0.17     Sequence
 HLA-DPA10103-DPB10401  490      KGFNCYFPLQSYGFQ  FPLQSYGFQ  6        0.5035
215.2     9.00  0.19     Sequence          WB
 HLA-DPA10103-DPB10401  491      GFNCYFPLQSYGFQP  LQSYGFQPX  7        0.5420
142.0     6.50  0.37     Sequence          WB
```

```
 HLA-DPA10103-DPB10401  492      FNCYFPLQSYGFQPT  LQSYGFQPT  6        0.6121
66.5     3.50  0.64     Sequence         WB
 HLA-DPA10103-DPB10401  493      NCYFPLQSYGFQPTY  LQSYGFQPT  5        0.6051
71.7     3.50  0.76     Sequence         WB
 HLA-DPA10103-DPB10401  494      CYFPLQSYGFQPTYG  LQSYGFQPT  4        0.5984
77.1     4.00  0.75     Sequence         WB
 HLA-DPA10103-DPB10401  495      YFPLQSYGFQPTYGV  LQSYGFQPT  3        0.5970
78.3     4.00  0.79     Sequence         WB
 HLA-DPA10103-DPB10401  496      FPLQSYGFQPTYGVG  LQSYGFQPT  2        0.4918
244.4    10.00  0.67     Sequence
 HLA-DPA10103-DPB10401  497      PLQSYGFQPTYGVGY  LQSYGFQPT  1        0.3642
971.8    25.00  0.41     Sequence
 HLA-DPA10103-DPB10401  498      LQSYGFQPTYGVGYQ  FQPTYGVGY  5        0.2925
2111.2    38.00  0.41     Sequence
 HLA-DPA10103-DPB10401  499      QSYGFQPTYGVGYQP  FQPTYGVGY  4        0.2593
3022.4    45.00  0.51     Sequence
 HLA-DPA10103-DPB10401  500      SYGFQPTYGVGYQPY  FQPTYGVGY  3        0.2693
2713.1    42.00  0.43     Sequence
 HLA-DPA10103-DPB10401  501      YGFQPTYGVGYQPYR  TYGVGYQPY  5        0.2642
2867.0    44.00  0.38     Sequence
 HLA-DPA10103-DPB10401  502      GFQPTYGVGYQPYRV  TYGVGYQPY  4        0.2532
3230.2    46.00  0.44     Sequence
 HLA-DPA10103-DPB10401  503      FQPTYGVGYQPYRVV  TYGVGYQPY  3        0.2775
2482.1    41.00  0.37     Sequence
 HLA-DPA10103-DPB10401  504      QPTYGVGYQPYRVVV  VGYQPYRVV  5        0.2750
2551.8    41.00  0.37     Sequence
 HLA-DPA10103-DPB10401  505      PTYGVGYQPYRVVVL  VGYQPYRVV  4        0.3244
1494.4    32.00  0.30     Sequence
 HLA-DPA10103-DPB10401  506      TYGVGYQPYRVVVLS  VGYQPYRVV  3        0.3294
1415.6    31.00  0.29     Sequence
 HLA-DPA10103-DPB10401  507      YGVGYQPYRVVVLSF  YQPYRVVVL  4        0.3787
830.8    23.00  0.20     Sequence
 HLA-DPA10103-DPB10401  508      GVGYQPYRVVVLSFE  YRVVVLSFE  6        0.4349
452.4    16.00  0.44     Sequence
 HLA-DPA10103-DPB10401  509      VGYQPYRVVVLSFEL  YRVVVLSFE  5        0.4811
274.3    11.00  0.42     Sequence
 HLA-DPA10103-DPB10401  510      GYQPYRVVVLSFELL  VVVLSFELL  6        0.5266
167.8     7.50  0.38     Sequence         WB
 HLA-DPA10103-DPB10401  511      YQPYRVVVLSFELLH  VVVLSFELL  5        0.5626
113.5     5.50  0.41     Sequence         WB
 HLA-DPA10103-DPB10401  512      QPYRVVVLSFELLHA  VVVLSFELL  4        0.5616
114.8     5.50  0.41     Sequence         WB
 HLA-DPA10103-DPB10401  513      PYRVVVLSFELLHAP  VVVLSFELL  3        0.5650
110.7     5.00  0.41     Sequence         WB
 HLA-DPA10103-DPB10401  514      YRVVVLSFELLHAPA  VVVLSFELL  2        0.5427
140.8     6.50  0.33     Sequence         WB
 HLA-DPA10103-DPB10401  515      RVVVLSFELLHAPAT  VLSFELLHA  3        0.4829
269.0    11.00  0.23     Sequence
 HLA-DPA10103-DPB10401  516      VVVLSFELLHAPATV  LSFELLHAP  3        0.4190
537.2    17.00  0.23     Sequence
 HLA-DPA10103-DPB10401  517      VVLSFELLHAPATVC  LSFELLHAP  2        0.3732
881.6    24.00  0.23     Sequence
 HLA-DPA10103-DPB10401  518      VLSFELLHAPATVCG  FELLHAPAT  3        0.2947
2061.1    37.00  0.22     Sequence
 HLA-DPA10103-DPB10401  519      LSFELLHAPATVCGP  LLHAPATVC  4        0.2326
4038.3    55.00  0.26     Sequence
 HLA-DPA10103-DPB10401  520      SFELLHAPATVCGPK  LLHAPATVC  3        0.2059
5389.8    60.00  0.37     Sequence
 HLA-DPA10103-DPB10401  521      FELLHAPATVCGPKK  LLHAPATVC  2        0.1579
9056.8    70.00  0.32     Sequence
 HLA-DPA10103-DPB10401  522      ELLHAPATVCGPKKS  HAPATVCGP  3        0.1070
15706.9    85.00  0.20     Sequence
 HLA-DPA10103-DPB10401  523      LLHAPATVCGPKKST  PATVCGPKK  4        0.0748
22267.9    95.00  0.23     Sequence
 HLA-DPA10103-DPB10401  524      LHAPATVCGPKKSTN  PATVCGPKK  3        0.0504
28991.7   100.00  0.34     Sequence
```

```
 HLA-DPA10103-DPB10401  525      HAPATVCGPKKSTNL  PATVCGPKK  2        0.0543
27771.2   100.00  0.22      Sequence
 HLA-DPA10103-DPB10401  526      APATVCGPKKSTNLV  CGPKKSTNL  5        0.0533
28086.4   100.00  0.25      Sequence
 HLA-DPA10103-DPB10401  527      PATVCGPKKSTNLVK  KKSTNLVKX  7        0.0746
22306.5    95.00  0.34      Sequence
 HLA-DPA10103-DPB10401  528      ATVCGPKKSTNLVKN  KKSTNLVKN  6        0.0908
18721.9    90.00  0.54      Sequence
 HLA-DPA10103-DPB10401  529      TVCGPKKSTNLVKNK  KKSTNLVKN  5        0.0920
18473.8    90.00  0.63      Sequence
 HLA-DPA10103-DPB10401  530      VCGPKKSTNLVKNKC  KKSTNLVKN  4        0.0946
17966.8    90.00  0.58      Sequence
 HLA-DPA10103-DPB10401  531      CGPKKSTNLVKNKCV  KKSTNLVKN  3        0.0965
17594.6    90.00  0.56      Sequence
 HLA-DPA10103-DPB10401  532      GPKKSTNLVKNKCVN  KKSTNLVKN  2        0.0871
19487.7    90.00  0.43      Sequence
 HLA-DPA10103-DPB10401  533      PKKSTNLVKNKCVNF  LVKNKCVNF  6        0.1771
7355.4    65.00  0.50     Sequence
 HLA-DPA10103-DPB10401  534      KKSTNLVKNKCVNFN  LVKNKCVNF  5        0.1742
7593.7    70.00  0.54     Sequence
 HLA-DPA10103-DPB10401  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4        0.2131
4985.8    60.00  0.47     Sequence
 HLA-DPA10103-DPB10401  536      STNLVKNKCVNFNFN  NKCVNFNFN  6        0.2609
2972.9    44.00  0.27     Sequence
 HLA-DPA10103-DPB10401  537      TNLVKNKCVNFNFNG  CVNFNFNGX  7        0.3028
1888.6    36.00  0.41     Sequence
 HLA-DPA10103-DPB10401  538      NLVKNKCVNFNFNGL  CVNFNFNGL  6        0.4659
323.3    12.00  0.65     Sequence
 HLA-DPA10103-DPB10401  539      LVKNKCVNFNFNGLT  CVNFNFNGL  5        0.4702
308.6    12.00  0.66     Sequence
 HLA-DPA10103-DPB10401  540      VKNKCVNFNFNGLTG  CVNFNFNGL  4        0.4410
423.5    15.00  0.70     Sequence
 HLA-DPA10103-DPB10401  541      KNKCVNFNFNGLTGT  CVNFNFNGL  3        0.4400
427.9    15.00  0.67     Sequence
 HLA-DPA10103-DPB10401  542      NKCVNFNFNGLTGTG  CVNFNFNGL  2        0.3861
766.5    22.00  0.61     Sequence
 HLA-DPA10103-DPB10401  543      KCVNFNFNGLTGTGV  CVNFNFNGL  1        0.3308
1395.6    30.00  0.41     Sequence
 HLA-DPA10103-DPB10401  544      CVNFNFNGLTGTGVL  CVNFNFNGL  0        0.2769
2500.0    41.00  0.28     Sequence
 HLA-DPA10103-DPB10401  545      VNFNFNGLTGTGVLT  LTGTGVLTX  7        0.2018
5630.6    60.00  0.35     Sequence
 HLA-DPA10103-DPB10401  546      NFNFNGLTGTGVLTE  LTGTGVLTE  6        0.2729
2610.6    42.00  0.68     Sequence
 HLA-DPA10103-DPB10401  547      FNFNGLTGTGVLTES  LTGTGVLTE  5        0.2660
2811.1    43.00  0.74     Sequence
 HLA-DPA10103-DPB10401  548      NFNGLTGTGVLTESN  LTGTGVLTE  4        0.2499
3347.6    47.00  0.76     Sequence
 HLA-DPA10103-DPB10401  549      FNGLTGTGVLTESNK  LTGTGVLTE  3        0.2435
3587.6    48.00  0.82     Sequence
 HLA-DPA10103-DPB10401  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.1977
5890.3    60.00  0.69     Sequence
 HLA-DPA10103-DPB10401  551      GLTGTGVLTESNKKF  LTGTGVLTE  1        0.1418
10779.3    75.00  0.42      Sequence
 HLA-DPA10103-DPB10401  552      LTGTGVLTESNKKFL  LTGTGVLTE  0        0.1458
10329.1    75.00  0.22      Sequence
 HLA-DPA10103-DPB10401  553      TGTGVLTESNKKFLP  ESNKKFLPX  7        0.1542
9424.0    75.00  0.40     Sequence
 HLA-DPA10103-DPB10401  554      GTGVLTESNKKFLPF  ESNKKFLPF  6        0.2512
3300.6    46.00  0.63     Sequence
 HLA-DPA10103-DPB10401  555      TGVLTESNKKFLPFQ  ESNKKFLPF  5        0.2790
2444.5    40.00  0.64     Sequence
 HLA-DPA10103-DPB10401  556      GVLTESNKKFLPFQQ  ESNKKFLPF  4        0.2991
1965.5    36.00  0.54     Sequence
 HLA-DPA10103-DPB10401  557      VLTESNKKFLPFQQF  KKFLPFQQF  6        0.4569
356.4    13.00  0.31     Sequence
```

```
 HLA-DPA10103-DPB10401  558      LTESNKKFLPFQQFG  KKFLPFQQF  5        0.4993
225.4     9.50  0.32     Sequence         WB
 HLA-DPA10103-DPB10401  559      TESNKKFLPFQQFGR  LPFQQFGRX  7        0.5579
119.5     5.50  0.38     Sequence         WB
 HLA-DPA10103-DPB10401  560      ESNKKFLPFQQFGRD  LPFQQFGRD  6        0.5620
114.3     5.50  0.40     Sequence         WB
 HLA-DPA10103-DPB10401  561      SNKKFLPFQQFGRDI  LPFQQFGRD  5        0.5801
93.9     4.50  0.41     Sequence         WB
 HLA-DPA10103-DPB10401  562      NKKFLPFQQFGRDIA  LPFQQFGRD  4        0.5907
83.8     4.00  0.43     Sequence         WB
 HLA-DPA10103-DPB10401  563      KKFLPFQQFGRDIAD  LPFQQFGRD  3        0.5759
98.4     4.50  0.44     Sequence         WB
 HLA-DPA10103-DPB10401  564      KFLPFQQFGRDIADT  LPFQQFGRD  2        0.4498
384.7    14.00  0.41     Sequence
 HLA-DPA10103-DPB10401  565      FLPFQQFGRDIADTT  FQQFGRDIA  3        0.2874
2229.9    39.00  0.31     Sequence
 HLA-DPA10103-DPB10401  566      LPFQQFGRDIADTTD  FQQFGRDIA  2        0.1679
8131.4    70.00  0.37     Sequence
 HLA-DPA10103-DPB10401  567      PFQQFGRDIADTTDA  FQQFGRDIA  1        0.1400
10989.1    75.00  0.29     Sequence
 HLA-DPA10103-DPB10401  568      FQQFGRDIADTTDAV  FGRDIADTT  3        0.1266
12702.5    80.00  0.40     Sequence
 HLA-DPA10103-DPB10401  569      QQFGRDIADTTDAVR  FGRDIADTT  2        0.0665
24337.6    95.00  0.30     Sequence
 HLA-DPA10103-DPB10401  570      QFGRDIADTTDAVRD  DIADTTDAV  4        0.0541
27856.7   100.00  0.21     Sequence
 HLA-DPA10103-DPB10401  571      FGRDIADTTDAVRDP  DIADTTDAV  3        0.0502
29057.9   100.00  0.26     Sequence
 HLA-DPA10103-DPB10401  572      GRDIADTTDAVRDPQ  DIADTTDAV  2        0.0430
31388.0   100.00  0.22     Sequence
 HLA-DPA10103-DPB10401  573      RDIADTTDAVRDPQT  IADTTDAVR  2        0.0435
31217.0   100.00  0.21     Sequence
 HLA-DPA10103-DPB10401  574      DIADTTDAVRDPQTL  DTTDAVRDP  3        0.0409
32112.5   100.00  0.17     Sequence
 HLA-DPA10103-DPB10401  575      IADTTDAVRDPQTLE  VRDPQTLEX  7        0.0422
31668.4   100.00  0.17     Sequence
 HLA-DPA10103-DPB10401  576      ADTTDAVRDPQTLEI  VRDPQTLEI  6        0.0843
20076.2    95.00  0.51     Sequence
 HLA-DPA10103-DPB10401  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5        0.1226
13265.4    80.00  0.35     Sequence
 HLA-DPA10103-DPB10401  578      TTDAVRDPQTLEILD  VRDPQTLEI  4        0.1232
13182.0    80.00  0.33     Sequence
 HLA-DPA10103-DPB10401  579      TDAVRDPQTLEILDI  PQTLEILDI  6        0.1761
7434.7    65.00  0.41     Sequence
 HLA-DPA10103-DPB10401  580      DAVRDPQTLEILDIT  PQTLEILDI  5        0.1991
5801.3    60.00  0.36     Sequence
 HLA-DPA10103-DPB10401  581      AVRDPQTLEILDITP  PQTLEILDI  4        0.2146
4905.2    55.00  0.31     Sequence
 HLA-DPA10103-DPB10401  582      VRDPQTLEILDITPC  PQTLEILDI  3        0.2256
4355.5    55.00  0.25     Sequence
 HLA-DPA10103-DPB10401  583      RDPQTLEILDITPCS  LEILDITPC  5        0.2280
4243.1    55.00  0.29     Sequence
 HLA-DPA10103-DPB10401  584      DPQTLEILDITPCSF  LEILDITPC  4        0.2823
2356.3    40.00  0.25     Sequence
 HLA-DPA10103-DPB10401  585      PQTLEILDITPCSFG  LDITPCSFG  6        0.2953
2048.0    37.00  0.31     Sequence
 HLA-DPA10103-DPB10401  586      QTLEILDITPCSFGG  LDITPCSFG  5        0.2835
2327.7    39.00  0.29     Sequence
 HLA-DPA10103-DPB10401  587      TLEILDITPCSFGGV  ITPCSFGGV  6        0.3405
1255.8    29.00  0.44     Sequence
 HLA-DPA10103-DPB10401  588      LEILDITPCSFGGVS  ITPCSFGGV  5        0.3230
1518.3    32.00  0.51     Sequence
 HLA-DPA10103-DPB10401  589      EILDITPCSFGGVSV  ITPCSFGGV  4        0.3242
1497.9    32.00  0.53     Sequence
 HLA-DPA10103-DPB10401  590      ILDITPCSFGGVSVI  ITPCSFGGV  3        0.3388
1279.9    29.00  0.46     Sequence
```

```
 HLA-DPA10103-DPB10401  591      LDITPCSFGGVSVIT  ITPCSFGGV  2        0.3109
1730.6    34.00  0.35     Sequence
 HLA-DPA10103-DPB10401  592      DITPCSFGGVSVITP  FGGVSVITP  6        0.3095
1756.4    34.00  0.43     Sequence
 HLA-DPA10103-DPB10401  593      ITPCSFGGVSVITPG  FGGVSVITP  5        0.2784
2460.2    40.00  0.48     Sequence
 HLA-DPA10103-DPB10401  594      TPCSFGGVSVITPGT  FGGVSVITP  4        0.2488
3389.1    47.00  0.55     Sequence
 HLA-DPA10103-DPB10401  595      PCSFGGVSVITPGTN  FGGVSVITP  3        0.2485
3398.4    47.00  0.56     Sequence
 HLA-DPA10103-DPB10401  596      CSFGGVSVITPGTNT  FGGVSVITP  2        0.1909
6335.6    65.00  0.47     Sequence
 HLA-DPA10103-DPB10401  597      SFGGVSVITPGTNTS  FGGVSVITP  1        0.1052
16017.0    85.00  0.32     Sequence
 HLA-DPA10103-DPB10401  598      FGGVSVITPGTNTSN  SVITPGTNT  4        0.0722
22892.1    95.00  0.26     Sequence
 HLA-DPA10103-DPB10401  599      GGVSVITPGTNTSNQ  SVITPGTNT  3        0.0490
29431.0    100.00  0.40     Sequence
 HLA-DPA10103-DPB10401  600      GVSVITPGTNTSNQV  SVITPGTNT  2        0.0468
30149.1    100.00  0.33     Sequence
 HLA-DPA10103-DPB10401  601      VSVITPGTNTSNQVA  GTNTSNQVA  6        0.0516
28607.5    100.00  0.17     Sequence
 HLA-DPA10103-DPB10401  602      SVITPGTNTSNQVAV  GTNTSNQVA  5        0.0430
31408.1    100.00  0.22     Sequence
 HLA-DPA10103-DPB10401  603      VITPGTNTSNQVAVL  NTSNQVAVL  6        0.0858
19764.8    90.00  0.49     Sequence
 HLA-DPA10103-DPB10401  604      ITPGTNTSNQVAVLY  NTSNQVAVL  5        0.1173
14055.8    85.00  0.47     Sequence
 HLA-DPA10103-DPB10401  605      TPGTNTSNQVAVLYQ  NTSNQVAVL  4        0.1398
11020.6    75.00  0.38     Sequence
 HLA-DPA10103-DPB10401  606      PGTNTSNQVAVLYQG  QVAVLYQGX  7        0.1487
10003.0    75.00  0.38     Sequence
 HLA-DPA10103-DPB10401  607      GTNTSNQVAVLYQGV  QVAVLYQGV  6        0.3197
1573.7    32.00  0.65     Sequence
 HLA-DPA10103-DPB10401  608      TNTSNQVAVLYQGVN  QVAVLYQGV  5        0.3284
1431.2    31.00  0.62     Sequence
 HLA-DPA10103-DPB10401  609      NTSNQVAVLYQGVNC  QVAVLYQGV  4        0.3381
1288.3    29.00  0.58     Sequence
 HLA-DPA10103-DPB10401  610      TSNQVAVLYQGVNCT  QVAVLYQGV  3        0.3449
1197.6    28.00  0.55     Sequence
 HLA-DPA10103-DPB10401  611      SNQVAVLYQGVNCTE  QVAVLYQGV  2        0.3381
1288.7    29.00  0.47     Sequence
 HLA-DPA10103-DPB10401  612      NQVAVLYQGVNCTEV  YQGVNCTEV  6        0.3342
1344.4    30.00  0.29     Sequence
 HLA-DPA10103-DPB10401  613      QVAVLYQGVNCTEVP  YQGVNCTEV  5        0.3187
1589.5    33.00  0.37     Sequence
 HLA-DPA10103-DPB10401  614      VAVLYQGVNCTEVPV  YQGVNCTEV  4        0.2829
2343.2    39.00  0.56     Sequence
 HLA-DPA10103-DPB10401  615      AVLYQGVNCTEVPVA  YQGVNCTEV  3        0.2645
2858.7    43.00  0.65     Sequence
 HLA-DPA10103-DPB10401  616      VLYQGVNCTEVPVAI  YQGVNCTEV  2        0.2423
3634.5    49.00  0.62     Sequence
 HLA-DPA10103-DPB10401  617      LYQGVNCTEVPVAIH  YQGVNCTEV  1        0.2133
4975.0    55.00  0.43     Sequence
 HLA-DPA10103-DPB10401  618      YQGVNCTEVPVAIHA  CTEVPVAIH  5        0.1664
8257.3    70.00  0.26     Sequence
 HLA-DPA10103-DPB10401  619      QGVNCTEVPVAIHAD  CTEVPVAIH  4        0.1262
12767.9    80.00  0.39     Sequence
 HLA-DPA10103-DPB10401  620      GVNCTEVPVAIHADQ  CTEVPVAIH  3        0.1236
13123.5    80.00  0.43     Sequence
 HLA-DPA10103-DPB10401  621      VNCTEVPVAIHADQL  CTEVPVAIH  2        0.1375
11289.8    80.00  0.31     Sequence
 HLA-DPA10103-DPB10401  622      NCTEVPVAIHADQLT  PVAIHADQL  5        0.1340
11726.2    80.00  0.17     Sequence
 HLA-DPA10103-DPB10401  623      CTEVPVAIHADQLTP  PVAIHADQL  4        0.1501
9852.2    75.00  0.19     Sequence
```

```
 HLA-DPA10103-DPB10401  624      TEVPVAIHADQLTPT  IHADQLTPT  6         0.1669
8219.6    70.00  0.43     Sequence
 HLA-DPA10103-DPB10401  625      EVPVAIHADQLTPTW  IHADQLTPT  5         0.1668
8229.4    70.00  0.50     Sequence
 HLA-DPA10103-DPB10401  626      VPVAIHADQLTPTWR  IHADQLTPT  4         0.1687
8060.0    70.00  0.54     Sequence
 HLA-DPA10103-DPB10401  627      PVAIHADQLTPTWRV  IHADQLTPT  3         0.1874
6585.2    65.00  0.44     Sequence
 HLA-DPA10103-DPB10401  628      VAIHADQLTPTWRVY  IHADQLTPT  2         0.2171
4774.1    55.00  0.26     Sequence
 HLA-DPA10103-DPB10401  629      AIHADQLTPTWRVYS  DQLTPTWRV  4         0.1965
5965.3    60.00  0.27     Sequence
 HLA-DPA10103-DPB10401  630      IHADQLTPTWRVYST  DQLTPTWRV  3         0.1810
7056.8    65.00  0.28     Sequence
 HLA-DPA10103-DPB10401  631      HADQLTPTWRVYSTG  DQLTPTWRV  2         0.1618
8686.2    70.00  0.27     Sequence
 HLA-DPA10103-DPB10401  632      ADQLTPTWRVYSTGS  LTPTWRVYS  3         0.1564
9209.1    75.00  0.27     Sequence
 HLA-DPA10103-DPB10401  633      DQLTPTWRVYSTGSN  LTPTWRVYS  2         0.1374
11309.0    80.00  0.25     Sequence
 HLA-DPA10103-DPB10401  634      QLTPTWRVYSTGSNV  RVYSTGSNV  6         0.1601
8846.6    70.00  0.44     Sequence
 HLA-DPA10103-DPB10401  635      LTPTWRVYSTGSNVF  RVYSTGSNV  5         0.1945
6095.5    60.00  0.41     Sequence
 HLA-DPA10103-DPB10401  636      TPTWRVYSTGSNVFQ  RVYSTGSNV  4         0.2173
4764.1    55.00  0.33     Sequence
 HLA-DPA10103-DPB10401  637      PTWRVYSTGSNVFQT  RVYSTGSNV  3         0.2300
4150.8    55.00  0.31     Sequence
 HLA-DPA10103-DPB10401  638      TWRVYSTGSNVFQTR  TGSNVFQTR  6         0.2448
3538.9    48.00  0.28     Sequence
 HLA-DPA10103-DPB10401  639      WRVYSTGSNVFQTRA  TGSNVFQTR  5         0.2417
3659.7    49.00  0.31     Sequence
 HLA-DPA10103-DPB10401  640      RVYSTGSNVFQTRAG  TGSNVFQTR  4         0.2112
5089.5    60.00  0.37     Sequence
 HLA-DPA10103-DPB10401  641      VYSTGSNVFQTRAGC  TGSNVFQTR  3         0.1688
8046.1    70.00  0.47     Sequence
 HLA-DPA10103-DPB10401  642      YSTGSNVFQTRAGCL  TGSNVFQTR  2         0.1894
6442.0    65.00  0.29     Sequence
 HLA-DPA10103-DPB10401  643      STGSNVFQTRAGCLI  FQTRAGCLI  6         0.2291
4190.0    55.00  0.34     Sequence
 HLA-DPA10103-DPB10401  644      TGSNVFQTRAGCLIG  FQTRAGCLI  5         0.2238
4438.1    55.00  0.33     Sequence
 HLA-DPA10103-DPB10401  645      GSNVFQTRAGCLIGA  FQTRAGCLI  4         0.2277
4255.7    55.00  0.31     Sequence
 HLA-DPA10103-DPB10401  646      SNVFQTRAGCLIGAE  RAGCLIGAE  6         0.2553
3155.7    45.00  0.22     Sequence
 HLA-DPA10103-DPB10401  647      NVFQTRAGCLIGAEY  RAGCLIGAE  5         0.2656
2824.1    43.00  0.26     Sequence
 HLA-DPA10103-DPB10401  648      VFQTRAGCLIGAEYV  RAGCLIGAE  4         0.2950
2055.1    37.00  0.26     Sequence
 HLA-DPA10103-DPB10401  649      FQTRAGCLIGAEYVN  LIGAEYVNX  7         0.3255
1476.5    31.00  0.41     Sequence
 HLA-DPA10103-DPB10401  650      QTRAGCLIGAEYVNN  LIGAEYVNN  6         0.3447
1200.0    28.00  0.60     Sequence
 HLA-DPA10103-DPB10401  651      TRAGCLIGAEYVNNS  LIGAEYVNN  5         0.3465
1177.0    28.00  0.61     Sequence
 HLA-DPA10103-DPB10401  652      RAGCLIGAEYVNNSY  LIGAEYVNN  4         0.3566
1054.7    26.00  0.62     Sequence
 HLA-DPA10103-DPB10401  653      AGCLIGAEYVNNSYE  LIGAEYVNN  3         0.3487
1149.1    27.00  0.68     Sequence
 HLA-DPA10103-DPB10401  654      GCLIGAEYVNNSYEC  LIGAEYVNN  2         0.3020
1904.4    36.00  0.54     Sequence
 HLA-DPA10103-DPB10401  655      CLIGAEYVNNSYECD  YVNNSYECD  6         0.2716
2647.6    42.00  0.49     Sequence
 HLA-DPA10103-DPB10401  656      LIGAEYVNNSYECDI  YVNNSYECD  5         0.2681
2747.8    43.00  0.68     Sequence
```

```
 HLA-DPA10103-DPB10401  657      IGAEYVNNSYECDIP  YVNNSYECD  4        0.2714
2651.6    42.00  0.70     Sequence
 HLA-DPA10103-DPB10401  658      GAEYVNNSYECDIPI  YVNNSYECD  3        0.2710
2664.2    42.00  0.71     Sequence
 HLA-DPA10103-DPB10401  659      AEYVNNSYECDIPIG  YVNNSYECD  2        0.2605
2986.0    44.00  0.63     Sequence
 HLA-DPA10103-DPB10401  660      EYVNNSYECDIPIGA  YVNNSYECD  1        0.1717
7799.5    70.00  0.42     Sequence
 HLA-DPA10103-DPB10401  661      YVNNSYECDIPIGAG  YVNNSYECD  0        0.1163
14202.3    85.00  0.23     Sequence
 HLA-DPA10103-DPB10401  662      VNNSYECDIPIGAGI  CDIPIGAGI  6        0.0953
17827.2    90.00  0.28     Sequence
 HLA-DPA10103-DPB10401  663      NNSYECDIPIGAGIC  CDIPIGAGI  5        0.0991
17116.7    90.00  0.29     Sequence
 HLA-DPA10103-DPB10401  664      NSYECDIPIGAGICA  CDIPIGAGI  4        0.0991
17108.2    90.00  0.28     Sequence
 HLA-DPA10103-DPB10401  665      SYECDIPIGAGICAS  CDIPIGAGI  3        0.1008
16806.9    90.00  0.29     Sequence
 HLA-DPA10103-DPB10401  666      YECDIPIGAGICASY  IGAGICASY  6        0.1422
10729.3    75.00  0.29     Sequence
 HLA-DPA10103-DPB10401  667      ECDIPIGAGICASYQ  IGAGICASY  5        0.1420
10758.3    75.00  0.32     Sequence
 HLA-DPA10103-DPB10401  668      CDIPIGAGICASYQT  IGAGICASY  4        0.1460
10296.6    75.00  0.31     Sequence
 HLA-DPA10103-DPB10401  669      DIPIGAGICASYQTQ  GICASYQTQ  6        0.1524
9609.2    75.00  0.39     Sequence
 HLA-DPA10103-DPB10401  670      IPIGAGICASYQTQT  GICASYQTQ  5        0.1630
8568.6    70.00  0.41     Sequence
 HLA-DPA10103-DPB10401  671      PIGAGICASYQTQTN  GICASYQTQ  4        0.1611
8751.3    70.00  0.43     Sequence
 HLA-DPA10103-DPB10401  672      IGAGICASYQTQTNS  GICASYQTQ  3        0.1498
9884.6    75.00  0.44     Sequence
 HLA-DPA10103-DPB10401  673      GAGICASYQTQTNSP  GICASYQTQ  2        0.1297
12291.3    80.00  0.33     Sequence
 HLA-DPA10103-DPB10401  674      AGICASYQTQTNSPR  CASYQTQTN  3        0.1138
14587.9    85.00  0.27     Sequence
 HLA-DPA10103-DPB10401  675      GICASYQTQTNSPRR  CASYQTQTN  2        0.1027
16464.0    90.00  0.22     Sequence
 HLA-DPA10103-DPB10401  676      ICASYQTQTNSPRRA  YQTQTNSPR  4        0.0940
18081.9    90.00  0.22     Sequence
 HLA-DPA10103-DPB10401  677      CASYQTQTNSPRRAR  YQTQTNSPR  3        0.0870
19513.0    90.00  0.28     Sequence
 HLA-DPA10103-DPB10401  678      ASYQTQTNSPRRARS  QTQTNSPRR  3        0.0804
20956.9    95.00  0.23     Sequence
 HLA-DPA10103-DPB10401  679      SYQTQTNSPRRARSV  QTQTNSPRR  2        0.0806
20896.0    95.00  0.19     Sequence
 HLA-DPA10103-DPB10401  680      YQTQTNSPRRARSVA  QTNSPRRAR  3        0.0733
22629.3    95.00  0.24     Sequence
 HLA-DPA10103-DPB10401  681      QTQTNSPRRARSVAS  TQTNSPRRA  1        0.0565
27134.7    100.00  0.16     Sequence
 HLA-DPA10103-DPB10401  682      TQTNSPRRARSVASQ  RRARSVASQ  6        0.0532
28120.8    100.00  0.22     Sequence
 HLA-DPA10103-DPB10401  683      QTNSPRRARSVASQS  RRARSVASQ  5        0.0524
28354.2    100.00  0.20     Sequence
 HLA-DPA10103-DPB10401  684      TNSPRRARSVASQSI  ARSVASQSI  6        0.1091
15356.4    85.00  0.56     Sequence
 HLA-DPA10103-DPB10401  685      NSPRRARSVASQSII  ARSVASQSI  5        0.1451
10399.3    75.00  0.47     Sequence
 HLA-DPA10103-DPB10401  686      SPRRARSVASQSIIA  ARSVASQSI  4        0.1712
7840.9    70.00  0.34     Sequence
 HLA-DPA10103-DPB10401  687      PRRARSVASQSIIAY  VASQSIIAY  6        0.2062
5373.5    60.00  0.41     Sequence
 HLA-DPA10103-DPB10401  688      RRARSVASQSIIAYT  VASQSIIAY  5        0.2201
4620.8    55.00  0.38     Sequence
 HLA-DPA10103-DPB10401  689      RARSVASQSIIAYTM  VASQSIIAY  4        0.2444
3551.3    48.00  0.37     Sequence
```

```
 HLA-DPA10103-DPB10401  690      ARSVASQSIIAYTMS  VASQSIIAY  3        0.2410
3685.8    49.00  0.31     Sequence
 HLA-DPA10103-DPB10401  691      RSVASQSIIAYTMSL  ASQSIIAYT  3        0.2648
2848.7    43.00  0.14     Sequence
 HLA-DPA10103-DPB10401  692      SVASQSIIAYTMSLG  IIAYTMSLG  6        0.2561
3131.7    45.00  0.19     Sequence
 HLA-DPA10103-DPB10401  693      VASQSIIAYTMSLGA  IAYTMSLGA  6        0.2870
2241.1    39.00  0.43     Sequence
 HLA-DPA10103-DPB10401  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.2908
2150.6    38.00  0.44     Sequence
 HLA-DPA10103-DPB10401  695      SQSIIAYTMSLGAEN  IAYTMSLGA  4        0.3055
1834.4    35.00  0.38     Sequence
 HLA-DPA10103-DPB10401  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.2790
2443.5    40.00  0.41     Sequence
 HLA-DPA10103-DPB10401  697      SIIAYTMSLGAENSV  IAYTMSLGA  2        0.2797
2424.5    40.00  0.43     Sequence
 HLA-DPA10103-DPB10401  698      IIAYTMSLGAENSVA  YTMSLGAEN  3        0.2224
4505.8    55.00  0.38     Sequence
 HLA-DPA10103-DPB10401  699      IAYTMSLGAENSVAY  YTMSLGAEN  2        0.1933
6173.9    65.00  0.38     Sequence
 HLA-DPA10103-DPB10401  700      AYTMSLGAENSVAYS  YTMSLGAEN  1        0.1554
9305.8    75.00  0.29     Sequence
 HLA-DPA10103-DPB10401  701      YTMSLGAENSVAYSN  LGAENSVAY  4        0.1266
12703.0    80.00  0.19     Sequence
 HLA-DPA10103-DPB10401  702      TMSLGAENSVAYSNN  LGAENSVAY  3        0.1068
15745.2    85.00  0.33     Sequence
 HLA-DPA10103-DPB10401  703      MSLGAENSVAYSNNS  ENSVAYSNN  5        0.1007
16820.0    90.00  0.32     Sequence
 HLA-DPA10103-DPB10401  704      SLGAENSVAYSNNSI  ENSVAYSNN  4        0.0975
17409.5    90.00  0.36     Sequence
 HLA-DPA10103-DPB10401  705      LGAENSVAYSNNSIA  ENSVAYSNN  3        0.1103
15156.2    85.00  0.28     Sequence
 HLA-DPA10103-DPB10401  706      GAENSVAYSNNSIAI  YSNNSIAIX  7        0.1440
10524.9    75.00  0.26     Sequence
 HLA-DPA10103-DPB10401  707      AENSVAYSNNSIAIP  YSNNSIAIP  6        0.1934
6168.6    65.00  0.41     Sequence
 HLA-DPA10103-DPB10401  708      ENSVAYSNNSIAIPT  YSNNSIAIP  5        0.1962
5982.5    60.00  0.41     Sequence
 HLA-DPA10103-DPB10401  709      NSVAYSNNSIAIPTN  YSNNSIAIP  4        0.1905
6362.4    65.00  0.41     Sequence
 HLA-DPA10103-DPB10401  710      SVAYSNNSIAIPTNF  YSNNSIAIP  3        0.1991
5799.1    60.00  0.44     Sequence
 HLA-DPA10103-DPB10401  711      VAYSNNSIAIPTNFT  YSNNSIAIP  2        0.1801
7121.7    65.00  0.42     Sequence
 HLA-DPA10103-DPB10401  712      AYSNNSIAIPTNFTI  AIPTNFTIX  7        0.1618
8681.4    70.00  0.28     Sequence
 HLA-DPA10103-DPB10401  713      YSNNSIAIPTNFTIS  AIPTNFTIS  6        0.1755
7490.4    65.00  0.50     Sequence
 HLA-DPA10103-DPB10401  714      SNNSIAIPTNFTISV  AIPTNFTIS  5        0.2066
5348.7    60.00  0.50     Sequence
 HLA-DPA10103-DPB10401  715      NNSIAIPTNFTISVT  AIPTNFTIS  4        0.2361
3888.2    50.00  0.41     Sequence
 HLA-DPA10103-DPB10401  716      NSIAIPTNFTISVTT  AIPTNFTIS  3        0.2312
4098.4    55.00  0.43     Sequence
 HLA-DPA10103-DPB10401  717      SIAIPTNFTISVTTE  AIPTNFTIS  2        0.2229
4481.6    55.00  0.38     Sequence
 HLA-DPA10103-DPB10401  718      IAIPTNFTISVTTEI  FTISVTTEI  6        0.2528
3243.4    46.00  0.34     Sequence
 HLA-DPA10103-DPB10401  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.2665
2798.4    43.00  0.42     Sequence
 HLA-DPA10103-DPB10401  720      IPTNFTISVTTEILP  FTISVTTEI  4        0.2908
2150.0    38.00  0.32     Sequence
 HLA-DPA10103-DPB10401  721      PTNFTISVTTEILPV  SVTTEILPV  6        0.3620
995.2    25.00  0.37     Sequence
 HLA-DPA10103-DPB10401  722      TNFTISVTTEILPVS  SVTTEILPV  5        0.3800
818.8    23.00  0.39     Sequence
```

```
 HLA-DPA10103-DPB10401  723      NFTISVTTEILPVSM  SVTTEILPV  4        0.3840
784.1    22.00  0.38     Sequence
 HLA-DPA10103-DPB10401  724      FTISVTTEILPVSMT  SVTTEILPV  3        0.3748
866.7    23.00  0.40     Sequence
 HLA-DPA10103-DPB10401  725      TISVTTEILPVSMTK  SVTTEILPV  2        0.3213
1545.9    32.00  0.40     Sequence
 HLA-DPA10103-DPB10401  726      ISVTTEILPVSMTKT  VTTEILPVS  2        0.2975
1999.3    37.00  0.31     Sequence
 HLA-DPA10103-DPB10401  727      SVTTEILPVSMTKTS  ILPVSMTKT  5        0.2134
4969.3    55.00  0.36     Sequence
 HLA-DPA10103-DPB10401  728      VTTEILPVSMTKTSV  ILPVSMTKT  4        0.1881
6532.8    65.00  0.44     Sequence
 HLA-DPA10103-DPB10401  729      TTEILPVSMTKTSVD  ILPVSMTKT  3        0.1637
8503.1    70.00  0.43     Sequence
 HLA-DPA10103-DPB10401  730      TEILPVSMTKTSVDC  ILPVSMTKT  2        0.1572
9128.6    70.00  0.43     Sequence
 HLA-DPA10103-DPB10401  731      EILPVSMTKTSVDCT  ILPVSMTKT  1        0.1452
10393.0    75.00  0.31     Sequence
 HLA-DPA10103-DPB10401  732      ILPVSMTKTSVDCTM  MTKTSVDCT  5        0.1132
14697.7    85.00  0.38     Sequence
 HLA-DPA10103-DPB10401  733      LPVSMTKTSVDCTMY  MTKTSVDCT  4        0.1369
11361.9    80.00  0.39     Sequence
 HLA-DPA10103-DPB10401  734      PVSMTKTSVDCTMYI  MTKTSVDCT  3        0.1560
9241.2    75.00  0.32     Sequence
 HLA-DPA10103-DPB10401  735      VSMTKTSVDCTMYIC  VDCTMYICX  7        0.2076
5290.1    60.00  0.35     Sequence
 HLA-DPA10103-DPB10401  736      SMTKTSVDCTMYICG  VDCTMYICG  6        0.2055
5413.4    60.00  0.51     Sequence
 HLA-DPA10103-DPB10401  737      MTKTSVDCTMYICGD  VDCTMYICG  5        0.2043
5484.7    60.00  0.55     Sequence
 HLA-DPA10103-DPB10401  738      TKTSVDCTMYICGDS  VDCTMYICG  4        0.2048
5452.5    60.00  0.52     Sequence
 HLA-DPA10103-DPB10401  739      KTSVDCTMYICGDST  VDCTMYICG  3        0.2039
5506.1    60.00  0.52     Sequence
 HLA-DPA10103-DPB10401  740      TSVDCTMYICGDSTE  VDCTMYICG  2        0.1573
9112.8    70.00  0.40     Sequence
 HLA-DPA10103-DPB10401  741      SVDCTMYICGDSTEC  VDCTMYICG  1        0.1318
12015.1    80.00  0.19     Sequence
 HLA-DPA10103-DPB10401  742      VDCTMYICGDSTECS  TMYICGDST  3        0.1054
15982.2    85.00  0.21     Sequence
 HLA-DPA10103-DPB10401  743      DCTMYICGDSTECSN  TMYICGDST  2        0.0929
18306.3    90.00  0.22     Sequence
 HLA-DPA10103-DPB10401  744      CTMYICGDSTECSNL  GDSTECSNL  6        0.1036
16290.6    85.00  0.18     Sequence
 HLA-DPA10103-DPB10401  745      TMYICGDSTECSNLL  GDSTECSNL  5        0.1031
16392.8    90.00  0.23     Sequence
 HLA-DPA10103-DPB10401  746      MYICGDSTECSNLLL  GDSTECSNL  4        0.1375
11297.4    80.00  0.17     Sequence
 HLA-DPA10103-DPB10401  747      YICGDSTECSNLLLQ  TECSNLLLQ  6        0.1650
8385.1    70.00  0.17     Sequence
 HLA-DPA10103-DPB10401  748      ICGDSTECSNLLLQY  ECSNLLLQY  6        0.2571
3094.9    45.00  0.28     Sequence
 HLA-DPA10103-DPB10401  749      CGDSTECSNLLLQYG  CSNLLLQYG  6        0.2564
3121.5    45.00  0.40     Sequence
 HLA-DPA10103-DPB10401  750      GDSTECSNLLLQYGS  CSNLLLQYG  5        0.2454
3513.7    48.00  0.40     Sequence
 HLA-DPA10103-DPB10401  751      DSTECSNLLLQYGSF  CSNLLLQYG  4        0.3019
1906.3    36.00  0.34     Sequence
 HLA-DPA10103-DPB10401  752      STECSNLLLQYGSFC  LLLQYGSFC  6        0.3633
981.1    25.00  0.25     Sequence
 HLA-DPA10103-DPB10401  753      TECSNLLLQYGSFCT  LLLQYGSFC  5        0.3875
755.4    22.00  0.26     Sequence
 HLA-DPA10103-DPB10401  754      ECSNLLLQYGSFCTQ  LQYGSFCTQ  6        0.4159
555.6    18.00  0.41     Sequence
 HLA-DPA10103-DPB10401  755      CSNLLLQYGSFCTQL  LQYGSFCTQ  5        0.4843
265.0    11.00  0.43     Sequence
```

```
 HLA-DPA10103-DPB10401  756      SNLLLQYGSFCTQLN  LQYGSFCTQ  4        0.4858
260.9    11.00  0.40     Sequence
 HLA-DPA10103-DPB10401  757      NLLLQYGSFCTQLNR  LQYGSFCTQ  3        0.4815
273.1    11.00  0.47     Sequence
 HLA-DPA10103-DPB10401  758      LLLQYGSFCTQLNRA  LQYGSFCTQ  2        0.4399
428.7    15.00  0.39     Sequence
 HLA-DPA10103-DPB10401  759      LLQYGSFCTQLNRAL  QYGSFCTQL  2        0.3876
754.2    21.00  0.22     Sequence
 HLA-DPA10103-DPB10401  760      LQYGSFCTQLNRALT  QYGSFCTQL  1        0.3223
1529.5    32.00  0.19     Sequence
 HLA-DPA10103-DPB10401  761      QYGSFCTQLNRALTG  CTQLNRALT  5        0.2566
3113.5    45.00  0.14     Sequence
 HLA-DPA10103-DPB10401  762      YGSFCTQLNRALTGI  CTQLNRALT  4        0.2077
5285.1    60.00  0.20     Sequence
 HLA-DPA10103-DPB10401  763      GSFCTQLNRALTGIA  CTQLNRALT  3        0.1821
6968.6    65.00  0.25     Sequence
 HLA-DPA10103-DPB10401  764      SFCTQLNRALTGIAV  CTQLNRALT  2        0.1926
6224.8    65.00  0.19     Sequence
 HLA-DPA10103-DPB10401  765      FCTQLNRALTGIAVE  LTGIAVEXX  8        0.2272
4278.9    55.00  0.17     Sequence
 HLA-DPA10103-DPB10401  766      CTQLNRALTGIAVEQ  LTGIAVEQX  7        0.2272
4281.5    55.00  0.28     Sequence
 HLA-DPA10103-DPB10401  767      TQLNRALTGIAVEQD  LTGIAVEQD  6        0.2227
4493.4    55.00  0.40     Sequence
 HLA-DPA10103-DPB10401  768      QLNRALTGIAVEQDK  LTGIAVEQD  5        0.2239
4435.6    55.00  0.47     Sequence
 HLA-DPA10103-DPB10401  769      LNRALTGIAVEQDKN  LTGIAVEQD  4        0.2179
4734.4    55.00  0.50     Sequence
 HLA-DPA10103-DPB10401  770      NRALTGIAVEQDKNT  LTGIAVEQD  3        0.2056
5406.9    60.00  0.56     Sequence
 HLA-DPA10103-DPB10401  771      RALTGIAVEQDKNTQ  LTGIAVEQD  2        0.1797
7156.0    65.00  0.52     Sequence
 HLA-DPA10103-DPB10401  772      ALTGIAVEQDKNTQE  LTGIAVEQD  1        0.0871
19477.8    90.00  0.32     Sequence
 HLA-DPA10103-DPB10401  773      LTGIAVEQDKNTQEV  VEQDKNTQE  5        0.0534
28060.9   100.00  0.17     Sequence
 HLA-DPA10103-DPB10401  774      TGIAVEQDKNTQEVF  VEQDKNTQE  4        0.0600
26126.4   100.00  0.24     Sequence
 HLA-DPA10103-DPB10401  775      GIAVEQDKNTQEVFA  DKNTQEVFA  6        0.0720
22937.0    95.00  0.28     Sequence
 HLA-DPA10103-DPB10401  776      IAVEQDKNTQEVFAQ  DKNTQEVFA  5        0.0843
20094.3    95.00  0.25     Sequence
 HLA-DPA10103-DPB10401  777      AVEQDKNTQEVFAQV  NTQEVFAQV  6        0.2439
3573.5    48.00  0.59     Sequence
 HLA-DPA10103-DPB10401  778      VEQDKNTQEVFAQVK  NTQEVFAQV  5        0.3056
1833.1    35.00  0.54     Sequence
 HLA-DPA10103-DPB10401  779      EQDKNTQEVFAQVKQ  NTQEVFAQV  4        0.3067
1810.3    35.00  0.48     Sequence
 HLA-DPA10103-DPB10401  780      QDKNTQEVFAQVKQI  NTQEVFAQV  3        0.3429
1224.1    28.00  0.41     Sequence
 HLA-DPA10103-DPB10401  781      DKNTQEVFAQVKQIY  NTQEVFAQV  2        0.3807
812.7    22.00  0.31     Sequence
 HLA-DPA10103-DPB10401  782      KNTQEVFAQVKQIYK  FAQVKQIYK  6        0.4037
633.9    19.00  0.40     Sequence
 HLA-DPA10103-DPB10401  783      NTQEVFAQVKQIYKT  FAQVKQIYK  5        0.3821
801.0    22.00  0.47     Sequence
 HLA-DPA10103-DPB10401  784      TQEVFAQVKQIYKTP  FAQVKQIYK  4        0.3634
980.3    25.00  0.56     Sequence
 HLA-DPA10103-DPB10401  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.3559
1063.3    26.00  0.56     Sequence
 HLA-DPA10103-DPB10401  786      EVFAQVKQIYKTPPI  FAQVKQIYK  2        0.3144
1666.0    33.00  0.47     Sequence
 HLA-DPA10103-DPB10401  787      VFAQVKQIYKTPPIK  FAQVKQIYK  1        0.2653
2833.9    43.00  0.34     Sequence
 HLA-DPA10103-DPB10401  788      FAQVKQIYKTPPIKD  YKTPPIKDX  7        0.2255
4360.4    55.00  0.20     Sequence
```

```
 HLA-DPA10103-DPB10401  789       AQVKQIYKTPPIKDF  YKTPPIKDF  6         0.2259
4338.3    55.00  0.51     Sequence
 HLA-DPA10103-DPB10401  790       QVKQIYKTPPIKDFG  YKTPPIKDF  5         0.2171
4771.8    55.00  0.50     Sequence
 HLA-DPA10103-DPB10401  791       VKQIYKTPPIKDFGG  YKTPPIKDF  4         0.2051
5436.4    60.00  0.51     Sequence
 HLA-DPA10103-DPB10401  792       KQIYKTPPIKDFGGF  YKTPPIKDF  3         0.1841
6821.1    65.00  0.63     Sequence
 HLA-DPA10103-DPB10401  793       QIYKTPPIKDFGGFN  YKTPPIKDF  2         0.1468
10213.5    75.00  0.54     Sequence
 HLA-DPA10103-DPB10401  794       IYKTPPIKDFGGFNF  IKDFGGFNF  6         0.2521
3270.4    46.00  0.35     Sequence
 HLA-DPA10103-DPB10401  795       YKTPPIKDFGGFNFS  FGGFNFSXX  8         0.3414
1244.2    29.00  0.39     Sequence
 HLA-DPA10103-DPB10401  796       KTPPIKDFGGFNFSQ  FGGFNFSQX  7         0.4348
452.6    16.00  0.55     Sequence
 HLA-DPA10103-DPB10401  797       TPPIKDFGGFNFSQI  FGGFNFSQI  6         0.6564
41.2     1.80  0.86     Sequence        SB
 HLA-DPA10103-DPB10401  798       PPIKDFGGFNFSQIL  FGGFNFSQI  5         0.6925
27.9     1.10  0.83     Sequence        SB
 HLA-DPA10103-DPB10401  799       PIKDFGGFNFSQILP  FGGFNFSQI  4         0.7050
24.3     1.00  0.80     Sequence        SB
 HLA-DPA10103-DPB10401  800       IKDFGGFNFSQILPD  FGGFNFSQI  3         0.7126
22.4     0.90  0.76     Sequence        SB
 HLA-DPA10103-DPB10401  801       KDFGGFNFSQILPDP  FGGFNFSQI  2         0.6440
47.1     2.50  0.64     Sequence        WB
 HLA-DPA10103-DPB10401  802       DFGGFNFSQILPDPS  FGGFNFSQI  1         0.5081
204.8     8.50  0.41     Sequence        WB
 HLA-DPA10103-DPB10401  803       FGGFNFSQILPDPSK  FNFSQILPD  3         0.4416
420.8    15.00  0.45     Sequence
 HLA-DPA10103-DPB10401  804       GGFNFSQILPDPSKP  FNFSQILPD  2         0.3404
1257.3    29.00  0.52     Sequence
 HLA-DPA10103-DPB10401  805       GFNFSQILPDPSKPS  FNFSQILPD  1         0.2968
2014.6    37.00  0.40     Sequence
 HLA-DPA10103-DPB10401  806       FNFSQILPDPSKPSK  FNFSQILPD  0         0.1752
7512.5    65.00  0.27     Sequence
 HLA-DPA10103-DPB10401  807       NFSQILPDPSKPSKR  FSQILPDPS  1         0.0888
19136.0    90.00  0.35     Sequence
 HLA-DPA10103-DPB10401  808       FSQILPDPSKPSKRS  FSQILPDPS  0         0.0712
23145.6    95.00  0.25     Sequence
 HLA-DPA10103-DPB10401  809       SQILPDPSKPSKRSF  ILPDPSKPS  2         0.0396
32562.4   100.00  0.34     Sequence
 HLA-DPA10103-DPB10401  810       QILPDPSKPSKRSFI  SKPSKRSFI  6         0.0530
28173.7   100.00  0.28     Sequence
 HLA-DPA10103-DPB10401  811       ILPDPSKPSKRSFIE  SKPSKRSFI  5         0.0551
27536.1   100.00  0.31     Sequence
 HLA-DPA10103-DPB10401  812       LPDPSKPSKRSFIED  SKPSKRSFI  4         0.0583
26606.2   100.00  0.23     Sequence
 HLA-DPA10103-DPB10401  813       PDPSKPSKRSFIEDL  SKRSFIEDL  6         0.1263
12752.3    80.00  0.49     Sequence
 HLA-DPA10103-DPB10401  814       DPSKPSKRSFIEDLL  SKRSFIEDL  5         0.2575
3084.2    45.00  0.29     Sequence
 HLA-DPA10103-DPB10401  815       PSKPSKRSFIEDLLF  FIEDLLFXX  8         0.3249
1487.1    31.00  0.29     Sequence
 HLA-DPA10103-DPB10401  816       SKPSKRSFIEDLLFN  FIEDLLFNX  7         0.4010
652.5    20.00  0.38     Sequence
 HLA-DPA10103-DPB10401  817       KPSKRSFIEDLLFNK  FIEDLLFNK  6         0.5422
141.7     6.50  0.46     Sequence        WB
 HLA-DPA10103-DPB10401  818       PSKRSFIEDLLFNKV  IEDLLFNKV  6         0.6805
31.7     1.40  0.61     Sequence        SB
 HLA-DPA10103-DPB10401  819       SKRSFIEDLLFNKVT  IEDLLFNKV  5         0.6838
30.6     1.30  0.61     Sequence        SB
 HLA-DPA10103-DPB10401  820       KRSFIEDLLFNKVTL  IEDLLFNKV  4         0.6945
27.3     1.10  0.62     Sequence        SB
 HLA-DPA10103-DPB10401  821       RSFIEDLLFNKVTLA  IEDLLFNKV  3         0.6715
35.0     1.50  0.65     Sequence        SB
```

```
 HLA-DPA10103-DPB10401  822      SFIEDLLFNKVTLAD  IEDLLFNKV  2        0.6246
58.1     3.00  0.59     Sequence         WB
 HLA-DPA10103-DPB10401  823      FIEDLLFNKVTLADA  IEDLLFNKV  1        0.5520
127.4     6.00  0.44     Sequence         WB
 HLA-DPA10103-DPB10401  824      IEDLLFNKVTLADAG  LLFNKVTLA  3        0.4057
620.6    19.00  0.34     Sequence
 HLA-DPA10103-DPB10401  825      EDLLFNKVTLADAGF  FNKVTLADA  4        0.3245
1493.5    31.00  0.38     Sequence
 HLA-DPA10103-DPB10401  826      DLLFNKVTLADAGFI  FNKVTLADA  3        0.3448
1199.2    28.00  0.36     Sequence
 HLA-DPA10103-DPB10401  827      LLFNKVTLADAGFIK  LADAGFIKX  7        0.3569
1052.3    26.00  0.31     Sequence
 HLA-DPA10103-DPB10401  828      LFNKVTLADAGFIKQ  LADAGFIKQ  6        0.3569
1051.4    26.00  0.60     Sequence
 HLA-DPA10103-DPB10401  829      FNKVTLADAGFIKQY  LADAGFIKQ  5        0.3505
1126.9    27.00  0.70     Sequence
 HLA-DPA10103-DPB10401  830      NKVTLADAGFIKQYG  LADAGFIKQ  4        0.3357
1322.5    30.00  0.73     Sequence
 HLA-DPA10103-DPB10401  831      KVTLADAGFIKQYGD  LADAGFIKQ  3        0.3433
1219.0    28.00  0.72     Sequence
 HLA-DPA10103-DPB10401  832      VTLADAGFIKQYGDC  LADAGFIKQ  2        0.2739
2582.7    41.00  0.56     Sequence
 HLA-DPA10103-DPB10401  833      TLADAGFIKQYGDCL  FIKQYGDCL  6        0.2353
3921.0    50.00  0.37     Sequence
 HLA-DPA10103-DPB10401  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.2025
5587.4    60.00  0.50     Sequence
 HLA-DPA10103-DPB10401  835      ADAGFIKQYGDCLGD  FIKQYGDCL  4        0.1914
6304.5    65.00  0.50     Sequence
 HLA-DPA10103-DPB10401  836      DAGFIKQYGDCLGDI  QYGDCLGDI  6        0.2462
3485.1    48.00  0.34     Sequence
 HLA-DPA10103-DPB10401  837      AGFIKQYGDCLGDIA  QYGDCLGDI  5        0.2854
2278.7    39.00  0.36     Sequence
 HLA-DPA10103-DPB10401  838      GFIKQYGDCLGDIAA  QYGDCLGDI  4        0.2668
2787.8    43.00  0.37     Sequence
 HLA-DPA10103-DPB10401  839      FIKQYGDCLGDIAAR  QYGDCLGDI  3        0.2566
3112.5    45.00  0.36     Sequence
 HLA-DPA10103-DPB10401  840      IKQYGDCLGDIAARD  CLGDIAARD  6        0.2045
5472.0    60.00  0.30     Sequence
 HLA-DPA10103-DPB10401  841      KQYGDCLGDIAARDL  CLGDIAARD  5        0.1978
5881.5    60.00  0.40     Sequence
 HLA-DPA10103-DPB10401  842      QYGDCLGDIAARDLI  CLGDIAARD  4        0.1883
6516.1    65.00  0.44     Sequence
 HLA-DPA10103-DPB10401  843      YGDCLGDIAARDLIC  CLGDIAARD  3        0.1744
7574.8    70.00  0.48     Sequence
 HLA-DPA10103-DPB10401  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.1447
10444.6    75.00  0.39     Sequence
 HLA-DPA10103-DPB10401  845      DCLGDIAARDLICAQ  CLGDIAARD  1        0.1344
11674.6    80.00  0.28     Sequence
 HLA-DPA10103-DPB10401  846      CLGDIAARDLICAQK  DIAARDLIC  3        0.1209
13520.2    85.00  0.21     Sequence
 HLA-DPA10103-DPB10401  847      LGDIAARDLICAQKF  RDLICAQKF  6        0.1258
12815.0    80.00  0.28     Sequence
 HLA-DPA10103-DPB10401  848      GDIAARDLICAQKFN  RDLICAQKF  5        0.1269
12660.6    80.00  0.26     Sequence
 HLA-DPA10103-DPB10401  849      DIAARDLICAQKFNG  LICAQKFNG  6        0.1329
11872.3    80.00  0.24     Sequence
 HLA-DPA10103-DPB10401  850      IAARDLICAQKFNGL  ICAQKFNGL  6        0.2846
2300.2    39.00  0.51     Sequence
 HLA-DPA10103-DPB10401  851      AARDLICAQKFNGLT  ICAQKFNGL  5        0.3051
1842.7    35.00  0.49     Sequence
 HLA-DPA10103-DPB10401  852      ARDLICAQKFNGLTV  ICAQKFNGL  4        0.3730
884.0    24.00  0.38     Sequence
 HLA-DPA10103-DPB10401  853      RDLICAQKFNGLTVL  ICAQKFNGL  3        0.4516
377.4    14.00  0.26     Sequence
 HLA-DPA10103-DPB10401  854      DLICAQKFNGLTVLP  FNGLTVLPX  7        0.5048
212.3     9.00  0.35     Sequence         WB
```

```
 HLA-DPA10103-DPB10401  855      LICAQKFNGLTVLPP  FNGLTVLPP  6         0.5387
147.0     6.50  0.48     Sequence         WB
 HLA-DPA10103-DPB10401  856      ICAQKFNGLTVLPPL  FNGLTVLPP  5         0.5548
123.6     5.50  0.51     Sequence         WB
 HLA-DPA10103-DPB10401  857      CAQKFNGLTVLPPLL  FNGLTVLPP  4         0.5555
122.7     5.50  0.58     Sequence         WB
 HLA-DPA10103-DPB10401  858      AQKFNGLTVLPPLLT  FNGLTVLPP  3         0.5496
130.8     6.00  0.57     Sequence         WB
 HLA-DPA10103-DPB10401  859      QKFNGLTVLPPLLTD  FNGLTVLPP  2         0.4918
244.4    10.00  0.51     Sequence
 HLA-DPA10103-DPB10401  860      KFNGLTVLPPLLTDE  FNGLTVLPP  1         0.3820
801.4    22.00  0.34     Sequence
 HLA-DPA10103-DPB10401  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3         0.2862
2259.9    39.00  0.28     Sequence
 HLA-DPA10103-DPB10401  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2         0.2258
4343.7    55.00  0.22     Sequence
 HLA-DPA10103-DPB10401  863      GLTVLPPLLTDEMIA  VLPPLLTDE  3         0.2152
4874.3    55.00  0.19     Sequence
 HLA-DPA10103-DPB10401  864      LTVLPPLLTDEMIAQ  LLTDEMIAQ  6         0.2433
3594.2    48.00  0.37     Sequence
 HLA-DPA10103-DPB10401  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5         0.2641
2869.7    44.00  0.39     Sequence
 HLA-DPA10103-DPB10401  866      VLPPLLTDEMIAQYT  LLTDEMIAQ  4         0.2560
3134.0    45.00  0.41     Sequence
 HLA-DPA10103-DPB10401  867      LPPLLTDEMIAQYTS  LLTDEMIAQ  3         0.2479
3420.5    47.00  0.41     Sequence
 HLA-DPA10103-DPB10401  868      PPLLTDEMIAQYTSA  LTDEMIAQY  3         0.2415
3664.6    49.00  0.41     Sequence
 HLA-DPA10103-DPB10401  869      PLLTDEMIAQYTSAL  LTDEMIAQY  2         0.2782
2464.1    40.00  0.29     Sequence
 HLA-DPA10103-DPB10401  870      LLTDEMIAQYTSALL  MIAQYTSAL  5         0.3519
1110.3    27.00  0.25     Sequence
 HLA-DPA10103-DPB10401  871      LTDEMIAQYTSALLA  QYTSALLAX  7         0.4014
649.9    20.00  0.22     Sequence
 HLA-DPA10103-DPB10401  872      TDEMIAQYTSALLAG  YTSALLAGX  7         0.4271
491.9    16.00  0.28     Sequence
 HLA-DPA10103-DPB10401  873      DEMIAQYTSALLAGT  YTSALLAGT  6         0.4597
345.8    13.00  0.43     Sequence
 HLA-DPA10103-DPB10401  874      EMIAQYTSALLAGTI  YTSALLAGT  5         0.4858
260.8    11.00  0.47     Sequence
 HLA-DPA10103-DPB10401  875      MIAQYTSALLAGTIT  YTSALLAGT  4         0.4729
299.7    12.00  0.54     Sequence
 HLA-DPA10103-DPB10401  876      IAQYTSALLAGTITS  YTSALLAGT  3         0.4445
407.9    15.00  0.62     Sequence
 HLA-DPA10103-DPB10401  877      AQYTSALLAGTITSG  YTSALLAGT  2         0.3568
1053.1    26.00  0.60     Sequence
 HLA-DPA10103-DPB10401  878      QYTSALLAGTITSGW  YTSALLAGT  1         0.2446
3545.8    48.00  0.34     Sequence
 HLA-DPA10103-DPB10401  879      YTSALLAGTITSGWT  LAGTITSGW  5         0.1838
6841.8    65.00  0.31     Sequence
 HLA-DPA10103-DPB10401  880      TSALLAGTITSGWTF  LAGTITSGW  4         0.1995
5776.7    60.00  0.30     Sequence
 HLA-DPA10103-DPB10401  881      SALLAGTITSGWTFG  LAGTITSGW  3         0.1910
6328.3    65.00  0.33     Sequence
 HLA-DPA10103-DPB10401  882      ALLAGTITSGWTFGA  LAGTITSGW  2         0.1940
6127.1    60.00  0.29     Sequence
 HLA-DPA10103-DPB10401  883      LLAGTITSGWTFGAG  TITSGWTFG  4         0.1697
7970.1    70.00  0.25     Sequence
 HLA-DPA10103-DPB10401  884      LAGTITSGWTFGAGA  TITSGWTFG  3         0.1654
8355.3    70.00  0.25     Sequence
 HLA-DPA10103-DPB10401  885      AGTITSGWTFGAGAA  TITSGWTFG  2         0.1482
10064.0    75.00  0.22     Sequence
 HLA-DPA10103-DPB10401  886      GTITSGWTFGAGAAL  WTFGAGAAL  6         0.1790
7210.5    65.00  0.20     Sequence
 HLA-DPA10103-DPB10401  887      TITSGWTFGAGAALQ  WTFGAGAAL  5         0.1974
5909.3    60.00  0.27     Sequence
```

```
 HLA-DPA10103-DPB10401  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.2698
2700.0    42.00  0.44     Sequence
 HLA-DPA10103-DPB10401  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.2908
2149.6    38.00  0.38     Sequence
 HLA-DPA10103-DPB10401  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.3070
1805.4    35.00  0.39     Sequence
 HLA-DPA10103-DPB10401  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.3107
1733.2    34.00  0.34     Sequence
 HLA-DPA10103-DPB10401  892      WTFGAGAALQIPFAM  GAGAALQIP  3        0.3136
1679.9    34.00  0.32     Sequence
 HLA-DPA10103-DPB10401  893      TFGAGAALQIPFAMQ  ALQIPFAMQ  6        0.2923
2116.8    38.00  0.25     Sequence
 HLA-DPA10103-DPB10401  894      FGAGAALQIPFAMQM  LQIPFAMQM  6        0.2949
2056.0    37.00  0.31     Sequence
 HLA-DPA10103-DPB10401  895      GAGAALQIPFAMQMA  LQIPFAMQM  5        0.3246
1492.5    31.00  0.33     Sequence
 HLA-DPA10103-DPB10401  896      AGAALQIPFAMQMAY  LQIPFAMQM  4        0.3398
1265.0    29.00  0.29     Sequence
 HLA-DPA10103-DPB10401  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.3470
1170.6    28.00  0.28     Sequence
 HLA-DPA10103-DPB10401  898      AALQIPFAMQMAYRF  FAMQMAYRF  6        0.4363
445.5    15.00  0.41     Sequence
 HLA-DPA10103-DPB10401  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.4511
379.6    14.00  0.44     Sequence
 HLA-DPA10103-DPB10401  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.4332
460.7    16.00  0.49     Sequence
 HLA-DPA10103-DPB10401  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.4627
334.9    13.00  0.37     Sequence
 HLA-DPA10103-DPB10401  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.4276
489.6    16.00  0.36     Sequence
 HLA-DPA10103-DPB10401  903      PFAMQMAYRFNGIGV  QMAYRFNGI  4        0.4183
541.3    17.00  0.33     Sequence
 HLA-DPA10103-DPB10401  904      FAMQMAYRFNGIGVT  QMAYRFNGI  3        0.4099
592.4    18.00  0.33     Sequence
 HLA-DPA10103-DPB10401  905      AMQMAYRFNGIGVTQ  YRFNGIGVT  5        0.3470
1170.1    28.00  0.32     Sequence
 HLA-DPA10103-DPB10401  906      MQMAYRFNGIGVTQN  YRFNGIGVT  4        0.3276
1443.3    31.00  0.35     Sequence
 HLA-DPA10103-DPB10401  907      QMAYRFNGIGVTQNV  YRFNGIGVT  3        0.3092
1763.1    34.00  0.38     Sequence
 HLA-DPA10103-DPB10401  908      MAYRFNGIGVTQNVL  YRFNGIGVT  2        0.2808
2395.7    40.00  0.35     Sequence
 HLA-DPA10103-DPB10401  909      AYRFNGIGVTQNVLY  FNGIGVTQN  3        0.2809
2392.3    40.00  0.37     Sequence
 HLA-DPA10103-DPB10401  910      YRFNGIGVTQNVLYE  FNGIGVTQN  2        0.2485
3398.2    47.00  0.25     Sequence
 HLA-DPA10103-DPB10401  911      RFNGIGVTQNVLYEN  GIGVTQNVL  3        0.2410
3684.8    49.00  0.16     Sequence
 HLA-DPA10103-DPB10401  912      FNGIGVTQNVLYENQ  TQNVLYENQ  6        0.2286
4214.6    55.00  0.31     Sequence
 HLA-DPA10103-DPB10401  913      NGIGVTQNVLYENQK  TQNVLYENQ  5        0.2219
4530.2    55.00  0.34     Sequence
 HLA-DPA10103-DPB10401  914      GIGVTQNVLYENQKL  TQNVLYENQ  4        0.2400
3724.8    49.00  0.32     Sequence
 HLA-DPA10103-DPB10401  915      IGVTQNVLYENQKLI  TQNVLYENQ  3        0.2758
2529.9    41.00  0.26     Sequence
 HLA-DPA10103-DPB10401  916      GVTQNVLYENQKLIA  LYENQKLIA  6        0.3152
1650.9    33.00  0.32     Sequence
 HLA-DPA10103-DPB10401  917      VTQNVLYENQKLIAN  LYENQKLIA  5        0.3085
1776.0    34.00  0.35     Sequence
 HLA-DPA10103-DPB10401  918      TQNVLYENQKLIANQ  LYENQKLIA  4        0.3004
1938.5    36.00  0.40     Sequence
 HLA-DPA10103-DPB10401  919      QNVLYENQKLIANQF  LYENQKLIA  3        0.3228
1520.5    32.00  0.36     Sequence
 HLA-DPA10103-DPB10401  920      NVLYENQKLIANQFN  LYENQKLIA  2        0.3335
1355.3    30.00  0.31     Sequence
```

```
 HLA-DPA10103-DPB10401  921      VLYENQKLIANQFNS  LIANQFNSX  7        0.3868
760.8    22.00  0.46     Sequence
 HLA-DPA10103-DPB10401  922      LYENQKLIANQFNSA  LIANQFNSA  6        0.5360
151.5     6.50  0.85     Sequence         WB
 HLA-DPA10103-DPB10401  923      YENQKLIANQFNSAI  LIANQFNSA  5        0.5658
109.8     5.00  0.87     Sequence         WB
 HLA-DPA10103-DPB10401  924      ENQKLIANQFNSAIG  LIANQFNSA  4        0.5577
119.7     5.50  0.85     Sequence         WB
 HLA-DPA10103-DPB10401  925      NQKLIANQFNSAIGK  LIANQFNSA  3        0.5610
115.6     5.50  0.88     Sequence         WB
 HLA-DPA10103-DPB10401  926      QKLIANQFNSAIGKI  LIANQFNSA  2        0.5040
214.2     9.00  0.68     Sequence         WB
 HLA-DPA10103-DPB10401  927      KLIANQFNSAIGKIQ  LIANQFNSA  1        0.3995
663.3    20.00  0.46     Sequence
 HLA-DPA10103-DPB10401  928      LIANQFNSAIGKIQD  FNSAIGKIQ  5        0.2991
1966.4    36.00  0.44     Sequence
 HLA-DPA10103-DPB10401  929      IANQFNSAIGKIQDS  FNSAIGKIQ  4        0.2070
5326.6    60.00  0.57     Sequence
 HLA-DPA10103-DPB10401  930      ANQFNSAIGKIQDSL  FNSAIGKIQ  3        0.1944
6105.4    60.00  0.63     Sequence
 HLA-DPA10103-DPB10401  931      NQFNSAIGKIQDSLS  FNSAIGKIQ  2        0.1746
7562.5    70.00  0.55     Sequence
 HLA-DPA10103-DPB10401  932      QFNSAIGKIQDSLSS  FNSAIGKIQ  1        0.1112
15005.2    85.00  0.34     Sequence
 HLA-DPA10103-DPB10401  933      FNSAIGKIQDSLSST  AIGKIQDSL  3        0.0937
18133.2    90.00  0.17     Sequence
 HLA-DPA10103-DPB10401  934      NSAIGKIQDSLSSTA  IQDSLSSTA  6        0.0986
17207.9    90.00  0.44     Sequence
 HLA-DPA10103-DPB10401  935      SAIGKIQDSLSSTAS  IQDSLSSTA  5        0.1021
16558.0    90.00  0.48     Sequence
 HLA-DPA10103-DPB10401  936      AIGKIQDSLSSTASA  IQDSLSSTA  4        0.1036
16294.8    85.00  0.47     Sequence
 HLA-DPA10103-DPB10401  937      IGKIQDSLSSTASAL  IQDSLSSTA  3        0.1403
10961.4    75.00  0.26     Sequence
 HLA-DPA10103-DPB10401  938      GKIQDSLSSTASALG  LSSTASALG  6        0.1408
10899.1    75.00  0.33     Sequence
 HLA-DPA10103-DPB10401  939      KIQDSLSSTASALGK  LSSTASALG  5        0.1425
10698.3    75.00  0.41     Sequence
 HLA-DPA10103-DPB10401  940      IQDSLSSTASALGKL  LSSTASALG  4        0.1534
9505.9    75.00  0.42     Sequence
 HLA-DPA10103-DPB10401  941      QDSLSSTASALGKLQ  LSSTASALG  3        0.1590
8954.8    70.00  0.41     Sequence
 HLA-DPA10103-DPB10401  942      DSLSSTASALGKLQD  LSSTASALG  2        0.1414
10833.5    75.00  0.38     Sequence
 HLA-DPA10103-DPB10401  943      SLSSTASALGKLQDV  STASALGKL  3        0.1268
12680.8    80.00  0.31     Sequence
 HLA-DPA10103-DPB10401  944      LSSTASALGKLQDVV  SALGKLQDV  5        0.1187
13837.3    85.00  0.29     Sequence
 HLA-DPA10103-DPB10401  945      SSTASALGKLQDVVN  SALGKLQDV  4        0.1047
16099.0    85.00  0.31     Sequence
 HLA-DPA10103-DPB10401  946      STASALGKLQDVVNQ  SALGKLQDV  3        0.0995
17043.1    90.00  0.34     Sequence
 HLA-DPA10103-DPB10401  947      TASALGKLQDVVNQN  SALGKLQDV  2        0.0944
17999.9    90.00  0.28     Sequence
 HLA-DPA10103-DPB10401  948      ASALGKLQDVVNQNA  LQDVVNQNA  6        0.0997
17003.5    90.00  0.29     Sequence
 HLA-DPA10103-DPB10401  949      SALGKLQDVVNQNAQ  LQDVVNQNA  5        0.0923
18426.1    90.00  0.38     Sequence
 HLA-DPA10103-DPB10401  950      ALGKLQDVVNQNAQA  LQDVVNQNA  4        0.0849
19964.5    95.00  0.47     Sequence
 HLA-DPA10103-DPB10401  951      LGKLQDVVNQNAQAL  LQDVVNQNA  3        0.0943
18020.3    90.00  0.35     Sequence
 HLA-DPA10103-DPB10401  952      GKLQDVVNQNAQALN  VVNQNAQAL  5        0.0973
17455.9    90.00  0.35     Sequence
 HLA-DPA10103-DPB10401  953      KLQDVVNQNAQALNT  VVNQNAQAL  4        0.0925
18369.8    90.00  0.34     Sequence
```

```
 HLA-DPA10103-DPB10401  954      LQDVVNQNAQALNTL  VVNQNAQAL  3        0.1072
15677.7    85.00  0.23     Sequence
 HLA-DPA10103-DPB10401  955      QDVVNQNAQALNTLV  QNAQALNTL  5        0.1165
14180.3    85.00  0.28     Sequence
 HLA-DPA10103-DPB10401  956      DVVNQNAQALNTLVK  QNAQALNTL  4        0.1179
13966.1    85.00  0.26     Sequence
 HLA-DPA10103-DPB10401  957      VVNQNAQALNTLVKQ  QALNTLVKQ  6        0.1240
13065.3    80.00  0.17     Sequence
 HLA-DPA10103-DPB10401  958      VNQNAQALNTLVKQL  ALNTLVKQL  6        0.1916
6291.8    65.00  0.34     Sequence
 HLA-DPA10103-DPB10401  959      NQNAQALNTLVKQLS  ALNTLVKQL  5        0.1980
5866.8    60.00  0.29     Sequence
 HLA-DPA10103-DPB10401  960      QNAQALNTLVKQLSS  ALNTLVKQL  4        0.1956
6025.2    60.00  0.29     Sequence
 HLA-DPA10103-DPB10401  961      NAQALNTLVKQLSSN  ALNTLVKQL  3        0.1876
6568.0    65.00  0.29     Sequence
 HLA-DPA10103-DPB10401  962      AQALNTLVKQLSSNF  LVKQLSSNF  6        0.2155
4855.9    55.00  0.27     Sequence
 HLA-DPA10103-DPB10401  963      QALNTLVKQLSSNFG  LVKQLSSNF  5        0.2005
5712.6    60.00  0.30     Sequence
 HLA-DPA10103-DPB10401  964      ALNTLVKQLSSNFGA  LVKQLSSNF  4        0.2060
5383.7    60.00  0.31     Sequence
 HLA-DPA10103-DPB10401  965      LNTLVKQLSSNFGAI  QLSSNFGAI  6        0.4276
489.3    16.00  0.56     Sequence
 HLA-DPA10103-DPB10401  966      NTLVKQLSSNFGAIS  QLSSNFGAI  5        0.4772
286.2    11.00  0.54     Sequence
 HLA-DPA10103-DPB10401  967      TLVKQLSSNFGAISS  QLSSNFGAI  4        0.4737
297.2    12.00  0.54     Sequence
 HLA-DPA10103-DPB10401  968      LVKQLSSNFGAISSV  QLSSNFGAI  3        0.4828
269.3    11.00  0.51     Sequence
 HLA-DPA10103-DPB10401  969      VKQLSSNFGAISSVL  QLSSNFGAI  2        0.4747
294.0    12.00  0.39     Sequence
 HLA-DPA10103-DPB10401  970      KQLSSNFGAISSVLN  LSSNFGAIS  2        0.4349
452.4    16.00  0.35     Sequence
 HLA-DPA10103-DPB10401  971      QLSSNFGAISSVLND  LSSNFGAIS  1        0.3472
1168.1    28.00  0.26     Sequence
 HLA-DPA10103-DPB10401  972      LSSNFGAISSVLNDI  AISSVLNDI  6        0.3084
1778.3    34.00  0.37     Sequence
 HLA-DPA10103-DPB10401  973      SSNFGAISSVLNDIL  AISSVLNDI  5        0.3381
1289.2    29.00  0.37     Sequence
 HLA-DPA10103-DPB10401  974      SNFGAISSVLNDILS  AISSVLNDI  4        0.3292
1418.8    31.00  0.35     Sequence
 HLA-DPA10103-DPB10401  975      NFGAISSVLNDILSR  AISSVLNDI  3        0.3217
1538.7    32.00  0.35     Sequence
 HLA-DPA10103-DPB10401  976      FGAISSVLNDILSRL  VLNDILSRL  6        0.3902
733.2    21.00  0.28     Sequence
 HLA-DPA10103-DPB10401  977      GAISSVLNDILSRLD  VLNDILSRL  5        0.3563
1059.1    26.00  0.31     Sequence
 HLA-DPA10103-DPB10401  978      AISSVLNDILSRLDK  VLNDILSRL  4        0.3465
1176.6    28.00  0.31     Sequence
 HLA-DPA10103-DPB10401  979      ISSVLNDILSRLDKV  DILSRLDKV  6        0.3538
1087.5    27.00  0.34     Sequence
 HLA-DPA10103-DPB10401  980      SSVLNDILSRLDKVE  DILSRLDKV  5        0.3274
1447.0    31.00  0.37     Sequence
 HLA-DPA10103-DPB10401  981      SVLNDILSRLDKVEA  DILSRLDKV  4        0.3091
1764.1    34.00  0.40     Sequence
 HLA-DPA10103-DPB10401  982      VLNDILSRLDKVEAE  DILSRLDKV  3        0.2650
2841.8    43.00  0.44     Sequence
 HLA-DPA10103-DPB10401  983      LNDILSRLDKVEAEV  DILSRLDKV  2        0.1648
8402.7    70.00  0.40     Sequence
 HLA-DPA10103-DPB10401  984      NDILSRLDKVEAEVQ  DILSRLDKV  1        0.1356
11524.8    80.00  0.27     Sequence
 HLA-DPA10103-DPB10401  985      DILSRLDKVEAEVQI  LDKVEAEVQ  5        0.1293
12342.6    80.00  0.15     Sequence
 HLA-DPA10103-DPB10401  986      ILSRLDKVEAEVQID  LDKVEAEVQ  4        0.1209
13522.2    85.00  0.19     Sequence
```

```
 HLA-DPA10103-DPB10401  987      LSRLDKVEAEVQIDR  VEAEVQIDR  6        0.1160
14250.3    85.00  0.22      Sequence
 HLA-DPA10103-DPB10401  988      SRLDKVEAEVQIDRL  EAEVQIDRL  6        0.1367
11388.6    80.00  0.29      Sequence
 HLA-DPA10103-DPB10401  989      RLDKVEAEVQIDRLI  EAEVQIDRL  5        0.1644
8444.1    70.00  0.27      Sequence
 HLA-DPA10103-DPB10401  990      LDKVEAEVQIDRLIT  EVQIDRLIT  6        0.2011
5675.2    60.00  0.22      Sequence
 HLA-DPA10103-DPB10401  991      DKVEAEVQIDRLITG  VQIDRLITG  6        0.2047
5457.8    60.00  0.32      Sequence
 HLA-DPA10103-DPB10401  992      KVEAEVQIDRLITGR  VQIDRLITG  5        0.2105
5129.3    60.00  0.37      Sequence
 HLA-DPA10103-DPB10401  993      VEAEVQIDRLITGRL  VQIDRLITG  4        0.2431
3602.4    48.00  0.33      Sequence
 HLA-DPA10103-DPB10401  994      EAEVQIDRLITGRLQ  VQIDRLITG  3        0.2480
3417.6    47.00  0.33      Sequence
 HLA-DPA10103-DPB10401  995      AEVQIDRLITGRLQS  VQIDRLITG  2        0.2581
3061.9    45.00  0.29      Sequence
 HLA-DPA10103-DPB10401  996      EVQIDRLITGRLQSL  LITGRLQSL  6        0.3847
778.3    22.00  0.65      Sequence
 HLA-DPA10103-DPB10401  997      VQIDRLITGRLQSLQ  LITGRLQSL  5        0.3894
740.2    21.00  0.69      Sequence
 HLA-DPA10103-DPB10401  998      QIDRLITGRLQSLQT  LITGRLQSL  4        0.3806
814.1    22.00  0.69      Sequence
 HLA-DPA10103-DPB10401  999      IDRLITGRLQSLQTY  LITGRLQSL  3        0.3802
817.5    23.00  0.69      Sequence
 HLA-DPA10103-DPB10401 1000      DRLITGRLQSLQTYV  LITGRLQSL  2        0.3691
921.3    24.00  0.54      Sequence
 HLA-DPA10103-DPB10401 1001      RLITGRLQSLQTYVT  LITGRLQSL  1        0.3673
940.0    24.00  0.31      Sequence
 HLA-DPA10103-DPB10401 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.3226
1523.6    32.00  0.35      Sequence
 HLA-DPA10103-DPB10401 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.2980
1989.1    36.00  0.41      Sequence
 HLA-DPA10103-DPB10401 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.3748
866.6    23.00  0.35      Sequence
 HLA-DPA10103-DPB10401 1005      GRLQSLQTYVTQQLI  LQTYVTQQL  5        0.4225
517.3    17.00  0.24      Sequence
 HLA-DPA10103-DPB10401 1006      RLQSLQTYVTQQLIR  YVTQQLIRX  7        0.4579
352.4    13.00  0.38      Sequence
 HLA-DPA10103-DPB10401 1007      LQSLQTYVTQQLIRA  YVTQQLIRA  6        0.4757
291.0    12.00  0.56      Sequence
 HLA-DPA10103-DPB10401 1008      QSLQTYVTQQLIRAA  YVTQQLIRA  5        0.4710
306.2    12.00  0.62      Sequence
 HLA-DPA10103-DPB10401 1009      SLQTYVTQQLIRAAE  YVTQQLIRA  4        0.4553
362.8    13.00  0.67      Sequence
 HLA-DPA10103-DPB10401 1010      LQTYVTQQLIRAAEI  YVTQQLIRA  3        0.4558
360.8    13.00  0.64      Sequence
 HLA-DPA10103-DPB10401 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.3723
890.4    24.00  0.51      Sequence
 HLA-DPA10103-DPB10401 1012      TYVTQQLIRAAEIRA  YVTQQLIRA  1        0.3044
1855.5    35.00  0.28      Sequence
 HLA-DPA10103-DPB10401 1013      YVTQQLIRAAEIRAS  IRAAEIRAS  6        0.2729
2609.5    42.00  0.37      Sequence
 HLA-DPA10103-DPB10401 1014      VTQQLIRAAEIRASA  IRAAEIRAS  5        0.2557
3145.4    45.00  0.44      Sequence
 HLA-DPA10103-DPB10401 1015      TQQLIRAAEIRASAN  IRAAEIRAS  4        0.2518
3277.7    46.00  0.41      Sequence
 HLA-DPA10103-DPB10401 1016      QQLIRAAEIRASANL  IRAAEIRAS  3        0.2470
3454.4    47.00  0.42      Sequence
 HLA-DPA10103-DPB10401 1017      QLIRAAEIRASANLA  IRAAEIRAS  2        0.1913
6313.8    65.00  0.27      Sequence
 HLA-DPA10103-DPB10401 1018      LIRAAEIRASANLAA  IRASANLAA  6        0.1957
6019.2    60.00  0.47      Sequence
 HLA-DPA10103-DPB10401 1019      IRAAEIRASANLAAI  RASANLAAI  6        0.2631
2901.7    44.00  0.48      Sequence
```

```
 HLA-DPA10103-DPB10401 1020      RAAEIRASANLAAIK  RASANLAAI  5        0.2723
2627.9    42.00  0.50     Sequence
 HLA-DPA10103-DPB10401 1021      AAEIRASANLAAIKM  RASANLAAI  4        0.2685
2736.5    43.00  0.47     Sequence
 HLA-DPA10103-DPB10401 1022      AEIRASANLAAIKMS  RASANLAAI  3        0.2648
2847.8    43.00  0.47     Sequence
 HLA-DPA10103-DPB10401 1023      EIRASANLAAIKMSE  RASANLAAI  2        0.2122
5033.0    60.00  0.40     Sequence
 HLA-DPA10103-DPB10401 1024      IRASANLAAIKMSEC  LAAIKMSEC  6        0.2072
5310.6    60.00  0.50     Sequence
 HLA-DPA10103-DPB10401 1025      RASANLAAIKMSECV  LAAIKMSEC  5        0.2229
4480.8    55.00  0.63     Sequence
 HLA-DPA10103-DPB10401 1026      ASANLAAIKMSECVL  LAAIKMSEC  4        0.2532
3229.9    46.00  0.57     Sequence
 HLA-DPA10103-DPB10401 1027      SANLAAIKMSECVLG  LAAIKMSEC  3        0.2691
2720.8    42.00  0.50     Sequence
 HLA-DPA10103-DPB10401 1028      ANLAAIKMSECVLGQ  LAAIKMSEC  2        0.2746
2562.3    41.00  0.37     Sequence
 HLA-DPA10103-DPB10401 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.2637
2884.5    44.00  0.22     Sequence
 HLA-DPA10103-DPB10401 1030      LAAIKMSECVLGQSK  KMSECVLGQ  4        0.2437
3579.7    48.00  0.28     Sequence
 HLA-DPA10103-DPB10401 1031      AAIKMSECVLGQSKR  KMSECVLGQ  3        0.2193
4659.5    55.00  0.32     Sequence
 HLA-DPA10103-DPB10401 1032      AIKMSECVLGQSKRV  KMSECVLGQ  2        0.2228
4489.1    55.00  0.28     Sequence
 HLA-DPA10103-DPB10401 1033      IKMSECVLGQSKRVD  CVLGQSKRV  5        0.1778
7300.3    65.00  0.26     Sequence
 HLA-DPA10103-DPB10401 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.1710
7862.6    70.00  0.32     Sequence
 HLA-DPA10103-DPB10401 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.1562
9222.8    75.00  0.42     Sequence
 HLA-DPA10103-DPB10401 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.1401
10983.2    75.00  0.34     Sequence
 HLA-DPA10103-DPB10401 1037      ECVLGQSKRVDFCGK  LGQSKRVDF  3        0.1291
12363.3    80.00  0.32     Sequence
 HLA-DPA10103-DPB10401 1038      CVLGQSKRVDFCGKG  LGQSKRVDF  2        0.1000
16952.5    90.00  0.34     Sequence
 HLA-DPA10103-DPB10401 1039      VLGQSKRVDFCGKGY  RVDFCGKGY  6        0.0954
17820.3    90.00  0.13     Sequence
 HLA-DPA10103-DPB10401 1040      LGQSKRVDFCGKGYH  KRVDFCGKG  4        0.1062
15849.0    85.00  0.16     Sequence
 HLA-DPA10103-DPB10401 1041      GQSKRVDFCGKGYHL  FCGKGYHLX  7        0.1419
10771.0    75.00  0.29     Sequence
 HLA-DPA10103-DPB10401 1042      QSKRVDFCGKGYHLM  FCGKGYHLM  6        0.2626
2919.0    44.00  0.47     Sequence
 HLA-DPA10103-DPB10401 1043      SKRVDFCGKGYHLMS  FCGKGYHLM  5        0.2892
2187.4    38.00  0.43     Sequence
 HLA-DPA10103-DPB10401 1044      KRVDFCGKGYHLMSF  FCGKGYHLM  4        0.3675
937.7    24.00  0.29     Sequence
 HLA-DPA10103-DPB10401 1045      RVDFCGKGYHLMSFP  FCGKGYHLM  3        0.3961
687.9    20.00  0.25     Sequence
 HLA-DPA10103-DPB10401 1046      VDFCGKGYHLMSFPQ  GKGYHLMSF  4        0.3994
663.7    20.00  0.23     Sequence
 HLA-DPA10103-DPB10401 1047      DFCGKGYHLMSFPQS  YHLMSFPQS  6        0.4136
569.5    18.00  0.41     Sequence
 HLA-DPA10103-DPB10401 1048      FCGKGYHLMSFPQSA  YHLMSFPQS  5        0.4121
578.6    18.00  0.44     Sequence
 HLA-DPA10103-DPB10401 1049      CGKGYHLMSFPQSAP  YHLMSFPQS  4        0.4089
599.0    19.00  0.47     Sequence
 HLA-DPA10103-DPB10401 1050      GKGYHLMSFPQSAPH  YHLMSFPQS  3        0.4018
647.1    20.00  0.47     Sequence
 HLA-DPA10103-DPB10401 1051      KGYHLMSFPQSAPHG  YHLMSFPQS  2        0.3729
884.1    24.00  0.41     Sequence
 HLA-DPA10103-DPB10401 1052      GYHLMSFPQSAPHGV  LMSFPQSAP  3        0.3100
1746.4    34.00  0.34     Sequence
```

```
 HLA-DPA10103-DPB10401 1053      YHLMSFPQSAPHGVV  LMSFPQSAP  2        0.2484
3403.3    47.00  0.32     Sequence
 HLA-DPA10103-DPB10401 1054      HLMSFPQSAPHGVVF  LMSFPQSAP  1        0.1976
5893.3    60.00  0.24     Sequence
 HLA-DPA10103-DPB10401 1055      LMSFPQSAPHGVVFL  PHGVVFLXX  8        0.2040
5500.9    60.00  0.21     Sequence
 HLA-DPA10103-DPB10401 1056      MSFPQSAPHGVVFLH  PHGVVFLHX  7        0.1810
7057.6    65.00  0.36     Sequence
 HLA-DPA10103-DPB10401 1057      SFPQSAPHGVVFLHV  PHGVVFLHV  6        0.3503
1129.7    27.00  0.69     Sequence
 HLA-DPA10103-DPB10401 1058      FPQSAPHGVVFLHVT  PHGVVFLHV  5        0.3877
753.4    21.00  0.67     Sequence
 HLA-DPA10103-DPB10401 1059      PQSAPHGVVFLHVTY  PHGVVFLHV  4        0.3964
686.2    20.00  0.63     Sequence
 HLA-DPA10103-DPB10401 1060      QSAPHGVVFLHVTYV  PHGVVFLHV  3        0.4065
614.9    19.00  0.57     Sequence
 HLA-DPA10103-DPB10401 1061      SAPHGVVFLHVTYVP  PHGVVFLHV  2        0.4224
517.6    17.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1062      APHGVVFLHVTYVPA  FLHVTYVPA  6        0.4357
448.3    15.00  0.35     Sequence
 HLA-DPA10103-DPB10401 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.4304
474.9    16.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.4121
578.6    18.00  0.44     Sequence
 HLA-DPA10103-DPB10401 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.4156
557.2    18.00  0.48     Sequence
 HLA-DPA10103-DPB10401 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.3871
758.3    22.00  0.43     Sequence
 HLA-DPA10103-DPB10401 1067      VFLHVTYVPAQEKNF  FLHVTYVPA  1        0.3487
1149.5    27.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1068      FLHVTYVPAQEKNFT  VTYVPAQEK  3        0.2575
3083.8    45.00  0.26     Sequence
 HLA-DPA10103-DPB10401 1069      LHVTYVPAQEKNFTT  YVPAQEKNF  4        0.1471
10177.7    75.00  0.23     Sequence
 HLA-DPA10103-DPB10401 1070      HVTYVPAQEKNFTTA  YVPAQEKNF  3        0.1206
13556.6    85.00  0.30     Sequence
 HLA-DPA10103-DPB10401 1071      VTYVPAQEKNFTTAP  AQEKNFTTA  5        0.1292
12350.2    80.00  0.35     Sequence
 HLA-DPA10103-DPB10401 1072      TYVPAQEKNFTTAPA  AQEKNFTTA  4        0.1247
12974.9    80.00  0.37     Sequence
 HLA-DPA10103-DPB10401 1073      YVPAQEKNFTTAPAI  AQEKNFTTA  3        0.1524
9611.4    75.00  0.31     Sequence
 HLA-DPA10103-DPB10401 1074      VPAQEKNFTTAPAIC  FTTAPAICX  7        0.1840
6832.1    65.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1075      PAQEKNFTTAPAICH  FTTAPAICH  6        0.2177
4740.5    55.00  0.52     Sequence
 HLA-DPA10103-DPB10401 1076      AQEKNFTTAPAICHD  FTTAPAICH  5        0.2149
4890.4    55.00  0.56     Sequence
 HLA-DPA10103-DPB10401 1077      QEKNFTTAPAICHDG  FTTAPAICH  4        0.2090
5208.1    60.00  0.57     Sequence
 HLA-DPA10103-DPB10401 1078      EKNFTTAPAICHDGK  FTTAPAICH  3        0.2002
5731.3    60.00  0.64     Sequence
 HLA-DPA10103-DPB10401 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.1734
7657.1    70.00  0.57     Sequence
 HLA-DPA10103-DPB10401 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.0869
19520.0    90.00  0.41     Sequence
 HLA-DPA10103-DPB10401 1081      FTTAPAICHDGKAHF  FTTAPAICH  0        0.0788
21320.1    95.00  0.25     Sequence
 HLA-DPA10103-DPB10401 1082      TTAPAICHDGKAHFP  DGKAHFPXX  8        0.0857
19780.2    90.00  0.23     Sequence
 HLA-DPA10103-DPB10401 1083      TAPAICHDGKAHFPR  DGKAHFPRX  7        0.0960
17692.3    90.00  0.31     Sequence
 HLA-DPA10103-DPB10401 1084      APAICHDGKAHFPRE  DGKAHFPRE  6        0.1144
14494.9    85.00  0.52     Sequence
 HLA-DPA10103-DPB10401 1085      PAICHDGKAHFPREG  DGKAHFPRE  5        0.1126
14794.2    85.00  0.49     Sequence
```

```
 HLA-DPA10103-DPB10401 1086      AICHDGKAHFPREGV  DGKAHFPRE  4         0.1223
13319.1    80.00  0.45      Sequence
 HLA-DPA10103-DPB10401 1087      ICHDGKAHFPREGVF  DGKAHFPRE  3         0.1349
11615.8    80.00  0.41      Sequence
 HLA-DPA10103-DPB10401 1088      CHDGKAHFPREGVFV  DGKAHFPRE  2         0.1471
10174.8    75.00  0.21      Sequence
 HLA-DPA10103-DPB10401 1089      HDGKAHFPREGVFVS  PREGVFVSX  7         0.1533
9516.4    75.00  0.22      Sequence
 HLA-DPA10103-DPB10401 1090      DGKAHFPREGVFVSN  PREGVFVSN  6         0.1657
8320.7    70.00  0.32      Sequence
 HLA-DPA10103-DPB10401 1091      GKAHFPREGVFVSNG  PREGVFVSN  5         0.1780
7286.5    65.00  0.29      Sequence
 HLA-DPA10103-DPB10401 1092      KAHFPREGVFVSNGT  PREGVFVSN  4         0.1788
7225.2    65.00  0.29      Sequence
 HLA-DPA10103-DPB10401 1093      AHFPREGVFVSNGTH  PREGVFVSN  3         0.1662
8280.8    70.00  0.28      Sequence
 HLA-DPA10103-DPB10401 1094      HFPREGVFVSNGTHW  REGVFVSNG  3         0.1875
6571.7    65.00  0.23      Sequence
 HLA-DPA10103-DPB10401 1095      FPREGVFVSNGTHWF  FVSNGTHWF  6         0.2593
3023.5    45.00  0.28      Sequence
 HLA-DPA10103-DPB10401 1096      PREGVFVSNGTHWFV  FVSNGTHWF  5         0.3081
1783.7    35.00  0.29      Sequence
 HLA-DPA10103-DPB10401 1097      REGVFVSNGTHWFVT  SNGTHWFVT  6         0.3254
1478.4    31.00  0.34      Sequence
 HLA-DPA10103-DPB10401 1098      EGVFVSNGTHWFVTQ  SNGTHWFVT  5         0.3458
1185.5    28.00  0.37      Sequence
 HLA-DPA10103-DPB10401 1099      GVFVSNGTHWFVTQR  SNGTHWFVT  4         0.3646
968.0    25.00  0.37      Sequence
 HLA-DPA10103-DPB10401 1100      VFVSNGTHWFVTQRN  SNGTHWFVT  3         0.3539
1086.5    27.00  0.41      Sequence
 HLA-DPA10103-DPB10401 1101      FVSNGTHWFVTQRNF  SNGTHWFVT  2         0.3113
1722.0    34.00  0.34      Sequence
 HLA-DPA10103-DPB10401 1102      VSNGTHWFVTQRNFY  FVTQRNFYX  7         0.3114
1720.7    34.00  0.22      Sequence
 HLA-DPA10103-DPB10401 1103      SNGTHWFVTQRNFYE  FVTQRNFYE  6         0.3411
1248.2    29.00  0.34      Sequence
 HLA-DPA10103-DPB10401 1104      NGTHWFVTQRNFYEP  FVTQRNFYE  5         0.3716
897.2    24.00  0.31      Sequence
 HLA-DPA10103-DPB10401 1105      GTHWFVTQRNFYEPQ  FVTQRNFYE  4         0.3804
815.4    22.00  0.31      Sequence
 HLA-DPA10103-DPB10401 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3         0.3986
670.2    20.00  0.34      Sequence
 HLA-DPA10103-DPB10401 1107      HWFVTQRNFYEPQII  FVTQRNFYE  2         0.3979
674.9    20.00  0.27      Sequence
 HLA-DPA10103-DPB10401 1108      WFVTQRNFYEPQIIT  VTQRNFYEP  2         0.3740
873.8    23.00  0.19      Sequence
 HLA-DPA10103-DPB10401 1109      FVTQRNFYEPQIITT  FYEPQIITT  6         0.3417
1240.3    28.00  0.34      Sequence
 HLA-DPA10103-DPB10401 1110      VTQRNFYEPQIITTD  FYEPQIITT  5         0.2887
2199.7    38.00  0.44      Sequence
 HLA-DPA10103-DPB10401 1111      TQRNFYEPQIITTDN  FYEPQIITT  4         0.2763
2516.4    41.00  0.47      Sequence
 HLA-DPA10103-DPB10401 1112      QRNFYEPQIITTDNT  FYEPQIITT  3         0.2705
2678.6    42.00  0.48      Sequence
 HLA-DPA10103-DPB10401 1113      RNFYEPQIITTDNTF  YEPQIITTD  3         0.2292
4185.7    55.00  0.34      Sequence
 HLA-DPA10103-DPB10401 1114      NFYEPQIITTDNTFV  YEPQIITTD  2         0.1992
5793.0    60.00  0.23      Sequence
 HLA-DPA10103-DPB10401 1115      FYEPQIITTDNTFVS  IITTDNTFV  5         0.1702
7929.1    70.00  0.30      Sequence
 HLA-DPA10103-DPB10401 1116      YEPQIITTDNTFVSG  IITTDNTFV  4         0.1539
9457.2    75.00  0.34      Sequence
 HLA-DPA10103-DPB10401 1117      EPQIITTDNTFVSGN  IITTDNTFV  3         0.1534
9507.3    75.00  0.34      Sequence
 HLA-DPA10103-DPB10401 1118      PQIITTDNTFVSGNC  IITTDNTFV  2         0.1585
9003.6    70.00  0.30      Sequence
```

```
 HLA-DPA10103-DPB10401 1119      QIITTDNTFVSGNCD  TTDNTFVSG  3        0.1560
9247.1    75.00  0.20      Sequence
 HLA-DPA10103-DPB10401 1120      IITTDNTFVSGNCDV  FVSGNCDVX  7        0.1506
9800.5    75.00  0.27      Sequence
 HLA-DPA10103-DPB10401 1121      ITTDNTFVSGNCDVV  FVSGNCDVV  6        0.2083
5252.7    60.00  0.69      Sequence
 HLA-DPA10103-DPB10401 1122      TTDNTFVSGNCDVVI  FVSGNCDVV  5        0.2331
4015.4    55.00  0.69      Sequence
 HLA-DPA10103-DPB10401 1123      TDNTFVSGNCDVVIG  FVSGNCDVV  4        0.2290
4195.1    55.00  0.68      Sequence
 HLA-DPA10103-DPB10401 1124      DNTFVSGNCDVVIGI  FVSGNCDVV  3        0.2381
3801.2    49.00  0.67      Sequence
 HLA-DPA10103-DPB10401 1125      NTFVSGNCDVVIGIV  FVSGNCDVV  2        0.2446
3543.6    48.00  0.57      Sequence
 HLA-DPA10103-DPB10401 1126      TFVSGNCDVVIGIVN  FVSGNCDVV  1        0.1972
5920.6    60.00  0.40      Sequence
 HLA-DPA10103-DPB10401 1127      FVSGNCDVVIGIVNN  FVSGNCDVV  0        0.1468
10214.8    75.00  0.25      Sequence
 HLA-DPA10103-DPB10401 1128      VSGNCDVVIGIVNNT  VVIGIVNNT  6        0.1216
13417.6    80.00  0.25      Sequence
 HLA-DPA10103-DPB10401 1129      SGNCDVVIGIVNNTV  VVIGIVNNT  5        0.1378
11258.6    80.00  0.26      Sequence
 HLA-DPA10103-DPB10401 1130      GNCDVVIGIVNNTVY  VVIGIVNNT  4        0.1598
8873.5    70.00  0.20      Sequence
 HLA-DPA10103-DPB10401 1131      NCDVVIGIVNNTVYD  VVIGIVNNT  3        0.1575
9100.4    70.00  0.22      Sequence
 HLA-DPA10103-DPB10401 1132      CDVVIGIVNNTVYDP  VNNTVYDPX  7        0.1764
7415.7    65.00  0.22      Sequence
 HLA-DPA10103-DPB10401 1133      DVVIGIVNNTVYDPL  VNNTVYDPL  6        0.2575
3083.5    45.00  0.55      Sequence
 HLA-DPA10103-DPB10401 1134      VVIGIVNNTVYDPLQ  VNNTVYDPL  5        0.2611
2966.7    44.00  0.56      Sequence
 HLA-DPA10103-DPB10401 1135      VIGIVNNTVYDPLQP  VNNTVYDPL  4        0.2721
2632.3    42.00  0.57      Sequence
 HLA-DPA10103-DPB10401 1136      IGIVNNTVYDPLQPE  VNNTVYDPL  3        0.2604
2989.2    44.00  0.58      Sequence
 HLA-DPA10103-DPB10401 1137      GIVNNTVYDPLQPEL  VNNTVYDPL  2        0.2557
3142.3    45.00  0.47      Sequence
 HLA-DPA10103-DPB10401 1138      IVNNTVYDPLQPELD  TVYDPLQPE  4        0.2239
4432.8    55.00  0.28      Sequence
 HLA-DPA10103-DPB10401 1139      VNNTVYDPLQPELDS  TVYDPLQPE  3        0.1905
6362.6    65.00  0.30      Sequence
 HLA-DPA10103-DPB10401 1140      NNTVYDPLQPELDSF  TVYDPLQPE  2        0.1632
8553.8    70.00  0.31      Sequence
 HLA-DPA10103-DPB10401 1141      NTVYDPLQPELDSFK  YDPLQPELD  3        0.1540
9446.5    75.00  0.23      Sequence
 HLA-DPA10103-DPB10401 1142      TVYDPLQPELDSFKE  LQPELDSFK  5        0.1443
10490.8    75.00  0.22      Sequence
 HLA-DPA10103-DPB10401 1143      VYDPLQPELDSFKEE  LQPELDSFK  4        0.1274
12602.5    80.00  0.28      Sequence
 HLA-DPA10103-DPB10401 1144      YDPLQPELDSFKEEL  PELDSFKEE  5        0.1335
11793.1    80.00  0.29      Sequence
 HLA-DPA10103-DPB10401 1145      DPLQPELDSFKEELD  PELDSFKEE  4        0.1276
12564.8    80.00  0.23      Sequence
 HLA-DPA10103-DPB10401 1146      PLQPELDSFKEELDK  PELDSFKEE  3        0.1296
12305.3    80.00  0.25      Sequence
 HLA-DPA10103-DPB10401 1147      LQPELDSFKEELDKY  LDSFKEELD  4        0.1375
11290.3    80.00  0.24      Sequence
 HLA-DPA10103-DPB10401 1148      QPELDSFKEELDKYF  FKEELDKYF  6        0.1655
8342.3    70.00  0.40      Sequence
 HLA-DPA10103-DPB10401 1149      PELDSFKEELDKYFK  FKEELDKYF  5        0.1693
8009.8    70.00  0.40      Sequence
 HLA-DPA10103-DPB10401 1150      ELDSFKEELDKYFKN  FKEELDKYF  4        0.1729
7699.2    70.00  0.34      Sequence
 HLA-DPA10103-DPB10401 1151      LDSFKEELDKYFKNH  FKEELDKYF  3        0.1701
7935.0    70.00  0.34      Sequence
```

```
 HLA-DPA10103-DPB10401 1152      DSFKEELDKYFKNHT  EELDKYFKN  4        0.1586
8992.0    70.00  0.28     Sequence
 HLA-DPA10103-DPB10401 1153      SFKEELDKYFKNHTS  EELDKYFKN  3        0.1624
8622.6    70.00  0.31     Sequence
 HLA-DPA10103-DPB10401 1154      FKEELDKYFKNHTSP  ELDKYFKNH  3        0.1523
9626.4    75.00  0.26     Sequence
 HLA-DPA10103-DPB10401 1155      KEELDKYFKNHTSPD  ELDKYFKNH  2        0.1072
15680.8    85.00  0.17     Sequence
 HLA-DPA10103-DPB10401 1156      EELDKYFKNHTSPDV  FKNHTSPDV  6        0.1297
12283.6    80.00  0.56     Sequence
 HLA-DPA10103-DPB10401 1157      ELDKYFKNHTSPDVD  FKNHTSPDV  5        0.1294
12333.8    80.00  0.57     Sequence
 HLA-DPA10103-DPB10401 1158      LDKYFKNHTSPDVDL  FKNHTSPDV  4        0.1419
10765.4    75.00  0.56     Sequence
 HLA-DPA10103-DPB10401 1159      DKYFKNHTSPDVDLG  FKNHTSPDV  3        0.1343
11695.7    80.00  0.59     Sequence
 HLA-DPA10103-DPB10401 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.1351
11590.2    80.00  0.52     Sequence
 HLA-DPA10103-DPB10401 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.0913
18616.1    90.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1162      FKNHTSPDVDLGDIS  HTSPDVDLG  3        0.0625
25433.2    100.00  0.34     Sequence
 HLA-DPA10103-DPB10401 1163      KNHTSPDVDLGDISG  HTSPDVDLG  2        0.0353
34136.1    100.00  0.26     Sequence
 HLA-DPA10103-DPB10401 1164      NHTSPDVDLGDISGI  VDLGDISGI  6        0.0323
35250.5    100.00  0.23     Sequence
 HLA-DPA10103-DPB10401 1165      HTSPDVDLGDISGIN  DLGDISGIN  6        0.0378
33217.6    100.00  0.28     Sequence
 HLA-DPA10103-DPB10401 1166      TSPDVDLGDISGINA  LGDISGINA  6        0.0447
30830.3    100.00  0.29     Sequence
 HLA-DPA10103-DPB10401 1167      SPDVDLGDISGINAS  LGDISGINA  5        0.0472
29992.9    100.00  0.28     Sequence
 HLA-DPA10103-DPB10401 1168      PDVDLGDISGINASF  DISGINASF  6        0.0680
23948.1    95.00  0.20     Sequence
 HLA-DPA10103-DPB10401 1169      DVDLGDISGINASFV  ISGINASFV  6        0.1210
13506.0    85.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1170      VDLGDISGINASFVN  ISGINASFV  5        0.1429
10658.2    75.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1171      DLGDISGINASFVNI  GINASFVNI  6        0.2492
3374.0    47.00  0.43     Sequence
 HLA-DPA10103-DPB10401 1172      LGDISGINASFVNIQ  GINASFVNI  5        0.2978
1993.9    37.00  0.40     Sequence
 HLA-DPA10103-DPB10401 1173      GDISGINASFVNIQK  GINASFVNI  4        0.2904
2159.4    38.00  0.40     Sequence
 HLA-DPA10103-DPB10401 1174      DISGINASFVNIQKE  GINASFVNI  3        0.2860
2265.6    39.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1175      ISGINASFVNIQKEI  GINASFVNI  2        0.3016
1913.9    36.00  0.31     Sequence
 HLA-DPA10103-DPB10401 1176      SGINASFVNIQKEID  FVNIQKEID  6        0.2732
2601.3    42.00  0.25     Sequence
 HLA-DPA10103-DPB10401 1177      GINASFVNIQKEIDR  FVNIQKEID  5        0.2506
3323.8    47.00  0.34     Sequence
 HLA-DPA10103-DPB10401 1178      INASFVNIQKEIDRL  FVNIQKEID  4        0.2369
3851.0    50.00  0.48     Sequence
 HLA-DPA10103-DPB10401 1179      NASFVNIQKEIDRLN  FVNIQKEID  3        0.2149
4886.1    55.00  0.54     Sequence
 HLA-DPA10103-DPB10401 1180      ASFVNIQKEIDRLNE  FVNIQKEID  2        0.2019
5629.6    60.00  0.52     Sequence
 HLA-DPA10103-DPB10401 1181      SFVNIQKEIDRLNEV  FVNIQKEID  1        0.1642
8461.4    70.00  0.27     Sequence
 HLA-DPA10103-DPB10401 1182      FVNIQKEIDRLNEVA  KEIDRLNEV  5        0.1349
11617.1    80.00  0.25     Sequence
 HLA-DPA10103-DPB10401 1183      VNIQKEIDRLNEVAK  KEIDRLNEV  4        0.1169
14111.9    85.00  0.34     Sequence
 HLA-DPA10103-DPB10401 1184      NIQKEIDRLNEVAKN  KEIDRLNEV  3        0.1114
14985.6    85.00  0.34     Sequence
```

```
 HLA-DPA10103-DPB10401 1185      IQKEIDRLNEVAKNL  DRLNEVAKN  5        0.1231
13195.7    80.00  0.31     Sequence
 HLA-DPA10103-DPB10401 1186      QKEIDRLNEVAKNLN  DRLNEVAKN  4        0.1155
14335.3    85.00  0.29     Sequence
 HLA-DPA10103-DPB10401 1187      KEIDRLNEVAKNLNE  DRLNEVAKN  3        0.1022
16543.8    90.00  0.28     Sequence
 HLA-DPA10103-DPB10401 1188      EIDRLNEVAKNLNES  DRLNEVAKN  2        0.0816
20670.5    95.00  0.26     Sequence
 HLA-DPA10103-DPB10401 1189      IDRLNEVAKNLNESL  VAKNLNESL  6        0.0935
18189.0    90.00  0.35     Sequence
 HLA-DPA10103-DPB10401 1190      DRLNEVAKNLNESLI  VAKNLNESL  5        0.1250
12928.5    80.00  0.34     Sequence
 HLA-DPA10103-DPB10401 1191      RLNEVAKNLNESLID  VAKNLNESL  4        0.1307
12150.4    80.00  0.31     Sequence
 HLA-DPA10103-DPB10401 1192      LNEVAKNLNESLIDL  LNESLIDLX  7        0.2007
5701.3    60.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1193      NEVAKNLNESLIDLQ  LNESLIDLQ  6        0.2449
3533.1    48.00  0.47     Sequence
 HLA-DPA10103-DPB10401 1194      EVAKNLNESLIDLQE  LNESLIDLQ  5        0.2394
3749.2    49.00  0.46     Sequence
 HLA-DPA10103-DPB10401 1195      VAKNLNESLIDLQEL  LNESLIDLQ  4        0.2642
2867.0    44.00  0.41     Sequence
 HLA-DPA10103-DPB10401 1196      AKNLNESLIDLQELG  LNESLIDLQ  3        0.2573
3088.4    45.00  0.43     Sequence
 HLA-DPA10103-DPB10401 1197      KNLNESLIDLQELGK  LNESLIDLQ  2        0.2417
3659.8    49.00  0.32     Sequence
 HLA-DPA10103-DPB10401 1198      NLNESLIDLQELGKY  LIDLQELGK  5        0.2166
4799.4    55.00  0.23     Sequence
 HLA-DPA10103-DPB10401 1199      LNESLIDLQELGKYE  LIDLQELGK  4        0.2020
5623.0    60.00  0.31     Sequence
 HLA-DPA10103-DPB10401 1200      NESLIDLQELGKYEQ  LIDLQELGK  3        0.1829
6909.3    65.00  0.31     Sequence
 HLA-DPA10103-DPB10401 1201      ESLIDLQELGKYEQY  LIDLQELGK  2        0.1912
6315.5    65.00  0.25     Sequence
 HLA-DPA10103-DPB10401 1202      SLIDLQELGKYEQYI  QELGKYEQY  5        0.1809
7064.2    65.00  0.16     Sequence
 HLA-DPA10103-DPB10401 1203      LIDLQELGKYEQYIK  GKYEQYIKX  7        0.1870
6607.6    65.00  0.22     Sequence
 HLA-DPA10103-DPB10401 1204      IDLQELGKYEQYIKW  GKYEQYIKW  6        0.2557
3145.1    45.00  0.52     Sequence
 HLA-DPA10103-DPB10401 1205      DLQELGKYEQYIKWP  GKYEQYIKW  5        0.3069
1806.8    35.00  0.50     Sequence
 HLA-DPA10103-DPB10401 1206      LQELGKYEQYIKWPW  GKYEQYIKW  4        0.4018
647.0    20.00  0.37     Sequence
 HLA-DPA10103-DPB10401 1207      QELGKYEQYIKWPWY  GKYEQYIKW  3        0.4340
456.9    16.00  0.29     Sequence
 HLA-DPA10103-DPB10401 1208      ELGKYEQYIKWPWYI  EQYIKWPWY  5        0.4641
329.7    13.00  0.26     Sequence
 HLA-DPA10103-DPB10401 1209      LGKYEQYIKWPWYIW  YIKWPWYIW  6        0.5159
188.2     8.00  0.22     Sequence         WB
 HLA-DPA10103-DPB10401 1210      GKYEQYIKWPWYIWL  IKWPWYIWL  6        0.5486
132.2     6.00  0.26     Sequence         WB
 HLA-DPA10103-DPB10401 1211      KYEQYIKWPWYIWLG  IKWPWYIWL  5        0.5509
129.0     6.00  0.26     Sequence         WB
 HLA-DPA10103-DPB10401 1212      YEQYIKWPWYIWLGF  IKWPWYIWL  4        0.5472
134.2     6.00  0.34     Sequence         WB
 HLA-DPA10103-DPB10401 1213      EQYIKWPWYIWLGFI  IKWPWYIWL  3        0.5352
152.8     7.00  0.34     Sequence         WB
 HLA-DPA10103-DPB10401 1214      QYIKWPWYIWLGFIA  IKWPWYIWL  2        0.5537
125.0     5.50  0.25     Sequence         WB
 HLA-DPA10103-DPB10401 1215      YIKWPWYIWLGFIAG  PWYIWLGFI  4        0.5144
191.3     8.00  0.23     Sequence         WB
 HLA-DPA10103-DPB10401 1216      IKWPWYIWLGFIAGL  IWLGFIAGL  6        0.4962
233.1     9.50  0.24     Sequence         WB
 HLA-DPA10103-DPB10401 1217      KWPWYIWLGFIAGLI  IWLGFIAGL  5        0.4687
313.6    12.00  0.29     Sequence
```

```
 HLA-DPA10103-DPB10401 1218      WPWYIWLGFIAGLIA  IWLGFIAGL  4         0.4395
430.2    15.00  0.35     Sequence
 HLA-DPA10103-DPB10401 1219      PWYIWLGFIAGLIAI  IWLGFIAGL  3         0.4360
446.8    15.00  0.36     Sequence
 HLA-DPA10103-DPB10401 1220      WYIWLGFIAGLIAIV  FIAGLIAIV  6         0.4393
431.1    15.00  0.26     Sequence
 HLA-DPA10103-DPB10401 1221      YIWLGFIAGLIAIVM  FIAGLIAIV  5         0.3662
950.7    25.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1222      IWLGFIAGLIAIVMV  FIAGLIAIV  4         0.3493
1142.2    27.00  0.47     Sequence
 HLA-DPA10103-DPB10401 1223      WLGFIAGLIAIVMVT  FIAGLIAIV  3         0.3302
1403.3    30.00  0.55     Sequence
 HLA-DPA10103-DPB10401 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2         0.2959
2034.9    37.00  0.56     Sequence
 HLA-DPA10103-DPB10401 1225      GFIAGLIAIVMVTIM  FIAGLIAIV  1         0.2709
2665.8    42.00  0.47     Sequence
 HLA-DPA10103-DPB10401 1226      FIAGLIAIVMVTIML  LIAIVMVTI  4         0.1832
6892.1    65.00  0.14     Sequence
 HLA-DPA10103-DPB10401 1227      IAGLIAIVMVTIMLC  LIAIVMVTI  3         0.1348
11627.7    80.00  0.35     Sequence
 HLA-DPA10103-DPB10401 1228      AGLIAIVMVTIMLCC  IAIVMVTIM  3         0.1306
12165.5    80.00  0.25     Sequence
 HLA-DPA10103-DPB10401 1229      GLIAIVMVTIMLCCM  IAIVMVTIM  2         0.1543
9417.0    75.00  0.21     Sequence
 HLA-DPA10103-DPB10401 1230      LIAIVMVTIMLCCMT  VMVTIMLCC  4         0.1268
12682.0    80.00  0.26     Sequence
 HLA-DPA10103-DPB10401 1231      IAIVMVTIMLCCMTS  VMVTIMLCC  3         0.1236
13124.0    80.00  0.27     Sequence
 HLA-DPA10103-DPB10401 1232      AIVMVTIMLCCMTSC  IMLCCMTSC  6         0.1504
9818.9    75.00  0.29     Sequence
 HLA-DPA10103-DPB10401 1233      IVMVTIMLCCMTSCC  IMLCCMTSC  5         0.1528
9576.1    75.00  0.36     Sequence
 HLA-DPA10103-DPB10401 1234      VMVTIMLCCMTSCCS  IMLCCMTSC  4         0.1669
8214.0    70.00  0.31     Sequence
 HLA-DPA10103-DPB10401 1235      MVTIMLCCMTSCCSC  CMTSCCSCX  7         0.1961
5991.7    60.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1236      VTIMLCCMTSCCSCL  CMTSCCSCL  6         0.2883
2208.1    38.00  0.67     Sequence
 HLA-DPA10103-DPB10401 1237      TIMLCCMTSCCSCLK  CMTSCCSCL  5         0.2934
2091.8    37.00  0.68     Sequence
 HLA-DPA10103-DPB10401 1238      IMLCCMTSCCSCLKG  CMTSCCSCL  4         0.2791
2441.0    40.00  0.68     Sequence
 HLA-DPA10103-DPB10401 1239      MLCCMTSCCSCLKGC  CMTSCCSCL  3         0.2738
2585.5    41.00  0.71     Sequence
 HLA-DPA10103-DPB10401 1240      LCCMTSCCSCLKGCC  CMTSCCSCL  2         0.2589
3035.4    45.00  0.63     Sequence
 HLA-DPA10103-DPB10401 1241      CCMTSCCSCLKGCCS  CMTSCCSCL  1         0.1807
7080.1    65.00  0.43     Sequence
 HLA-DPA10103-DPB10401 1242      CMTSCCSCLKGCCSC  CMTSCCSCL  0         0.1363
11439.1    80.00  0.28     Sequence
 HLA-DPA10103-DPB10401 1243      MTSCCSCLKGCCSCG  CLKGCCSCG  6         0.1016
16659.3    90.00  0.23     Sequence
 HLA-DPA10103-DPB10401 1244      TSCCSCLKGCCSCGS  CLKGCCSCG  5         0.0887
19149.7    90.00  0.27     Sequence
 HLA-DPA10103-DPB10401 1245      SCCSCLKGCCSCGSC  CLKGCCSCG  4         0.0865
19616.5    90.00  0.31     Sequence
 HLA-DPA10103-DPB10401 1246      CCSCLKGCCSCGSCC  CLKGCCSCG  3         0.0864
19622.7    90.00  0.29     Sequence
 HLA-DPA10103-DPB10401 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3         0.0867
19566.7    90.00  0.35     Sequence
 HLA-DPA10103-DPB10401 1248      SCLKGCCSCGSCCKF  CSCGSCCKF  6         0.1185
13868.5    85.00  0.33     Sequence
 HLA-DPA10103-DPB10401 1249      CLKGCCSCGSCCKFD  CSCGSCCKF  5         0.1037
16284.0    85.00  0.36     Sequence
 HLA-DPA10103-DPB10401 1250      LKGCCSCGSCCKFDE  CSCGSCCKF  4         0.1047
16113.1    85.00  0.33     Sequence
```

```
 HLA-DPA10103-DPB10401 1251      KGCCSCGSCCKFDED  GSCCKFDED  6        0.1098
15241.7    85.00  0.34     Sequence
 HLA-DPA10103-DPB10401 1252      GCCSCGSCCKFDEDD  GSCCKFDED  5        0.1010
16764.6    90.00  0.36     Sequence
 HLA-DPA10103-DPB10401 1253      CCSCGSCCKFDEDDS  GSCCKFDED  4        0.1018
16625.0    90.00  0.37     Sequence
 HLA-DPA10103-DPB10401 1254      CSCGSCCKFDEDDSE  GSCCKFDED  3        0.0841
20131.7    95.00  0.44     Sequence
 HLA-DPA10103-DPB10401 1255      SCGSCCKFDEDDSEP  GSCCKFDED  2        0.0703
23362.0    95.00  0.35     Sequence
 HLA-DPA10103-DPB10401 1256      CGSCCKFDEDDSEPV  FDEDDSEPV  6        0.0812
20769.6    95.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1257      GSCCKFDEDDSEPVL  FDEDDSEPV  5        0.0916
18554.4    90.00  0.47     Sequence
 HLA-DPA10103-DPB10401 1258      SCCKFDEDDSEPVLK  FDEDDSEPV  4        0.0935
18176.2    90.00  0.44     Sequence
 HLA-DPA10103-DPB10401 1259      CCKFDEDDSEPVLKG  FDEDDSEPV  3        0.0935
18171.1    90.00  0.38     Sequence
 HLA-DPA10103-DPB10401 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.0987
17192.4    90.00  0.32     Sequence
 HLA-DPA10103-DPB10401 1261      KFDEDDSEPVLKGVK  DDSEPVLKG  4        0.0910
18689.1    90.00  0.35     Sequence
 HLA-DPA10103-DPB10401 1262      FDEDDSEPVLKGVKL  DDSEPVLKG  3        0.0927
18337.0    90.00  0.33     Sequence
 HLA-DPA10103-DPB10401 1263      DEDDSEPVLKGVKLH  LKGVKLHXX  8        0.1055
15973.6    85.00  0.25     Sequence
 HLA-DPA10103-DPB10401 1264      EDDSEPVLKGVKLHY  LKGVKLHYX  7        0.2026
5586.5    60.00  0.44     Sequence
 HLA-DPA10103-DPB10401 1265      DDSEPVLKGVKLHYT  LKGVKLHYT  6        0.3008
1930.8    36.00  0.66     Sequence
 HLA-DPA10301-DPB10402    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3        0.3264
1462.4    46.00  0.23     Sequence
 HLA-DPA10301-DPB10402    2      SPIKEMFVFLVLLPL  MFVFLVLLP  5        0.3901
734.1    32.00  0.45     Sequence
 HLA-DPA10301-DPB10402    3      PIKEMFVFLVLLPLV  MFVFLVLLP  4        0.3860
767.6    33.00  0.48     Sequence
 HLA-DPA10301-DPB10402    4      IKEMFVFLVLLPLVS  MFVFLVLLP  3        0.4264
495.8    26.00  0.44     Sequence
 HLA-DPA10301-DPB10402    5      KEMFVFLVLLPLVSS  FLVLLPLVS  5        0.4779
284.0    17.00  0.50     Sequence
 HLA-DPA10301-DPB10402    6      EMFVFLVLLPLVSSQ  FLVLLPLVS  4        0.4932
240.7    15.00  0.54     Sequence
 HLA-DPA10301-DPB10402    7      MFVFLVLLPLVSSQC  FLVLLPLVS  3        0.4796
278.8    17.00  0.61     Sequence
 HLA-DPA10301-DPB10402    8      FVFLVLLPLVSSQCV  FLVLLPLVS  2        0.4999
223.9    14.00  0.60     Sequence
 HLA-DPA10301-DPB10402    9      VFLVLLPLVSSQCVN  FLVLLPLVS  1        0.4891
251.6    16.00  0.51     Sequence
 HLA-DPA10301-DPB10402   10      FLVLLPLVSSQCVNF  FLVLLPLVS  0        0.4692
311.9    19.00  0.34     Sequence
 HLA-DPA10301-DPB10402   11      LVLLPLVSSQCVNFT  PLVSSQCVN  4        0.4184
540.8    27.00  0.35     Sequence
 HLA-DPA10301-DPB10402   12      VLLPLVSSQCVNFTN  PLVSSQCVN  3        0.3693
919.5    37.00  0.42     Sequence
 HLA-DPA10301-DPB10402   13      LLPLVSSQCVNFTNR  PLVSSQCVN  2        0.3690
922.7    37.00  0.44     Sequence
 HLA-DPA10301-DPB10402   14      LPLVSSQCVNFTNRT  PLVSSQCVN  1        0.3407
1253.5    43.00  0.44     Sequence
 HLA-DPA10301-DPB10402   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.2523
3262.5    65.00  0.31     Sequence
 HLA-DPA10301-DPB10402   16      LVSSQCVNFTNRTQL  SSQCVNFTN  2        0.2159
4836.0    70.00  0.23     Sequence
 HLA-DPA10301-DPB10402   17      VSSQCVNFTNRTQLP  CVNFTNRTQ  4        0.2015
5651.0    75.00  0.25     Sequence
 HLA-DPA10301-DPB10402   18      SSQCVNFTNRTQLPS  CVNFTNRTQ  3        0.1971
5928.5    75.00  0.30     Sequence
```

```
 HLA-DPA10301-DPB10402   19      SQCVNFTNRTQLPSA  CVNFTNRTQ  2        0.2028
5572.7    75.00  0.31     Sequence
 HLA-DPA10301-DPB10402   20      QCVNFTNRTQLPSAY  FTNRTQLPS  4        0.2000
5740.8    75.00  0.21     Sequence
 HLA-DPA10301-DPB10402   21      CVNFTNRTQLPSAYT  FTNRTQLPS  3        0.1960
5994.6    75.00  0.26     Sequence
 HLA-DPA10301-DPB10402   22      VNFTNRTQLPSAYTN  FTNRTQLPS  2        0.1811
7046.4    80.00  0.26     Sequence
 HLA-DPA10301-DPB10402   23      NFTNRTQLPSAYTNS  FTNRTQLPS  1        0.1172
14066.2    90.00  0.15     Sequence
 HLA-DPA10301-DPB10402   24      FTNRTQLPSAYTNSF  QLPSAYTNS  5        0.1531
9543.4    85.00  0.25     Sequence
 HLA-DPA10301-DPB10402   25      TNRTQLPSAYTNSFT  PSAYTNSFT  6        0.1806
7087.2    80.00  0.29     Sequence
 HLA-DPA10301-DPB10402   26      NRTQLPSAYTNSFTR  PSAYTNSFT  5        0.2163
4814.2    70.00  0.31     Sequence
 HLA-DPA10301-DPB10402   27      RTQLPSAYTNSFTRG  SAYTNSFTR  5        0.2129
4993.5    75.00  0.29     Sequence
 HLA-DPA10301-DPB10402   28      TQLPSAYTNSFTRGV  SAYTNSFTR  4        0.2463
3481.4    65.00  0.34     Sequence
 HLA-DPA10301-DPB10402   29      QLPSAYTNSFTRGVY  SAYTNSFTR  3        0.2791
2439.3    60.00  0.32     Sequence
 HLA-DPA10301-DPB10402   30      LPSAYTNSFTRGVYY  SAYTNSFTR  2        0.2899
2170.5    55.00  0.31     Sequence
 HLA-DPA10301-DPB10402   31      PSAYTNSFTRGVYYP  AYTNSFTRG  2        0.2640
2874.1    60.00  0.28     Sequence
 HLA-DPA10301-DPB10402   32      SAYTNSFTRGVYYPD  SFTRGVYYP  5        0.2441
3565.4    65.00  0.23     Sequence
 HLA-DPA10301-DPB10402   33      AYTNSFTRGVYYPDK  SFTRGVYYP  4        0.2386
3782.9    65.00  0.35     Sequence
 HLA-DPA10301-DPB10402   34      YTNSFTRGVYYPDKV  SFTRGVYYP  3        0.2410
3685.7    65.00  0.40     Sequence
 HLA-DPA10301-DPB10402   35      TNSFTRGVYYPDKVF  SFTRGVYYP  2        0.2294
4177.2    70.00  0.49     Sequence
 HLA-DPA10301-DPB10402   36      NSFTRGVYYPDKVFR  SFTRGVYYP  1        0.2330
4020.3    70.00  0.36     Sequence
 HLA-DPA10301-DPB10402   37      SFTRGVYYPDKVFRS  VYYPDKVFR  5        0.2610
2969.3    60.00  0.28     Sequence
 HLA-DPA10301-DPB10402   38      FTRGVYYPDKVFRSS  VYYPDKVFR  4        0.2780
2468.7    60.00  0.32     Sequence
 HLA-DPA10301-DPB10402   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.2963
2026.0    55.00  0.41     Sequence
 HLA-DPA10301-DPB10402   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.3398
1264.8    43.00  0.37     Sequence
 HLA-DPA10301-DPB10402   41      GVYYPDKVFRSSVLH  YYPDKVFRS  2        0.4062
617.1    29.00  0.22     Sequence
 HLA-DPA10301-DPB10402   42      VYYPDKVFRSSVLHS  VFRSSVLHS  6        0.5078
205.6    13.00  0.47     Sequence
 HLA-DPA10301-DPB10402   43      YYPDKVFRSSVLHST  VFRSSVLHS  5        0.6008
75.1     4.50  0.70     Sequence         WB
 HLA-DPA10301-DPB10402   44      YPDKVFRSSVLHSTQ  VFRSSVLHS  4        0.6298
54.9     3.00  0.78     Sequence         WB
 HLA-DPA10301-DPB10402   45      PDKVFRSSVLHSTQD  VFRSSVLHS  3        0.6275
56.3     3.00  0.79     Sequence         WB
 HLA-DPA10301-DPB10402   46      DKVFRSSVLHSTQDL  VFRSSVLHS  2        0.6436
47.3     2.50  0.80     Sequence         WB
 HLA-DPA10301-DPB10402   47      KVFRSSVLHSTQDLF  VFRSSVLHS  1        0.6113
67.1     4.00  0.69     Sequence         WB
 HLA-DPA10301-DPB10402   48      VFRSSVLHSTQDLFL  VFRSSVLHS  0        0.5175
185.0    12.00  0.46     Sequence
 HLA-DPA10301-DPB10402   49      FRSSVLHSTQDLFLP  LHSTQDLFL  5        0.4553
362.5    21.00  0.28     Sequence
 HLA-DPA10301-DPB10402   50      RSSVLHSTQDLFLPF  HSTQDLFLP  5        0.4522
375.0    21.00  0.35     Sequence
 HLA-DPA10301-DPB10402   51      SSVLHSTQDLFLPFF  HSTQDLFLP  4        0.4955
234.7    15.00  0.34     Sequence
```

```
 HLA-DPA10301-DPB10402   52      SVLHSTQDLFLPFFS  HSTQDLFLP  3        0.5443
138.4     9.00  0.34     Sequence         WB
 HLA-DPA10301-DPB10402   53      VLHSTQDLFLPFFSN  HSTQDLFLP  2        0.5592
117.9     7.50  0.32     Sequence         WB
 HLA-DPA10301-DPB10402   54      LHSTQDLFLPFFSNV  QDLFLPFFS  4        0.5888
85.5     5.50  0.22     Sequence         WB
 HLA-DPA10301-DPB10402   55      HSTQDLFLPFFSNVT  LFLPFFSNV  5        0.6081
69.4     4.00  0.32     Sequence         WB
 HLA-DPA10301-DPB10402   56      STQDLFLPFFSNVTW  LFLPFFSNV  4        0.6122
66.4     4.00  0.35     Sequence         WB
 HLA-DPA10301-DPB10402   57      TQDLFLPFFSNVTWF  LFLPFFSNV  3        0.6138
65.3     4.00  0.37     Sequence         WB
 HLA-DPA10301-DPB10402   58      QDLFLPFFSNVTWFH  LFLPFFSNV  2        0.5925
82.2     5.00  0.37     Sequence         WB
 HLA-DPA10301-DPB10402   59      DLFLPFFSNVTWFHA  FFSNVTWFH  5        0.6035
72.9     4.50  0.22     Sequence         WB
 HLA-DPA10301-DPB10402   60      LFLPFFSNVTWFHAI  FFSNVTWFH  4        0.6043
72.3     4.50  0.33     Sequence         WB
 HLA-DPA10301-DPB10402   61      FLPFFSNVTWFHAIH  FFSNVTWFH  3        0.6119
66.7     4.00  0.36     Sequence         WB
 HLA-DPA10301-DPB10402   62      LPFFSNVTWFHAIHV  FFSNVTWFH  2        0.6060
71.0     4.50  0.36     Sequence         WB
 HLA-DPA10301-DPB10402   63      PFFSNVTWFHAIHVS  FSNVTWFHA  2        0.6023
73.9     4.50  0.41     Sequence         WB
 HLA-DPA10301-DPB10402   64      FFSNVTWFHAIHVSG  FSNVTWFHA  1        0.5540
124.6     8.00  0.35     Sequence         WB
 HLA-DPA10301-DPB10402   65      FSNVTWFHAIHVSGT  VTWFHAIHV  3        0.4352
450.7    24.00  0.22     Sequence
 HLA-DPA10301-DPB10402   66      SNVTWFHAIHVSGTN  VTWFHAIHV  2        0.3572
1048.7    39.00  0.31     Sequence
 HLA-DPA10301-DPB10402   67      NVTWFHAIHVSGTNG  VTWFHAIHV  1        0.3141
1671.1    48.00  0.28     Sequence
 HLA-DPA10301-DPB10402   68      VTWFHAIHVSGTNGT  WFHAIHVSG  2        0.2608
2973.9    60.00  0.35     Sequence
 HLA-DPA10301-DPB10402   69      TWFHAIHVSGTNGTK  WFHAIHVSG  1        0.1926
6222.3    75.00  0.39     Sequence
 HLA-DPA10301-DPB10402   70      WFHAIHVSGTNGTKR  WFHAIHVSG  0        0.1788
7225.4    80.00  0.29     Sequence
 HLA-DPA10301-DPB10402   71      FHAIHVSGTNGTKRF  HVSGTNGTK  4        0.1451
10401.9    85.00  0.27     Sequence
 HLA-DPA10301-DPB10402   72      HAIHVSGTNGTKRFD  HVSGTNGTK  3        0.1050
16047.4    95.00  0.44     Sequence
 HLA-DPA10301-DPB10402   73      AIHVSGTNGTKRFDN  HVSGTNGTK  2        0.0998
16985.3    95.00  0.50     Sequence
 HLA-DPA10301-DPB10402   74      IHVSGTNGTKRFDNP  HVSGTNGTK  1        0.0838
20191.3   100.00  0.44     Sequence
 HLA-DPA10301-DPB10402   75      HVSGTNGTKRFDNPV  HVSGTNGTK  0        0.0615
25692.4   100.00  0.28     Sequence
 HLA-DPA10301-DPB10402   76      VSGTNGTKRFDNPVL  KRFDNPVLX  7        0.1164
14184.4    95.00  0.24     Sequence
 HLA-DPA10301-DPB10402   77      SGTNGTKRFDNPVLP  KRFDNPVLP  6        0.1505
9809.1    85.00  0.37     Sequence
 HLA-DPA10301-DPB10402   78      GTNGTKRFDNPVLPF  KRFDNPVLP  5        0.2159
4833.3    70.00  0.52     Sequence
 HLA-DPA10301-DPB10402   79      TNGTKRFDNPVLPFN  KRFDNPVLP  4        0.2389
3769.5    65.00  0.49     Sequence
 HLA-DPA10301-DPB10402   80      NGTKRFDNPVLPFND  KRFDNPVLP  3        0.2486
3396.1    65.00  0.46     Sequence
 HLA-DPA10301-DPB10402   81      GTKRFDNPVLPFNDG  KRFDNPVLP  2        0.2465
3473.5    65.00  0.47     Sequence
 HLA-DPA10301-DPB10402   82      TKRFDNPVLPFNDGV  KRFDNPVLP  1        0.2585
3048.6    60.00  0.41     Sequence
 HLA-DPA10301-DPB10402   83      KRFDNPVLPFNDGVY  KRFDNPVLP  0        0.2299
4155.7    70.00  0.17     Sequence
 HLA-DPA10301-DPB10402   84      RFDNPVLPFNDGVYF  VLPFNDGVY  5        0.2393
3753.0    65.00  0.19     Sequence
```

```
 HLA-DPA10301-DPB10402   85      FDNPVLPFNDGVYFA  PFNDGVYFA  6         0.2711
2662.6    60.00  0.22     Sequence
 HLA-DPA10301-DPB10402   86      DNPVLPFNDGVYFAS  PFNDGVYFA  5         0.3282
1435.0    45.00  0.35     Sequence
 HLA-DPA10301-DPB10402   87      NPVLPFNDGVYFAST  PFNDGVYFA  4         0.3585
1033.6    39.00  0.36     Sequence
 HLA-DPA10301-DPB10402   88      PVLPFNDGVYFASTE  PFNDGVYFA  3         0.3791
827.1    35.00  0.38     Sequence
 HLA-DPA10301-DPB10402   89      VLPFNDGVYFASTEK  PFNDGVYFA  2         0.3957
690.8    31.00  0.40     Sequence
 HLA-DPA10301-DPB10402   90      LPFNDGVYFASTEKS  FNDGVYFAS  2         0.3758
857.5    35.00  0.38     Sequence
 HLA-DPA10301-DPB10402   91      PFNDGVYFASTEKSN  FNDGVYFAS  1         0.3287
1427.2    45.00  0.25     Sequence
 HLA-DPA10301-DPB10402   92      FNDGVYFASTEKSNI  YFASTEKSN  5         0.3382
1287.1    43.00  0.44     Sequence
 HLA-DPA10301-DPB10402   93      NDGVYFASTEKSNII  YFASTEKSN  4         0.3378
1292.8    43.00  0.51     Sequence
 HLA-DPA10301-DPB10402   94      DGVYFASTEKSNIIR  YFASTEKSN  3         0.3555
1067.5    40.00  0.52     Sequence
 HLA-DPA10301-DPB10402   95      GVYFASTEKSNIIRG  YFASTEKSN  2         0.3486
1150.2    41.00  0.54     Sequence
 HLA-DPA10301-DPB10402   96      VYFASTEKSNIIRGW  YFASTEKSN  1         0.3173
1615.1    48.00  0.46     Sequence
 HLA-DPA10301-DPB10402   97      YFASTEKSNIIRGWI  YFASTEKSN  0         0.2405
3707.2    65.00  0.29     Sequence
 HLA-DPA10301-DPB10402   98      FASTEKSNIIRGWIF  TEKSNIIRG  3         0.1959
6006.2    75.00  0.30     Sequence
 HLA-DPA10301-DPB10402   99      ASTEKSNIIRGWIFG  TEKSNIIRG  2         0.1842
6813.0    80.00  0.30     Sequence
 HLA-DPA10301-DPB10402  100      STEKSNIIRGWIFGT  NIIRGWIFG  5         0.3133
1685.3    48.00  0.37     Sequence
 HLA-DPA10301-DPB10402  101      TEKSNIIRGWIFGTT  IIRGWIFGT  5         0.3578
1041.2    39.00  0.44     Sequence
 HLA-DPA10301-DPB10402  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4         0.3998
661.1    31.00  0.48     Sequence
 HLA-DPA10301-DPB10402  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3         0.4021
644.7    30.00  0.47     Sequence
 HLA-DPA10301-DPB10402  104      SNIIRGWIFGTTLDS  IIRGWIFGT  2         0.4106
588.4    29.00  0.42     Sequence
 HLA-DPA10301-DPB10402  105      NIIRGWIFGTTLDSK  IIRGWIFGT  1         0.4071
610.7    29.00  0.29     Sequence
 HLA-DPA10301-DPB10402  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4         0.3749
866.0    36.00  0.34     Sequence
 HLA-DPA10301-DPB10402  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3         0.3474
1165.8    41.00  0.46     Sequence
 HLA-DPA10301-DPB10402  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2         0.3523
1105.2    40.00  0.49     Sequence
 HLA-DPA10301-DPB10402  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1         0.3227
1523.1    46.00  0.43     Sequence
 HLA-DPA10301-DPB10402  110      WIFGTTLDSKTQSLL  WIFGTTLDS  0         0.3116
1717.0    49.00  0.34     Sequence
 HLA-DPA10301-DPB10402  111      IFGTTLDSKTQSLLI  DSKTQSLLI  6         0.2382
3797.1    65.00  0.25     Sequence
 HLA-DPA10301-DPB10402  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5         0.3591
1026.5    39.00  0.46     Sequence
 HLA-DPA10301-DPB10402  113      GTTLDSKTQSLLIVN  DSKTQSLLI  4         0.3909
727.8    32.00  0.41     Sequence
 HLA-DPA10301-DPB10402  114      TTLDSKTQSLLIVNN  DSKTQSLLI  3         0.4156
557.1    28.00  0.37     Sequence
 HLA-DPA10301-DPB10402  115      TLDSKTQSLLIVNNA  DSKTQSLLI  2         0.4318
467.9    25.00  0.34     Sequence
 HLA-DPA10301-DPB10402  116      LDSKTQSLLIVNNAT  DSKTQSLLI  1         0.4284
485.3    25.00  0.31     Sequence
 HLA-DPA10301-DPB10402  117      DSKTQSLLIVNNATN  KTQSLLIVN  2         0.3984
671.4    31.00  0.19     Sequence
```

```
 HLA-DPA10301-DPB10402  118       SKTQSLLIVNNATNV  TQSLLIVNN  2        0.3752
862.9    35.00  0.23     Sequence
 HLA-DPA10301-DPB10402  119       KTQSLLIVNNATNVV  LLIVNNATN  4        0.3237
1506.4    46.00  0.22     Sequence
 HLA-DPA10301-DPB10402  120       TQSLLIVNNATNVVI  LLIVNNATN  3        0.3227
1523.2    46.00  0.29     Sequence
 HLA-DPA10301-DPB10402  121       QSLLIVNNATNVVIK  LLIVNNATN  2        0.3266
1459.6    46.00  0.28     Sequence
 HLA-DPA10301-DPB10402  122       SLLIVNNATNVVIKV  LLIVNNATN  1        0.3343
1343.4    44.00  0.22     Sequence
 HLA-DPA10301-DPB10402  123       LLIVNNATNVVIKVC  VNNATNVVI  3        0.3180
1601.5    47.00  0.34     Sequence
 HLA-DPA10301-DPB10402  124       LIVNNATNVVIKVCE  VNNATNVVI  2        0.3003
1939.9    55.00  0.35     Sequence
 HLA-DPA10301-DPB10402  125       IVNNATNVVIKVCEF  NNATNVVIK  2        0.2781
2466.5    60.00  0.22     Sequence
 HLA-DPA10301-DPB10402  126       VNNATNVVIKVCEFQ  NATNVVIKV  2        0.2723
2626.6    60.00  0.19     Sequence
 HLA-DPA10301-DPB10402  127       NNATNVVIKVCEFQF  VIKVCEFQF  6        0.3304
1401.7    45.00  0.36     Sequence
 HLA-DPA10301-DPB10402  128       NATNVVIKVCEFQFC  VIKVCEFQF  5        0.3801
818.6    34.00  0.47     Sequence
 HLA-DPA10301-DPB10402  129       ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.4078
606.3    29.00  0.56     Sequence
 HLA-DPA10301-DPB10402  130       TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.4560
360.0    21.00  0.50     Sequence
 HLA-DPA10301-DPB10402  131       NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.4678
316.9    19.00  0.47     Sequence
 HLA-DPA10301-DPB10402  132       VVIKVCEFQFCNYPF  VIKVCEFQF  1        0.4799
277.9    17.00  0.41     Sequence
 HLA-DPA10301-DPB10402  133       VIKVCEFQFCNYPFL  VCEFQFCNY  3        0.5567
121.1     8.00  0.17     Sequence         WB
 HLA-DPA10301-DPB10402  134       IKVCEFQFCNYPFLG  QFCNYPFLG  6        0.5364
150.8    10.00  0.29     Sequence
 HLA-DPA10301-DPB10402  135       KVCEFQFCNYPFLGV  QFCNYPFLG  5        0.6140
65.1     4.00  0.43     Sequence         WB
 HLA-DPA10301-DPB10402  136       VCEFQFCNYPFLGVY  QFCNYPFLG  4        0.6366
51.0     3.00  0.47     Sequence         WB
 HLA-DPA10301-DPB10402  137       CEFQFCNYPFLGVYY  QFCNYPFLG  3        0.6568
41.0     1.80  0.47     Sequence         SB
 HLA-DPA10301-DPB10402  138       EFQFCNYPFLGVYYH  QFCNYPFLG  2        0.6625
38.6     1.70  0.48     Sequence         SB
 HLA-DPA10301-DPB10402  139       FQFCNYPFLGVYYHK  QFCNYPFLG  1        0.6803
31.8     1.20  0.40     Sequence         SB
 HLA-DPA10301-DPB10402  140       QFCNYPFLGVYYHKN  PFLGVYYHK  5        0.6211
60.3     3.50  0.49     Sequence         WB
 HLA-DPA10301-DPB10402  141       FCNYPFLGVYYHKNN  PFLGVYYHK  4        0.6102
67.9     4.00  0.56     Sequence         WB
 HLA-DPA10301-DPB10402  142       CNYPFLGVYYHKNNK  PFLGVYYHK  3        0.5997
76.1     4.50  0.64     Sequence         WB
 HLA-DPA10301-DPB10402  143       NYPFLGVYYHKNNKS  PFLGVYYHK  2        0.6030
73.4     4.50  0.65     Sequence         WB
 HLA-DPA10301-DPB10402  144       YPFLGVYYHKNNKSW  PFLGVYYHK  1        0.5496
130.7     8.50  0.64     Sequence         WB
 HLA-DPA10301-DPB10402  145       PFLGVYYHKNNKSWM  PFLGVYYHK  0        0.4354
449.8    24.00  0.46     Sequence
 HLA-DPA10301-DPB10402  146       FLGVYYHKNNKSWME  XFLGVYYHK -1        0.2735
2592.8    60.00  0.22     Sequence
 HLA-DPA10301-DPB10402  147       LGVYYHKNNKSWMES  VYYHKNNKS  2        0.1127
14763.2    95.00  0.17     Sequence
 HLA-DPA10301-DPB10402  148       GVYYHKNNKSWMESE  KNNKSWMES  5        0.1105
15122.6    95.00  0.19     Sequence
 HLA-DPA10301-DPB10402  149       VYYHKNNKSWMESEF  KNNKSWMES  4        0.1164
14191.7    95.00  0.25     Sequence
 HLA-DPA10301-DPB10402  150       YYHKNNKSWMESEFR  SWMESEFRX  7        0.1382
11211.6    90.00  0.17     Sequence
```

```
 HLA-DPA10301-DPB10402  151      YHKNNKSWMESEFRV  SWMESEFRV  6        0.2506
3320.4    65.00  0.44     Sequence
 HLA-DPA10301-DPB10402  152      HKNNKSWMESEFRVY  SWMESEFRV  5        0.3963
686.8    31.00   0.55     Sequence
 HLA-DPA10301-DPB10402  153      KNNKSWMESEFRVYS  SWMESEFRV  4        0.4379
437.9    24.00   0.57     Sequence
 HLA-DPA10301-DPB10402  154      NNKSWMESEFRVYSS  SWMESEFRV  3        0.4530
371.7    21.00   0.57     Sequence
 HLA-DPA10301-DPB10402  155      NKSWMESEFRVYSSA  SWMESEFRV  2        0.4609
341.3    20.00   0.57     Sequence
 HLA-DPA10301-DPB10402  156      KSWMESEFRVYSSAN  SWMESEFRV  1        0.4494
386.4    22.00   0.54     Sequence
 HLA-DPA10301-DPB10402  157      SWMESEFRVYSSANN  SWMESEFRV  0        0.3976
677.0    31.00   0.40     Sequence
 HLA-DPA10301-DPB10402  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.2949
2057.2    55.00  0.18     Sequence
 HLA-DPA10301-DPB10402  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.2150
4883.2    70.00  0.40     Sequence
 HLA-DPA10301-DPB10402  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.2190
4677.1    70.00  0.41     Sequence
 HLA-DPA10301-DPB10402  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.2235
4455.8    70.00  0.40     Sequence
 HLA-DPA10301-DPB10402  162      EFRVYSSANNCTFEY  FRVYSSANN  1        0.2120
5046.7    75.00  0.31     Sequence
 HLA-DPA10301-DPB10402  163      FRVYSSANNCTFEYV  SANNCTFEY  5        0.2372
3839.9    65.00  0.28     Sequence
 HLA-DPA10301-DPB10402  164      RVYSSANNCTFEYVS  SANNCTFEY  4        0.2639
2876.4    60.00  0.37     Sequence
 HLA-DPA10301-DPB10402  165      VYSSANNCTFEYVSQ  NCTFEYVSQ  6        0.2993
1960.7    55.00  0.38     Sequence
 HLA-DPA10301-DPB10402  166      YSSANNCTFEYVSQP  NCTFEYVSQ  5        0.3241
1499.6    46.00  0.47     Sequence
 HLA-DPA10301-DPB10402  167      SSANNCTFEYVSQPF  NCTFEYVSQ  4        0.3522
1107.1    40.00  0.52     Sequence
 HLA-DPA10301-DPB10402  168      SANNCTFEYVSQPFL  NCTFEYVSQ  3        0.4941
238.4    15.00   0.29     Sequence
 HLA-DPA10301-DPB10402  169      ANNCTFEYVSQPFLM  EYVSQPFLM  6        0.5853
88.9      5.50  0.46     Sequence         WB
 HLA-DPA10301-DPB10402  170      NNCTFEYVSQPFLMD  EYVSQPFLM  5        0.6875
29.4     1.00   0.66     Sequence         SB
 HLA-DPA10301-DPB10402  171      NCTFEYVSQPFLMDL  EYVSQPFLM  4        0.7203
20.6     0.50  0.70      Sequence         SB
 HLA-DPA10301-DPB10402  172      CTFEYVSQPFLMDLE  EYVSQPFLM  3        0.7287
18.8     0.50  0.69      Sequence         SB
 HLA-DPA10301-DPB10402  173      TFEYVSQPFLMDLEG  EYVSQPFLM  2        0.7276
19.0     0.50  0.69      Sequence         SB
 HLA-DPA10301-DPB10402  174      FEYVSQPFLMDLEGK  EYVSQPFLM  1        0.7168
21.4     0.60  0.69      Sequence         SB
 HLA-DPA10301-DPB10402  175      EYVSQPFLMDLEGKQ  EYVSQPFLM  0        0.5288
163.7    11.00   0.45     Sequence
 HLA-DPA10301-DPB10402  176      YVSQPFLMDLEGKQG  PFLMDLEGK  4        0.3949
697.1    32.00   0.18     Sequence
 HLA-DPA10301-DPB10402  177      VSQPFLMDLEGKQGN  PFLMDLEGK  3        0.3102
1742.9    49.00  0.29     Sequence
 HLA-DPA10301-DPB10402  178      SQPFLMDLEGKQGNF  FLMDLEGKQ  3        0.3087
1771.2    49.00  0.28     Sequence
 HLA-DPA10301-DPB10402  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2        0.3037
1871.1    55.00  0.31     Sequence
 HLA-DPA10301-DPB10402  180      PFLMDLEGKQGNFKN  LMDLEGKQG  2        0.2590
3032.5    60.00  0.29     Sequence
 HLA-DPA10301-DPB10402  181      FLMDLEGKQGNFKNL  LMDLEGKQG  1        0.2287
4211.9    70.00  0.32     Sequence
 HLA-DPA10301-DPB10402  182      LMDLEGKQGNFKNLS  GKQGNFKNL  5        0.1245
13003.8    90.00  0.20     Sequence
 HLA-DPA10301-DPB10402  183      MDLEGKQGNFKNLSE  GKQGNFKNL  4        0.1182
13919.6    90.00  0.28     Sequence
```

```
 HLA-DPA10301-DPB10402  184      DLEGKQGNFKNLSEF  GKQGNFKNL  3        0.1315
12052.3    90.00  0.28     Sequence
 HLA-DPA10301-DPB10402  185      LEGKQGNFKNLSEFV  GKQGNFKNL  2        0.1690
8032.8    80.00  0.19     Sequence
 HLA-DPA10301-DPB10402  186      EGKQGNFKNLSEFVF  NFKNLSEFV  5        0.2477
3428.8    65.00  0.31     Sequence
 HLA-DPA10301-DPB10402  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5        0.3146
1661.8    48.00  0.22     Sequence
 HLA-DPA10301-DPB10402  188      KQGNFKNLSEFVFKN  NLSEFVFKN  6        0.3785
832.9    35.00  0.29    Sequence
 HLA-DPA10301-DPB10402  189      QGNFKNLSEFVFKNI  NLSEFVFKN  5        0.4509
380.2    21.00  0.40    Sequence
 HLA-DPA10301-DPB10402  190      GNFKNLSEFVFKNID  NLSEFVFKN  4        0.4554
362.5    21.00  0.41    Sequence
 HLA-DPA10301-DPB10402  191      NFKNLSEFVFKNIDG  NLSEFVFKN  3        0.4496
385.6    22.00  0.39    Sequence
 HLA-DPA10301-DPB10402  192      FKNLSEFVFKNIDGY  NLSEFVFKN  2        0.4557
361.1    21.00  0.37    Sequence
 HLA-DPA10301-DPB10402  193      KNLSEFVFKNIDGYF  EFVFKNIDG  4        0.4228
515.8    26.00  0.31    Sequence
 HLA-DPA10301-DPB10402  194      NLSEFVFKNIDGYFK  EFVFKNIDG  3        0.3899
735.7    33.00  0.45    Sequence
 HLA-DPA10301-DPB10402  195      LSEFVFKNIDGYFKI  EFVFKNIDG  2        0.3934
708.8    32.00  0.49    Sequence
 HLA-DPA10301-DPB10402  196      SEFVFKNIDGYFKIY  EFVFKNIDG  1        0.3879
752.3    33.00  0.44    Sequence
 HLA-DPA10301-DPB10402  197      EFVFKNIDGYFKIYS  VFKNIDGYF  2        0.3672
940.3    37.00  0.20    Sequence
 HLA-DPA10301-DPB10402  198      FVFKNIDGYFKIYSK  KNIDGYFKI  3        0.3542
1083.3    40.00  0.22     Sequence
 HLA-DPA10301-DPB10402  199      VFKNIDGYFKIYSKH  KNIDGYFKI  2        0.3077
1790.9    50.00  0.34     Sequence
 HLA-DPA10301-DPB10402  200      FKNIDGYFKIYSKHT  IDGYFKIYS  3        0.3245
1492.6    46.00  0.27     Sequence
 HLA-DPA10301-DPB10402  201      KNIDGYFKIYSKHTP  IDGYFKIYS  2        0.3246
1491.6    46.00  0.22     Sequence
 HLA-DPA10301-DPB10402  202      NIDGYFKIYSKHTPI  YFKIYSKHT  4        0.3258
1472.5    46.00  0.29     Sequence
 HLA-DPA10301-DPB10402  203      IDGYFKIYSKHTPIN  YFKIYSKHT  3        0.3203
1562.2    47.00  0.32     Sequence
 HLA-DPA10301-DPB10402  204      DGYFKIYSKHTPINL  YFKIYSKHT  2        0.3280
1437.2    45.00  0.27     Sequence
 HLA-DPA10301-DPB10402  205      GYFKIYSKHTPINLV  YSKHTPINL  5        0.4101
591.4    29.00  0.28    Sequence
 HLA-DPA10301-DPB10402  206      YFKIYSKHTPINLVR  YSKHTPINL  4        0.4738
297.0    18.00  0.35    Sequence
 HLA-DPA10301-DPB10402  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.4494
386.5    22.00  0.40    Sequence
 HLA-DPA10301-DPB10402  208      KIYSKHTPINLVRDL  YSKHTPINL  2        0.4727
300.6    18.00  0.39    Sequence
 HLA-DPA10301-DPB10402  209      IYSKHTPINLVRDLP  KHTPINLVR  3        0.4687
313.9    19.00  0.36    Sequence
 HLA-DPA10301-DPB10402  210      YSKHTPINLVRDLPQ  KHTPINLVR  2        0.4614
339.7    20.00  0.38    Sequence
 HLA-DPA10301-DPB10402  211      SKHTPINLVRDLPQG  KHTPINLVR  1        0.4191
536.4    27.00  0.38    Sequence
 HLA-DPA10301-DPB10402  212      KHTPINLVRDLPQGF  PINLVRDLP  3        0.2752
2546.8    60.00  0.23     Sequence
 HLA-DPA10301-DPB10402  213      HTPINLVRDLPQGFS  PINLVRDLP  2        0.2134
4969.5    70.00  0.29     Sequence
 HLA-DPA10301-DPB10402  214      TPINLVRDLPQGFSA  PINLVRDLP  1        0.2135
4960.7    70.00  0.28     Sequence
 HLA-DPA10301-DPB10402  215      PINLVRDLPQGFSAL  RDLPQGFSA  5        0.2270
4289.1    70.00  0.22     Sequence
 HLA-DPA10301-DPB10402  216      INLVRDLPQGFSALE  RDLPQGFSA  4        0.2465
3471.2    65.00  0.28     Sequence
```

```
 HLA-DPA10301-DPB10402  217       NLVRDLPQGFSALEP  RDLPQGFSA  3         0.2635
2889.7    60.00  0.27     Sequence
 HLA-DPA10301-DPB10402  218       LVRDLPQGFSALEPL  PQGFSALEP  5         0.3348
1336.2    44.00  0.30     Sequence
 HLA-DPA10301-DPB10402  219       VRDLPQGFSALEPLV  PQGFSALEP  4         0.3956
691.8    31.00  0.30     Sequence
 HLA-DPA10301-DPB10402  220       RDLPQGFSALEPLVD  FSALEPLVD  6         0.4305
474.3    25.00  0.28     Sequence
 HLA-DPA10301-DPB10402  221       DLPQGFSALEPLVDL  FSALEPLVD  5         0.4846
264.1    16.00  0.42     Sequence
 HLA-DPA10301-DPB10402  222       LPQGFSALEPLVDLP  FSALEPLVD  4         0.4977
229.3    15.00  0.49     Sequence
 HLA-DPA10301-DPB10402  223       PQGFSALEPLVDLPI  FSALEPLVD  3         0.5196
181.0    12.00  0.48     Sequence
 HLA-DPA10301-DPB10402  224       QGFSALEPLVDLPIG  FSALEPLVD  2         0.5145
191.2    12.00  0.49     Sequence
 HLA-DPA10301-DPB10402  225       GFSALEPLVDLPIGI  FSALEPLVD  1         0.4706
307.2    18.00  0.40     Sequence
 HLA-DPA10301-DPB10402  226       FSALEPLVDLPIGIN  PLVDLPIGI  5         0.4718
303.4    18.00  0.47     Sequence
 HLA-DPA10301-DPB10402  227       SALEPLVDLPIGINI  PLVDLPIGI  4         0.4590
348.4    20.00  0.62     Sequence
 HLA-DPA10301-DPB10402  228       ALEPLVDLPIGINIT  PLVDLPIGI  3         0.4582
351.6    20.00  0.69     Sequence
 HLA-DPA10301-DPB10402  229       LEPLVDLPIGINITR  PLVDLPIGI  2         0.4669
319.9    19.00  0.69     Sequence
 HLA-DPA10301-DPB10402  230       EPLVDLPIGINITRF  PLVDLPIGI  1         0.4413
421.9    23.00  0.60     Sequence
 HLA-DPA10301-DPB10402  231       PLVDLPIGINITRFQ  PLVDLPIGI  0         0.3653
960.1    37.00  0.36     Sequence
 HLA-DPA10301-DPB10402  232       LVDLPIGINITRFQT  VDLPIGINI  1         0.3113
1722.8    49.00  0.22     Sequence
 HLA-DPA10301-DPB10402  233       VDLPIGINITRFQTL  GINITRFQT  5         0.3859
768.7    33.00  0.57     Sequence
 HLA-DPA10301-DPB10402  234       DLPIGINITRFQTLL  GINITRFQT  4         0.4757
290.9    18.00  0.59     Sequence
 HLA-DPA10301-DPB10402  235       LPIGINITRFQTLLA  GINITRFQT  3         0.5633
112.7     7.50  0.47     Sequence        WB
 HLA-DPA10301-DPB10402  236       PIGINITRFQTLLAL  ITRFQTLLA  5         0.5913
83.3     5.00  0.34     Sequence        WB
 HLA-DPA10301-DPB10402  237       IGINITRFQTLLALH  ITRFQTLLA  4         0.6168
63.2     3.50  0.34     Sequence        WB
 HLA-DPA10301-DPB10402  238       GINITRFQTLLALHR  ITRFQTLLA  3         0.6726
34.6     1.40  0.29     Sequence        SB
 HLA-DPA10301-DPB10402  239       INITRFQTLLALHRS  ITRFQTLLA  2         0.6868
29.6     1.10  0.25     Sequence        SB
 HLA-DPA10301-DPB10402  240       NITRFQTLLALHRSY  RFQTLLALH  3         0.6847
30.3     1.10  0.32     Sequence        SB
 HLA-DPA10301-DPB10402  241       ITRFQTLLALHRSYL  RFQTLLALH  2         0.6836
30.7     1.10  0.34     Sequence        SB
 HLA-DPA10301-DPB10402  242       TRFQTLLALHRSYLT  FQTLLALHR  2         0.6650
37.5     1.60  0.29     Sequence        SB
 HLA-DPA10301-DPB10402  243       RFQTLLALHRSYLTP  TLLALHRSY  3         0.6472
45.5     2.50  0.20     Sequence        WB
 HLA-DPA10301-DPB10402  244       FQTLLALHRSYLTPG  TLLALHRSY  2         0.5737
100.8     6.50  0.33     Sequence        WB
 HLA-DPA10301-DPB10402  245       QTLLALHRSYLTPGD  TLLALHRSY  1         0.4702
308.7    18.00  0.41     Sequence
 HLA-DPA10301-DPB10402  246       TLLALHRSYLTPGDS  ALHRSYLTP  3         0.4075
608.5    29.00  0.30     Sequence
 HLA-DPA10301-DPB10402  247       LLALHRSYLTPGDSS  ALHRSYLTP  2         0.3580
1039.1    39.00  0.42     Sequence
 HLA-DPA10301-DPB10402  248       LALHRSYLTPGDSSS  ALHRSYLTP  1         0.2177
4743.5    70.00  0.50     Sequence
 HLA-DPA10301-DPB10402  249       ALHRSYLTPGDSSSG  ALHRSYLTP  0         0.1413
10844.0    90.00  0.34     Sequence
```

```
 HLA-DPA10301-DPB10402  250      LHRSYLTPGDSSSGW  RSYLTPGDS  2        0.1074
15634.9    95.00  0.32     Sequence
 HLA-DPA10301-DPB10402  251      HRSYLTPGDSSSGWT  RSYLTPGDS  1        0.0774
21650.2   100.00  0.28     Sequence
 HLA-DPA10301-DPB10402  252      RSYLTPGDSSSGWTA  YLTPGDSSS  2        0.0686
23790.8   100.00  0.38     Sequence
 HLA-DPA10301-DPB10402  253      SYLTPGDSSSGWTAG  YLTPGDSSS  1        0.0545
27713.3   100.00  0.36     Sequence
 HLA-DPA10301-DPB10402  254      YLTPGDSSSGWTAGA  YLTPGDSSS  0        0.0440
31059.3   100.00  0.21     Sequence
 HLA-DPA10301-DPB10402  255      LTPGDSSSGWTAGAA  GDSSSGWTA  3        0.0355
34050.5   100.00  0.21     Sequence
 HLA-DPA10301-DPB10402  256      TPGDSSSGWTAGAAA  SSGWTAGAA  5        0.0426
31547.7   100.00  0.22     Sequence
 HLA-DPA10301-DPB10402  257      PGDSSSGWTAGAAAY  SGWTAGAAA  5        0.0530
28189.9   100.00  0.28     Sequence
 HLA-DPA10301-DPB10402  258      GDSSSGWTAGAAAYY  SGWTAGAAA  4        0.0707
23267.7   100.00  0.24     Sequence
 HLA-DPA10301-DPB10402  259      DSSSGWTAGAAAYYV  SGWTAGAAA  3        0.0932
18246.8    95.00  0.19     Sequence
 HLA-DPA10301-DPB10402  260      SSSGWTAGAAAYYVG  SGWTAGAAA  2        0.0958
17732.0    95.00  0.22     Sequence
 HLA-DPA10301-DPB10402  261      SSGWTAGAAAYYVGY  WTAGAAAYY  3        0.1056
15957.0    95.00  0.23     Sequence
 HLA-DPA10301-DPB10402  262      SGWTAGAAAYYVGYL  GAAAYYVGY  5        0.2089
5218.9    75.00  0.26    Sequence
 HLA-DPA10301-DPB10402  263      GWTAGAAAYYVGYLQ  AAYYVGYLQ  6        0.2895
2181.3    55.00  0.34    Sequence
 HLA-DPA10301-DPB10402  264      WTAGAAAYYVGYLQP  AYYVGYLQP  6        0.4003
657.6    31.00  0.38    Sequence
 HLA-DPA10301-DPB10402  265      TAGAAAYYVGYLQPR  AYYVGYLQP  5        0.5141
191.9    12.00  0.61    Sequence
 HLA-DPA10301-DPB10402  266      AGAAAYYVGYLQPRT  AYYVGYLQP  4        0.5497
130.7     8.50  0.62    Sequence         WB
 HLA-DPA10301-DPB10402  267      GAAAYYVGYLQPRTF  AYYVGYLQP  3        0.5766
97.6     6.00  0.61    Sequence         WB
 HLA-DPA10301-DPB10402  268      AAAYYVGYLQPRTFL  AYYVGYLQP  2        0.5916
83.0     5.00  0.60    Sequence         WB
 HLA-DPA10301-DPB10402  269      AAYYVGYLQPRTFLL  AYYVGYLQP  1        0.5888
85.5     5.50  0.51    Sequence         WB
 HLA-DPA10301-DPB10402  270      AYYVGYLQPRTFLLK  AYYVGYLQP  0        0.5524
126.9     8.00  0.34    Sequence         WB
 HLA-DPA10301-DPB10402  271      YYVGYLQPRTFLLKY  YLQPRTFLL  4        0.5020
218.7    14.00  0.34    Sequence
 HLA-DPA10301-DPB10402  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.4582
351.5    20.00  0.38    Sequence
 HLA-DPA10301-DPB10402  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.4364
445.2    24.00  0.42    Sequence
 HLA-DPA10301-DPB10402  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.4142
565.5    28.00  0.38    Sequence
 HLA-DPA10301-DPB10402  275      YLQPRTFLLKYNENG  LQPRTFLLK  1        0.3280
1437.6    45.00  0.22    Sequence
 HLA-DPA10301-DPB10402  276      LQPRTFLLKYNENGT  TFLLKYNEN  4        0.2800
2415.6    60.00  0.23    Sequence
 HLA-DPA10301-DPB10402  277      QPRTFLLKYNENGTI  TFLLKYNEN  3        0.2876
2225.5    55.00  0.26    Sequence
 HLA-DPA10301-DPB10402  278      PRTFLLKYNENGTIT  TFLLKYNEN  2        0.2872
2235.4    55.00  0.26    Sequence
 HLA-DPA10301-DPB10402  279      RTFLLKYNENGTITD  LLKYNENGT  3        0.2878
2222.1    55.00  0.28    Sequence
 HLA-DPA10301-DPB10402  280      TFLLKYNENGTITDA  LLKYNENGT  2        0.2571
3097.0    65.00  0.35    Sequence
 HLA-DPA10301-DPB10402  281      FLLKYNENGTITDAV  LLKYNENGT  1        0.2329
4023.8    70.00  0.38    Sequence
 HLA-DPA10301-DPB10402  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.1676
8152.8    80.00  0.29    Sequence
```

```
 HLA-DPA10301-DPB10402  283      LKYNENGTITDAVDC  LKYNENGTI  0        0.1150
14402.5    95.00  0.28     Sequence
 HLA-DPA10301-DPB10402  284      KYNENGTITDAVDCA  NENGTITDA  2        0.0869
19520.4   100.00  0.17     Sequence
 HLA-DPA10301-DPB10402  285      YNENGTITDAVDCAL  TITDAVDCA  5        0.0968
17539.6    95.00  0.28     Sequence
 HLA-DPA10301-DPB10402  286      NENGTITDAVDCALD  TITDAVDCA  4        0.1076
15607.5    95.00  0.28     Sequence
 HLA-DPA10301-DPB10402  287      ENGTITDAVDCALDP  TITDAVDCA  3        0.1232
13191.0    90.00  0.26     Sequence
 HLA-DPA10301-DPB10402  288      NGTITDAVDCALDPL  DAVDCALDP  5        0.1618
8681.0    85.00  0.24     Sequence
 HLA-DPA10301-DPB10402  289      GTITDAVDCALDPLS  DAVDCALDP  4        0.1951
6057.5    75.00  0.24     Sequence
 HLA-DPA10301-DPB10402  290      TITDAVDCALDPLSE  DCALDPLSE  6        0.2213
4563.2    70.00  0.29     Sequence
 HLA-DPA10301-DPB10402  291      ITDAVDCALDPLSET  DCALDPLSE  5        0.2538
3208.0    65.00  0.50     Sequence
 HLA-DPA10301-DPB10402  292      TDAVDCALDPLSETK  DCALDPLSE  4        0.2588
3040.0    60.00  0.56     Sequence
 HLA-DPA10301-DPB10402  293      DAVDCALDPLSETKC  DCALDPLSE  3        0.2619
2940.5    60.00  0.57     Sequence
 HLA-DPA10301-DPB10402  294      AVDCALDPLSETKCT  DCALDPLSE  2        0.2660
2813.5    60.00  0.61     Sequence
 HLA-DPA10301-DPB10402  295      VDCALDPLSETKCTL  DCALDPLSE  1        0.2399
3730.6    65.00  0.54     Sequence
 HLA-DPA10301-DPB10402  296      DCALDPLSETKCTLK  DCALDPLSE  0        0.1939
6136.2    75.00  0.22     Sequence
 HLA-DPA10301-DPB10402  297      CALDPLSETKCTLKS  PLSETKCTL  4        0.1907
6352.0    75.00  0.29     Sequence
 HLA-DPA10301-DPB10402  298      ALDPLSETKCTLKSF  PLSETKCTL  3        0.1967
5954.5    75.00  0.29     Sequence
 HLA-DPA10301-DPB10402  299      LDPLSETKCTLKSFT  PLSETKCTL  2        0.2223
4511.0    70.00  0.23     Sequence
 HLA-DPA10301-DPB10402  300      DPLSETKCTLKSFTV  KCTLKSFTV  6        0.2338
3984.4    70.00  0.18     Sequence
 HLA-DPA10301-DPB10402  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.2796
2427.6    60.00  0.36     Sequence
 HLA-DPA10301-DPB10402  302      LSETKCTLKSFTVEK  KCTLKSFTV  4        0.3264
1462.2    46.00  0.44     Sequence
 HLA-DPA10301-DPB10402  303      SETKCTLKSFTVEKG  TLKSFTVEK  5        0.3465
1177.6    41.00  0.37     Sequence
 HLA-DPA10301-DPB10402  304      ETKCTLKSFTVEKGI  TLKSFTVEK  4        0.3807
812.7    34.00  0.42    Sequence
 HLA-DPA10301-DPB10402  305      TKCTLKSFTVEKGIY  TLKSFTVEK  3        0.3758
857.0    35.00  0.44    Sequence
 HLA-DPA10301-DPB10402  306      KCTLKSFTVEKGIYQ  TLKSFTVEK  2        0.3719
893.8    36.00  0.44    Sequence
 HLA-DPA10301-DPB10402  307      CTLKSFTVEKGIYQT  TLKSFTVEK  1        0.3646
967.5    38.00  0.37    Sequence
 HLA-DPA10301-DPB10402  308      TLKSFTVEKGIYQTS  SFTVEKGIY  3        0.3382
1287.5    43.00  0.31     Sequence
 HLA-DPA10301-DPB10402  309      LKSFTVEKGIYQTSN  SFTVEKGIY  2        0.3046
1852.3    50.00  0.43     Sequence
 HLA-DPA10301-DPB10402  310      KSFTVEKGIYQTSNF  SFTVEKGIY  1        0.2874
2231.4    55.00  0.41     Sequence
 HLA-DPA10301-DPB10402  311      SFTVEKGIYQTSNFR  TVEKGIYQT  2        0.2548
3173.5    65.00  0.22     Sequence
 HLA-DPA10301-DPB10402  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.3917
721.7    32.00  0.44    Sequence
 HLA-DPA10301-DPB10402  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.4967
231.6    15.00  0.62    Sequence
 HLA-DPA10301-DPB10402  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.5372
149.5     9.50  0.64    Sequence         WB
 HLA-DPA10301-DPB10402  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.5525
126.8     8.00  0.64    Sequence         WB
```

```
 HLA-DPA10301-DPB10402  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.5523
126.9     8.00  0.64     Sequence         WB
 HLA-DPA10301-DPB10402  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.5110
198.4    13.00  0.62     Sequence
 HLA-DPA10301-DPB10402  318      IYQTSNFRVQPTESI  IYQTSNFRV  0        0.4746
294.2    18.00  0.47     Sequence
 HLA-DPA10301-DPB10402  319      YQTSNFRVQPTESIV  NFRVQPTES  4        0.3352
1330.1    44.00  0.33     Sequence
 HLA-DPA10301-DPB10402  320      QTSNFRVQPTESIVR  NFRVQPTES  3        0.3106
1736.2    49.00  0.47     Sequence
 HLA-DPA10301-DPB10402  321      TSNFRVQPTESIVRF  NFRVQPTES  2        0.3338
1350.6    44.00  0.44     Sequence
 HLA-DPA10301-DPB10402  322      SNFRVQPTESIVRFP  NFRVQPTES  1        0.3475
1164.7    41.00  0.42     Sequence
 HLA-DPA10301-DPB10402  323      NFRVQPTESIVRFPN  RVQPTESIV  2        0.3272
1450.9    46.00  0.26     Sequence
 HLA-DPA10301-DPB10402  324      FRVQPTESIVRFPNI  RVQPTESIV  1        0.3107
1734.5    49.00  0.28     Sequence
 HLA-DPA10301-DPB10402  325      RVQPTESIVRFPNIT  VQPTESIVR  1        0.2306
4126.0    70.00  0.19     Sequence
 HLA-DPA10301-DPB10402  326      VQPTESIVRFPNITN  IVRFPNITN  6        0.2516
3285.2    65.00  0.28     Sequence
 HLA-DPA10301-DPB10402  327      QPTESIVRFPNITNL  IVRFPNITN  5        0.3006
1933.5    55.00  0.43     Sequence
 HLA-DPA10301-DPB10402  328      PTESIVRFPNITNLC  IVRFPNITN  4        0.3238
1504.0    46.00  0.44     Sequence
 HLA-DPA10301-DPB10402  329      TESIVRFPNITNLCP  IVRFPNITN  3        0.3413
1245.1    43.00  0.42     Sequence
 HLA-DPA10301-DPB10402  330      ESIVRFPNITNLCPF  IVRFPNITN  2        0.3527
1100.2    40.00  0.40     Sequence
 HLA-DPA10301-DPB10402  331      SIVRFPNITNLCPFG  IVRFPNITN  1        0.3339
1348.8    44.00  0.37     Sequence
 HLA-DPA10301-DPB10402  332      IVRFPNITNLCPFGE  FPNITNLCP  3        0.3255
1477.4    46.00  0.19     Sequence
 HLA-DPA10301-DPB10402  333      VRFPNITNLCPFGEV  ITNLCPFGE  5        0.3183
1597.6    47.00  0.26     Sequence
 HLA-DPA10301-DPB10402  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.3094
1759.2    49.00  0.31     Sequence
 HLA-DPA10301-DPB10402  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.2980
1990.1    55.00  0.31     Sequence
 HLA-DPA10301-DPB10402  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.3000
1945.9    55.00  0.31     Sequence
 HLA-DPA10301-DPB10402  337      NITNLCPFGEVFNAT  CPFGEVFNA  5        0.3270
1453.8    46.00  0.30     Sequence
 HLA-DPA10301-DPB10402  338      ITNLCPFGEVFNATR  CPFGEVFNA  4        0.3677
935.6    37.00  0.35     Sequence
 HLA-DPA10301-DPB10402  339      TNLCPFGEVFNATRF  CPFGEVFNA  3        0.3828
795.0    34.00  0.38     Sequence
 HLA-DPA10301-DPB10402  340      NLCPFGEVFNATRFA  CPFGEVFNA  2        0.4118
580.5    28.00  0.34     Sequence
 HLA-DPA10301-DPB10402  341      LCPFGEVFNATRFAS  VFNATRFAS  6        0.4467
398.2    22.00  0.41     Sequence
 HLA-DPA10301-DPB10402  342      CPFGEVFNATRFASV  VFNATRFAS  5        0.5384
147.6     9.50  0.65     Sequence         WB
 HLA-DPA10301-DPB10402  343      PFGEVFNATRFASVY  VFNATRFAS  4        0.5936
81.2     5.00  0.74     Sequence         WB
 HLA-DPA10301-DPB10402  344      FGEVFNATRFASVYA  VFNATRFAS  3        0.6701
35.5     1.50  0.70     Sequence         SB
 HLA-DPA10301-DPB10402  345      GEVFNATRFASVYAW  VFNATRFAS  2        0.6678
36.4     1.50  0.68     Sequence         SB
 HLA-DPA10301-DPB10402  346      EVFNATRFASVYAWN  VFNATRFAS  1        0.6475
45.3     2.50  0.57     Sequence         WB
 HLA-DPA10301-DPB10402  347      VFNATRFASVYAWNR  RFASVYAWN  5        0.6036
72.9     4.50  0.28     Sequence         WB
 HLA-DPA10301-DPB10402  348      FNATRFASVYAWNRK  RFASVYAWN  4        0.5707
104.0     6.50  0.43     Sequence         WB
```

```
 HLA-DPA10301-DPB10402  349      NATRFASVYAWNRKR  RFASVYAWN  3        0.5278
165.5    11.00  0.60     Sequence
 HLA-DPA10301-DPB10402  350      ATRFASVYAWNRKRI  RFASVYAWN  2        0.5230
174.3    11.00  0.58     Sequence
 HLA-DPA10301-DPB10402  351      TRFASVYAWNRKRIS  RFASVYAWN  1        0.4441
409.2    23.00  0.47     Sequence
 HLA-DPA10301-DPB10402  352      RFASVYAWNRKRISN  RFASVYAWN  0        0.3907
729.9    32.00  0.30     Sequence
 HLA-DPA10301-DPB10402  353      FASVYAWNRKRISNC  VYAWNRKRI  3        0.3337
1351.4    44.00  0.41     Sequence
 HLA-DPA10301-DPB10402  354      ASVYAWNRKRISNCV  VYAWNRKRI  2        0.2657
2820.2    60.00  0.47     Sequence
 HLA-DPA10301-DPB10402  355      SVYAWNRKRISNCVA  VYAWNRKRI  1        0.2650
2843.3    60.00  0.43     Sequence
 HLA-DPA10301-DPB10402  356      VYAWNRKRISNCVAD  VYAWNRKRI  0        0.2346
3948.9    70.00  0.32     Sequence
 HLA-DPA10301-DPB10402  357      YAWNRKRISNCVADY  KRISNCVAD  5        0.1547
9372.8    85.00  0.22     Sequence
 HLA-DPA10301-DPB10402  358      AWNRKRISNCVADYS  KRISNCVAD  4        0.1358
11507.3    90.00  0.32     Sequence
 HLA-DPA10301-DPB10402  359      WNRKRISNCVADYSV  KRISNCVAD  3        0.1469
10202.0    85.00  0.35     Sequence
 HLA-DPA10301-DPB10402  360      NRKRISNCVADYSVL  KRISNCVAD  2        0.1793
7185.8    80.00  0.28     Sequence
 HLA-DPA10301-DPB10402  361      RKRISNCVADYSVLY  NCVADYSVL  5        0.2349
3935.4    70.00  0.31     Sequence
 HLA-DPA10301-DPB10402  362      KRISNCVADYSVLYN  CVADYSVLY  5        0.2803
2409.6    60.00  0.28     Sequence
 HLA-DPA10301-DPB10402  363      RISNCVADYSVLYNS  CVADYSVLY  4        0.2950
2054.4    55.00  0.31     Sequence
 HLA-DPA10301-DPB10402  364      ISNCVADYSVLYNSA  VADYSVLYN  4        0.3076
1792.3    50.00  0.28     Sequence
 HLA-DPA10301-DPB10402  365      SNCVADYSVLYNSAS  VADYSVLYN  3        0.3015
1915.6    55.00  0.27     Sequence
 HLA-DPA10301-DPB10402  366      NCVADYSVLYNSASF  VADYSVLYN  2        0.3021
1902.7    55.00  0.27     Sequence
 HLA-DPA10301-DPB10402  367      CVADYSVLYNSASFS  VADYSVLYN  1        0.2891
2191.1    55.00  0.22     Sequence
 HLA-DPA10301-DPB10402  368      VADYSVLYNSASFST  LYNSASFST  6        0.3069
1807.1    50.00  0.31     Sequence
 HLA-DPA10301-DPB10402  369      ADYSVLYNSASFSTF  LYNSASFST  5        0.3485
1152.3    41.00  0.50     Sequence
 HLA-DPA10301-DPB10402  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.3783
834.6    35.00  0.56     Sequence
 HLA-DPA10301-DPB10402  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.3998
661.3    31.00  0.57     Sequence
 HLA-DPA10301-DPB10402  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.4078
606.6    29.00  0.60     Sequence
 HLA-DPA10301-DPB10402  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.3562
1059.9    39.00  0.51     Sequence
 HLA-DPA10301-DPB10402  374      LYNSASFSTFKCYGV  SFSTFKCYG  5        0.3467
1173.9    41.00  0.23     Sequence
 HLA-DPA10301-DPB10402  375      YNSASFSTFKCYGVS  SFSTFKCYG  4        0.3071
1802.6    50.00  0.37     Sequence
 HLA-DPA10301-DPB10402  376      NSASFSTFKCYGVSP  SFSTFKCYG  3        0.3090
1766.5    49.00  0.44     Sequence
 HLA-DPA10301-DPB10402  377      SASFSTFKCYGVSPT  SFSTFKCYG  2        0.3345
1340.0    44.00  0.40     Sequence
 HLA-DPA10301-DPB10402  378      ASFSTFKCYGVSPTK  SFSTFKCYG  1        0.3392
1274.2    43.00  0.34     Sequence
 HLA-DPA10301-DPB10402  379      SFSTFKCYGVSPTKL  KCYGVSPTK  5        0.3574
1046.4    39.00  0.22     Sequence
 HLA-DPA10301-DPB10402  380      FSTFKCYGVSPTKLN  KCYGVSPTK  4        0.3519
1110.0    40.00  0.28     Sequence
 HLA-DPA10301-DPB10402  381      STFKCYGVSPTKLND  KCYGVSPTK  3        0.3172
1616.1    48.00  0.33     Sequence
```

```
 HLA-DPA10301-DPB10402  382      TFKCYGVSPTKLNDL  KCYGVSPTK  2        0.3348
1336.2    44.00  0.31     Sequence
 HLA-DPA10301-DPB10402  383      FKCYGVSPTKLNDLC  GVSPTKLND  4        0.3061
1823.0    50.00  0.28     Sequence
 HLA-DPA10301-DPB10402  384      KCYGVSPTKLNDLCF  GVSPTKLND  3        0.3017
1911.3    55.00  0.38     Sequence
 HLA-DPA10301-DPB10402  385      CYGVSPTKLNDLCFT  GVSPTKLND  2        0.3124
1702.9    49.00  0.31     Sequence
 HLA-DPA10301-DPB10402  386      YGVSPTKLNDLCFTN  KLNDLCFTN  6        0.3316
1382.3    45.00  0.34     Sequence
 HLA-DPA10301-DPB10402  387      GVSPTKLNDLCFTNV  KLNDLCFTN  5        0.3920
719.1    32.00  0.56     Sequence
 HLA-DPA10301-DPB10402  388      VSPTKLNDLCFTNVY  KLNDLCFTN  4        0.4486
390.1    22.00  0.51     Sequence
 HLA-DPA10301-DPB10402  389      SPTKLNDLCFTNVYA  KLNDLCFTN  3        0.4838
266.3    16.00  0.50     Sequence
 HLA-DPA10301-DPB10402  390      PTKLNDLCFTNVYAD  KLNDLCFTN  2        0.4914
245.3    15.00  0.48     Sequence
 HLA-DPA10301-DPB10402  391      TKLNDLCFTNVYADS  KLNDLCFTN  1        0.4878
255.2    16.00  0.37     Sequence
 HLA-DPA10301-DPB10402  392      KLNDLCFTNVYADSF  DLCFTNVYA  3        0.5007
222.0    14.00  0.29     Sequence
 HLA-DPA10301-DPB10402  393      LNDLCFTNVYADSFV  CFTNVYADS  4        0.5149
190.3    12.00  0.38     Sequence
 HLA-DPA10301-DPB10402  394      NDLCFTNVYADSFVI  CFTNVYADS  3        0.5352
152.8    10.00  0.37     Sequence
 HLA-DPA10301-DPB10402  395      DLCFTNVYADSFVIR  CFTNVYADS  2        0.5346
153.9    10.00  0.36     Sequence
 HLA-DPA10301-DPB10402  396      LCFTNVYADSFVIRG  CFTNVYADS  1        0.5072
206.7    13.00  0.34     Sequence
 HLA-DPA10301-DPB10402  397      CFTNVYADSFVIRGD  NVYADSFVI  3        0.4798
278.2    17.00  0.30     Sequence
 HLA-DPA10301-DPB10402  398      FTNVYADSFVIRGDE  NVYADSFVI  2        0.4486
389.9    22.00  0.34     Sequence
 HLA-DPA10301-DPB10402  399      TNVYADSFVIRGDEV  VYADSFVIR  2        0.3391
1274.6    43.00  0.41     Sequence
 HLA-DPA10301-DPB10402  400      NVYADSFVIRGDEVR  VYADSFVIR  1        0.3016
1914.1    55.00  0.35     Sequence
 HLA-DPA10301-DPB10402  401      VYADSFVIRGDEVRQ  SFVIRGDEV  4        0.2640
2874.6    60.00  0.20     Sequence
 HLA-DPA10301-DPB10402  402      YADSFVIRGDEVRQI  VIRGDEVRQ  5        0.2751
2547.3    60.00  0.41     Sequence
 HLA-DPA10301-DPB10402  403      ADSFVIRGDEVRQIA  VIRGDEVRQ  4        0.2828
2344.7    55.00  0.49     Sequence
 HLA-DPA10301-DPB10402  404      DSFVIRGDEVRQIAP  VIRGDEVRQ  3        0.2942
2072.2    55.00  0.50     Sequence
 HLA-DPA10301-DPB10402  405      SFVIRGDEVRQIAPG  VIRGDEVRQ  2        0.2975
2000.1    55.00  0.54     Sequence
 HLA-DPA10301-DPB10402  406      FVIRGDEVRQIAPGQ  VIRGDEVRQ  1        0.2659
2815.4    60.00  0.54     Sequence
 HLA-DPA10301-DPB10402  407      VIRGDEVRQIAPGQT  VIRGDEVRQ  0        0.1730
7694.1    80.00  0.35     Sequence
 HLA-DPA10301-DPB10402  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.1139
14579.2    95.00  0.22     Sequence
 HLA-DPA10301-DPB10402  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.0769
21760.4   100.00  0.37     Sequence
 HLA-DPA10301-DPB10402  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.0784
21401.7   100.00  0.36     Sequence
 HLA-DPA10301-DPB10402  411      DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.0883
19236.9    95.00  0.31     Sequence
 HLA-DPA10301-DPB10402  412      EVRQIAPGQTGTIAD  VRQIAPGQT  1        0.0945
17980.4    95.00  0.28     Sequence
 HLA-DPA10301-DPB10402  413      VRQIAPGQTGTIADY  PGQTGTIAD  5        0.0796
21127.7   100.00  0.23     Sequence
 HLA-DPA10301-DPB10402  414      RQIAPGQTGTIADYN  PGQTGTIAD  4        0.0689
23725.0   100.00  0.28     Sequence
```

```
 HLA-DPA10301-DPB10402  415      QIAPGQTGTIADYNY  PGQTGTIAD  3        0.0717
23006.6   100.00  0.29     Sequence
 HLA-DPA10301-DPB10402  416      IAPGQTGTIADYNYK  PGQTGTIAD  2        0.0777
21559.5   100.00  0.23     Sequence
 HLA-DPA10301-DPB10402  417      APGQTGTIADYNYKL  TIADYNYKL  6        0.1379
11248.5    90.00  0.24     Sequence
 HLA-DPA10301-DPB10402  418      PGQTGTIADYNYKLP  IADYNYKLP  6        0.1956
6021.1    75.00  0.24     Sequence
 HLA-DPA10301-DPB10402  419      GQTGTIADYNYKLPD  IADYNYKLP  5        0.2020
5618.6    75.00  0.26     Sequence
 HLA-DPA10301-DPB10402  420      QTGTIADYNYKLPDD  IADYNYKLP  4        0.1998
5758.1    75.00  0.25     Sequence
 HLA-DPA10301-DPB10402  421      TGTIADYNYKLPDDF  IADYNYKLP  3        0.2012
5668.4    75.00  0.25     Sequence
 HLA-DPA10301-DPB10402  422      GTIADYNYKLPDDFT  IADYNYKLP  2        0.1952
6048.6    75.00  0.27     Sequence
 HLA-DPA10301-DPB10402  423      TIADYNYKLPDDFTG  IADYNYKLP  1        0.1749
7536.5    80.00  0.26     Sequence
 HLA-DPA10301-DPB10402  424      IADYNYKLPDDFTGC  YKLPDDFTG  5        0.1258
12824.7    90.00  0.33     Sequence
 HLA-DPA10301-DPB10402  425      ADYNYKLPDDFTGCV  YKLPDDFTG  4        0.1422
10737.2    90.00  0.42     Sequence
 HLA-DPA10301-DPB10402  426      DYNYKLPDDFTGCVI  PDDFTGCVI  6        0.1942
6113.8    75.00  0.28     Sequence
 HLA-DPA10301-DPB10402  427      YNYKLPDDFTGCVIA  PDDFTGCVI  5        0.2297
4163.5    70.00  0.29     Sequence
 HLA-DPA10301-DPB10402  428      NYKLPDDFTGCVIAW  PDDFTGCVI  4        0.2451
3526.9    65.00  0.28     Sequence
 HLA-DPA10301-DPB10402  429      YKLPDDFTGCVIAWN  DFTGCVIAW  5        0.2558
3140.1    65.00  0.32     Sequence
 HLA-DPA10301-DPB10402  430      KLPDDFTGCVIAWNS  DFTGCVIAW  4        0.2562
3125.5    65.00  0.41     Sequence
 HLA-DPA10301-DPB10402  431      LPDDFTGCVIAWNSN  DFTGCVIAW  3        0.2425
3625.0    65.00  0.46     Sequence
 HLA-DPA10301-DPB10402  432      PDDFTGCVIAWNSNN  DFTGCVIAW  2        0.2268
4297.4    70.00  0.50     Sequence
 HLA-DPA10301-DPB10402  433      DDFTGCVIAWNSNNL  DFTGCVIAW  1        0.2534
3222.1    65.00  0.28     Sequence
 HLA-DPA10301-DPB10402  434      DFTGCVIAWNSNNLD  VIAWNSNNL  5        0.2492
3373.2    65.00  0.19     Sequence
 HLA-DPA10301-DPB10402  435      FTGCVIAWNSNNLDS  VIAWNSNNL  4        0.2645
2856.7    60.00  0.22     Sequence
 HLA-DPA10301-DPB10402  436      TGCVIAWNSNNLDSK  AWNSNNLDS  5        0.2737
2587.7    60.00  0.29     Sequence
 HLA-DPA10301-DPB10402  437      GCVIAWNSNNLDSKV  AWNSNNLDS  4        0.2803
2410.0    60.00  0.32     Sequence
 HLA-DPA10301-DPB10402  438      CVIAWNSNNLDSKVG  AWNSNNLDS  3        0.2777
2478.4    60.00  0.34     Sequence
 HLA-DPA10301-DPB10402  439      VIAWNSNNLDSKVGG  AWNSNNLDS  2        0.2608
2976.1    60.00  0.38     Sequence
 HLA-DPA10301-DPB10402  440      IAWNSNNLDSKVGGN  AWNSNNLDS  1        0.1251
12913.5    90.00  0.55     Sequence
 HLA-DPA10301-DPB10402  441      AWNSNNLDSKVGGNY  AWNSNNLDS  0        0.0747
22292.5   100.00  0.35     Sequence
 HLA-DPA10301-DPB10402  442      WNSNNLDSKVGGNYN  NNLDSKVGG  3        0.0530
28164.0   100.00  0.19     Sequence
 HLA-DPA10301-DPB10402  443      NSNNLDSKVGGNYNY  NNLDSKVGG  2        0.0505
28965.4   100.00  0.25     Sequence
 HLA-DPA10301-DPB10402  444      SNNLDSKVGGNYNYL  SKVGGNYNY  5        0.0867
19562.5   100.00  0.34     Sequence
 HLA-DPA10301-DPB10402  445      NNLDSKVGGNYNYLY  SKVGGNYNY  4        0.1242
13035.6    90.00  0.31     Sequence
 HLA-DPA10301-DPB10402  446      NLDSKVGGNYNYLYR  GGNYNYLYR  6        0.1644
8440.4    85.00  0.31     Sequence
 HLA-DPA10301-DPB10402  447      LDSKVGGNYNYLYRL  GGNYNYLYR  5        0.2143
4922.8    70.00  0.38     Sequence
```

```
 HLA-DPA10301-DPB10402  448      DSKVGGNYNYLYRLF  GGNYNYLYR  4        0.2556
3146.4    65.00  0.35      Sequence
 HLA-DPA10301-DPB10402  449      SKVGGNYNYLYRLFR  GGNYNYLYR  3        0.3057
1829.6    50.00  0.28      Sequence
 HLA-DPA10301-DPB10402  450      KVGGNYNYLYRLFRK  NYLYRLFRK  6        0.3776
841.1    35.00  0.35     Sequence
 HLA-DPA10301-DPB10402  451      VGGNYNYLYRLFRKS  NYLYRLFRK  5        0.4719
303.1    18.00  0.59     Sequence
 HLA-DPA10301-DPB10402  452      GGNYNYLYRLFRKSN  NYLYRLFRK  4        0.4941
238.4    15.00  0.57     Sequence
 HLA-DPA10301-DPB10402  453      GNYNYLYRLFRKSNL  NYLYRLFRK  3        0.5205
179.1    12.00  0.54     Sequence
 HLA-DPA10301-DPB10402  454      NYNYLYRLFRKSNLK  NYLYRLFRK  2        0.5449
137.5     9.00  0.52     Sequence         WB
 HLA-DPA10301-DPB10402  455      YNYLYRLFRKSNLKP  NYLYRLFRK  1        0.5421
141.8     9.00  0.44     Sequence         WB
 HLA-DPA10301-DPB10402  456      NYLYRLFRKSNLKPF  LFRKSNLKP  5        0.5440
138.9     9.00  0.40     Sequence         WB
 HLA-DPA10301-DPB10402  457      YLYRLFRKSNLKPFE  LFRKSNLKP  4        0.5234
173.7    11.00  0.56     Sequence
 HLA-DPA10301-DPB10402  458      LYRLFRKSNLKPFER  LFRKSNLKP  3        0.5246
171.4    11.00  0.67     Sequence
 HLA-DPA10301-DPB10402  459      YRLFRKSNLKPFERD  LFRKSNLKP  2        0.5138
192.6    12.00  0.65     Sequence
 HLA-DPA10301-DPB10402  460      RLFRKSNLKPFERDI  LFRKSNLKP  1        0.4758
290.6    18.00  0.62     Sequence
 HLA-DPA10301-DPB10402  461      LFRKSNLKPFERDIS  LFRKSNLKP  0        0.3685
927.4    37.00  0.41     Sequence
 HLA-DPA10301-DPB10402  462      FRKSNLKPFERDIST  KSNLKPFER  2        0.2688
2729.7    60.00  0.37      Sequence
 HLA-DPA10301-DPB10402  463      RKSNLKPFERDISTE  KSNLKPFER  1        0.1642
8463.4    85.00  0.40      Sequence
 HLA-DPA10301-DPB10402  464      KSNLKPFERDISTEI  LKPFERDIS  3        0.1836
6855.9    80.00  0.16      Sequence
 HLA-DPA10301-DPB10402  465      SNLKPFERDISTEIY  FERDISTEI  5        0.2045
5470.5    75.00  0.18      Sequence
 HLA-DPA10301-DPB10402  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.2331
4013.9    70.00  0.17      Sequence
 HLA-DPA10301-DPB10402  467      LKPFERDISTEIYQA  DISTEIYQA  6        0.2700
2692.9    60.00  0.25      Sequence
 HLA-DPA10301-DPB10402  468      KPFERDISTEIYQAG  DISTEIYQA  5        0.2638
2878.6    60.00  0.34      Sequence
 HLA-DPA10301-DPB10402  469      PFERDISTEIYQAGS  DISTEIYQA  4        0.2601
2997.2    60.00  0.43      Sequence
 HLA-DPA10301-DPB10402  470      FERDISTEIYQAGST  DISTEIYQA  3        0.2614
2956.7    60.00  0.50      Sequence
 HLA-DPA10301-DPB10402  471      ERDISTEIYQAGSTP  DISTEIYQA  2        0.2238
4440.0    70.00  0.65      Sequence
 HLA-DPA10301-DPB10402  472      RDISTEIYQAGSTPC  DISTEIYQA  1        0.1964
5970.5    75.00  0.58      Sequence
 HLA-DPA10301-DPB10402  473      DISTEIYQAGSTPCN  DISTEIYQA  0        0.1290
12381.3    90.00  0.33     Sequence
 HLA-DPA10301-DPB10402  474      ISTEIYQAGSTPCNG  QAGSTPCNG  6        0.0993
17082.5    95.00  0.22     Sequence
 HLA-DPA10301-DPB10402  475      STEIYQAGSTPCNGV  QAGSTPCNG  5        0.1111
15034.1    95.00  0.32     Sequence
 HLA-DPA10301-DPB10402  476      TEIYQAGSTPCNGVK  QAGSTPCNG  4        0.1156
14318.3    95.00  0.43     Sequence
 HLA-DPA10301-DPB10402  477      EIYQAGSTPCNGVKG  QAGSTPCNG  3        0.1150
14401.9    95.00  0.44     Sequence
 HLA-DPA10301-DPB10402  478      IYQAGSTPCNGVKGF  QAGSTPCNG  2        0.1167
14140.0    95.00  0.47     Sequence
 HLA-DPA10301-DPB10402  479      YQAGSTPCNGVKGFN  QAGSTPCNG  1        0.0853
19872.9   100.00  0.44     Sequence
 HLA-DPA10301-DPB10402  480      QAGSTPCNGVKGFNC  PCNGVKGFN  5        0.0620
25559.0   100.00  0.33     Sequence
```

```
 HLA-DPA10301-DPB10402  481      AGSTPCNGVKGFNCY  PCNGVKGFN  4        0.0722
22895.1   100.00  0.38     Sequence
 HLA-DPA10301-DPB10402  482      GSTPCNGVKGFNCYF  GVKGFNCYF  6        0.0931
18267.9    95.00  0.26     Sequence
 HLA-DPA10301-DPB10402  483      STPCNGVKGFNCYFP  GVKGFNCYF  5        0.1119
14899.4    95.00  0.32     Sequence
 HLA-DPA10301-DPB10402  484      TPCNGVKGFNCYFPL  GVKGFNCYF  4        0.1458
10318.8    85.00  0.28     Sequence
 HLA-DPA10301-DPB10402  485      PCNGVKGFNCYFPLQ  VKGFNCYFP  4        0.1868
6628.3    80.00  0.26     Sequence
 HLA-DPA10301-DPB10402  486      CNGVKGFNCYFPLQS  FNCYFPLQS  6        0.3041
1862.6    50.00  0.28     Sequence
 HLA-DPA10301-DPB10402  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5        0.3391
1275.4    43.00  0.37    Sequence
 HLA-DPA10301-DPB10402  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4        0.3348
1335.9    44.00  0.40    Sequence
 HLA-DPA10301-DPB10402  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3        0.3480
1158.3    41.00  0.41    Sequence
 HLA-DPA10301-DPB10402  490      KGFNCYFPLQSYGFQ  FNCYFPLQS  2        0.3838
786.1    34.00  0.34    Sequence
 HLA-DPA10301-DPB10402  491      GFNCYFPLQSYGFQP  PLQSYGFQP  6        0.3880
751.6    33.00  0.28    Sequence
 HLA-DPA10301-DPB10402  492      FNCYFPLQSYGFQPT  PLQSYGFQP  5        0.4374
440.4    24.00  0.46    Sequence
 HLA-DPA10301-DPB10402  493      NCYFPLQSYGFQPTY  PLQSYGFQP  4        0.4087
600.3    29.00  0.58    Sequence
 HLA-DPA10301-DPB10402  494      CYFPLQSYGFQPTYG  PLQSYGFQP  3        0.3971
680.5    31.00  0.61    Sequence
 HLA-DPA10301-DPB10402  495      YFPLQSYGFQPTYGV  PLQSYGFQP  2        0.4030
638.8    30.00  0.65    Sequence
 HLA-DPA10301-DPB10402  496      FPLQSYGFQPTYGVG  PLQSYGFQP  1        0.3681
932.0    37.00  0.67    Sequence
 HLA-DPA10301-DPB10402  497      PLQSYGFQPTYGVGY  PLQSYGFQP  0        0.2574
3087.9    65.00  0.36    Sequence
 HLA-DPA10301-DPB10402  498      LQSYGFQPTYGVGYQ  GFQPTYGVG  4        0.2258
4343.3    70.00  0.41    Sequence
 HLA-DPA10301-DPB10402  499      QSYGFQPTYGVGYQP  GFQPTYGVG  3        0.2178
4736.2    70.00  0.52    Sequence
 HLA-DPA10301-DPB10402  500      SYGFQPTYGVGYQPY  GFQPTYGVG  2        0.2117
5062.4    75.00  0.51    Sequence
 HLA-DPA10301-DPB10402  501      YGFQPTYGVGYQPYR  GFQPTYGVG  1        0.2087
5230.1    75.00  0.47    Sequence
 HLA-DPA10301-DPB10402  502      GFQPTYGVGYQPYRV  PTYGVGYQP  3        0.2036
5521.4    75.00  0.34    Sequence
 HLA-DPA10301-DPB10402  503      FQPTYGVGYQPYRVV  GVGYQPYRV  5        0.2451
3525.6    65.00  0.30    Sequence
 HLA-DPA10301-DPB10402  504      QPTYGVGYQPYRVVV  GVGYQPYRV  4        0.2595
3018.1    60.00  0.38    Sequence
 HLA-DPA10301-DPB10402  505      PTYGVGYQPYRVVVL  GVGYQPYRV  3        0.2938
2082.3    55.00  0.38    Sequence
 HLA-DPA10301-DPB10402  506      TYGVGYQPYRVVVLS  GVGYQPYRV  2        0.3101
1745.4    49.00  0.34    Sequence
 HLA-DPA10301-DPB10402  507      YGVGYQPYRVVVLSF  GYQPYRVVV  3        0.3402
1260.6    43.00  0.29    Sequence
 HLA-DPA10301-DPB10402  508      GVGYQPYRVVVLSFE  GYQPYRVVV  2        0.3554
1068.4    40.00  0.27    Sequence
 HLA-DPA10301-DPB10402  509      VGYQPYRVVVLSFEL  RVVVLSFEL  6        0.4101
591.5    29.00  0.34    Sequence
 HLA-DPA10301-DPB10402  510      GYQPYRVVVLSFELL  RVVVLSFEL  5        0.5491
131.4     8.50  0.58    Sequence         WB
 HLA-DPA10301-DPB10402  511      YQPYRVVVLSFELLH  RVVVLSFEL  4        0.6263
57.0     3.00  0.50    Sequence         WB
 HLA-DPA10301-DPB10402  512      QPYRVVVLSFELLHA  RVVVLSFEL  3        0.7484
15.2     0.25  0.28    Sequence         SB
 HLA-DPA10301-DPB10402  513      PYRVVVLSFELLHAP  RVVVLSFEL  2        0.7711
11.9     0.15  0.28    Sequence         SB
```

```
 HLA-DPA10301-DPB10402  514      YRVVVLSFELLHAPA  VLSFELLHA  4         0.7762
11.3     0.12  0.41     Sequence         SB
 HLA-DPA10301-DPB10402  515      RVVVLSFELLHAPAT  VLSFELLHA  3         0.7403
16.6     0.40  0.47     Sequence         SB
 HLA-DPA10301-DPB10402  516      VVVLSFELLHAPATV  VLSFELLHA  2         0.7192
20.9     0.60  0.48     Sequence         SB
 HLA-DPA10301-DPB10402  517      VVLSFELLHAPATVC  VLSFELLHA  1         0.6563
41.2     1.80  0.49     Sequence         SB
 HLA-DPA10301-DPB10402  518      VLSFELLHAPATVCG  VLSFELLHA  0         0.5395
145.8     9.50  0.32     Sequence         WB
 HLA-DPA10301-DPB10402  519      LSFELLHAPATVCGP  ELLHAPATV  3         0.3594
1023.6    39.00  0.50     Sequence
 HLA-DPA10301-DPB10402  520      SFELLHAPATVCGPK  ELLHAPATV  2         0.3437
1213.4    42.00  0.60     Sequence
 HLA-DPA10301-DPB10402  521      FELLHAPATVCGPKK  ELLHAPATV  1         0.3231
1515.3    46.00  0.55     Sequence
 HLA-DPA10301-DPB10402  522      ELLHAPATVCGPKKS  ELLHAPATV  0         0.2413
3673.8    65.00  0.40     Sequence
 HLA-DPA10301-DPB10402  523      LLHAPATVCGPKKST  LHAPATVCG  1         0.1921
6254.2    75.00  0.31     Sequence
 HLA-DPA10301-DPB10402  524      LHAPATVCGPKKSTN  PATVCGPKK  3         0.0892
19056.7    95.00  0.28     Sequence
 HLA-DPA10301-DPB10402  525      HAPATVCGPKKSTNL  PATVCGPKK  2         0.0790
21264.4   100.00  0.31     Sequence
 HLA-DPA10301-DPB10402  526      APATVCGPKKSTNLV  ATVCGPKKS  2         0.0843
20085.8   100.00  0.26     Sequence
 HLA-DPA10301-DPB10402  527      PATVCGPKKSTNLVK  PKKSTNLVK  6         0.1050
16047.0    95.00  0.32     Sequence
 HLA-DPA10301-DPB10402  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5         0.1432
10617.7    85.00  0.56     Sequence
 HLA-DPA10301-DPB10402  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4         0.1716
7807.5    80.00  0.54     Sequence
 HLA-DPA10301-DPB10402  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3         0.1824
6947.4    80.00  0.53     Sequence
 HLA-DPA10301-DPB10402  531      CGPKKSTNLVKNKCV  PKKSTNLVK  2         0.1954
6035.9    75.00  0.48     Sequence
 HLA-DPA10301-DPB10402  532      GPKKSTNLVKNKCVN  PKKSTNLVK  1         0.1959
6006.0    75.00  0.44     Sequence
 HLA-DPA10301-DPB10402  533      PKKSTNLVKNKCVNF  PKKSTNLVK  0         0.2106
5123.9    75.00  0.28     Sequence
 HLA-DPA10301-DPB10402  534      KKSTNLVKNKCVNFN  NLVKNKCVN  4         0.1905
6363.0    75.00  0.31     Sequence
 HLA-DPA10301-DPB10402  535      KSTNLVKNKCVNFNF  LVKNKCVNF  4         0.1984
5846.0    75.00  0.37     Sequence
 HLA-DPA10301-DPB10402  536      STNLVKNKCVNFNFN  LVKNKCVNF  3         0.2198
4638.2    70.00  0.29     Sequence
 HLA-DPA10301-DPB10402  537      TNLVKNKCVNFNFNG  KCVNFNFNG  6         0.2234
4458.1    70.00  0.26     Sequence
 HLA-DPA10301-DPB10402  538      NLVKNKCVNFNFNGL  KCVNFNFNG  5         0.3456
1187.9    42.00  0.52     Sequence
 HLA-DPA10301-DPB10402  539      LVKNKCVNFNFNGLT  KCVNFNFNG  4         0.3797
822.1    35.00  0.51     Sequence
 HLA-DPA10301-DPB10402  540      VKNKCVNFNFNGLTG  KCVNFNFNG  3         0.3769
847.5    35.00  0.49     Sequence
 HLA-DPA10301-DPB10402  541      KNKCVNFNFNGLTGT  KCVNFNFNG  2         0.4071
610.9    29.00  0.47     Sequence
 HLA-DPA10301-DPB10402  542      NKCVNFNFNGLTGTG  KCVNFNFNG  1         0.3778
839.3    35.00  0.41     Sequence
 HLA-DPA10301-DPB10402  543      KCVNFNFNGLTGTGV  NFNFNGLTG  3         0.3406
1255.0    43.00  0.40     Sequence
 HLA-DPA10301-DPB10402  544      CVNFNFNGLTGTGVL  NFNFNGLTG  2         0.3586
1032.9    39.00  0.31     Sequence
 HLA-DPA10301-DPB10402  545      VNFNFNGLTGTGVLT  GLTGTGVLT  6         0.3617
998.0    38.00  0.43     Sequence
 HLA-DPA10301-DPB10402  546      NFNFNGLTGTGVLTE  GLTGTGVLT  5         0.4032
637.6    30.00  0.56     Sequence
```

```
 HLA-DPA10301-DPB10402  547      FNFNGLTGTGVLTES  GLTGTGVLT  4        0.4088
599.7    29.00  0.65     Sequence
 HLA-DPA10301-DPB10402  548      NFNGLTGTGVLTESN  GLTGTGVLT  3        0.3948
697.9    32.00  0.69     Sequence
 HLA-DPA10301-DPB10402  549      FNGLTGTGVLTESNK  GLTGTGVLT  2        0.4013
650.3    30.00  0.71     Sequence
 HLA-DPA10301-DPB10402  550      NGLTGTGVLTESNKK  GLTGTGVLT  1        0.3669
943.6    37.00  0.68     Sequence
 HLA-DPA10301-DPB10402  551      GLTGTGVLTESNKKF  GLTGTGVLT  0        0.2246
4400.2    70.00  0.40     Sequence
 HLA-DPA10301-DPB10402  552      LTGTGVLTESNKKFL  GVLTESNKK  4        0.1817
7003.3    80.00  0.16     Sequence
 HLA-DPA10301-DPB10402  553      TGTGVLTESNKKFLP  TESNKKFLP  6        0.1763
7423.9    80.00  0.25     Sequence
 HLA-DPA10301-DPB10402  554      GTGVLTESNKKFLPF  TESNKKFLP  5        0.2016
5643.1    75.00  0.31     Sequence
 HLA-DPA10301-DPB10402  555      TGVLTESNKKFLPFQ  TESNKKFLP  4        0.2486
3395.3    65.00  0.28     Sequence
 HLA-DPA10301-DPB10402  556      GVLTESNKKFLPFQQ  NKKFLPFQQ  6        0.2909
2147.3    55.00  0.32     Sequence
 HLA-DPA10301-DPB10402  557      VLTESNKKFLPFQQF  NKKFLPFQQ  5        0.3617
998.4    38.00  0.50     Sequence
 HLA-DPA10301-DPB10402  558      LTESNKKFLPFQQFG  NKKFLPFQQ  4        0.3771
845.5    35.00  0.48     Sequence
 HLA-DPA10301-DPB10402  559      TESNKKFLPFQQFGR  NKKFLPFQQ  3        0.4505
382.0    22.00  0.34     Sequence
 HLA-DPA10301-DPB10402  560      ESNKKFLPFQQFGRD  FLPFQQFGR  5        0.4658
323.8    19.00  0.41     Sequence
 HLA-DPA10301-DPB10402  561      SNKKFLPFQQFGRDI  FLPFQQFGR  4        0.4958
233.9    15.00  0.44     Sequence
 HLA-DPA10301-DPB10402  562      NKKFLPFQQFGRDIA  FLPFQQFGR  3        0.4810
274.6    17.00  0.45     Sequence
 HLA-DPA10301-DPB10402  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.4636
331.6    19.00  0.46     Sequence
 HLA-DPA10301-DPB10402  564      KFLPFQQFGRDIADT  FLPFQQFGR  1        0.3827
795.2    34.00  0.36     Sequence
 HLA-DPA10301-DPB10402  565      FLPFQQFGRDIADTT  FLPFQQFGR  0        0.2913
2139.6    55.00  0.16     Sequence
 HLA-DPA10301-DPB10402  566      LPFQQFGRDIADTTD  QQFGRDIAD  3        0.2371
3846.4    65.00  0.29     Sequence
 HLA-DPA10301-DPB10402  567      PFQQFGRDIADTTDA  QQFGRDIAD  2        0.2332
4011.6    70.00  0.32     Sequence
 HLA-DPA10301-DPB10402  568      FQQFGRDIADTTDAV  QFGRDIADT  2        0.2112
5090.2    75.00  0.29     Sequence
 HLA-DPA10301-DPB10402  569      QQFGRDIADTTDAVR  QFGRDIADT  1        0.1191
13789.2    90.00  0.28     Sequence
 HLA-DPA10301-DPB10402  570      QFGRDIADTTDAVRD  DIADTTDAV  4        0.1084
15466.9    95.00  0.17     Sequence
 HLA-DPA10301-DPB10402  571      FGRDIADTTDAVRDP  DIADTTDAV  3        0.0934
18198.3    95.00  0.27     Sequence
 HLA-DPA10301-DPB10402  572      GRDIADTTDAVRDPQ  DIADTTDAV  2        0.0733
22617.6   100.00  0.38     Sequence
 HLA-DPA10301-DPB10402  573      RDIADTTDAVRDPQT  DIADTTDAV  1        0.0746
22308.4   100.00  0.34     Sequence
 HLA-DPA10301-DPB10402  574      DIADTTDAVRDPQTL  DIADTTDAV  0        0.0632
25245.4   100.00  0.24     Sequence
 HLA-DPA10301-DPB10402  575      IADTTDAVRDPQTLE  ADTTDAVRD  1        0.0534
28052.7   100.00  0.12     Sequence
 HLA-DPA10301-DPB10402  576      ADTTDAVRDPQTLEI  VRDPQTLEI  6        0.0759
21985.0   100.00  0.38     Sequence
 HLA-DPA10301-DPB10402  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5        0.2330
4020.3    70.00  0.50     Sequence
 HLA-DPA10301-DPB10402  578      TTDAVRDPQTLEILD  VRDPQTLEI  4        0.2663
2803.2    60.00  0.47     Sequence
 HLA-DPA10301-DPB10402  579      TDAVRDPQTLEILDI  PQTLEILDI  6        0.4701
309.1    18.00  0.38     Sequence
```

```
 HLA-DPA10301-DPB10402  580      DAVRDPQTLEILDIT  PQTLEILDI  5        0.5549
123.5     8.00  0.38     Sequence         WB
 HLA-DPA10301-DPB10402  581      AVRDPQTLEILDITP  PQTLEILDI  4        0.6034
73.1     4.50  0.40     Sequence         WB
 HLA-DPA10301-DPB10402  582      VRDPQTLEILDITPC  PQTLEILDI  3        0.6107
67.5     4.00  0.38     Sequence         WB
 HLA-DPA10301-DPB10402  583      RDPQTLEILDITPCS  PQTLEILDI  2        0.6086
69.0     4.00  0.39     Sequence         WB
 HLA-DPA10301-DPB10402  584      DPQTLEILDITPCSF  TLEILDITP  3        0.5712
103.5     6.50  0.38     Sequence         WB
 HLA-DPA10301-DPB10402  585      PQTLEILDITPCSFG  TLEILDITP  2        0.5421
141.8     9.00  0.41     Sequence         WB
 HLA-DPA10301-DPB10402  586      QTLEILDITPCSFGG  TLEILDITP  1        0.4477
393.9    22.00  0.55     Sequence
 HLA-DPA10301-DPB10402  587      TLEILDITPCSFGGV  ILDITPCSF  3        0.3388
1278.7    43.00  0.38     Sequence
 HLA-DPA10301-DPB10402  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.2851
2287.8    55.00  0.45     Sequence
 HLA-DPA10301-DPB10402  589      EILDITPCSFGGVSV  ILDITPCSF  1        0.2751
2547.3    60.00  0.38     Sequence
 HLA-DPA10301-DPB10402  590      ILDITPCSFGGVSVI  PCSFGGVSV  5        0.2681
2749.8    60.00  0.25     Sequence
 HLA-DPA10301-DPB10402  591      LDITPCSFGGVSVIT  PCSFGGVSV  4        0.2720
2635.1    60.00  0.34     Sequence
 HLA-DPA10301-DPB10402  592      DITPCSFGGVSVITP  PCSFGGVSV  3        0.2819
2368.3    55.00  0.37     Sequence
 HLA-DPA10301-DPB10402  593      ITPCSFGGVSVITPG  PCSFGGVSV  2        0.2760
2524.6    60.00  0.38     Sequence
 HLA-DPA10301-DPB10402  594      TPCSFGGVSVITPGT  SFGGVSVIT  3        0.2684
2738.6    60.00  0.31     Sequence
 HLA-DPA10301-DPB10402  595      PCSFGGVSVITPGTN  SFGGVSVIT  2        0.2446
3543.9    65.00  0.39     Sequence
 HLA-DPA10301-DPB10402  596      CSFGGVSVITPGTNT  SFGGVSVIT  1        0.1920
6262.5    75.00  0.35     Sequence
 HLA-DPA10301-DPB10402  597      SFGGVSVITPGTNTS  SFGGVSVIT  0        0.1211
13488.6    90.00  0.25     Sequence
 HLA-DPA10301-DPB10402  598      FGGVSVITPGTNTSN  VSVITPGTN  3        0.0854
19849.4   100.00  0.29     Sequence
 HLA-DPA10301-DPB10402  599      GGVSVITPGTNTSNQ  VSVITPGTN  2        0.0685
23838.5   100.00  0.30     Sequence
 HLA-DPA10301-DPB10402  600      GVSVITPGTNTSNQV  VSVITPGTN  1        0.0745
22325.3   100.00  0.22     Sequence
 HLA-DPA10301-DPB10402  601      VSVITPGTNTSNQVA  VITPGTNTS  2        0.0702
23394.6   100.00  0.19     Sequence
 HLA-DPA10301-DPB10402  602      SVITPGTNTSNQVAV  TNTSNQVAV  6        0.0707
23270.2   100.00  0.20     Sequence
 HLA-DPA10301-DPB10402  603      VITPGTNTSNQVAVL  TNTSNQVAV  5        0.1101
15191.5    95.00  0.39     Sequence
 HLA-DPA10301-DPB10402  604      ITPGTNTSNQVAVLY  TNTSNQVAV  4        0.1424
10711.6    90.00  0.41     Sequence
 HLA-DPA10301-DPB10402  605      TPGTNTSNQVAVLYQ  SNQVAVLYQ  6        0.2028
5569.7    75.00  0.25     Sequence
 HLA-DPA10301-DPB10402  606      PGTNTSNQVAVLYQG  SNQVAVLYQ  5        0.2043
5481.7    75.00  0.24     Sequence
 HLA-DPA10301-DPB10402  607      GTNTSNQVAVLYQGV  NQVAVLYQG  5        0.2474
3438.1    65.00  0.31     Sequence
 HLA-DPA10301-DPB10402  608      TNTSNQVAVLYQGVN  NQVAVLYQG  4        0.2881
2213.3    55.00  0.28     Sequence
 HLA-DPA10301-DPB10402  609      NTSNQVAVLYQGVNC  NQVAVLYQG  3        0.3123
1704.5    49.00  0.29     Sequence
 HLA-DPA10301-DPB10402  610      TSNQVAVLYQGVNCT  AVLYQGVNC  5        0.3749
866.1    36.00  0.27     Sequence
 HLA-DPA10301-DPB10402  611      SNQVAVLYQGVNCTE  AVLYQGVNC  4        0.3990
666.7    31.00  0.31     Sequence
 HLA-DPA10301-DPB10402  612      NQVAVLYQGVNCTEV  AVLYQGVNC  3        0.4062
617.3    29.00  0.32     Sequence
```

```
 HLA-DPA10301-DPB10402  613      QVAVLYQGVNCTEVP  AVLYQGVNC  2        0.4122
578.4    28.00  0.34     Sequence
 HLA-DPA10301-DPB10402  614      VAVLYQGVNCTEVPV  LYQGVNCTE  3        0.4142
565.7    28.00  0.34     Sequence
 HLA-DPA10301-DPB10402  615      AVLYQGVNCTEVPVA  LYQGVNCTE  2        0.3929
712.5    32.00  0.41     Sequence
 HLA-DPA10301-DPB10402  616      VLYQGVNCTEVPVAI  LYQGVNCTE  1        0.3543
1082.0    40.00  0.45     Sequence
 HLA-DPA10301-DPB10402  617      LYQGVNCTEVPVAIH  NCTEVPVAI  5        0.2507
3319.8    65.00  0.26     Sequence
 HLA-DPA10301-DPB10402  618      YQGVNCTEVPVAIHA  NCTEVPVAI  4        0.2355
3911.0    70.00  0.36     Sequence
 HLA-DPA10301-DPB10402  619      QGVNCTEVPVAIHAD  NCTEVPVAI  3        0.2014
5656.2    75.00  0.50     Sequence
 HLA-DPA10301-DPB10402  620      GVNCTEVPVAIHADQ  NCTEVPVAI  2        0.2042
5486.8    75.00  0.51     Sequence
 HLA-DPA10301-DPB10402  621      VNCTEVPVAIHADQL  NCTEVPVAI  1        0.2186
4695.9    70.00  0.40     Sequence
 HLA-DPA10301-DPB10402  622      NCTEVPVAIHADQLT  TEVPVAIHA  2        0.1933
6176.9    75.00  0.23     Sequence
 HLA-DPA10301-DPB10402  623      CTEVPVAIHADQLTP  TEVPVAIHA  1        0.1845
6788.7    80.00  0.25     Sequence
 HLA-DPA10301-DPB10402  624      TEVPVAIHADQLTPT  AIHADQLTP  5        0.1890
6468.4    80.00  0.37     Sequence
 HLA-DPA10301-DPB10402  625      EVPVAIHADQLTPTW  AIHADQLTP  4        0.1858
6694.6    80.00  0.44     Sequence
 HLA-DPA10301-DPB10402  626      VPVAIHADQLTPTWR  AIHADQLTP  3        0.1963
5977.6    75.00  0.51     Sequence
 HLA-DPA10301-DPB10402  627      PVAIHADQLTPTWRV  AIHADQLTP  2        0.2043
5484.0    75.00  0.50     Sequence
 HLA-DPA10301-DPB10402  628      VAIHADQLTPTWRVY  AIHADQLTP  1        0.2098
5168.3    75.00  0.37     Sequence
 HLA-DPA10301-DPB10402  629      AIHADQLTPTWRVYS  ADQLTPTWR  3        0.2008
5697.0    75.00  0.19     Sequence
 HLA-DPA10301-DPB10402  630      IHADQLTPTWRVYST  ADQLTPTWR  2        0.2038
5510.6    75.00  0.20     Sequence
 HLA-DPA10301-DPB10402  631      HADQLTPTWRVYSTG  QLTPTWRVY  3        0.1764
7411.8    80.00  0.28     Sequence
 HLA-DPA10301-DPB10402  632      ADQLTPTWRVYSTGS  QLTPTWRVY  2        0.1709
7867.1    80.00  0.30     Sequence
 HLA-DPA10301-DPB10402  633      DQLTPTWRVYSTGSN  LTPTWRVYS  2        0.1618
8686.8    85.00  0.30     Sequence
 HLA-DPA10301-DPB10402  634      QLTPTWRVYSTGSNV  LTPTWRVYS  1        0.1530
9548.3    85.00  0.22     Sequence
 HLA-DPA10301-DPB10402  635      LTPTWRVYSTGSNVF  RVYSTGSNV  5        0.2263
4323.0    70.00  0.36     Sequence
 HLA-DPA10301-DPB10402  636      TPTWRVYSTGSNVFQ  RVYSTGSNV  4        0.2723
2627.2    60.00  0.37     Sequence
 HLA-DPA10301-DPB10402  637      PTWRVYSTGSNVFQT  RVYSTGSNV  3        0.3073
1798.3    50.00  0.32     Sequence
 HLA-DPA10301-DPB10402  638      TWRVYSTGSNVFQTR  RVYSTGSNV  2        0.3392
1274.4    43.00  0.31     Sequence
 HLA-DPA10301-DPB10402  639      WRVYSTGSNVFQTRA  STGSNVFQT  4        0.3485
1152.1    41.00  0.28     Sequence
 HLA-DPA10301-DPB10402  640      RVYSTGSNVFQTRAG  STGSNVFQT  3        0.3334
1355.9    44.00  0.29     Sequence
 HLA-DPA10301-DPB10402  641      VYSTGSNVFQTRAGC  STGSNVFQT  2        0.2981
1986.6    55.00  0.38     Sequence
 HLA-DPA10301-DPB10402  642      YSTGSNVFQTRAGCL  STGSNVFQT  1        0.2005
5715.0    75.00  0.34     Sequence
 HLA-DPA10301-DPB10402  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.3230
1518.2    46.00  0.26     Sequence
 HLA-DPA10301-DPB10402  644      TGSNVFQTRAGCLIG  QTRAGCLIG  6        0.3643
971.2    38.00  0.28     Sequence
 HLA-DPA10301-DPB10402  645      GSNVFQTRAGCLIGA  QTRAGCLIG  5        0.4037
634.1    30.00  0.26     Sequence
```

```
 HLA-DPA10301-DPB10402  646      SNVFQTRAGCLIGAE  TRAGCLIGA  5        0.4199
531.9    27.00  0.22     Sequence
 HLA-DPA10301-DPB10402  647      NVFQTRAGCLIGAEY  TRAGCLIGA  4        0.4253
501.7    26.00  0.24     Sequence
 HLA-DPA10301-DPB10402  648      VFQTRAGCLIGAEYV  TRAGCLIGA  3        0.4207
527.4    27.00  0.25     Sequence
 HLA-DPA10301-DPB10402  649      FQTRAGCLIGAEYVN  TRAGCLIGA  2        0.3881
750.3    33.00  0.28     Sequence
 HLA-DPA10301-DPB10402  650      QTRAGCLIGAEYVNN  TRAGCLIGA  1        0.3106
1735.9    49.00  0.23     Sequence
 HLA-DPA10301-DPB10402  651      TRAGCLIGAEYVNNS  LIGAEYVNN  5        0.3068
1808.3    50.00  0.41     Sequence
 HLA-DPA10301-DPB10402  652      RAGCLIGAEYVNNSY  LIGAEYVNN  4        0.3282
1435.2    45.00  0.44     Sequence
 HLA-DPA10301-DPB10402  653      AGCLIGAEYVNNSYE  LIGAEYVNN  3        0.3354
1326.6    44.00  0.46     Sequence
 HLA-DPA10301-DPB10402  654      GCLIGAEYVNNSYEC  LIGAEYVNN  2        0.3305
1399.5    45.00  0.47     Sequence
 HLA-DPA10301-DPB10402  655      CLIGAEYVNNSYECD  LIGAEYVNN  1        0.2853
2282.5    55.00  0.41     Sequence
 HLA-DPA10301-DPB10402  656      LIGAEYVNNSYECDI  EYVNNSYEC  4        0.2424
3629.4    65.00  0.31     Sequence
 HLA-DPA10301-DPB10402  657      IGAEYVNNSYECDIP  EYVNNSYEC  3        0.1972
5922.9    75.00  0.49     Sequence
 HLA-DPA10301-DPB10402  658      GAEYVNNSYECDIPI  EYVNNSYEC  2        0.1992
5796.1    75.00  0.50     Sequence
 HLA-DPA10301-DPB10402  659      AEYVNNSYECDIPIG  EYVNNSYEC  1        0.1997
5764.6    75.00  0.45     Sequence
 HLA-DPA10301-DPB10402  660      EYVNNSYECDIPIGA  EYVNNSYEC  0        0.1798
7143.1    80.00  0.25     Sequence
 HLA-DPA10301-DPB10402  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.1387
11154.2    90.00  0.19     Sequence
 HLA-DPA10301-DPB10402  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.1325
11927.5    90.00  0.23     Sequence
 HLA-DPA10301-DPB10402  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.1304
12201.1    90.00  0.25     Sequence
 HLA-DPA10301-DPB10402  664      NSYECDIPIGAGICA  YECDIPIGA  2        0.1363
11441.1    90.00  0.24     Sequence
 HLA-DPA10301-DPB10402  665      SYECDIPIGAGICAS  YECDIPIGA  1        0.1455
10356.1    85.00  0.17     Sequence
 HLA-DPA10301-DPB10402  666      YECDIPIGAGICASY  IPIGAGICA  4        0.1481
10067.5    85.00  0.22     Sequence
 HLA-DPA10301-DPB10402  667      ECDIPIGAGICASYQ  IPIGAGICA  3        0.1438
10555.0    85.00  0.26     Sequence
 HLA-DPA10301-DPB10402  668      CDIPIGAGICASYQT  IPIGAGICA  2        0.1495
9924.1    85.00  0.28     Sequence
 HLA-DPA10301-DPB10402  669      DIPIGAGICASYQTQ  IPIGAGICA  1        0.1529
9563.4    85.00  0.27     Sequence
 HLA-DPA10301-DPB10402  670      IPIGAGICASYQTQT  IGAGICASY  2        0.1541
9440.5    85.00  0.24     Sequence
 HLA-DPA10301-DPB10402  671      PIGAGICASYQTQTN  ICASYQTQT  5        0.1129
14730.9    95.00  0.23     Sequence
 HLA-DPA10301-DPB10402  672      IGAGICASYQTQTNS  ICASYQTQT  4        0.1008
16804.9    95.00  0.32     Sequence
 HLA-DPA10301-DPB10402  673      GAGICASYQTQTNSP  ICASYQTQT  3        0.1015
16676.7    95.00  0.34     Sequence
 HLA-DPA10301-DPB10402  674      AGICASYQTQTNSPR  ICASYQTQT  2        0.1075
15628.4    95.00  0.33     Sequence
 HLA-DPA10301-DPB10402  675      GICASYQTQTNSPRR  ICASYQTQT  1        0.1058
15907.9    95.00  0.23     Sequence
 HLA-DPA10301-DPB10402  676      ICASYQTQTNSPRRA  SYQTQTNSP  3        0.1135
14646.6    95.00  0.23     Sequence
 HLA-DPA10301-DPB10402  677      CASYQTQTNSPRRAR  QTQTNSPRR  4        0.1121
14867.2    95.00  0.28     Sequence
 HLA-DPA10301-DPB10402  678      ASYQTQTNSPRRARS  QTQTNSPRR  3        0.1113
14988.0    95.00  0.26     Sequence
```

```
 HLA-DPA10301-DPB10402  679      SYQTQTNSPRRARSV  QTQTNSPRR  2        0.1030
16409.4    95.00  0.31     Sequence
 HLA-DPA10301-DPB10402  680      YQTQTNSPRRARSVA  TQTNSPRRA  2        0.0908
18729.4    95.00  0.28     Sequence
 HLA-DPA10301-DPB10402  681      QTQTNSPRRARSVAS  TQTNSPRRA  1        0.0715
23077.6   100.00  0.30     Sequence
 HLA-DPA10301-DPB10402  682      TQTNSPRRARSVASQ  PRRARSVAS  5        0.0628
25347.8   100.00  0.30     Sequence
 HLA-DPA10301-DPB10402  683      QTNSPRRARSVASQS  PRRARSVAS  4        0.0603
26041.1   100.00  0.37     Sequence
 HLA-DPA10301-DPB10402  684      TNSPRRARSVASQSI  PRRARSVAS  3        0.0709
23214.1   100.00  0.31     Sequence
 HLA-DPA10301-DPB10402  685      NSPRRARSVASQSII  SVASQSIIX  7        0.1235
13136.9    90.00  0.22     Sequence
 HLA-DPA10301-DPB10402  686      SPRRARSVASQSIIA  SVASQSIIA  6        0.1722
7757.8    80.00  0.41     Sequence
 HLA-DPA10301-DPB10402  687      PRRARSVASQSIIAY  SVASQSIIA  5        0.2275
4263.3    70.00  0.55     Sequence
 HLA-DPA10301-DPB10402  688      RRARSVASQSIIAYT  SVASQSIIA  4        0.2571
3095.2    65.00  0.51     Sequence
 HLA-DPA10301-DPB10402  689      RARSVASQSIIAYTM  SVASQSIIA  3        0.3129
1692.2    48.00  0.47     Sequence
 HLA-DPA10301-DPB10402  690      ARSVASQSIIAYTMS  SVASQSIIA  2        0.3254
1479.6    46.00  0.44     Sequence
 HLA-DPA10301-DPB10402  691      RSVASQSIIAYTMSL  SVASQSIIA  1        0.3590
1028.5    39.00  0.29     Sequence
 HLA-DPA10301-DPB10402  692      SVASQSIIAYTMSLG  IIAYTMSLG  6        0.3844
781.2    34.00  0.28     Sequence
 HLA-DPA10301-DPB10402  693      VASQSIIAYTMSLGA  IIAYTMSLG  5        0.4297
478.5    25.00  0.39     Sequence
 HLA-DPA10301-DPB10402  694      ASQSIIAYTMSLGAE  IIAYTMSLG  4        0.4536
369.2    21.00  0.41     Sequence
 HLA-DPA10301-DPB10402  695      SQSIIAYTMSLGAEN  IIAYTMSLG  3        0.4676
317.5    19.00  0.43     Sequence
 HLA-DPA10301-DPB10402  696      QSIIAYTMSLGAENS  IIAYTMSLG  2        0.4497
385.5    22.00  0.44     Sequence
 HLA-DPA10301-DPB10402  697      SIIAYTMSLGAENSV  IIAYTMSLG  1        0.4287
483.8    25.00  0.39     Sequence
 HLA-DPA10301-DPB10402  698      IIAYTMSLGAENSVA  IAYTMSLGA  1        0.3389
1278.3    43.00  0.25     Sequence
 HLA-DPA10301-DPB10402  699      IAYTMSLGAENSVAY  YTMSLGAEN  2        0.2680
2752.7    60.00  0.29     Sequence
 HLA-DPA10301-DPB10402  700      AYTMSLGAENSVAYS  YTMSLGAEN  1        0.2026
5581.1    75.00  0.28     Sequence
 HLA-DPA10301-DPB10402  701      YTMSLGAENSVAYSN  SLGAENSVA  3        0.1772
7353.8    80.00  0.36     Sequence
 HLA-DPA10301-DPB10402  702      TMSLGAENSVAYSNN  SLGAENSVA  2        0.1515
9710.6    85.00  0.49     Sequence
 HLA-DPA10301-DPB10402  703      MSLGAENSVAYSNNS  SLGAENSVA  1        0.1334
11809.2    90.00  0.47     Sequence
 HLA-DPA10301-DPB10402  704      SLGAENSVAYSNNSI  LGAENSVAY  1        0.1015
16667.8    95.00  0.22     Sequence
 HLA-DPA10301-DPB10402  705      LGAENSVAYSNNSIA  SVAYSNNSI  5        0.1385
11177.2    90.00  0.38     Sequence
 HLA-DPA10301-DPB10402  706      GAENSVAYSNNSIAI  AYSNNSIAI  6        0.2288
4206.3    70.00  0.38     Sequence
 HLA-DPA10301-DPB10402  707      AENSVAYSNNSIAIP  AYSNNSIAI  5        0.2744
2569.0    60.00  0.48     Sequence
 HLA-DPA10301-DPB10402  708      ENSVAYSNNSIAIPT  AYSNNSIAI  4        0.2992
1962.7    55.00  0.49     Sequence
 HLA-DPA10301-DPB10402  709      NSVAYSNNSIAIPTN  AYSNNSIAI  3        0.3004
1938.8    55.00  0.50     Sequence
 HLA-DPA10301-DPB10402  710      SVAYSNNSIAIPTNF  AYSNNSIAI  2        0.3003
1941.0    55.00  0.53     Sequence
 HLA-DPA10301-DPB10402  711      VAYSNNSIAIPTNFT  AYSNNSIAI  1        0.2835
2325.9    55.00  0.53     Sequence
```

```
 HLA-DPA10301-DPB10402  712      AYSNNSIAIPTNFTI  AYSNNSIAI  0        0.2244
4412.5    70.00  0.34     Sequence
 HLA-DPA10301-DPB10402  713      YSNNSIAIPTNFTIS  IAIPTNFTI  5        0.1845
6790.9    80.00  0.43     Sequence
 HLA-DPA10301-DPB10402  714      SNNSIAIPTNFTISV  IAIPTNFTI  4        0.2424
3629.3    65.00  0.46     Sequence
 HLA-DPA10301-DPB10402  715      NNSIAIPTNFTISVT  IAIPTNFTI  3        0.3021
1903.5    55.00  0.38     Sequence
 HLA-DPA10301-DPB10402  716      NSIAIPTNFTISVTT  IAIPTNFTI  2        0.3141
1670.5    48.00  0.35     Sequence
 HLA-DPA10301-DPB10402  717      SIAIPTNFTISVTTE  IAIPTNFTI  1        0.3133
1686.5    48.00  0.34     Sequence
 HLA-DPA10301-DPB10402  718      IAIPTNFTISVTTEI  PTNFTISVT  3        0.3081
1783.7    50.00  0.22     Sequence
 HLA-DPA10301-DPB10402  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.3626
988.5    38.00  0.25     Sequence
 HLA-DPA10301-DPB10402  720      IPTNFTISVTTEILP  ISVTTEILP  6        0.4044
628.9    30.00  0.23     Sequence
 HLA-DPA10301-DPB10402  721      PTNFTISVTTEILPV  ISVTTEILP  5        0.4884
253.5    16.00  0.46     Sequence
 HLA-DPA10301-DPB10402  722      TNFTISVTTEILPVS  ISVTTEILP  4        0.5197
180.6    12.00  0.47     Sequence
 HLA-DPA10301-DPB10402  723      NFTISVTTEILPVSM  ISVTTEILP  3        0.5588
118.4     7.50  0.47     Sequence         WB
 HLA-DPA10301-DPB10402  724      FTISVTTEILPVSMT  ISVTTEILP  2        0.5658
109.7     7.00  0.46     Sequence         WB
 HLA-DPA10301-DPB10402  725      TISVTTEILPVSMTK  ISVTTEILP  1        0.5367
150.3     9.50  0.46     Sequence         WB
 HLA-DPA10301-DPB10402  726      ISVTTEILPVSMTKT  TTEILPVSM  3        0.4943
237.9    15.00  0.22     Sequence
 HLA-DPA10301-DPB10402  727      SVTTEILPVSMTKTS  TTEILPVSM  2        0.4519
376.1    21.00  0.28     Sequence
 HLA-DPA10301-DPB10402  728      VTTEILPVSMTKTSV  EILPVSMTK  3        0.4260
497.9    26.00  0.44     Sequence
 HLA-DPA10301-DPB10402  729      TTEILPVSMTKTSVD  EILPVSMTK  2        0.3908
728.9    32.00  0.49     Sequence
 HLA-DPA10301-DPB10402  730      TEILPVSMTKTSVDC  EILPVSMTK  1        0.3422
1232.7    42.00  0.47     Sequence
 HLA-DPA10301-DPB10402  731      EILPVSMTKTSVDCT  EILPVSMTK  0        0.2955
2043.0    55.00  0.34     Sequence
 HLA-DPA10301-DPB10402  732      ILPVSMTKTSVDCTM  PVSMTKTSV  2        0.2122
5030.6    75.00  0.23     Sequence
 HLA-DPA10301-DPB10402  733      LPVSMTKTSVDCTMY  SMTKTSVDC  3        0.1398
11016.5    90.00  0.21     Sequence
 HLA-DPA10301-DPB10402  734      PVSMTKTSVDCTMYI  TKTSVDCTM  4        0.1849
6761.9    80.00  0.22     Sequence
 HLA-DPA10301-DPB10402  735      VSMTKTSVDCTMYIC  TSVDCTMYI  5        0.2322
4051.8    70.00  0.26     Sequence
 HLA-DPA10301-DPB10402  736      SMTKTSVDCTMYICG  TSVDCTMYI  4        0.2270
4287.2    70.00  0.26     Sequence
 HLA-DPA10301-DPB10402  737      MTKTSVDCTMYICGD  TSVDCTMYI  3        0.2248
4393.5    70.00  0.27     Sequence
 HLA-DPA10301-DPB10402  738      TKTSVDCTMYICGDS  TSVDCTMYI  2        0.2242
4420.7    70.00  0.26     Sequence
 HLA-DPA10301-DPB10402  739      KTSVDCTMYICGDST  SVDCTMYIC  2        0.2293
4181.7    70.00  0.25     Sequence
 HLA-DPA10301-DPB10402  740      TSVDCTMYICGDSTE  VDCTMYICG  2        0.2062
5373.1    75.00  0.24     Sequence
 HLA-DPA10301-DPB10402  741      SVDCTMYICGDSTEC  CTMYICGDS  3        0.1648
8404.0    85.00  0.26     Sequence
 HLA-DPA10301-DPB10402  742      VDCTMYICGDSTECS  CTMYICGDS  2        0.1439
10539.3    85.00  0.29     Sequence
 HLA-DPA10301-DPB10402  743      DCTMYICGDSTECSN  TMYICGDST  2        0.1365
11411.5    90.00  0.23     Sequence
 HLA-DPA10301-DPB10402  744      CTMYICGDSTECSNL  TMYICGDST  1        0.1463
10266.0    85.00  0.23     Sequence
```

```
 HLA-DPA10301-DPB10402  745      TMYICGDSTECSNLL  YICGDSTEC  2        0.1481
10072.9    85.00  0.18     Sequence
 HLA-DPA10301-DPB10402  746      MYICGDSTECSNLLL  STECSNLLL  6        0.2044
5477.5    75.00  0.25     Sequence
 HLA-DPA10301-DPB10402  747      YICGDSTECSNLLLQ  STECSNLLL  5        0.2690
2721.4    60.00  0.29     Sequence
 HLA-DPA10301-DPB10402  748      ICGDSTECSNLLLQY  TECSNLLLQ  5        0.3356
1324.1    44.00  0.27     Sequence
 HLA-DPA10301-DPB10402  749      CGDSTECSNLLLQYG  ECSNLLLQY  5        0.3352
1329.8    44.00  0.35     Sequence
 HLA-DPA10301-DPB10402  750      GDSTECSNLLLQYGS  ECSNLLLQY  4        0.3489
1147.2    41.00  0.39     Sequence
 HLA-DPA10301-DPB10402  751      DSTECSNLLLQYGSF  ECSNLLLQY  3        0.3684
928.6    37.00  0.37     Sequence
 HLA-DPA10301-DPB10402  752      STECSNLLLQYGSFC  ECSNLLLQY  2        0.4099
593.0    29.00  0.31     Sequence
 HLA-DPA10301-DPB10402  753      TECSNLLLQYGSFCT  LLQYGSFCT  6        0.4567
357.1    21.00  0.34     Sequence
 HLA-DPA10301-DPB10402  754      ECSNLLLQYGSFCTQ  LLQYGSFCT  5        0.4947
236.7    15.00  0.50     Sequence
 HLA-DPA10301-DPB10402  755      CSNLLLQYGSFCTQL  LLQYGSFCT  4        0.5324
157.5    10.00  0.53     Sequence
 HLA-DPA10301-DPB10402  756      SNLLLQYGSFCTQLN  LLQYGSFCT  3        0.5482
132.8     8.50  0.50     Sequence         WB
 HLA-DPA10301-DPB10402  757      NLLLQYGSFCTQLNR  LLQYGSFCT  2        0.5570
120.7     8.00  0.54     Sequence         WB
 HLA-DPA10301-DPB10402  758      LLLQYGSFCTQLNRA  LLQYGSFCT  1        0.5501
130.1     8.50  0.50     Sequence         WB
 HLA-DPA10301-DPB10402  759      LLQYGSFCTQLNRAL  LLQYGSFCT  0        0.4898
249.7    16.00  0.26     Sequence
 HLA-DPA10301-DPB10402  760      LQYGSFCTQLNRALT  GSFCTQLNR  3        0.4442
408.8    23.00  0.23     Sequence
 HLA-DPA10301-DPB10402  761      QYGSFCTQLNRALTG  GSFCTQLNR  2        0.4156
557.5    28.00  0.25     Sequence
 HLA-DPA10301-DPB10402  762      YGSFCTQLNRALTGI  CTQLNRALT  4        0.4193
535.4    27.00  0.25     Sequence
 HLA-DPA10301-DPB10402  763      GSFCTQLNRALTGIA  CTQLNRALT  3        0.4133
571.6    28.00  0.29     Sequence
 HLA-DPA10301-DPB10402  764      SFCTQLNRALTGIAV  CTQLNRALT  2        0.4260
497.8    26.00  0.28     Sequence
 HLA-DPA10301-DPB10402  765      FCTQLNRALTGIAVE  NRALTGIAV  5        0.4118
580.6    28.00  0.22     Sequence
 HLA-DPA10301-DPB10402  766      CTQLNRALTGIAVEQ  NRALTGIAV  4        0.3569
1051.9    39.00  0.38     Sequence
 HLA-DPA10301-DPB10402  767      TQLNRALTGIAVEQD  NRALTGIAV  3        0.3571
1048.9    39.00  0.38     Sequence
 HLA-DPA10301-DPB10402  768      QLNRALTGIAVEQDK  ALTGIAVEQ  4        0.3747
867.8    36.00  0.37     Sequence
 HLA-DPA10301-DPB10402  769      LNRALTGIAVEQDKN  ALTGIAVEQ  3        0.3526
1101.7    40.00  0.47     Sequence
 HLA-DPA10301-DPB10402  770      NRALTGIAVEQDKNT  ALTGIAVEQ  2        0.3093
1760.9    49.00  0.62     Sequence
 HLA-DPA10301-DPB10402  771      RALTGIAVEQDKNTQ  ALTGIAVEQ  1        0.2816
2374.8    55.00  0.65     Sequence
 HLA-DPA10301-DPB10402  772      ALTGIAVEQDKNTQE  ALTGIAVEQ  0        0.1678
8139.9    80.00  0.44     Sequence
 HLA-DPA10301-DPB10402  773      LTGIAVEQDKNTQEV  GIAVEQDKN  2        0.0988
17171.0    95.00  0.35     Sequence
 HLA-DPA10301-DPB10402  774      TGIAVEQDKNTQEVF  GIAVEQDKN  1        0.0743
22373.9   100.00  0.37     Sequence
 HLA-DPA10301-DPB10402  775      GIAVEQDKNTQEVFA  DKNTQEVFA  6        0.0773
21673.7   100.00  0.19     Sequence
 HLA-DPA10301-DPB10402  776      IAVEQDKNTQEVFAQ  KNTQEVFAQ  6        0.1001
16934.7    95.00  0.34     Sequence
 HLA-DPA10301-DPB10402  777      AVEQDKNTQEVFAQV  KNTQEVFAQ  5        0.1598
8877.0    85.00  0.55     Sequence
```

```
 HLA-DPA10301-DPB10402  778      VEQDKNTQEVFAQVK  KNTQEVFAQ  4        0.2356
3905.5    70.00  0.51     Sequence
 HLA-DPA10301-DPB10402  779      EQDKNTQEVFAQVKQ  KNTQEVFAQ  3        0.2509
3310.8    65.00  0.45     Sequence
 HLA-DPA10301-DPB10402  780      QDKNTQEVFAQVKQI  KNTQEVFAQ  2        0.2845
2301.3    55.00  0.34     Sequence
 HLA-DPA10301-DPB10402  781      DKNTQEVFAQVKQIY  KNTQEVFAQ  1        0.3004
1937.5    55.00  0.25     Sequence
 HLA-DPA10301-DPB10402  782      KNTQEVFAQVKQIYK  VFAQVKQIY  5        0.3422
1233.1    42.00  0.20     Sequence
 HLA-DPA10301-DPB10402  783      NTQEVFAQVKQIYKT  FAQVKQIYK  5        0.3587
1031.7    39.00  0.31     Sequence
 HLA-DPA10301-DPB10402  784      TQEVFAQVKQIYKTP  FAQVKQIYK  4        0.3735
878.5    36.00  0.33     Sequence
 HLA-DPA10301-DPB10402  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.3481
1157.1    41.00  0.38     Sequence
 HLA-DPA10301-DPB10402  786      EVFAQVKQIYKTPPI  FAQVKQIYK  2        0.3316
1382.3    45.00  0.38     Sequence
 HLA-DPA10301-DPB10402  787      VFAQVKQIYKTPPIK  FAQVKQIYK  1        0.3061
1822.0    50.00  0.29     Sequence
 HLA-DPA10301-DPB10402  788      FAQVKQIYKTPPIKD  IYKTPPIKD  6        0.2854
2279.6    55.00  0.23     Sequence
 HLA-DPA10301-DPB10402  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.2733
2598.1    60.00  0.44     Sequence
 HLA-DPA10301-DPB10402  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.2695
2706.8    60.00  0.47     Sequence
 HLA-DPA10301-DPB10402  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.2697
2703.1    60.00  0.50     Sequence
 HLA-DPA10301-DPB10402  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.2559
3137.8    65.00  0.58     Sequence
 HLA-DPA10301-DPB10402  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.1829
6914.5    80.00  0.55     Sequence
 HLA-DPA10301-DPB10402  794      IYKTPPIKDFGGFNF  IYKTPPIKD  0        0.1764
7411.5    80.00  0.23     Sequence
 HLA-DPA10301-DPB10402  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.2004
5716.2    75.00  0.27     Sequence
 HLA-DPA10301-DPB10402  796      KTPPIKDFGGFNFSQ  DFGGFNFSQ  6        0.2508
3315.9    65.00  0.46     Sequence
 HLA-DPA10301-DPB10402  797      TPPIKDFGGFNFSQI  DFGGFNFSQ  5        0.3845
780.6    34.00  0.62     Sequence
 HLA-DPA10301-DPB10402  798      PPIKDFGGFNFSQIL  DFGGFNFSQ  4        0.4572
355.3    20.00  0.56     Sequence
 HLA-DPA10301-DPB10402  799      PIKDFGGFNFSQILP  DFGGFNFSQ  3        0.4876
255.8    16.00  0.52     Sequence
 HLA-DPA10301-DPB10402  800      IKDFGGFNFSQILPD  DFGGFNFSQ  2        0.4879
254.9    16.00  0.51     Sequence
 HLA-DPA10301-DPB10402  801      KDFGGFNFSQILPDP  DFGGFNFSQ  1        0.4645
328.4    19.00  0.43     Sequence
 HLA-DPA10301-DPB10402  802      DFGGFNFSQILPDPS  GFNFSQILP  3        0.4131
572.8    28.00  0.43     Sequence
 HLA-DPA10301-DPB10402  803      FGGFNFSQILPDPSK  GFNFSQILP  2        0.3890
743.0    33.00  0.49     Sequence
 HLA-DPA10301-DPB10402  804      GGFNFSQILPDPSKP  GFNFSQILP  1        0.3322
1373.6    44.00  0.57     Sequence
 HLA-DPA10301-DPB10402  805      GFNFSQILPDPSKPS  GFNFSQILP  0        0.2487
3390.6    65.00  0.31     Sequence
 HLA-DPA10301-DPB10402  806      FNFSQILPDPSKPSK  NFSQILPDP  1        0.1824
6944.8    80.00  0.29     Sequence
 HLA-DPA10301-DPB10402  807      NFSQILPDPSKPSKR  QILPDPSKP  3        0.1420
10758.9    90.00  0.32     Sequence
 HLA-DPA10301-DPB10402  808      FSQILPDPSKPSKRS  QILPDPSKP  2        0.1134
14656.4    95.00  0.44     Sequence
 HLA-DPA10301-DPB10402  809      SQILPDPSKPSKRSF  QILPDPSKP  1        0.0812
20776.5   100.00  0.47     Sequence
 HLA-DPA10301-DPB10402  810      QILPDPSKPSKRSFI  QILPDPSKP  0        0.0684
23850.9   100.00  0.28     Sequence
```

```
 HLA-DPA10301-DPB10402  811      ILPDPSKPSKRSFIE  PDPSKPSKR  2        0.0615
25694.4   100.00  0.21     Sequence
 HLA-DPA10301-DPB10402  812      LPDPSKPSKRSFIED  PSKRSFIED  6        0.0646
24864.0   100.00  0.31     Sequence
 HLA-DPA10301-DPB10402  813      PDPSKPSKRSFIEDL  PSKRSFIED  5        0.1671
8201.9    80.00  0.47     Sequence
 HLA-DPA10301-DPB10402  814      DPSKPSKRSFIEDLL  PSKRSFIED  4        0.2871
2237.0    55.00  0.44     Sequence
 HLA-DPA10301-DPB10402  815      PSKPSKRSFIEDLLF  PSKRSFIED  3        0.3574
1046.3    39.00  0.32     Sequence
 HLA-DPA10301-DPB10402  816      SKPSKRSFIEDLLFN  SFIEDLLFN  6        0.4492
387.4    22.00  0.31    Sequence
 HLA-DPA10301-DPB10402  817      KPSKRSFIEDLLFNK  SFIEDLLFN  5        0.6363
51.2     3.00  0.38    Sequence         WB
 HLA-DPA10301-DPB10402  818      PSKRSFIEDLLFNKV  FIEDLLFNK  5        0.7192
20.9     0.60  0.56    Sequence         SB
 HLA-DPA10301-DPB10402  819      SKRSFIEDLLFNKVT  FIEDLLFNK  4        0.7354
17.5     0.40  0.57    Sequence         SB
 HLA-DPA10301-DPB10402  820      KRSFIEDLLFNKVTL  FIEDLLFNK  3        0.7534
14.4     0.25  0.60    Sequence         SB
 HLA-DPA10301-DPB10402  821      RSFIEDLLFNKVTLA  FIEDLLFNK  2        0.7471
15.4     0.30  0.57    Sequence         SB
 HLA-DPA10301-DPB10402  822      SFIEDLLFNKVTLAD  FIEDLLFNK  1        0.7177
21.2     0.60  0.54    Sequence         SB
 HLA-DPA10301-DPB10402  823      FIEDLLFNKVTLADA  DLLFNKVTL  3        0.6354
51.7     3.00  0.26    Sequence         WB
 HLA-DPA10301-DPB10402  824      IEDLLFNKVTLADAG  DLLFNKVTL  2        0.5278
165.5    11.00  0.42    Sequence
 HLA-DPA10301-DPB10402  825      EDLLFNKVTLADAGF  DLLFNKVTL  1        0.4975
229.7    15.00  0.44    Sequence
 HLA-DPA10301-DPB10402  826      DLLFNKVTLADAGFI  LFNKVTLAD  2        0.4631
333.3    20.00  0.37    Sequence
 HLA-DPA10301-DPB10402  827      LLFNKVTLADAGFIK  LFNKVTLAD  1        0.4244
506.8    26.00  0.28    Sequence
 HLA-DPA10301-DPB10402  828      LFNKVTLADAGFIKQ  TLADAGFIK  5        0.4257
499.6    26.00  0.52    Sequence
 HLA-DPA10301-DPB10402  829      FNKVTLADAGFIKQY  TLADAGFIK  4        0.4448
406.5    22.00  0.56    Sequence
 HLA-DPA10301-DPB10402  830      NKVTLADAGFIKQYG  TLADAGFIK  3        0.4198
532.3    27.00  0.62    Sequence
 HLA-DPA10301-DPB10402  831      KVTLADAGFIKQYGD  TLADAGFIK  2        0.4211
525.0    27.00  0.62    Sequence
 HLA-DPA10301-DPB10402  832      VTLADAGFIKQYGDC  TLADAGFIK  1        0.3864
764.2    33.00  0.57    Sequence
 HLA-DPA10301-DPB10402  833      TLADAGFIKQYGDCL  TLADAGFIK  0        0.3484
1153.1    41.00  0.26     Sequence
 HLA-DPA10301-DPB10402  834      LADAGFIKQYGDCLG  GFIKQYGDC  4        0.3101
1745.4    49.00  0.25     Sequence
 HLA-DPA10301-DPB10402  835      ADAGFIKQYGDCLGD  IKQYGDCLG  5        0.3029
1886.5    55.00  0.30     Sequence
 HLA-DPA10301-DPB10402  836      DAGFIKQYGDCLGDI  KQYGDCLGD  5        0.3666
946.5    37.00  0.31    Sequence
 HLA-DPA10301-DPB10402  837      AGFIKQYGDCLGDIA  KQYGDCLGD  4        0.3988
668.7    31.00  0.28    Sequence
 HLA-DPA10301-DPB10402  838      GFIKQYGDCLGDIAA  KQYGDCLGD  3        0.4118
580.7    28.00  0.31    Sequence
 HLA-DPA10301-DPB10402  839      FIKQYGDCLGDIAAR  KQYGDCLGD  2        0.4160
555.0    28.00  0.33    Sequence
 HLA-DPA10301-DPB10402  840      IKQYGDCLGDIAARD  KQYGDCLGD  1        0.3124
1701.8    49.00  0.34     Sequence
 HLA-DPA10301-DPB10402  841      KQYGDCLGDIAARDL  QYGDCLGDI  1        0.2870
2241.3    55.00  0.22     Sequence
 HLA-DPA10301-DPB10402  842      QYGDCLGDIAARDLI  DCLGDIAAR  3        0.2637
2883.5    60.00  0.19     Sequence
 HLA-DPA10301-DPB10402  843      YGDCLGDIAARDLIC  DCLGDIAAR  2        0.2206
4593.7    70.00  0.28     Sequence
```

```
 HLA-DPA10301-DPB10402  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.2175
4755.1    70.00  0.23     Sequence
 HLA-DPA10301-DPB10402  845      DCLGDIAARDLICAQ  DIAARDLIC  4        0.2248
4389.9    70.00  0.26     Sequence
 HLA-DPA10301-DPB10402  846      CLGDIAARDLICAQK  DIAARDLIC  3        0.2263
4321.4    70.00  0.32     Sequence
 HLA-DPA10301-DPB10402  847      LGDIAARDLICAQKF  DIAARDLIC  2        0.2434
3592.0    65.00  0.26     Sequence
 HLA-DPA10301-DPB10402  848      GDIAARDLICAQKFN  IAARDLICA  2        0.2346
3950.8    70.00  0.28     Sequence
 HLA-DPA10301-DPB10402  849      DIAARDLICAQKFNG  LICAQKFNG  6        0.2363
3879.0    65.00  0.24     Sequence
 HLA-DPA10301-DPB10402  850      IAARDLICAQKFNGL  LICAQKFNG  5        0.2771
2494.8    60.00  0.53     Sequence
 HLA-DPA10301-DPB10402  851      AARDLICAQKFNGLT  LICAQKFNG  4        0.2909
2148.7    55.00  0.57     Sequence
 HLA-DPA10301-DPB10402  852      ARDLICAQKFNGLTV  LICAQKFNG  3        0.3600
1016.6    39.00  0.47     Sequence
 HLA-DPA10301-DPB10402  853      RDLICAQKFNGLTVL  LICAQKFNG  2        0.4914
245.5    15.00  0.24     Sequence
 HLA-DPA10301-DPB10402  854      DLICAQKFNGLTVLP  AQKFNGLTV  4        0.5233
173.8    11.00  0.35     Sequence
 HLA-DPA10301-DPB10402  855      LICAQKFNGLTVLPP  KFNGLTVLP  5        0.5367
150.3     9.50  0.35     Sequence         WB
 HLA-DPA10301-DPB10402  856      ICAQKFNGLTVLPPL  KFNGLTVLP  4        0.5449
137.5     9.00  0.42     Sequence         WB
 HLA-DPA10301-DPB10402  857      CAQKFNGLTVLPPLL  KFNGLTVLP  3        0.5604
116.4     7.50  0.41     Sequence         WB
 HLA-DPA10301-DPB10402  858      AQKFNGLTVLPPLLT  KFNGLTVLP  2        0.6075
69.9     4.00  0.35     Sequence         WB
 HLA-DPA10301-DPB10402  859      QKFNGLTVLPPLLTD  KFNGLTVLP  1        0.5887
85.6     5.50  0.31     Sequence         WB
 HLA-DPA10301-DPB10402  860      KFNGLTVLPPLLTDE  LTVLPPLLT  4        0.4957
234.2    15.00  0.32     Sequence
 HLA-DPA10301-DPB10402  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3        0.4960
233.5    15.00  0.36     Sequence
 HLA-DPA10301-DPB10402  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.5014
220.3    14.00  0.36     Sequence
 HLA-DPA10301-DPB10402  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.5283
164.6    11.00  0.23     Sequence
 HLA-DPA10301-DPB10402  864      LTVLPPLLTDEMIAQ  LLTDEMIAQ  6        0.5976
77.8     5.00  0.41     Sequence         WB
 HLA-DPA10301-DPB10402  865      TVLPPLLTDEMIAQY  LLTDEMIAQ  5        0.6131
65.8     4.00  0.50     Sequence         WB
 HLA-DPA10301-DPB10402  866      VLPPLLTDEMIAQYT  LLTDEMIAQ  4        0.6319
53.7     3.00  0.52     Sequence         WB
 HLA-DPA10301-DPB10402  867      LPPLLTDEMIAQYTS  LLTDEMIAQ  3        0.6382
50.1     2.50  0.54     Sequence         WB
 HLA-DPA10301-DPB10402  868      PPLLTDEMIAQYTSA  LLTDEMIAQ  2        0.6235
58.8     3.50  0.56     Sequence         WB
 HLA-DPA10301-DPB10402  869      PLLTDEMIAQYTSAL  LLTDEMIAQ  1        0.5718
102.9     6.50  0.44     Sequence         WB
 HLA-DPA10301-DPB10402  870      LLTDEMIAQYTSALL  EMIAQYTSA  4        0.4722
302.2    18.00  0.19     Sequence
 HLA-DPA10301-DPB10402  871      LTDEMIAQYTSALLA  IAQYTSALL  5        0.4448
406.1    22.00  0.35     Sequence
 HLA-DPA10301-DPB10402  872      TDEMIAQYTSALLAG  IAQYTSALL  4        0.4541
367.5    21.00  0.34     Sequence
 HLA-DPA10301-DPB10402  873      DEMIAQYTSALLAGT  IAQYTSALL  3        0.4972
230.6    15.00  0.29     Sequence
 HLA-DPA10301-DPB10402  874      EMIAQYTSALLAGTI  QYTSALLAG  4        0.5235
173.3    11.00  0.38     Sequence
 HLA-DPA10301-DPB10402  875      MIAQYTSALLAGTIT  QYTSALLAG  3        0.5196
180.8    12.00  0.40     Sequence
 HLA-DPA10301-DPB10402  876      IAQYTSALLAGTITS  QYTSALLAG  2        0.4873
256.5    16.00  0.47     Sequence
```

```
 HLA-DPA10301-DPB10402  877      AQYTSALLAGTITSG  QYTSALLAG  1        0.4354
450.0    24.00  0.50     Sequence
 HLA-DPA10301-DPB10402  878      QYTSALLAGTITSGW  QYTSALLAG  0        0.3691
921.3    37.00  0.36     Sequence
 HLA-DPA10301-DPB10402  879      YTSALLAGTITSGWT  ALLAGTITS  3        0.3135
1682.6    48.00  0.26     Sequence
 HLA-DPA10301-DPB10402  880      TSALLAGTITSGWTF  LLAGTITSG  3        0.2804
2405.3    60.00  0.44     Sequence
 HLA-DPA10301-DPB10402  881      SALLAGTITSGWTFG  LLAGTITSG  2        0.2923
2115.3    55.00  0.44     Sequence
 HLA-DPA10301-DPB10402  882      ALLAGTITSGWTFGA  LLAGTITSG  1        0.2483
3404.0    65.00  0.35     Sequence
 HLA-DPA10301-DPB10402  883      LLAGTITSGWTFGAG  TITSGWTFG  4        0.1481
10066.5    85.00  0.19     Sequence
 HLA-DPA10301-DPB10402  884      LAGTITSGWTFGAGA  TITSGWTFG  3        0.1298
12275.0    90.00  0.27     Sequence
 HLA-DPA10301-DPB10402  885      AGTITSGWTFGAGAA  TITSGWTFG  2        0.1331
11839.7    90.00  0.28     Sequence
 HLA-DPA10301-DPB10402  886      GTITSGWTFGAGAAL  ITSGWTFGA  2        0.1688
8048.2    80.00  0.22     Sequence
 HLA-DPA10301-DPB10402  887      TITSGWTFGAGAALQ  FGAGAALQX  7        0.1950
6060.3    75.00  0.16     Sequence
 HLA-DPA10301-DPB10402  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.2764
2512.3    60.00  0.38     Sequence
 HLA-DPA10301-DPB10402  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.3124
1703.0    49.00  0.41     Sequence
 HLA-DPA10301-DPB10402  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.3348
1336.5    44.00  0.44     Sequence
 HLA-DPA10301-DPB10402  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.3447
1199.8    42.00  0.43     Sequence
 HLA-DPA10301-DPB10402  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.3630
985.0    38.00  0.40     Sequence
 HLA-DPA10301-DPB10402  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.3593
1024.3    39.00  0.29     Sequence
 HLA-DPA10301-DPB10402  894      FGAGAALQIPFAMQM  ALQIPFAMQ  5        0.3756
859.3    35.00  0.28     Sequence
 HLA-DPA10301-DPB10402  895      GAGAALQIPFAMQMA  ALQIPFAMQ  4        0.3635
979.6    38.00  0.37     Sequence
 HLA-DPA10301-DPB10402  896      AGAALQIPFAMQMAY  ALQIPFAMQ  3        0.3823
798.9    34.00  0.37     Sequence
 HLA-DPA10301-DPB10402  897      GAALQIPFAMQMAYR  ALQIPFAMQ  2        0.3944
701.3    32.00  0.35     Sequence
 HLA-DPA10301-DPB10402  898      AALQIPFAMQMAYRF  ALQIPFAMQ  1        0.4166
551.5    27.00  0.26     Sequence
 HLA-DPA10301-DPB10402  899      ALQIPFAMQMAYRFN  PFAMQMAYR  4        0.4056
621.2    29.00  0.25     Sequence
 HLA-DPA10301-DPB10402  900      LQIPFAMQMAYRFNG  PFAMQMAYR  3        0.3717
896.4    36.00  0.31     Sequence
 HLA-DPA10301-DPB10402  901      QIPFAMQMAYRFNGI  PFAMQMAYR  2        0.3750
865.1    36.00  0.32     Sequence
 HLA-DPA10301-DPB10402  902      IPFAMQMAYRFNGIG  MQMAYRFNG  4        0.3543
1082.0    40.00  0.26     Sequence
 HLA-DPA10301-DPB10402  903      PFAMQMAYRFNGIGV  MQMAYRFNG  3        0.3862
766.2    33.00  0.28     Sequence
 HLA-DPA10301-DPB10402  904      FAMQMAYRFNGIGVT  AYRFNGIGV  5        0.4571
355.8    20.00  0.38     Sequence
 HLA-DPA10301-DPB10402  905      AMQMAYRFNGIGVTQ  AYRFNGIGV  4        0.4717
303.7    18.00  0.45     Sequence
 HLA-DPA10301-DPB10402  906      MQMAYRFNGIGVTQN  AYRFNGIGV  3        0.4753
292.1    18.00  0.49     Sequence
 HLA-DPA10301-DPB10402  907      QMAYRFNGIGVTQNV  AYRFNGIGV  2        0.4775
285.4    17.00  0.50     Sequence
 HLA-DPA10301-DPB10402  908      MAYRFNGIGVTQNVL  AYRFNGIGV  1        0.4693
311.7    19.00  0.49     Sequence
 HLA-DPA10301-DPB10402  909      AYRFNGIGVTQNVLY  RFNGIGVTQ  2        0.4528
372.6    21.00  0.40     Sequence
```

```
 HLA-DPA10301-DPB10402  910      YRFNGIGVTQNVLYE  RFNGIGVTQ  1        0.3597
1019.9    39.00  0.35     Sequence
 HLA-DPA10301-DPB10402  911      RFNGIGVTQNVLYEN  IGVTQNVLY  4        0.2409
3688.1    65.00  0.26     Sequence
 HLA-DPA10301-DPB10402  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.2457
3504.2    65.00  0.30     Sequence
 HLA-DPA10301-DPB10402  913      NGIGVTQNVLYENQK  IGVTQNVLY  2        0.2575
3081.6    65.00  0.28     Sequence
 HLA-DPA10301-DPB10402  914      GIGVTQNVLYENQKL  GVTQNVLYE  2        0.2732
2601.7    60.00  0.27     Sequence
 HLA-DPA10301-DPB10402  915      IGVTQNVLYENQKLI  NVLYENQKL  5        0.3674
938.8    37.00  0.25     Sequence
 HLA-DPA10301-DPB10402  916      GVTQNVLYENQKLIA  VLYENQKLI  5        0.4285
484.7    25.00  0.20     Sequence
 HLA-DPA10301-DPB10402  917      VTQNVLYENQKLIAN  LYENQKLIA  5        0.4578
353.2    20.00  0.38     Sequence
 HLA-DPA10301-DPB10402  918      TQNVLYENQKLIANQ  LYENQKLIA  4        0.4753
292.1    18.00  0.43     Sequence
 HLA-DPA10301-DPB10402  919      QNVLYENQKLIANQF  LYENQKLIA  3        0.4873
256.5    16.00  0.44     Sequence
 HLA-DPA10301-DPB10402  920      NVLYENQKLIANQFN  LYENQKLIA  2        0.4886
253.0    16.00  0.41     Sequence
 HLA-DPA10301-DPB10402  921      VLYENQKLIANQFNS  LYENQKLIA  1        0.5002
223.2    14.00  0.35     Sequence
 HLA-DPA10301-DPB10402  922      LYENQKLIANQFNSA  KLIANQFNS  5        0.4630
333.6    20.00  0.66     Sequence
 HLA-DPA10301-DPB10402  923      YENQKLIANQFNSAI  KLIANQFNS  4        0.4924
242.8    15.00  0.73     Sequence
 HLA-DPA10301-DPB10402  924      ENQKLIANQFNSAIG  KLIANQFNS  3        0.4979
228.8    14.00  0.71     Sequence
 HLA-DPA10301-DPB10402  925      NQKLIANQFNSAIGK  KLIANQFNS  2        0.5014
220.2    14.00  0.69     Sequence
 HLA-DPA10301-DPB10402  926      QKLIANQFNSAIGKI  KLIANQFNS  1        0.4832
268.2    17.00  0.57     Sequence
 HLA-DPA10301-DPB10402  927      KLIANQFNSAIGKIQ  KLIANQFNS  0        0.4193
535.4    27.00  0.37     Sequence
 HLA-DPA10301-DPB10402  928      LIANQFNSAIGKIQD  QFNSAIGKI  4        0.3266
1459.6    46.00  0.28     Sequence
 HLA-DPA10301-DPB10402  929      IANQFNSAIGKIQDS  QFNSAIGKI  3        0.2746
2562.0    60.00  0.41     Sequence
 HLA-DPA10301-DPB10402  930      ANQFNSAIGKIQDSL  QFNSAIGKI  2        0.2767
2505.3    60.00  0.43     Sequence
 HLA-DPA10301-DPB10402  931      NQFNSAIGKIQDSLS  QFNSAIGKI  1        0.2632
2897.6    60.00  0.35     Sequence
 HLA-DPA10301-DPB10402  932      QFNSAIGKIQDSLSS  QFNSAIGKI  0        0.2471
3448.9    65.00  0.29     Sequence
 HLA-DPA10301-DPB10402  933      FNSAIGKIQDSLSST  GKIQDSLSS  5        0.1976
5895.5    75.00  0.20     Sequence
 HLA-DPA10301-DPB10402  934      NSAIGKIQDSLSSTA  GKIQDSLSS  4        0.1593
8925.6    85.00  0.28     Sequence
 HLA-DPA10301-DPB10402  935      SAIGKIQDSLSSTAS  KIQDSLSST  4        0.1698
7963.4    80.00  0.28     Sequence
 HLA-DPA10301-DPB10402  936      AIGKIQDSLSSTASA  KIQDSLSST  3        0.1749
7538.7    80.00  0.31     Sequence
 HLA-DPA10301-DPB10402  937      IGKIQDSLSSTASAL  KIQDSLSST  2        0.1800
7133.5    80.00  0.27     Sequence
 HLA-DPA10301-DPB10402  938      GKIQDSLSSTASALG  KIQDSLSST  1        0.1715
7814.9    80.00  0.26     Sequence
 HLA-DPA10301-DPB10402  939      KIQDSLSSTASALGK  SLSSTASAL  4        0.1656
8330.6    85.00  0.15     Sequence
 HLA-DPA10301-DPB10402  940      IQDSLSSTASALGKL  SSTASALGK  5        0.1950
6061.3    75.00  0.31     Sequence
 HLA-DPA10301-DPB10402  941      QDSLSSTASALGKLQ  SSTASALGK  4        0.2469
3458.2    65.00  0.37     Sequence
 HLA-DPA10301-DPB10402  942      DSLSSTASALGKLQD  SSTASALGK  3        0.2491
3378.2    65.00  0.36     Sequence
```

```
 HLA-DPA10301-DPB10402  943       SLSSTASALGKLQDV  SSTASALGK  2         0.2653
2832.7    60.00  0.35     Sequence
 HLA-DPA10301-DPB10402  944       LSSTASALGKLQDVV  SSTASALGK  1         0.2654
2829.7    60.00  0.26     Sequence
 HLA-DPA10301-DPB10402  945       SSTASALGKLQDVVN  ASALGKLQD  3         0.2560
3133.9    65.00  0.26     Sequence
 HLA-DPA10301-DPB10402  946       STASALGKLQDVVNQ  ASALGKLQD  2         0.2473
3443.8    65.00  0.25     Sequence
 HLA-DPA10301-DPB10402  947       TASALGKLQDVVNQN  ASALGKLQD  1         0.1937
6150.8    75.00  0.20     Sequence
 HLA-DPA10301-DPB10402  948       ASALGKLQDVVNQNA  ALGKLQDVV  2         0.1681
8110.4    80.00  0.23     Sequence
 HLA-DPA10301-DPB10402  949       SALGKLQDVVNQNAQ  KLQDVVNQN  4         0.1694
7998.6    80.00  0.22     Sequence
 HLA-DPA10301-DPB10402  950       ALGKLQDVVNQNAQA  KLQDVVNQN  3         0.1544
9407.7    85.00  0.29     Sequence
 HLA-DPA10301-DPB10402  951       LGKLQDVVNQNAQAL  KLQDVVNQN  2         0.1474
10149.6    85.00  0.34     Sequence
 HLA-DPA10301-DPB10402  952       GKLQDVVNQNAQALN  KLQDVVNQN  1         0.1333
11816.9    90.00  0.31     Sequence
 HLA-DPA10301-DPB10402  953       KLQDVVNQNAQALNT  DVVNQNAQA  3         0.1234
13150.0    90.00  0.28     Sequence
 HLA-DPA10301-DPB10402  954       LQDVVNQNAQALNTL  NQNAQALNT  5         0.1584
9005.6    85.00  0.26     Sequence
 HLA-DPA10301-DPB10402  955       QDVVNQNAQALNTLV  NQNAQALNT  4         0.2040
5503.0    75.00  0.29     Sequence
 HLA-DPA10301-DPB10402  956       DVVNQNAQALNTLVK  AQALNTLVK  6         0.2644
2860.3    60.00  0.31     Sequence
 HLA-DPA10301-DPB10402  957       VVNQNAQALNTLVKQ  AQALNTLVK  5         0.3060
1824.0    50.00  0.38     Sequence
 HLA-DPA10301-DPB10402  958       VNQNAQALNTLVKQL  AQALNTLVK  4         0.3558
1064.2    39.00  0.36     Sequence
 HLA-DPA10301-DPB10402  959       NQNAQALNTLVKQLS  AQALNTLVK  3         0.3777
839.8    35.00  0.33     Sequence
 HLA-DPA10301-DPB10402  960       QNAQALNTLVKQLSS  AQALNTLVK  2         0.3822
799.7    34.00  0.34     Sequence
 HLA-DPA10301-DPB10402  961       NAQALNTLVKQLSSN  QALNTLVKQ  2         0.3349
1334.2    44.00  0.26     Sequence
 HLA-DPA10301-DPB10402  962       AQALNTLVKQLSSNF  ALNTLVKQL  2         0.3233
1512.5    46.00  0.22     Sequence
 HLA-DPA10301-DPB10402  963       QALNTLVKQLSSNFG  ALNTLVKQL  1         0.2769
2499.2    60.00  0.20     Sequence
 HLA-DPA10301-DPB10402  964       ALNTLVKQLSSNFGA  TLVKQLSSN  3         0.2510
3308.7    65.00  0.22     Sequence
 HLA-DPA10301-DPB10402  965       LNTLVKQLSSNFGAI  KQLSSNFGA  5         0.3057
1829.6    50.00  0.25     Sequence
 HLA-DPA10301-DPB10402  966       NTLVKQLSSNFGAIS  KQLSSNFGA  4         0.3441
1208.2    42.00  0.31     Sequence
 HLA-DPA10301-DPB10402  967       TLVKQLSSNFGAISS  KQLSSNFGA  3         0.3665
948.2    37.00  0.31     Sequence
 HLA-DPA10301-DPB10402  968       LVKQLSSNFGAISSV  QLSSNFGAI  3         0.3915
723.2    32.00  0.34     Sequence
 HLA-DPA10301-DPB10402  969       VKQLSSNFGAISSVL  QLSSNFGAI  2         0.3903
732.9    32.00  0.34     Sequence
 HLA-DPA10301-DPB10402  970       KQLSSNFGAISSVLN  QLSSNFGAI  1         0.3840
784.4    34.00  0.28     Sequence
 HLA-DPA10301-DPB10402  971       QLSSNFGAISSVLND  FGAISSVLN  5         0.3360
1318.8    44.00  0.20     Sequence
 HLA-DPA10301-DPB10402  972       LSSNFGAISSVLNDI  FGAISSVLN  4         0.3168
1623.8    48.00  0.30     Sequence
 HLA-DPA10301-DPB10402  973       SSNFGAISSVLNDIL  GAISSVLND  4         0.3940
704.0    32.00  0.28     Sequence
 HLA-DPA10301-DPB10402  974       SNFGAISSVLNDILS  GAISSVLND  3         0.4103
590.0    29.00  0.26     Sequence
 HLA-DPA10301-DPB10402  975       NFGAISSVLNDILSR  GAISSVLND  2         0.4376
439.4    24.00  0.19     Sequence
```

```
 HLA-DPA10301-DPB10402  976      FGAISSVLNDILSRL  SVLNDILSR  5        0.4897
249.9    16.00  0.31     Sequence
 HLA-DPA10301-DPB10402  977      GAISSVLNDILSRLD  SVLNDILSR  4        0.4759
290.1    18.00  0.34     Sequence
 HLA-DPA10301-DPB10402  978      AISSVLNDILSRLDK  SVLNDILSR  3        0.4866
258.6    16.00  0.39     Sequence
 HLA-DPA10301-DPB10402  979      ISSVLNDILSRLDKV  SVLNDILSR  2        0.4903
248.4    16.00  0.42     Sequence
 HLA-DPA10301-DPB10402  980      SSVLNDILSRLDKVE  SVLNDILSR  1        0.4282
486.3    25.00  0.34     Sequence
 HLA-DPA10301-DPB10402  981      SVLNDILSRLDKVEA  VLNDILSRL  1        0.4093
596.8    29.00  0.21     Sequence
 HLA-DPA10301-DPB10402  982      VLNDILSRLDKVEAE  NDILSRLDK  2        0.3680
932.8    37.00  0.21     Sequence
 HLA-DPA10301-DPB10402  983      LNDILSRLDKVEAEV  LSRLDKVEA  4        0.3105
1736.9    49.00  0.28     Sequence
 HLA-DPA10301-DPB10402  984      NDILSRLDKVEAEVQ  LSRLDKVEA  3        0.3052
1839.5    50.00  0.31     Sequence
 HLA-DPA10301-DPB10402  985      DILSRLDKVEAEVQI  LSRLDKVEA  2        0.3083
1779.5    50.00  0.31     Sequence
 HLA-DPA10301-DPB10402  986      ILSRLDKVEAEVQID  LSRLDKVEA  1        0.2465
3472.0    65.00  0.29     Sequence
 HLA-DPA10301-DPB10402  987      LSRLDKVEAEVQIDR  RLDKVEAEV  2        0.1989
5813.8    75.00  0.36     Sequence
 HLA-DPA10301-DPB10402  988      SRLDKVEAEVQIDRL  RLDKVEAEV  1        0.1943
6106.4    75.00  0.29     Sequence
 HLA-DPA10301-DPB10402  989      RLDKVEAEVQIDRLI  VEAEVQIDR  4        0.2248
4391.1    70.00  0.23     Sequence
 HLA-DPA10301-DPB10402  990      LDKVEAEVQIDRLIT  EVQIDRLIT  6        0.2881
2214.0    55.00  0.38     Sequence
 HLA-DPA10301-DPB10402  991      DKVEAEVQIDRLITG  EVQIDRLIT  5        0.2915
2134.2    55.00  0.47     Sequence
 HLA-DPA10301-DPB10402  992      KVEAEVQIDRLITGR  EVQIDRLIT  4        0.3050
1843.6    50.00  0.56     Sequence
 HLA-DPA10301-DPB10402  993      VEAEVQIDRLITGRL  EVQIDRLIT  3        0.3536
1089.9    40.00  0.49     Sequence
 HLA-DPA10301-DPB10402  994      EAEVQIDRLITGRLQ  EVQIDRLIT  2        0.3611
1005.1    38.00  0.44     Sequence
 HLA-DPA10301-DPB10402  995      AEVQIDRLITGRLQS  EVQIDRLIT  1        0.3718
895.5    36.00  0.37     Sequence
 HLA-DPA10301-DPB10402  996      EVQIDRLITGRLQSL  RLITGRLQS  5        0.4166
551.3    27.00  0.53     Sequence
 HLA-DPA10301-DPB10402  997      VQIDRLITGRLQSLQ  RLITGRLQS  4        0.4174
546.6    27.00  0.62     Sequence
 HLA-DPA10301-DPB10402  998      QIDRLITGRLQSLQT  RLITGRLQS  3        0.4320
466.6    25.00  0.61     Sequence
 HLA-DPA10301-DPB10402  999      IDRLITGRLQSLQTY  RLITGRLQS  2        0.4449
405.8    22.00  0.59     Sequence
 HLA-DPA10301-DPB10402 1000      DRLITGRLQSLQTYV  RLITGRLQS  1        0.4307
473.5    25.00  0.46     Sequence
 HLA-DPA10301-DPB10402 1001      RLITGRLQSLQTYVT  RLITGRLQS  0        0.4276
489.7    25.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1002      LITGRLQSLQTYVTQ  RLQSLQTYV  4        0.3775
841.2    35.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1003      ITGRLQSLQTYVTQQ  RLQSLQTYV  3        0.3438
1212.3    42.00  0.44     Sequence
 HLA-DPA10301-DPB10402 1004      TGRLQSLQTYVTQQL  RLQSLQTYV  2        0.3597
1019.8    39.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1005      GRLQSLQTYVTQQLI  RLQSLQTYV  1        0.4116
581.7    28.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1006      RLQSLQTYVTQQLIR  TYVTQQLIR  6        0.4658
323.7    19.00  0.37     Sequence
 HLA-DPA10301-DPB10402 1007      LQSLQTYVTQQLIRA  TYVTQQLIR  5        0.5684
106.7     7.00  0.57     Sequence         WB
 HLA-DPA10301-DPB10402 1008      QSLQTYVTQQLIRAA  TYVTQQLIR  4        0.6104
67.7     4.00  0.58     Sequence         WB
```

```
 HLA-DPA10301-DPB10402 1009      SLQTYVTQQLIRAAE  TYVTQQLIR  3        0.6214
60.1     3.50  0.57     Sequence         WB
 HLA-DPA10301-DPB10402 1010      LQTYVTQQLIRAAEI  TYVTQQLIR  2        0.6325
53.3     3.00  0.56     Sequence         WB
 HLA-DPA10301-DPB10402 1011      QTYVTQQLIRAAEIR  TYVTQQLIR  1        0.6223
59.5     3.50  0.51     Sequence         WB
 HLA-DPA10301-DPB10402 1012      TYVTQQLIRAAEIRA  YVTQQLIRA  1        0.5339
155.0    10.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1013      YVTQQLIRAAEIRAS  LIRAAEIRA  5        0.4792
280.1    17.00  0.43     Sequence
 HLA-DPA10301-DPB10402 1014      VTQQLIRAAEIRASA  LIRAAEIRA  4        0.4294
480.2    25.00  0.65     Sequence
 HLA-DPA10301-DPB10402 1015      TQQLIRAAEIRASAN  LIRAAEIRA  3        0.4285
484.5    25.00  0.71     Sequence
 HLA-DPA10301-DPB10402 1016      QQLIRAAEIRASANL  LIRAAEIRA  2        0.4320
466.7    25.00  0.72     Sequence
 HLA-DPA10301-DPB10402 1017      QLIRAAEIRASANLA  LIRAAEIRA  1        0.3958
690.2    31.00  0.63     Sequence
 HLA-DPA10301-DPB10402 1018      LIRAAEIRASANLAA  LIRAAEIRA  0        0.3070
1803.7    50.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.2647
2852.1    60.00  0.57     Sequence
 HLA-DPA10301-DPB10402 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.2998
1951.7    55.00  0.60     Sequence
 HLA-DPA10301-DPB10402 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.3384
1284.3    43.00  0.55     Sequence
 HLA-DPA10301-DPB10402 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.3563
1058.7    39.00  0.52     Sequence
 HLA-DPA10301-DPB10402 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.3397
1266.4    43.00  0.45     Sequence
 HLA-DPA10301-DPB10402 1024      IRASANLAAIKMSEC  NLAAIKMSE  5        0.3211
1549.2    47.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1025      RASANLAAIKMSECV  NLAAIKMSE  4        0.3208
1554.4    47.00  0.49     Sequence
 HLA-DPA10301-DPB10402 1026      ASANLAAIKMSECVL  NLAAIKMSE  3        0.3370
1304.4    43.00  0.55     Sequence
 HLA-DPA10301-DPB10402 1027      SANLAAIKMSECVLG  NLAAIKMSE  2        0.3514
1116.7    40.00  0.50     Sequence
 HLA-DPA10301-DPB10402 1028      ANLAAIKMSECVLGQ  NLAAIKMSE  1        0.3330
1361.9    44.00  0.37     Sequence
 HLA-DPA10301-DPB10402 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.3199
1569.5    47.00  0.25     Sequence
 HLA-DPA10301-DPB10402 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.3013
1919.1    55.00  0.39     Sequence
 HLA-DPA10301-DPB10402 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.2968
2014.8    55.00  0.44     Sequence
 HLA-DPA10301-DPB10402 1032      AIKMSECVLGQSKRV  IKMSECVLG  1        0.2790
2444.1    60.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1033      IKMSECVLGQSKRVD  IKMSECVLG  0        0.2343
3961.9    70.00  0.29     Sequence
 HLA-DPA10301-DPB10402 1034      KMSECVLGQSKRVDF  CVLGQSKRV  4        0.1760
7447.5    80.00  0.23     Sequence
 HLA-DPA10301-DPB10402 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.1460
10304.6    85.00  0.36     Sequence
 HLA-DPA10301-DPB10402 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.1378
11255.9    90.00  0.38     Sequence
 HLA-DPA10301-DPB10402 1037      ECVLGQSKRVDFCGK  CVLGQSKRV  1        0.1288
12413.7    90.00  0.35     Sequence
 HLA-DPA10301-DPB10402 1038      CVLGQSKRVDFCGKG  CVLGQSKRV  0        0.1127
14763.8    95.00  0.24     Sequence
 HLA-DPA10301-DPB10402 1039      VLGQSKRVDFCGKGY  SKRVDFCGK  4        0.0848
19973.8   100.00  0.17     Sequence
 HLA-DPA10301-DPB10402 1040      LGQSKRVDFCGKGYH  RVDFCGKGY  5        0.0993
17077.3    95.00  0.22     Sequence
 HLA-DPA10301-DPB10402 1041      GQSKRVDFCGKGYHL  DFCGKGYHL  6        0.1306
12166.0    90.00  0.25     Sequence
```

```
 HLA-DPA10301-DPB10402 1042      QSKRVDFCGKGYHLM  DFCGKGYHL  5        0.2285
4217.3    70.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1043      SKRVDFCGKGYHLMS  DFCGKGYHL  4        0.2654
2829.0    60.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1044      KRVDFCGKGYHLMSF  CGKGYHLMS  5        0.2955
2042.9    55.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1045      RVDFCGKGYHLMSFP  CGKGYHLMS  4        0.3146
1661.8    48.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1046      VDFCGKGYHLMSFPQ  CGKGYHLMS  3        0.3079
1787.1    50.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1047      DFCGKGYHLMSFPQS  CGKGYHLMS  2        0.3110
1727.8    49.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1048      FCGKGYHLMSFPQSA  CGKGYHLMS  1        0.3111
1725.9    49.00  0.27     Sequence
 HLA-DPA10301-DPB10402 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.2938
2082.3    55.00  0.29     Sequence
 HLA-DPA10301-DPB10402 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.2996
1954.4    55.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.2916
2132.5    55.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.2695
2709.1    60.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1053      YHLMSFPQSAPHGVV  HLMSFPQSA  1        0.2216
4545.3    70.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1054      HLMSFPQSAPHGVVF  LMSFPQSAP  1        0.1531
9545.4    85.00  0.19     Sequence
 HLA-DPA10301-DPB10402 1055      LMSFPQSAPHGVVFL  FPQSAPHGV  3        0.1455
10359.5    85.00  0.17     Sequence
 HLA-DPA10301-DPB10402 1056      MSFPQSAPHGVVFLH  APHGVVFLH  6        0.1543
9422.0    85.00  0.13     Sequence
 HLA-DPA10301-DPB10402 1057      SFPQSAPHGVVFLHV  PHGVVFLHV  6        0.2845
2301.6    55.00  0.33     Sequence
 HLA-DPA10301-DPB10402 1058      FPQSAPHGVVFLHVT  PHGVVFLHV  5        0.3941
703.0    32.00  0.38     Sequence
 HLA-DPA10301-DPB10402 1059      PQSAPHGVVFLHVTY  PHGVVFLHV  4        0.4402
426.9    23.00  0.38     Sequence
 HLA-DPA10301-DPB10402 1060      QSAPHGVVFLHVTYV  GVVFLHVTY  5        0.4822
271.2    17.00  0.37     Sequence
 HLA-DPA10301-DPB10402 1061      SAPHGVVFLHVTYVP  GVVFLHVTY  4        0.4902
248.6    16.00  0.38     Sequence
 HLA-DPA10301-DPB10402 1062      APHGVVFLHVTYVPA  GVVFLHVTY  3        0.5159
188.3    12.00  0.35     Sequence
 HLA-DPA10301-DPB10402 1063      PHGVVFLHVTYVPAQ  GVVFLHVTY  2        0.5174
185.3    12.00  0.35     Sequence
 HLA-DPA10301-DPB10402 1064      HGVVFLHVTYVPAQE  GVVFLHVTY  1        0.4960
233.4    15.00  0.30     Sequence
 HLA-DPA10301-DPB10402 1065      GVVFLHVTYVPAQEK  VFLHVTYVP  2        0.4563
359.0    21.00  0.38     Sequence
 HLA-DPA10301-DPB10402 1066      VVFLHVTYVPAQEKN  VFLHVTYVP  1        0.4282
486.4    25.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1067      VFLHVTYVPAQEKNF  HVTYVPAQE  3        0.3829
793.7    34.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1068      FLHVTYVPAQEKNFT  HVTYVPAQE  2        0.3277
1441.9    45.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1069      LHVTYVPAQEKNFTT  HVTYVPAQE  1        0.2162
4821.1    70.00  0.51     Sequence
 HLA-DPA10301-DPB10402 1070      HVTYVPAQEKNFTTA  HVTYVPAQE  0        0.1288
12408.0    90.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1071      VTYVPAQEKNFTTAP  PAQEKNFTT  4        0.1038
16271.5    95.00  0.26     Sequence
 HLA-DPA10301-DPB10402 1072      TYVPAQEKNFTTAPA  PAQEKNFTT  3        0.0966
17583.1    95.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1073      YVPAQEKNFTTAPAI  PAQEKNFTT  2        0.1217
13397.6    90.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1074      VPAQEKNFTTAPAIC  NFTTAPAIC  6        0.1504
9818.3    85.00  0.35     Sequence
```

```
 HLA-DPA10301-DPB10402 1075      PAQEKNFTTAPAICH  NFTTAPAIC  5        0.2285
4220.1    70.00  0.43     Sequence
 HLA-DPA10301-DPB10402 1076      AQEKNFTTAPAICHD  NFTTAPAIC  4        0.2535
3217.7    65.00  0.43     Sequence
 HLA-DPA10301-DPB10402 1077      QEKNFTTAPAICHDG  NFTTAPAIC  3        0.2541
3199.8    65.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1078      EKNFTTAPAICHDGK  NFTTAPAIC  2        0.2674
2769.4    60.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1079      KNFTTAPAICHDGKA  FTTAPAICH  2        0.2567
3109.5    65.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1080      NFTTAPAICHDGKAH  FTTAPAICH  1        0.1762
7430.2    80.00  0.29     Sequence
 HLA-DPA10301-DPB10402 1081      FTTAPAICHDGKAHF  TTAPAICHD  1        0.1573
9116.7    85.00  0.26     Sequence
 HLA-DPA10301-DPB10402 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.0920
18486.2    95.00  0.26     Sequence
 HLA-DPA10301-DPB10402 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.0936
18152.6    95.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.0970
17502.9    95.00  0.35     Sequence
 HLA-DPA10301-DPB10402 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.0959
17714.1    95.00  0.36     Sequence
 HLA-DPA10301-DPB10402 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.1041
16212.7    95.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1087      ICHDGKAHFPREGVF  GKAHFPREG  4        0.1016
16660.4    95.00  0.25     Sequence
 HLA-DPA10301-DPB10402 1088      CHDGKAHFPREGVFV  HFPREGVFV  6        0.1131
14703.4    95.00  0.35     Sequence
 HLA-DPA10301-DPB10402 1089      HDGKAHFPREGVFVS  HFPREGVFV  5        0.1853
6730.7    80.00  0.38     Sequence
 HLA-DPA10301-DPB10402 1090      DGKAHFPREGVFVSN  HFPREGVFV  4        0.2073
5307.8    75.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1091      GKAHFPREGVFVSNG  HFPREGVFV  3        0.2067
5341.7    75.00  0.29     Sequence
 HLA-DPA10301-DPB10402 1092      KAHFPREGVFVSNGT  HFPREGVFV  2        0.2189
4682.3    70.00  0.30     Sequence
 HLA-DPA10301-DPB10402 1093      AHFPREGVFVSNGTH  PREGVFVSN  3        0.2096
5174.7    75.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1094      HFPREGVFVSNGTHW  PREGVFVSN  2        0.2050
5444.0    75.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1095      FPREGVFVSNGTHWF  PREGVFVSN  1        0.1985
5835.1    75.00  0.25     Sequence
 HLA-DPA10301-DPB10402 1096      PREGVFVSNGTHWFV  VFVSNGTHW  4        0.1987
5825.4    75.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1097      REGVFVSNGTHWFVT  VSNGTHWFV  5        0.2236
4446.8    70.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1098      EGVFVSNGTHWFVTQ  VSNGTHWFV  4        0.2369
3854.8    65.00  0.36     Sequence
 HLA-DPA10301-DPB10402 1099      GVFVSNGTHWFVTQR  VSNGTHWFV  3        0.2511
3303.5    65.00  0.35     Sequence
 HLA-DPA10301-DPB10402 1100      VFVSNGTHWFVTQRN  VSNGTHWFV  2        0.2397
3736.7    65.00  0.38     Sequence
 HLA-DPA10301-DPB10402 1101      FVSNGTHWFVTQRNF  VSNGTHWFV  1        0.2069
5327.4    75.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1102      VSNGTHWFVTQRNFY  HWFVTQRNF  5        0.2095
5184.4    75.00  0.16     Sequence
 HLA-DPA10301-DPB10402 1103      SNGTHWFVTQRNFYE  WFVTQRNFY  5        0.2443
3554.9    65.00  0.26     Sequence
 HLA-DPA10301-DPB10402 1104      NGTHWFVTQRNFYEP  WFVTQRNFY  4        0.2736
2590.8    60.00  0.25     Sequence
 HLA-DPA10301-DPB10402 1105      GTHWFVTQRNFYEPQ  FVTQRNFYE  4        0.2991
1966.3    55.00  0.29     Sequence
 HLA-DPA10301-DPB10402 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3        0.3250
1485.7    46.00  0.29     Sequence
 HLA-DPA10301-DPB10402 1107      HWFVTQRNFYEPQII  FVTQRNFYE  2        0.3615
1000.9    38.00  0.25     Sequence
```

```
 HLA-DPA10301-DPB10402 1108      WFVTQRNFYEPQIIT  VTQRNFYEP  2        0.3780
837.0    35.00  0.16     Sequence
 HLA-DPA10301-DPB10402 1109      FVTQRNFYEPQIITT  NFYEPQIIT  5        0.4233
512.8    26.00  0.36     Sequence
 HLA-DPA10301-DPB10402 1110      VTQRNFYEPQIITTD  NFYEPQIIT  4        0.4164
552.2    27.00  0.39     Sequence
 HLA-DPA10301-DPB10402 1111      TQRNFYEPQIITTDN  NFYEPQIIT  3        0.4246
505.7    26.00  0.38     Sequence
 HLA-DPA10301-DPB10402 1112      QRNFYEPQIITTDNT  FYEPQIITT  3        0.4165
551.7    27.00  0.40     Sequence
 HLA-DPA10301-DPB10402 1113      RNFYEPQIITTDNTF  FYEPQIITT  2        0.3977
676.3    31.00  0.47     Sequence
 HLA-DPA10301-DPB10402 1114      NFYEPQIITTDNTFV  FYEPQIITT  1        0.3206
1557.6    47.00  0.44     Sequence
 HLA-DPA10301-DPB10402 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.2570
3098.2    65.00  0.25     Sequence
 HLA-DPA10301-DPB10402 1116      YEPQIITTDNTFVSG  IITTDNTFV  4        0.2099
5158.8    75.00  0.36     Sequence
 HLA-DPA10301-DPB10402 1117      EPQIITTDNTFVSGN  IITTDNTFV  3        0.2179
4734.1    70.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1118      PQIITTDNTFVSGNC  IITTDNTFV  2        0.2127
5008.0    75.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1119      QIITTDNTFVSGNCD  IITTDNTFV  1        0.2064
5357.5    75.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.1933
6173.5    75.00  0.23     Sequence
 HLA-DPA10301-DPB10402 1121      ITTDNTFVSGNCDVV  TFVSGNCDV  5        0.2357
3904.4    70.00  0.47     Sequence
 HLA-DPA10301-DPB10402 1122      TTDNTFVSGNCDVVI  TFVSGNCDV  4        0.2693
2712.1    60.00  0.52     Sequence
 HLA-DPA10301-DPB10402 1123      TDNTFVSGNCDVVIG  TFVSGNCDV  3        0.2670
2781.8    60.00  0.51     Sequence
 HLA-DPA10301-DPB10402 1124      DNTFVSGNCDVVIGI  TFVSGNCDV  2        0.2931
2097.5    55.00  0.48     Sequence
 HLA-DPA10301-DPB10402 1125      NTFVSGNCDVVIGIV  TFVSGNCDV  1        0.3097
1752.4    49.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1126      TFVSGNCDVVIGIVN  TFVSGNCDV  0        0.2979
1990.6    55.00  0.25     Sequence
 HLA-DPA10301-DPB10402 1127      FVSGNCDVVIGIVNN  CDVVIGIVN  5        0.2856
2275.8    55.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1128      VSGNCDVVIGIVNNT  CDVVIGIVN  4        0.2493
3370.7    65.00  0.39     Sequence
 HLA-DPA10301-DPB10402 1129      SGNCDVVIGIVNNTV  CDVVIGIVN  3        0.2760
2523.7    60.00  0.35     Sequence
 HLA-DPA10301-DPB10402 1130      GNCDVVIGIVNNTVY  CDVVIGIVN  2        0.2974
2001.7    55.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1131      NCDVVIGIVNNTVYD  CDVVIGIVN  1        0.2793
2434.2    60.00  0.23     Sequence
 HLA-DPA10301-DPB10402 1132      CDVVIGIVNNTVYDP  DVVIGIVNN  1        0.2425
3627.6    65.00  0.27     Sequence
 HLA-DPA10301-DPB10402 1133      DVVIGIVNNTVYDPL  VIGIVNNTV  2        0.2293
4183.2    70.00  0.18     Sequence
 HLA-DPA10301-DPB10402 1134      VVIGIVNNTVYDPLQ  IVNNTVYDP  4        0.2163
4812.9    70.00  0.20     Sequence
 HLA-DPA10301-DPB10402 1135      VIGIVNNTVYDPLQP  NTVYDPLQP  6        0.2348
3941.8    70.00  0.35     Sequence
 HLA-DPA10301-DPB10402 1136      IGIVNNTVYDPLQPE  NTVYDPLQP  5        0.2447
3539.2    65.00  0.51     Sequence
 HLA-DPA10301-DPB10402 1137      GIVNNTVYDPLQPEL  NTVYDPLQP  4        0.2621
2933.8    60.00  0.60     Sequence
 HLA-DPA10301-DPB10402 1138      IVNNTVYDPLQPELD  NTVYDPLQP  3        0.2659
2813.8    60.00  0.60     Sequence
 HLA-DPA10301-DPB10402 1139      VNNTVYDPLQPELDS  NTVYDPLQP  2        0.2630
2905.5    60.00  0.62     Sequence
 HLA-DPA10301-DPB10402 1140      NNTVYDPLQPELDSF  NTVYDPLQP  1        0.2469
3459.2    65.00  0.51     Sequence
```

```
 HLA-DPA10301-DPB10402 1141      NTVYDPLQPELDSFK  NTVYDPLQP  0        0.2000
5741.9    75.00  0.27     Sequence
 HLA-DPA10301-DPB10402 1142      TVYDPLQPELDSFKE  VYDPLQPEL  1        0.1755
7488.2    80.00  0.25     Sequence
 HLA-DPA10301-DPB10402 1143      VYDPLQPELDSFKEE  PLQPELDSF  3        0.1611
8751.9    85.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1144      YDPLQPELDSFKEEL  PLQPELDSF  2        0.1721
7769.1    80.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1145      DPLQPELDSFKEELD  ELDSFKEEL  5        0.1833
6880.7    80.00  0.24     Sequence
 HLA-DPA10301-DPB10402 1146      PLQPELDSFKEELDK  ELDSFKEEL  4        0.1857
6703.2    80.00  0.29     Sequence
 HLA-DPA10301-DPB10402 1147      LQPELDSFKEELDKY  ELDSFKEEL  3        0.1928
6210.5    75.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1148      QPELDSFKEELDKYF  ELDSFKEEL  2        0.2204
4606.6    70.00  0.25     Sequence
 HLA-DPA10301-DPB10402 1149      PELDSFKEELDKYFK  SFKEELDKY  4        0.2299
4157.9    70.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1150      ELDSFKEELDKYFKN  SFKEELDKY  3        0.2301
4147.5    70.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1151      LDSFKEELDKYFKNH  SFKEELDKY  2        0.2154
4860.8    70.00  0.38     Sequence
 HLA-DPA10301-DPB10402 1152      DSFKEELDKYFKNHT  EELDKYFKN  4        0.2258
4344.9    70.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1153      SFKEELDKYFKNHTS  EELDKYFKN  3        0.2290
4196.0    70.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1154      FKEELDKYFKNHTSP  EELDKYFKN  2        0.2178
4737.3    70.00  0.35     Sequence
 HLA-DPA10301-DPB10402 1155      KEELDKYFKNHTSPD  EELDKYFKN  1        0.1681
8108.2    80.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1156      EELDKYFKNHTSPDV  ELDKYFKNH  1        0.1494
9933.9    85.00  0.22     Sequence
 HLA-DPA10301-DPB10402 1157      ELDKYFKNHTSPDVD  KYFKNHTSP  3        0.1333
11824.9    90.00  0.22     Sequence
 HLA-DPA10301-DPB10402 1158      LDKYFKNHTSPDVDL  KYFKNHTSP  2        0.1307
12155.4    90.00  0.25     Sequence
 HLA-DPA10301-DPB10402 1159      DKYFKNHTSPDVDLG  YFKNHTSPD  2        0.1019
16600.3    95.00  0.17     Sequence
 HLA-DPA10301-DPB10402 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.0913
18611.6    95.00  0.20     Sequence
 HLA-DPA10301-DPB10402 1161      YFKNHTSPDVDLGDI  NHTSPDVDL  3        0.0805
20915.7   100.00  0.20     Sequence
 HLA-DPA10301-DPB10402 1162      FKNHTSPDVDLGDIS  NHTSPDVDL  2        0.0788
21304.2   100.00  0.23     Sequence
 HLA-DPA10301-DPB10402 1163      KNHTSPDVDLGDISG  NHTSPDVDL  1        0.0694
23591.6   100.00  0.23     Sequence
 HLA-DPA10301-DPB10402 1164      NHTSPDVDLGDISGI  DVDLGDISG  5        0.0946
17974.8    95.00  0.25     Sequence
 HLA-DPA10301-DPB10402 1165      HTSPDVDLGDISGIN  DVDLGDISG  4        0.1045
16148.8    95.00  0.27     Sequence
 HLA-DPA10301-DPB10402 1166      TSPDVDLGDISGINA  DLGDISGIN  5        0.1212
13479.7    90.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1167      SPDVDLGDISGINAS  DLGDISGIN  4        0.1354
11553.4    90.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1168      PDVDLGDISGINASF  DLGDISGIN  3        0.1407
10914.1    90.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1169      DVDLGDISGINASFV  DLGDISGIN  2        0.1595
8903.0    85.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1170      VDLGDISGINASFVN  LGDISGINA  2        0.1669
8218.6    80.00  0.18     Sequence
 HLA-DPA10301-DPB10402 1171      DLGDISGINASFVNI  GINASFVNI  6        0.2084
5245.2    75.00  0.37     Sequence
 HLA-DPA10301-DPB10402 1172      LGDISGINASFVNIQ  GINASFVNI  5        0.2928
2103.7    55.00  0.45     Sequence
 HLA-DPA10301-DPB10402 1173      GDISGINASFVNIQK  GINASFVNI  4        0.3323
1372.1    44.00  0.48     Sequence
```

```
 HLA-DPA10301-DPB10402 1174      DISGINASFVNIQKE  GINASFVNI  3        0.3432
1220.3    42.00  0.45     Sequence
 HLA-DPA10301-DPB10402 1175      ISGINASFVNIQKEI  GINASFVNI  2        0.3775
842.0    35.00  0.40     Sequence
 HLA-DPA10301-DPB10402 1176      SGINASFVNIQKEID  GINASFVNI  1        0.3972
679.8    31.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1177      GINASFVNIQKEIDR  SFVNIQKEI  4        0.3938
705.7    32.00  0.37     Sequence
 HLA-DPA10301-DPB10402 1178      INASFVNIQKEIDRL  SFVNIQKEI  3        0.3902
733.8    32.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1179      NASFVNIQKEIDRLN  SFVNIQKEI  2        0.3404
1257.9    43.00  0.52     Sequence
 HLA-DPA10301-DPB10402 1180      ASFVNIQKEIDRLNE  SFVNIQKEI  1        0.3253
1480.3    46.00  0.51     Sequence
 HLA-DPA10301-DPB10402 1181      SFVNIQKEIDRLNEV  SFVNIQKEI  0        0.2884
2207.6    55.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1182      FVNIQKEIDRLNEVA  QKEIDRLNE  4        0.2310
4104.8    70.00  0.22     Sequence
 HLA-DPA10301-DPB10402 1183      VNIQKEIDRLNEVAK  QKEIDRLNE  3        0.2107
5113.4    75.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1184      NIQKEIDRLNEVAKN  QKEIDRLNE  2        0.2198
4636.2    70.00  0.23     Sequence
 HLA-DPA10301-DPB10402 1185      IQKEIDRLNEVAKNL  EIDRLNEVA  3        0.2328
4027.2    70.00  0.26     Sequence
 HLA-DPA10301-DPB10402 1186      QKEIDRLNEVAKNLN  EIDRLNEVA  2        0.2247
4397.7    70.00  0.25     Sequence
 HLA-DPA10301-DPB10402 1187      KEIDRLNEVAKNLNE  EIDRLNEVA  1        0.2152
4874.2    70.00  0.26     Sequence
 HLA-DPA10301-DPB10402 1188      EIDRLNEVAKNLNES  DRLNEVAKN  2        0.1714
7827.8    80.00  0.21     Sequence
 HLA-DPA10301-DPB10402 1189      IDRLNEVAKNLNESL  NEVAKNLNE  4        0.1694
7996.7    80.00  0.20     Sequence
 HLA-DPA10301-DPB10402 1190      DRLNEVAKNLNESLI  NEVAKNLNE  3        0.1848
6771.4    80.00  0.23     Sequence
 HLA-DPA10301-DPB10402 1191      RLNEVAKNLNESLID  NEVAKNLNE  2        0.2014
5656.7    75.00  0.22     Sequence
 HLA-DPA10301-DPB10402 1192      LNEVAKNLNESLIDL  NLNESLIDL  6        0.2747
2559.4    60.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1193      NEVAKNLNESLIDLQ  NLNESLIDL  5        0.3250
1484.9    46.00  0.37     Sequence
 HLA-DPA10301-DPB10402 1194      EVAKNLNESLIDLQE  NLNESLIDL  4        0.3355
1325.5    44.00  0.39     Sequence
 HLA-DPA10301-DPB10402 1195      VAKNLNESLIDLQEL  NLNESLIDL  3        0.3757
858.1    35.00  0.36     Sequence
 HLA-DPA10301-DPB10402 1196      AKNLNESLIDLQELG  NLNESLIDL  2        0.3752
862.4    35.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1197      KNLNESLIDLQELGK  NLNESLIDL  1        0.3781
835.9    35.00  0.23     Sequence
 HLA-DPA10301-DPB10402 1198      NLNESLIDLQELGKY  LIDLQELGK  5        0.3645
968.8    38.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1199      LNESLIDLQELGKYE  LIDLQELGK  4        0.3513
1117.7    40.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1200      NESLIDLQELGKYEQ  LIDLQELGK  3        0.3516
1114.2    40.00  0.43     Sequence
 HLA-DPA10301-DPB10402 1201      ESLIDLQELGKYEQY  LIDLQELGK  2        0.3580
1039.1    39.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1202      SLIDLQELGKYEQYI  LIDLQELGK  1        0.2837
2321.6    55.00  0.36     Sequence
 HLA-DPA10301-DPB10402 1203      LIDLQELGKYEQYIK  DLQELGKYE  2        0.2391
3761.7    65.00  0.22     Sequence
 HLA-DPA10301-DPB10402 1204      IDLQELGKYEQYIKW  LGKYEQYIK  5        0.2072
5314.8    75.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1205      DLQELGKYEQYIKWP  LGKYEQYIK  4        0.1956
6024.0    75.00  0.40     Sequence
 HLA-DPA10301-DPB10402 1206      LQELGKYEQYIKWPW  LGKYEQYIK  3        0.1996
5767.4    75.00  0.42     Sequence
```

```
 HLA-DPA10301-DPB10402 1207      QELGKYEQYIKWPWY  LGKYEQYIK  2        0.2105
5124.0    75.00  0.40     Sequence
 HLA-DPA10301-DPB10402 1208      ELGKYEQYIKWPWYI  LGKYEQYIK  1        0.2493
3368.8    65.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1209      LGKYEQYIKWPWYIW  YIKWPWYIW  6        0.3319
1378.3    44.00  0.30     Sequence
 HLA-DPA10301-DPB10402 1210      GKYEQYIKWPWYIWL  YIKWPWYIW  5        0.3841
783.8    34.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1211      KYEQYIKWPWYIWLG  YIKWPWYIW  4        0.3870
759.8    33.00  0.36     Sequence
 HLA-DPA10301-DPB10402 1212      YEQYIKWPWYIWLGF  YIKWPWYIW  3        0.4006
655.7    30.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1213      EQYIKWPWYIWLGFI  YIKWPWYIW  2        0.4186
539.3    27.00  0.29     Sequence
 HLA-DPA10301-DPB10402 1214      QYIKWPWYIWLGFIA  WYIWLGFIA  6        0.4398
428.9    23.00  0.20     Sequence
 HLA-DPA10301-DPB10402 1215      YIKWPWYIWLGFIAG  WYIWLGFIA  5        0.4120
579.2    28.00  0.29     Sequence
 HLA-DPA10301-DPB10402 1216      IKWPWYIWLGFIAGL  YIWLGFIAG  5        0.4396
429.6    23.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1217      KWPWYIWLGFIAGLI  YIWLGFIAG  4        0.4650
326.5    19.00  0.46     Sequence
 HLA-DPA10301-DPB10402 1218      WPWYIWLGFIAGLIA  YIWLGFIAG  3        0.4709
306.4    18.00  0.47     Sequence
 HLA-DPA10301-DPB10402 1219      PWYIWLGFIAGLIAI  YIWLGFIAG  2        0.4663
322.2    19.00  0.46     Sequence
 HLA-DPA10301-DPB10402 1220      WYIWLGFIAGLIAIV  YIWLGFIAG  1        0.4597
345.9    20.00  0.37     Sequence
 HLA-DPA10301-DPB10402 1221      YIWLGFIAGLIAIVM  GFIAGLIAI  4        0.4102
591.0    29.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1222      IWLGFIAGLIAIVMV  GFIAGLIAI  3        0.3746
868.4    36.00  0.42     Sequence
 HLA-DPA10301-DPB10402 1223      WLGFIAGLIAIVMVT  GFIAGLIAI  2        0.3555
1068.3    40.00  0.54     Sequence
 HLA-DPA10301-DPB10402 1224      LGFIAGLIAIVMVTI  GFIAGLIAI  1        0.3344
1341.1    44.00  0.52     Sequence
 HLA-DPA10301-DPB10402 1225      GFIAGLIAIVMVTIM  GFIAGLIAI  0        0.2817
2372.0    55.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1226      FIAGLIAIVMVTIML  GLIAIVMVT  3        0.2334
4001.9    70.00  0.16     Sequence
 HLA-DPA10301-DPB10402 1227      IAGLIAIVMVTIMLC  AIVMVTIML  5        0.2152
4873.1    70.00  0.26     Sequence
 HLA-DPA10301-DPB10402 1228      AGLIAIVMVTIMLCC  IVMVTIMLC  5        0.2501
3341.0    65.00  0.26     Sequence
 HLA-DPA10301-DPB10402 1229      GLIAIVMVTIMLCCM  IVMVTIMLC  4        0.2798
2422.2    60.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1230      LIAIVMVTIMLCCMT  VMVTIMLCC  4        0.2862
2259.7    55.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1231      IAIVMVTIMLCCMTS  VMVTIMLCC  3        0.3006
1934.4    55.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1232      AIVMVTIMLCCMTSC  VMVTIMLCC  2        0.3099
1748.3    49.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1233      IVMVTIMLCCMTSCC  TIMLCCMTS  4        0.3116
1716.4    49.00  0.32     Sequence
 HLA-DPA10301-DPB10402 1234      VMVTIMLCCMTSCCS  TIMLCCMTS  3        0.2995
1957.8    55.00  0.39     Sequence
 HLA-DPA10301-DPB10402 1235      MVTIMLCCMTSCCSC  TIMLCCMTS  2        0.2881
2215.3    55.00  0.44     Sequence
 HLA-DPA10301-DPB10402 1236      VTIMLCCMTSCCSCL  TIMLCCMTS  1        0.3056
1831.2    50.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1237      TIMLCCMTSCCSCLK  CCMTSCCSC  4        0.3329
1362.9    44.00  0.23     Sequence
 HLA-DPA10301-DPB10402 1238      IMLCCMTSCCSCLKG  CCMTSCCSC  3        0.2953
2048.8    55.00  0.26     Sequence
 HLA-DPA10301-DPB10402 1239      MLCCMTSCCSCLKGC  CCMTSCCSC  2        0.2734
2596.7    60.00  0.34     Sequence
```

```
 HLA-DPA10301-DPB10402 1240      LCCMTSCCSCLKGCC  CCMTSCCSC  1         0.2484
3403.5    65.00  0.36     Sequence
 HLA-DPA10301-DPB10402 1241      CCMTSCCSCLKGCCS  CCMTSCCSC  0         0.2216
4548.5    70.00  0.26     Sequence
 HLA-DPA10301-DPB10402 1242      CMTSCCSCLKGCCSC  XCMTSCCSC -1         0.1951
6058.5    75.00  0.21     Sequence
 HLA-DPA10301-DPB10402 1243      MTSCCSCLKGCCSCG  TSCCSCLKG  1         0.1305
12177.6    90.00  0.21     Sequence
 HLA-DPA10301-DPB10402 1244      TSCCSCLKGCCSCGS  CLKGCCSCG  5         0.0993
17074.0    95.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1245      SCCSCLKGCCSCGSC  CLKGCCSCG  4         0.0923
18412.4    95.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1246      CCSCLKGCCSCGSCC  CLKGCCSCG  3         0.0873
19442.6   100.00  0.40     Sequence
 HLA-DPA10301-DPB10402 1247      CSCLKGCCSCGSCCK  CLKGCCSCG  2         0.0911
18657.2    95.00  0.43     Sequence
 HLA-DPA10301-DPB10402 1248      SCLKGCCSCGSCCKF  CLKGCCSCG  1         0.0945
17977.9    95.00  0.35     Sequence
 HLA-DPA10301-DPB10402 1249      CLKGCCSCGSCCKFD  CCSCGSCCK  4         0.0769
21764.6   100.00  0.22     Sequence
 HLA-DPA10301-DPB10402 1250      LKGCCSCGSCCKFDE  CCSCGSCCK  3         0.0709
23210.1   100.00  0.26     Sequence
 HLA-DPA10301-DPB10402 1251      KGCCSCGSCCKFDED  CCSCGSCCK  2         0.0691
23669.6   100.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1252      GCCSCGSCCKFDEDD  CGSCCKFDE  4         0.0674
24109.3   100.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1253      CCSCGSCCKFDEDDS  CGSCCKFDE  3         0.0743
22385.3   100.00  0.28     Sequence
 HLA-DPA10301-DPB10402 1254      CSCGSCCKFDEDDSE  CGSCCKFDE  2         0.0700
23453.4   100.00  0.31     Sequence
 HLA-DPA10301-DPB10402 1255      SCGSCCKFDEDDSEP  CCKFDEDDS  4         0.0615
25693.0   100.00  0.29     Sequence
 HLA-DPA10301-DPB10402 1256      CGSCCKFDEDDSEPV  KFDEDDSEP  5         0.0832
20321.5   100.00  0.39     Sequence
 HLA-DPA10301-DPB10402 1257      GSCCKFDEDDSEPVL  KFDEDDSEP  4         0.1047
16097.8    95.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1258      SCCKFDEDDSEPVLK  KFDEDDSEP  3         0.1331
11839.0    90.00  0.35     Sequence
 HLA-DPA10301-DPB10402 1259      CCKFDEDDSEPVLKG  EDDSEPVLK  5         0.1325
11925.7    90.00  0.42     Sequence
 HLA-DPA10301-DPB10402 1260      CKFDEDDSEPVLKGV  EDDSEPVLK  4         0.1397
11027.9    90.00  0.46     Sequence
 HLA-DPA10301-DPB10402 1261      KFDEDDSEPVLKGVK  EDDSEPVLK  3         0.1494
9932.8    85.00  0.47     Sequence
 HLA-DPA10301-DPB10402 1262      FDEDDSEPVLKGVKL  EDDSEPVLK  2         0.1886
6494.0    80.00  0.41     Sequence
 HLA-DPA10301-DPB10402 1263      DEDDSEPVLKGVKLH  VLKGVKLHX  7         0.2625
2920.5    60.00  0.34     Sequence
 HLA-DPA10301-DPB10402 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6         0.4247
505.3    26.00  0.63     Sequence
 HLA-DPA10301-DPB10402 1265      DDSEPVLKGVKLHYT  VLKGVKLHY  5         0.5310
160.0    11.00  0.83     Sequence
 HLA-DPA10201-DPB10501    1      PSPIKEMFVFLVLLP  IKEMFVFLV  3         0.3008
1929.1    33.00  0.36     Sequence
 HLA-DPA10201-DPB10501    2      SPIKEMFVFLVLLPL  IKEMFVFLV  2         0.3220
1534.6    29.00  0.32     Sequence
 HLA-DPA10201-DPB10501    3      PIKEMFVFLVLLPLV  IKEMFVFLV  1         0.3149
1657.7    30.00  0.34     Sequence
 HLA-DPA10201-DPB10501    4      IKEMFVFLVLLPLVS  IKEMFVFLV  0         0.3254
1478.9    28.00  0.22     Sequence
 HLA-DPA10201-DPB10501    5      KEMFVFLVLLPLVSS  FLVLLPLVS  5         0.2968
2016.0    34.00  0.23     Sequence
 HLA-DPA10201-DPB10501    6      EMFVFLVLLPLVSSQ  FLVLLPLVS  4         0.2730
2607.3    41.00  0.28     Sequence
 HLA-DPA10201-DPB10501    7      MFVFLVLLPLVSSQC  FLVLLPLVS  3         0.2768
2501.9    40.00  0.31     Sequence
```

```
 HLA-DPA10201-DPB10501    8       FVFLVLLPLVSSQCV  FLVLLPLVS  2        0.2784
2458.0    39.00  0.30     Sequence
 HLA-DPA10201-DPB10501    9       VFLVLLPLVSSQCVN  FLVLLPLVS  1        0.2553
3157.4    46.00  0.29     Sequence
 HLA-DPA10201-DPB10501   10       FLVLLPLVSSQCVNF  LLPLVSSQC  3        0.2690
2722.4    42.00  0.16     Sequence
 HLA-DPA10201-DPB10501   11       LVLLPLVSSQCVNFT  LLPLVSSQC  2        0.2326
4036.4    55.00  0.21     Sequence
 HLA-DPA10201-DPB10501   12       VLLPLVSSQCVNFTN  PLVSSQCVN  3        0.2323
4050.8    55.00  0.31     Sequence
 HLA-DPA10201-DPB10501   13       LLPLVSSQCVNFTNR  PLVSSQCVN  2        0.2099
5162.8    60.00  0.34     Sequence
 HLA-DPA10201-DPB10501   14       LPLVSSQCVNFTNRT  PLVSSQCVN  1        0.1947
6082.7    65.00  0.30     Sequence
 HLA-DPA10201-DPB10501   15       PLVSSQCVNFTNRTQ  SSQCVNFTN  3        0.1751
7516.3    70.00  0.25     Sequence
 HLA-DPA10201-DPB10501   16       LVSSQCVNFTNRTQL  SSQCVNFTN  2        0.1815
7012.7    70.00  0.26     Sequence
 HLA-DPA10201-DPB10501   17       VSSQCVNFTNRTQLP  SSQCVNFTN  1        0.1732
7677.7    75.00  0.28     Sequence
 HLA-DPA10201-DPB10501   18       SSQCVNFTNRTQLPS  CVNFTNRTQ  3        0.1695
7992.2    75.00  0.21     Sequence
 HLA-DPA10201-DPB10501   19       SQCVNFTNRTQLPSA  CVNFTNRTQ  2        0.1513
9729.1    80.00  0.26     Sequence
 HLA-DPA10201-DPB10501   20       QCVNFTNRTQLPSAY  VNFTNRTQL  2        0.1416
10801.7    80.00  0.26     Sequence
 HLA-DPA10201-DPB10501   21       CVNFTNRTQLPSAYT  VNFTNRTQL  1        0.1214
13447.8    90.00  0.28     Sequence
 HLA-DPA10201-DPB10501   22       VNFTNRTQLPSAYTN  VNFTNRTQL  0        0.1120
14886.4    90.00  0.21     Sequence
 HLA-DPA10201-DPB10501   23       NFTNRTQLPSAYTNS  TQLPSAYTN  5        0.1013
16715.3    95.00  0.25     Sequence
 HLA-DPA10201-DPB10501   24       FTNRTQLPSAYTNSF  TQLPSAYTN  4        0.1464
10258.1    80.00  0.26     Sequence
 HLA-DPA10201-DPB10501   25       TNRTQLPSAYTNSFT  TQLPSAYTN  3        0.1579
9058.0    75.00  0.26     Sequence
 HLA-DPA10201-DPB10501   26       NRTQLPSAYTNSFTR  TQLPSAYTN  2        0.1928
6210.6    65.00  0.21     Sequence
 HLA-DPA10201-DPB10501   27       RTQLPSAYTNSFTRG  SAYTNSFTR  5        0.1974
5904.7    65.00  0.23     Sequence
 HLA-DPA10201-DPB10501   28       TQLPSAYTNSFTRGV  SAYTNSFTR  4        0.1962
5982.7    65.00  0.30     Sequence
 HLA-DPA10201-DPB10501   29       QLPSAYTNSFTRGVY  SAYTNSFTR  3        0.1868
6628.8    70.00  0.34     Sequence
 HLA-DPA10201-DPB10501   30       LPSAYTNSFTRGVYY  SAYTNSFTR  2        0.1776
7318.1    70.00  0.34     Sequence
 HLA-DPA10201-DPB10501   31       PSAYTNSFTRGVYYP  SAYTNSFTR  1        0.1683
8090.2    75.00  0.28     Sequence
 HLA-DPA10201-DPB10501   32       SAYTNSFTRGVYYPD  SAYTNSFTR  0        0.1872
6596.6    70.00  0.21     Sequence
 HLA-DPA10201-DPB10501   33       AYTNSFTRGVYYPDK  SFTRGVYYP  4        0.1782
7275.2    70.00  0.26     Sequence
 HLA-DPA10201-DPB10501   34       YTNSFTRGVYYPDKV  SFTRGVYYP  3        0.1844
6801.8    70.00  0.28     Sequence
 HLA-DPA10201-DPB10501   35       TNSFTRGVYYPDKVF  SFTRGVYYP  2        0.1974
5908.8    65.00  0.28     Sequence
 HLA-DPA10201-DPB10501   36       NSFTRGVYYPDKVFR  VYYPDKVFR  6        0.2692
2716.4    42.00  0.22     Sequence
 HLA-DPA10201-DPB10501   37       SFTRGVYYPDKVFRS  VYYPDKVFR  5        0.2999
1948.4    34.00  0.31     Sequence
 HLA-DPA10201-DPB10501   38       FTRGVYYPDKVFRSS  VYYPDKVFR  4        0.3115
1719.3    31.00  0.33     Sequence
 HLA-DPA10201-DPB10501   39       TRGVYYPDKVFRSSV  VYYPDKVFR  3        0.3131
1689.8    31.00  0.33     Sequence
 HLA-DPA10201-DPB10501   40       RGVYYPDKVFRSSVL  VYYPDKVFR  2        0.3452
1194.0    24.00  0.28     Sequence
```

```
 HLA-DPA10201-DPB10501   41      GVYYPDKVFRSSVLH  DKVFRSSVL  5        0.3855
771.7    16.00  0.37     Sequence
 HLA-DPA10201-DPB10501   42      VYYPDKVFRSSVLHS  DKVFRSSVL  4        0.4240
509.1    11.00  0.37     Sequence
 HLA-DPA10201-DPB10501   43      YYPDKVFRSSVLHST  DKVFRSSVL  3        0.4404
426.2     9.00  0.42     Sequence         WB
 HLA-DPA10201-DPB10501   44      YPDKVFRSSVLHSTQ  DKVFRSSVL  2        0.4448
406.4     8.50  0.43     Sequence         WB
 HLA-DPA10201-DPB10501   45      PDKVFRSSVLHSTQD  VFRSSVLHS  3        0.4309
472.2    10.00  0.43     Sequence
 HLA-DPA10201-DPB10501   46      DKVFRSSVLHSTQDL  VFRSSVLHS  2        0.4321
466.1    10.00  0.44     Sequence
 HLA-DPA10201-DPB10501   47      KVFRSSVLHSTQDLF  VFRSSVLHS  1        0.3838
786.4    17.00  0.50     Sequence
 HLA-DPA10201-DPB10501   48      VFRSSVLHSTQDLFL  VFRSSVLHS  0        0.2901
2167.7    36.00  0.35     Sequence
 HLA-DPA10201-DPB10501   49      FRSSVLHSTQDLFLP  LHSTQDLFL  5        0.2399
3731.7    50.00  0.19     Sequence
 HLA-DPA10201-DPB10501   50      RSSVLHSTQDLFLPF  HSTQDLFLP  5        0.3341
1345.6    26.00  0.44     Sequence
 HLA-DPA10201-DPB10501   51      SSVLHSTQDLFLPFF  HSTQDLFLP  4        0.3860
767.4    16.00  0.39     Sequence
 HLA-DPA10201-DPB10501   52      SVLHSTQDLFLPFFS  HSTQDLFLP  3        0.4302
475.8    10.00  0.34     Sequence
 HLA-DPA10201-DPB10501   53      VLHSTQDLFLPFFSN  QDLFLPFFS  5        0.4470
396.7     8.50  0.33     Sequence         WB
 HLA-DPA10201-DPB10501   54      LHSTQDLFLPFFSNV  QDLFLPFFS  4        0.4417
420.3     9.00  0.35     Sequence         WB
 HLA-DPA10201-DPB10501   55      HSTQDLFLPFFSNVT  QDLFLPFFS  3        0.4104
589.6    13.00  0.42     Sequence
 HLA-DPA10201-DPB10501   56      STQDLFLPFFSNVTW  QDLFLPFFS  2        0.3844
780.9    17.00  0.46     Sequence
 HLA-DPA10201-DPB10501   57      TQDLFLPFFSNVTWF  QDLFLPFFS  1        0.3539
1085.9    22.00  0.43     Sequence
 HLA-DPA10201-DPB10501   58      QDLFLPFFSNVTWFH  DLFLPFFSN  1        0.3449
1197.9    24.00  0.22     Sequence
 HLA-DPA10201-DPB10501   59      DLFLPFFSNVTWFHA  FSNVTWFHA  6        0.3533
1093.3    22.00  0.24     Sequence
 HLA-DPA10201-DPB10501   60      LFLPFFSNVTWFHAI  FSNVTWFHA  5        0.3475
1164.2    23.00  0.32     Sequence
 HLA-DPA10201-DPB10501   61      FLPFFSNVTWFHAIH  FSNVTWFHA  4        0.3463
1179.1    23.00  0.35     Sequence
 HLA-DPA10201-DPB10501   62      LPFFSNVTWFHAIHV  FSNVTWFHA  3        0.3456
1188.0    24.00  0.35     Sequence
 HLA-DPA10201-DPB10501   63      PFFSNVTWFHAIHVS  FSNVTWFHA  2        0.3290
1422.7    27.00  0.37     Sequence
 HLA-DPA10201-DPB10501   64      FFSNVTWFHAIHVSG  FSNVTWFHA  1        0.3046
1852.6    33.00  0.38     Sequence
 HLA-DPA10201-DPB10501   65      FSNVTWFHAIHVSGT  FSNVTWFHA  0        0.2220
4528.6    60.00  0.29     Sequence
 HLA-DPA10201-DPB10501   66      SNVTWFHAIHVSGTN  VTWFHAIHV  2        0.1587
8979.5    75.00  0.41     Sequence
 HLA-DPA10201-DPB10501   67      NVTWFHAIHVSGTNG  VTWFHAIHV  1        0.1413
10842.8    80.00  0.41     Sequence
 HLA-DPA10201-DPB10501   68      VTWFHAIHVSGTNGT  VTWFHAIHV  0        0.1061
15868.5    90.00  0.28     Sequence
 HLA-DPA10201-DPB10501   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.0862
19675.4    95.00  0.17     Sequence
 HLA-DPA10201-DPB10501   70      WFHAIHVSGTNGTKR  HVSGTNGTK  5        0.0860
19725.1    95.00  0.22     Sequence
 HLA-DPA10201-DPB10501   71      FHAIHVSGTNGTKRF  VSGTNGTKR  5        0.0943
18021.7    95.00  0.30     Sequence
 HLA-DPA10201-DPB10501   72      HAIHVSGTNGTKRFD  VSGTNGTKR  4        0.0875
19405.2    95.00  0.34     Sequence
 HLA-DPA10201-DPB10501   73      AIHVSGTNGTKRFDN  VSGTNGTKR  3        0.0873
19440.9    95.00  0.36     Sequence
```

```
 HLA-DPA10201-DPB10501   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.0815
20693.5    95.00  0.39     Sequence
 HLA-DPA10201-DPB10501   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.0835
20265.2    95.00  0.37     Sequence
 HLA-DPA10201-DPB10501   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.1719
7788.2    75.00  0.43     Sequence
 HLA-DPA10201-DPB10501   77      SGTNGTKRFDNPVLP  TKRFDNPVL  5        0.2252
4372.6    55.00  0.50     Sequence
 HLA-DPA10201-DPB10501   78      GTNGTKRFDNPVLPF  TKRFDNPVL  4        0.3352
1330.3    26.00  0.43     Sequence
 HLA-DPA10201-DPB10501   79      TNGTKRFDNPVLPFN  KRFDNPVLP  4        0.3758
857.4    18.00  0.40     Sequence
 HLA-DPA10201-DPB10501   80      NGTKRFDNPVLPFND  KRFDNPVLP  3        0.3787
830.7    18.00  0.39     Sequence
 HLA-DPA10201-DPB10501   81      GTKRFDNPVLPFNDG  KRFDNPVLP  2        0.3728
885.4    19.00  0.40     Sequence
 HLA-DPA10201-DPB10501   82      TKRFDNPVLPFNDGV  KRFDNPVLP  1        0.3653
960.1    20.00  0.40     Sequence
 HLA-DPA10201-DPB10501   83      KRFDNPVLPFNDGVY  KRFDNPVLP  0        0.2775
2484.4    40.00  0.30     Sequence
 HLA-DPA10201-DPB10501   84      RFDNPVLPFNDGVYF  VLPFNDGVY  5        0.2377
3819.4    55.00  0.17     Sequence
 HLA-DPA10201-DPB10501   85      FDNPVLPFNDGVYFA  VLPFNDGVY  4        0.2110
5098.5    60.00  0.26     Sequence
 HLA-DPA10201-DPB10501   86      DNPVLPFNDGVYFAS  PFNDGVYFA  5        0.2485
3399.5    48.00  0.26     Sequence
 HLA-DPA10201-DPB10501   87      NPVLPFNDGVYFAST  FNDGVYFAS  5        0.2663
2804.0    43.00  0.26     Sequence
 HLA-DPA10201-DPB10501   88      PVLPFNDGVYFASTE  FNDGVYFAS  4        0.2772
2491.2    40.00  0.25     Sequence
 HLA-DPA10201-DPB10501   89      VLPFNDGVYFASTEK  FNDGVYFAS  3        0.3118
1713.0    31.00  0.22     Sequence
 HLA-DPA10201-DPB10501   90      LPFNDGVYFASTEKS  GVYFASTEK  5        0.3750
864.4    18.00  0.34     Sequence
 HLA-DPA10201-DPB10501   91      PFNDGVYFASTEKSN  GVYFASTEK  4        0.3902
733.3    16.00  0.41     Sequence
 HLA-DPA10201-DPB10501   92      FNDGVYFASTEKSNI  GVYFASTEK  3        0.4112
584.8    13.00  0.41     Sequence
 HLA-DPA10201-DPB10501   93      NDGVYFASTEKSNII  GVYFASTEK  2        0.4035
635.6    14.00  0.44     Sequence
 HLA-DPA10201-DPB10501   94      DGVYFASTEKSNIIR  GVYFASTEK  1        0.4105
589.2    13.00  0.41     Sequence
 HLA-DPA10201-DPB10501   95      GVYFASTEKSNIIRG  GVYFASTEK  0        0.3908
729.2    16.00  0.34     Sequence
 HLA-DPA10201-DPB10501   96      VYFASTEKSNIIRGW  YFASTEKSN  1        0.3170
1619.4    30.00  0.26     Sequence
 HLA-DPA10201-DPB10501   97      YFASTEKSNIIRGWI  YFASTEKSN  0        0.2015
5650.7    65.00  0.25     Sequence
 HLA-DPA10201-DPB10501   98      FASTEKSNIIRGWIF  TEKSNIIRG  3        0.1607
8784.9    75.00  0.25     Sequence
 HLA-DPA10201-DPB10501   99      ASTEKSNIIRGWIFG  SNIIRGWIF  5        0.1324
11929.6    85.00  0.23     Sequence
 HLA-DPA10201-DPB10501  100      STEKSNIIRGWIFGT  SNIIRGWIF  4        0.1554
9309.5    80.00  0.25     Sequence
 HLA-DPA10201-DPB10501  101      TEKSNIIRGWIFGTT  SNIIRGWIF  3        0.1795
7171.6    70.00  0.23     Sequence
 HLA-DPA10201-DPB10501  102      EKSNIIRGWIFGTTL  IIRGWIFGT  4        0.1966
5957.4    65.00  0.24     Sequence
 HLA-DPA10201-DPB10501  103      KSNIIRGWIFGTTLD  IIRGWIFGT  3        0.1996
5769.6    65.00  0.23     Sequence
 HLA-DPA10201-DPB10501  104      SNIIRGWIFGTTLDS  IIRGWIFGT  2        0.2124
5022.3    60.00  0.17     Sequence
 HLA-DPA10201-DPB10501  105      NIIRGWIFGTTLDSK  WIFGTTLDS  5        0.2339
3979.7    55.00  0.30     Sequence
 HLA-DPA10201-DPB10501  106      IIRGWIFGTTLDSKT  WIFGTTLDS  4        0.2362
3883.7    55.00  0.32     Sequence
```

```
 HLA-DPA10201-DPB10501  107      IRGWIFGTTLDSKTQ  WIFGTTLDS  3        0.2304
4133.5    55.00  0.37     Sequence
 HLA-DPA10201-DPB10501  108      RGWIFGTTLDSKTQS  WIFGTTLDS  2        0.2228
4488.4    60.00  0.41     Sequence
 HLA-DPA10201-DPB10501  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1        0.1838
6845.0    70.00  0.43     Sequence
 HLA-DPA10201-DPB10501  110      WIFGTTLDSKTQSLL  WIFGTTLDS  0        0.1669
8213.2    75.00  0.37     Sequence
 HLA-DPA10201-DPB10501  111      IFGTTLDSKTQSLLI  FGTTLDSKT  1        0.1539
9462.0    80.00  0.22     Sequence
 HLA-DPA10201-DPB10501  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5        0.1711
7851.3    75.00  0.29     Sequence
 HLA-DPA10201-DPB10501  113      GTTLDSKTQSLLIVN  SKTQSLLIV  5        0.2352
3924.6    55.00  0.45     Sequence
 HLA-DPA10201-DPB10501  114      TTLDSKTQSLLIVNN  SKTQSLLIV  4        0.2686
2734.8    42.00  0.43     Sequence
 HLA-DPA10201-DPB10501  115      TLDSKTQSLLIVNNA  SKTQSLLIV  3        0.2952
2049.3    35.00  0.40     Sequence
 HLA-DPA10201-DPB10501  116      LDSKTQSLLIVNNAT  SKTQSLLIV  2        0.3180
1601.4    29.00  0.36     Sequence
 HLA-DPA10201-DPB10501  117      DSKTQSLLIVNNATN  SKTQSLLIV  1        0.3217
1538.5    29.00  0.30     Sequence
 HLA-DPA10201-DPB10501  118      SKTQSLLIVNNATNV  SKTQSLLIV  0        0.3223
1530.0    28.00  0.25     Sequence
 HLA-DPA10201-DPB10501  119      KTQSLLIVNNATNVV  LLIVNNATN  4        0.2965
2022.2    35.00  0.22     Sequence
 HLA-DPA10201-DPB10501  120      TQSLLIVNNATNVVI  LLIVNNATN  3        0.2629
2907.9    44.00  0.28     Sequence
 HLA-DPA10201-DPB10501  121      QSLLIVNNATNVVIK  LLIVNNATN  2        0.2530
3236.1    47.00  0.31     Sequence
 HLA-DPA10201-DPB10501  122      SLLIVNNATNVVIKV  LLIVNNATN  1        0.2362
3883.8    55.00  0.26     Sequence
 HLA-DPA10201-DPB10501  123      LLIVNNATNVVIKVC  LLIVNNATN  0        0.2049
5447.5    65.00  0.18     Sequence
 HLA-DPA10201-DPB10501  124      LIVNNATNVVIKVCE  NNATNVVIK  3        0.1670
8207.2    75.00  0.26     Sequence
 HLA-DPA10201-DPB10501  125      IVNNATNVVIKVCEF  NNATNVVIK  2        0.1659
8308.5    75.00  0.27     Sequence
 HLA-DPA10201-DPB10501  126      VNNATNVVIKVCEFQ  NNATNVVIK  1        0.1603
8829.1    75.00  0.26     Sequence
 HLA-DPA10201-DPB10501  127      NNATNVVIKVCEFQF  VIKVCEFQF  6        0.2034
5533.2    65.00  0.23     Sequence
 HLA-DPA10201-DPB10501  128      NATNVVIKVCEFQFC  VIKVCEFQF  5        0.2615
2953.0    44.00  0.37     Sequence
 HLA-DPA10201-DPB10501  129      ATNVVIKVCEFQFCN  VIKVCEFQF  4        0.3013
1920.2    33.00  0.36     Sequence
 HLA-DPA10201-DPB10501  130      TNVVIKVCEFQFCNY  VIKVCEFQF  3        0.3361
1316.8    25.00  0.29     Sequence
 HLA-DPA10201-DPB10501  131      NVVIKVCEFQFCNYP  VIKVCEFQF  2        0.3340
1347.2    26.00  0.32     Sequence
 HLA-DPA10201-DPB10501  132      VVIKVCEFQFCNYPF  VIKVCEFQF  1        0.3413
1245.5    24.00  0.31     Sequence
 HLA-DPA10201-DPB10501  133      VIKVCEFQFCNYPFL  IKVCEFQFC  1        0.3484
1152.7    23.00  0.26     Sequence
 HLA-DPA10201-DPB10501  134      IKVCEFQFCNYPFLG  IKVCEFQFC  0        0.3048
1847.9    32.00  0.21     Sequence
 HLA-DPA10201-DPB10501  135      KVCEFQFCNYPFLGV  QFCNYPFLG  5        0.2940
2077.6    35.00  0.22     Sequence
 HLA-DPA10201-DPB10501  136      VCEFQFCNYPFLGVY  QFCNYPFLG  4        0.2869
2242.8    37.00  0.28     Sequence
 HLA-DPA10201-DPB10501  137      CEFQFCNYPFLGVYY  QFCNYPFLG  3        0.2883
2210.3    37.00  0.29     Sequence
 HLA-DPA10201-DPB10501  138      EFQFCNYPFLGVYYH  QFCNYPFLG  2        0.3156
1643.7    30.00  0.26     Sequence
 HLA-DPA10201-DPB10501  139      FQFCNYPFLGVYYHK  PFLGVYYHK  6        0.3747
867.9    18.00  0.20     Sequence
```

```
 HLA-DPA10201-DPB10501  140      QFCNYPFLGVYYHKN  PFLGVYYHK  5        0.4243
507.3    11.00  0.41     Sequence
 HLA-DPA10201-DPB10501  141      FCNYPFLGVYYHKNN  PFLGVYYHK  4        0.4178
544.1    12.00  0.45     Sequence
 HLA-DPA10201-DPB10501  142      CNYPFLGVYYHKNNK  PFLGVYYHK  3        0.4148
562.2    12.00  0.46     Sequence
 HLA-DPA10201-DPB10501  143      NYPFLGVYYHKNNKS  PFLGVYYHK  2        0.4017
647.6    14.00  0.50     Sequence
 HLA-DPA10201-DPB10501  144      YPFLGVYYHKNNKSW  PFLGVYYHK  1        0.3872
758.1    16.00  0.49     Sequence
 HLA-DPA10201-DPB10501  145      PFLGVYYHKNNKSWM  PFLGVYYHK  0        0.3269
1454.4    27.00  0.41     Sequence
 HLA-DPA10201-DPB10501  146      FLGVYYHKNNKSWME  XFLGVYYHK -1        0.2419
3650.8    50.00  0.20     Sequence
 HLA-DPA10201-DPB10501  147      LGVYYHKNNKSWMES  GVYYHKNNK  1        0.1349
11611.2    85.00  0.22     Sequence
 HLA-DPA10201-DPB10501  148      GVYYHKNNKSWMESE  HKNNKSWME  4        0.1104
15134.5    90.00  0.23     Sequence
 HLA-DPA10201-DPB10501  149      VYYHKNNKSWMESEF  HKNNKSWME  3        0.1252
12908.2    85.00  0.31     Sequence
 HLA-DPA10201-DPB10501  150      YYHKNNKSWMESEFR  NKSWMESEF  5        0.1660
8295.4    75.00  0.31     Sequence
 HLA-DPA10201-DPB10501  151      YHKNNKSWMESEFRV  NKSWMESEF  4        0.2082
5256.0    60.00  0.32     Sequence
 HLA-DPA10201-DPB10501  152      HKNNKSWMESEFRVY  SWMESEFRV  5        0.2902
2163.3    36.00  0.37     Sequence
 HLA-DPA10201-DPB10501  153      KNNKSWMESEFRVYS  SWMESEFRV  4        0.3160
1638.0    30.00  0.34     Sequence
 HLA-DPA10201-DPB10501  154      NNKSWMESEFRVYSS  SWMESEFRV  3        0.3200
1567.7    29.00  0.34     Sequence
 HLA-DPA10201-DPB10501  155      NKSWMESEFRVYSSA  SWMESEFRV  2        0.3266
1459.0    27.00  0.32     Sequence
 HLA-DPA10201-DPB10501  156      KSWMESEFRVYSSAN  SWMESEFRV  1        0.3068
1808.8    32.00  0.31     Sequence
 HLA-DPA10201-DPB10501  157      SWMESEFRVYSSANN  ESEFRVYSS  3        0.2813
2383.1    39.00  0.23     Sequence
 HLA-DPA10201-DPB10501  158      WMESEFRVYSSANNC  FRVYSSANN  5        0.2680
2751.1    42.00  0.26     Sequence
 HLA-DPA10201-DPB10501  159      MESEFRVYSSANNCT  FRVYSSANN  4        0.2482
3409.6    48.00  0.38     Sequence
 HLA-DPA10201-DPB10501  160      ESEFRVYSSANNCTF  FRVYSSANN  3        0.2547
3178.3    46.00  0.51     Sequence
 HLA-DPA10201-DPB10501  161      SEFRVYSSANNCTFE  FRVYSSANN  2        0.2533
3225.9    46.00  0.54     Sequence
 HLA-DPA10201-DPB10501  162      EFRVYSSANNCTFEY  FRVYSSANN  1        0.2376
3822.5    55.00  0.55     Sequence
 HLA-DPA10201-DPB10501  163      FRVYSSANNCTFEYV  FRVYSSANN  0        0.2074
5298.9    60.00  0.47     Sequence
 HLA-DPA10201-DPB10501  164      RVYSSANNCTFEYVS  SANNCTFEY  4        0.1345
11666.3    85.00  0.20     Sequence
 HLA-DPA10201-DPB10501  165      VYSSANNCTFEYVSQ  NCTFEYVSQ  6        0.1204
13595.9    90.00  0.19     Sequence
 HLA-DPA10201-DPB10501  166      YSSANNCTFEYVSQP  NCTFEYVSQ  5        0.1163
14200.4    90.00  0.28     Sequence
 HLA-DPA10201-DPB10501  167      SSANNCTFEYVSQPF  NCTFEYVSQ  4        0.1261
12779.5    85.00  0.34     Sequence
 HLA-DPA10201-DPB10501  168      SANNCTFEYVSQPFL  NCTFEYVSQ  3        0.1890
6469.6    70.00  0.28     Sequence
 HLA-DPA10201-DPB10501  169      ANNCTFEYVSQPFLM  EYVSQPFLM  6        0.2385
3787.9    55.00  0.23     Sequence
 HLA-DPA10201-DPB10501  170      NNCTFEYVSQPFLMD  EYVSQPFLM  5        0.2708
2668.8    41.00  0.30     Sequence
 HLA-DPA10201-DPB10501  171      NCTFEYVSQPFLMDL  EYVSQPFLM  4        0.2973
2005.1    34.00  0.29     Sequence
 HLA-DPA10201-DPB10501  172      CTFEYVSQPFLMDLE  EYVSQPFLM  3        0.2981
1987.8    34.00  0.31     Sequence
```

```
 HLA-DPA10201-DPB10501  173      TFEYVSQPFLMDLEG  EYVSQPFLM  2        0.2948
2058.6    35.00  0.31     Sequence
 HLA-DPA10201-DPB10501  174      FEYVSQPFLMDLEGK  EYVSQPFLM  1        0.2904
2158.6    36.00  0.28     Sequence
 HLA-DPA10201-DPB10501  175      EYVSQPFLMDLEGKQ  YVSQPFLMD  1        0.2676
2764.5    42.00  0.28     Sequence
 HLA-DPA10201-DPB10501  176      YVSQPFLMDLEGKQG  QPFLMDLEG  3        0.2395
3747.9    55.00  0.20     Sequence
 HLA-DPA10201-DPB10501  177      VSQPFLMDLEGKQGN  FLMDLEGKQ  4        0.2222
4517.2    60.00  0.25     Sequence
 HLA-DPA10201-DPB10501  178      SQPFLMDLEGKQGNF  FLMDLEGKQ  3        0.2260
4333.7    55.00  0.28     Sequence
 HLA-DPA10201-DPB10501  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2        0.2238
4440.8    55.00  0.28     Sequence
 HLA-DPA10201-DPB10501  180      PFLMDLEGKQGNFKN  FLMDLEGKQ  1        0.2140
4933.5    60.00  0.25     Sequence
 HLA-DPA10201-DPB10501  181      FLMDLEGKQGNFKNL  LMDLEGKQG  1        0.2113
5083.5    60.00  0.22     Sequence
 HLA-DPA10201-DPB10501  182      LMDLEGKQGNFKNLS  EGKQGNFKN  4        0.1481
10067.6    80.00  0.35     Sequence
 HLA-DPA10201-DPB10501  183      MDLEGKQGNFKNLSE  EGKQGNFKN  3        0.1326
11910.6    85.00  0.37     Sequence
 HLA-DPA10201-DPB10501  184      DLEGKQGNFKNLSEF  EGKQGNFKN  2        0.1554
9306.3    80.00  0.32     Sequence
 HLA-DPA10201-DPB10501  185      LEGKQGNFKNLSEFV  QGNFKNLSE  4        0.2251
4379.9    55.00  0.16     Sequence
 HLA-DPA10201-DPB10501  186      EGKQGNFKNLSEFVF  FKNLSEFVF  6        0.4128
574.4    13.00  0.58     Sequence
 HLA-DPA10201-DPB10501  187      GKQGNFKNLSEFVFK  FKNLSEFVF  5        0.5282
164.8     3.00  0.68     Sequence         WB
 HLA-DPA10201-DPB10501  188      KQGNFKNLSEFVFKN  FKNLSEFVF  4        0.5893
85.1      1.10  0.60     Sequence         SB
 HLA-DPA10201-DPB10501  189      QGNFKNLSEFVFKNI  FKNLSEFVF  3        0.6492
44.5      0.30  0.48     Sequence         SB
 HLA-DPA10201-DPB10501  190      GNFKNLSEFVFKNID  FKNLSEFVF  2        0.6402
49.1      0.40  0.44     Sequence         SB
 HLA-DPA10201-DPB10501  191      NFKNLSEFVFKNIDG  FKNLSEFVF  1        0.6332
52.9      0.50  0.44     Sequence         SB
 HLA-DPA10201-DPB10501  192      FKNLSEFVFKNIDGY  FKNLSEFVF  0        0.6018
74.3      0.90  0.34     Sequence         SB
 HLA-DPA10201-DPB10501  193      KNLSEFVFKNIDGYF  NLSEFVFKN  1        0.4874
256.4     5.50  0.32     Sequence         WB
 HLA-DPA10201-DPB10501  194      NLSEFVFKNIDGYFK  FKNIDGYFK  6        0.5382
147.9     2.50  0.37     Sequence         WB
 HLA-DPA10201-DPB10501  195      LSEFVFKNIDGYFKI  FKNIDGYFK  5        0.5658
109.8     1.60  0.55     Sequence         SB
 HLA-DPA10201-DPB10501  196      SEFVFKNIDGYFKIY  FKNIDGYFK  4        0.5951
80.0      1.00  0.58     Sequence         SB
 HLA-DPA10201-DPB10501  197      EFVFKNIDGYFKIYS  FKNIDGYFK  3        0.6066
70.6      0.80  0.58     Sequence         SB
 HLA-DPA10201-DPB10501  198      FVFKNIDGYFKIYSK  FKNIDGYFK  2        0.6129
65.9      0.70  0.60     Sequence         SB
 HLA-DPA10201-DPB10501  199      VFKNIDGYFKIYSKH  FKNIDGYFK  1        0.5854
88.8      1.10  0.56     Sequence         SB
 HLA-DPA10201-DPB10501  200      FKNIDGYFKIYSKHT  FKNIDGYFK  0        0.5680
107.1     1.50  0.49     Sequence         SB
 HLA-DPA10201-DPB10501  201      KNIDGYFKIYSKHTP  DGYFKIYSK  3        0.3734
880.0    18.00  0.26     Sequence
 HLA-DPA10201-DPB10501  202      NIDGYFKIYSKHTPI  FKIYSKHTP  5        0.3486
1150.8    23.00  0.26     Sequence
 HLA-DPA10201-DPB10501  203      IDGYFKIYSKHTPIN  FKIYSKHTP  4        0.3535
1090.6    22.00  0.31     Sequence
 HLA-DPA10201-DPB10501  204      DGYFKIYSKHTPINL  FKIYSKHTP  3        0.3629
985.7    20.00  0.31     Sequence
 HLA-DPA10201-DPB10501  205      GYFKIYSKHTPINLV  FKIYSKHTP  2        0.3734
880.1    18.00  0.30     Sequence
```

```
 HLA-DPA10201-DPB10501  206      YFKIYSKHTPINLVR  FKIYSKHTP  1        0.3527
1101.0    22.00  0.34     Sequence
 HLA-DPA10201-DPB10501  207      FKIYSKHTPINLVRD  YSKHTPINL  3        0.2967
2017.5    34.00  0.25     Sequence
 HLA-DPA10201-DPB10501  208      KIYSKHTPINLVRDL  YSKHTPINL  2        0.2600
3002.2    45.00  0.28     Sequence
 HLA-DPA10201-DPB10501  209      IYSKHTPINLVRDLP  YSKHTPINL  1        0.2239
4433.5    55.00  0.27     Sequence
 HLA-DPA10201-DPB10501  210      YSKHTPINLVRDLPQ  KHTPINLVR  2        0.1946
6087.0    65.00  0.30     Sequence
 HLA-DPA10201-DPB10501  211      SKHTPINLVRDLPQG  KHTPINLVR  1        0.1626
8606.0    75.00  0.26     Sequence
 HLA-DPA10201-DPB10501  212      KHTPINLVRDLPQGF  KHTPINLVR  0        0.1579
9054.2    75.00  0.21     Sequence
 HLA-DPA10201-DPB10501  213      HTPINLVRDLPQGFS  INLVRDLPQ  3        0.1462
10276.3    80.00  0.24     Sequence
 HLA-DPA10201-DPB10501  214      TPINLVRDLPQGFSA  INLVRDLPQ  2        0.1537
9482.7    80.00  0.22     Sequence
 HLA-DPA10201-DPB10501  215      PINLVRDLPQGFSAL  INLVRDLPQ  1        0.1628
8590.1    75.00  0.22     Sequence
 HLA-DPA10201-DPB10501  216      INLVRDLPQGFSALE  LPQGFSALE  6        0.1836
6858.8    70.00  0.16     Sequence
 HLA-DPA10201-DPB10501  217      NLVRDLPQGFSALEP  LPQGFSALE  5        0.1733
7664.4    75.00  0.22     Sequence
 HLA-DPA10201-DPB10501  218      LVRDLPQGFSALEPL  PQGFSALEP  5        0.2075
5298.6    60.00  0.31     Sequence
 HLA-DPA10201-DPB10501  219      VRDLPQGFSALEPLV  PQGFSALEP  4        0.2432
3600.5    49.00  0.28     Sequence
 HLA-DPA10201-DPB10501  220      RDLPQGFSALEPLVD  FSALEPLVD  6        0.2892
2188.9    36.00  0.34     Sequence
 HLA-DPA10201-DPB10501  221      DLPQGFSALEPLVDL  FSALEPLVD  5        0.3140
1673.4    30.00  0.47     Sequence
 HLA-DPA10201-DPB10501  222      LPQGFSALEPLVDLP  FSALEPLVD  4        0.3227
1522.9    28.00  0.47     Sequence
 HLA-DPA10201-DPB10501  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.3266
1459.3    27.00  0.48     Sequence
 HLA-DPA10201-DPB10501  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.3296
1412.5    27.00  0.45     Sequence
 HLA-DPA10201-DPB10501  225      GFSALEPLVDLPIGI  FSALEPLVD  1        0.2999
1948.0    34.00  0.44     Sequence
 HLA-DPA10201-DPB10501  226      FSALEPLVDLPIGIN  FSALEPLVD  0        0.2783
2462.5    39.00  0.31     Sequence
 HLA-DPA10201-DPB10501  227      SALEPLVDLPIGINI  PLVDLPIGI  4        0.2390
3767.9    55.00  0.22     Sequence
 HLA-DPA10201-DPB10501  228      ALEPLVDLPIGINIT  LVDLPIGIN  4        0.2323
4050.2    55.00  0.22     Sequence
 HLA-DPA10201-DPB10501  229      LEPLVDLPIGINITR  LVDLPIGIN  3        0.2622
2928.7    44.00  0.19     Sequence
 HLA-DPA10201-DPB10501  230      EPLVDLPIGINITRF  LPIGINITR  5        0.2837
2323.1    38.00  0.33     Sequence
 HLA-DPA10201-DPB10501  231      PLVDLPIGINITRFQ  LPIGINITR  4        0.2808
2397.2    39.00  0.39     Sequence
 HLA-DPA10201-DPB10501  232      LVDLPIGINITRFQT  LPIGINITR  3        0.2877
2224.3    37.00  0.39     Sequence
 HLA-DPA10201-DPB10501  233      VDLPIGINITRFQTL  LPIGINITR  2        0.3084
1777.4    32.00  0.33     Sequence
 HLA-DPA10201-DPB10501  234      DLPIGINITRFQTLL  GINITRFQT  4        0.3346
1339.1    26.00  0.33     Sequence
 HLA-DPA10201-DPB10501  235      LPIGINITRFQTLLA  ITRFQTLLA  6        0.3956
691.6    15.00  0.28     Sequence
 HLA-DPA10201-DPB10501  236      PIGINITRFQTLLAL  ITRFQTLLA  5        0.4181
542.5    12.00  0.41     Sequence
 HLA-DPA10201-DPB10501  237      IGINITRFQTLLALH  ITRFQTLLA  4        0.4482
391.8     8.50  0.41     Sequence         WB
 HLA-DPA10201-DPB10501  238      GINITRFQTLLALHR  ITRFQTLLA  3        0.5318
158.5     3.00  0.32     Sequence         WB
```

```
 HLA-DPA10201-DPB10501  239      INITRFQTLLALHRS  FQTLLALHR  5         0.5566
121.3     1.80  0.31     Sequence         SB
 HLA-DPA10201-DPB10501  240      NITRFQTLLALHRSY  FQTLLALHR  4         0.5705
104.3     1.50  0.35     Sequence         SB
 HLA-DPA10201-DPB10501  241      ITRFQTLLALHRSYL  FQTLLALHR  3         0.5637
112.2     1.60  0.38     Sequence         SB
 HLA-DPA10201-DPB10501  242      TRFQTLLALHRSYLT  FQTLLALHR  2         0.5454
136.8     2.50  0.47     Sequence         WB
 HLA-DPA10201-DPB10501  243      RFQTLLALHRSYLTP  FQTLLALHR  1         0.5118
196.8     4.00  0.50     Sequence         WB
 HLA-DPA10201-DPB10501  244      FQTLLALHRSYLTPG  FQTLLALHR  0         0.4335
459.4    10.00  0.41     Sequence
 HLA-DPA10201-DPB10501  245      QTLLALHRSYLTPGD  QTLLALHRS  0         0.2850
2288.8    38.00  0.28     Sequence
 HLA-DPA10201-DPB10501  246      TLLALHRSYLTPGDS  LLALHRSYL  1         0.2247
4395.6    55.00  0.25     Sequence
 HLA-DPA10201-DPB10501  247      LLALHRSYLTPGDSS  LALHRSYLT  1         0.1602
8838.7    75.00  0.35     Sequence
 HLA-DPA10201-DPB10501  248      LALHRSYLTPGDSSS  LALHRSYLT  0         0.1030
16410.0    90.00  0.31     Sequence
 HLA-DPA10201-DPB10501  249      ALHRSYLTPGDSSSG  HRSYLTPGD  2         0.0594
26281.2   100.00  0.23     Sequence
 HLA-DPA10201-DPB10501  250      LHRSYLTPGDSSSGW  HRSYLTPGD  1         0.0539
27895.9   100.00  0.23     Sequence
 HLA-DPA10201-DPB10501  251      HRSYLTPGDSSSGWT  RSYLTPGDS  1         0.0439
31101.0   100.00  0.30     Sequence
 HLA-DPA10201-DPB10501  252      RSYLTPGDSSSGWTA  RSYLTPGDS  0         0.0342
34545.9   100.00  0.25     Sequence
 HLA-DPA10201-DPB10501  253      SYLTPGDSSSGWTAG  YLTPGDSSS  1         0.0292
36460.8   100.00  0.24     Sequence
 HLA-DPA10201-DPB10501  254      YLTPGDSSSGWTAGA  PGDSSSGWT  3         0.0237
38706.4   100.00  0.16     Sequence
 HLA-DPA10201-DPB10501  255      LTPGDSSSGWTAGAA  SSGWTAGAA  6         0.0269
37371.0   100.00  0.24     Sequence
 HLA-DPA10201-DPB10501  256      TPGDSSSGWTAGAAA  SSGWTAGAA  5         0.0344
34479.1   100.00  0.31     Sequence
 HLA-DPA10201-DPB10501  257      PGDSSSGWTAGAAAY  SSGWTAGAA  4         0.0435
31246.0   100.00  0.32     Sequence
 HLA-DPA10201-DPB10501  258      GDSSSGWTAGAAAYY  SGWTAGAAA  4         0.0650
24748.6   100.00  0.25     Sequence
 HLA-DPA10201-DPB10501  259      DSSSGWTAGAAAYYV  WTAGAAAYY  5         0.0802
20996.9    95.00  0.17     Sequence
 HLA-DPA10201-DPB10501  260      SSSGWTAGAAAYYVG  WTAGAAAYY  4         0.0905
18778.1    95.00  0.14     Sequence
 HLA-DPA10201-DPB10501  261      SSGWTAGAAAYYVGY  AGAAAYYVG  5         0.1153
14357.9    90.00  0.37     Sequence
 HLA-DPA10201-DPB10501  262      SGWTAGAAAYYVGYL  AGAAAYYVG  4         0.1358
11507.8    85.00  0.37     Sequence
 HLA-DPA10201-DPB10501  263      GWTAGAAAYYVGYLQ  AAYYVGYLQ  6         0.1840
6827.4    70.00  0.29     Sequence
 HLA-DPA10201-DPB10501  264      WTAGAAAYYVGYLQP  AAYYVGYLQ  5         0.2099
5157.4    60.00  0.36     Sequence
 HLA-DPA10201-DPB10501  265      TAGAAAYYVGYLQPR  AAYYVGYLQ  4         0.2381
3804.2    55.00  0.38     Sequence
 HLA-DPA10201-DPB10501  266      AGAAAYYVGYLQPRT  AYYVGYLQP  4         0.2591
3030.6    45.00  0.33     Sequence
 HLA-DPA10201-DPB10501  267      GAAAYYVGYLQPRTF  AYYVGYLQP  3         0.3060
1824.6    32.00  0.31     Sequence
 HLA-DPA10201-DPB10501  268      AAAYYVGYLQPRTFL  AYYVGYLQP  2         0.3463
1179.4    23.00  0.24     Sequence
 HLA-DPA10201-DPB10501  269      AAYYVGYLQPRTFLL  YLQPRTFLL  6         0.4259
498.5    11.00  0.29     Sequence
 HLA-DPA10201-DPB10501  270      AYYVGYLQPRTFLLK  YLQPRTFLL  5         0.4544
366.2     8.00  0.34     Sequence         WB
 HLA-DPA10201-DPB10501  271      YYVGYLQPRTFLLKY  YLQPRTFLL  4         0.4688
313.2     6.50  0.37     Sequence         WB
```

```
 HLA-DPA10201-DPB10501  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.4604
343.2     7.50  0.38     Sequence         WB
 HLA-DPA10201-DPB10501  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.4482
391.6     8.50  0.36     Sequence         WB
 HLA-DPA10201-DPB10501  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.4391
432.3     9.00  0.34     Sequence         WB
 HLA-DPA10201-DPB10501  275      YLQPRTFLLKYNENG  YLQPRTFLL  0        0.4029
639.4    14.00  0.19     Sequence
 HLA-DPA10201-DPB10501  276      LQPRTFLLKYNENGT  RTFLLKYNE  3        0.3391
1275.8    25.00  0.24     Sequence
 HLA-DPA10201-DPB10501  277      QPRTFLLKYNENGTI  RTFLLKYNE  2        0.3291
1420.2    27.00  0.28     Sequence
 HLA-DPA10201-DPB10501  278      PRTFLLKYNENGTIT  RTFLLKYNE  1        0.3096
1753.7    31.00  0.29     Sequence
 HLA-DPA10201-DPB10501  279      RTFLLKYNENGTITD  TFLLKYNEN  1        0.2880
2217.6    37.00  0.24     Sequence
 HLA-DPA10201-DPB10501  280      TFLLKYNENGTITDA  TFLLKYNEN  0        0.2391
3764.0    55.00  0.23     Sequence
 HLA-DPA10201-DPB10501  281      FLLKYNENGTITDAV  LLKYNENGT  1        0.2042
5490.9    65.00  0.28     Sequence
 HLA-DPA10201-DPB10501  282      LLKYNENGTITDAVD  LKYNENGTI  1        0.1261
12780.3    85.00  0.41     Sequence
 HLA-DPA10201-DPB10501  283      LKYNENGTITDAVDC  LKYNENGTI  0        0.0800
21031.7    95.00  0.31     Sequence
 HLA-DPA10201-DPB10501  284      KYNENGTITDAVDCA  GTITDAVDC  5        0.0567
27087.5   100.00  0.23     Sequence
 HLA-DPA10201-DPB10501  285      YNENGTITDAVDCAL  GTITDAVDC  4        0.0663
24401.4   100.00  0.28     Sequence
 HLA-DPA10201-DPB10501  286      NENGTITDAVDCALD  GTITDAVDC  3        0.0706
23281.8   100.00  0.28     Sequence
 HLA-DPA10201-DPB10501  287      ENGTITDAVDCALDP  GTITDAVDC  2        0.0754
22109.2   100.00  0.27     Sequence
 HLA-DPA10201-DPB10501  288      NGTITDAVDCALDPL  GTITDAVDC  1        0.0894
18997.0    95.00  0.20     Sequence
 HLA-DPA10201-DPB10501  289      GTITDAVDCALDPLS  DAVDCALDP  4        0.1039
16237.6    90.00  0.17     Sequence
 HLA-DPA10201-DPB10501  290      TITDAVDCALDPLSE  VDCALDPLS  5        0.1156
14312.1    90.00  0.14     Sequence
 HLA-DPA10201-DPB10501  291      ITDAVDCALDPLSET  DCALDPLSE  5        0.1132
14692.6    90.00  0.28     Sequence
 HLA-DPA10201-DPB10501  292      TDAVDCALDPLSETK  DCALDPLSE  4        0.1124
14824.2    90.00  0.34     Sequence
 HLA-DPA10201-DPB10501  293      DAVDCALDPLSETKC  DCALDPLSE  3        0.1151
14390.7    90.00  0.32     Sequence
 HLA-DPA10201-DPB10501  294      AVDCALDPLSETKCT  DCALDPLSE  2        0.1176
14014.7    90.00  0.34     Sequence
 HLA-DPA10201-DPB10501  295      VDCALDPLSETKCTL  DCALDPLSE  1        0.1244
13016.0    85.00  0.29     Sequence
 HLA-DPA10201-DPB10501  296      DCALDPLSETKCTLK  LSETKCTLK  6        0.1318
12013.6    85.00  0.18     Sequence
 HLA-DPA10201-DPB10501  297      CALDPLSETKCTLKS  LSETKCTLK  5        0.1440
10523.9    80.00  0.29     Sequence
 HLA-DPA10201-DPB10501  298      ALDPLSETKCTLKSF  LSETKCTLK  4        0.1845
6793.0    70.00  0.31     Sequence
 HLA-DPA10201-DPB10501  299      LDPLSETKCTLKSFT  LSETKCTLK  3        0.2035
5528.0    65.00  0.28     Sequence
 HLA-DPA10201-DPB10501  300      DPLSETKCTLKSFTV  LSETKCTLK  2        0.2209
4579.4    60.00  0.22     Sequence
 HLA-DPA10201-DPB10501  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.2307
4122.2    55.00  0.23     Sequence
 HLA-DPA10201-DPB10501  302      LSETKCTLKSFTVEK  KCTLKSFTV  4        0.3228
1521.0    28.00  0.22     Sequence
 HLA-DPA10201-DPB10501  303      SETKCTLKSFTVEKG  LKSFTVEKG  6        0.3785
832.4    18.00  0.29     Sequence
 HLA-DPA10201-DPB10501  304      ETKCTLKSFTVEKGI  LKSFTVEKG  5        0.4357
448.2     9.50  0.44     Sequence         WB
```

```
 HLA-DPA10201-DPB10501  305      TKCTLKSFTVEKGIY  LKSFTVEKG  4        0.4645
328.3     7.00  0.47     Sequence         WB
 HLA-DPA10201-DPB10501  306      KCTLKSFTVEKGIYQ  LKSFTVEKG  3        0.4623
336.4     7.00  0.51     Sequence         WB
 HLA-DPA10201-DPB10501  307      CTLKSFTVEKGIYQT  LKSFTVEKG  2        0.4476
394.3     8.50  0.54     Sequence         WB
 HLA-DPA10201-DPB10501  308      TLKSFTVEKGIYQTS  LKSFTVEKG  1        0.4271
492.0    11.00  0.54     Sequence
 HLA-DPA10201-DPB10501  309      LKSFTVEKGIYQTSN  LKSFTVEKG  0        0.2968
2015.1    34.00  0.43     Sequence
 HLA-DPA10201-DPB10501  310      KSFTVEKGIYQTSNF  SFTVEKGIY  1        0.2345
3952.4    55.00  0.22     Sequence
 HLA-DPA10201-DPB10501  311      SFTVEKGIYQTSNFR  KGIYQTSNF  5        0.2261
4331.7    55.00  0.19     Sequence
 HLA-DPA10201-DPB10501  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.3012
1921.2    33.00  0.37     Sequence
 HLA-DPA10201-DPB10501  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.3340
1347.2    26.00  0.56     Sequence
 HLA-DPA10201-DPB10501  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.3439
1210.7    24.00  0.56     Sequence
 HLA-DPA10201-DPB10501  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.3456
1189.0    24.00  0.60     Sequence
 HLA-DPA10201-DPB10501  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.3320
1376.2    26.00  0.60     Sequence
 HLA-DPA10201-DPB10501  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.2819
2366.8    38.00  0.58     Sequence
 HLA-DPA10201-DPB10501  318      IYQTSNFRVQPTESI  IYQTSNFRV  0        0.2006
5707.3    65.00  0.39     Sequence
 HLA-DPA10201-DPB10501  319      YQTSNFRVQPTESIV  NFRVQPTES  4        0.1448
10438.6    80.00  0.26     Sequence
 HLA-DPA10201-DPB10501  320      QTSNFRVQPTESIVR  VQPTESIVR  6        0.1804
7101.1    70.00  0.32     Sequence
 HLA-DPA10201-DPB10501  321      TSNFRVQPTESIVRF  VQPTESIVR  5        0.2199
4631.2    60.00  0.41     Sequence
 HLA-DPA10201-DPB10501  322      SNFRVQPTESIVRFP  VQPTESIVR  4        0.2278
4251.5    55.00  0.40     Sequence
 HLA-DPA10201-DPB10501  323      NFRVQPTESIVRFPN  VQPTESIVR  3        0.2417
3656.8    50.00  0.40     Sequence
 HLA-DPA10201-DPB10501  324      FRVQPTESIVRFPNI  VQPTESIVR  2        0.2476
3430.9    48.00  0.41     Sequence
 HLA-DPA10201-DPB10501  325      RVQPTESIVRFPNIT  VQPTESIVR  1        0.2240
4429.2    55.00  0.37     Sequence
 HLA-DPA10201-DPB10501  326      VQPTESIVRFPNITN  IVRFPNITN  6        0.2164
4811.7    60.00  0.22     Sequence
 HLA-DPA10201-DPB10501  327      QPTESIVRFPNITNL  IVRFPNITN  5        0.2264
4317.1    55.00  0.41     Sequence
 HLA-DPA10201-DPB10501  328      PTESIVRFPNITNLC  IVRFPNITN  4        0.2240
4430.2    55.00  0.43     Sequence
 HLA-DPA10201-DPB10501  329      TESIVRFPNITNLCP  IVRFPNITN  3        0.2265
4309.6    55.00  0.46     Sequence
 HLA-DPA10201-DPB10501  330      ESIVRFPNITNLCPF  IVRFPNITN  2        0.2276
4262.9    55.00  0.47     Sequence
 HLA-DPA10201-DPB10501  331      SIVRFPNITNLCPFG  IVRFPNITN  1        0.2190
4673.8    60.00  0.47     Sequence
 HLA-DPA10201-DPB10501  332      IVRFPNITNLCPFGE  IVRFPNITN  0        0.2112
5087.3    60.00  0.29     Sequence
 HLA-DPA10201-DPB10501  333      VRFPNITNLCPFGEV  ITNLCPFGE  5        0.1851
6745.1    70.00  0.31     Sequence
 HLA-DPA10201-DPB10501  334      RFPNITNLCPFGEVF  ITNLCPFGE  4        0.1770
7366.5    70.00  0.37     Sequence
 HLA-DPA10201-DPB10501  335      FPNITNLCPFGEVFN  ITNLCPFGE  3        0.1810
7056.5    70.00  0.35     Sequence
 HLA-DPA10201-DPB10501  336      PNITNLCPFGEVFNA  ITNLCPFGE  2        0.1846
6782.1    70.00  0.29     Sequence
 HLA-DPA10201-DPB10501  337      NITNLCPFGEVFNAT  CPFGEVFNA  5        0.1930
6195.5    65.00  0.32     Sequence
```

```
 HLA-DPA10201-DPB10501  338      ITNLCPFGEVFNATR  CPFGEVFNA  4        0.2155
4857.4    60.00  0.31     Sequence
 HLA-DPA10201-DPB10501  339      TNLCPFGEVFNATRF  CPFGEVFNA  3        0.2426
3621.9    50.00  0.32     Sequence
 HLA-DPA10201-DPB10501  340      NLCPFGEVFNATRFA  GEVFNATRF  5        0.2719
2637.4    41.00  0.25     Sequence
 HLA-DPA10201-DPB10501  341      LCPFGEVFNATRFAS  VFNATRFAS  6        0.3285
1430.0    27.00  0.31     Sequence
 HLA-DPA10201-DPB10501  342      CPFGEVFNATRFASV  VFNATRFAS  5        0.4129
573.6    13.00  0.47     Sequence
 HLA-DPA10201-DPB10501  343      PFGEVFNATRFASVY  VFNATRFAS  4        0.4338
457.7    10.00  0.47     Sequence
 HLA-DPA10201-DPB10501  344      FGEVFNATRFASVYA  VFNATRFAS  3        0.4700
309.4     6.50  0.47     Sequence         WB
 HLA-DPA10201-DPB10501  345      GEVFNATRFASVYAW  VFNATRFAS  2        0.4486
390.0     8.50  0.47     Sequence         WB
 HLA-DPA10201-DPB10501  346      EVFNATRFASVYAWN  VFNATRFAS  1        0.4336
458.7    10.00  0.44     Sequence
 HLA-DPA10201-DPB10501  347      VFNATRFASVYAWNR  VFNATRFAS  0        0.4016
648.5    14.00  0.31     Sequence
 HLA-DPA10201-DPB10501  348      FNATRFASVYAWNRK  TRFASVYAW  3        0.3633
981.3    20.00  0.23     Sequence
 HLA-DPA10201-DPB10501  349      NATRFASVYAWNRKR  TRFASVYAW  2        0.3595
1022.9    21.00  0.23     Sequence
 HLA-DPA10201-DPB10501  350      ATRFASVYAWNRKRI  ASVYAWNRK  4        0.3730
883.9    18.00  0.23     Sequence
 HLA-DPA10201-DPB10501  351      TRFASVYAWNRKRIS  ASVYAWNRK  3        0.3474
1165.6    23.00  0.30     Sequence
 HLA-DPA10201-DPB10501  352      RFASVYAWNRKRISN  ASVYAWNRK  2        0.3338
1350.8    26.00  0.35     Sequence
 HLA-DPA10201-DPB10501  353      FASVYAWNRKRISNC  ASVYAWNRK  1        0.2956
2042.5    35.00  0.38     Sequence
 HLA-DPA10201-DPB10501  354      ASVYAWNRKRISNCV  VYAWNRKRI  2        0.2414
3669.7    50.00  0.31     Sequence
 HLA-DPA10201-DPB10501  355      SVYAWNRKRISNCVA  VYAWNRKRI  1        0.2264
4315.2    55.00  0.32     Sequence
 HLA-DPA10201-DPB10501  356      VYAWNRKRISNCVAD  RKRISNCVA  5        0.1894
6443.1    70.00  0.30     Sequence
 HLA-DPA10201-DPB10501  357      YAWNRKRISNCVADY  RKRISNCVA  4        0.1891
6464.8    70.00  0.38     Sequence
 HLA-DPA10201-DPB10501  358      AWNRKRISNCVADYS  RKRISNCVA  3        0.1969
5942.0    65.00  0.37     Sequence
 HLA-DPA10201-DPB10501  359      WNRKRISNCVADYSV  RKRISNCVA  2        0.2116
5064.2    60.00  0.36     Sequence
 HLA-DPA10201-DPB10501  360      NRKRISNCVADYSVL  KRISNCVAD  2        0.2232
4470.6    55.00  0.32     Sequence
 HLA-DPA10201-DPB10501  361      RKRISNCVADYSVLY  KRISNCVAD  1        0.2430
3606.8    49.00  0.31     Sequence
 HLA-DPA10201-DPB10501  362      KRISNCVADYSVLYN  NCVADYSVL  4        0.2258
4346.5    55.00  0.19     Sequence
 HLA-DPA10201-DPB10501  363      RISNCVADYSVLYNS  VADYSVLYN  5        0.2265
4313.3    55.00  0.35     Sequence
 HLA-DPA10201-DPB10501  364      ISNCVADYSVLYNSA  VADYSVLYN  4        0.2247
4394.6    55.00  0.37     Sequence
 HLA-DPA10201-DPB10501  365      SNCVADYSVLYNSAS  VADYSVLYN  3        0.2231
4474.6    55.00  0.36     Sequence
 HLA-DPA10201-DPB10501  366      NCVADYSVLYNSASF  VADYSVLYN  2        0.2290
4198.2    55.00  0.33     Sequence
 HLA-DPA10201-DPB10501  367      CVADYSVLYNSASFS  VADYSVLYN  1        0.2350
3931.9    55.00  0.28     Sequence
 HLA-DPA10201-DPB10501  368      VADYSVLYNSASFST  LYNSASFST  6        0.2401
3720.3    50.00  0.24     Sequence
 HLA-DPA10201-DPB10501  369      ADYSVLYNSASFSTF  LYNSASFST  5        0.2957
2038.6    35.00  0.43     Sequence
 HLA-DPA10201-DPB10501  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.3488
1147.8    23.00  0.40     Sequence
```

```
 HLA-DPA10201-DPB10501  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.3902
733.9    16.00  0.34     Sequence
 HLA-DPA10201-DPB10501  372      SVLYNSASFSTFKCY  SASFSTFKC  5        0.4223
518.4    11.00  0.42     Sequence
 HLA-DPA10201-DPB10501  373      VLYNSASFSTFKCYG  SASFSTFKC  4        0.4100
591.8    13.00  0.46     Sequence
 HLA-DPA10201-DPB10501  374      LYNSASFSTFKCYGV  SASFSTFKC  3        0.3989
667.9    14.00  0.54     Sequence
 HLA-DPA10201-DPB10501  375      YNSASFSTFKCYGVS  SASFSTFKC  2        0.3765
850.7    18.00  0.61     Sequence
 HLA-DPA10201-DPB10501  376      NSASFSTFKCYGVSP  SASFSTFKC  1        0.3374
1299.4    25.00  0.59     Sequence
 HLA-DPA10201-DPB10501  377      SASFSTFKCYGVSPT  SASFSTFKC  0        0.2790
2442.6    39.00  0.43     Sequence
 HLA-DPA10201-DPB10501  378      ASFSTFKCYGVSPTK  FSTFKCYGV  2        0.2322
4054.1    55.00  0.22     Sequence
 HLA-DPA10201-DPB10501  379      SFSTFKCYGVSPTKL  FKCYGVSPT  4        0.2175
4751.3    60.00  0.22     Sequence
 HLA-DPA10201-DPB10501  380      FSTFKCYGVSPTKLN  FKCYGVSPT  3        0.2091
5202.7    60.00  0.22     Sequence
 HLA-DPA10201-DPB10501  381      STFKCYGVSPTKLND  FKCYGVSPT  2        0.1876
6568.3    70.00  0.26     Sequence
 HLA-DPA10201-DPB10501  382      TFKCYGVSPTKLNDL  FKCYGVSPT  1        0.1935
6159.9    65.00  0.25     Sequence
 HLA-DPA10201-DPB10501  383      FKCYGVSPTKLNDLC  KCYGVSPTK  1        0.1711
7851.0    75.00  0.25     Sequence
 HLA-DPA10201-DPB10501  384      KCYGVSPTKLNDLCF  KCYGVSPTK  0        0.1529
9558.2    80.00  0.18     Sequence
 HLA-DPA10201-DPB10501  385      CYGVSPTKLNDLCFT  PTKLNDLCF  5        0.1585
9001.9    75.00  0.25     Sequence
 HLA-DPA10201-DPB10501  386      YGVSPTKLNDLCFTN  PTKLNDLCF  4        0.1724
7745.1    75.00  0.31     Sequence
 HLA-DPA10201-DPB10501  387      GVSPTKLNDLCFTNV  KLNDLCFTN  5        0.2099
5160.2    60.00  0.34     Sequence
 HLA-DPA10201-DPB10501  388      VSPTKLNDLCFTNVY  KLNDLCFTN  4        0.2435
3587.7    49.00  0.31     Sequence
 HLA-DPA10201-DPB10501  389      SPTKLNDLCFTNVYA  KLNDLCFTN  3        0.2621
2934.1    44.00  0.28     Sequence
 HLA-DPA10201-DPB10501  390      PTKLNDLCFTNVYAD  KLNDLCFTN  2        0.2730
2607.3    41.00  0.23     Sequence
 HLA-DPA10201-DPB10501  391      TKLNDLCFTNVYADS  KLNDLCFTN  1        0.2658
2819.1    43.00  0.24     Sequence
 HLA-DPA10201-DPB10501  392      KLNDLCFTNVYADSF  DLCFTNVYA  3        0.2785
2457.6    39.00  0.22     Sequence
 HLA-DPA10201-DPB10501  393      LNDLCFTNVYADSFV  DLCFTNVYA  2        0.2631
2901.7    44.00  0.21     Sequence
 HLA-DPA10201-DPB10501  394      NDLCFTNVYADSFVI  LCFTNVYAD  2        0.2836
2325.6    38.00  0.22     Sequence
 HLA-DPA10201-DPB10501  395      DLCFTNVYADSFVIR  NVYADSFVI  5        0.3189
1586.4    29.00  0.29     Sequence
 HLA-DPA10201-DPB10501  396      LCFTNVYADSFVIRG  NVYADSFVI  4        0.3017
1911.7    33.00  0.33     Sequence
 HLA-DPA10201-DPB10501  397      CFTNVYADSFVIRGD  NVYADSFVI  3        0.2864
2254.6    37.00  0.39     Sequence
 HLA-DPA10201-DPB10501  398      FTNVYADSFVIRGDE  NVYADSFVI  2        0.2762
2518.6    40.00  0.42     Sequence
 HLA-DPA10201-DPB10501  399      TNVYADSFVIRGDEV  NVYADSFVI  1        0.2312
4096.8    55.00  0.41     Sequence
 HLA-DPA10201-DPB10501  400      NVYADSFVIRGDEVR  NVYADSFVI  0        0.2048
5452.8    65.00  0.31     Sequence
 HLA-DPA10201-DPB10501  401      VYADSFVIRGDEVRQ  VIRGDEVRQ  6        0.1883
6518.6    70.00  0.23     Sequence
 HLA-DPA10201-DPB10501  402      YADSFVIRGDEVRQI  VIRGDEVRQ  5        0.1798
7142.8    70.00  0.47     Sequence
 HLA-DPA10201-DPB10501  403      ADSFVIRGDEVRQIA  VIRGDEVRQ  4        0.1832
6886.9    70.00  0.54     Sequence
```

```
 HLA-DPA10201-DPB10501  404      DSFVIRGDEVRQIAP  VIRGDEVRQ  3        0.1844
6800.2    70.00  0.54     Sequence
 HLA-DPA10201-DPB10501  405      SFVIRGDEVRQIAPG  VIRGDEVRQ  2        0.1853
6735.1    70.00  0.55     Sequence
 HLA-DPA10201-DPB10501  406      FVIRGDEVRQIAPGQ  VIRGDEVRQ  1        0.1671
8195.0    75.00  0.52     Sequence
 HLA-DPA10201-DPB10501  407      VIRGDEVRQIAPGQT  VIRGDEVRQ  0        0.1215
13433.5    90.00  0.41     Sequence
 HLA-DPA10201-DPB10501  408      IRGDEVRQIAPGQTG  VRQIAPGQT  5        0.0736
22557.7   100.00  0.40     Sequence
 HLA-DPA10201-DPB10501  409      RGDEVRQIAPGQTGT  VRQIAPGQT  4        0.0729
22719.1   100.00  0.50     Sequence
 HLA-DPA10201-DPB10501  410      GDEVRQIAPGQTGTI  VRQIAPGQT  3        0.0887
19159.0    95.00  0.47     Sequence
 HLA-DPA10201-DPB10501  411      DEVRQIAPGQTGTIA  VRQIAPGQT  2        0.0947
17941.6    95.00  0.44     Sequence
 HLA-DPA10201-DPB10501  412      EVRQIAPGQTGTIAD  VRQIAPGQT  1        0.0996
17016.8    95.00  0.43     Sequence
 HLA-DPA10201-DPB10501  413      VRQIAPGQTGTIADY  VRQIAPGQT  0        0.0846
20010.7    95.00  0.24     Sequence
 HLA-DPA10201-DPB10501  414      RQIAPGQTGTIADYN  PGQTGTIAD  4        0.0649
24784.8   100.00  0.31     Sequence
 HLA-DPA10201-DPB10501  415      QIAPGQTGTIADYNY  PGQTGTIAD  3        0.0653
24667.6   100.00  0.28     Sequence
 HLA-DPA10201-DPB10501  416      IAPGQTGTIADYNYK  TGTIADYNY  5        0.0801
21009.8    95.00  0.25     Sequence
 HLA-DPA10201-DPB10501  417      APGQTGTIADYNYKL  GTIADYNYK  5        0.1298
12269.3    85.00  0.25     Sequence
 HLA-DPA10201-DPB10501  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.1454
10370.7    80.00  0.25     Sequence
 HLA-DPA10201-DPB10501  419      GQTGTIADYNYKLPD  IADYNYKLP  5        0.1415
10818.9    80.00  0.21     Sequence
 HLA-DPA10201-DPB10501  420      QTGTIADYNYKLPDD  IADYNYKLP  4        0.1377
11269.3    85.00  0.22     Sequence
 HLA-DPA10201-DPB10501  421      TGTIADYNYKLPDDF  IADYNYKLP  3        0.1408
10902.3    80.00  0.23     Sequence
 HLA-DPA10201-DPB10501  422      GTIADYNYKLPDDFT  IADYNYKLP  2        0.1386
11162.2    85.00  0.24     Sequence
 HLA-DPA10201-DPB10501  423      TIADYNYKLPDDFTG  YKLPDDFTG  6        0.1634
8533.7    75.00  0.32     Sequence
 HLA-DPA10201-DPB10501  424      IADYNYKLPDDFTGC  YKLPDDFTG  5        0.1670
8206.0    75.00  0.57     Sequence
 HLA-DPA10201-DPB10501  425      ADYNYKLPDDFTGCV  YKLPDDFTG  4        0.1883
6515.3    70.00  0.54     Sequence
 HLA-DPA10201-DPB10501  426      DYNYKLPDDFTGCVI  YKLPDDFTG  3        0.2067
5339.7    65.00  0.51     Sequence
 HLA-DPA10201-DPB10501  427      YNYKLPDDFTGCVIA  YKLPDDFTG  2        0.2182
4716.5    60.00  0.50     Sequence
 HLA-DPA10201-DPB10501  428      NYKLPDDFTGCVIAW  YKLPDDFTG  1        0.2127
5004.9    60.00  0.41     Sequence
 HLA-DPA10201-DPB10501  429      YKLPDDFTGCVIAWN  YKLPDDFTG  0        0.2171
4771.4    60.00  0.29     Sequence
 HLA-DPA10201-DPB10501  430      KLPDDFTGCVIAWNS  DFTGCVIAW  4        0.1811
7048.3    70.00  0.22     Sequence
 HLA-DPA10201-DPB10501  431      LPDDFTGCVIAWNSN  DFTGCVIAW  3        0.1663
8273.3    75.00  0.24     Sequence
 HLA-DPA10201-DPB10501  432      PDDFTGCVIAWNSNN  DFTGCVIAW  2        0.1604
8813.5    75.00  0.24     Sequence
 HLA-DPA10201-DPB10501  433      DDFTGCVIAWNSNNL  DFTGCVIAW  1        0.1671
8196.3    75.00  0.19     Sequence
 HLA-DPA10201-DPB10501  434      DFTGCVIAWNSNNLD  DFTGCVIAW  0        0.1651
8377.5    75.00  0.12     Sequence
 HLA-DPA10201-DPB10501  435      FTGCVIAWNSNNLDS  VIAWNSNNL  4        0.1492
9948.4    80.00  0.25     Sequence
 HLA-DPA10201-DPB10501  436      TGCVIAWNSNNLDSK  VIAWNSNNL  3        0.1229
13220.4    85.00  0.26     Sequence
```

```
 HLA-DPA10201-DPB10501  437      GCVIAWNSNNLDSKV  VIAWNSNNL  2        0.1122
14855.0    90.00  0.28     Sequence
 HLA-DPA10201-DPB10501  438      CVIAWNSNNLDSKVG  VIAWNSNNL  1        0.1079
15555.2    90.00  0.29     Sequence
 HLA-DPA10201-DPB10501  439      VIAWNSNNLDSKVGG  VIAWNSNNL  0        0.0829
20394.8    95.00  0.25     Sequence
 HLA-DPA10201-DPB10501  440      IAWNSNNLDSKVGGN  AWNSNNLDS  1        0.0501
29078.4   100.00  0.22     Sequence
 HLA-DPA10201-DPB10501  441      AWNSNNLDSKVGGNY  SNNLDSKVG  3        0.0517
28579.0   100.00  0.22     Sequence
 HLA-DPA10201-DPB10501  442      WNSNNLDSKVGGNYN  SNNLDSKVG  2        0.0531
28156.1   100.00  0.23     Sequence
 HLA-DPA10201-DPB10501  443      NSNNLDSKVGGNYNY  SKVGGNYNY  6        0.0733
22610.0   100.00  0.28     Sequence
 HLA-DPA10201-DPB10501  444      SNNLDSKVGGNYNYL  SKVGGNYNY  5        0.1512
9743.0    80.00  0.50     Sequence
 HLA-DPA10201-DPB10501  445      NNLDSKVGGNYNYLY  SKVGGNYNY  4        0.1855
6720.7    70.00  0.47     Sequence
 HLA-DPA10201-DPB10501  446      NLDSKVGGNYNYLYR  SKVGGNYNY  3        0.2249
4387.1    55.00  0.44     Sequence
 HLA-DPA10201-DPB10501  447      LDSKVGGNYNYLYRL  SKVGGNYNY  2        0.2484
3403.5    48.00  0.39     Sequence
 HLA-DPA10201-DPB10501  448      DSKVGGNYNYLYRLF  SKVGGNYNY  1        0.2678
2756.8    42.00  0.32     Sequence
 HLA-DPA10201-DPB10501  449      SKVGGNYNYLYRLFR  YNYLYRLFR  6        0.3407
1253.5    25.00  0.25     Sequence
 HLA-DPA10201-DPB10501  450      KVGGNYNYLYRLFRK  NYLYRLFRK  6        0.4451
404.9     8.50  0.34     Sequence          WB
 HLA-DPA10201-DPB10501  451      VGGNYNYLYRLFRKS  NYLYRLFRK  5        0.5446
138.0     2.50  0.51     Sequence          WB
 HLA-DPA10201-DPB10501  452      GGNYNYLYRLFRKSN  NYLYRLFRK  4        0.5590
118.1     1.80  0.50     Sequence          SB
 HLA-DPA10201-DPB10501  453      GNYNYLYRLFRKSNL  NYLYRLFRK  3        0.5805
93.6     1.20  0.49     Sequence          SB
 HLA-DPA10201-DPB10501  454      NYNYLYRLFRKSNLK  NYLYRLFRK  2        0.5982
77.3     0.90  0.48     Sequence          SB
 HLA-DPA10201-DPB10501  455      YNYLYRLFRKSNLKP  NYLYRLFRK  1        0.6042
72.4     0.80  0.44     Sequence          SB
 HLA-DPA10201-DPB10501  456      NYLYRLFRKSNLKPF  NYLYRLFRK  0        0.5943
80.6     1.00  0.29     Sequence          SB
 HLA-DPA10201-DPB10501  457      YLYRLFRKSNLKPFE  LFRKSNLKP  4        0.5485
132.3     2.50  0.35     Sequence          WB
 HLA-DPA10201-DPB10501  458      LYRLFRKSNLKPFER  LFRKSNLKP  3        0.5152
189.8     3.50  0.41     Sequence          WB
 HLA-DPA10201-DPB10501  459      YRLFRKSNLKPFERD  LFRKSNLKP  2        0.4864
259.0     5.50  0.44     Sequence          WB
 HLA-DPA10201-DPB10501  460      RLFRKSNLKPFERDI  LFRKSNLKP  1        0.4336
458.7    10.00  0.46     Sequence
 HLA-DPA10201-DPB10501  461      LFRKSNLKPFERDIS  LFRKSNLKP  0        0.3609
1007.4    21.00  0.33     Sequence
 HLA-DPA10201-DPB10501  462      FRKSNLKPFERDIST  KSNLKPFER  2        0.3007
1931.9    33.00  0.34     Sequence
 HLA-DPA10201-DPB10501  463      RKSNLKPFERDISTE  LKPFERDIS  4        0.2278
4251.4    55.00  0.38     Sequence
 HLA-DPA10201-DPB10501  464      KSNLKPFERDISTEI  LKPFERDIS  3        0.2093
5194.9    60.00  0.47     Sequence
 HLA-DPA10201-DPB10501  465      SNLKPFERDISTEIY  LKPFERDIS  2        0.2020
5618.4    65.00  0.41     Sequence
 HLA-DPA10201-DPB10501  466      NLKPFERDISTEIYQ  LKPFERDIS  1        0.2045
5472.1    65.00  0.32     Sequence
 HLA-DPA10201-DPB10501  467      LKPFERDISTEIYQA  ERDISTEIY  4        0.2167
4792.6    60.00  0.23     Sequence
 HLA-DPA10201-DPB10501  468      KPFERDISTEIYQAG  DISTEIYQA  5        0.2317
4076.7    55.00  0.34     Sequence
 HLA-DPA10201-DPB10501  469      PFERDISTEIYQAGS  DISTEIYQA  4        0.2275
4265.0    55.00  0.38     Sequence
```

```
 HLA-DPA10201-DPB10501  470      FERDISTEIYQAGST  DISTEIYQA  3         0.2277
4256.4    55.00  0.38     Sequence
 HLA-DPA10201-DPB10501  471      ERDISTEIYQAGSTP  DISTEIYQA  2         0.1886
6496.8    70.00  0.49     Sequence
 HLA-DPA10201-DPB10501  472      RDISTEIYQAGSTPC  DISTEIYQA  1         0.1523
9620.1    80.00  0.56     Sequence
 HLA-DPA10201-DPB10501  473      DISTEIYQAGSTPCN  DISTEIYQA  0         0.0979
17343.9    95.00  0.40     Sequence
 HLA-DPA10201-DPB10501  474      ISTEIYQAGSTPCNG  EIYQAGSTP  3         0.0744
22351.9   100.00  0.14     Sequence
 HLA-DPA10201-DPB10501  475      STEIYQAGSTPCNGV  YQAGSTPCN  4         0.0655
24601.8   100.00  0.25     Sequence
 HLA-DPA10201-DPB10501  476      TEIYQAGSTPCNGVK  YQAGSTPCN  3         0.0699
23482.1   100.00  0.28     Sequence
 HLA-DPA10201-DPB10501  477      EIYQAGSTPCNGVKG  YQAGSTPCN  2         0.0614
25741.9   100.00  0.31     Sequence
 HLA-DPA10201-DPB10501  478      IYQAGSTPCNGVKGF  YQAGSTPCN  1         0.0627
25376.1   100.00  0.28     Sequence
 HLA-DPA10201-DPB10501  479      YQAGSTPCNGVKGFN  PCNGVKGFN  6         0.0597
26212.4   100.00  0.17     Sequence
 HLA-DPA10201-DPB10501  480      QAGSTPCNGVKGFNC  PCNGVKGFN  5         0.0554
27461.7   100.00  0.29     Sequence
 HLA-DPA10201-DPB10501  481      AGSTPCNGVKGFNCY  PCNGVKGFN  4         0.0717
23016.8   100.00  0.26     Sequence
 HLA-DPA10201-DPB10501  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4         0.1066
15786.5    90.00  0.28     Sequence
 HLA-DPA10201-DPB10501  483      STPCNGVKGFNCYFP  VKGFNCYFP  6         0.1808
7070.7    70.00  0.43     Sequence
 HLA-DPA10201-DPB10501  484      TPCNGVKGFNCYFPL  VKGFNCYFP  5         0.2397
3739.4    50.00  0.60     Sequence
 HLA-DPA10201-DPB10501  485      PCNGVKGFNCYFPLQ  VKGFNCYFP  4         0.2756
2533.8    40.00  0.54     Sequence
 HLA-DPA10201-DPB10501  486      CNGVKGFNCYFPLQS  VKGFNCYFP  3         0.3261
1468.0    28.00  0.46     Sequence
 HLA-DPA10201-DPB10501  487      NGVKGFNCYFPLQSY  FNCYFPLQS  5         0.3525
1102.9    22.00  0.35     Sequence
 HLA-DPA10201-DPB10501  488      GVKGFNCYFPLQSYG  FNCYFPLQS  4         0.3503
1130.2    23.00  0.38     Sequence
 HLA-DPA10201-DPB10501  489      VKGFNCYFPLQSYGF  FNCYFPLQS  3         0.3574
1046.2    21.00  0.38     Sequence
 HLA-DPA10201-DPB10501  490      KGFNCYFPLQSYGFQ  FNCYFPLQS  2         0.3266
1459.4    27.00  0.43     Sequence
 HLA-DPA10201-DPB10501  491      GFNCYFPLQSYGFQP  FNCYFPLQS  1         0.2979
1991.1    34.00  0.43     Sequence
 HLA-DPA10201-DPB10501  492      FNCYFPLQSYGFQPT  FNCYFPLQS  0         0.2675
2767.5    42.00  0.29     Sequence
 HLA-DPA10201-DPB10501  493      NCYFPLQSYGFQPTY  PLQSYGFQP  4         0.2247
4395.4    55.00  0.28     Sequence
 HLA-DPA10201-DPB10501  494      CYFPLQSYGFQPTYG  PLQSYGFQP  3         0.2003
5722.3    65.00  0.28     Sequence
 HLA-DPA10201-DPB10501  495      YFPLQSYGFQPTYGV  PLQSYGFQP  2         0.1779
7292.4    70.00  0.32     Sequence
 HLA-DPA10201-DPB10501  496      FPLQSYGFQPTYGVG  PLQSYGFQP  1         0.1479
10087.5    80.00  0.33     Sequence
 HLA-DPA10201-DPB10501  497      PLQSYGFQPTYGVGY  PLQSYGFQP  0         0.1365
11421.2    85.00  0.19     Sequence
 HLA-DPA10201-DPB10501  498      LQSYGFQPTYGVGYQ  GFQPTYGVG  4         0.1345
11671.0    85.00  0.17     Sequence
 HLA-DPA10201-DPB10501  499      QSYGFQPTYGVGYQP  GFQPTYGVG  3         0.1291
12366.1    85.00  0.20     Sequence
 HLA-DPA10201-DPB10501  500      SYGFQPTYGVGYQPY  PTYGVGYQP  5         0.1338
11761.7    85.00  0.26     Sequence
 HLA-DPA10201-DPB10501  501      YGFQPTYGVGYQPYR  PTYGVGYQP  4         0.1580
9050.7    75.00  0.31     Sequence
 HLA-DPA10201-DPB10501  502      GFQPTYGVGYQPYRV  GVGYQPYRV  6         0.1771
7359.7    70.00  0.23     Sequence
```

```
 HLA-DPA10201-DPB10501  503      FQPTYGVGYQPYRVV  GVGYQPYRV  5         0.1990
5802.9    65.00  0.36     Sequence
 HLA-DPA10201-DPB10501  504      QPTYGVGYQPYRVVV  GVGYQPYRV  4         0.1972
5920.3    65.00  0.40     Sequence
 HLA-DPA10201-DPB10501  505      PTYGVGYQPYRVVVL  GVGYQPYRV  3         0.2128
5001.4    60.00  0.38     Sequence
 HLA-DPA10201-DPB10501  506      TYGVGYQPYRVVVLS  GVGYQPYRV  2         0.2201
4622.5    60.00  0.34     Sequence
 HLA-DPA10201-DPB10501  507      YGVGYQPYRVVVLSF  GVGYQPYRV  1         0.2352
3926.2    55.00  0.27     Sequence
 HLA-DPA10201-DPB10501  508      GVGYQPYRVVVLSFE  PYRVVVLSF  5         0.2672
2777.1    42.00  0.23     Sequence
 HLA-DPA10201-DPB10501  509      VGYQPYRVVVLSFEL  YRVVVLSFE  5         0.3111
1725.5    31.00  0.23     Sequence
 HLA-DPA10201-DPB10501  510      GYQPYRVVVLSFELL  YRVVVLSFE  4         0.3299
1408.5    27.00  0.24     Sequence
 HLA-DPA10201-DPB10501  511      YQPYRVVVLSFELLH  YRVVVLSFE  3         0.3635
979.0    20.00  0.23     Sequence
 HLA-DPA10201-DPB10501  512      QPYRVVVLSFELLHA  RVVVLSFEL  3         0.3998
660.9    14.00  0.17     Sequence
 HLA-DPA10201-DPB10501  513      PYRVVVLSFELLHAP  VLSFELLHA  5         0.4037
633.8    14.00  0.25     Sequence
 HLA-DPA10201-DPB10501  514      YRVVVLSFELLHAPA  VLSFELLHA  4         0.4061
617.5    13.00  0.30     Sequence
 HLA-DPA10201-DPB10501  515      RVVVLSFELLHAPAT  VLSFELLHA  3         0.3662
951.3    20.00  0.39     Sequence
 HLA-DPA10201-DPB10501  516      VVVLSFELLHAPATV  VLSFELLHA  2         0.3372
1302.2    25.00  0.44     Sequence
 HLA-DPA10201-DPB10501  517      VVLSFELLHAPATVC  VLSFELLHA  1         0.3126
1698.0    31.00  0.47     Sequence
 HLA-DPA10201-DPB10501  518      VLSFELLHAPATVCG  VLSFELLHA  0         0.2484
3403.7    48.00  0.40     Sequence
 HLA-DPA10201-DPB10501  519      LSFELLHAPATVCGP  FELLHAPAT  2         0.1711
7848.9    75.00  0.26     Sequence
 HLA-DPA10201-DPB10501  520      SFELLHAPATVCGPK  FELLHAPAT  1         0.1562
9227.6    80.00  0.27     Sequence
 HLA-DPA10201-DPB10501  521      FELLHAPATVCGPKK  LLHAPATVC  2         0.1445
10474.2    80.00  0.31     Sequence
 HLA-DPA10201-DPB10501  522      ELLHAPATVCGPKKS  LLHAPATVC  1         0.1103
15155.2    90.00  0.35     Sequence
 HLA-DPA10201-DPB10501  523      LLHAPATVCGPKKST  LLHAPATVC  0         0.1075
15625.6    90.00  0.22     Sequence
 HLA-DPA10201-DPB10501  524      LHAPATVCGPKKSTN  ATVCGPKKS  4         0.0914
18602.6    95.00  0.29     Sequence
 HLA-DPA10201-DPB10501  525      HAPATVCGPKKSTNL  ATVCGPKKS  3         0.0870
19510.3    95.00  0.35     Sequence
 HLA-DPA10201-DPB10501  526      APATVCGPKKSTNLV  ATVCGPKKS  2         0.1009
16791.1    95.00  0.31     Sequence
 HLA-DPA10201-DPB10501  527      PATVCGPKKSTNLVK  PKKSTNLVK  6         0.1975
5902.1    65.00  0.49     Sequence
 HLA-DPA10201-DPB10501  528      ATVCGPKKSTNLVKN  PKKSTNLVK  5         0.2905
2157.2    36.00  0.64     Sequence
 HLA-DPA10201-DPB10501  529      TVCGPKKSTNLVKNK  PKKSTNLVK  4         0.3202
1564.1    29.00  0.64     Sequence
 HLA-DPA10201-DPB10501  530      VCGPKKSTNLVKNKC  PKKSTNLVK  3         0.3243
1497.1    28.00  0.65     Sequence
 HLA-DPA10201-DPB10501  531      CGPKKSTNLVKNKCV  PKKSTNLVK  2         0.3254
1478.2    28.00  0.63     Sequence
 HLA-DPA10201-DPB10501  532      GPKKSTNLVKNKCVN  PKKSTNLVK  1         0.3162
1634.5    30.00  0.59     Sequence
 HLA-DPA10201-DPB10501  533      PKKSTNLVKNKCVNF  PKKSTNLVK  0         0.2925
2110.1    36.00  0.48     Sequence
 HLA-DPA10201-DPB10501  534      KKSTNLVKNKCVNFN  KKSTNLVKN  0         0.2117
5062.7    60.00  0.23     Sequence
 HLA-DPA10201-DPB10501  535      KSTNLVKNKCVNFNF  KNKCVNFNF  6         0.1925
6229.5    65.00  0.23     Sequence
```

```
 HLA-DPA10201-DPB10501  536      STNLVKNKCVNFNFN  KNKCVNFNF  5        0.2240
4430.3    55.00  0.32     Sequence
 HLA-DPA10201-DPB10501  537      TNLVKNKCVNFNFNG  KNKCVNFNF  4        0.2353
3922.0    55.00  0.33     Sequence
 HLA-DPA10201-DPB10501  538      NLVKNKCVNFNFNGL  KNKCVNFNF  3        0.2580
3065.4    45.00  0.30     Sequence
 HLA-DPA10201-DPB10501  539      LVKNKCVNFNFNGLT  KNKCVNFNF  2        0.2571
3095.2    45.00  0.33     Sequence
 HLA-DPA10201-DPB10501  540      VKNKCVNFNFNGLTG  KNKCVNFNF  1        0.2421
3640.2    50.00  0.29     Sequence
 HLA-DPA10201-DPB10501  541      KNKCVNFNFNGLTGT  KNKCVNFNF  0        0.2186
4698.3    60.00  0.26     Sequence
 HLA-DPA10201-DPB10501  542      NKCVNFNFNGLTGTG  KCVNFNFNG  1        0.1829
6914.1    70.00  0.28     Sequence
 HLA-DPA10201-DPB10501  543      KCVNFNFNGLTGTGV  NFNFNGLTG  3        0.1519
9664.5    80.00  0.30     Sequence
 HLA-DPA10201-DPB10501  544      CVNFNFNGLTGTGVL  NFNFNGLTG  2        0.1323
11951.3    85.00  0.35     Sequence
 HLA-DPA10201-DPB10501  545      VNFNFNGLTGTGVLT  NFNFNGLTG  1        0.1299
12257.6    85.00  0.31     Sequence
 HLA-DPA10201-DPB10501  546      NFNFNGLTGTGVLTE  GLTGTGVLT  5        0.1298
12269.3    85.00  0.28     Sequence
 HLA-DPA10201-DPB10501  547      FNFNGLTGTGVLTES  GLTGTGVLT  4        0.1247
12977.5    85.00  0.32     Sequence
 HLA-DPA10201-DPB10501  548      NFNGLTGTGVLTESN  GLTGTGVLT  3        0.1196
13703.7    90.00  0.31     Sequence
 HLA-DPA10201-DPB10501  549      FNGLTGTGVLTESNK  GLTGTGVLT  2        0.1391
11096.4    85.00  0.31     Sequence
 HLA-DPA10201-DPB10501  550      NGLTGTGVLTESNKK  GVLTESNKK  6        0.1974
5909.5    65.00  0.32     Sequence
 HLA-DPA10201-DPB10501  551      GLTGTGVLTESNKKF  GVLTESNKK  5        0.3168
1622.3    30.00  0.56     Sequence
 HLA-DPA10201-DPB10501  552      LTGTGVLTESNKKFL  GVLTESNKK  4        0.3763
852.9    18.00  0.48     Sequence
 HLA-DPA10201-DPB10501  553      TGTGVLTESNKKFLP  GVLTESNKK  3        0.3885
747.5    16.00  0.47     Sequence
 HLA-DPA10201-DPB10501  554      GTGVLTESNKKFLPF  GVLTESNKK  2        0.4194
534.8    12.00  0.45     Sequence
 HLA-DPA10201-DPB10501  555      TGVLTESNKKFLPFQ  GVLTESNKK  1        0.4702
308.7     6.50  0.38     Sequence         WB
 HLA-DPA10201-DPB10501  556      GVLTESNKKFLPFQQ  NKKFLPFQQ  6        0.4965
232.3     4.50  0.31     Sequence         WB
 HLA-DPA10201-DPB10501  557      VLTESNKKFLPFQQF  NKKFLPFQQ  5        0.5281
164.9     3.00  0.49     Sequence         WB
 HLA-DPA10201-DPB10501  558      LTESNKKFLPFQQFG  NKKFLPFQQ  4        0.5172
185.5     3.50  0.51     Sequence         WB
 HLA-DPA10201-DPB10501  559      TESNKKFLPFQQFGR  NKKFLPFQQ  3        0.5588
118.4     1.80  0.47     Sequence         SB
 HLA-DPA10201-DPB10501  560      ESNKKFLPFQQFGRD  NKKFLPFQQ  2        0.5653
110.3     1.60  0.41     Sequence         SB
 HLA-DPA10201-DPB10501  561      SNKKFLPFQQFGRDI  NKKFLPFQQ  1        0.5639
112.0     1.60  0.40     Sequence         SB
 HLA-DPA10201-DPB10501  562      NKKFLPFQQFGRDIA  NKKFLPFQQ  0        0.5023
218.1     4.50  0.28     Sequence         WB
 HLA-DPA10201-DPB10501  563      KKFLPFQQFGRDIAD  FLPFQQFGR  2        0.4350
451.7     9.50  0.34     Sequence         WB
 HLA-DPA10201-DPB10501  564      KFLPFQQFGRDIADT  FLPFQQFGR  1        0.3283
1433.8    27.00  0.39     Sequence
 HLA-DPA10201-DPB10501  565      FLPFQQFGRDIADTT  FLPFQQFGR  0        0.2093
5192.0    60.00  0.32     Sequence
 HLA-DPA10201-DPB10501  566      LPFQQFGRDIADTTD  FQQFGRDIA  2        0.1170
14104.9    90.00  0.45     Sequence
 HLA-DPA10201-DPB10501  567      PFQQFGRDIADTTDA  FQQFGRDIA  1        0.1104
15140.1    90.00  0.45     Sequence
 HLA-DPA10201-DPB10501  568      FQQFGRDIADTTDAV  FQQFGRDIA  0        0.0962
17656.2    95.00  0.36     Sequence
```

```
 HLA-DPA10201-DPB10501  569       QQFGRDIADTTDAVR  RDIADTTDA  4         0.0602
26078.1   100.00  0.18      Sequence
 HLA-DPA10201-DPB10501  570       QFGRDIADTTDAVRD  IADTTDAVR  5         0.0532
28130.8   100.00  0.26      Sequence
 HLA-DPA10201-DPB10501  571       FGRDIADTTDAVRDP  IADTTDAVR  4         0.0524
28376.6   100.00  0.29      Sequence
 HLA-DPA10201-DPB10501  572       GRDIADTTDAVRDPQ  IADTTDAVR  3         0.0485
29577.5   100.00  0.35      Sequence
 HLA-DPA10201-DPB10501  573       RDIADTTDAVRDPQT  IADTTDAVR  2         0.0481
29705.2   100.00  0.40      Sequence
 HLA-DPA10201-DPB10501  574       DIADTTDAVRDPQTL  IADTTDAVR  1         0.0408
32143.1   100.00  0.38      Sequence
 HLA-DPA10201-DPB10501  575       IADTTDAVRDPQTLE  IADTTDAVR  0         0.0410
32070.1   100.00  0.27      Sequence
 HLA-DPA10201-DPB10501  576       ADTTDAVRDPQTLEI  AVRDPQTLE  5         0.0583
26612.2   100.00  0.29      Sequence
 HLA-DPA10201-DPB10501  577       DTTDAVRDPQTLEIL  VRDPQTLEI  5         0.0811
20786.2    95.00  0.44      Sequence
 HLA-DPA10201-DPB10501  578       TTDAVRDPQTLEILD  VRDPQTLEI  4         0.1028
16448.0    90.00  0.37      Sequence
 HLA-DPA10201-DPB10501  579       TDAVRDPQTLEILDI  VRDPQTLEI  3         0.1321
11976.0    85.00  0.25      Sequence
 HLA-DPA10201-DPB10501  580       DAVRDPQTLEILDIT  PQTLEILDI  5         0.1598
8876.0     75.00  0.30     Sequence
 HLA-DPA10201-DPB10501  581       AVRDPQTLEILDITP  PQTLEILDI  4         0.1715
7818.7     75.00  0.31     Sequence
 HLA-DPA10201-DPB10501  582       VRDPQTLEILDITPC  PQTLEILDI  3         0.1728
7712.0     75.00  0.32     Sequence
 HLA-DPA10201-DPB10501  583       RDPQTLEILDITPCS  PQTLEILDI  2         0.1716
7809.3     75.00  0.32     Sequence
 HLA-DPA10201-DPB10501  584       DPQTLEILDITPCSF  PQTLEILDI  1         0.1928
6207.2     65.00  0.25     Sequence
 HLA-DPA10201-DPB10501  585       PQTLEILDITPCSFG  LEILDITPC  3         0.1903
6380.9     70.00  0.25     Sequence
 HLA-DPA10201-DPB10501  586       QTLEILDITPCSFGG  LEILDITPC  2         0.1824
6944.7     70.00  0.25     Sequence
 HLA-DPA10201-DPB10501  587       TLEILDITPCSFGGV  LEILDITPC  1         0.1752
7511.3     70.00  0.25     Sequence
 HLA-DPA10201-DPB10501  588       LEILDITPCSFGGVS  ILDITPCSF  2         0.1637
8506.5     75.00  0.28     Sequence
 HLA-DPA10201-DPB10501  589       EILDITPCSFGGVSV  ILDITPCSF  1         0.1368
11380.7    85.00  0.30      Sequence
 HLA-DPA10201-DPB10501  590       ILDITPCSFGGVSVI  PCSFGGVSV  5         0.1243
13034.5    85.00  0.21      Sequence
 HLA-DPA10201-DPB10501  591       LDITPCSFGGVSVIT  PCSFGGVSV  4         0.1079
15563.1    90.00  0.26      Sequence
 HLA-DPA10201-DPB10501  592       DITPCSFGGVSVITP  PCSFGGVSV  3         0.1057
15928.4    90.00  0.29      Sequence
 HLA-DPA10201-DPB10501  593       ITPCSFGGVSVITPG  PCSFGGVSV  2         0.1037
16289.0    90.00  0.29      Sequence
 HLA-DPA10201-DPB10501  594       TPCSFGGVSVITPGT  PCSFGGVSV  1         0.1051
16038.0    90.00  0.23      Sequence
 HLA-DPA10201-DPB10501  595       PCSFGGVSVITPGTN  VSVITPGTN  6         0.1101
15188.7    90.00  0.23      Sequence
 HLA-DPA10201-DPB10501  596       CSFGGVSVITPGTNT  VSVITPGTN  5         0.1078
15567.8    90.00  0.29      Sequence
 HLA-DPA10201-DPB10501  597       SFGGVSVITPGTNTS  VSVITPGTN  4         0.0982
17284.2    95.00  0.34      Sequence
 HLA-DPA10201-DPB10501  598       FGGVSVITPGTNTSN  VSVITPGTN  3         0.0921
18457.8    95.00  0.40      Sequence
 HLA-DPA10201-DPB10501  599       GGVSVITPGTNTSNQ  VSVITPGTN  2         0.0835
20259.1    95.00  0.41      Sequence
 HLA-DPA10201-DPB10501  600       GVSVITPGTNTSNQV  VSVITPGTN  1         0.0855
19834.4    95.00  0.41      Sequence
 HLA-DPA10201-DPB10501  601       VSVITPGTNTSNQVA  VSVITPGTN  0         0.0687
23782.1   100.00  0.31      Sequence
```

```
 HLA-DPA10201-DPB10501  602      SVITPGTNTSNQVAV  VITPGTNTS  1        0.0502
29031.2   100.00  0.20     Sequence
 HLA-DPA10201-DPB10501  603      VITPGTNTSNQVAVL  PGTNTSNQV  3        0.0465
30240.9   100.00  0.12     Sequence
 HLA-DPA10201-DPB10501  604      ITPGTNTSNQVAVLY  TSNQVAVLY  6        0.0546
27690.8   100.00  0.20     Sequence
 HLA-DPA10201-DPB10501  605      TPGTNTSNQVAVLYQ  SNQVAVLYQ  6        0.0727
22757.8   100.00  0.28     Sequence
 HLA-DPA10201-DPB10501  606      PGTNTSNQVAVLYQG  SNQVAVLYQ  5        0.0950
17881.7    95.00  0.40     Sequence
 HLA-DPA10201-DPB10501  607      GTNTSNQVAVLYQGV  NQVAVLYQG  5        0.1538
9465.7    80.00  0.38     Sequence
 HLA-DPA10201-DPB10501  608      TNTSNQVAVLYQGVN  NQVAVLYQG  4        0.1739
7616.5    75.00  0.35     Sequence
 HLA-DPA10201-DPB10501  609      NTSNQVAVLYQGVNC  NQVAVLYQG  3        0.1831
6897.7    70.00  0.34     Sequence
 HLA-DPA10201-DPB10501  610      TSNQVAVLYQGVNCT  NQVAVLYQG  2        0.1968
5944.0    65.00  0.28     Sequence
 HLA-DPA10201-DPB10501  611      SNQVAVLYQGVNCTE  NQVAVLYQG  1        0.1953
6045.1    65.00  0.25     Sequence
 HLA-DPA10201-DPB10501  612      NQVAVLYQGVNCTEV  AVLYQGVNC  3        0.1820
6979.8    70.00  0.31     Sequence
 HLA-DPA10201-DPB10501  613      QVAVLYQGVNCTEVP  AVLYQGVNC  2        0.1646
8424.6    75.00  0.32     Sequence
 HLA-DPA10201-DPB10501  614      VAVLYQGVNCTEVPV  AVLYQGVNC  1        0.1423
10722.6    80.00  0.31     Sequence
 HLA-DPA10201-DPB10501  615      AVLYQGVNCTEVPVA  AVLYQGVNC  0        0.1426
10684.7    80.00  0.26     Sequence
 HLA-DPA10201-DPB10501  616      VLYQGVNCTEVPVAI  VNCTEVPVA  5        0.1237
13116.1    85.00  0.26     Sequence
 HLA-DPA10201-DPB10501  617      LYQGVNCTEVPVAIH  VNCTEVPVA  4        0.0985
17215.1    95.00  0.34     Sequence
 HLA-DPA10201-DPB10501  618      YQGVNCTEVPVAIHA  VNCTEVPVA  3        0.1140
14565.3    90.00  0.32     Sequence
 HLA-DPA10201-DPB10501  619      QGVNCTEVPVAIHAD  VNCTEVPVA  2        0.1134
14654.8    90.00  0.29     Sequence
 HLA-DPA10201-DPB10501  620      GVNCTEVPVAIHADQ  VNCTEVPVA  1        0.1135
14647.0    90.00  0.25     Sequence
 HLA-DPA10201-DPB10501  621      VNCTEVPVAIHADQL  TEVPVAIHA  3        0.1135
14635.9    90.00  0.26     Sequence
 HLA-DPA10201-DPB10501  622      NCTEVPVAIHADQLT  TEVPVAIHA  2        0.1002
16910.3    95.00  0.31     Sequence
 HLA-DPA10201-DPB10501  623      CTEVPVAIHADQLTP  TEVPVAIHA  1        0.1009
16783.6    95.00  0.31     Sequence
 HLA-DPA10201-DPB10501  624      TEVPVAIHADQLTPT  AIHADQLTP  5        0.1018
16619.4    95.00  0.22     Sequence
 HLA-DPA10201-DPB10501  625      EVPVAIHADQLTPTW  AIHADQLTP  4        0.0832
20330.5    95.00  0.31     Sequence
 HLA-DPA10201-DPB10501  626      VPVAIHADQLTPTWR  AIHADQLTP  3        0.1021
16571.6    90.00  0.34     Sequence
 HLA-DPA10201-DPB10501  627      PVAIHADQLTPTWRV  ADQLTPTWR  5        0.1055
15966.3    90.00  0.30     Sequence
 HLA-DPA10201-DPB10501  628      VAIHADQLTPTWRVY  ADQLTPTWR  4        0.1209
13521.8    90.00  0.30     Sequence
 HLA-DPA10201-DPB10501  629      AIHADQLTPTWRVYS  ADQLTPTWR  3        0.1200
13646.7    90.00  0.29     Sequence
 HLA-DPA10201-DPB10501  630      IHADQLTPTWRVYST  DQLTPTWRV  3        0.1263
12756.2    85.00  0.28     Sequence
 HLA-DPA10201-DPB10501  631      HADQLTPTWRVYSTG  DQLTPTWRV  2        0.1302
12227.9    85.00  0.28     Sequence
 HLA-DPA10201-DPB10501  632      ADQLTPTWRVYSTGS  DQLTPTWRV  1        0.1294
12334.3    85.00  0.27     Sequence
 HLA-DPA10201-DPB10501  633      DQLTPTWRVYSTGSN  TPTWRVYST  3        0.1249
12946.0    85.00  0.19     Sequence
 HLA-DPA10201-DPB10501  634      QLTPTWRVYSTGSNV  WRVYSTGSN  5        0.1288
12405.3    85.00  0.24     Sequence
```

```
 HLA-DPA10201-DPB10501  635      LTPTWRVYSTGSNVF  WRVYSTGSN  4        0.1487
10003.9    80.00  0.26     Sequence
 HLA-DPA10201-DPB10501  636      TPTWRVYSTGSNVFQ  WRVYSTGSN  3        0.1648
8405.5    75.00  0.23     Sequence
 HLA-DPA10201-DPB10501  637      PTWRVYSTGSNVFQT  RVYSTGSNV  3        0.1749
7535.6    70.00  0.29     Sequence
 HLA-DPA10201-DPB10501  638      TWRVYSTGSNVFQTR  RVYSTGSNV  2        0.1882
6523.2    70.00  0.29     Sequence
 HLA-DPA10201-DPB10501  639      WRVYSTGSNVFQTRA  RVYSTGSNV  1        0.1836
6857.6    70.00  0.28     Sequence
 HLA-DPA10201-DPB10501  640      RVYSTGSNVFQTRAG  RVYSTGSNV  0        0.1534
9513.3    80.00  0.23     Sequence
 HLA-DPA10201-DPB10501  641      VYSTGSNVFQTRAGC  STGSNVFQT  2        0.1224
13301.4    85.00  0.26     Sequence
 HLA-DPA10201-DPB10501  642      YSTGSNVFQTRAGCL  STGSNVFQT  1        0.0994
17059.7    95.00  0.25     Sequence
 HLA-DPA10201-DPB10501  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.1051
16038.0    90.00  0.25     Sequence
 HLA-DPA10201-DPB10501  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.1179
13955.2    90.00  0.22     Sequence
 HLA-DPA10201-DPB10501  645      GSNVFQTRAGCLIGA  QTRAGCLIG  5        0.1391
11104.2    85.00  0.26     Sequence
 HLA-DPA10201-DPB10501  646      SNVFQTRAGCLIGAE  QTRAGCLIG  4        0.1587
8982.3    75.00  0.25     Sequence
 HLA-DPA10201-DPB10501  647      NVFQTRAGCLIGAEY  QTRAGCLIG  3        0.1765
7404.6    70.00  0.29     Sequence
 HLA-DPA10201-DPB10501  648      VFQTRAGCLIGAEYV  QTRAGCLIG  2        0.1879
6547.5    70.00  0.29     Sequence
 HLA-DPA10201-DPB10501  649      FQTRAGCLIGAEYVN  QTRAGCLIG  1        0.2081
5260.6    60.00  0.25     Sequence
 HLA-DPA10201-DPB10501  650      QTRAGCLIGAEYVNN  CLIGAEYVN  5        0.2181
4721.0    60.00  0.25     Sequence
 HLA-DPA10201-DPB10501  651      TRAGCLIGAEYVNNS  CLIGAEYVN  4        0.2240
4430.0    55.00  0.31     Sequence
 HLA-DPA10201-DPB10501  652      RAGCLIGAEYVNNSY  CLIGAEYVN  3        0.2250
4384.5    55.00  0.32     Sequence
 HLA-DPA10201-DPB10501  653      AGCLIGAEYVNNSYE  CLIGAEYVN  2        0.2140
4937.0    60.00  0.31     Sequence
 HLA-DPA10201-DPB10501  654      GCLIGAEYVNNSYEC  CLIGAEYVN  1        0.2027
5577.0    65.00  0.31     Sequence
 HLA-DPA10201-DPB10501  655      CLIGAEYVNNSYECD  LIGAEYVNN  1        0.1829
6908.5    70.00  0.32     Sequence
 HLA-DPA10201-DPB10501  656      LIGAEYVNNSYECDI  LIGAEYVNN  0        0.1305
12178.3    85.00  0.28     Sequence
 HLA-DPA10201-DPB10501  657      IGAEYVNNSYECDIP  EYVNNSYEC  3        0.0859
19747.3    95.00  0.32     Sequence
 HLA-DPA10201-DPB10501  658      GAEYVNNSYECDIPI  EYVNNSYEC  2        0.0835
20255.4    95.00  0.35     Sequence
 HLA-DPA10201-DPB10501  659      AEYVNNSYECDIPIG  EYVNNSYEC  1        0.0909
18702.5    95.00  0.29     Sequence
 HLA-DPA10201-DPB10501  660      EYVNNSYECDIPIGA  SYECDIPIG  5        0.1031
16391.9    90.00  0.22     Sequence
 HLA-DPA10201-DPB10501  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.1026
16480.1    90.00  0.27     Sequence
 HLA-DPA10201-DPB10501  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.1114
14979.3    90.00  0.34     Sequence
 HLA-DPA10201-DPB10501  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.1132
14687.8    90.00  0.28     Sequence
 HLA-DPA10201-DPB10501  664      NSYECDIPIGAGICA  YECDIPIGA  2        0.1242
13037.6    85.00  0.21     Sequence
 HLA-DPA10201-DPB10501  665      SYECDIPIGAGICAS  YECDIPIGA  1        0.1256
12844.8    85.00  0.20     Sequence
 HLA-DPA10201-DPB10501  666      YECDIPIGAGICASY  IPIGAGICA  4        0.1270
12658.8    85.00  0.27     Sequence
 HLA-DPA10201-DPB10501  667      ECDIPIGAGICASYQ  IPIGAGICA  3        0.1214
13449.7    90.00  0.34     Sequence
```

```
 HLA-DPA10201-DPB10501  668      CDIPIGAGICASYQT  IPIGAGICA  2               0.1217
13394.4    90.00  0.35     Sequence
 HLA-DPA10201-DPB10501  669      DIPIGAGICASYQTQ  IPIGAGICA  1               0.1268
12683.0    85.00  0.31     Sequence
 HLA-DPA10201-DPB10501  670      IPIGAGICASYQTQT  AGICASYQT  4               0.1294
12327.0    85.00  0.31     Sequence
 HLA-DPA10201-DPB10501  671      PIGAGICASYQTQTN  AGICASYQT  3               0.1037
16282.6    90.00  0.43     Sequence
 HLA-DPA10201-DPB10501  672      IGAGICASYQTQTNS  AGICASYQT  2               0.0916
18562.2    95.00  0.47     Sequence
 HLA-DPA10201-DPB10501  673      GAGICASYQTQTNSP  AGICASYQT  1               0.0816
20681.9    95.00  0.44     Sequence
 HLA-DPA10201-DPB10501  674      AGICASYQTQTNSPR  AGICASYQT  0               0.0856
19796.9    95.00  0.33     Sequence
 HLA-DPA10201-DPB10501  675      GICASYQTQTNSPRR  QTQTNSPRR  6               0.1009
16787.1    95.00  0.28     Sequence
 HLA-DPA10201-DPB10501  676      ICASYQTQTNSPRRA  QTQTNSPRR  5               0.0974
17421.4    95.00  0.35     Sequence
 HLA-DPA10201-DPB10501  677      CASYQTQTNSPRRAR  QTQTNSPRR  4               0.0952
17846.5    95.00  0.38     Sequence
 HLA-DPA10201-DPB10501  678      ASYQTQTNSPRRARS  QTQTNSPRR  3               0.0943
18026.2    95.00  0.38     Sequence
 HLA-DPA10201-DPB10501  679      SYQTQTNSPRRARSV  QTQTNSPRR  2               0.0936
18151.5    95.00  0.38     Sequence
 HLA-DPA10201-DPB10501  680      YQTQTNSPRRARSVA  QTQTNSPRR  1               0.0887
19158.2    95.00  0.38     Sequence
 HLA-DPA10201-DPB10501  681      QTQTNSPRRARSVAS  QTQTNSPRR  0               0.0785
21374.9    95.00  0.22     Sequence
 HLA-DPA10201-DPB10501  682      TQTNSPRRARSVASQ  PRRARSVAS  5               0.0649
24785.3   100.00  0.40     Sequence
 HLA-DPA10201-DPB10501  683      QTNSPRRARSVASQS  PRRARSVAS  4               0.0695
23584.0   100.00  0.41     Sequence
 HLA-DPA10201-DPB10501  684      TNSPRRARSVASQSI  PRRARSVAS  3               0.0792
21224.4    95.00  0.37     Sequence
 HLA-DPA10201-DPB10501  685      NSPRRARSVASQSII  PRRARSVAS  2               0.1014
16692.5    95.00  0.26     Sequence
 HLA-DPA10201-DPB10501  686      SPRRARSVASQSIIA  ARSVASQSI  4               0.1305
12178.5    85.00  0.19     Sequence
 HLA-DPA10201-DPB10501  687      PRRARSVASQSIIAY  SVASQSIIA  5               0.1647
8417.8    75.00  0.32     Sequence
 HLA-DPA10201-DPB10501  688      RRARSVASQSIIAYT  SVASQSIIA  4               0.1856
6709.2    70.00  0.34     Sequence
 HLA-DPA10201-DPB10501  689      RARSVASQSIIAYTM  SVASQSIIA  3               0.2319
4065.5    55.00  0.27     Sequence
 HLA-DPA10201-DPB10501  690      ARSVASQSIIAYTMS  SQSIIAYTM  5               0.2771
2494.0    40.00  0.25     Sequence
 HLA-DPA10201-DPB10501  691      RSVASQSIIAYTMSL  QSIIAYTMS  5               0.3133
1686.4    30.00  0.25     Sequence
 HLA-DPA10201-DPB10501  692      SVASQSIIAYTMSLG  QSIIAYTMS  4               0.3066
1812.0    32.00  0.28     Sequence
 HLA-DPA10201-DPB10501  693      VASQSIIAYTMSLGA  QSIIAYTMS  3               0.3305
1399.2    27.00  0.26     Sequence
 HLA-DPA10201-DPB10501  694      ASQSIIAYTMSLGAE  QSIIAYTMS  2               0.3308
1394.3    27.00  0.25     Sequence
 HLA-DPA10201-DPB10501  695      SQSIIAYTMSLGAEN  QSIIAYTMS  1               0.3357
1323.5    26.00  0.25     Sequence
 HLA-DPA10201-DPB10501  696      QSIIAYTMSLGAENS  IIAYTMSLG  2               0.2962
2028.6    35.00  0.30     Sequence
 HLA-DPA10201-DPB10501  697      SIIAYTMSLGAENSV  IIAYTMSLG  1               0.2464
3477.6    48.00  0.34     Sequence
 HLA-DPA10201-DPB10501  698      IIAYTMSLGAENSVA  IIAYTMSLG  0               0.2131
4983.4    60.00  0.25     Sequence
 HLA-DPA10201-DPB10501  699      IAYTMSLGAENSVAY  YTMSLGAEN  2               0.1915
6297.0    65.00  0.19     Sequence
 HLA-DPA10201-DPB10501  700      AYTMSLGAENSVAYS  YTMSLGAEN  1               0.1648
8405.6    75.00  0.24     Sequence
```

```
 HLA-DPA10201-DPB10501  701      YTMSLGAENSVAYSN  SLGAENSVA  3        0.1649
8400.7    75.00  0.24     Sequence
 HLA-DPA10201-DPB10501  702      TMSLGAENSVAYSNN  SLGAENSVA  2        0.1484
10043.0    80.00  0.25     Sequence
 HLA-DPA10201-DPB10501  703      MSLGAENSVAYSNNS  SLGAENSVA  1        0.1351
11595.7    85.00  0.24     Sequence
 HLA-DPA10201-DPB10501  704      SLGAENSVAYSNNSI  AENSVAYSN  3        0.1237
13110.5    85.00  0.20     Sequence
 HLA-DPA10201-DPB10501  705      LGAENSVAYSNNSIA  AENSVAYSN  2        0.1124
14816.8    90.00  0.22     Sequence
 HLA-DPA10201-DPB10501  706      GAENSVAYSNNSIAI  VAYSNNSIA  5        0.1107
15087.1    90.00  0.25     Sequence
 HLA-DPA10201-DPB10501  707      AENSVAYSNNSIAIP  VAYSNNSIA  4        0.1150
14406.4    90.00  0.25     Sequence
 HLA-DPA10201-DPB10501  708      ENSVAYSNNSIAIPT  VAYSNNSIA  3        0.1040
16230.4    90.00  0.28     Sequence
 HLA-DPA10201-DPB10501  709      NSVAYSNNSIAIPTN  VAYSNNSIA  2        0.0995
17035.0    95.00  0.30     Sequence
 HLA-DPA10201-DPB10501  710      SVAYSNNSIAIPTNF  VAYSNNSIA  1        0.1088
15411.1    90.00  0.23     Sequence
 HLA-DPA10201-DPB10501  711      VAYSNNSIAIPTNFT  NSIAIPTNF  5        0.1226
13265.1    85.00  0.23     Sequence
 HLA-DPA10201-DPB10501  712      AYSNNSIAIPTNFTI  NSIAIPTNF  4        0.1542
9429.6    80.00  0.24     Sequence
 HLA-DPA10201-DPB10501  713      YSNNSIAIPTNFTIS  IAIPTNFTI  5        0.1627
8597.3    75.00  0.28     Sequence
 HLA-DPA10201-DPB10501  714      SNNSIAIPTNFTISV  IAIPTNFTI  4        0.1914
6305.2    65.00  0.23     Sequence
 HLA-DPA10201-DPB10501  715      NNSIAIPTNFTISVT  IAIPTNFTI  3        0.2082
5256.0    60.00  0.22     Sequence
 HLA-DPA10201-DPB10501  716      NSIAIPTNFTISVTT  PTNFTISVT  5        0.2190
4677.8    60.00  0.25     Sequence
 HLA-DPA10201-DPB10501  717      SIAIPTNFTISVTTE  PTNFTISVT  4        0.2130
4989.9    60.00  0.26     Sequence
 HLA-DPA10201-DPB10501  718      IAIPTNFTISVTTEI  PTNFTISVT  3        0.2210
4577.4    60.00  0.30     Sequence
 HLA-DPA10201-DPB10501  719      AIPTNFTISVTTEIL  PTNFTISVT  2        0.2326
4034.3    55.00  0.31     Sequence
 HLA-DPA10201-DPB10501  720      IPTNFTISVTTEILP  PTNFTISVT  1        0.2417
3659.6    50.00  0.27     Sequence
 HLA-DPA10201-DPB10501  721      PTNFTISVTTEILPV  ISVTTEILP  5        0.2446
3546.6    49.00  0.25     Sequence
 HLA-DPA10201-DPB10501  722      TNFTISVTTEILPVS  ISVTTEILP  4        0.2488
3387.7    48.00  0.34     Sequence
 HLA-DPA10201-DPB10501  723      NFTISVTTEILPVSM  ISVTTEILP  3        0.2545
3185.8    46.00  0.38     Sequence
 HLA-DPA10201-DPB10501  724      FTISVTTEILPVSMT  ISVTTEILP  2        0.2458
3498.7    49.00  0.38     Sequence
 HLA-DPA10201-DPB10501  725      TISVTTEILPVSMTK  ISVTTEILP  1        0.2686
2732.8    42.00  0.28     Sequence
 HLA-DPA10201-DPB10501  726      ISVTTEILPVSMTKT  EILPVSMTK  5        0.2923
2114.7    36.00  0.37     Sequence
 HLA-DPA10201-DPB10501  727      SVTTEILPVSMTKTS  EILPVSMTK  4        0.3048
1848.4    32.00  0.43     Sequence
 HLA-DPA10201-DPB10501  728      VTTEILPVSMTKTSV  EILPVSMTK  3        0.3122
1705.8    31.00  0.45     Sequence
 HLA-DPA10201-DPB10501  729      TTEILPVSMTKTSVD  EILPVSMTK  2        0.3004
1937.8    34.00  0.46     Sequence
 HLA-DPA10201-DPB10501  730      TEILPVSMTKTSVDC  EILPVSMTK  1        0.2872
2236.7    37.00  0.47     Sequence
 HLA-DPA10201-DPB10501  731      EILPVSMTKTSVDCT  EILPVSMTK  0        0.2570
3099.2    45.00  0.44     Sequence
 HLA-DPA10201-DPB10501  732      ILPVSMTKTSVDCTM  ILPVSMTKT  0        0.1452
10386.1    80.00  0.22     Sequence
 HLA-DPA10201-DPB10501  733      LPVSMTKTSVDCTMY  TKTSVDCTM  5        0.1034
16332.7    90.00  0.19     Sequence
```

```
 HLA-DPA10201-DPB10501  734       PVSMTKTSVDCTMYI  KTSVDCTMY  5         0.1122
14851.0    90.00  0.28     Sequence
 HLA-DPA10201-DPB10501  735       VSMTKTSVDCTMYIC  KTSVDCTMY  4         0.1382
11206.2    85.00  0.28     Sequence
 HLA-DPA10201-DPB10501  736       SMTKTSVDCTMYICG  SVDCTMYIC  5         0.1788
7223.3    70.00  0.34     Sequence
 HLA-DPA10201-DPB10501  737       MTKTSVDCTMYICGD  SVDCTMYIC  4         0.1814
7027.1    70.00  0.35     Sequence
 HLA-DPA10201-DPB10501  738       TKTSVDCTMYICGDS  SVDCTMYIC  3         0.1819
6985.8    70.00  0.37     Sequence
 HLA-DPA10201-DPB10501  739       KTSVDCTMYICGDST  SVDCTMYIC  2         0.1668
8223.6    75.00  0.44     Sequence
 HLA-DPA10201-DPB10501  740       TSVDCTMYICGDSTE  SVDCTMYIC  1         0.1533
9517.7    80.00  0.44     Sequence
 HLA-DPA10201-DPB10501  741       SVDCTMYICGDSTEC  SVDCTMYIC  0         0.1337
11769.6    85.00  0.31     Sequence
 HLA-DPA10201-DPB10501  742       VDCTMYICGDSTECS  YICGDSTEC  5         0.1097
15254.9    90.00  0.23     Sequence
 HLA-DPA10201-DPB10501  743       DCTMYICGDSTECSN  YICGDSTEC  4         0.0793
21201.2    95.00  0.35     Sequence
 HLA-DPA10201-DPB10501  744       CTMYICGDSTECSNL  YICGDSTEC  3         0.0814
20718.9    95.00  0.38     Sequence
 HLA-DPA10201-DPB10501  745       TMYICGDSTECSNLL  YICGDSTEC  2         0.0836
20236.1    95.00  0.41     Sequence
 HLA-DPA10201-DPB10501  746       MYICGDSTECSNLLL  YICGDSTEC  1         0.0855
19826.3    95.00  0.33     Sequence
 HLA-DPA10201-DPB10501  747       YICGDSTECSNLLLQ  STECSNLLL  5         0.1010
16768.8    95.00  0.32     Sequence
 HLA-DPA10201-DPB10501  748       ICGDSTECSNLLLQY  TECSNLLLQ  5         0.1275
12587.3    85.00  0.37     Sequence
 HLA-DPA10201-DPB10501  749       CGDSTECSNLLLQYG  TECSNLLLQ  4         0.1407
10909.5    85.00  0.35     Sequence
 HLA-DPA10201-DPB10501  750       GDSTECSNLLLQYGS  TECSNLLLQ  3         0.1621
8658.2    75.00  0.31     Sequence
 HLA-DPA10201-DPB10501  751       DSTECSNLLLQYGSF  TECSNLLLQ  2         0.1980
5872.3    65.00  0.22     Sequence
 HLA-DPA10201-DPB10501  752       STECSNLLLQYGSFC  SNLLLQYGS  4         0.2109
5106.3    60.00  0.28     Sequence
 HLA-DPA10201-DPB10501  753       TECSNLLLQYGSFCT  LLQYGSFCT  6         0.2431
3602.7    49.00  0.26     Sequence
 HLA-DPA10201-DPB10501  754       ECSNLLLQYGSFCTQ  LLQYGSFCT  5         0.2454
3513.0    49.00  0.38     Sequence
 HLA-DPA10201-DPB10501  755       CSNLLLQYGSFCTQL  LLQYGSFCT  4         0.2516
3285.0    47.00  0.43     Sequence
 HLA-DPA10201-DPB10501  756       SNLLLQYGSFCTQLN  LLQYGSFCT  3         0.2587
3043.9    45.00  0.43     Sequence
 HLA-DPA10201-DPB10501  757       NLLLQYGSFCTQLNR  LLQYGSFCT  2         0.2697
2700.7    42.00  0.46     Sequence
 HLA-DPA10201-DPB10501  758       LLLQYGSFCTQLNRA  LLQYGSFCT  1         0.2572
3093.8    45.00  0.41     Sequence
 HLA-DPA10201-DPB10501  759       LLQYGSFCTQLNRAL  LLQYGSFCT  0         0.2613
2957.8    44.00  0.28     Sequence
 HLA-DPA10201-DPB10501  760       LQYGSFCTQLNRALT  GSFCTQLNR  3         0.2344
3956.9    55.00  0.32     Sequence
 HLA-DPA10201-DPB10501  761       QYGSFCTQLNRALTG  GSFCTQLNR  2         0.2205
4602.0    60.00  0.34     Sequence
 HLA-DPA10201-DPB10501  762       YGSFCTQLNRALTGI  GSFCTQLNR  1         0.2131
4983.3    60.00  0.28     Sequence
 HLA-DPA10201-DPB10501  763       GSFCTQLNRALTGIA  GSFCTQLNR  0         0.2004
5718.2    65.00  0.22     Sequence
 HLA-DPA10201-DPB10501  764       SFCTQLNRALTGIAV  CTQLNRALT  2         0.2076
5289.0    60.00  0.21     Sequence
 HLA-DPA10201-DPB10501  765       FCTQLNRALTGIAVE  NRALTGIAV  5         0.1952
6051.5    65.00  0.19     Sequence
 HLA-DPA10201-DPB10501  766       CTQLNRALTGIAVEQ  NRALTGIAV  4         0.1961
5990.1    65.00  0.25     Sequence
```

```
 HLA-DPA10201-DPB10501  767      TQLNRALTGIAVEQD  NRALTGIAV  3        0.1997
5759.9    65.00  0.25     Sequence
 HLA-DPA10201-DPB10501  768      QLNRALTGIAVEQDK  NRALTGIAV  2        0.2013
5666.0    65.00  0.29     Sequence
 HLA-DPA10201-DPB10501  769      LNRALTGIAVEQDKN  NRALTGIAV  1        0.1846
6784.8    70.00  0.31     Sequence
 HLA-DPA10201-DPB10501  770      NRALTGIAVEQDKNT  NRALTGIAV  0        0.1717
7805.3    75.00  0.33     Sequence
 HLA-DPA10201-DPB10501  771      RALTGIAVEQDKNTQ  ALTGIAVEQ  1        0.1394
11061.2    85.00  0.28     Sequence
 HLA-DPA10201-DPB10501  772      ALTGIAVEQDKNTQE  GIAVEQDKN  3        0.1032
16361.0    90.00  0.22     Sequence
 HLA-DPA10201-DPB10501  773      LTGIAVEQDKNTQEV  GIAVEQDKN  2        0.0716
23048.2   100.00  0.37     Sequence
 HLA-DPA10201-DPB10501  774      TGIAVEQDKNTQEVF  GIAVEQDKN  1        0.0621
25548.0   100.00  0.29     Sequence
 HLA-DPA10201-DPB10501  775      GIAVEQDKNTQEVFA  DKNTQEVFA  6        0.0789
21296.6    95.00  0.23     Sequence
 HLA-DPA10201-DPB10501  776      IAVEQDKNTQEVFAQ  KNTQEVFAQ  6        0.1040
16236.2    90.00  0.26     Sequence
 HLA-DPA10201-DPB10501  777      AVEQDKNTQEVFAQV  KNTQEVFAQ  5        0.1386
11163.5    85.00  0.42     Sequence
 HLA-DPA10201-DPB10501  778      VEQDKNTQEVFAQVK  KNTQEVFAQ  4        0.1806
7084.9    70.00  0.38     Sequence
 HLA-DPA10201-DPB10501  779      EQDKNTQEVFAQVKQ  KNTQEVFAQ  3        0.2204
4608.1    60.00  0.29     Sequence
 HLA-DPA10201-DPB10501  780      QDKNTQEVFAQVKQI  QEVFAQVKQ  5        0.2547
3176.8    46.00  0.41     Sequence
 HLA-DPA10201-DPB10501  781      DKNTQEVFAQVKQIY  QEVFAQVKQ  4        0.2700
2693.0    42.00  0.40     Sequence
 HLA-DPA10201-DPB10501  782      KNTQEVFAQVKQIYK  QEVFAQVKQ  3        0.2922
2117.6    36.00  0.38     Sequence
 HLA-DPA10201-DPB10501  783      NTQEVFAQVKQIYKT  QEVFAQVKQ  2        0.2886
2202.4    37.00  0.34     Sequence
 HLA-DPA10201-DPB10501  784      TQEVFAQVKQIYKTP  QEVFAQVKQ  1        0.2818
2369.1    38.00  0.31     Sequence
 HLA-DPA10201-DPB10501  785      QEVFAQVKQIYKTPP  FAQVKQIYK  3        0.2452
3523.8    49.00  0.25     Sequence
 HLA-DPA10201-DPB10501  786      EVFAQVKQIYKTPPI  FAQVKQIYK  2        0.2118
5057.4    60.00  0.30     Sequence
 HLA-DPA10201-DPB10501  787      VFAQVKQIYKTPPIK  FAQVKQIYK  1        0.2445
3547.8    49.00  0.22     Sequence
 HLA-DPA10201-DPB10501  788      FAQVKQIYKTPPIKD  QIYKTPPIK  5        0.2762
2517.4    40.00  0.24     Sequence
 HLA-DPA10201-DPB10501  789      AQVKQIYKTPPIKDF  IYKTPPIKD  5        0.3183
1597.7    29.00  0.46     Sequence
 HLA-DPA10201-DPB10501  790      QVKQIYKTPPIKDFG  IYKTPPIKD  4        0.3213
1545.7    29.00  0.44     Sequence
 HLA-DPA10201-DPB10501  791      VKQIYKTPPIKDFGG  IYKTPPIKD  3        0.3168
1623.6    30.00  0.46     Sequence
 HLA-DPA10201-DPB10501  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.3039
1865.6    33.00  0.46     Sequence
 HLA-DPA10201-DPB10501  793      QIYKTPPIKDFGGFN  IYKTPPIKD  1        0.2540
3202.1    46.00  0.43     Sequence
 HLA-DPA10201-DPB10501  794      IYKTPPIKDFGGFNF  IKDFGGFNF  6        0.2501
3339.5    47.00  0.39     Sequence
 HLA-DPA10201-DPB10501  795      YKTPPIKDFGGFNFS  IKDFGGFNF  5        0.2821
2362.4    38.00  0.62     Sequence
 HLA-DPA10201-DPB10501  796      KTPPIKDFGGFNFSQ  IKDFGGFNF  4        0.3038
1867.7    33.00  0.66     Sequence
 HLA-DPA10201-DPB10501  797      TPPIKDFGGFNFSQI  IKDFGGFNF  3        0.3374
1299.4    25.00  0.59     Sequence
 HLA-DPA10201-DPB10501  798      PPIKDFGGFNFSQIL  IKDFGGFNF  2        0.3577
1043.1    21.00  0.54     Sequence
 HLA-DPA10201-DPB10501  799      PIKDFGGFNFSQILP  IKDFGGFNF  1        0.3699
913.7    19.00  0.50     Sequence
```

```
 HLA-DPA10201-DPB10501  800      IKDFGGFNFSQILPD  IKDFGGFNF  0         0.3575
1044.8    21.00  0.40     Sequence
 HLA-DPA10201-DPB10501  801      KDFGGFNFSQILPDP  GFNFSQILP  4         0.2971
2008.0    34.00  0.38     Sequence
 HLA-DPA10201-DPB10501  802      DFGGFNFSQILPDPS  GFNFSQILP  3         0.2603
2990.3    44.00  0.41     Sequence
 HLA-DPA10201-DPB10501  803      FGGFNFSQILPDPSK  GFNFSQILP  2         0.2743
2569.5    40.00  0.39     Sequence
 HLA-DPA10201-DPB10501  804      GGFNFSQILPDPSKP  GFNFSQILP  1         0.2444
3553.7    49.00  0.39     Sequence
 HLA-DPA10201-DPB10501  805      GFNFSQILPDPSKPS  GFNFSQILP  0         0.2258
4343.8    55.00  0.34     Sequence
 HLA-DPA10201-DPB10501  806      FNFSQILPDPSKPSK  QILPDPSKP  4         0.1859
6691.0    70.00  0.26     Sequence
 HLA-DPA10201-DPB10501  807      NFSQILPDPSKPSKR  QILPDPSKP  3         0.1465
10245.5    80.00  0.38     Sequence
 HLA-DPA10201-DPB10501  808      FSQILPDPSKPSKRS  QILPDPSKP  2         0.1358
11501.4    85.00  0.39     Sequence
 HLA-DPA10201-DPB10501  809      SQILPDPSKPSKRSF  QILPDPSKP  1         0.1204
13582.6    90.00  0.37     Sequence
 HLA-DPA10201-DPB10501  810      QILPDPSKPSKRSFI  QILPDPSKP  0         0.0988
17163.0    95.00  0.29     Sequence
 HLA-DPA10201-DPB10501  811      ILPDPSKPSKRSFIE  KPSKRSFIE  6         0.1081
15518.4    90.00  0.25     Sequence
 HLA-DPA10201-DPB10501  812      LPDPSKPSKRSFIED  KPSKRSFIE  5         0.1104
15145.0    90.00  0.32     Sequence
 HLA-DPA10201-DPB10501  813      PDPSKPSKRSFIEDL  KPSKRSFIE  4         0.1317
12027.7    85.00  0.32     Sequence
 HLA-DPA10201-DPB10501  814      DPSKPSKRSFIEDLL  KRSFIEDLL  6         0.2338
3983.7    55.00  0.26     Sequence
 HLA-DPA10201-DPB10501  815      PSKPSKRSFIEDLLF  KRSFIEDLL  5         0.3135
1681.6    30.00  0.34     Sequence
 HLA-DPA10201-DPB10501  816      SKPSKRSFIEDLLFN  RSFIEDLLF  5         0.3757
858.0    18.00  0.34     Sequence
 HLA-DPA10201-DPB10501  817      KPSKRSFIEDLLFNK  RSFIEDLLF  4         0.5034
215.5     4.50  0.27     Sequence         WB
 HLA-DPA10201-DPB10501  818      PSKRSFIEDLLFNKV  FIEDLLFNK  5         0.5706
104.1     1.50  0.38     Sequence         SB
 HLA-DPA10201-DPB10501  819      SKRSFIEDLLFNKVT  FIEDLLFNK  4         0.5813
92.8     1.20  0.38     Sequence         SB
 HLA-DPA10201-DPB10501  820      KRSFIEDLLFNKVTL  FIEDLLFNK  3         0.5808
93.3     1.20  0.38     Sequence         SB
 HLA-DPA10201-DPB10501  821      RSFIEDLLFNKVTLA  FIEDLLFNK  2         0.5378
148.6     2.50  0.43     Sequence         WB
 HLA-DPA10201-DPB10501  822      SFIEDLLFNKVTLAD  FIEDLLFNK  1         0.4988
226.6     4.50  0.44     Sequence         WB
 HLA-DPA10201-DPB10501  823      FIEDLLFNKVTLADA  FIEDLLFNK  0         0.4360
446.9     9.50  0.40     Sequence         WB
 HLA-DPA10201-DPB10501  824      IEDLLFNKVTLADAG  DLLFNKVTL  2         0.3134
1683.6    30.00  0.29     Sequence
 HLA-DPA10201-DPB10501  825      EDLLFNKVTLADAGF  DLLFNKVTL  1         0.2790
2442.8    39.00  0.28     Sequence
 HLA-DPA10201-DPB10501  826      DLLFNKVTLADAGFI  LFNKVTLAD  2         0.2915
2135.0    36.00  0.23     Sequence
 HLA-DPA10201-DPB10501  827      LLFNKVTLADAGFIK  TLADAGFIK  6         0.2949
2056.1    35.00  0.21     Sequence
 HLA-DPA10201-DPB10501  828      LFNKVTLADAGFIKQ  TLADAGFIK  5         0.3155
1646.0    30.00  0.41     Sequence
 HLA-DPA10201-DPB10501  829      FNKVTLADAGFIKQY  TLADAGFIK  4         0.3282
1434.7    27.00  0.43     Sequence
 HLA-DPA10201-DPB10501  830      NKVTLADAGFIKQYG  TLADAGFIK  3         0.3199
1569.5    29.00  0.43     Sequence
 HLA-DPA10201-DPB10501  831      KVTLADAGFIKQYGD  TLADAGFIK  2         0.3132
1688.0    31.00  0.46     Sequence
 HLA-DPA10201-DPB10501  832      VTLADAGFIKQYGDC  TLADAGFIK  1         0.2797
2424.4    39.00  0.47     Sequence
```

```
 HLA-DPA10201-DPB10501  833      TLADAGFIKQYGDCL  TLADAGFIK  0         0.2456
3506.5    49.00  0.40     Sequence
 HLA-DPA10201-DPB10501  834      LADAGFIKQYGDCLG  IKQYGDCLG  6         0.1933
6175.4    65.00  0.30     Sequence
 HLA-DPA10201-DPB10501  835      ADAGFIKQYGDCLGD  IKQYGDCLG  5         0.1661
8288.2    75.00  0.46     Sequence
 HLA-DPA10201-DPB10501  836      DAGFIKQYGDCLGDI  IKQYGDCLG  4         0.1746
7559.2    70.00  0.48     Sequence
 HLA-DPA10201-DPB10501  837      AGFIKQYGDCLGDIA  IKQYGDCLG  3         0.1824
6946.4    70.00  0.50     Sequence
 HLA-DPA10201-DPB10501  838      GFIKQYGDCLGDIAA  IKQYGDCLG  2         0.1833
6879.5    70.00  0.50     Sequence
 HLA-DPA10201-DPB10501  839      FIKQYGDCLGDIAAR  IKQYGDCLG  1         0.1822
6961.9    70.00  0.50     Sequence
 HLA-DPA10201-DPB10501  840      IKQYGDCLGDIAARD  IKQYGDCLG  0         0.1200
13645.4    90.00  0.35     Sequence
 HLA-DPA10201-DPB10501  841      KQYGDCLGDIAARDL  DCLGDIAAR  4         0.0920
18485.4    95.00  0.29     Sequence
 HLA-DPA10201-DPB10501  842      QYGDCLGDIAARDLI  DCLGDIAAR  3         0.0948
17931.7    95.00  0.28     Sequence
 HLA-DPA10201-DPB10501  843      YGDCLGDIAARDLIC  DCLGDIAAR  2         0.0973
17442.5    95.00  0.28     Sequence
 HLA-DPA10201-DPB10501  844      GDCLGDIAARDLICA  DIAARDLIC  5         0.1004
16865.6    95.00  0.21     Sequence
 HLA-DPA10201-DPB10501  845      DCLGDIAARDLICAQ  DIAARDLIC  4         0.1054
15975.8    90.00  0.24     Sequence
 HLA-DPA10201-DPB10501  846      CLGDIAARDLICAQK  DIAARDLIC  3         0.1215
13432.4    90.00  0.26     Sequence
 HLA-DPA10201-DPB10501  847      LGDIAARDLICAQKF  ARDLICAQK  5         0.1598
8873.0    75.00  0.38     Sequence
 HLA-DPA10201-DPB10501  848      GDIAARDLICAQKFN  ARDLICAQK  4         0.1998
5754.4    65.00  0.36     Sequence
 HLA-DPA10201-DPB10501  849      DIAARDLICAQKFNG  ARDLICAQK  3         0.2501
3341.0    47.00  0.26     Sequence
 HLA-DPA10201-DPB10501  850      IAARDLICAQKFNGL  LICAQKFNG  5         0.2970
2010.5    34.00  0.47     Sequence
 HLA-DPA10201-DPB10501  851      AARDLICAQKFNGLT  LICAQKFNG  4         0.3060
1823.5    32.00  0.49     Sequence
 HLA-DPA10201-DPB10501  852      ARDLICAQKFNGLTV  LICAQKFNG  3         0.3333
1357.4    26.00  0.45     Sequence
 HLA-DPA10201-DPB10501  853      RDLICAQKFNGLTVL  LICAQKFNG  2         0.3666
947.3    20.00  0.39     Sequence
 HLA-DPA10201-DPB10501  854      DLICAQKFNGLTVLP  AQKFNGLTV  4         0.3701
912.0    19.00  0.30     Sequence
 HLA-DPA10201-DPB10501  855      LICAQKFNGLTVLPP  AQKFNGLTV  3         0.3548
1075.6    22.00  0.34     Sequence
 HLA-DPA10201-DPB10501  856      ICAQKFNGLTVLPPL  AQKFNGLTV  2         0.3479
1159.9    23.00  0.38     Sequence
 HLA-DPA10201-DPB10501  857      CAQKFNGLTVLPPLL  AQKFNGLTV  1         0.3467
1174.8    23.00  0.31     Sequence
 HLA-DPA10201-DPB10501  858      AQKFNGLTVLPPLLT  AQKFNGLTV  0         0.3694
919.1    19.00  0.22     Sequence
 HLA-DPA10201-DPB10501  859      QKFNGLTVLPPLLTD  LTVLPPLLT  5         0.3382
1287.4    25.00  0.28     Sequence
 HLA-DPA10201-DPB10501  860      KFNGLTVLPPLLTDE  LTVLPPLLT  4         0.2804
2405.6    39.00  0.39     Sequence
 HLA-DPA10201-DPB10501  861      FNGLTVLPPLLTDEM  LTVLPPLLT  3         0.2329
4025.3    55.00  0.52     Sequence
 HLA-DPA10201-DPB10501  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2         0.2225
4501.7    60.00  0.55     Sequence
 HLA-DPA10201-DPB10501  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1         0.2287
4209.1    55.00  0.43     Sequence
 HLA-DPA10201-DPB10501  864      LTVLPPLLTDEMIAQ  PLLTDEMIA  5         0.2393
3754.3    55.00  0.28     Sequence
 HLA-DPA10201-DPB10501  865      TVLPPLLTDEMIAQY  PLLTDEMIA  4         0.2361
3886.9    55.00  0.33     Sequence
```

```
 HLA-DPA10201-DPB10501  866      VLPPLLTDEMIAQYT  PLLTDEMIA  3        0.2354
3916.3    55.00  0.37     Sequence
 HLA-DPA10201-DPB10501  867      LPPLLTDEMIAQYTS  PLLTDEMIA  2        0.2343
3963.4    55.00  0.38     Sequence
 HLA-DPA10201-DPB10501  868      PPLLTDEMIAQYTSA  PLLTDEMIA  1        0.2266
4306.5    55.00  0.34     Sequence
 HLA-DPA10201-DPB10501  869      PLLTDEMIAQYTSAL  LLTDEMIAQ  1        0.2066
5345.8    65.00  0.34     Sequence
 HLA-DPA10201-DPB10501  870      LLTDEMIAQYTSALL  IAQYTSALL  6        0.2243
4417.9    55.00  0.25     Sequence
 HLA-DPA10201-DPB10501  871      LTDEMIAQYTSALLA  IAQYTSALL  5        0.2528
3245.7    47.00  0.38     Sequence
 HLA-DPA10201-DPB10501  872      TDEMIAQYTSALLAG  IAQYTSALL  4        0.2811
2388.1    39.00  0.38     Sequence
 HLA-DPA10201-DPB10501  873      DEMIAQYTSALLAGT  IAQYTSALL  3        0.3185
1593.4    29.00  0.34     Sequence
 HLA-DPA10201-DPB10501  874      EMIAQYTSALLAGTI  IAQYTSALL  2        0.3486
1150.7    23.00  0.33     Sequence
 HLA-DPA10201-DPB10501  875      MIAQYTSALLAGTIT  AQYTSALLA  2        0.3481
1156.7    23.00  0.34     Sequence
 HLA-DPA10201-DPB10501  876      IAQYTSALLAGTITS  AQYTSALLA  1        0.3283
1433.1    27.00  0.32     Sequence
 HLA-DPA10201-DPB10501  877      AQYTSALLAGTITSG  QYTSALLAG  1        0.2672
2775.8    42.00  0.24     Sequence
 HLA-DPA10201-DPB10501  878      QYTSALLAGTITSGW  SALLAGTIT  3        0.2418
3655.2    50.00  0.25     Sequence
 HLA-DPA10201-DPB10501  879      YTSALLAGTITSGWT  ALLAGTITS  3        0.2319
4068.6    55.00  0.31     Sequence
 HLA-DPA10201-DPB10501  880      TSALLAGTITSGWTF  ALLAGTITS  2        0.2152
4874.8    60.00  0.33     Sequence
 HLA-DPA10201-DPB10501  881      SALLAGTITSGWTFG  ALLAGTITS  1        0.2011
5673.8    65.00  0.35     Sequence
 HLA-DPA10201-DPB10501  882      ALLAGTITSGWTFGA  ALLAGTITS  0        0.1696
7978.0    75.00  0.31     Sequence
 HLA-DPA10201-DPB10501  883      LLAGTITSGWTFGAG  LLAGTITSG  0        0.1108
15077.6    90.00  0.17     Sequence
 HLA-DPA10201-DPB10501  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.0936
18164.8    95.00  0.25     Sequence
 HLA-DPA10201-DPB10501  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.0884
19216.7    95.00  0.28     Sequence
 HLA-DPA10201-DPB10501  886      GTITSGWTFGAGAAL  ITSGWTFGA  2        0.0994
17064.0    95.00  0.25     Sequence
 HLA-DPA10201-DPB10501  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.1185
13874.0    90.00  0.19     Sequence
 HLA-DPA10201-DPB10501  888      ITSGWTFGAGAALQI  FGAGAALQI  6        0.1490
9969.5    80.00  0.29     Sequence
 HLA-DPA10201-DPB10501  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.1524
9607.7    80.00  0.36     Sequence
 HLA-DPA10201-DPB10501  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.1824
6950.8    70.00  0.39     Sequence
 HLA-DPA10201-DPB10501  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.1980
5866.5    65.00  0.35     Sequence
 HLA-DPA10201-DPB10501  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.2199
4632.3    60.00  0.31     Sequence
 HLA-DPA10201-DPB10501  893      TFGAGAALQIPFAMQ  FGAGAALQI  1        0.2174
4759.6    60.00  0.28     Sequence
 HLA-DPA10201-DPB10501  894      FGAGAALQIPFAMQM  AALQIPFAM  4        0.2171
4771.4    60.00  0.22     Sequence
 HLA-DPA10201-DPB10501  895      GAGAALQIPFAMQMA  AALQIPFAM  3        0.2248
4389.8    55.00  0.23     Sequence
 HLA-DPA10201-DPB10501  896      AGAALQIPFAMQMAY  LQIPFAMQM  4        0.2605
2985.9    44.00  0.27     Sequence
 HLA-DPA10201-DPB10501  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.2823
2356.9    38.00  0.25     Sequence
 HLA-DPA10201-DPB10501  898      AALQIPFAMQMAYRF  LQIPFAMQM  2        0.3286
1428.2    27.00  0.20     Sequence
```

```
 HLA-DPA10201-DPB10501  899      ALQIPFAMQMAYRFN  FAMQMAYRF  5        0.3478
1161.0    23.00  0.26     Sequence
 HLA-DPA10201-DPB10501  900      LQIPFAMQMAYRFNG  FAMQMAYRF  4        0.3521
1107.9    22.00  0.23     Sequence
 HLA-DPA10201-DPB10501  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.3450
1195.7    24.00  0.29     Sequence
 HLA-DPA10201-DPB10501  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.3195
1577.1    29.00  0.28     Sequence
 HLA-DPA10201-DPB10501  903      PFAMQMAYRFNGIGV  MQMAYRFNG  3        0.3048
1847.6    32.00  0.30     Sequence
 HLA-DPA10201-DPB10501  904      FAMQMAYRFNGIGVT  MQMAYRFNG  2        0.2952
2051.2    35.00  0.35     Sequence
 HLA-DPA10201-DPB10501  905      AMQMAYRFNGIGVTQ  MQMAYRFNG  1        0.2397
3739.6    50.00  0.38     Sequence
 HLA-DPA10201-DPB10501  906      MQMAYRFNGIGVTQN  MQMAYRFNG  0        0.1886
6494.6    70.00  0.27     Sequence
 HLA-DPA10201-DPB10501  907      QMAYRFNGIGVTQNV  YRFNGIGVT  3        0.1591
8937.2    75.00  0.20     Sequence
 HLA-DPA10201-DPB10501  908      MAYRFNGIGVTQNVL  YRFNGIGVT  2        0.1597
8881.5    75.00  0.22     Sequence
 HLA-DPA10201-DPB10501  909      AYRFNGIGVTQNVLY  YRFNGIGVT  1        0.1875
6571.7    70.00  0.17     Sequence
 HLA-DPA10201-DPB10501  910      YRFNGIGVTQNVLYE  IGVTQNVLY  5        0.1768
7378.7    70.00  0.19     Sequence
 HLA-DPA10201-DPB10501  911      RFNGIGVTQNVLYEN  IGVTQNVLY  4        0.1861
6674.6    70.00  0.22     Sequence
 HLA-DPA10201-DPB10501  912      FNGIGVTQNVLYENQ  IGVTQNVLY  3        0.1834
6876.0    70.00  0.24     Sequence
 HLA-DPA10201-DPB10501  913      NGIGVTQNVLYENQK  GVTQNVLYE  3        0.1886
6494.1    70.00  0.26     Sequence
 HLA-DPA10201-DPB10501  914      GIGVTQNVLYENQKL  QNVLYENQK  5        0.2237
4442.3    55.00  0.18     Sequence
 HLA-DPA10201-DPB10501  915      IGVTQNVLYENQKLI  NVLYENQKL  5        0.3024
1896.2    33.00  0.38     Sequence
 HLA-DPA10201-DPB10501  916      GVTQNVLYENQKLIA  NVLYENQKL  4        0.3416
1241.6    24.00  0.34     Sequence
 HLA-DPA10201-DPB10501  917      VTQNVLYENQKLIAN  NVLYENQKL  3        0.3539
1086.5    22.00  0.34     Sequence
 HLA-DPA10201-DPB10501  918      TQNVLYENQKLIANQ  NVLYENQKL  2        0.3566
1054.9    21.00  0.34     Sequence
 HLA-DPA10201-DPB10501  919      QNVLYENQKLIANQF  NVLYENQKL  1        0.3663
950.1    20.00  0.29     Sequence
 HLA-DPA10201-DPB10501  920      NVLYENQKLIANQFN  LYENQKLIA  2        0.3606
1010.4    21.00  0.32     Sequence
 HLA-DPA10201-DPB10501  921      VLYENQKLIANQFNS  LYENQKLIA  1        0.3625
990.3    20.00  0.22     Sequence
 HLA-DPA10201-DPB10501  922      LYENQKLIANQFNSA  KLIANQFNS  5        0.3731
882.4    18.00  0.40     Sequence
 HLA-DPA10201-DPB10501  923      YENQKLIANQFNSAI  KLIANQFNS  4        0.3979
674.7    15.00  0.41     Sequence
 HLA-DPA10201-DPB10501  924      ENQKLIANQFNSAIG  KLIANQFNS  3        0.4020
645.9    14.00  0.41     Sequence
 HLA-DPA10201-DPB10501  925      NQKLIANQFNSAIGK  KLIANQFNS  2        0.4068
612.8    13.00  0.40     Sequence
 HLA-DPA10201-DPB10501  926      QKLIANQFNSAIGKI  KLIANQFNS  1        0.3886
746.5    16.00  0.40     Sequence
 HLA-DPA10201-DPB10501  927      KLIANQFNSAIGKIQ  KLIANQFNS  0        0.3299
1408.2    27.00  0.35     Sequence
 HLA-DPA10201-DPB10501  928      LIANQFNSAIGKIQD  ANQFNSAIG  2        0.2506
3323.3    47.00  0.33     Sequence
 HLA-DPA10201-DPB10501  929      IANQFNSAIGKIQDS  ANQFNSAIG  1        0.1984
5843.7    65.00  0.31     Sequence
 HLA-DPA10201-DPB10501  930      ANQFNSAIGKIQDSL  QFNSAIGKI  2        0.1906
6361.5    70.00  0.26     Sequence
 HLA-DPA10201-DPB10501  931      NQFNSAIGKIQDSLS  IGKIQDSLS  6        0.1922
6246.2    65.00  0.24     Sequence
```

```
 HLA-DPA10201-DPB10501  932      QFNSAIGKIQDSLSS  IGKIQDSLS  5        0.2118
5057.2    60.00  0.32     Sequence
 HLA-DPA10201-DPB10501  933      FNSAIGKIQDSLSST  GKIQDSLSS  5        0.2352
3922.8    55.00  0.38     Sequence
 HLA-DPA10201-DPB10501  934      NSAIGKIQDSLSSTA  GKIQDSLSS  4        0.2478
3423.0    48.00  0.44     Sequence
 HLA-DPA10201-DPB10501  935      SAIGKIQDSLSSTAS  GKIQDSLSS  3        0.2550
3167.5    46.00  0.45     Sequence
 HLA-DPA10201-DPB10501  936      AIGKIQDSLSSTASA  GKIQDSLSS  2        0.2496
3359.3    48.00  0.46     Sequence
 HLA-DPA10201-DPB10501  937      IGKIQDSLSSTASAL  GKIQDSLSS  1        0.2202
4618.4    60.00  0.46     Sequence
 HLA-DPA10201-DPB10501  938      GKIQDSLSSTASALG  GKIQDSLSS  0        0.1644
8441.2    75.00  0.40     Sequence
 HLA-DPA10201-DPB10501  939      KIQDSLSSTASALGK  LSSTASALG  5        0.1327
11899.4    85.00  0.20     Sequence
 HLA-DPA10201-DPB10501  940      IQDSLSSTASALGKL  SSTASALGK  5        0.1243
13026.9    85.00  0.29     Sequence
 HLA-DPA10201-DPB10501  941      QDSLSSTASALGKLQ  SSTASALGK  4        0.1326
11905.1    85.00  0.32     Sequence
 HLA-DPA10201-DPB10501  942      DSLSSTASALGKLQD  SSTASALGK  3        0.1324
11938.9    85.00  0.32     Sequence
 HLA-DPA10201-DPB10501  943      SLSSTASALGKLQDV  SSTASALGK  2        0.1420
10762.5    80.00  0.31     Sequence
 HLA-DPA10201-DPB10501  944      LSSTASALGKLQDVV  ASALGKLQD  4        0.1455
10354.9    80.00  0.28     Sequence
 HLA-DPA10201-DPB10501  945      SSTASALGKLQDVVN  ASALGKLQD  3        0.1730
7688.5    75.00  0.25     Sequence
 HLA-DPA10201-DPB10501  946      STASALGKLQDVVNQ  LGKLQDVVN  5        0.1893
6446.7    70.00  0.28     Sequence
 HLA-DPA10201-DPB10501  947      TASALGKLQDVVNQN  LGKLQDVVN  4        0.2013
5666.2    65.00  0.28     Sequence
 HLA-DPA10201-DPB10501  948      ASALGKLQDVVNQNA  GKLQDVVNQ  4        0.2109
5102.0    60.00  0.36     Sequence
 HLA-DPA10201-DPB10501  949      SALGKLQDVVNQNAQ  GKLQDVVNQ  3        0.2137
4951.9    60.00  0.38     Sequence
 HLA-DPA10201-DPB10501  950      ALGKLQDVVNQNAQA  GKLQDVVNQ  2        0.2055
5411.9    65.00  0.40     Sequence
 HLA-DPA10201-DPB10501  951      LGKLQDVVNQNAQAL  GKLQDVVNQ  1        0.1787
7228.3    70.00  0.42     Sequence
 HLA-DPA10201-DPB10501  952      GKLQDVVNQNAQALN  GKLQDVVNQ  0        0.1228
13237.6    85.00  0.32     Sequence
 HLA-DPA10201-DPB10501  953      KLQDVVNQNAQALNT  LQDVVNQNA  1        0.0991
17105.2    95.00  0.20     Sequence
 HLA-DPA10201-DPB10501  954      LQDVVNQNAQALNTL  NQNAQALNT  5        0.0817
20666.0    95.00  0.22     Sequence
 HLA-DPA10201-DPB10501  955      QDVVNQNAQALNTLV  NQNAQALNT  4        0.0898
18928.0    95.00  0.26     Sequence
 HLA-DPA10201-DPB10501  956      DVVNQNAQALNTLVK  AQALNTLVK  6        0.1835
6866.8    70.00  0.44     Sequence
 HLA-DPA10201-DPB10501  957      VVNQNAQALNTLVKQ  AQALNTLVK  5        0.2571
3097.3    45.00  0.62     Sequence
 HLA-DPA10201-DPB10501  958      VNQNAQALNTLVKQL  AQALNTLVK  4        0.3063
1818.9    32.00  0.61     Sequence
 HLA-DPA10201-DPB10501  959      NQNAQALNTLVKQLS  AQALNTLVK  3        0.3241
1499.1    28.00  0.56     Sequence
 HLA-DPA10201-DPB10501  960      QNAQALNTLVKQLSS  AQALNTLVK  2        0.3271
1451.4    27.00  0.56     Sequence
 HLA-DPA10201-DPB10501  961      NAQALNTLVKQLSSN  AQALNTLVK  1        0.3147
1660.9    30.00  0.53     Sequence
 HLA-DPA10201-DPB10501  962      AQALNTLVKQLSSNF  AQALNTLVK  0        0.3050
1843.9    32.00  0.47     Sequence
 HLA-DPA10201-DPB10501  963      QALNTLVKQLSSNFG  LNTLVKQLS  2        0.2418
3652.8    50.00  0.23     Sequence
 HLA-DPA10201-DPB10501  964      ALNTLVKQLSSNFGA  VKQLSSNFG  5        0.2287
4209.6    55.00  0.22     Sequence
```

```
 HLA-DPA10201-DPB10501  965      LNTLVKQLSSNFGAI  VKQLSSNFG  4        0.2499
3348.6    47.00  0.25     Sequence
 HLA-DPA10201-DPB10501  966      NTLVKQLSSNFGAIS  VKQLSSNFG  3        0.2480
3416.1    48.00  0.31     Sequence
 HLA-DPA10201-DPB10501  967      TLVKQLSSNFGAISS  VKQLSSNFG  2        0.2514
3293.9    47.00  0.30     Sequence
 HLA-DPA10201-DPB10501  968      LVKQLSSNFGAISSV  KQLSSNFGA  2        0.2452
3520.5    49.00  0.32     Sequence
 HLA-DPA10201-DPB10501  969      VKQLSSNFGAISSVL  KQLSSNFGA  1        0.2113
5080.5    60.00  0.33     Sequence
 HLA-DPA10201-DPB10501  970      KQLSSNFGAISSVLN  FGAISSVLN  6        0.1859
6688.5    70.00  0.22     Sequence
 HLA-DPA10201-DPB10501  971      QLSSNFGAISSVLND  FGAISSVLN  5        0.1703
7920.9    75.00  0.37     Sequence
 HLA-DPA10201-DPB10501  972      LSSNFGAISSVLNDI  FGAISSVLN  4        0.1775
7324.4    70.00  0.41     Sequence
 HLA-DPA10201-DPB10501  973      SSNFGAISSVLNDIL  FGAISSVLN  3        0.1940
6130.9    65.00  0.40     Sequence
 HLA-DPA10201-DPB10501  974      SNFGAISSVLNDILS  FGAISSVLN  2        0.2129
4996.8    60.00  0.31     Sequence
 HLA-DPA10201-DPB10501  975      NFGAISSVLNDILSR  FGAISSVLN  1        0.2321
4057.2    55.00  0.26     Sequence
 HLA-DPA10201-DPB10501  976      FGAISSVLNDILSRL  SSVLNDILS  4        0.2564
3121.3    46.00  0.26     Sequence
 HLA-DPA10201-DPB10501  977      GAISSVLNDILSRLD  SSVLNDILS  3        0.2324
4045.5    55.00  0.35     Sequence
 HLA-DPA10201-DPB10501  978      AISSVLNDILSRLDK  SSVLNDILS  2        0.2440
3566.2    49.00  0.36     Sequence
 HLA-DPA10201-DPB10501  979      ISSVLNDILSRLDKV  SSVLNDILS  1        0.2591
3030.5    45.00  0.30     Sequence
 HLA-DPA10201-DPB10501  980      SSVLNDILSRLDKVE  SSVLNDILS  0        0.2444
3552.8    49.00  0.25     Sequence
 HLA-DPA10201-DPB10501  981      SVLNDILSRLDKVEA  NDILSRLDK  3        0.2377
3819.9    55.00  0.20     Sequence
 HLA-DPA10201-DPB10501  982      VLNDILSRLDKVEAE  LSRLDKVEA  5        0.2293
4180.9    55.00  0.28     Sequence
 HLA-DPA10201-DPB10501  983      LNDILSRLDKVEAEV  LSRLDKVEA  4        0.2181
4724.3    60.00  0.36     Sequence
 HLA-DPA10201-DPB10501  984      NDILSRLDKVEAEVQ  LSRLDKVEA  3        0.2141
4928.9    60.00  0.40     Sequence
 HLA-DPA10201-DPB10501  985      DILSRLDKVEAEVQI  LSRLDKVEA  2        0.2114
5076.8    60.00  0.37     Sequence
 HLA-DPA10201-DPB10501  986      ILSRLDKVEAEVQID  LSRLDKVEA  1        0.1894
6444.0    70.00  0.38     Sequence
 HLA-DPA10201-DPB10501  987      LSRLDKVEAEVQIDR  LDKVEAEVQ  3        0.1620
8664.4    75.00  0.24     Sequence
 HLA-DPA10201-DPB10501  988      SRLDKVEAEVQIDRL  LDKVEAEVQ  2        0.1523
9619.7    80.00  0.31     Sequence
 HLA-DPA10201-DPB10501  989      RLDKVEAEVQIDRLI  LDKVEAEVQ  1        0.1760
7445.0    70.00  0.25     Sequence
 HLA-DPA10201-DPB10501  990      LDKVEAEVQIDRLIT  EVQIDRLIT  6        0.1852
6742.1    70.00  0.27     Sequence
 HLA-DPA10201-DPB10501  991      DKVEAEVQIDRLITG  EVQIDRLIT  5        0.1956
6024.0    65.00  0.50     Sequence
 HLA-DPA10201-DPB10501  992      KVEAEVQIDRLITGR  EVQIDRLIT  4        0.2209
4580.8    60.00  0.54     Sequence
 HLA-DPA10201-DPB10501  993      VEAEVQIDRLITGRL  EVQIDRLIT  3        0.2529
3241.5    47.00  0.51     Sequence
 HLA-DPA10201-DPB10501  994      EAEVQIDRLITGRLQ  EVQIDRLIT  2        0.2672
2776.4    42.00  0.47     Sequence
 HLA-DPA10201-DPB10501  995      AEVQIDRLITGRLQS  EVQIDRLIT  1        0.2898
2174.5    36.00  0.32     Sequence
 HLA-DPA10201-DPB10501  996      EVQIDRLITGRLQSL  RLITGRLQS  5        0.3092
1762.1    31.00  0.32     Sequence
 HLA-DPA10201-DPB10501  997      VQIDRLITGRLQSLQ  RLITGRLQS  4        0.3024
1896.2    33.00  0.36     Sequence
```

```
 HLA-DPA10201-DPB10501  998      QIDRLITGRLQSLQT  RLITGRLQS  3        0.2925
2110.7    36.00  0.41     Sequence
 HLA-DPA10201-DPB10501  999      IDRLITGRLQSLQTY  RLITGRLQS  2        0.2809
2393.8    39.00  0.40     Sequence
 HLA-DPA10201-DPB10501 1000      DRLITGRLQSLQTYV  RLITGRLQS  1        0.2574
3087.5    45.00  0.40     Sequence
 HLA-DPA10201-DPB10501 1001      RLITGRLQSLQTYVT  RLITGRLQS  0        0.2818
2370.2    38.00  0.25     Sequence
 HLA-DPA10201-DPB10501 1002      LITGRLQSLQTYVTQ  LQSLQTYVT  5        0.2804
2406.1    39.00  0.42     Sequence
 HLA-DPA10201-DPB10501 1003      ITGRLQSLQTYVTQQ  LQSLQTYVT  4        0.2913
2139.4    36.00  0.41     Sequence
 HLA-DPA10201-DPB10501 1004      TGRLQSLQTYVTQQL  LQSLQTYVT  3        0.3103
1741.9    31.00  0.39     Sequence
 HLA-DPA10201-DPB10501 1005      GRLQSLQTYVTQQLI  LQSLQTYVT  2        0.3233
1512.2    28.00  0.35     Sequence
 HLA-DPA10201-DPB10501 1006      RLQSLQTYVTQQLIR  LQSLQTYVT  1        0.3474
1165.0    23.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1007      LQSLQTYVTQQLIRA  TYVTQQLIR  5        0.3485
1151.9    23.00  0.25     Sequence
 HLA-DPA10201-DPB10501 1008      QSLQTYVTQQLIRAA  TYVTQQLIR  4        0.3415
1242.6    24.00  0.34     Sequence
 HLA-DPA10201-DPB10501 1009      SLQTYVTQQLIRAAE  TYVTQQLIR  3        0.3441
1208.5    24.00  0.35     Sequence
 HLA-DPA10201-DPB10501 1010      LQTYVTQQLIRAAEI  TYVTQQLIR  2        0.3321
1375.9    26.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1011      QTYVTQQLIRAAEIR  YVTQQLIRA  2        0.3244
1494.7    28.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1012      TYVTQQLIRAAEIRA  LIRAAEIRA  6        0.3629
986.0    20.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1013      YVTQQLIRAAEIRAS  LIRAAEIRA  5        0.3674
939.0    19.00  0.50     Sequence
 HLA-DPA10201-DPB10501 1014      VTQQLIRAAEIRASA  LIRAAEIRA  4        0.3792
826.0    17.00  0.52     Sequence
 HLA-DPA10201-DPB10501 1015      TQQLIRAAEIRASAN  LIRAAEIRA  3        0.3829
794.1    17.00  0.53     Sequence
 HLA-DPA10201-DPB10501 1016      QQLIRAAEIRASANL  LIRAAEIRA  2        0.3811
809.3    17.00  0.54     Sequence
 HLA-DPA10201-DPB10501 1017      QLIRAAEIRASANLA  LIRAAEIRA  1        0.3674
938.8    19.00  0.52     Sequence
 HLA-DPA10201-DPB10501 1018      LIRAAEIRASANLAA  LIRAAEIRA  0        0.3204
1560.4    29.00  0.34     Sequence
 HLA-DPA10201-DPB10501 1019      IRAAEIRASANLAAI  IRASANLAA  5        0.3108
1731.1    31.00  0.49     Sequence
 HLA-DPA10201-DPB10501 1020      RAAEIRASANLAAIK  IRASANLAA  4        0.3472
1168.5    23.00  0.54     Sequence
 HLA-DPA10201-DPB10501 1021      AAEIRASANLAAIKM  IRASANLAA  3        0.3661
951.9    20.00  0.52     Sequence
 HLA-DPA10201-DPB10501 1022      AEIRASANLAAIKMS  IRASANLAA  2        0.3753
861.9    18.00  0.51     Sequence
 HLA-DPA10201-DPB10501 1023      EIRASANLAAIKMSE  IRASANLAA  1        0.3593
1025.2    21.00  0.49     Sequence
 HLA-DPA10201-DPB10501 1024      IRASANLAAIKMSEC  IRASANLAA  0        0.2994
1958.5    34.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1025      RASANLAAIKMSECV  SANLAAIKM  2        0.2543
3192.7    46.00  0.27     Sequence
 HLA-DPA10201-DPB10501 1026      ASANLAAIKMSECVL  SANLAAIKM  1        0.2859
2266.5    37.00  0.19     Sequence
 HLA-DPA10201-DPB10501 1027      SANLAAIKMSECVLG  IKMSECVLG  6        0.3551
1072.1    22.00  0.30     Sequence
 HLA-DPA10201-DPB10501 1028      ANLAAIKMSECVLGQ  IKMSECVLG  5        0.3961
688.2    15.00  0.45     Sequence
 HLA-DPA10201-DPB10501 1029      NLAAIKMSECVLGQS  IKMSECVLG  4        0.4176
545.4    12.00  0.49     Sequence
 HLA-DPA10201-DPB10501 1030      LAAIKMSECVLGQSK  IKMSECVLG  3        0.4380
437.2     9.50  0.48     Sequence          WB
```

```
 HLA-DPA10201-DPB10501 1031      AAIKMSECVLGQSKR  IKMSECVLG  2        0.4428
415.1     9.00  0.51     Sequence         WB
 HLA-DPA10201-DPB10501 1032      AIKMSECVLGQSKRV  IKMSECVLG  1        0.4385
435.1     9.50  0.50     Sequence         WB
 HLA-DPA10201-DPB10501 1033      IKMSECVLGQSKRVD  IKMSECVLG  0        0.3452
1193.7    24.00  0.40     Sequence
 HLA-DPA10201-DPB10501 1034      KMSECVLGQSKRVDF  ECVLGQSKR  3        0.2432
3599.0    49.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1035      MSECVLGQSKRVDFC  ECVLGQSKR  2        0.1954
6036.5    65.00  0.44     Sequence
 HLA-DPA10201-DPB10501 1036      SECVLGQSKRVDFCG  ECVLGQSKR  1        0.1856
6714.4    70.00  0.45     Sequence
 HLA-DPA10201-DPB10501 1037      ECVLGQSKRVDFCGK  ECVLGQSKR  0        0.1760
7445.2    70.00  0.34     Sequence
 HLA-DPA10201-DPB10501 1038      CVLGQSKRVDFCGKG  SKRVDFCGK  5        0.1490
9970.7    80.00  0.20     Sequence
 HLA-DPA10201-DPB10501 1039      VLGQSKRVDFCGKGY  SKRVDFCGK  4        0.1220
13354.0    90.00  0.27     Sequence
 HLA-DPA10201-DPB10501 1040      LGQSKRVDFCGKGYH  SKRVDFCGK  3        0.1316
12034.7    85.00  0.30     Sequence
 HLA-DPA10201-DPB10501 1041      GQSKRVDFCGKGYHL  SKRVDFCGK  2        0.1398
11021.5    85.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1042      QSKRVDFCGKGYHLM  SKRVDFCGK  1        0.1593
8917.4    75.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1043      SKRVDFCGKGYHLMS  DFCGKGYHL  4        0.1802
7115.9    70.00  0.23     Sequence
 HLA-DPA10201-DPB10501 1044      KRVDFCGKGYHLMSF  CGKGYHLMS  5        0.1998
5753.5    65.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1045      RVDFCGKGYHLMSFP  CGKGYHLMS  4        0.2131
4983.2    60.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1046      VDFCGKGYHLMSFPQ  CGKGYHLMS  3        0.2350
3933.5    55.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1047      DFCGKGYHLMSFPQS  GKGYHLMSF  3        0.2491
3375.8    48.00  0.25     Sequence
 HLA-DPA10201-DPB10501 1048      FCGKGYHLMSFPQSA  GKGYHLMSF  2        0.2608
2973.7    44.00  0.23     Sequence
 HLA-DPA10201-DPB10501 1049      CGKGYHLMSFPQSAP  GKGYHLMSF  1        0.2473
3443.7    48.00  0.19     Sequence
 HLA-DPA10201-DPB10501 1050      GKGYHLMSFPQSAPH  YHLMSFPQS  3        0.2324
4043.3    55.00  0.24     Sequence
 HLA-DPA10201-DPB10501 1051      KGYHLMSFPQSAPHG  YHLMSFPQS  2        0.2153
4866.4    60.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1052      GYHLMSFPQSAPHGV  YHLMSFPQS  1        0.1747
7548.1    70.00  0.30     Sequence
 HLA-DPA10201-DPB10501 1053      YHLMSFPQSAPHGVV  LMSFPQSAP  2        0.1415
10818.7    80.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1054      HLMSFPQSAPHGVVF  LMSFPQSAP  1        0.1125
14806.7    90.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1055      LMSFPQSAPHGVVFL  LMSFPQSAP  0        0.1040
16219.9    90.00  0.23     Sequence
 HLA-DPA10201-DPB10501 1056      MSFPQSAPHGVVFLH  APHGVVFLH  6        0.1262
12757.8    85.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1057      SFPQSAPHGVVFLHV  APHGVVFLH  5        0.1557
9277.4    80.00  0.46     Sequence
 HLA-DPA10201-DPB10501 1058      FPQSAPHGVVFLHVT  APHGVVFLH  4        0.1690
8032.3    75.00  0.44     Sequence
 HLA-DPA10201-DPB10501 1059      PQSAPHGVVFLHVTY  APHGVVFLH  3        0.1835
6864.9    70.00  0.40     Sequence
 HLA-DPA10201-DPB10501 1060      QSAPHGVVFLHVTYV  APHGVVFLH  2        0.1913
6309.0    65.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1061      SAPHGVVFLHVTYVP  APHGVVFLH  1        0.1953
6042.7    65.00  0.32     Sequence
 HLA-DPA10201-DPB10501 1062      APHGVVFLHVTYVPA  APHGVVFLH  0        0.2013
5661.4    65.00  0.19     Sequence
 HLA-DPA10201-DPB10501 1063      PHGVVFLHVTYVPAQ  VFLHVTYVP  4        0.1829
6908.2    70.00  0.23     Sequence
```

```
 HLA-DPA10201-DPB10501 1064      HGVVFLHVTYVPAQE  VFLHVTYVP  3        0.1908
6341.5    65.00  0.21     Sequence
 HLA-DPA10201-DPB10501 1065      GVVFLHVTYVPAQEK  HVTYVPAQE  5        0.2062
5373.4    65.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1066      VVFLHVTYVPAQEKN  HVTYVPAQE  4        0.2149
4890.8    60.00  0.25     Sequence
 HLA-DPA10201-DPB10501 1067      VFLHVTYVPAQEKNF  HVTYVPAQE  3        0.2501
3341.5    47.00  0.25     Sequence
 HLA-DPA10201-DPB10501 1068      FLHVTYVPAQEKNFT  HVTYVPAQE  2        0.2498
3352.6    47.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1069      LHVTYVPAQEKNFTT  HVTYVPAQE  1        0.2243
4418.0    55.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1070      HVTYVPAQEKNFTTA  TYVPAQEKN  2        0.2025
5590.8    65.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1071      VTYVPAQEKNFTTAP  TYVPAQEKN  1        0.1875
6578.4    70.00  0.24     Sequence
 HLA-DPA10201-DPB10501 1072      TYVPAQEKNFTTAPA  TYVPAQEKN  0        0.1692
8015.1    75.00  0.20     Sequence
 HLA-DPA10201-DPB10501 1073      YVPAQEKNFTTAPAI  EKNFTTAPA  5        0.1791
7198.4    70.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1074      VPAQEKNFTTAPAIC  EKNFTTAPA  4        0.1882
6524.0    70.00  0.42     Sequence
 HLA-DPA10201-DPB10501 1075      PAQEKNFTTAPAICH  EKNFTTAPA  3        0.2054
5419.6    65.00  0.44     Sequence
 HLA-DPA10201-DPB10501 1076      AQEKNFTTAPAICHD  EKNFTTAPA  2        0.2069
5327.7    60.00  0.41     Sequence
 HLA-DPA10201-DPB10501 1077      QEKNFTTAPAICHDG  EKNFTTAPA  1        0.2031
5555.1    65.00  0.41     Sequence
 HLA-DPA10201-DPB10501 1078      EKNFTTAPAICHDGK  EKNFTTAPA  0        0.1796
7165.1    70.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1079      KNFTTAPAICHDGKA  NFTTAPAIC  1        0.1500
9868.8    80.00  0.32     Sequence
 HLA-DPA10201-DPB10501 1080      NFTTAPAICHDGKAH  NFTTAPAIC  0        0.0929
18291.4    95.00  0.33     Sequence
 HLA-DPA10201-DPB10501 1081      FTTAPAICHDGKAHF  ICHDGKAHF  6        0.0904
18798.5    95.00  0.19     Sequence
 HLA-DPA10201-DPB10501 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.0776
21596.6    95.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1083      TAPAICHDGKAHFPR  ICHDGKAHF  4        0.0892
19050.3    95.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1084      APAICHDGKAHFPRE  ICHDGKAHF  3        0.0917
18546.7    95.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1085      PAICHDGKAHFPREG  ICHDGKAHF  2        0.0871
19480.1    95.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1086      AICHDGKAHFPREGV  ICHDGKAHF  1        0.0924
18406.0    95.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1087      ICHDGKAHFPREGVF  GKAHFPREG  4        0.0847
20001.9    95.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1088      CHDGKAHFPREGVFV  GKAHFPREG  3        0.0815
20697.6    95.00  0.24     Sequence
 HLA-DPA10201-DPB10501 1089      HDGKAHFPREGVFVS  FPREGVFVS  6        0.1670
8212.5    75.00  0.43     Sequence
 HLA-DPA10201-DPB10501 1090      DGKAHFPREGVFVSN  FPREGVFVS  5        0.2151
4880.4    60.00  0.54     Sequence
 HLA-DPA10201-DPB10501 1091      GKAHFPREGVFVSNG  FPREGVFVS  4        0.2293
4184.9    55.00  0.54     Sequence
 HLA-DPA10201-DPB10501 1092      KAHFPREGVFVSNGT  FPREGVFVS  3        0.2430
3606.9    49.00  0.51     Sequence
 HLA-DPA10201-DPB10501 1093      AHFPREGVFVSNGTH  FPREGVFVS  2        0.2346
3948.4    55.00  0.49     Sequence
 HLA-DPA10201-DPB10501 1094      HFPREGVFVSNGTHW  FPREGVFVS  1        0.2396
3741.9    50.00  0.46     Sequence
 HLA-DPA10201-DPB10501 1095      FPREGVFVSNGTHWF  FPREGVFVS  0        0.2388
3775.0    55.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1096      PREGVFVSNGTHWFV  VFVSNGTHW  4        0.1883
6520.7    70.00  0.34     Sequence
```

```
 HLA-DPA10201-DPB10501 1097      REGVFVSNGTHWFVT  VFVSNGTHW  3        0.1898
6412.1    70.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1098      EGVFVSNGTHWFVTQ  VFVSNGTHW  2        0.1869
6614.7    70.00  0.37     Sequence
 HLA-DPA10201-DPB10501 1099      GVFVSNGTHWFVTQR  VFVSNGTHW  1        0.1988
5816.7    65.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1100      VFVSNGTHWFVTQRN  VFVSNGTHW  0        0.1920
6265.4    65.00  0.20     Sequence
 HLA-DPA10201-DPB10501 1101      FVSNGTHWFVTQRNF  THWFVTQRN  5        0.2071
5318.8    60.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1102      VSNGTHWFVTQRNFY  THWFVTQRN  4        0.2407
3699.6    50.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1103      SNGTHWFVTQRNFYE  FVTQRNFYE  6        0.2931
2097.6    35.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1104      NGTHWFVTQRNFYEP  FVTQRNFYE  5        0.3119
1712.3    31.00  0.30     Sequence
 HLA-DPA10201-DPB10501 1105      GTHWFVTQRNFYEPQ  FVTQRNFYE  4        0.3155
1645.8    30.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3        0.3144
1665.2    30.00  0.32     Sequence
 HLA-DPA10201-DPB10501 1107      HWFVTQRNFYEPQII  FVTQRNFYE  2        0.3333
1357.9    26.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1108      WFVTQRNFYEPQIIT  FVTQRNFYE  1        0.3286
1429.3    27.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1109      FVTQRNFYEPQIITT  RNFYEPQII  4        0.3271
1452.0    27.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1110      VTQRNFYEPQIITTD  RNFYEPQII  3        0.2729
2610.1    41.00  0.32     Sequence
 HLA-DPA10201-DPB10501 1111      TQRNFYEPQIITTDN  RNFYEPQII  2        0.2722
2628.4    41.00  0.34     Sequence
 HLA-DPA10201-DPB10501 1112      QRNFYEPQIITTDNT  RNFYEPQII  1        0.2637
2881.8    43.00  0.34     Sequence
 HLA-DPA10201-DPB10501 1113      RNFYEPQIITTDNTF  NFYEPQIIT  1        0.2201
4618.8    60.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1114      NFYEPQIITTDNTFV  NFYEPQIIT  0        0.1872
6598.4    70.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1115      FYEPQIITTDNTFVS  IITTDNTFV  5        0.1822
6959.6    70.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1116      YEPQIITTDNTFVSG  ITTDNTFVS  5        0.1725
7734.4    75.00  0.34     Sequence
 HLA-DPA10201-DPB10501 1117      EPQIITTDNTFVSGN  ITTDNTFVS  4        0.1735
7646.9    75.00  0.37     Sequence
 HLA-DPA10201-DPB10501 1118      PQIITTDNTFVSGNC  ITTDNTFVS  3        0.1793
7182.8    70.00  0.37     Sequence
 HLA-DPA10201-DPB10501 1119      QIITTDNTFVSGNCD  ITTDNTFVS  2        0.1729
7701.7    75.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.1365
11414.5    85.00  0.41     Sequence
 HLA-DPA10201-DPB10501 1121      ITTDNTFVSGNCDVV  ITTDNTFVS  0        0.1081
15526.1    90.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1122      TTDNTFVSGNCDVVI  DNTFVSGNC  2        0.0931
18253.9    95.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1123      TDNTFVSGNCDVVIG  DNTFVSGNC  1        0.0927
18347.3    95.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1124      DNTFVSGNCDVVIGI  DNTFVSGNC  0        0.1010
16763.0    95.00  0.21     Sequence
 HLA-DPA10201-DPB10501 1125      NTFVSGNCDVVIGIV  SGNCDVVIG  4        0.1088
15412.0    90.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1126      TFVSGNCDVVIGIVN  SGNCDVVIG  3        0.1098
15240.0    90.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1127      FVSGNCDVVIGIVNN  CDVVIGIVN  5        0.1145
14484.4    90.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1128      VSGNCDVVIGIVNNT  CDVVIGIVN  4        0.1282
12490.1    85.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1129      SGNCDVVIGIVNNTV  CDVVIGIVN  3        0.1446
10459.0    80.00  0.25     Sequence
```

```
 HLA-DPA10201-DPB10501 1130      GNCDVVIGIVNNTVY  DVVIGIVNN  3        0.1608
8778.9    75.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1131      NCDVVIGIVNNTVYD  DVVIGIVNN  2        0.1640
8475.6    75.00  0.23     Sequence
 HLA-DPA10201-DPB10501 1132      CDVVIGIVNNTVYDP  DVVIGIVNN  1        0.1615
8714.1    75.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1133      DVVIGIVNNTVYDPL  IVNNTVYDP  5        0.1631
8557.5    75.00  0.21     Sequence
 HLA-DPA10201-DPB10501 1134      VVIGIVNNTVYDPLQ  IVNNTVYDP  4        0.1656
8335.5    75.00  0.23     Sequence
 HLA-DPA10201-DPB10501 1135      VIGIVNNTVYDPLQP  IVNNTVYDP  3        0.1652
8368.0    75.00  0.25     Sequence
 HLA-DPA10201-DPB10501 1136      IGIVNNTVYDPLQPE  NTVYDPLQP  5        0.1563
9212.6    80.00  0.35     Sequence
 HLA-DPA10201-DPB10501 1137      GIVNNTVYDPLQPEL  NTVYDPLQP  4        0.1659
8305.7    75.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1138      IVNNTVYDPLQPELD  NTVYDPLQP  3        0.1656
8330.8    75.00  0.41     Sequence
 HLA-DPA10201-DPB10501 1139      VNNTVYDPLQPELDS  NTVYDPLQP  2        0.1566
9187.9    80.00  0.44     Sequence
 HLA-DPA10201-DPB10501 1140      NNTVYDPLQPELDSF  NTVYDPLQP  1        0.1618
8679.7    75.00  0.35     Sequence
 HLA-DPA10201-DPB10501 1141      NTVYDPLQPELDSFK  NTVYDPLQP  0        0.1715
7815.2    75.00  0.23     Sequence
 HLA-DPA10201-DPB10501 1142      TVYDPLQPELDSFKE  QPELDSFKE  6        0.2117
5062.9    60.00  0.34     Sequence
 HLA-DPA10201-DPB10501 1143      VYDPLQPELDSFKEE  QPELDSFKE  5        0.2142
4927.7    60.00  0.41     Sequence
 HLA-DPA10201-DPB10501 1144      YDPLQPELDSFKEEL  QPELDSFKE  4        0.2133
4972.1    60.00  0.46     Sequence
 HLA-DPA10201-DPB10501 1145      DPLQPELDSFKEELD  QPELDSFKE  3        0.2079
5275.5    60.00  0.47     Sequence
 HLA-DPA10201-DPB10501 1146      PLQPELDSFKEELDK  QPELDSFKE  2        0.2147
4896.7    60.00  0.47     Sequence
 HLA-DPA10201-DPB10501 1147      LQPELDSFKEELDKY  QPELDSFKE  1        0.2397
3737.2    50.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1148      QPELDSFKEELDKYF  DSFKEELDK  4        0.2751
2549.0    40.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1149      PELDSFKEELDKYFK  KEELDKYFK  6        0.3317
1382.0    26.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1150      ELDSFKEELDKYFKN  KEELDKYFK  5        0.3793
825.7    17.00  0.37     Sequence
 HLA-DPA10201-DPB10501 1151      LDSFKEELDKYFKNH  KEELDKYFK  4        0.3912
725.8    16.00  0.40     Sequence
 HLA-DPA10201-DPB10501 1152      DSFKEELDKYFKNHT  KEELDKYFK  3        0.4006
655.7    14.00  0.41     Sequence
 HLA-DPA10201-DPB10501 1153      SFKEELDKYFKNHTS  KEELDKYFK  2        0.4018
646.8    14.00  0.41     Sequence
 HLA-DPA10201-DPB10501 1154      FKEELDKYFKNHTSP  KEELDKYFK  1        0.3530
1097.0    22.00  0.45     Sequence
 HLA-DPA10201-DPB10501 1155      KEELDKYFKNHTSPD  KEELDKYFK  0        0.2826
2349.9    38.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1156      EELDKYFKNHTSPDV  EELDKYFKN  0        0.1821
6968.3    70.00  0.34     Sequence
 HLA-DPA10201-DPB10501 1157      ELDKYFKNHTSPDVD  LDKYFKNHT  1        0.1309
12129.5    85.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1158      LDKYFKNHTSPDVDL  DKYFKNHTS  1        0.1015
16676.3    95.00  0.32     Sequence
 HLA-DPA10201-DPB10501 1159      DKYFKNHTSPDVDLG  DKYFKNHTS  0        0.0753
22141.5   100.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1160      KYFKNHTSPDVDLGD  FKNHTSPDV  2        0.0698
23486.5   100.00  0.23     Sequence
 HLA-DPA10201-DPB10501 1161      YFKNHTSPDVDLGDI  FKNHTSPDV  1        0.0534
28050.6   100.00  0.27     Sequence
 HLA-DPA10201-DPB10501 1162      FKNHTSPDVDLGDIS  KNHTSPDVD  1        0.0432
31334.8   100.00  0.22     Sequence
```

```
 HLA-DPA10201-DPB10501 1163      KNHTSPDVDLGDISG  HTSPDVDLG  2        0.0306
35897.9   100.00  0.17     Sequence
 HLA-DPA10201-DPB10501 1164      NHTSPDVDLGDISGI  DVDLGDISG  5        0.0343
34489.5   100.00  0.20     Sequence
 HLA-DPA10201-DPB10501 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.0385
32972.6   100.00  0.21     Sequence
 HLA-DPA10201-DPB10501 1166      TSPDVDLGDISGINA  LGDISGINA  6        0.0418
31817.8   100.00  0.18     Sequence
 HLA-DPA10201-DPB10501 1167      SPDVDLGDISGINAS  LGDISGINA  5        0.0454
30591.0   100.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1168      PDVDLGDISGINASF  LGDISGINA  4        0.0577
26781.5   100.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1169      DVDLGDISGINASFV  LGDISGINA  3        0.0820
20580.8    95.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1170      VDLGDISGINASFVN  SGINASFVN  6        0.1142
14532.6    90.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1171      DLGDISGINASFVNI  SGINASFVN  5        0.1357
11515.0    85.00  0.43     Sequence
 HLA-DPA10201-DPB10501 1172      LGDISGINASFVNIQ  SGINASFVN  4        0.1515
9704.9    80.00  0.40     Sequence
 HLA-DPA10201-DPB10501 1173      GDISGINASFVNIQK  SGINASFVN  3        0.1934
6165.5    65.00  0.34     Sequence
 HLA-DPA10201-DPB10501 1174      DISGINASFVNIQKE  NASFVNIQK  5        0.2185
4703.9    60.00  0.27     Sequence
 HLA-DPA10201-DPB10501 1175      ISGINASFVNIQKEI  NASFVNIQK  4        0.2477
3428.1    48.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1176      SGINASFVNIQKEID  NASFVNIQK  3        0.2589
3036.1    45.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1177      GINASFVNIQKEIDR  NASFVNIQK  2        0.2596
3015.4    45.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1178      INASFVNIQKEIDRL  NASFVNIQK  1        0.2769
2498.0    40.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1179      NASFVNIQKEIDRLN  NASFVNIQK  0        0.2806
2400.2    39.00  0.20     Sequence
 HLA-DPA10201-DPB10501 1180      ASFVNIQKEIDRLNE  QKEIDRLNE  6        0.2691
2720.2    42.00  0.20     Sequence
 HLA-DPA10201-DPB10501 1181      SFVNIQKEIDRLNEV  QKEIDRLNE  5        0.2702
2686.9    42.00  0.36     Sequence
 HLA-DPA10201-DPB10501 1182      FVNIQKEIDRLNEVA  QKEIDRLNE  4        0.2606
2980.5    44.00  0.43     Sequence
 HLA-DPA10201-DPB10501 1183      VNIQKEIDRLNEVAK  QKEIDRLNE  3        0.2471
3450.4    48.00  0.43     Sequence
 HLA-DPA10201-DPB10501 1184      NIQKEIDRLNEVAKN  QKEIDRLNE  2        0.2492
3371.6    48.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1185      IQKEIDRLNEVAKNL  QKEIDRLNE  1        0.2593
3022.5    45.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1186      QKEIDRLNEVAKNLN  DRLNEVAKN  4        0.2446
3543.2    49.00  0.33     Sequence
 HLA-DPA10201-DPB10501 1187      KEIDRLNEVAKNLNE  DRLNEVAKN  3        0.2316
4080.0    55.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1188      EIDRLNEVAKNLNES  DRLNEVAKN  2        0.2208
4587.4    60.00  0.40     Sequence
 HLA-DPA10201-DPB10501 1189      IDRLNEVAKNLNESL  DRLNEVAKN  1        0.2332
4010.5    55.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1190      DRLNEVAKNLNESLI  AKNLNESLI  6        0.2522
3264.8    47.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1191      RLNEVAKNLNESLID  AKNLNESLI  5        0.2733
2598.5    41.00  0.37     Sequence
 HLA-DPA10201-DPB10501 1192      LNEVAKNLNESLIDL  AKNLNESLI  4        0.2726
2617.9    41.00  0.41     Sequence
 HLA-DPA10201-DPB10501 1193      NEVAKNLNESLIDLQ  AKNLNESLI  3        0.2772
2490.5    40.00  0.41     Sequence
 HLA-DPA10201-DPB10501 1194      EVAKNLNESLIDLQE  AKNLNESLI  2        0.2754
2540.3    40.00  0.42     Sequence
 HLA-DPA10201-DPB10501 1195      VAKNLNESLIDLQEL  AKNLNESLI  1        0.2704
2681.7    42.00  0.44     Sequence
```

```
 HLA-DPA10201-DPB10501 1196      AKNLNESLIDLQELG  AKNLNESLI  0        0.2303
4139.2    55.00  0.33     Sequence
 HLA-DPA10201-DPB10501 1197      KNLNESLIDLQELGK  LIDLQELGK  6        0.2124
5022.6    60.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1198      NLNESLIDLQELGKY  LIDLQELGK  5        0.2462
3483.0    49.00  0.50     Sequence
 HLA-DPA10201-DPB10501 1199      LNESLIDLQELGKYE  LIDLQELGK  4        0.2570
3100.7    45.00  0.50     Sequence
 HLA-DPA10201-DPB10501 1200      NESLIDLQELGKYEQ  LIDLQELGK  3        0.2726
2617.3    41.00  0.46     Sequence
 HLA-DPA10201-DPB10501 1201      ESLIDLQELGKYEQY  LIDLQELGK  2        0.2877
2224.6    37.00  0.41     Sequence
 HLA-DPA10201-DPB10501 1202      SLIDLQELGKYEQYI  LIDLQELGK  1        0.2959
2035.4    35.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1203      LIDLQELGKYEQYIK  LGKYEQYIK  6        0.3782
835.1    18.00  0.36     Sequence
 HLA-DPA10201-DPB10501 1204      IDLQELGKYEQYIKW  LGKYEQYIK  5        0.4097
594.0    13.00  0.53     Sequence
 HLA-DPA10201-DPB10501 1205      DLQELGKYEQYIKWP  LGKYEQYIK  4        0.4276
489.4    11.00  0.56     Sequence
 HLA-DPA10201-DPB10501 1206      LQELGKYEQYIKWPW  LGKYEQYIK  3        0.4400
428.0     9.00  0.57     Sequence         WB
 HLA-DPA10201-DPB10501 1207      QELGKYEQYIKWPWY  LGKYEQYIK  2        0.4366
444.0     9.50  0.57     Sequence         WB
 HLA-DPA10201-DPB10501 1208      ELGKYEQYIKWPWYI  LGKYEQYIK  1        0.4293
480.5    11.00  0.55     Sequence
 HLA-DPA10201-DPB10501 1209      LGKYEQYIKWPWYIW  LGKYEQYIK  0        0.3955
692.8    15.00  0.44     Sequence
 HLA-DPA10201-DPB10501 1210      GKYEQYIKWPWYIWL  YIKWPWYIW  5        0.3293
1417.0    27.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1211      KYEQYIKWPWYIWLG  YIKWPWYIW  4        0.3091
1763.6    31.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1212      YEQYIKWPWYIWLGF  YIKWPWYIW  3        0.3040
1863.3    33.00  0.44     Sequence
 HLA-DPA10201-DPB10501 1213      EQYIKWPWYIWLGFI  YIKWPWYIW  2        0.2990
1966.8    34.00  0.43     Sequence
 HLA-DPA10201-DPB10501 1214      QYIKWPWYIWLGFIA  YIKWPWYIW  1        0.3364
1313.6    25.00  0.32     Sequence
 HLA-DPA10201-DPB10501 1215      YIKWPWYIWLGFIAG  WYIWLGFIA  5        0.3502
1130.9    23.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1216      IKWPWYIWLGFIAGL  WYIWLGFIA  4        0.3483
1154.8    23.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1217      KWPWYIWLGFIAGLI  WYIWLGFIA  3        0.3499
1134.2    23.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1218      WPWYIWLGFIAGLIA  WYIWLGFIA  2        0.3415
1241.9    24.00  0.33     Sequence
 HLA-DPA10201-DPB10501 1219      PWYIWLGFIAGLIAI  WYIWLGFIA  1        0.3393
1272.2    25.00  0.30     Sequence
 HLA-DPA10201-DPB10501 1220      WYIWLGFIAGLIAIV  WYIWLGFIA  0        0.3373
1299.8    25.00  0.25     Sequence
 HLA-DPA10201-DPB10501 1221      YIWLGFIAGLIAIVM  LGFIAGLIA  3        0.2815
2378.7    38.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1222      IWLGFIAGLIAIVMV  LGFIAGLIA  2        0.2382
3800.7    55.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1223      WLGFIAGLIAIVMVT  LGFIAGLIA  1        0.2258
4343.3    55.00  0.26     Sequence
 HLA-DPA10201-DPB10501 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.2021
5613.3    65.00  0.21     Sequence
 HLA-DPA10201-DPB10501 1225      GFIAGLIAIVMVTIM  FIAGLIAIV  1        0.1809
7063.4    70.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1226      FIAGLIAIVMVTIML  GLIAIVMVT  3        0.1757
7473.3    70.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1227      IAGLIAIVMVTIMLC  GLIAIVMVT  2        0.1561
9238.2    80.00  0.30     Sequence
 HLA-DPA10201-DPB10501 1228      AGLIAIVMVTIMLCC  GLIAIVMVT  1        0.1515
9704.7    80.00  0.27     Sequence
```

```
 HLA-DPA10201-DPB10501 1229      GLIAIVMVTIMLCCM  IVMVTIMLC  4        0.1483
10043.9    80.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1230      LIAIVMVTIMLCCMT  IVMVTIMLC  3        0.1416
10804.5    80.00  0.35     Sequence
 HLA-DPA10201-DPB10501 1231      IAIVMVTIMLCCMTS  IVMVTIMLC  2        0.1403
10953.2    85.00  0.37     Sequence
 HLA-DPA10201-DPB10501 1232      AIVMVTIMLCCMTSC  IVMVTIMLC  1        0.1406
10922.9    85.00  0.32     Sequence
 HLA-DPA10201-DPB10501 1233      IVMVTIMLCCMTSCC  IVMVTIMLC  0        0.1203
13606.2    90.00  0.19     Sequence
 HLA-DPA10201-DPB10501 1234      VMVTIMLCCMTSCCS  TIMLCCMTS  3        0.1202
13618.5    90.00  0.17     Sequence
 HLA-DPA10201-DPB10501 1235      MVTIMLCCMTSCCSC  TIMLCCMTS  2        0.1084
15466.6    90.00  0.20     Sequence
 HLA-DPA10201-DPB10501 1236      VTIMLCCMTSCCSCL  TIMLCCMTS  1        0.1018
16625.7    95.00  0.19     Sequence
 HLA-DPA10201-DPB10501 1237      TIMLCCMTSCCSCLK  MTSCCSCLK  6        0.1229
13225.3    85.00  0.18     Sequence
 HLA-DPA10201-DPB10501 1238      IMLCCMTSCCSCLKG  MTSCCSCLK  5        0.1239
13085.7    85.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1239      MLCCMTSCCSCLKGC  MTSCCSCLK  4        0.1226
13275.8    85.00  0.34     Sequence
 HLA-DPA10201-DPB10501 1240      LCCMTSCCSCLKGCC  MTSCCSCLK  3        0.1240
13071.1    85.00  0.37     Sequence
 HLA-DPA10201-DPB10501 1241      CCMTSCCSCLKGCCS  MTSCCSCLK  2        0.1168
14127.0    90.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1242      CMTSCCSCLKGCCSC  MTSCCSCLK  1        0.1150
14414.8    90.00  0.38     Sequence
 HLA-DPA10201-DPB10501 1243      MTSCCSCLKGCCSCG  MTSCCSCLK  0        0.1050
16054.5    90.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1244      TSCCSCLKGCCSCGS  TSCCSCLKG  0        0.0663
24389.5   100.00  0.25     Sequence
 HLA-DPA10201-DPB10501 1245      SCCSCLKGCCSCGSC  CSCLKGCCS  2        0.0595
26277.2   100.00  0.19     Sequence
 HLA-DPA10201-DPB10501 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.0499
29152.4   100.00  0.23     Sequence
 HLA-DPA10201-DPB10501 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.0482
29689.1   100.00  0.25     Sequence
 HLA-DPA10201-DPB10501 1248      SCLKGCCSCGSCCKF  CCSCGSCCK  5        0.0646
24848.7   100.00  0.23     Sequence
 HLA-DPA10201-DPB10501 1249      CLKGCCSCGSCCKFD  CCSCGSCCK  4        0.0644
24902.8   100.00  0.27     Sequence
 HLA-DPA10201-DPB10501 1250      LKGCCSCGSCCKFDE  CCSCGSCCK  3        0.0629
25327.2   100.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1251      KGCCSCGSCCKFDED  CCSCGSCCK  2        0.0581
26656.6   100.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1252      GCCSCGSCCKFDEDD  CCSCGSCCK  1        0.0545
27722.9   100.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1253      CCSCGSCCKFDEDDS  CCSCGSCCK  0        0.0510
28790.4   100.00  0.25     Sequence
 HLA-DPA10201-DPB10501 1254      CSCGSCCKFDEDDSE  CGSCCKFDE  2        0.0430
31409.4   100.00  0.20     Sequence
 HLA-DPA10201-DPB10501 1255      SCGSCCKFDEDDSEP  CCKFDEDDS  4        0.0356
34030.3   100.00  0.22     Sequence
 HLA-DPA10201-DPB10501 1256      CGSCCKFDEDDSEPV  KFDEDDSEP  5        0.0476
29887.6   100.00  0.28     Sequence
 HLA-DPA10201-DPB10501 1257      GSCCKFDEDDSEPVL  KFDEDDSEP  4        0.0542
27820.2   100.00  0.29     Sequence
 HLA-DPA10201-DPB10501 1258      SCCKFDEDDSEPVLK  EDDSEPVLK  6        0.0844
20062.3    95.00  0.34     Sequence
 HLA-DPA10201-DPB10501 1259      CCKFDEDDSEPVLKG  EDDSEPVLK  5        0.0862
19666.7    95.00  0.46     Sequence
 HLA-DPA10201-DPB10501 1260      CKFDEDDSEPVLKGV  EDDSEPVLK  4        0.0920
18486.4    95.00  0.44     Sequence
 HLA-DPA10201-DPB10501 1261      KFDEDDSEPVLKGVK  EDDSEPVLK  3        0.1027
16451.7    90.00  0.42     Sequence
```

```
 HLA-DPA10201-DPB10501 1262      FDEDDSEPVLKGVKL  EDDSEPVLK  2        0.1178
13978.0    90.00  0.35     Sequence
 HLA-DPA10201-DPB10501 1263      DEDDSEPVLKGVKLH  EPVLKGVKL  5        0.1641
8472.7    75.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1264      EDDSEPVLKGVKLHY  VLKGVKLHY  6        0.2665
2798.2    43.00  0.31     Sequence
 HLA-DPA10201-DPB10501 1265      DDSEPVLKGVKLHYT  VLKGVKLHY  5        0.3051
1841.4    32.00  0.36     Sequence
 HLA-DPA10201-DPB11401    1      PSPIKEMFVFLVLLP  KEMFVFLVL  4        0.2843
2307.7    20.00  0.37     Sequence
 HLA-DPA10201-DPB11401    2      SPIKEMFVFLVLLPL  KEMFVFLVL  3        0.3097
1752.5    16.00  0.34     Sequence
 HLA-DPA10201-DPB11401    3      PIKEMFVFLVLLPLV  KEMFVFLVL  2        0.3110
1728.0    16.00  0.34     Sequence
 HLA-DPA10201-DPB11401    4      IKEMFVFLVLLPLVS  KEMFVFLVL  1        0.2843
2308.0    20.00  0.27     Sequence
 HLA-DPA10201-DPB11401    5      KEMFVFLVLLPLVSS  FVFLVLLPL  3        0.2392
3759.9    31.00  0.26     Sequence
 HLA-DPA10201-DPB11401    6      EMFVFLVLLPLVSSQ  FVFLVLLPL  2        0.2026
5585.2    42.00  0.30     Sequence
 HLA-DPA10201-DPB11401    7      MFVFLVLLPLVSSQC  FVFLVLLPL  1        0.2028
5573.1    42.00  0.27     Sequence
 HLA-DPA10201-DPB11401    8      FVFLVLLPLVSSQCV  FLVLLPLVS  2        0.1942
6116.5    45.00  0.30     Sequence
 HLA-DPA10201-DPB11401    9      VFLVLLPLVSSQCVN  FLVLLPLVS  1        0.1572
9123.6    60.00  0.31     Sequence
 HLA-DPA10201-DPB11401   10      FLVLLPLVSSQCVNF  VLLPLVSSQ  2        0.1300
12250.9    70.00  0.23     Sequence
 HLA-DPA10201-DPB11401   11      LVLLPLVSSQCVNFT  LPLVSSQCV  3        0.1036
16297.8    80.00  0.19     Sequence
 HLA-DPA10201-DPB11401   12      VLLPLVSSQCVNFTN  LPLVSSQCV  2        0.0960
17692.1    85.00  0.23     Sequence
 HLA-DPA10201-DPB11401   13      LLPLVSSQCVNFTNR  LVSSQCVNF  3        0.0855
19816.8    85.00  0.29     Sequence
 HLA-DPA10201-DPB11401   14      LPLVSSQCVNFTNRT  LVSSQCVNF  2        0.0821
20561.2    90.00  0.32     Sequence
 HLA-DPA10201-DPB11401   15      PLVSSQCVNFTNRTQ  LVSSQCVNF  1        0.0704
23336.0    90.00  0.28     Sequence
 HLA-DPA10201-DPB11401   16      LVSSQCVNFTNRTQL  VNFTNRTQL  6        0.0754
22107.6    90.00  0.31     Sequence
 HLA-DPA10201-DPB11401   17      VSSQCVNFTNRTQLP  VNFTNRTQL  5        0.0900
18876.3    85.00  0.47     Sequence
 HLA-DPA10201-DPB11401   18      SSQCVNFTNRTQLPS  VNFTNRTQL  4        0.0994
17049.6    80.00  0.50     Sequence
 HLA-DPA10201-DPB11401   19      SQCVNFTNRTQLPSA  VNFTNRTQL  3        0.1116
14949.6    80.00  0.48     Sequence
 HLA-DPA10201-DPB11401   20      QCVNFTNRTQLPSAY  VNFTNRTQL  2        0.1172
14063.7    75.00  0.41     Sequence
 HLA-DPA10201-DPB11401   21      CVNFTNRTQLPSAYT  RTQLPSAYT  6        0.1467
10218.9    65.00  0.31     Sequence
 HLA-DPA10201-DPB11401   22      VNFTNRTQLPSAYTN  RTQLPSAYT  5        0.1510
9761.7    60.00  0.46     Sequence
 HLA-DPA10201-DPB11401   23      NFTNRTQLPSAYTNS  RTQLPSAYT  4        0.1494
9930.6    65.00  0.54     Sequence
 HLA-DPA10201-DPB11401   24      FTNRTQLPSAYTNSF  RTQLPSAYT  3        0.1609
8767.0    60.00  0.50     Sequence
 HLA-DPA10201-DPB11401   25      TNRTQLPSAYTNSFT  RTQLPSAYT  2        0.1497
9902.6    65.00  0.49     Sequence
 HLA-DPA10201-DPB11401   26      NRTQLPSAYTNSFTR  RTQLPSAYT  1        0.1455
10355.6    65.00  0.41     Sequence
 HLA-DPA10201-DPB11401   27      RTQLPSAYTNSFTRG  RTQLPSAYT  0        0.1281
12499.4    70.00  0.33     Sequence
 HLA-DPA10201-DPB11401   28      TQLPSAYTNSFTRGV  SAYTNSFTR  4        0.0912
18634.8    85.00  0.32     Sequence
 HLA-DPA10201-DPB11401   29      QLPSAYTNSFTRGVY  SAYTNSFTR  3        0.1051
16037.1    80.00  0.31     Sequence
```

```
 HLA-DPA10201-DPB11401   30      LPSAYTNSFTRGVYY  SAYTNSFTR  2        0.1084
15467.9    80.00  0.30     Sequence
 HLA-DPA10201-DPB11401   31      PSAYTNSFTRGVYYP  SAYTNSFTR  1        0.1352
11578.9    70.00  0.21     Sequence
 HLA-DPA10201-DPB11401   32      SAYTNSFTRGVYYPD  SFTRGVYYP  5        0.1324
11935.5    70.00  0.18     Sequence
 HLA-DPA10201-DPB11401   33      AYTNSFTRGVYYPDK  SFTRGVYYP  4        0.1369
11365.5    70.00  0.22     Sequence
 HLA-DPA10201-DPB11401   34      YTNSFTRGVYYPDKV  SFTRGVYYP  3        0.1583
9016.6    60.00  0.23     Sequence
 HLA-DPA10201-DPB11401   35      TNSFTRGVYYPDKVF  SFTRGVYYP  2        0.1590
8950.5    60.00  0.20     Sequence
 HLA-DPA10201-DPB11401   36      NSFTRGVYYPDKVFR  RGVYYPDKV  4        0.1746
7560.5    55.00  0.21     Sequence
 HLA-DPA10201-DPB11401   37      SFTRGVYYPDKVFRS  RGVYYPDKV  3        0.1851
6749.6    48.00  0.19     Sequence
 HLA-DPA10201-DPB11401   38      FTRGVYYPDKVFRSS  YYPDKVFRS  5        0.1642
8464.7    55.00  0.25     Sequence
 HLA-DPA10201-DPB11401   39      TRGVYYPDKVFRSSV  YYPDKVFRS  4        0.1678
8137.5    55.00  0.28     Sequence
 HLA-DPA10201-DPB11401   40      RGVYYPDKVFRSSVL  YYPDKVFRS  3        0.1903
6382.2    46.00  0.27     Sequence
 HLA-DPA10201-DPB11401   41      GVYYPDKVFRSSVLH  KVFRSSVLH  6        0.2628
2912.3    25.00  0.34     Sequence
 HLA-DPA10201-DPB11401   42      VYYPDKVFRSSVLHS  KVFRSSVLH  5        0.3178
1606.5    15.00  0.32     Sequence
 HLA-DPA10201-DPB11401   43      YYPDKVFRSSVLHST  KVFRSSVLH  4        0.3737
877.2     8.00  0.29     Sequence         WB
 HLA-DPA10201-DPB11401   44      YPDKVFRSSVLHSTQ  KVFRSSVLH  3        0.3981
673.2     6.00  0.28     Sequence         WB
 HLA-DPA10201-DPB11401   45      PDKVFRSSVLHSTQD  KVFRSSVLH  2        0.3882
749.7     6.50  0.28     Sequence         WB
 HLA-DPA10201-DPB11401   46      DKVFRSSVLHSTQDL  KVFRSSVLH  1        0.4016
648.1     5.50  0.22     Sequence         WB
 HLA-DPA10201-DPB11401   47      KVFRSSVLHSTQDLF  FRSSVLHST  2        0.4159
555.7     5.00  0.18     Sequence         WB
 HLA-DPA10201-DPB11401   48      VFRSSVLHSTQDLFL  RSSVLHSTQ  2        0.3294
1416.1    13.00  0.22     Sequence
 HLA-DPA10201-DPB11401   49      FRSSVLHSTQDLFLP  SVLHSTQDL  3        0.2795
2429.5    21.00  0.31     Sequence
 HLA-DPA10201-DPB11401   50      RSSVLHSTQDLFLPF  SVLHSTQDL  2        0.2213
4558.9    36.00  0.33     Sequence
 HLA-DPA10201-DPB11401   51      SSVLHSTQDLFLPFF  LHSTQDLFL  3        0.2198
4638.3    36.00  0.25     Sequence
 HLA-DPA10201-DPB11401   52      SVLHSTQDLFLPFFS  LHSTQDLFL  2        0.2241
4424.3    35.00  0.21     Sequence
 HLA-DPA10201-DPB11401   53      VLHSTQDLFLPFFSN  STQDLFLPF  3        0.1845
6792.0    48.00  0.25     Sequence
 HLA-DPA10201-DPB11401   54      LHSTQDLFLPFFSNV  STQDLFLPF  2        0.1820
6979.0    49.00  0.23     Sequence
 HLA-DPA10201-DPB11401   55      HSTQDLFLPFFSNVT  LFLPFFSNV  5        0.1902
6383.0    46.00  0.26     Sequence
 HLA-DPA10201-DPB11401   56      STQDLFLPFFSNVTW  LFLPFFSNV  4        0.1843
6805.3    48.00  0.31     Sequence
 HLA-DPA10201-DPB11401   57      TQDLFLPFFSNVTWF  LFLPFFSNV  3        0.1925
6229.3    45.00  0.32     Sequence
 HLA-DPA10201-DPB11401   58      QDLFLPFFSNVTWFH  PFFSNVTWF  5        0.2339
3979.3    32.00  0.26     Sequence
 HLA-DPA10201-DPB11401   59      DLFLPFFSNVTWFHA  PFFSNVTWF  4        0.2788
2449.4    21.00  0.26     Sequence
 HLA-DPA10201-DPB11401   60      LFLPFFSNVTWFHAI  FSNVTWFHA  5        0.3147
1660.3    15.00  0.22     Sequence
 HLA-DPA10201-DPB11401   61      FLPFFSNVTWFHAIH  SNVTWFHAI  5        0.3391
1274.8    12.00  0.25     Sequence
 HLA-DPA10201-DPB11401   62      LPFFSNVTWFHAIHV  SNVTWFHAI  4        0.3718
895.1     8.00  0.25     Sequence         WB
```

```
 HLA-DPA10201-DPB11401   63      PFFSNVTWFHAIHVS  SNVTWFHAI  3        0.3914
723.8     6.50  0.23     Sequence         WB
 HLA-DPA10201-DPB11401   64      FFSNVTWFHAIHVSG  SNVTWFHAI  2        0.3682
931.0     8.50  0.25     Sequence         WB
 HLA-DPA10201-DPB11401   65      FSNVTWFHAIHVSGT  VTWFHAIHV  3        0.3196
1575.5    14.00  0.31     Sequence
 HLA-DPA10201-DPB11401   66      SNVTWFHAIHVSGTN  VTWFHAIHV  2        0.2859
2268.6    20.00  0.34     Sequence
 HLA-DPA10201-DPB11401   67      NVTWFHAIHVSGTNG  VTWFHAIHV  1        0.2489
3384.2    28.00  0.32     Sequence
 HLA-DPA10201-DPB11401   68      VTWFHAIHVSGTNGT  VTWFHAIHV  0        0.2144
4916.5    38.00  0.25     Sequence
 HLA-DPA10201-DPB11401   69      TWFHAIHVSGTNGTK  FHAIHVSGT  2        0.1696
7984.0    55.00  0.25     Sequence
 HLA-DPA10201-DPB11401   70      WFHAIHVSGTNGTKR  FHAIHVSGT  1        0.1419
10770.8    65.00  0.30     Sequence
 HLA-DPA10201-DPB11401   71      FHAIHVSGTNGTKRF  AIHVSGTNG  2        0.1141
14541.2    75.00  0.26     Sequence
 HLA-DPA10201-DPB11401   72      HAIHVSGTNGTKRFD  AIHVSGTNG  1        0.0771
21713.6    90.00  0.29     Sequence
 HLA-DPA10201-DPB11401   73      AIHVSGTNGTKRFDN  AIHVSGTNG  0        0.0681
23934.4    95.00  0.26     Sequence
 HLA-DPA10201-DPB11401   74      IHVSGTNGTKRFDNP  VSGTNGTKR  2        0.0493
29335.0   100.00  0.34     Sequence
 HLA-DPA10201-DPB11401   75      HVSGTNGTKRFDNPV  VSGTNGTKR  1        0.0385
32968.7   100.00  0.38     Sequence
 HLA-DPA10201-DPB11401   76      VSGTNGTKRFDNPVL  TKRFDNPVL  6        0.0922
18435.3    85.00  0.28     Sequence
 HLA-DPA10201-DPB11401   77      SGTNGTKRFDNPVLP  KRFDNPVLP  6        0.1994
5782.2    43.00  0.54     Sequence
 HLA-DPA10201-DPB11401   78      GTNGTKRFDNPVLPF  KRFDNPVLP  5        0.3309
1393.3    13.00  0.41     Sequence
 HLA-DPA10201-DPB11401   79      TNGTKRFDNPVLPFN  RFDNPVLPF  5        0.3487
1149.1    11.00  0.46     Sequence
 HLA-DPA10201-DPB11401   80      NGTKRFDNPVLPFND  RFDNPVLPF  4        0.3419
1237.1    11.00  0.47     Sequence
 HLA-DPA10201-DPB11401   81      GTKRFDNPVLPFNDG  KRFDNPVLP  2        0.3385
1283.1    12.00  0.43     Sequence
 HLA-DPA10201-DPB11401   82      TKRFDNPVLPFNDGV  RFDNPVLPF  2        0.3384
1285.4    12.00  0.44     Sequence
 HLA-DPA10201-DPB11401   83      KRFDNPVLPFNDGVY  RFDNPVLPF  1        0.2583
3055.5    26.00  0.44     Sequence
 HLA-DPA10201-DPB11401   84      RFDNPVLPFNDGVYF  RFDNPVLPF  0        0.1485
10021.9    65.00  0.49     Sequence
 HLA-DPA10201-DPB11401   85      FDNPVLPFNDGVYFA  PFNDGVYFA  6        0.0960
17687.1    85.00  0.34     Sequence
 HLA-DPA10201-DPB11401   86      DNPVLPFNDGVYFAS  PFNDGVYFA  5        0.1226
13270.0    75.00  0.40     Sequence
 HLA-DPA10201-DPB11401   87      NPVLPFNDGVYFAST  PFNDGVYFA  4        0.1371
11345.4    70.00  0.40     Sequence
 HLA-DPA10201-DPB11401   88      PVLPFNDGVYFASTE  PFNDGVYFA  3        0.1433
10611.2    65.00  0.37     Sequence
 HLA-DPA10201-DPB11401   89      VLPFNDGVYFASTEK  PFNDGVYFA  2        0.1494
9932.9    65.00  0.33     Sequence
 HLA-DPA10201-DPB11401   90      LPFNDGVYFASTEKS  PFNDGVYFA  1        0.1323
11954.2    70.00  0.19     Sequence
 HLA-DPA10201-DPB11401   91      PFNDGVYFASTEKSN  VYFASTEKS  5        0.1418
10777.2    65.00  0.28     Sequence
 HLA-DPA10201-DPB11401   92      FNDGVYFASTEKSNI  VYFASTEKS  4        0.1585
8997.4    60.00  0.28     Sequence
 HLA-DPA10201-DPB11401   93      NDGVYFASTEKSNII  FASTEKSNI  5        0.1948
6074.1    44.00  0.36     Sequence
 HLA-DPA10201-DPB11401   94      DGVYFASTEKSNIIR  FASTEKSNI  4        0.2224
4506.3    35.00  0.34     Sequence
 HLA-DPA10201-DPB11401   95      GVYFASTEKSNIIRG  FASTEKSNI  3        0.2179
4733.0    37.00  0.32     Sequence
```

```
 HLA-DPA10201-DPB11401   96      VYFASTEKSNIIRGW  FASTEKSNI  2        0.2132
4978.1    38.00  0.34     Sequence
 HLA-DPA10201-DPB11401   97      YFASTEKSNIIRGWI  FASTEKSNI  1        0.1832
6891.2    48.00  0.31     Sequence
 HLA-DPA10201-DPB11401   98      FASTEKSNIIRGWIF  KSNIIRGWI  5        0.1507
9796.1    65.00  0.24     Sequence
 HLA-DPA10201-DPB11401   99      ASTEKSNIIRGWIFG  KSNIIRGWI  4        0.1206
13555.2    75.00  0.33     Sequence
 HLA-DPA10201-DPB11401  100      STEKSNIIRGWIFGT  KSNIIRGWI  3        0.1276
12574.2    70.00  0.31     Sequence
 HLA-DPA10201-DPB11401  101      TEKSNIIRGWIFGTT  KSNIIRGWI  2        0.1502
9849.5    65.00  0.26     Sequence
 HLA-DPA10201-DPB11401  102      EKSNIIRGWIFGTTL  RGWIFGTTL  6        0.1846
6784.3    48.00  0.35     Sequence
 HLA-DPA10201-DPB11401  103      KSNIIRGWIFGTTLD  RGWIFGTTL  5        0.1958
6007.3    44.00  0.45     Sequence
 HLA-DPA10201-DPB11401  104      SNIIRGWIFGTTLDS  RGWIFGTTL  4        0.2044
5477.4    41.00  0.44     Sequence
 HLA-DPA10201-DPB11401  105      NIIRGWIFGTTLDSK  RGWIFGTTL  3        0.2202
4618.1    36.00  0.43     Sequence
 HLA-DPA10201-DPB11401  106      IIRGWIFGTTLDSKT  RGWIFGTTL  2        0.2249
4385.4    35.00  0.44     Sequence
 HLA-DPA10201-DPB11401  107      IRGWIFGTTLDSKTQ  RGWIFGTTL  1        0.1893
6446.1    46.00  0.39     Sequence
 HLA-DPA10201-DPB11401  108      RGWIFGTTLDSKTQS  RGWIFGTTL  0        0.1534
9513.9    60.00  0.31     Sequence
 HLA-DPA10201-DPB11401  109      GWIFGTTLDSKTQSL  WIFGTTLDS  1        0.0908
18718.7    85.00  0.25     Sequence
 HLA-DPA10201-DPB11401  110      WIFGTTLDSKTQSLL  TLDSKTQSL  5        0.0964
17617.0    85.00  0.28     Sequence
 HLA-DPA10201-DPB11401  111      IFGTTLDSKTQSLLI  TLDSKTQSL  4        0.1162
14218.9    75.00  0.34     Sequence
 HLA-DPA10201-DPB11401  112      FGTTLDSKTQSLLIV  DSKTQSLLI  5        0.1678
8136.3    55.00  0.32     Sequence
 HLA-DPA10201-DPB11401  113      GTTLDSKTQSLLIVN  KTQSLLIVN  6        0.2122
5031.1    39.00  0.28     Sequence
 HLA-DPA10201-DPB11401  114      TTLDSKTQSLLIVNN  KTQSLLIVN  5        0.2248
4392.0    35.00  0.32     Sequence
 HLA-DPA10201-DPB11401  115      TLDSKTQSLLIVNNA  KTQSLLIVN  4        0.2446
3546.2    29.00  0.35     Sequence
 HLA-DPA10201-DPB11401  116      LDSKTQSLLIVNNAT  KTQSLLIVN  3        0.2410
3686.6    30.00  0.37     Sequence
 HLA-DPA10201-DPB11401  117      DSKTQSLLIVNNATN  KTQSLLIVN  2        0.2339
3979.0    32.00  0.35     Sequence
 HLA-DPA10201-DPB11401  118      SKTQSLLIVNNATNV  KTQSLLIVN  1        0.2477
3427.0    29.00  0.26     Sequence
 HLA-DPA10201-DPB11401  119      KTQSLLIVNNATNVV  LIVNNATNV  5        0.2329
4024.8    32.00  0.31     Sequence
 HLA-DPA10201-DPB11401  120      TQSLLIVNNATNVVI  LIVNNATNV  4        0.2128
4998.6    38.00  0.47     Sequence
 HLA-DPA10201-DPB11401  121      QSLLIVNNATNVVIK  LIVNNATNV  3        0.2270
4289.0    34.00  0.46     Sequence
 HLA-DPA10201-DPB11401  122      SLLIVNNATNVVIKV  LIVNNATNV  2        0.2366
3867.2    31.00  0.44     Sequence
 HLA-DPA10201-DPB11401  123      LLIVNNATNVVIKVC  LIVNNATNV  1        0.2305
4128.0    33.00  0.41     Sequence
 HLA-DPA10201-DPB11401  124      LIVNNATNVVIKVCE  LIVNNATNV  0        0.1894
6441.1    46.00  0.34     Sequence
 HLA-DPA10201-DPB11401  125      IVNNATNVVIKVCEF  NNATNVVIK  2        0.1439
10543.4    65.00  0.19     Sequence
 HLA-DPA10201-DPB11401  126      VNNATNVVIKVCEFQ  NATNVVIKV  2        0.1086
15444.0    80.00  0.28     Sequence
 HLA-DPA10201-DPB11401  127      NNATNVVIKVCEFQF  ATNVVIKVC  2        0.1106
15106.2    80.00  0.19     Sequence
 HLA-DPA10201-DPB11401  128      NATNVVIKVCEFQFC  NVVIKVCEF  3        0.1165
14170.3    75.00  0.15     Sequence
```

```
 HLA-DPA10201-DPB11401  129      ATNVVIKVCEFQFCN  NVVIKVCEF  2        0.1164
14183.2    75.00  0.16     Sequence
 HLA-DPA10201-DPB11401  130      TNVVIKVCEFQFCNY  KVCEFQFCN  5        0.1085
15462.6    80.00  0.31     Sequence
 HLA-DPA10201-DPB11401  131      NVVIKVCEFQFCNYP  KVCEFQFCN  4        0.1088
15404.3    80.00  0.34     Sequence
 HLA-DPA10201-DPB11401  132      VVIKVCEFQFCNYPF  KVCEFQFCN  3        0.1119
14900.1    80.00  0.37     Sequence
 HLA-DPA10201-DPB11401  133      VIKVCEFQFCNYPFL  KVCEFQFCN  2        0.1258
12819.5    70.00  0.37     Sequence
 HLA-DPA10201-DPB11401  134      IKVCEFQFCNYPFLG  FQFCNYPFL  5        0.1193
13750.0    75.00  0.22     Sequence
 HLA-DPA10201-DPB11401  135      KVCEFQFCNYPFLGV  QFCNYPFLG  5        0.1558
9264.6    60.00  0.26     Sequence
 HLA-DPA10201-DPB11401  136      VCEFQFCNYPFLGVY  FCNYPFLGV  5        0.1658
8317.4    55.00  0.33     Sequence
 HLA-DPA10201-DPB11401  137      CEFQFCNYPFLGVYY  FCNYPFLGV  4        0.1781
7281.1    50.00  0.32     Sequence
 HLA-DPA10201-DPB11401  138      EFQFCNYPFLGVYYH  FCNYPFLGV  3        0.1846
6786.5    48.00  0.32     Sequence
 HLA-DPA10201-DPB11401  139      FQFCNYPFLGVYYHK  FCNYPFLGV  2        0.1859
6692.1    47.00  0.28     Sequence
 HLA-DPA10201-DPB11401  140      QFCNYPFLGVYYHKN  FCNYPFLGV  1        0.1614
8720.6    60.00  0.25     Sequence
 HLA-DPA10201-DPB11401  141      FCNYPFLGVYYHKNN  PFLGVYYHK  4        0.1344
11676.8    70.00  0.20     Sequence
 HLA-DPA10201-DPB11401  142      CNYPFLGVYYHKNNK  PFLGVYYHK  3        0.1057
15936.5    80.00  0.32     Sequence
 HLA-DPA10201-DPB11401  143      NYPFLGVYYHKNNKS  PFLGVYYHK  2        0.0972
17467.1    85.00  0.34     Sequence
 HLA-DPA10201-DPB11401  144      YPFLGVYYHKNNKSW  FLGVYYHKN  2        0.0891
19065.8    85.00  0.28     Sequence
 HLA-DPA10201-DPB11401  145      PFLGVYYHKNNKSWM  FLGVYYHKN  1        0.0752
22164.6    90.00  0.25     Sequence
 HLA-DPA10201-DPB11401  146      FLGVYYHKNNKSWME  HKNNKSWME  6        0.0600
26135.1    95.00  0.14     Sequence
 HLA-DPA10201-DPB11401  147      LGVYYHKNNKSWMES  HKNNKSWME  5        0.0579
26733.1    95.00  0.27     Sequence
 HLA-DPA10201-DPB11401  148      GVYYHKNNKSWMESE  KNNKSWMES  5        0.0596
26239.1    95.00  0.28     Sequence
 HLA-DPA10201-DPB11401  149      VYYHKNNKSWMESEF  KNNKSWMES  4        0.0704
23354.7    90.00  0.31     Sequence
 HLA-DPA10201-DPB11401  150      YYHKNNKSWMESEFR  KSWMESEFR  6        0.1031
16378.7    80.00  0.37     Sequence
 HLA-DPA10201-DPB11401  151      YHKNNKSWMESEFRV  KSWMESEFR  5        0.1423
10727.1    65.00  0.49     Sequence
 HLA-DPA10201-DPB11401  152      HKNNKSWMESEFRVY  KSWMESEFR  4        0.1725
7730.7    55.00  0.42     Sequence
 HLA-DPA10201-DPB11401  153      KNNKSWMESEFRVYS  KSWMESEFR  3        0.1823
6955.7    49.00  0.40     Sequence
 HLA-DPA10201-DPB11401  154      NNKSWMESEFRVYSS  KSWMESEFR  2        0.1787
7231.8    50.00  0.37     Sequence
 HLA-DPA10201-DPB11401  155      NKSWMESEFRVYSSA  KSWMESEFR  1        0.1798
7144.5    49.00  0.34     Sequence
 HLA-DPA10201-DPB11401  156      KSWMESEFRVYSSAN  SWMESEFRV  1        0.2022
5608.9    42.00  0.25     Sequence
 HLA-DPA10201-DPB11401  157      SWMESEFRVYSSANN  RVYSSANNX  7        0.2515
3289.3    28.00  0.19     Sequence
 HLA-DPA10201-DPB11401  158      WMESEFRVYSSANNC  RVYSSANNC  6        0.3426
1227.2    11.00  0.49     Sequence
 HLA-DPA10201-DPB11401  159      MESEFRVYSSANNCT  RVYSSANNC  5        0.3876
754.3     6.50  0.56     Sequence          WB
 HLA-DPA10201-DPB11401  160      ESEFRVYSSANNCTF  RVYSSANNC  4        0.4184
540.4     4.50  0.58     Sequence          WB
 HLA-DPA10201-DPB11401  161      SEFRVYSSANNCTFE  RVYSSANNC  3        0.4279
487.8     4.00  0.58     Sequence          WB
```

```
 HLA-DPA10201-DPB11401  162      EFRVYSSANNCTFEY  RVYSSANNC  2        0.4323
464.9     4.00  0.61     Sequence         WB
 HLA-DPA10201-DPB11401  163      FRVYSSANNCTFEYV  RVYSSANNC  1        0.3413
1245.3    11.00  0.56     Sequence
 HLA-DPA10201-DPB11401  164      RVYSSANNCTFEYVS  RVYSSANNC  0        0.1504
9818.4    65.00  0.52     Sequence
 HLA-DPA10201-DPB11401  165      VYSSANNCTFEYVSQ  SSANNCTFE  2        0.0391
32749.4   100.00  0.17     Sequence
 HLA-DPA10201-DPB11401  166      YSSANNCTFEYVSQP  ANNCTFEYV  3        0.0313
35629.3   100.00  0.22     Sequence
 HLA-DPA10201-DPB11401  167      SSANNCTFEYVSQPF  TFEYVSQPF  6        0.0497
29217.2   100.00  0.35     Sequence
 HLA-DPA10201-DPB11401  168      SANNCTFEYVSQPFL  FEYVSQPFL  6        0.1175
14021.5    75.00  0.33     Sequence
 HLA-DPA10201-DPB11401  169      ANNCTFEYVSQPFLM  EYVSQPFLM  6        0.2181
4723.0    37.00  0.44     Sequence
 HLA-DPA10201-DPB11401  170      NNCTFEYVSQPFLMD  EYVSQPFLM  5        0.2673
2774.0    24.00  0.51     Sequence
 HLA-DPA10201-DPB11401  171      NCTFEYVSQPFLMDL  EYVSQPFLM  4        0.3330
1362.3    12.00  0.47     Sequence
 HLA-DPA10201-DPB11401  172      CTFEYVSQPFLMDLE  EYVSQPFLM  3        0.3413
1245.0    11.00  0.44     Sequence
 HLA-DPA10201-DPB11401  173      TFEYVSQPFLMDLEG  EYVSQPFLM  2        0.3346
1338.9    12.00  0.47     Sequence
 HLA-DPA10201-DPB11401  174      FEYVSQPFLMDLEGK  EYVSQPFLM  1        0.3090
1765.6    16.00  0.46     Sequence
 HLA-DPA10201-DPB11401  175      EYVSQPFLMDLEGKQ  EYVSQPFLM  0        0.2311
4104.4    33.00  0.42     Sequence
 HLA-DPA10201-DPB11401  176      YVSQPFLMDLEGKQG  YVSQPFLMD  0        0.1425
10696.3    65.00  0.25     Sequence
 HLA-DPA10201-DPB11401  177      VSQPFLMDLEGKQGN  PFLMDLEGK  3        0.0884
19217.6    85.00  0.25     Sequence
 HLA-DPA10201-DPB11401  178      SQPFLMDLEGKQGNF  PFLMDLEGK  2        0.0774
21646.5    90.00  0.31     Sequence
 HLA-DPA10201-DPB11401  179      QPFLMDLEGKQGNFK  FLMDLEGKQ  2        0.0669
24248.5    95.00  0.28     Sequence
 HLA-DPA10201-DPB11401  180      PFLMDLEGKQGNFKN  FLMDLEGKQ  1        0.0649
24771.4    95.00  0.31     Sequence
 HLA-DPA10201-DPB11401  181      FLMDLEGKQGNFKNL  GKQGNFKNL  6        0.0589
26425.7    95.00  0.18     Sequence
 HLA-DPA10201-DPB11401  182      LMDLEGKQGNFKNLS  GKQGNFKNL  5        0.0666
24310.5    95.00  0.43     Sequence
 HLA-DPA10201-DPB11401  183      MDLEGKQGNFKNLSE  GKQGNFKNL  4        0.0740
22461.5    90.00  0.41     Sequence
 HLA-DPA10201-DPB11401  184      DLEGKQGNFKNLSEF  GKQGNFKNL  3        0.0789
21296.4    90.00  0.38     Sequence
 HLA-DPA10201-DPB11401  185      LEGKQGNFKNLSEFV  GKQGNFKNL  2        0.1115
14970.0    80.00  0.31     Sequence
 HLA-DPA10201-DPB11401  186      EGKQGNFKNLSEFVF  NFKNLSEFV  5        0.1476
10129.5    65.00  0.22     Sequence
 HLA-DPA10201-DPB11401  187      GKQGNFKNLSEFVFK  KNLSEFVFK  6        0.1897
6418.8    46.00  0.29     Sequence
 HLA-DPA10201-DPB11401  188      KQGNFKNLSEFVFKN  KNLSEFVFK  5        0.2100
5152.6    39.00  0.36     Sequence
 HLA-DPA10201-DPB11401  189      QGNFKNLSEFVFKNI  KNLSEFVFK  4        0.2482
3409.9    28.00  0.34     Sequence
 HLA-DPA10201-DPB11401  190      GNFKNLSEFVFKNID  KNLSEFVFK  3        0.2422
3636.6    30.00  0.34     Sequence
 HLA-DPA10201-DPB11401  191      NFKNLSEFVFKNIDG  KNLSEFVFK  2        0.2407
3696.0    30.00  0.37     Sequence
 HLA-DPA10201-DPB11401  192      FKNLSEFVFKNIDGY  KNLSEFVFK  1        0.2125
5015.5    38.00  0.43     Sequence
 HLA-DPA10201-DPB11401  193      KNLSEFVFKNIDGYF  KNLSEFVFK  0        0.1673
8180.0    55.00  0.35     Sequence
 HLA-DPA10201-DPB11401  194      NLSEFVFKNIDGYFK  FKNIDGYFK  6        0.1404
10949.7    65.00  0.19     Sequence
```

```
 HLA-DPA10201-DPB11401  195      LSEFVFKNIDGYFKI  KNIDGYFKI  6        0.2273
4274.5    34.00  0.47     Sequence
 HLA-DPA10201-DPB11401  196      SEFVFKNIDGYFKIY  KNIDGYFKI  5        0.2888
2198.5    20.00  0.62     Sequence
 HLA-DPA10201-DPB11401  197      EFVFKNIDGYFKIYS  KNIDGYFKI  4        0.3119
1711.6    16.00  0.62     Sequence
 HLA-DPA10201-DPB11401  198      FVFKNIDGYFKIYSK  KNIDGYFKI  3        0.3224
1527.4    14.00  0.63     Sequence
 HLA-DPA10201-DPB11401  199      VFKNIDGYFKIYSKH  KNIDGYFKI  2        0.3053
1838.6    17.00  0.66     Sequence
 HLA-DPA10201-DPB11401  200      FKNIDGYFKIYSKHT  KNIDGYFKI  1        0.2844
2304.7    20.00  0.61     Sequence
 HLA-DPA10201-DPB11401  201      KNIDGYFKIYSKHTP  KNIDGYFKI  0        0.2438
3576.9    30.00  0.48     Sequence
 HLA-DPA10201-DPB11401  202      NIDGYFKIYSKHTPI  KIYSKHTPI  6        0.2939
2079.0    19.00  0.62     Sequence
 HLA-DPA10201-DPB11401  203      IDGYFKIYSKHTPIN  KIYSKHTPI  5        0.3671
941.7     8.50  0.71    Sequence         WB
 HLA-DPA10201-DPB11401  204      DGYFKIYSKHTPINL  KIYSKHTPI  4        0.4457
402.3     3.50  0.67    Sequence         WB
 HLA-DPA10201-DPB11401  205      GYFKIYSKHTPINLV  KIYSKHTPI  3        0.4955
234.8     1.60  0.62    Sequence         SB
 HLA-DPA10201-DPB11401  206      YFKIYSKHTPINLVR  KIYSKHTPI  2        0.5298
161.9     0.90  0.58    Sequence         SB
 HLA-DPA10201-DPB11401  207      FKIYSKHTPINLVRD  KIYSKHTPI  1        0.4894
250.8     1.70  0.50    Sequence         SB
 HLA-DPA10201-DPB11401  208      KIYSKHTPINLVRDL  KIYSKHTPI  0        0.4370
442.0     3.50  0.35    Sequence         WB
 HLA-DPA10201-DPB11401  209      IYSKHTPINLVRDLP  SKHTPINLV  2        0.3259
1470.7    13.00  0.31     Sequence
 HLA-DPA10201-DPB11401  210      YSKHTPINLVRDLPQ  SKHTPINLV  1        0.2931
2096.5    19.00  0.34     Sequence
 HLA-DPA10201-DPB11401  211      SKHTPINLVRDLPQG  SKHTPINLV  0        0.2265
4312.5    34.00  0.32     Sequence
 HLA-DPA10201-DPB11401  212      KHTPINLVRDLPQGF  KHTPINLVR  0        0.1726
7727.4    55.00  0.18     Sequence
 HLA-DPA10201-DPB11401  213      HTPINLVRDLPQGFS  LVRDLPQGF  5        0.1444
10479.4    65.00  0.27     Sequence
 HLA-DPA10201-DPB11401  214      TPINLVRDLPQGFSA  LVRDLPQGF  4        0.1744
7577.0    55.00  0.27     Sequence
 HLA-DPA10201-DPB11401  215      PINLVRDLPQGFSAL  RDLPQGFSA  5        0.2088
5220.0    40.00  0.35     Sequence
 HLA-DPA10201-DPB11401  216      INLVRDLPQGFSALE  RDLPQGFSA  4        0.2186
4694.4    37.00  0.34     Sequence
 HLA-DPA10201-DPB11401  217      NLVRDLPQGFSALEP  RDLPQGFSA  3        0.2180
4727.8    37.00  0.34     Sequence
 HLA-DPA10201-DPB11401  218      LVRDLPQGFSALEPL  RDLPQGFSA  2        0.2232
4470.0    35.00  0.31     Sequence
 HLA-DPA10201-DPB11401  219      VRDLPQGFSALEPLV  QGFSALEPL  5        0.2531
3233.4    27.00  0.35     Sequence
 HLA-DPA10201-DPB11401  220      RDLPQGFSALEPLVD  QGFSALEPL  4        0.2720
2635.7    23.00  0.34     Sequence
 HLA-DPA10201-DPB11401  221      DLPQGFSALEPLVDL  QGFSALEPL  3        0.3308
1395.0    13.00  0.30     Sequence
 HLA-DPA10201-DPB11401  222      LPQGFSALEPLVDLP  QGFSALEPL  2        0.3472
1168.5    11.00  0.28     Sequence
 HLA-DPA10201-DPB11401  223      PQGFSALEPLVDLPI  FSALEPLVD  3        0.3626
988.8     9.00  0.25    Sequence         WB
 HLA-DPA10201-DPB11401  224      QGFSALEPLVDLPIG  FSALEPLVD  2        0.3524
1104.6    10.00  0.27     Sequence
 HLA-DPA10201-DPB11401  225      GFSALEPLVDLPIGI  FSALEPLVD  1        0.3138
1676.2    15.00  0.25     Sequence
 HLA-DPA10201-DPB11401  226      FSALEPLVDLPIGIN  SALEPLVDL  1        0.2501
3340.0    28.00  0.26     Sequence
 HLA-DPA10201-DPB11401  227      SALEPLVDLPIGINI  PLVDLPIGI  4        0.2163
4816.9    37.00  0.23     Sequence
```

```
 HLA-DPA10201-DPB11401  228      ALEPLVDLPIGINIT  PLVDLPIGI  3        0.2082
5255.1    40.00  0.28     Sequence
 HLA-DPA10201-DPB11401  229      LEPLVDLPIGINITR  PLVDLPIGI  2        0.2136
4958.2    38.00  0.28     Sequence
 HLA-DPA10201-DPB11401  230      EPLVDLPIGINITRF  PLVDLPIGI  1        0.2161
4826.0    37.00  0.22     Sequence
 HLA-DPA10201-DPB11401  231      PLVDLPIGINITRFQ  PLVDLPIGI  0        0.2136
4957.8    38.00  0.22     Sequence
 HLA-DPA10201-DPB11401  232      LVDLPIGINITRFQT  PIGINITRF  4        0.1895
6433.1    46.00  0.24     Sequence
 HLA-DPA10201-DPB11401  233      VDLPIGINITRFQTL  INITRFQTL  6        0.2068
5338.7    40.00  0.23     Sequence
 HLA-DPA10201-DPB11401  234      DLPIGINITRFQTLL  INITRFQTL  5        0.2464
3475.5    29.00  0.38     Sequence
 HLA-DPA10201-DPB11401  235      LPIGINITRFQTLLA  INITRFQTL  4        0.2914
2136.9    19.00  0.43     Sequence
 HLA-DPA10201-DPB11401  236      PIGINITRFQTLLAL  INITRFQTL  3        0.3375
1297.6    12.00  0.34     Sequence
 HLA-DPA10201-DPB11401  237      IGINITRFQTLLALH  TRFQTLLAL  5        0.4142
565.7     5.00  0.27    Sequence         WB
 HLA-DPA10201-DPB11401  238      GINITRFQTLLALHR  RFQTLLALH  5        0.4685
314.5     2.50  0.28    Sequence         WB
 HLA-DPA10201-DPB11401  239      INITRFQTLLALHRS  RFQTLLALH  4        0.4753
292.2     2.50  0.28    Sequence         WB
 HLA-DPA10201-DPB11401  240      NITRFQTLLALHRSY  RFQTLLALH  3        0.4689
313.1     2.50  0.32    Sequence         WB
 HLA-DPA10201-DPB11401  241      ITRFQTLLALHRSYL  RFQTLLALH  2        0.4716
304.1     2.50  0.31    Sequence         WB
 HLA-DPA10201-DPB11401  242      TRFQTLLALHRSYLT  FQTLLALHR  2        0.4411
422.9     3.50  0.26    Sequence         WB
 HLA-DPA10201-DPB11401  243      RFQTLLALHRSYLTP  FQTLLALHR  1        0.3878
752.8     6.50  0.29    Sequence         WB
 HLA-DPA10201-DPB11401  244      FQTLLALHRSYLTPG  FQTLLALHR  0        0.2325
4039.3    33.00  0.32     Sequence
 HLA-DPA10201-DPB11401  245      QTLLALHRSYLTPGD  LLALHRSYL  2        0.1420
10762.2    65.00  0.24     Sequence
 HLA-DPA10201-DPB11401  246      TLLALHRSYLTPGDS  RSYLTPGDS  6        0.1286
12441.3    70.00  0.22     Sequence
 HLA-DPA10201-DPB11401  247      LLALHRSYLTPGDSS  RSYLTPGDS  5        0.1293
12348.6    70.00  0.28     Sequence
 HLA-DPA10201-DPB11401  248      LALHRSYLTPGDSSS  RSYLTPGDS  4        0.1219
13365.6    75.00  0.40     Sequence
 HLA-DPA10201-DPB11401  249      ALHRSYLTPGDSSSG  RSYLTPGDS  3        0.1072
15672.5    80.00  0.47     Sequence
 HLA-DPA10201-DPB11401  250      LHRSYLTPGDSSSGW  RSYLTPGDS  2        0.0914
18601.0    85.00  0.52     Sequence
 HLA-DPA10201-DPB11401  251      HRSYLTPGDSSSGWT  RSYLTPGDS  1        0.0769
21762.0    90.00  0.47     Sequence
 HLA-DPA10201-DPB11401  252      RSYLTPGDSSSGWTA  RSYLTPGDS  0        0.0475
29922.3    100.00  0.40     Sequence
 HLA-DPA10201-DPB11401  253      SYLTPGDSSSGWTAG  SYLTPGDSS  0        0.0216
39594.2    100.00  0.34     Sequence
 HLA-DPA10201-DPB11401  254      YLTPGDSSSGWTAGA  DSSSGWTAG  5        0.0153
42366.2    100.00  0.15     Sequence
 HLA-DPA10201-DPB11401  255      LTPGDSSSGWTAGAA  SSGWTAGAA  6        0.0209
39878.0    100.00  0.23     Sequence
 HLA-DPA10201-DPB11401  256      TPGDSSSGWTAGAAA  SGWTAGAAA  6        0.0346
34382.2    100.00  0.33     Sequence
 HLA-DPA10201-DPB11401  257      PGDSSSGWTAGAAAY  SGWTAGAAA  5        0.0500
29117.1    100.00  0.38     Sequence
 HLA-DPA10201-DPB11401  258      GDSSSGWTAGAAAYY  SGWTAGAAA  4        0.0609
25860.3    95.00  0.32     Sequence
 HLA-DPA10201-DPB11401  259      DSSSGWTAGAAAYYV  SGWTAGAAA  3        0.0818
20628.3    90.00  0.27     Sequence
 HLA-DPA10201-DPB11401  260      SSSGWTAGAAAYYVG  SGWTAGAAA  2        0.0865
19601.7    85.00  0.28     Sequence
```

```
 HLA-DPA10201-DPB11401  261      SSGWTAGAAAYYVGY  TAGAAAYYV  4        0.0883
19241.1    85.00  0.20     Sequence
 HLA-DPA10201-DPB11401  262      SGWTAGAAAYYVGYL  TAGAAAYYV  3        0.0987
17188.5    85.00  0.23     Sequence
 HLA-DPA10201-DPB11401  263      GWTAGAAAYYVGYLQ  TAGAAAYYV  2        0.1021
16571.4    80.00  0.24     Sequence
 HLA-DPA10201-DPB11401  264      WTAGAAAYYVGYLQP  AYYVGYLQP  6        0.1195
13720.7    75.00  0.26     Sequence
 HLA-DPA10201-DPB11401  265      TAGAAAYYVGYLQPR  AYYVGYLQP  5        0.1387
11151.8    65.00  0.32     Sequence
 HLA-DPA10201-DPB11401  266      AGAAAYYVGYLQPRT  AYYVGYLQP  4        0.1515
9707.2    60.00  0.31     Sequence
 HLA-DPA10201-DPB11401  267      GAAAYYVGYLQPRTF  AYYVGYLQP  3        0.1757
7467.4    55.00  0.28     Sequence
 HLA-DPA10201-DPB11401  268      AAAYYVGYLQPRTFL  AYYVGYLQP  2        0.2173
4764.9    37.00  0.25     Sequence
 HLA-DPA10201-DPB11401  269      AAYYVGYLQPRTFLL  YLQPRTFLL  6        0.2785
2456.2    21.00  0.20     Sequence
 HLA-DPA10201-DPB11401  270      AYYVGYLQPRTFLLK  YLQPRTFLL  5        0.3110
1728.4    16.00  0.35     Sequence
 HLA-DPA10201-DPB11401  271      YYVGYLQPRTFLLKY  YLQPRTFLL  4        0.3120
1709.9    16.00  0.38     Sequence
 HLA-DPA10201-DPB11401  272      YVGYLQPRTFLLKYN  YLQPRTFLL  3        0.2987
1974.0    18.00  0.41     Sequence
 HLA-DPA10201-DPB11401  273      VGYLQPRTFLLKYNE  YLQPRTFLL  2        0.2785
2455.4    21.00  0.41     Sequence
 HLA-DPA10201-DPB11401  274      GYLQPRTFLLKYNEN  YLQPRTFLL  1        0.2587
3043.9    26.00  0.35     Sequence
 HLA-DPA10201-DPB11401  275      YLQPRTFLLKYNENG  YLQPRTFLL  0        0.1947
6079.4    44.00  0.32     Sequence
 HLA-DPA10201-DPB11401  276      LQPRTFLLKYNENGT  RTFLLKYNE  3        0.1547
9375.8    60.00  0.41     Sequence
 HLA-DPA10201-DPB11401  277      QPRTFLLKYNENGTI  RTFLLKYNE  2        0.1571
9137.5    60.00  0.42     Sequence
 HLA-DPA10201-DPB11401  278      PRTFLLKYNENGTIT  KYNENGTIT  6        0.1882
6523.6    47.00  0.38     Sequence
 HLA-DPA10201-DPB11401  279      RTFLLKYNENGTITD  KYNENGTIT  5        0.1886
6500.4    46.00  0.46     Sequence
 HLA-DPA10201-DPB11401  280      TFLLKYNENGTITDA  KYNENGTIT  4        0.1955
6031.5    44.00  0.56     Sequence
 HLA-DPA10201-DPB11401  281      FLLKYNENGTITDAV  KYNENGTIT  3        0.2078
5276.3    40.00  0.57     Sequence
 HLA-DPA10201-DPB11401  282      LLKYNENGTITDAVD  KYNENGTIT  2        0.1878
6557.1    47.00  0.57     Sequence
 HLA-DPA10201-DPB11401  283      LKYNENGTITDAVDC  KYNENGTIT  1        0.1443
10489.8    65.00  0.50     Sequence
 HLA-DPA10201-DPB11401  284      KYNENGTITDAVDCA  KYNENGTIT  0        0.0932
18234.3    85.00  0.37     Sequence
 HLA-DPA10201-DPB11401  285      YNENGTITDAVDCAL  GTITDAVDC  4        0.0833
20295.5    90.00  0.31     Sequence
 HLA-DPA10201-DPB11401  286      NENGTITDAVDCALD  ITDAVDCAL  5        0.0866
19599.1    85.00  0.27     Sequence
 HLA-DPA10201-DPB11401  287      ENGTITDAVDCALDP  ITDAVDCAL  4        0.0890
19080.0    85.00  0.26     Sequence
 HLA-DPA10201-DPB11401  288      NGTITDAVDCALDPL  ITDAVDCAL  3        0.1021
16570.7    80.00  0.25     Sequence
 HLA-DPA10201-DPB11401  289      GTITDAVDCALDPLS  ITDAVDCAL  2        0.1082
15509.8    80.00  0.22     Sequence
 HLA-DPA10201-DPB11401  290      TITDAVDCALDPLSE  ITDAVDCAL  1        0.0977
17380.8    85.00  0.23     Sequence
 HLA-DPA10201-DPB11401  291      ITDAVDCALDPLSET  AVDCALDPL  3        0.0834
20270.1    90.00  0.28     Sequence
 HLA-DPA10201-DPB11401  292      TDAVDCALDPLSETK  AVDCALDPL  2        0.0677
24028.3    95.00  0.29     Sequence
 HLA-DPA10201-DPB11401  293      DAVDCALDPLSETKC  AVDCALDPL  1        0.0662
24422.5    95.00  0.24     Sequence
```

```
 HLA-DPA10201-DPB11401  294      AVDCALDPLSETKCT  CALDPLSET  3        0.0655
24620.4    95.00  0.25     Sequence
 HLA-DPA10201-DPB11401  295      VDCALDPLSETKCTL  CALDPLSET  2        0.0640
25027.6    95.00  0.31     Sequence
 HLA-DPA10201-DPB11401  296      DCALDPLSETKCTLK  PLSETKCTL  5        0.0885
19201.4    85.00  0.33     Sequence
 HLA-DPA10201-DPB11401  297      CALDPLSETKCTLKS  PLSETKCTL  4        0.0962
17653.1    85.00  0.38     Sequence
 HLA-DPA10201-DPB11401  298      ALDPLSETKCTLKSF  PLSETKCTL  3        0.0947
17945.0    85.00  0.41     Sequence
 HLA-DPA10201-DPB11401  299      LDPLSETKCTLKSFT  PLSETKCTL  2        0.1042
16200.7    80.00  0.38     Sequence
 HLA-DPA10201-DPB11401  300      DPLSETKCTLKSFTV  KCTLKSFTV  6        0.1520
9658.6    60.00  0.47    Sequence
 HLA-DPA10201-DPB11401  301      PLSETKCTLKSFTVE  KCTLKSFTV  5        0.1708
7875.1    55.00  0.54    Sequence
 HLA-DPA10201-DPB11401  302      LSETKCTLKSFTVEK  KCTLKSFTV  4        0.1918
6273.7    45.00  0.57    Sequence
 HLA-DPA10201-DPB11401  303      SETKCTLKSFTVEKG  KCTLKSFTV  3        0.2076
5292.1    40.00  0.43    Sequence
 HLA-DPA10201-DPB11401  304      ETKCTLKSFTVEKGI  KSFTVEKGI  6        0.2857
2271.9    20.00  0.40    Sequence
 HLA-DPA10201-DPB11401  305      TKCTLKSFTVEKGIY  KSFTVEKGI  5        0.3170
1619.3    15.00  0.49    Sequence
 HLA-DPA10201-DPB11401  306      KCTLKSFTVEKGIYQ  KSFTVEKGI  4        0.3296
1413.9    13.00  0.54    Sequence
 HLA-DPA10201-DPB11401  307      CTLKSFTVEKGIYQT  KSFTVEKGI  3        0.3212
1546.8    14.00  0.55    Sequence
 HLA-DPA10201-DPB11401  308      TLKSFTVEKGIYQTS  KSFTVEKGI  2        0.3198
1571.4    14.00  0.58    Sequence
 HLA-DPA10201-DPB11401  309      LKSFTVEKGIYQTSN  KSFTVEKGI  1        0.2767
2503.8    22.00  0.52    Sequence
 HLA-DPA10201-DPB11401  310      KSFTVEKGIYQTSNF  KSFTVEKGI  0        0.2329
4022.3    32.00  0.41    Sequence
 HLA-DPA10201-DPB11401  311      SFTVEKGIYQTSNFR  FTVEKGIYQ  1        0.1228
13245.8    75.00  0.28     Sequence
 HLA-DPA10201-DPB11401  312      FTVEKGIYQTSNFRV  IYQTSNFRV  6        0.1696
7982.0    55.00  0.27    Sequence
 HLA-DPA10201-DPB11401  313      TVEKGIYQTSNFRVQ  IYQTSNFRV  5        0.1964
5969.2    44.00  0.44    Sequence
 HLA-DPA10201-DPB11401  314      VEKGIYQTSNFRVQP  IYQTSNFRV  4        0.2029
5564.3    42.00  0.45    Sequence
 HLA-DPA10201-DPB11401  315      EKGIYQTSNFRVQPT  IYQTSNFRV  3        0.2073
5307.9    40.00  0.46    Sequence
 HLA-DPA10201-DPB11401  316      KGIYQTSNFRVQPTE  IYQTSNFRV  2        0.2027
5578.0    42.00  0.44    Sequence
 HLA-DPA10201-DPB11401  317      GIYQTSNFRVQPTES  IYQTSNFRV  1        0.1680
8120.4    55.00  0.46    Sequence
 HLA-DPA10201-DPB11401  318      IYQTSNFRVQPTESI  FRVQPTESI  6        0.2084
5245.6    40.00  0.31    Sequence
 HLA-DPA10201-DPB11401  319      YQTSNFRVQPTESIV  FRVQPTESI  5        0.2940
2078.3    19.00  0.41    Sequence
 HLA-DPA10201-DPB11401  320      QTSNFRVQPTESIVR  FRVQPTESI  4        0.3605
1011.4     9.00  0.36    Sequence          WB
 HLA-DPA10201-DPB11401  321      TSNFRVQPTESIVRF  RVQPTESIV  4        0.3861
766.5     7.00  0.38    Sequence          WB
 HLA-DPA10201-DPB11401  322      SNFRVQPTESIVRFP  RVQPTESIV  3        0.3894
740.0     6.50  0.38    Sequence          WB
 HLA-DPA10201-DPB11401  323      NFRVQPTESIVRFPN  RVQPTESIV  2        0.3839
785.5     7.00  0.40    Sequence          WB
 HLA-DPA10201-DPB11401  324      FRVQPTESIVRFPNI  RVQPTESIV  1        0.3645
968.9     8.50  0.38    Sequence          WB
 HLA-DPA10201-DPB11401  325      RVQPTESIVRFPNIT  RVQPTESIV  0        0.2357
3902.3    32.00  0.31    Sequence
 HLA-DPA10201-DPB11401  326      VQPTESIVRFPNITN  ESIVRFPNI  4        0.1565
9193.1    60.00  0.30    Sequence
```

```
 HLA-DPA10201-DPB11401  327      QPTESIVRFPNITNL  VRFPNITNL  6        0.1951
6055.0    44.00  0.35     Sequence
 HLA-DPA10201-DPB11401  328      PTESIVRFPNITNLC  VRFPNITNL  5        0.2442
3559.3    29.00  0.47     Sequence
 HLA-DPA10201-DPB11401  329      TESIVRFPNITNLCP  VRFPNITNL  4        0.2498
3351.5    28.00  0.49     Sequence
 HLA-DPA10201-DPB11401  330      ESIVRFPNITNLCPF  VRFPNITNL  3        0.2637
2884.2    25.00  0.51     Sequence
 HLA-DPA10201-DPB11401  331      SIVRFPNITNLCPFG  VRFPNITNL  2        0.2611
2964.6    25.00  0.56     Sequence
 HLA-DPA10201-DPB11401  332      IVRFPNITNLCPFGE  VRFPNITNL  1        0.2416
3661.4    30.00  0.54     Sequence
 HLA-DPA10201-DPB11401  333      VRFPNITNLCPFGEV  VRFPNITNL  0        0.1907
6349.6    46.00  0.44     Sequence
 HLA-DPA10201-DPB11401  334      RFPNITNLCPFGEVF  PNITNLCPF  2        0.1201
13629.3    75.00  0.28     Sequence
 HLA-DPA10201-DPB11401  335      FPNITNLCPFGEVFN  PNITNLCPF  1        0.0783
21428.4    90.00  0.25     Sequence
 HLA-DPA10201-DPB11401  336      PNITNLCPFGEVFNA  TNLCPFGEV  3        0.0744
22357.7    90.00  0.25     Sequence
 HLA-DPA10201-DPB11401  337      NITNLCPFGEVFNAT  TNLCPFGEV  2        0.0755
22092.3    90.00  0.22     Sequence
 HLA-DPA10201-DPB11401  338      ITNLCPFGEVFNATR  PFGEVFNAT  5        0.0938
18112.8    85.00  0.30     Sequence
 HLA-DPA10201-DPB11401  339      TNLCPFGEVFNATRF  PFGEVFNAT  4        0.1052
16023.6    80.00  0.29     Sequence
 HLA-DPA10201-DPB11401  340      NLCPFGEVFNATRFA  GEVFNATRF  5        0.1509
9773.8    60.00  0.25     Sequence
 HLA-DPA10201-DPB11401  341      LCPFGEVFNATRFAS  EVFNATRFA  5        0.2041
5493.9    41.00  0.26     Sequence
 HLA-DPA10201-DPB11401  342      CPFGEVFNATRFASV  FNATRFASV  6        0.3072
1801.5    16.00  0.34     Sequence
 HLA-DPA10201-DPB11401  343      PFGEVFNATRFASVY  FNATRFASV  5        0.3682
931.1     8.50  0.47     Sequence          WB
 HLA-DPA10201-DPB11401  344      FGEVFNATRFASVYA  FNATRFASV  4        0.4266
494.6     4.00  0.47     Sequence          WB
 HLA-DPA10201-DPB11401  345      GEVFNATRFASVYAW  FNATRFASV  3        0.4148
562.4     5.00  0.50     Sequence          WB
 HLA-DPA10201-DPB11401  346      EVFNATRFASVYAWN  FNATRFASV  2        0.4145
563.9     5.00  0.48     Sequence          WB
 HLA-DPA10201-DPB11401  347      VFNATRFASVYAWNR  FNATRFASV  1        0.3855
771.9     7.00  0.41     Sequence          WB
 HLA-DPA10201-DPB11401  348      FNATRFASVYAWNRK  RFASVYAWN  4        0.3420
1236.2    11.00  0.31     Sequence
 HLA-DPA10201-DPB11401  349      NATRFASVYAWNRKR  RFASVYAWN  3        0.2986
1977.2    18.00  0.38     Sequence
 HLA-DPA10201-DPB11401  350      ATRFASVYAWNRKRI  RFASVYAWN  2        0.3038
1868.5    17.00  0.37     Sequence
 HLA-DPA10201-DPB11401  351      TRFASVYAWNRKRIS  FASVYAWNR  2        0.2556
3147.7    27.00  0.26     Sequence
 HLA-DPA10201-DPB11401  352      RFASVYAWNRKRISN  FASVYAWNR  1        0.2231
4473.9    35.00  0.27     Sequence
 HLA-DPA10201-DPB11401  353      FASVYAWNRKRISNC  VYAWNRKRI  3        0.1589
8956.1    60.00  0.28     Sequence
 HLA-DPA10201-DPB11401  354      ASVYAWNRKRISNCV  VYAWNRKRI  2        0.1117
14933.8    80.00  0.38     Sequence
 HLA-DPA10201-DPB11401  355      SVYAWNRKRISNCVA  RKRISNCVA  6        0.1673
8178.6    55.00  0.28     Sequence
 HLA-DPA10201-DPB11401  356      VYAWNRKRISNCVAD  KRISNCVAD  6        0.2046
5465.9    41.00  0.28     Sequence
 HLA-DPA10201-DPB11401  357      YAWNRKRISNCVADY  KRISNCVAD  5        0.2428
3613.2    30.00  0.31     Sequence
 HLA-DPA10201-DPB11401  358      AWNRKRISNCVADYS  KRISNCVAD  4        0.2648
2849.6    24.00  0.31     Sequence
 HLA-DPA10201-DPB11401  359      WNRKRISNCVADYSV  KRISNCVAD  3        0.2896
2177.8    19.00  0.31     Sequence
```

```
 HLA-DPA10201-DPB11401  360      NRKRISNCVADYSVL  KRISNCVAD  2        0.3034
1876.6    17.00  0.28    Sequence
 HLA-DPA10201-DPB11401  361      RKRISNCVADYSVLY  RISNCVADY  2        0.2970
2010.6    18.00  0.40    Sequence
 HLA-DPA10201-DPB11401  362      KRISNCVADYSVLYN  RISNCVADY  1        0.2134
4966.5    38.00  0.35    Sequence
 HLA-DPA10201-DPB11401  363      RISNCVADYSVLYNS  RISNCVADY  0        0.1318
12011.9    70.00  0.31    Sequence
 HLA-DPA10201-DPB11401  364      ISNCVADYSVLYNSA  CVADYSVLY  3        0.0960
17690.2    85.00  0.26    Sequence
 HLA-DPA10201-DPB11401  365      SNCVADYSVLYNSAS  CVADYSVLY  2        0.0983
17262.5    85.00  0.22    Sequence
 HLA-DPA10201-DPB11401  366      NCVADYSVLYNSASF  CVADYSVLY  1        0.1002
16909.6    80.00  0.20    Sequence
 HLA-DPA10201-DPB11401  367      CVADYSVLYNSASFS  VLYNSASFS  6        0.1067
15762.9    80.00  0.19    Sequence
 HLA-DPA10201-DPB11401  368      VADYSVLYNSASFST  LYNSASFST  6        0.1499
9878.0    65.00  0.35    Sequence
 HLA-DPA10201-DPB11401  369      ADYSVLYNSASFSTF  LYNSASFST  5        0.1806
7085.8    49.00  0.44    Sequence
 HLA-DPA10201-DPB11401  370      DYSVLYNSASFSTFK  LYNSASFST  4        0.2070
5322.9    40.00  0.42    Sequence
 HLA-DPA10201-DPB11401  371      YSVLYNSASFSTFKC  LYNSASFST  3        0.2236
4449.8    35.00  0.41    Sequence
 HLA-DPA10201-DPB11401  372      SVLYNSASFSTFKCY  LYNSASFST  2        0.2092
5197.6    39.00  0.41    Sequence
 HLA-DPA10201-DPB11401  373      VLYNSASFSTFKCYG  LYNSASFST  1        0.1786
7240.1    50.00  0.38    Sequence
 HLA-DPA10201-DPB11401  374      LYNSASFSTFKCYGV  LYNSASFST  0        0.1313
12078.9    70.00  0.31    Sequence
 HLA-DPA10201-DPB11401  375      YNSASFSTFKCYGVS  SASFSTFKC  2        0.0885
19191.6    85.00  0.12    Sequence
 HLA-DPA10201-DPB11401  376      NSASFSTFKCYGVSP  FSTFKCYGV  4        0.0958
17730.2    85.00  0.18    Sequence
 HLA-DPA10201-DPB11401  377      SASFSTFKCYGVSPT  FKCYGVSPT  6        0.1587
8977.2    60.00  0.23    Sequence
 HLA-DPA10201-DPB11401  378      ASFSTFKCYGVSPTK  KCYGVSPTK  6        0.2014
5657.7    42.00  0.32    Sequence
 HLA-DPA10201-DPB11401  379      SFSTFKCYGVSPTKL  KCYGVSPTK  5        0.2849
2292.1    20.00  0.31    Sequence
 HLA-DPA10201-DPB11401  380      FSTFKCYGVSPTKLN  CYGVSPTKL  5        0.3341
1346.7    12.00  0.34    Sequence
 HLA-DPA10201-DPB11401  381      STFKCYGVSPTKLND  CYGVSPTKL  4        0.3320
1377.2    13.00  0.35    Sequence
 HLA-DPA10201-DPB11401  382      TFKCYGVSPTKLNDL  CYGVSPTKL  3        0.3511
1120.4    10.00  0.38    Sequence
 HLA-DPA10201-DPB11401  383      FKCYGVSPTKLNDLC  CYGVSPTKL  2        0.3066
1811.8    16.00  0.46    Sequence
 HLA-DPA10201-DPB11401  384      KCYGVSPTKLNDLCF  CYGVSPTKL  1        0.2182
4717.6    37.00  0.47    Sequence
 HLA-DPA10201-DPB11401  385      CYGVSPTKLNDLCFT  CYGVSPTKL  0        0.1693
8004.8    55.00  0.43    Sequence
 HLA-DPA10201-DPB11401  386      YGVSPTKLNDLCFTN  KLNDLCFTN  6        0.1148
14436.5    75.00  0.23    Sequence
 HLA-DPA10201-DPB11401  387      GVSPTKLNDLCFTNV  KLNDLCFTN  5        0.1037
16274.0    80.00  0.34    Sequence
 HLA-DPA10201-DPB11401  388      VSPTKLNDLCFTNVY  KLNDLCFTN  4        0.1154
14343.7    75.00  0.40    Sequence
 HLA-DPA10201-DPB11401  389      SPTKLNDLCFTNVYA  KLNDLCFTN  3        0.1173
14059.6    75.00  0.41    Sequence
 HLA-DPA10201-DPB11401  390      PTKLNDLCFTNVYAD  KLNDLCFTN  2        0.1156
14321.5    75.00  0.41    Sequence
 HLA-DPA10201-DPB11401  391      TKLNDLCFTNVYADS  KLNDLCFTN  1        0.0928
18313.6    85.00  0.31    Sequence
 HLA-DPA10201-DPB11401  392      KLNDLCFTNVYADSF  KLNDLCFTN  0        0.0885
19188.9    85.00  0.19    Sequence
```

```
 HLA-DPA10201-DPB11401  393      LNDLCFTNVYADSFV  FTNVYADSF  5        0.0938
18126.5    85.00  0.28     Sequence
 HLA-DPA10201-DPB11401  394      NDLCFTNVYADSFVI  NVYADSFVI  6        0.1326
11914.1    70.00  0.35     Sequence
 HLA-DPA10201-DPB11401  395      DLCFTNVYADSFVIR  NVYADSFVI  5        0.2051
5438.0    41.00  0.38     Sequence
 HLA-DPA10201-DPB11401  396      LCFTNVYADSFVIRG  NVYADSFVI  4        0.2201
4620.5    36.00  0.37     Sequence
 HLA-DPA10201-DPB11401  397      CFTNVYADSFVIRGD  NVYADSFVI  3        0.2120
5044.5    39.00  0.38     Sequence
 HLA-DPA10201-DPB11401  398      FTNVYADSFVIRGDE  NVYADSFVI  2        0.1998
5758.2    43.00  0.40     Sequence
 HLA-DPA10201-DPB11401  399      TNVYADSFVIRGDEV  NVYADSFVI  1        0.1761
7434.4    55.00  0.31     Sequence
 HLA-DPA10201-DPB11401  400      NVYADSFVIRGDEVR  NVYADSFVI  0        0.1764
7412.6    55.00  0.25     Sequence
 HLA-DPA10201-DPB11401  401      VYADSFVIRGDEVRQ  SFVIRGDEV  4        0.1500
9868.1    65.00  0.23     Sequence
 HLA-DPA10201-DPB11401  402      YADSFVIRGDEVRQI  SFVIRGDEV  3        0.1654
8348.3    55.00  0.25     Sequence
 HLA-DPA10201-DPB11401  403      ADSFVIRGDEVRQIA  IRGDEVRQI  5        0.1771
7359.9    55.00  0.30     Sequence
 HLA-DPA10201-DPB11401  404      DSFVIRGDEVRQIAP  IRGDEVRQI  4        0.1772
7353.7    50.00  0.31     Sequence
 HLA-DPA10201-DPB11401  405      SFVIRGDEVRQIAPG  IRGDEVRQI  3        0.1739
7618.3    55.00  0.28     Sequence
 HLA-DPA10201-DPB11401  406      FVIRGDEVRQIAPGQ  IRGDEVRQI  2        0.1489
9980.0    65.00  0.34     Sequence
 HLA-DPA10201-DPB11401  407      VIRGDEVRQIAPGQT  IRGDEVRQI  1        0.1336
11787.3    70.00  0.30     Sequence
 HLA-DPA10201-DPB11401  408      IRGDEVRQIAPGQTG  RQIAPGQTG  6        0.1189
13813.4    75.00  0.25     Sequence
 HLA-DPA10201-DPB11401  409      RGDEVRQIAPGQTGT  RQIAPGQTG  5        0.1100
15203.8    80.00  0.40     Sequence
 HLA-DPA10201-DPB11401  410      GDEVRQIAPGQTGTI  RQIAPGQTG  4        0.1258
12819.3    70.00  0.42     Sequence
 HLA-DPA10201-DPB11401  411      DEVRQIAPGQTGTIA  RQIAPGQTG  3        0.1391
11096.1    65.00  0.42     Sequence
 HLA-DPA10201-DPB11401  412      EVRQIAPGQTGTIAD  RQIAPGQTG  2        0.1517
9681.4    60.00  0.47     Sequence
 HLA-DPA10201-DPB11401  413      VRQIAPGQTGTIADY  RQIAPGQTG  1        0.1222
13330.5    75.00  0.44     Sequence
 HLA-DPA10201-DPB11401  414      RQIAPGQTGTIADYN  RQIAPGQTG  0        0.0755
22098.5    90.00  0.37     Sequence
 HLA-DPA10201-DPB11401  415      QIAPGQTGTIADYNY  IAPGQTGTI  1        0.0366
33651.3   100.00  0.23     Sequence
 HLA-DPA10201-DPB11401  416      IAPGQTGTIADYNYK  QTGTIADYN  4        0.0328
35060.7   100.00  0.25     Sequence
 HLA-DPA10201-DPB11401  417      APGQTGTIADYNYKL  QTGTIADYN  3        0.0446
30856.3   100.00  0.24     Sequence
 HLA-DPA10201-DPB11401  418      PGQTGTIADYNYKLP  TIADYNYKL  5        0.0619
25593.1    95.00  0.39     Sequence
 HLA-DPA10201-DPB11401  419      GQTGTIADYNYKLPD  TIADYNYKL  4        0.0643
24944.3    95.00  0.40     Sequence
 HLA-DPA10201-DPB11401  420      QTGTIADYNYKLPDD  TIADYNYKL  3        0.0560
27267.5    95.00  0.40     Sequence
 HLA-DPA10201-DPB11401  421      TGTIADYNYKLPDDF  TIADYNYKL  2        0.0546
27698.9    95.00  0.39     Sequence
 HLA-DPA10201-DPB11401  422      GTIADYNYKLPDDFT  TIADYNYKL  1        0.0546
27703.1    95.00  0.32     Sequence
 HLA-DPA10201-DPB11401  423      TIADYNYKLPDDFTG  TIADYNYKL  0        0.0541
27860.0    95.00  0.26     Sequence
 HLA-DPA10201-DPB11401  424      IADYNYKLPDDFTGC  KLPDDFTGC  6        0.0581
26673.3    95.00  0.28     Sequence
 HLA-DPA10201-DPB11401  425      ADYNYKLPDDFTGCV  KLPDDFTGC  5        0.0696
23537.1    90.00  0.43     Sequence
```

```
 HLA-DPA10201-DPB11401  426      DYNYKLPDDFTGCVI  KLPDDFTGC  4        0.0927
18329.3    85.00  0.39     Sequence
 HLA-DPA10201-DPB11401  427      YNYKLPDDFTGCVIA  KLPDDFTGC  3        0.1073
15653.5    80.00  0.38     Sequence
 HLA-DPA10201-DPB11401  428      NYKLPDDFTGCVIAW  KLPDDFTGC  2        0.1119
14904.1    80.00  0.33     Sequence
 HLA-DPA10201-DPB11401  429      YKLPDDFTGCVIAWN  KLPDDFTGC  1        0.1063
15829.2    80.00  0.29     Sequence
 HLA-DPA10201-DPB11401  430      KLPDDFTGCVIAWNS  PDDFTGCVI  2        0.0893
19027.6    85.00  0.19     Sequence
 HLA-DPA10201-DPB11401  431      LPDDFTGCVIAWNSN  DDFTGCVIA  2        0.0703
23357.0    90.00  0.20     Sequence
 HLA-DPA10201-DPB11401  432      PDDFTGCVIAWNSNN  DFTGCVIAW  2        0.0674
24114.8    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401  433      DDFTGCVIAWNSNNL  VIAWNSNNL  6        0.0978
17348.3    85.00  0.31     Sequence
 HLA-DPA10201-DPB11401  434      DFTGCVIAWNSNNLD  VIAWNSNNL  5        0.1089
15396.8    80.00  0.41     Sequence
 HLA-DPA10201-DPB11401  435      FTGCVIAWNSNNLDS  VIAWNSNNL  4        0.1128
14753.3    75.00  0.44     Sequence
 HLA-DPA10201-DPB11401  436      TGCVIAWNSNNLDSK  VIAWNSNNL  3        0.1050
16061.3    80.00  0.50     Sequence
 HLA-DPA10201-DPB11401  437      GCVIAWNSNNLDSKV  VIAWNSNNL  2        0.1009
16790.7    80.00  0.53     Sequence
 HLA-DPA10201-DPB11401  438      CVIAWNSNNLDSKVG  VIAWNSNNL  1        0.0946
17962.0    85.00  0.52     Sequence
 HLA-DPA10201-DPB11401  439      VIAWNSNNLDSKVGG  VIAWNSNNL  0        0.0807
20871.6    90.00  0.52     Sequence
 HLA-DPA10201-DPB11401  440      IAWNSNNLDSKVGGN  AWNSNNLDS  1        0.0309
35801.7   100.00  0.18     Sequence
 HLA-DPA10201-DPB11401  441      AWNSNNLDSKVGGNY  NNLDSKVGG  4        0.0208
39904.8   100.00  0.16     Sequence
 HLA-DPA10201-DPB11401  442      WNSNNLDSKVGGNYN  NNLDSKVGG  3        0.0211
39790.9   100.00  0.16     Sequence
 HLA-DPA10201-DPB11401  443      NSNNLDSKVGGNYNY  NNLDSKVGG  2        0.0223
39270.8   100.00  0.17     Sequence
 HLA-DPA10201-DPB11401  444      SNNLDSKVGGNYNYL  KVGGNYNYL  6        0.0664
24368.9    95.00  0.49     Sequence
 HLA-DPA10201-DPB11401  445      NNLDSKVGGNYNYLY  KVGGNYNYL  5        0.0861
19705.6    85.00  0.62     Sequence
 HLA-DPA10201-DPB11401  446      NLDSKVGGNYNYLYR  KVGGNYNYL  4        0.0970
17497.4    85.00  0.62     Sequence
 HLA-DPA10201-DPB11401  447      LDSKVGGNYNYLYRL  KVGGNYNYL  3        0.1164
14184.9    75.00  0.59     Sequence
 HLA-DPA10201-DPB11401  448      DSKVGGNYNYLYRLF  KVGGNYNYL  2        0.1342
11701.4    70.00  0.46     Sequence
 HLA-DPA10201-DPB11401  449      SKVGGNYNYLYRLFR  KVGGNYNYL  1        0.1539
9460.4    60.00  0.38     Sequence
 HLA-DPA10201-DPB11401  450      KVGGNYNYLYRLFRK  KVGGNYNYL  0        0.1482
10060.7    65.00  0.28     Sequence
 HLA-DPA10201-DPB11401  451      VGGNYNYLYRLFRKS  GNYNYLYRL  2        0.1179
13960.9    75.00  0.25     Sequence
 HLA-DPA10201-DPB11401  452      GGNYNYLYRLFRKSN  YLYRLFRKS  5        0.1381
11224.7    70.00  0.29     Sequence
 HLA-DPA10201-DPB11401  453      GNYNYLYRLFRKSNL  YRLFRKSNL  6        0.1970
5935.0    44.00  0.25     Sequence
 HLA-DPA10201-DPB11401  454      NYNYLYRLFRKSNLK  YRLFRKSNL  5        0.2680
2752.9    24.00  0.31     Sequence
 HLA-DPA10201-DPB11401  455      YNYLYRLFRKSNLKP  RLFRKSNLK  5        0.3114
1720.8    16.00  0.34     Sequence
 HLA-DPA10201-DPB11401  456      NYLYRLFRKSNLKPF  RLFRKSNLK  4        0.3829
793.7     7.00  0.32     Sequence         WB
 HLA-DPA10201-DPB11401  457      YLYRLFRKSNLKPFE  RLFRKSNLK  3        0.4003
657.4     6.00  0.31     Sequence         WB
 HLA-DPA10201-DPB11401  458      LYRLFRKSNLKPFER  FRKSNLKPF  4        0.4015
649.3     5.50  0.25     Sequence         WB
```

```
 HLA-DPA10201-DPB11401  459      YRLFRKSNLKPFERD  FRKSNLKPF  3        0.3626
989.2     9.00  0.29     Sequence         WB
 HLA-DPA10201-DPB11401  460      RLFRKSNLKPFERDI  FRKSNLKPF  2        0.3172
1615.4    15.00  0.34     Sequence
 HLA-DPA10201-DPB11401  461      LFRKSNLKPFERDIS  FRKSNLKPF  1        0.2543
3191.5    27.00  0.37     Sequence
 HLA-DPA10201-DPB11401  462      FRKSNLKPFERDIST  FRKSNLKPF  0        0.1902
6383.5    46.00  0.31     Sequence
 HLA-DPA10201-DPB11401  463      RKSNLKPFERDISTE  KSNLKPFER  1        0.1079
15565.6    80.00  0.29     Sequence
 HLA-DPA10201-DPB11401  464      KSNLKPFERDISTEI  KPFERDIST  4        0.1179
13959.0    75.00  0.22     Sequence
 HLA-DPA10201-DPB11401  465      SNLKPFERDISTEIY  FERDISTEI  5        0.1432
10623.9    65.00  0.37     Sequence
 HLA-DPA10201-DPB11401  466      NLKPFERDISTEIYQ  FERDISTEI  4        0.1602
8837.2    60.00  0.32     Sequence
 HLA-DPA10201-DPB11401  467      LKPFERDISTEIYQA  FERDISTEI  3        0.1770
7364.6    55.00  0.34     Sequence
 HLA-DPA10201-DPB11401  468      KPFERDISTEIYQAG  FERDISTEI  2        0.1671
8198.6    55.00  0.32     Sequence
 HLA-DPA10201-DPB11401  469      PFERDISTEIYQAGS  FERDISTEI  1        0.1503
9828.8    65.00  0.32     Sequence
 HLA-DPA10201-DPB11401  470      FERDISTEIYQAGST  FERDISTEI  0        0.1320
11981.8    70.00  0.21     Sequence
 HLA-DPA10201-DPB11401  471      ERDISTEIYQAGSTP  ISTEIYQAG  3        0.1001
16924.8    80.00  0.23     Sequence
 HLA-DPA10201-DPB11401  472      RDISTEIYQAGSTPC  ISTEIYQAG  2        0.0823
20524.3    90.00  0.28     Sequence
 HLA-DPA10201-DPB11401  473      DISTEIYQAGSTPCN  ISTEIYQAG  1        0.0676
24069.1    95.00  0.28     Sequence
 HLA-DPA10201-DPB11401  474      ISTEIYQAGSTPCNG  ISTEIYQAG  0        0.0611
25812.8    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401  475      STEIYQAGSTPCNGV  IYQAGSTPC  3        0.0558
27351.1    95.00  0.28     Sequence
 HLA-DPA10201-DPB11401  476      TEIYQAGSTPCNGVK  IYQAGSTPC  2        0.0508
28869.9    95.00  0.32     Sequence
 HLA-DPA10201-DPB11401  477      EIYQAGSTPCNGVKG  IYQAGSTPC  1        0.0439
31087.6   100.00  0.31     Sequence
 HLA-DPA10201-DPB11401  478      IYQAGSTPCNGVKGF  IYQAGSTPC  0        0.0403
32341.9   100.00  0.25     Sequence
 HLA-DPA10201-DPB11401  479      YQAGSTPCNGVKGFN  QAGSTPCNG  1        0.0288
36618.1   100.00  0.27     Sequence
 HLA-DPA10201-DPB11401  480      QAGSTPCNGVKGFNC  CNGVKGFNC  6        0.0232
38887.8   100.00  0.20     Sequence
 HLA-DPA10201-DPB11401  481      AGSTPCNGVKGFNCY  CNGVKGFNC  5        0.0276
37109.5   100.00  0.34     Sequence
 HLA-DPA10201-DPB11401  482      GSTPCNGVKGFNCYF  CNGVKGFNC  4        0.0306
35924.3   100.00  0.37     Sequence
 HLA-DPA10201-DPB11401  483      STPCNGVKGFNCYFP  CNGVKGFNC  3        0.0369
33537.9   100.00  0.31     Sequence
 HLA-DPA10201-DPB11401  484      TPCNGVKGFNCYFPL  KGFNCYFPL  6        0.0921
18448.8    85.00  0.48     Sequence
 HLA-DPA10201-DPB11401  485      PCNGVKGFNCYFPLQ  KGFNCYFPL  5        0.1384
11180.9    65.00  0.54     Sequence
 HLA-DPA10201-DPB11401  486      CNGVKGFNCYFPLQS  KGFNCYFPL  4        0.1824
6946.3    49.00  0.48     Sequence
 HLA-DPA10201-DPB11401  487      NGVKGFNCYFPLQSY  KGFNCYFPL  3        0.1933
6172.8    45.00  0.46     Sequence
 HLA-DPA10201-DPB11401  488      GVKGFNCYFPLQSYG  KGFNCYFPL  2        0.1901
6396.3    46.00  0.47     Sequence
 HLA-DPA10201-DPB11401  489      VKGFNCYFPLQSYGF  KGFNCYFPL  1        0.2012
5666.4    42.00  0.42     Sequence
 HLA-DPA10201-DPB11401  490      KGFNCYFPLQSYGFQ  KGFNCYFPL  0        0.1875
6573.1    47.00  0.34     Sequence
 HLA-DPA10201-DPB11401  491      GFNCYFPLQSYGFQP  NCYFPLQSY  2        0.1321
11971.8    70.00  0.22     Sequence
```

```
 HLA-DPA10201-DPB11401  492      FNCYFPLQSYGFQPT  CYFPLQSYG  2        0.1273
12614.1    70.00  0.14     Sequence
 HLA-DPA10201-DPB11401  493      NCYFPLQSYGFQPTY  LQSYGFQPT  5        0.1170
14106.1    75.00  0.35     Sequence
 HLA-DPA10201-DPB11401  494      CYFPLQSYGFQPTYG  LQSYGFQPT  4        0.1128
14760.8    75.00  0.35     Sequence
 HLA-DPA10201-DPB11401  495      YFPLQSYGFQPTYGV  LQSYGFQPT  3        0.1200
13651.1    75.00  0.35     Sequence
 HLA-DPA10201-DPB11401  496      FPLQSYGFQPTYGVG  LQSYGFQPT  2        0.1070
15718.3    80.00  0.35     Sequence
 HLA-DPA10201-DPB11401  497      PLQSYGFQPTYGVGY  LQSYGFQPT  1        0.0984
17250.4    85.00  0.28     Sequence
 HLA-DPA10201-DPB11401  498      LQSYGFQPTYGVGYQ  YGFQPTYGV  3        0.0809
20833.7    90.00  0.20     Sequence
 HLA-DPA10201-DPB11401  499      QSYGFQPTYGVGYQP  YGFQPTYGV  2        0.0627
25379.4    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401  500      SYGFQPTYGVGYQPY  TYGVGYQPY  6        0.0684
23865.3    95.00  0.17     Sequence
 HLA-DPA10201-DPB11401  501      YGFQPTYGVGYQPYR  TYGVGYQPY  5        0.0813
20753.2    90.00  0.31     Sequence
 HLA-DPA10201-DPB11401  502      GFQPTYGVGYQPYRV  TYGVGYQPY  4        0.0850
19922.4    85.00  0.36     Sequence
 HLA-DPA10201-DPB11401  503      FQPTYGVGYQPYRVV  TYGVGYQPY  3        0.1213
13455.8    75.00  0.30     Sequence
 HLA-DPA10201-DPB11401  504      QPTYGVGYQPYRVVV  VGYQPYRVV  5        0.1339
11745.4    70.00  0.22     Sequence
 HLA-DPA10201-DPB11401  505      PTYGVGYQPYRVVVL  VGYQPYRVV  4        0.1614
8718.2    60.00  0.26     Sequence
 HLA-DPA10201-DPB11401  506      TYGVGYQPYRVVVLS  VGYQPYRVV  3        0.1750
7529.8    55.00  0.27     Sequence
 HLA-DPA10201-DPB11401  507      YGVGYQPYRVVVLSF  PYRVVVLSF  6        0.2177
4740.8    37.00  0.22     Sequence
 HLA-DPA10201-DPB11401  508      GVGYQPYRVVVLSFE  YRVVVLSFE  6        0.2792
2439.2    21.00  0.26     Sequence
 HLA-DPA10201-DPB11401  509      VGYQPYRVVVLSFEL  RVVVLSFEL  6        0.3991
665.9     6.00  0.45     Sequence         WB
 HLA-DPA10201-DPB11401  510      GYQPYRVVVLSFELL  RVVVLSFEL  5        0.4615
339.3     3.00  0.54     Sequence         WB
 HLA-DPA10201-DPB11401  511      YQPYRVVVLSFELLH  RVVVLSFEL  4        0.4915
245.1     1.60  0.50     Sequence         SB
 HLA-DPA10201-DPB11401  512      QPYRVVVLSFELLHA  RVVVLSFEL  3        0.5056
210.5     1.30  0.48     Sequence         SB
 HLA-DPA10201-DPB11401  513      PYRVVVLSFELLHAP  RVVVLSFEL  2        0.5060
209.6     1.30  0.49     Sequence         SB
 HLA-DPA10201-DPB11401  514      YRVVVLSFELLHAPA  RVVVLSFEL  1        0.4457
402.5     3.50  0.43     Sequence         WB
 HLA-DPA10201-DPB11401  515      RVVVLSFELLHAPAT  RVVVLSFEL  0        0.3549
1074.9     9.50  0.36     Sequence         WB
 HLA-DPA10201-DPB11401  516      VVVLSFELLHAPATV  VVVLSFELL  0        0.2253
4366.5    35.00  0.19     Sequence
 HLA-DPA10201-DPB11401  517      VVLSFELLHAPATVC  ELLHAPATV  5        0.2106
5118.8    39.00  0.25     Sequence
 HLA-DPA10201-DPB11401  518      VLSFELLHAPATVCG  ELLHAPATV  4        0.1839
6833.6    48.00  0.28     Sequence
 HLA-DPA10201-DPB11401  519      LSFELLHAPATVCGP  ELLHAPATV  3        0.1725
7736.2    55.00  0.34     Sequence
 HLA-DPA10201-DPB11401  520      SFELLHAPATVCGPK  ELLHAPATV  2        0.1737
7630.9    55.00  0.36     Sequence
 HLA-DPA10201-DPB11401  521      FELLHAPATVCGPKK  LLHAPATVC  2        0.1518
9674.1    60.00  0.34     Sequence
 HLA-DPA10201-DPB11401  522      ELLHAPATVCGPKKS  LLHAPATVC  1        0.1163
14199.8    75.00  0.30     Sequence
 HLA-DPA10201-DPB11401  523      LLHAPATVCGPKKST  LLHAPATVC  0        0.0767
21812.9    90.00  0.22     Sequence
 HLA-DPA10201-DPB11401  524      LHAPATVCGPKKSTN  PATVCGPKK  3        0.0504
28977.0    95.00  0.22     Sequence
```

```
 HLA-DPA10201-DPB11401  525      HAPATVCGPKKSTNL  ATVCGPKKS  3        0.0491
29377.9   100.00  0.31     Sequence
 HLA-DPA10201-DPB11401  526      APATVCGPKKSTNLV  ATVCGPKKS  2        0.0654
24646.8    95.00  0.24     Sequence
 HLA-DPA10201-DPB11401  527      PATVCGPKKSTNLVK  KKSTNLVKX  7        0.1310
12113.2    70.00  0.18     Sequence
 HLA-DPA10201-DPB11401  528      ATVCGPKKSTNLVKN  KKSTNLVKN  6        0.2103
5135.2    39.00  0.50     Sequence
 HLA-DPA10201-DPB11401  529      TVCGPKKSTNLVKNK  KKSTNLVKN  5        0.2590
3032.1    26.00  0.54     Sequence
 HLA-DPA10201-DPB11401  530      VCGPKKSTNLVKNKC  KKSTNLVKN  4        0.2662
2805.1    24.00  0.52     Sequence
 HLA-DPA10201-DPB11401  531      CGPKKSTNLVKNKCV  KKSTNLVKN  3        0.2819
2368.9    21.00  0.52     Sequence
 HLA-DPA10201-DPB11401  532      GPKKSTNLVKNKCVN  KKSTNLVKN  2        0.2816
2375.1    21.00  0.51     Sequence
 HLA-DPA10201-DPB11401  533      PKKSTNLVKNKCVNF  KKSTNLVKN  1        0.2637
2882.4    25.00  0.47     Sequence
 HLA-DPA10201-DPB11401  534      KKSTNLVKNKCVNFN  KKSTNLVKN  0        0.1799
7137.0    49.00  0.41     Sequence
 HLA-DPA10201-DPB11401  535      KSTNLVKNKCVNFNF  KSTNLVKNK  0        0.0752
22155.9    90.00  0.30     Sequence
 HLA-DPA10201-DPB11401  536      STNLVKNKCVNFNFN  KNKCVNFNF  5        0.0497
29208.3   100.00  0.26     Sequence
 HLA-DPA10201-DPB11401  537      TNLVKNKCVNFNFNG  KNKCVNFNF  4        0.0548
27628.6    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401  538      NLVKNKCVNFNFNGL  CVNFNFNGL  6        0.0908
18722.5    85.00  0.23     Sequence
 HLA-DPA10201-DPB11401  539      LVKNKCVNFNFNGLT  CVNFNFNGL  5        0.1064
15811.6    80.00  0.31     Sequence
 HLA-DPA10201-DPB11401  540      VKNKCVNFNFNGLTG  CVNFNFNGL  4        0.0995
17036.7    80.00  0.29     Sequence
 HLA-DPA10201-DPB11401  541      KNKCVNFNFNGLTGT  CVNFNFNGL  3        0.1015
16665.3    80.00  0.31     Sequence
 HLA-DPA10201-DPB11401  542      NKCVNFNFNGLTGTG  CVNFNFNGL  2        0.0844
20072.5    90.00  0.32     Sequence
 HLA-DPA10201-DPB11401  543      KCVNFNFNGLTGTGV  CVNFNFNGL  1        0.0964
17622.4    85.00  0.25     Sequence
 HLA-DPA10201-DPB11401  544      CVNFNFNGLTGTGVL  FNGLTGTGV  5        0.1064
15805.3    80.00  0.28     Sequence
 HLA-DPA10201-DPB11401  545      VNFNFNGLTGTGVLT  FNGLTGTGV  4        0.1116
14945.6    80.00  0.30     Sequence
 HLA-DPA10201-DPB11401  546      NFNFNGLTGTGVLTE  FNGLTGTGV  3        0.1233
13172.2    75.00  0.25     Sequence
 HLA-DPA10201-DPB11401  547      FNFNGLTGTGVLTES  FNGLTGTGV  2        0.1262
12762.1    70.00  0.23     Sequence
 HLA-DPA10201-DPB11401  548      NFNGLTGTGVLTESN  FNGLTGTGV  1        0.1090
15365.7    80.00  0.22     Sequence
 HLA-DPA10201-DPB11401  549      FNGLTGTGVLTESNK  LTGTGVLTE  3        0.1035
16322.8    80.00  0.29     Sequence
 HLA-DPA10201-DPB11401  550      NGLTGTGVLTESNKK  LTGTGVLTE  2        0.0837
20219.7    90.00  0.34     Sequence
 HLA-DPA10201-DPB11401  551      GLTGTGVLTESNKKF  LTGTGVLTE  1        0.0806
20893.1    90.00  0.29     Sequence
 HLA-DPA10201-DPB11401  552      LTGTGVLTESNKKFL  LTESNKKFL  6        0.1059
15892.2    80.00  0.25     Sequence
 HLA-DPA10201-DPB11401  553      TGTGVLTESNKKFLP  LTESNKKFL  5        0.1079
15563.0    80.00  0.34     Sequence
 HLA-DPA10201-DPB11401  554      GTGVLTESNKKFLPF  LTESNKKFL  4        0.1189
13817.4    75.00  0.32     Sequence
 HLA-DPA10201-DPB11401  555      TGVLTESNKKFLPFQ  LTESNKKFL  3        0.1329
11867.4    70.00  0.28     Sequence
 HLA-DPA10201-DPB11401  556      GVLTESNKKFLPFQQ  LTESNKKFL  2        0.1492
9948.6    65.00  0.25     Sequence
 HLA-DPA10201-DPB11401  557      VLTESNKKFLPFQQF  KKFLPFQQF  6        0.2625
2919.4    25.00  0.56     Sequence
```

```
 HLA-DPA10201-DPB11401  558      LTESNKKFLPFQQFG  KKFLPFQQF  5        0.2769
2498.6    22.00  0.57     Sequence
 HLA-DPA10201-DPB11401  559      TESNKKFLPFQQFGR  KKFLPFQQF  4        0.3107
1733.6    16.00  0.58     Sequence
 HLA-DPA10201-DPB11401  560      ESNKKFLPFQQFGRD  KKFLPFQQF  3        0.3077
1791.4    16.00  0.57     Sequence
 HLA-DPA10201-DPB11401  561      SNKKFLPFQQFGRDI  KKFLPFQQF  2        0.3235
1510.2    14.00  0.51     Sequence
 HLA-DPA10201-DPB11401  562      NKKFLPFQQFGRDIA  KKFLPFQQF  1        0.3149
1656.7    15.00  0.48     Sequence
 HLA-DPA10201-DPB11401  563      KKFLPFQQFGRDIAD  KKFLPFQQF  0        0.2703
2684.0    23.00  0.41     Sequence
 HLA-DPA10201-DPB11401  564      KFLPFQQFGRDIADT  KFLPFQQFG  0        0.1439
10540.4    65.00  0.27     Sequence
 HLA-DPA10201-DPB11401  565      FLPFQQFGRDIADTT  PFQQFGRDI  2        0.0886
19165.9    85.00  0.22     Sequence
 HLA-DPA10201-DPB11401  566      LPFQQFGRDIADTTD  QFGRDIADT  4        0.0679
23983.1    95.00  0.27     Sequence
 HLA-DPA10201-DPB11401  567      PFQQFGRDIADTTDA  QFGRDIADT  3        0.0739
22482.4    90.00  0.25     Sequence
 HLA-DPA10201-DPB11401  568      FQQFGRDIADTTDAV  QFGRDIADT  2        0.0733
22623.2    90.00  0.23     Sequence
 HLA-DPA10201-DPB11401  569      QQFGRDIADTTDAVR  DIADTTDAV  5        0.0787
21337.0    90.00  0.20     Sequence
 HLA-DPA10201-DPB11401  570      QFGRDIADTTDAVRD  DIADTTDAV  4        0.0792
21232.4    90.00  0.22     Sequence
 HLA-DPA10201-DPB11401  571      FGRDIADTTDAVRDP  DIADTTDAV  3        0.0752
22166.2    90.00  0.22     Sequence
 HLA-DPA10201-DPB11401  572      GRDIADTTDAVRDPQ  DIADTTDAV  2        0.0678
24016.3    95.00  0.25     Sequence
 HLA-DPA10201-DPB11401  573      RDIADTTDAVRDPQT  DIADTTDAV  1        0.0696
23536.6    90.00  0.25     Sequence
 HLA-DPA10201-DPB11401  574      DIADTTDAVRDPQTL  DIADTTDAV  0        0.0523
28396.5    95.00  0.25     Sequence
 HLA-DPA10201-DPB11401  575      IADTTDAVRDPQTLE  DAVRDPQTL  5        0.0588
26477.5    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401  576      ADTTDAVRDPQTLEI  VRDPQTLEI  6        0.0898
18926.6    85.00  0.46     Sequence
 HLA-DPA10201-DPB11401  577      DTTDAVRDPQTLEIL  VRDPQTLEI  5        0.1370
11354.5    70.00  0.44     Sequence
 HLA-DPA10201-DPB11401  578      TTDAVRDPQTLEILD  RDPQTLEIL  5        0.1461
10291.8    65.00  0.33     Sequence
 HLA-DPA10201-DPB11401  579      TDAVRDPQTLEILDI  RDPQTLEIL  4        0.1827
6928.1    48.00  0.32     Sequence
 HLA-DPA10201-DPB11401  580      DAVRDPQTLEILDIT  RDPQTLEIL  3        0.1983
5851.3    43.00  0.27     Sequence
 HLA-DPA10201-DPB11401  581      AVRDPQTLEILDITP  RDPQTLEIL  2        0.2069
5332.5    40.00  0.28     Sequence
 HLA-DPA10201-DPB11401  582      VRDPQTLEILDITPC  PQTLEILDI  3        0.1798
7149.8    49.00  0.26     Sequence
 HLA-DPA10201-DPB11401  583      RDPQTLEILDITPCS  PQTLEILDI  2        0.1589
8960.4    60.00  0.34     Sequence
 HLA-DPA10201-DPB11401  584      DPQTLEILDITPCSF  PQTLEILDI  1        0.1413
10833.9    65.00  0.25     Sequence
 HLA-DPA10201-DPB11401  585      PQTLEILDITPCSFG  PQTLEILDI  0        0.1403
10961.8    65.00  0.22     Sequence
 HLA-DPA10201-DPB11401  586      QTLEILDITPCSFGG  LEILDITPC  2        0.1153
14354.4    75.00  0.27     Sequence
 HLA-DPA10201-DPB11401  587      TLEILDITPCSFGGV  LEILDITPC  1        0.1101
15190.3    80.00  0.28     Sequence
 HLA-DPA10201-DPB11401  588      LEILDITPCSFGGVS  ILDITPCSF  2        0.0922
18436.9    85.00  0.28     Sequence
 HLA-DPA10201-DPB11401  589      EILDITPCSFGGVSV  ILDITPCSF  1        0.0769
21765.5    90.00  0.25     Sequence
 HLA-DPA10201-DPB11401  590      ILDITPCSFGGVSVI  CSFGGVSVI  6        0.0854
19844.5    85.00  0.23     Sequence
```

```
 HLA-DPA10201-DPB11401  591      LDITPCSFGGVSVIT  CSFGGVSVI  5        0.0978
17354.8    85.00  0.37     Sequence
 HLA-DPA10201-DPB11401  592      DITPCSFGGVSVITP  CSFGGVSVI  4        0.1150
14415.3    75.00  0.34     Sequence
 HLA-DPA10201-DPB11401  593      ITPCSFGGVSVITPG  CSFGGVSVI  3        0.1133
14677.5    75.00  0.33     Sequence
 HLA-DPA10201-DPB11401  594      TPCSFGGVSVITPGT  CSFGGVSVI  2        0.1210
13497.7    75.00  0.31     Sequence
 HLA-DPA10201-DPB11401  595      PCSFGGVSVITPGTN  CSFGGVSVI  1        0.1231
13202.9    75.00  0.25     Sequence
 HLA-DPA10201-DPB11401  596      CSFGGVSVITPGTNT  CSFGGVSVI  0        0.1229
13230.5    75.00  0.19     Sequence
 HLA-DPA10201-DPB11401  597      SFGGVSVITPGTNTS  SVITPGTNT  5        0.1111
15023.7    80.00  0.27     Sequence
 HLA-DPA10201-DPB11401  598      FGGVSVITPGTNTSN  SVITPGTNT  4        0.1096
15271.4    80.00  0.33     Sequence
 HLA-DPA10201-DPB11401  599      GGVSVITPGTNTSNQ  SVITPGTNT  3        0.0956
17769.4    85.00  0.41     Sequence
 HLA-DPA10201-DPB11401  600      GVSVITPGTNTSNQV  SVITPGTNT  2        0.0984
17246.4    85.00  0.44     Sequence
 HLA-DPA10201-DPB11401  601      VSVITPGTNTSNQVA  SVITPGTNT  1        0.0853
19858.0    85.00  0.47     Sequence
 HLA-DPA10201-DPB11401  602      SVITPGTNTSNQVAV  SVITPGTNT  0        0.0592
26362.6    95.00  0.41     Sequence
 HLA-DPA10201-DPB11401  603      VITPGTNTSNQVAVL  NTSNQVAVL  6        0.0500
29112.4    95.00  0.28     Sequence
 HLA-DPA10201-DPB11401  604      ITPGTNTSNQVAVLY  NTSNQVAVL  5        0.0680
23956.9    95.00  0.39     Sequence
 HLA-DPA10201-DPB11401  605      TPGTNTSNQVAVLYQ  NTSNQVAVL  4        0.1029
16425.2    80.00  0.33     Sequence
 HLA-DPA10201-DPB11401  606      PGTNTSNQVAVLYQG  NTSNQVAVL  3        0.1019
16598.9    80.00  0.28     Sequence
 HLA-DPA10201-DPB11401  607      GTNTSNQVAVLYQGV  QVAVLYQGV  6        0.1456
10350.0    65.00  0.40     Sequence
 HLA-DPA10201-DPB11401  608      TNTSNQVAVLYQGVN  QVAVLYQGV  5        0.1675
8166.1    55.00  0.49     Sequence
 HLA-DPA10201-DPB11401  609      NTSNQVAVLYQGVNC  QVAVLYQGV  4        0.1773
7346.2    50.00  0.49     Sequence
 HLA-DPA10201-DPB11401  610      TSNQVAVLYQGVNCT  QVAVLYQGV  3        0.1824
6947.9    49.00  0.49     Sequence
 HLA-DPA10201-DPB11401  611      SNQVAVLYQGVNCTE  QVAVLYQGV  2        0.1715
7820.6    55.00  0.54     Sequence
 HLA-DPA10201-DPB11401  612      NQVAVLYQGVNCTEV  QVAVLYQGV  1        0.1475
10138.6    65.00  0.42     Sequence
 HLA-DPA10201-DPB11401  613      QVAVLYQGVNCTEVP  QVAVLYQGV  0        0.1379
11247.4    70.00  0.34     Sequence
 HLA-DPA10201-DPB11401  614      VAVLYQGVNCTEVPV  YQGVNCTEV  4        0.0995
17030.4    80.00  0.25     Sequence
 HLA-DPA10201-DPB11401  615      AVLYQGVNCTEVPVA  YQGVNCTEV  3        0.1027
16460.5    80.00  0.28     Sequence
 HLA-DPA10201-DPB11401  616      VLYQGVNCTEVPVAI  VNCTEVPVA  5        0.1113
14999.2    80.00  0.23     Sequence
 HLA-DPA10201-DPB11401  617      LYQGVNCTEVPVAIH  CTEVPVAIH  6        0.1499
9872.0    65.00  0.22     Sequence
 HLA-DPA10201-DPB11401  618      YQGVNCTEVPVAIHA  CTEVPVAIH  5        0.1916
6291.1    45.00  0.28     Sequence
 HLA-DPA10201-DPB11401  619      QGVNCTEVPVAIHAD  CTEVPVAIH  4        0.1989
5814.3    43.00  0.26     Sequence
 HLA-DPA10201-DPB11401  620      GVNCTEVPVAIHADQ  CTEVPVAIH  3        0.2061
5379.4    41.00  0.26     Sequence
 HLA-DPA10201-DPB11401  621      VNCTEVPVAIHADQL  CTEVPVAIH  2        0.2338
3985.2    32.00  0.22     Sequence
 HLA-DPA10201-DPB11401  622      NCTEVPVAIHADQLT  PVAIHADQL  5        0.2397
3737.0    31.00  0.22     Sequence
 HLA-DPA10201-DPB11401  623      CTEVPVAIHADQLTP  PVAIHADQL  4        0.2319
4065.2    33.00  0.22     Sequence
```

```
 HLA-DPA10201-DPB11401  624      TEVPVAIHADQLTPT  PVAIHADQL  3        0.1842
6814.8    48.00  0.35     Sequence
 HLA-DPA10201-DPB11401  625      EVPVAIHADQLTPTW  PVAIHADQL  2        0.1701
7935.7    55.00  0.38     Sequence
 HLA-DPA10201-DPB11401  626      VPVAIHADQLTPTWR  PVAIHADQL  1        0.1536
9484.0    60.00  0.35     Sequence
 HLA-DPA10201-DPB11401  627      PVAIHADQLTPTWRV  PVAIHADQL  0        0.1404
10944.4    65.00  0.25     Sequence
 HLA-DPA10201-DPB11401  628      VAIHADQLTPTWRVY  IHADQLTPT  2        0.1150
14403.4    75.00  0.29     Sequence
 HLA-DPA10201-DPB11401  629      AIHADQLTPTWRVYS  IHADQLTPT  1        0.1016
16659.3    80.00  0.32     Sequence
 HLA-DPA10201-DPB11401  630      IHADQLTPTWRVYST  DQLTPTWRV  3        0.0817
20666.5    90.00  0.32     Sequence
 HLA-DPA10201-DPB11401  631      HADQLTPTWRVYSTG  DQLTPTWRV  2        0.0667
24291.5    95.00  0.38     Sequence
 HLA-DPA10201-DPB11401  632      ADQLTPTWRVYSTGS  DQLTPTWRV  1        0.0650
24756.1    95.00  0.35     Sequence
 HLA-DPA10201-DPB11401  633      DQLTPTWRVYSTGSN  DQLTPTWRV  0        0.0803
20979.9    90.00  0.25     Sequence
 HLA-DPA10201-DPB11401  634      QLTPTWRVYSTGSNV  RVYSTGSNV  6        0.2169
4782.6    37.00  0.65     Sequence
 HLA-DPA10201-DPB11401  635      LTPTWRVYSTGSNVF  RVYSTGSNV  5        0.2989
1970.0    18.00  0.68     Sequence
 HLA-DPA10201-DPB11401  636      TPTWRVYSTGSNVFQ  RVYSTGSNV  4        0.3326
1368.4    13.00  0.64     Sequence
 HLA-DPA10201-DPB11401  637      PTWRVYSTGSNVFQT  RVYSTGSNV  3        0.3510
1121.3    10.00  0.63     Sequence
 HLA-DPA10201-DPB11401  638      TWRVYSTGSNVFQTR  RVYSTGSNV  2        0.3643
970.7     8.50  0.63     Sequence         WB
 HLA-DPA10201-DPB11401  639      WRVYSTGSNVFQTRA  RVYSTGSNV  1        0.3509
1121.8    10.00  0.60     Sequence
 HLA-DPA10201-DPB11401  640      RVYSTGSNVFQTRAG  RVYSTGSNV  0        0.2968
2014.3    18.00  0.53     Sequence
 HLA-DPA10201-DPB11401  641      VYSTGSNVFQTRAGC  STGSNVFQT  2        0.1105
15128.0    80.00  0.31     Sequence
 HLA-DPA10201-DPB11401  642      YSTGSNVFQTRAGCL  VFQTRAGCL  6        0.0853
19872.9    85.00  0.26     Sequence
 HLA-DPA10201-DPB11401  643      STGSNVFQTRAGCLI  VFQTRAGCL  5        0.1174
14042.0    75.00  0.42     Sequence
 HLA-DPA10201-DPB11401  644      TGSNVFQTRAGCLIG  VFQTRAGCL  4        0.1279
12526.9    70.00  0.37     Sequence
 HLA-DPA10201-DPB11401  645      GSNVFQTRAGCLIGA  VFQTRAGCL  3        0.1483
10048.3    65.00  0.31     Sequence
 HLA-DPA10201-DPB11401  646      SNVFQTRAGCLIGAE  VFQTRAGCL  2        0.1670
8210.6    55.00  0.27     Sequence
 HLA-DPA10201-DPB11401  647      NVFQTRAGCLIGAEY  VFQTRAGCL  1        0.1730
7690.7    55.00  0.23     Sequence
 HLA-DPA10201-DPB11401  648      VFQTRAGCLIGAEYV  RAGCLIGAE  4        0.1826
6935.9    48.00  0.21     Sequence
 HLA-DPA10201-DPB11401  649      FQTRAGCLIGAEYVN  RAGCLIGAE  3        0.1791
7200.0    50.00  0.28     Sequence
 HLA-DPA10201-DPB11401  650      QTRAGCLIGAEYVNN  GCLIGAEYV  4        0.1573
9119.1    60.00  0.29     Sequence
 HLA-DPA10201-DPB11401  651      TRAGCLIGAEYVNNS  GCLIGAEYV  3        0.1411
10868.3    65.00  0.31     Sequence
 HLA-DPA10201-DPB11401  652      RAGCLIGAEYVNNSY  GCLIGAEYV  2        0.1331
11846.6    70.00  0.38     Sequence
 HLA-DPA10201-DPB11401  653      AGCLIGAEYVNNSYE  GCLIGAEYV  1        0.1062
15844.8    80.00  0.37     Sequence
 HLA-DPA10201-DPB11401  654      GCLIGAEYVNNSYEC  GCLIGAEYV  0        0.0981
17291.8    85.00  0.32     Sequence
 HLA-DPA10201-DPB11401  655      CLIGAEYVNNSYECD  LIGAEYVNN  1        0.0709
23213.1    90.00  0.31     Sequence
 HLA-DPA10201-DPB11401  656      LIGAEYVNNSYECDI  EYVNNSYEC  4        0.0495
29264.9   100.00  0.24     Sequence
```

```
 HLA-DPA10201-DPB11401  657      IGAEYVNNSYECDIP  EYVNNSYEC  3        0.0411
32045.5   100.00  0.31     Sequence
 HLA-DPA10201-DPB11401  658      GAEYVNNSYECDIPI  EYVNNSYEC  2        0.0444
30932.2   100.00  0.31     Sequence
 HLA-DPA10201-DPB11401  659      AEYVNNSYECDIPIG  EYVNNSYEC  1        0.0534
28055.4    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401  660      EYVNNSYECDIPIGA  YECDIPIGA  6        0.0762
21930.3    90.00  0.24     Sequence
 HLA-DPA10201-DPB11401  661      YVNNSYECDIPIGAG  YECDIPIGA  5        0.0733
22626.9    90.00  0.30     Sequence
 HLA-DPA10201-DPB11401  662      VNNSYECDIPIGAGI  YECDIPIGA  4        0.0917
18537.7    85.00  0.31     Sequence
 HLA-DPA10201-DPB11401  663      NNSYECDIPIGAGIC  YECDIPIGA  3        0.1010
16766.4    80.00  0.26     Sequence
 HLA-DPA10201-DPB11401  664      NSYECDIPIGAGICA  ECDIPIGAG  3        0.1128
14758.9    75.00  0.18     Sequence
 HLA-DPA10201-DPB11401  665      SYECDIPIGAGICAS  CDIPIGAGI  3        0.1182
13910.1    75.00  0.19     Sequence
 HLA-DPA10201-DPB11401  666      YECDIPIGAGICASY  CDIPIGAGI  2        0.1009
16786.2    80.00  0.21     Sequence
 HLA-DPA10201-DPB11401  667      ECDIPIGAGICASYQ  PIGAGICAS  4        0.0906
18756.4    85.00  0.22     Sequence
 HLA-DPA10201-DPB11401  668      CDIPIGAGICASYQT  PIGAGICAS  3        0.0867
19565.0    85.00  0.28     Sequence
 HLA-DPA10201-DPB11401  669      DIPIGAGICASYQTQ  PIGAGICAS  2        0.0739
22481.2    90.00  0.28     Sequence
 HLA-DPA10201-DPB11401  670      IPIGAGICASYQTQT  PIGAGICAS  1        0.0666
24310.5    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401  671      PIGAGICASYQTQTN  GICASYQTQ  4        0.0574
26868.0    95.00  0.19     Sequence
 HLA-DPA10201-DPB11401  672      IGAGICASYQTQTNS  GICASYQTQ  3        0.0509
28814.1    95.00  0.25     Sequence
 HLA-DPA10201-DPB11401  673      GAGICASYQTQTNSP  GICASYQTQ  2        0.0486
29546.8   100.00  0.25     Sequence
 HLA-DPA10201-DPB11401  674      AGICASYQTQTNSPR  CASYQTQTN  3        0.0530
28174.7    95.00  0.19     Sequence
 HLA-DPA10201-DPB11401  675      GICASYQTQTNSPRR  CASYQTQTN  2        0.0559
27312.6    95.00  0.19     Sequence
 HLA-DPA10201-DPB11401  676      ICASYQTQTNSPRRA  QTQTNSPRR  5        0.0512
28724.1    95.00  0.19     Sequence
 HLA-DPA10201-DPB11401  677      CASYQTQTNSPRRAR  QTQTNSPRR  4        0.0527
28280.0    95.00  0.19     Sequence
 HLA-DPA10201-DPB11401  678      ASYQTQTNSPRRARS  QTQTNSPRR  3        0.0527
28263.8    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401  679      SYQTQTNSPRRARSV  QTQTNSPRR  2        0.0621
25543.3    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401  680      YQTQTNSPRRARSVA  TQTNSPRRA  2        0.0640
25008.9    95.00  0.31     Sequence
 HLA-DPA10201-DPB11401  681      QTQTNSPRRARSVAS  PRRARSVAS  6        0.0803
20975.5    90.00  0.26     Sequence
 HLA-DPA10201-DPB11401  682      TQTNSPRRARSVASQ  RRARSVASQ  6        0.1587
8979.7    60.00  0.49     Sequence
 HLA-DPA10201-DPB11401  683      QTNSPRRARSVASQS  RRARSVASQ  5        0.2092
5202.0    40.00  0.44     Sequence
 HLA-DPA10201-DPB11401  684      TNSPRRARSVASQSI  RRARSVASQ  4        0.2914
2137.6    19.00  0.29     Sequence
 HLA-DPA10201-DPB11401  685      NSPRRARSVASQSII  ARSVASQSI  5        0.4084
602.2     5.50  0.34     Sequence         WB
 HLA-DPA10201-DPB11401  686      SPRRARSVASQSIIA  ARSVASQSI  4        0.4536
369.2     3.00  0.31     Sequence         WB
 HLA-DPA10201-DPB11401  687      PRRARSVASQSIIAY  ARSVASQSI  3        0.4816
272.9     1.90  0.28     Sequence         SB
 HLA-DPA10201-DPB11401  688      RRARSVASQSIIAYT  ARSVASQSI  2        0.4821
271.5     1.90  0.25     Sequence         SB
 HLA-DPA10201-DPB11401  689      RARSVASQSIIAYTM  RSVASQSII  2        0.4290
482.3     4.00  0.36     Sequence         WB
```

```
 HLA-DPA10201-DPB11401  690      ARSVASQSIIAYTMS  RSVASQSII  1        0.3917
721.7     6.50  0.35     Sequence         WB
 HLA-DPA10201-DPB11401  691      RSVASQSIIAYTMSL  RSVASQSII  0        0.3386
1281.9    12.00  0.32     Sequence
 HLA-DPA10201-DPB11401  692      SVASQSIIAYTMSLG  SQSIIAYTM  3        0.2213
4560.7    36.00  0.23     Sequence
 HLA-DPA10201-DPB11401  693      VASQSIIAYTMSLGA  IAYTMSLGA  6        0.2469
3456.0    29.00  0.24     Sequence
 HLA-DPA10201-DPB11401  694      ASQSIIAYTMSLGAE  IAYTMSLGA  5        0.2790
2443.5    21.00  0.31     Sequence
 HLA-DPA10201-DPB11401  695      SQSIIAYTMSLGAEN  IAYTMSLGA  4        0.2852
2285.3    20.00  0.34     Sequence
 HLA-DPA10201-DPB11401  696      QSIIAYTMSLGAENS  IAYTMSLGA  3        0.2808
2395.8    21.00  0.37     Sequence
 HLA-DPA10201-DPB11401  697      SIIAYTMSLGAENSV  IAYTMSLGA  2        0.2918
2127.4    19.00  0.34     Sequence
 HLA-DPA10201-DPB11401  698      IIAYTMSLGAENSVA  IAYTMSLGA  1        0.2873
2234.4    20.00  0.32     Sequence
 HLA-DPA10201-DPB11401  699      IAYTMSLGAENSVAY  IAYTMSLGA  0        0.2581
3062.3    26.00  0.25     Sequence
 HLA-DPA10201-DPB11401  700      AYTMSLGAENSVAYS  TMSLGAENS  2        0.2026
5585.1    42.00  0.33     Sequence
 HLA-DPA10201-DPB11401  701      YTMSLGAENSVAYSN  TMSLGAENS  1        0.1123
14837.2    80.00  0.37     Sequence
 HLA-DPA10201-DPB11401  702      TMSLGAENSVAYSNN  TMSLGAENS  0        0.0609
25868.4    95.00  0.28     Sequence
 HLA-DPA10201-DPB11401  703      MSLGAENSVAYSNNS  LGAENSVAY  2        0.0473
29956.9   100.00  0.25     Sequence
 HLA-DPA10201-DPB11401  704      SLGAENSVAYSNNSI  GAENSVAYS  2        0.0453
30612.9   100.00  0.20     Sequence
 HLA-DPA10201-DPB11401  705      LGAENSVAYSNNSIA  SVAYSNNSI  5        0.0597
26207.3    95.00  0.25     Sequence
 HLA-DPA10201-DPB11401  706      GAENSVAYSNNSIAI  AYSNNSIAI  6        0.1168
14136.0    75.00  0.49     Sequence
 HLA-DPA10201-DPB11401  707      AENSVAYSNNSIAIP  AYSNNSIAI  5        0.1465
10244.3    65.00  0.52     Sequence
 HLA-DPA10201-DPB11401  708      ENSVAYSNNSIAIPT  AYSNNSIAI  4        0.1631
8561.6    60.00  0.51     Sequence
 HLA-DPA10201-DPB11401  709      NSVAYSNNSIAIPTN  AYSNNSIAI  3        0.1726
7726.5    55.00  0.47     Sequence
 HLA-DPA10201-DPB11401  710      SVAYSNNSIAIPTNF  AYSNNSIAI  2        0.1798
7144.4    49.00  0.47     Sequence
 HLA-DPA10201-DPB11401  711      VAYSNNSIAIPTNFT  AYSNNSIAI  1        0.1693
8004.4    55.00  0.41     Sequence
 HLA-DPA10201-DPB11401  712      AYSNNSIAIPTNFTI  AYSNNSIAI  0        0.1794
7175.6    50.00  0.28     Sequence
 HLA-DPA10201-DPB11401  713      YSNNSIAIPTNFTIS  SIAIPTNFT  4        0.1682
8106.2    55.00  0.25     Sequence
 HLA-DPA10201-DPB11401  714      SNNSIAIPTNFTISV  AIPTNFTIS  5        0.2071
5317.6    40.00  0.28     Sequence
 HLA-DPA10201-DPB11401  715      NNSIAIPTNFTISVT  AIPTNFTIS  4        0.2236
4451.4    35.00  0.26     Sequence
 HLA-DPA10201-DPB11401  716      NSIAIPTNFTISVTT  AIPTNFTIS  3        0.2332
4008.3    32.00  0.26     Sequence
 HLA-DPA10201-DPB11401  717      SIAIPTNFTISVTTE  AIPTNFTIS  2        0.2362
3882.8    32.00  0.25     Sequence
 HLA-DPA10201-DPB11401  718      IAIPTNFTISVTTEI  PTNFTISVT  3        0.2652
2837.2    24.00  0.14     Sequence
 HLA-DPA10201-DPB11401  719      AIPTNFTISVTTEIL  FTISVTTEI  5        0.2923
2115.8    19.00  0.25     Sequence
 HLA-DPA10201-DPB11401  720      IPTNFTISVTTEILP  TISVTTEIL  5        0.2967
2017.3    18.00  0.25     Sequence
 HLA-DPA10201-DPB11401  721      PTNFTISVTTEILPV  TISVTTEIL  4        0.3206
1558.0    14.00  0.31     Sequence
 HLA-DPA10201-DPB11401  722      TNFTISVTTEILPVS  TISVTTEIL  3        0.3210
1550.5    14.00  0.28     Sequence
```

```
 HLA-DPA10201-DPB11401  723      NFTISVTTEILPVSM  SVTTEILPV  4        0.3368
1307.3    12.00  0.25     Sequence
 HLA-DPA10201-DPB11401  724      FTISVTTEILPVSMT  SVTTEILPV  3        0.3198
1571.7    14.00  0.32     Sequence
 HLA-DPA10201-DPB11401  725      TISVTTEILPVSMTK  SVTTEILPV  2        0.2962
2027.9    18.00  0.35     Sequence
 HLA-DPA10201-DPB11401  726      ISVTTEILPVSMTKT  SVTTEILPV  1        0.2760
2523.3    22.00  0.31     Sequence
 HLA-DPA10201-DPB11401  727      SVTTEILPVSMTKTS  EILPVSMTK  4        0.2564
3119.4    26.00  0.31     Sequence
 HLA-DPA10201-DPB11401  728      VTTEILPVSMTKTSV  EILPVSMTK  3        0.2408
3691.8    30.00  0.40     Sequence
 HLA-DPA10201-DPB11401  729      TTEILPVSMTKTSVD  EILPVSMTK  2        0.2136
4958.7    38.00  0.41     Sequence
 HLA-DPA10201-DPB11401  730      TEILPVSMTKTSVDC  EILPVSMTK  1        0.1639
8492.3    55.00  0.31     Sequence
 HLA-DPA10201-DPB11401  731      EILPVSMTKTSVDCT  EILPVSMTK  0        0.1394
11066.3    65.00  0.29     Sequence
 HLA-DPA10201-DPB11401  732      ILPVSMTKTSVDCTM  PVSMTKTSV  2        0.1220
13349.5    75.00  0.23     Sequence
 HLA-DPA10201-DPB11401  733      LPVSMTKTSVDCTMY  KTSVDCTMY  6        0.1329
11864.6    70.00  0.29     Sequence
 HLA-DPA10201-DPB11401  734      PVSMTKTSVDCTMYI  KTSVDCTMY  5        0.1530
9553.7    60.00  0.40     Sequence
 HLA-DPA10201-DPB11401  735      VSMTKTSVDCTMYIC  KTSVDCTMY  4        0.1629
8579.5    60.00  0.44     Sequence
 HLA-DPA10201-DPB11401  736      SMTKTSVDCTMYICG  KTSVDCTMY  3        0.1536
9492.4    60.00  0.42     Sequence
 HLA-DPA10201-DPB11401  737      MTKTSVDCTMYICGD  KTSVDCTMY  2        0.1495
9916.2    65.00  0.46     Sequence
 HLA-DPA10201-DPB11401  738      TKTSVDCTMYICGDS  KTSVDCTMY  1        0.1106
15113.7    80.00  0.40     Sequence
 HLA-DPA10201-DPB11401  739      KTSVDCTMYICGDST  KTSVDCTMY  0        0.0665
24355.5    95.00  0.31     Sequence
 HLA-DPA10201-DPB11401  740      TSVDCTMYICGDSTE  TSVDCTMYI  0        0.0369
33540.8   100.00  0.20     Sequence
 HLA-DPA10201-DPB11401  741      SVDCTMYICGDSTEC  TMYICGDST  4        0.0338
34675.9   100.00  0.27     Sequence
 HLA-DPA10201-DPB11401  742      VDCTMYICGDSTECS  TMYICGDST  3        0.0292
36436.3   100.00  0.28     Sequence
 HLA-DPA10201-DPB11401  743      DCTMYICGDSTECSN  TMYICGDST  2        0.0297
36242.1   100.00  0.29     Sequence
 HLA-DPA10201-DPB11401  744      CTMYICGDSTECSNL  YICGDSTEC  3        0.0321
35335.3   100.00  0.28     Sequence
 HLA-DPA10201-DPB11401  745      TMYICGDSTECSNLL  YICGDSTEC  2        0.0309
35804.4   100.00  0.31     Sequence
 HLA-DPA10201-DPB11401  746      MYICGDSTECSNLLL  STECSNLLL  6        0.0406
32234.7   100.00  0.17     Sequence
 HLA-DPA10201-DPB11401  747      YICGDSTECSNLLLQ  STECSNLLL  5        0.0529
28200.3    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401  748      ICGDSTECSNLLLQY  TECSNLLLQ  5        0.0686
23813.5    95.00  0.26     Sequence
 HLA-DPA10201-DPB11401  749      CGDSTECSNLLLQYG  ECSNLLLQY  5        0.0642
24956.8    95.00  0.28     Sequence
 HLA-DPA10201-DPB11401  750      GDSTECSNLLLQYGS  ECSNLLLQY  4        0.0679
23995.6    95.00  0.26     Sequence
 HLA-DPA10201-DPB11401  751      DSTECSNLLLQYGSF  ECSNLLLQY  3        0.0721
22909.4    90.00  0.27     Sequence
 HLA-DPA10201-DPB11401  752      STECSNLLLQYGSFC  ECSNLLLQY  2        0.0779
21514.3    90.00  0.28     Sequence
 HLA-DPA10201-DPB11401  753      TECSNLLLQYGSFCT  ECSNLLLQY  1        0.0712
23149.4    90.00  0.19     Sequence
 HLA-DPA10201-DPB11401  754      ECSNLLLQYGSFCTQ  LLLQYGSFC  4        0.0673
24150.5    95.00  0.19     Sequence
 HLA-DPA10201-DPB11401  755      CSNLLLQYGSFCTQL  QYGSFCTQL  6        0.0948
17932.0    85.00  0.23     Sequence
```

```
 HLA-DPA10201-DPB11401  756       SNLLLQYGSFCTQLN  QYGSFCTQL  5        0.1024
16507.5    80.00  0.26     Sequence
 HLA-DPA10201-DPB11401  757       NLLLQYGSFCTQLNR  QYGSFCTQL  4        0.1107
15095.6    80.00  0.29     Sequence
 HLA-DPA10201-DPB11401  758       LLLQYGSFCTQLNRA  QYGSFCTQL  3        0.1175
14021.0    75.00  0.28     Sequence
 HLA-DPA10201-DPB11401  759       LLQYGSFCTQLNRAL  QYGSFCTQL  2        0.1476
10122.8    65.00  0.24     Sequence
 HLA-DPA10201-DPB11401  760       LQYGSFCTQLNRALT  FCTQLNRAL  5        0.1596
8893.9    60.00  0.22     Sequence
 HLA-DPA10201-DPB11401  761       QYGSFCTQLNRALTG  FCTQLNRAL  4        0.1539
9462.3    60.00  0.22     Sequence
 HLA-DPA10201-DPB11401  762       YGSFCTQLNRALTGI  QLNRALTGI  6        0.1943
6109.0    44.00  0.22     Sequence
 HLA-DPA10201-DPB11401  763       GSFCTQLNRALTGIA  QLNRALTGI  5        0.2145
4910.7    38.00  0.26     Sequence
 HLA-DPA10201-DPB11401  764       SFCTQLNRALTGIAV  QLNRALTGI  4        0.2705
2679.9    23.00  0.24     Sequence
 HLA-DPA10201-DPB11401  765       FCTQLNRALTGIAVE  RALTGIAVE  6        0.3234
1510.4    14.00  0.35     Sequence
 HLA-DPA10201-DPB11401  766       CTQLNRALTGIAVEQ  RALTGIAVE  5        0.3457
1187.0    11.00  0.50     Sequence
 HLA-DPA10201-DPB11401  767       TQLNRALTGIAVEQD  RALTGIAVE  4        0.3475
1163.8    11.00  0.51     Sequence
 HLA-DPA10201-DPB11401  768       QLNRALTGIAVEQDK  RALTGIAVE  3        0.3583
1036.4     9.50  0.54     Sequence         WB
 HLA-DPA10201-DPB11401  769       LNRALTGIAVEQDKN  RALTGIAVE  2        0.3273
1449.2    13.00  0.62     Sequence
 HLA-DPA10201-DPB11401  770       NRALTGIAVEQDKNT  RALTGIAVE  1        0.2909
2147.4    19.00  0.52     Sequence
 HLA-DPA10201-DPB11401  771       RALTGIAVEQDKNTQ  RALTGIAVE  0        0.2422
3639.8    30.00  0.48     Sequence
 HLA-DPA10201-DPB11401  772       ALTGIAVEQDKNTQE  ALTGIAVEQ  0        0.0707
23274.2    90.00  0.31     Sequence
 HLA-DPA10201-DPB11401  773       LTGIAVEQDKNTQEV  IAVEQDKNT  3        0.0346
34396.0    100.00 0.25     Sequence
 HLA-DPA10201-DPB11401  774       TGIAVEQDKNTQEVF  IAVEQDKNT  2        0.0328
35070.9    100.00 0.29     Sequence
 HLA-DPA10201-DPB11401  775       GIAVEQDKNTQEVFA  EQDKNTQEV  4        0.0403
32334.9    100.00 0.20     Sequence
 HLA-DPA10201-DPB11401  776       IAVEQDKNTQEVFAQ  KNTQEVFAQ  6        0.0696
23549.6    90.00  0.50     Sequence
 HLA-DPA10201-DPB11401  777       AVEQDKNTQEVFAQV  KNTQEVFAQ  5        0.0964
17619.7    85.00  0.56     Sequence
 HLA-DPA10201-DPB11401  778       VEQDKNTQEVFAQVK  KNTQEVFAQ  4        0.1463
10273.9    65.00  0.46     Sequence
 HLA-DPA10201-DPB11401  779       EQDKNTQEVFAQVKQ  KNTQEVFAQ  3        0.1680
8119.1    55.00  0.38     Sequence
 HLA-DPA10201-DPB11401  780       QDKNTQEVFAQVKQI  EVFAQVKQI  6        0.2074
5301.1    40.00  0.29     Sequence
 HLA-DPA10201-DPB11401  781       DKNTQEVFAQVKQIY  EVFAQVKQI  5        0.2363
3876.4    31.00  0.37     Sequence
 HLA-DPA10201-DPB11401  782       KNTQEVFAQVKQIYK  EVFAQVKQI  4        0.2705
2679.1    23.00  0.34     Sequence
 HLA-DPA10201-DPB11401  783       NTQEVFAQVKQIYKT  EVFAQVKQI  3        0.2636
2887.5    25.00  0.37     Sequence
 HLA-DPA10201-DPB11401  784       TQEVFAQVKQIYKTP  EVFAQVKQI  2        0.2651
2838.8    24.00  0.36     Sequence
 HLA-DPA10201-DPB11401  785       QEVFAQVKQIYKTPP  EVFAQVKQI  1        0.2193
4662.2    36.00  0.27     Sequence
 HLA-DPA10201-DPB11401  786       EVFAQVKQIYKTPPI  KQIYKTPPI  6        0.2275
4264.4    34.00  0.22     Sequence
 HLA-DPA10201-DPB11401  787       VFAQVKQIYKTPPIK  KQIYKTPPI  5        0.2448
3537.4    29.00  0.34     Sequence
 HLA-DPA10201-DPB11401  788       FAQVKQIYKTPPIKD  KQIYKTPPI  4        0.2503
3332.1    28.00  0.37     Sequence
```

```
 HLA-DPA10201-DPB11401  789      AQVKQIYKTPPIKDF  KQIYKTPPI  3        0.2837
2321.0    20.00  0.31     Sequence
 HLA-DPA10201-DPB11401  790      QVKQIYKTPPIKDFG  KQIYKTPPI  2        0.2772
2489.9    22.00  0.30     Sequence
 HLA-DPA10201-DPB11401  791      VKQIYKTPPIKDFGG  KQIYKTPPI  1        0.2607
2979.5    25.00  0.31     Sequence
 HLA-DPA10201-DPB11401  792      KQIYKTPPIKDFGGF  IYKTPPIKD  2        0.2404
3711.3    30.00  0.25     Sequence
 HLA-DPA10201-DPB11401  793      QIYKTPPIKDFGGFN  YKTPPIKDF  2        0.1739
7620.0    55.00  0.34     Sequence
 HLA-DPA10201-DPB11401  794      IYKTPPIKDFGGFNF  YKTPPIKDF  1        0.1353
11569.9    70.00  0.29     Sequence
 HLA-DPA10201-DPB11401  795      YKTPPIKDFGGFNFS  KDFGGFNFS  6        0.1003
16884.2    80.00  0.23     Sequence
 HLA-DPA10201-DPB11401  796      KTPPIKDFGGFNFSQ  KDFGGFNFS  5        0.0877
19353.0    85.00  0.40     Sequence
 HLA-DPA10201-DPB11401  797      TPPIKDFGGFNFSQI  KDFGGFNFS  4        0.1201
13639.3    75.00  0.36     Sequence
 HLA-DPA10201-DPB11401  798      PPIKDFGGFNFSQIL  KDFGGFNFS  3        0.1427
10675.0    65.00  0.31     Sequence
 HLA-DPA10201-DPB11401  799      PIKDFGGFNFSQILP  KDFGGFNFS  2        0.1705
7901.0    55.00  0.25     Sequence
 HLA-DPA10201-DPB11401  800      IKDFGGFNFSQILPD  FGGFNFSQI  3        0.1656
8334.7    55.00  0.17     Sequence
 HLA-DPA10201-DPB11401  801      KDFGGFNFSQILPDP  FNFSQILPD  5        0.1734
7657.0    55.00  0.28     Sequence
 HLA-DPA10201-DPB11401  802      DFGGFNFSQILPDPS  FNFSQILPD  4        0.1663
8273.0    55.00  0.31     Sequence
 HLA-DPA10201-DPB11401  803      FGGFNFSQILPDPSK  FNFSQILPD  3        0.1747
7553.6    55.00  0.34     Sequence
 HLA-DPA10201-DPB11401  804      GGFNFSQILPDPSKP  FNFSQILPD  2        0.1578
9069.6    60.00  0.36     Sequence
 HLA-DPA10201-DPB11401  805      GFNFSQILPDPSKPS  FNFSQILPD  1        0.1428
10666.8    65.00  0.38     Sequence
 HLA-DPA10201-DPB11401  806      FNFSQILPDPSKPSK  FNFSQILPD  0        0.1181
13928.9    75.00  0.27     Sequence
 HLA-DPA10201-DPB11401  807      NFSQILPDPSKPSKR  QILPDPSKP  3        0.0965
17604.5    85.00  0.28     Sequence
 HLA-DPA10201-DPB11401  808      FSQILPDPSKPSKRS  QILPDPSKP  2        0.0839
20169.6    90.00  0.34     Sequence
 HLA-DPA10201-DPB11401  809      SQILPDPSKPSKRSF  ILPDPSKPS  2        0.0609
25866.7    95.00  0.34     Sequence
 HLA-DPA10201-DPB11401  810      QILPDPSKPSKRSFI  ILPDPSKPS  1        0.0574
26880.5    95.00  0.34     Sequence
 HLA-DPA10201-DPB11401  811      ILPDPSKPSKRSFIE  KPSKRSFIE  6        0.0615
25691.6    95.00  0.36     Sequence
 HLA-DPA10201-DPB11401  812      LPDPSKPSKRSFIED  KPSKRSFIE  5        0.0606
25966.0    95.00  0.41     Sequence
 HLA-DPA10201-DPB11401  813      PDPSKPSKRSFIEDL  KPSKRSFIE  4        0.1180
13954.7    75.00  0.30     Sequence
 HLA-DPA10201-DPB11401  814      DPSKPSKRSFIEDLL  KRSFIEDLL  6        0.2444
3551.7    29.00  0.35     Sequence
 HLA-DPA10201-DPB11401  815      PSKPSKRSFIEDLLF  KRSFIEDLL  5        0.2848
2293.4    20.00  0.37     Sequence
 HLA-DPA10201-DPB11401  816      SKPSKRSFIEDLLFN  KRSFIEDLL  4        0.2969
2012.8    18.00  0.35     Sequence
 HLA-DPA10201-DPB11401  817      KPSKRSFIEDLLFNK  KRSFIEDLL  3        0.3177
1607.5    15.00  0.31     Sequence
 HLA-DPA10201-DPB11401  818      PSKRSFIEDLLFNKV  RSFIEDLLF  3        0.3266
1459.9    13.00  0.25     Sequence
 HLA-DPA10201-DPB11401  819      SKRSFIEDLLFNKVT  RSFIEDLLF  2        0.3341
1345.6    12.00  0.25     Sequence
 HLA-DPA10201-DPB11401  820      KRSFIEDLLFNKVTL  RSFIEDLLF  1        0.3026
1893.3    17.00  0.20     Sequence
 HLA-DPA10201-DPB11401  821      RSFIEDLLFNKVTLA  FIEDLLFNK  2        0.2302
4143.4    33.00  0.26     Sequence
```

```
 HLA-DPA10201-DPB11401  822      SFIEDLLFNKVTLAD  IEDLLFNKV  2        0.1972
5918.2    43.00  0.28     Sequence
 HLA-DPA10201-DPB11401  823      FIEDLLFNKVTLADA  IEDLLFNKV  1        0.1783
7264.6    50.00  0.22     Sequence
 HLA-DPA10201-DPB11401  824      IEDLLFNKVTLADAG  LLFNKVTLA  3        0.1428
10661.8    65.00  0.18     Sequence
 HLA-DPA10201-DPB11401  825      EDLLFNKVTLADAGF  KVTLADAGF  6        0.1592
8935.2    60.00  0.28     Sequence
 HLA-DPA10201-DPB11401  826      DLLFNKVTLADAGFI  KVTLADAGF  5        0.1910
6330.6    46.00  0.34     Sequence
 HLA-DPA10201-DPB11401  827      LLFNKVTLADAGFIK  KVTLADAGF  4        0.2272
4281.0    34.00  0.32     Sequence
 HLA-DPA10201-DPB11401  828      LFNKVTLADAGFIKQ  KVTLADAGF  3        0.2366
3864.0    31.00  0.34     Sequence
 HLA-DPA10201-DPB11401  829      FNKVTLADAGFIKQY  KVTLADAGF  2        0.2399
3731.1    31.00  0.32     Sequence
 HLA-DPA10201-DPB11401  830      NKVTLADAGFIKQYG  TLADAGFIK  3        0.2021
5614.4    42.00  0.22     Sequence
 HLA-DPA10201-DPB11401  831      KVTLADAGFIKQYGD  TLADAGFIK  2        0.1925
6227.9    45.00  0.28     Sequence
 HLA-DPA10201-DPB11401  832      VTLADAGFIKQYGDC  TLADAGFIK  1        0.1260
12795.4    70.00  0.30     Sequence
 HLA-DPA10201-DPB11401  833      TLADAGFIKQYGDCL  LADAGFIKQ  1        0.1159
14272.8    75.00  0.22     Sequence
 HLA-DPA10201-DPB11401  834      LADAGFIKQYGDCLG  FIKQYGDCL  5        0.0941
18063.7    85.00  0.26     Sequence
 HLA-DPA10201-DPB11401  835      ADAGFIKQYGDCLGD  KQYGDCLGD  6        0.0927
18338.8    85.00  0.28     Sequence
 HLA-DPA10201-DPB11401  836      DAGFIKQYGDCLGDI  KQYGDCLGD  5        0.1226
13263.3    75.00  0.30     Sequence
 HLA-DPA10201-DPB11401  837      AGFIKQYGDCLGDIA  KQYGDCLGD  4        0.1425
10701.1    65.00  0.31     Sequence
 HLA-DPA10201-DPB11401  838      GFIKQYGDCLGDIAA  KQYGDCLGD  3        0.1461
10289.9    65.00  0.32     Sequence
 HLA-DPA10201-DPB11401  839      FIKQYGDCLGDIAAR  KQYGDCLGD  2        0.1494
9924.6    65.00  0.34     Sequence
 HLA-DPA10201-DPB11401  840      IKQYGDCLGDIAARD  QYGDCLGDI  2        0.0898
18916.8    85.00  0.35     Sequence
 HLA-DPA10201-DPB11401  841      KQYGDCLGDIAARDL  QYGDCLGDI  1        0.0782
21456.7    90.00  0.26     Sequence
 HLA-DPA10201-DPB11401  842      QYGDCLGDIAARDLI  CLGDIAARD  4        0.0782
21446.9    90.00  0.30     Sequence
 HLA-DPA10201-DPB11401  843      YGDCLGDIAARDLIC  CLGDIAARD  3        0.0715
23075.9    90.00  0.37     Sequence
 HLA-DPA10201-DPB11401  844      GDCLGDIAARDLICA  CLGDIAARD  2        0.0767
21805.6    90.00  0.34     Sequence
 HLA-DPA10201-DPB11401  845      DCLGDIAARDLICAQ  CLGDIAARD  1        0.0811
20799.9    90.00  0.26     Sequence
 HLA-DPA10201-DPB11401  846      CLGDIAARDLICAQK  LGDIAARDL  1        0.0875
19401.2    85.00  0.19     Sequence
 HLA-DPA10201-DPB11401  847      LGDIAARDLICAQKF  RDLICAQKF  6        0.1249
12947.8    75.00  0.41     Sequence
 HLA-DPA10201-DPB11401  848      GDIAARDLICAQKFN  RDLICAQKF  5        0.1433
10605.5    65.00  0.57     Sequence
 HLA-DPA10201-DPB11401  849      DIAARDLICAQKFNG  RDLICAQKF  4        0.1443
10489.0    65.00  0.51     Sequence
 HLA-DPA10201-DPB11401  850      IAARDLICAQKFNGL  RDLICAQKF  3        0.1825
6937.0    49.00  0.48     Sequence
 HLA-DPA10201-DPB11401  851      AARDLICAQKFNGLT  RDLICAQKF  2        0.1907
6350.7    46.00  0.43     Sequence
 HLA-DPA10201-DPB11401  852      ARDLICAQKFNGLTV  RDLICAQKF  1        0.2362
3882.9    32.00  0.31     Sequence
 HLA-DPA10201-DPB11401  853      RDLICAQKFNGLTVL  QKFNGLTVL  6        0.2726
2619.0    23.00  0.16     Sequence
 HLA-DPA10201-DPB11401  854      DLICAQKFNGLTVLP  QKFNGLTVL  5        0.3103
1741.5    16.00  0.28     Sequence
```

```
 HLA-DPA10201-DPB11401  855      LICAQKFNGLTVLPP  KFNGLTVLP  5        0.3300
1407.0    13.00  0.32     Sequence
 HLA-DPA10201-DPB11401  856      ICAQKFNGLTVLPPL  KFNGLTVLP  4        0.3714
899.1     8.00  0.35     Sequence         WB
 HLA-DPA10201-DPB11401  857      CAQKFNGLTVLPPLL  KFNGLTVLP  3        0.3999
660.6     6.00  0.34     Sequence         WB
 HLA-DPA10201-DPB11401  858      AQKFNGLTVLPPLLT  KFNGLTVLP  2        0.4234
512.1     4.50  0.32     Sequence         WB
 HLA-DPA10201-DPB11401  859      QKFNGLTVLPPLLTD  KFNGLTVLP  1        0.3769
846.9     7.50  0.23     Sequence         WB
 HLA-DPA10201-DPB11401  860      KFNGLTVLPPLLTDE  GLTVLPPLL  3        0.3050
1844.0    17.00  0.19     Sequence
 HLA-DPA10201-DPB11401  861      FNGLTVLPPLLTDEM  GLTVLPPLL  2        0.2299
4154.1    33.00  0.29     Sequence
 HLA-DPA10201-DPB11401  862      NGLTVLPPLLTDEMI  LTVLPPLLT  2        0.2041
5495.3    41.00  0.32     Sequence
 HLA-DPA10201-DPB11401  863      GLTVLPPLLTDEMIA  LTVLPPLLT  1        0.1862
6665.1    47.00  0.32     Sequence
 HLA-DPA10201-DPB11401  864      LTVLPPLLTDEMIAQ  LTVLPPLLT  0        0.1271
12640.6    70.00  0.29     Sequence
 HLA-DPA10201-DPB11401  865      TVLPPLLTDEMIAQY  PLLTDEMIA  4        0.1009
16775.8    80.00  0.32     Sequence
 HLA-DPA10201-DPB11401  866      VLPPLLTDEMIAQYT  PLLTDEMIA  3        0.0991
17107.8    80.00  0.34     Sequence
 HLA-DPA10201-DPB11401  867      LPPLLTDEMIAQYTS  PLLTDEMIA  2        0.0986
17200.2    85.00  0.34     Sequence
 HLA-DPA10201-DPB11401  868      PPLLTDEMIAQYTSA  LTDEMIAQY  3        0.0966
17585.6    85.00  0.26     Sequence
 HLA-DPA10201-DPB11401  869      PLLTDEMIAQYTSAL  LTDEMIAQY  2        0.1241
13056.0    75.00  0.22     Sequence
 HLA-DPA10201-DPB11401  870      LLTDEMIAQYTSALL  IAQYTSALL  6        0.1838
6841.1    48.00  0.24     Sequence
 HLA-DPA10201-DPB11401  871      LTDEMIAQYTSALLA  AQYTSALLA  6        0.2719
2637.0    23.00  0.35     Sequence
 HLA-DPA10201-DPB11401  872      TDEMIAQYTSALLAG  AQYTSALLA  5        0.2967
2017.2    18.00  0.36     Sequence
 HLA-DPA10201-DPB11401  873      DEMIAQYTSALLAGT  AQYTSALLA  4        0.3269
1455.8    13.00  0.39     Sequence
 HLA-DPA10201-DPB11401  874      EMIAQYTSALLAGTI  AQYTSALLA  3        0.3660
952.9     8.50  0.37     Sequence         WB
 HLA-DPA10201-DPB11401  875      MIAQYTSALLAGTIT  AQYTSALLA  2        0.3695
917.2     8.00  0.41     Sequence         WB
 HLA-DPA10201-DPB11401  876      IAQYTSALLAGTITS  AQYTSALLA  1        0.3475
1164.9    11.00  0.38     Sequence
 HLA-DPA10201-DPB11401  877      AQYTSALLAGTITSG  AQYTSALLA  0        0.2806
2400.0    21.00  0.29     Sequence
 HLA-DPA10201-DPB11401  878      QYTSALLAGTITSGW  QYTSALLAG  0        0.2040
5499.6    41.00  0.26     Sequence
 HLA-DPA10201-DPB11401  879      YTSALLAGTITSGWT  SALLAGTIT  2        0.1381
11225.6    70.00  0.20     Sequence
 HLA-DPA10201-DPB11401  880      TSALLAGTITSGWTF  SALLAGTIT  1        0.1105
15122.7    80.00  0.23     Sequence
 HLA-DPA10201-DPB11401  881      SALLAGTITSGWTFG  LLAGTITSG  2        0.0967
17562.8    85.00  0.29     Sequence
 HLA-DPA10201-DPB11401  882      ALLAGTITSGWTFGA  LLAGTITSG  1        0.0889
19117.4    85.00  0.25     Sequence
 HLA-DPA10201-DPB11401  883      LLAGTITSGWTFGAG  LLAGTITSG  0        0.0619
25597.0    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401  884      LAGTITSGWTFGAGA  ITSGWTFGA  4        0.0579
26717.0    95.00  0.23     Sequence
 HLA-DPA10201-DPB11401  885      AGTITSGWTFGAGAA  ITSGWTFGA  3        0.0678
24013.0    95.00  0.25     Sequence
 HLA-DPA10201-DPB11401  886      GTITSGWTFGAGAAL  WTFGAGAAL  6        0.0980
17322.4    85.00  0.30     Sequence
 HLA-DPA10201-DPB11401  887      TITSGWTFGAGAALQ  WTFGAGAAL  5        0.1621
8658.6    60.00  0.41     Sequence
```

```
 HLA-DPA10201-DPB11401  888      ITSGWTFGAGAALQI  WTFGAGAAL  4        0.2218
4536.3    36.00  0.29     Sequence
 HLA-DPA10201-DPB11401  889      TSGWTFGAGAALQIP  FGAGAALQI  5        0.2332
4008.7    32.00  0.34     Sequence
 HLA-DPA10201-DPB11401  890      SGWTFGAGAALQIPF  FGAGAALQI  4        0.2465
3473.8    29.00  0.37     Sequence
 HLA-DPA10201-DPB11401  891      GWTFGAGAALQIPFA  FGAGAALQI  3        0.2510
3309.0    28.00  0.36     Sequence
 HLA-DPA10201-DPB11401  892      WTFGAGAALQIPFAM  FGAGAALQI  2        0.2632
2899.6    25.00  0.39     Sequence
 HLA-DPA10201-DPB11401  893      TFGAGAALQIPFAMQ  AALQIPFAM  5        0.2658
2817.3    24.00  0.22     Sequence
 HLA-DPA10201-DPB11401  894      FGAGAALQIPFAMQM  AALQIPFAM  4        0.2958
2037.9    18.00  0.23     Sequence
 HLA-DPA10201-DPB11401  895      GAGAALQIPFAMQMA  LQIPFAMQM  5        0.3279
1439.4    13.00  0.28     Sequence
 HLA-DPA10201-DPB11401  896      AGAALQIPFAMQMAY  LQIPFAMQM  4        0.3420
1236.1    11.00  0.23     Sequence
 HLA-DPA10201-DPB11401  897      GAALQIPFAMQMAYR  LQIPFAMQM  3        0.3567
1054.4     9.50  0.28     Sequence         WB
 HLA-DPA10201-DPB11401  898      AALQIPFAMQMAYRF  LQIPFAMQM  2        0.3628
986.4     9.00  0.26     Sequence         WB
 HLA-DPA10201-DPB11401  899      ALQIPFAMQMAYRFN  LQIPFAMQM  1        0.3338
1350.2    12.00  0.29     Sequence
 HLA-DPA10201-DPB11401  900      LQIPFAMQMAYRFNG  LQIPFAMQM  0        0.2596
3012.8    26.00  0.22     Sequence
 HLA-DPA10201-DPB11401  901      QIPFAMQMAYRFNGI  FAMQMAYRF  3        0.2179
4731.7    37.00  0.35     Sequence
 HLA-DPA10201-DPB11401  902      IPFAMQMAYRFNGIG  FAMQMAYRF  2        0.1748
7542.6    55.00  0.43     Sequence
 HLA-DPA10201-DPB11401  903      PFAMQMAYRFNGIGV  FAMQMAYRF  1        0.1909
6338.9    46.00  0.35     Sequence
 HLA-DPA10201-DPB11401  904      FAMQMAYRFNGIGVT  FAMQMAYRF  0        0.2151
4875.5    38.00  0.22     Sequence
 HLA-DPA10201-DPB11401  905      AMQMAYRFNGIGVTQ  RFNGIGVTQ  6        0.2328
4027.6    32.00  0.32     Sequence
 HLA-DPA10201-DPB11401  906      MQMAYRFNGIGVTQN  RFNGIGVTQ  5        0.2436
3584.2    30.00  0.40     Sequence
 HLA-DPA10201-DPB11401  907      QMAYRFNGIGVTQNV  RFNGIGVTQ  4        0.2690
2723.4    23.00  0.43     Sequence
 HLA-DPA10201-DPB11401  908      MAYRFNGIGVTQNVL  RFNGIGVTQ  3        0.2888
2197.9    20.00  0.44     Sequence
 HLA-DPA10201-DPB11401  909      AYRFNGIGVTQNVLY  RFNGIGVTQ  2        0.2949
2057.8    18.00  0.44     Sequence
 HLA-DPA10201-DPB11401  910      YRFNGIGVTQNVLYE  RFNGIGVTQ  1        0.2512
3301.0    28.00  0.37     Sequence
 HLA-DPA10201-DPB11401  911      RFNGIGVTQNVLYEN  RFNGIGVTQ  0        0.1677
8147.2    55.00  0.27     Sequence
 HLA-DPA10201-DPB11401  912      FNGIGVTQNVLYENQ  GIGVTQNVL  2        0.1126
14787.5    75.00  0.29     Sequence
 HLA-DPA10201-DPB11401  913      NGIGVTQNVLYENQK  GIGVTQNVL  1        0.0967
17558.2    85.00  0.27     Sequence
 HLA-DPA10201-DPB11401  914      GIGVTQNVLYENQKL  GVTQNVLYE  2        0.0977
17379.8    85.00  0.26     Sequence
 HLA-DPA10201-DPB11401  915      IGVTQNVLYENQKLI  VLYENQKLI  6        0.1123
14830.3    80.00  0.35     Sequence
 HLA-DPA10201-DPB11401  916      GVTQNVLYENQKLIA  VLYENQKLI  5        0.1531
9537.4    60.00  0.40     Sequence
 HLA-DPA10201-DPB11401  917      VTQNVLYENQKLIAN  VLYENQKLI  4        0.1657
8326.1    55.00  0.38     Sequence
 HLA-DPA10201-DPB11401  918      TQNVLYENQKLIANQ  VLYENQKLI  3        0.1677
8148.4    55.00  0.41     Sequence
 HLA-DPA10201-DPB11401  919      QNVLYENQKLIANQF  VLYENQKLI  2        0.1776
7317.5    50.00  0.38     Sequence
 HLA-DPA10201-DPB11401  920      NVLYENQKLIANQFN  VLYENQKLI  1        0.1797
7154.0    50.00  0.32     Sequence
```

```
 HLA-DPA10201-DPB11401  921      VLYENQKLIANQFNS  KLIANQFNS  6        0.1946
6087.9    44.00  0.23     Sequence
 HLA-DPA10201-DPB11401  922      LYENQKLIANQFNSA  KLIANQFNS  5        0.2023
5604.8    42.00  0.38     Sequence
 HLA-DPA10201-DPB11401  923      YENQKLIANQFNSAI  KLIANQFNS  4        0.2416
3662.7    30.00  0.42     Sequence
 HLA-DPA10201-DPB11401  924      ENQKLIANQFNSAIG  KLIANQFNS  3        0.2344
3958.0    32.00  0.38     Sequence
 HLA-DPA10201-DPB11401  925      NQKLIANQFNSAIGK  KLIANQFNS  2        0.2464
3474.9    29.00  0.37     Sequence
 HLA-DPA10201-DPB11401  926      QKLIANQFNSAIGKI  QFNSAIGKI  6        0.2871
2237.2    20.00  0.26     Sequence
 HLA-DPA10201-DPB11401  927      KLIANQFNSAIGKIQ  QFNSAIGKI  5        0.2886
2201.7    20.00  0.32     Sequence
 HLA-DPA10201-DPB11401  928      LIANQFNSAIGKIQD  QFNSAIGKI  4        0.2473
3444.7    29.00  0.40     Sequence
 HLA-DPA10201-DPB11401  929      IANQFNSAIGKIQDS  QFNSAIGKI  3        0.2460
3492.5    29.00  0.44     Sequence
 HLA-DPA10201-DPB11401  930      ANQFNSAIGKIQDSL  QFNSAIGKI  2        0.2458
3498.0    29.00  0.43     Sequence
 HLA-DPA10201-DPB11401  931      NQFNSAIGKIQDSLS  QFNSAIGKI  1        0.2275
4265.9    34.00  0.38     Sequence
 HLA-DPA10201-DPB11401  932      QFNSAIGKIQDSLSS  QFNSAIGKI  0        0.2024
5594.5    42.00  0.31     Sequence
 HLA-DPA10201-DPB11401  933      FNSAIGKIQDSLSST  KIQDSLSST  6        0.1535
9503.5    60.00  0.26     Sequence
 HLA-DPA10201-DPB11401  934      NSAIGKIQDSLSSTA  KIQDSLSST  5        0.1576
9089.2    60.00  0.47     Sequence
 HLA-DPA10201-DPB11401  935      SAIGKIQDSLSSTAS  KIQDSLSST  4        0.1704
7915.6    55.00  0.46     Sequence
 HLA-DPA10201-DPB11401  936      AIGKIQDSLSSTASA  KIQDSLSST  3        0.1772
7351.4    50.00  0.49     Sequence
 HLA-DPA10201-DPB11401  937      IGKIQDSLSSTASAL  KIQDSLSST  2        0.1992
5792.1    43.00  0.38     Sequence
 HLA-DPA10201-DPB11401  938      GKIQDSLSSTASALG  SLSSTASAL  5        0.1979
5873.1    43.00  0.31     Sequence
 HLA-DPA10201-DPB11401  939      KIQDSLSSTASALGK  SLSSTASAL  4        0.2083
5252.3    40.00  0.39     Sequence
 HLA-DPA10201-DPB11401  940      IQDSLSSTASALGKL  SLSSTASAL  3        0.2261
4329.2    34.00  0.49     Sequence
 HLA-DPA10201-DPB11401  941      QDSLSSTASALGKLQ  SLSSTASAL  2        0.2372
3839.1    31.00  0.43     Sequence
 HLA-DPA10201-DPB11401  942      DSLSSTASALGKLQD  SLSSTASAL  1        0.2342
3965.5    32.00  0.41     Sequence
 HLA-DPA10201-DPB11401  943      SLSSTASALGKLQDV  SLSSTASAL  0        0.2440
3567.5    29.00  0.37     Sequence
 HLA-DPA10201-DPB11401  944      LSSTASALGKLQDVV  STASALGKL  2        0.1797
7150.8    49.00  0.43     Sequence
 HLA-DPA10201-DPB11401  945      SSTASALGKLQDVVN  STASALGKL  1        0.1540
9443.9    60.00  0.34     Sequence
 HLA-DPA10201-DPB11401  946      STASALGKLQDVVNQ  STASALGKL  0        0.1420
10757.0    65.00  0.28     Sequence
 HLA-DPA10201-DPB11401  947      TASALGKLQDVVNQN  SALGKLQDV  2        0.1155
14323.4    75.00  0.24     Sequence
 HLA-DPA10201-DPB11401  948      ASALGKLQDVVNQNA  KLQDVVNQN  5        0.1089
15382.8    80.00  0.28     Sequence
 HLA-DPA10201-DPB11401  949      SALGKLQDVVNQNAQ  KLQDVVNQN  4        0.1123
14842.5    80.00  0.35     Sequence
 HLA-DPA10201-DPB11401  950      ALGKLQDVVNQNAQA  KLQDVVNQN  3        0.1095
15283.8    80.00  0.38     Sequence
 HLA-DPA10201-DPB11401  951      LGKLQDVVNQNAQAL  VVNQNAQAL  6        0.1470
10195.3    65.00  0.29     Sequence
 HLA-DPA10201-DPB11401  952      GKLQDVVNQNAQALN  VVNQNAQAL  5        0.1749
7537.4    55.00  0.46     Sequence
 HLA-DPA10201-DPB11401  953      KLQDVVNQNAQALNT  VVNQNAQAL  4        0.1759
7454.0    55.00  0.50     Sequence
```

```
 HLA-DPA10201-DPB11401  954      LQDVVNQNAQALNTL  VVNQNAQAL  3        0.1880
6541.9    47.00  0.56     Sequence
 HLA-DPA10201-DPB11401  955      QDVVNQNAQALNTLV  VVNQNAQAL  2        0.1998
5758.1    43.00  0.50     Sequence
 HLA-DPA10201-DPB11401  956      DVVNQNAQALNTLVK  VVNQNAQAL  1        0.2050
5443.5    41.00  0.46     Sequence
 HLA-DPA10201-DPB11401  957      VVNQNAQALNTLVKQ  VVNQNAQAL  0        0.2021
5617.4    42.00  0.40     Sequence
 HLA-DPA10201-DPB11401  958      VNQNAQALNTLVKQL  ALNTLVKQL  6        0.1692
8015.4    55.00  0.22     Sequence
 HLA-DPA10201-DPB11401  959      NQNAQALNTLVKQLS  ALNTLVKQL  5        0.1732
7679.4    55.00  0.36     Sequence
 HLA-DPA10201-DPB11401  960      QNAQALNTLVKQLSS  ALNTLVKQL  4        0.1770
7370.2    55.00  0.37     Sequence
 HLA-DPA10201-DPB11401  961      NAQALNTLVKQLSSN  ALNTLVKQL  3        0.1685
8080.0    55.00  0.40     Sequence
 HLA-DPA10201-DPB11401  962      AQALNTLVKQLSSNF  ALNTLVKQL  2        0.1721
7765.3    55.00  0.40     Sequence
 HLA-DPA10201-DPB11401  963      QALNTLVKQLSSNFG  ALNTLVKQL  1        0.1420
10761.1    65.00  0.33     Sequence
 HLA-DPA10201-DPB11401  964      ALNTLVKQLSSNFGA  NTLVKQLSS  2        0.1375
11294.1    70.00  0.22     Sequence
 HLA-DPA10201-DPB11401  965      LNTLVKQLSSNFGAI  KQLSSNFGA  5        0.1545
9398.3    60.00  0.25     Sequence
 HLA-DPA10201-DPB11401  966      NTLVKQLSSNFGAIS  QLSSNFGAI  5        0.1873
6592.6    47.00  0.36     Sequence
 HLA-DPA10201-DPB11401  967      TLVKQLSSNFGAISS  QLSSNFGAI  4        0.2046
5462.3    41.00  0.35     Sequence
 HLA-DPA10201-DPB11401  968      LVKQLSSNFGAISSV  QLSSNFGAI  3        0.2135
4962.0    38.00  0.39     Sequence
 HLA-DPA10201-DPB11401  969      VKQLSSNFGAISSVL  QLSSNFGAI  2        0.2519
3275.4    27.00  0.31     Sequence
 HLA-DPA10201-DPB11401  970      KQLSSNFGAISSVLN  NFGAISSVL  5        0.2637
2881.5    25.00  0.23     Sequence
 HLA-DPA10201-DPB11401  971      QLSSNFGAISSVLND  NFGAISSVL  4        0.2390
3766.6    31.00  0.26     Sequence
 HLA-DPA10201-DPB11401  972      LSSNFGAISSVLNDI  NFGAISSVL  3        0.2434
3590.0    30.00  0.28     Sequence
 HLA-DPA10201-DPB11401  973      SSNFGAISSVLNDIL  NFGAISSVL  2        0.2474
3439.0    29.00  0.27     Sequence
 HLA-DPA10201-DPB11401  974      SNFGAISSVLNDILS  NFGAISSVL  1        0.2450
3528.4    29.00  0.23     Sequence
 HLA-DPA10201-DPB11401  975      NFGAISSVLNDILSR  NFGAISSVL  0        0.2310
4107.3    33.00  0.19     Sequence
 HLA-DPA10201-DPB11401  976      FGAISSVLNDILSRL  AISSVLNDI  2        0.1962
5985.9    44.00  0.19     Sequence
 HLA-DPA10201-DPB11401  977      GAISSVLNDILSRLD  VLNDILSRL  5        0.1538
9465.4    60.00  0.31     Sequence
 HLA-DPA10201-DPB11401  978      AISSVLNDILSRLDK  VLNDILSRL  4        0.1514
9718.6    60.00  0.38     Sequence
 HLA-DPA10201-DPB11401  979      ISSVLNDILSRLDKV  VLNDILSRL  3        0.1429
10652.9    65.00  0.47     Sequence
 HLA-DPA10201-DPB11401  980      SSVLNDILSRLDKVE  VLNDILSRL  2        0.1317
12020.5    70.00  0.47     Sequence
 HLA-DPA10201-DPB11401  981      SVLNDILSRLDKVEA  VLNDILSRL  1        0.1343
11696.1    70.00  0.38     Sequence
 HLA-DPA10201-DPB11401  982      VLNDILSRLDKVEAE  VLNDILSRL  0        0.1158
14276.7    75.00  0.31     Sequence
 HLA-DPA10201-DPB11401  983      LNDILSRLDKVEAEV  RLDKVEAEV  6        0.1484
10041.5    65.00  0.38     Sequence
 HLA-DPA10201-DPB11401  984      NDILSRLDKVEAEVQ  RLDKVEAEV  5        0.1746
7563.3    55.00  0.38     Sequence
 HLA-DPA10201-DPB11401  985      DILSRLDKVEAEVQI  RLDKVEAEV  4        0.2150
4882.4    38.00  0.37     Sequence
 HLA-DPA10201-DPB11401  986      ILSRLDKVEAEVQID  RLDKVEAEV  3        0.2319
4065.1    33.00  0.31     Sequence
```

```
 HLA-DPA10201-DPB11401  987      LSRLDKVEAEVQIDR  KVEAEVQID  5        0.2401
3721.3    30.00  0.28     Sequence
 HLA-DPA10201-DPB11401  988      SRLDKVEAEVQIDRL  KVEAEVQID  4        0.2543
3192.5    27.00  0.38     Sequence
 HLA-DPA10201-DPB11401  989      RLDKVEAEVQIDRLI  KVEAEVQID  3        0.2748
2555.8    22.00  0.45     Sequence
 HLA-DPA10201-DPB11401  990      LDKVEAEVQIDRLIT  KVEAEVQID  2        0.2431
3604.3    30.00  0.49     Sequence
 HLA-DPA10201-DPB11401  991      DKVEAEVQIDRLITG  KVEAEVQID  1        0.2145
4911.0    38.00  0.43     Sequence
 HLA-DPA10201-DPB11401  992      KVEAEVQIDRLITGR  KVEAEVQID  0        0.1981
5860.6    43.00  0.34     Sequence
 HLA-DPA10201-DPB11401  993      VEAEVQIDRLITGRL  EAEVQIDRL  1        0.1485
10027.7    65.00  0.11     Sequence
 HLA-DPA10201-DPB11401  994      EAEVQIDRLITGRLQ  QIDRLITGR  4        0.1552
9330.8    60.00  0.19     Sequence
 HLA-DPA10201-DPB11401  995      AEVQIDRLITGRLQS  RLITGRLQS  6        0.1925
6230.3    45.00  0.29     Sequence
 HLA-DPA10201-DPB11401  996      EVQIDRLITGRLQSL  RLITGRLQS  5        0.2287
4211.0    34.00  0.40     Sequence
 HLA-DPA10201-DPB11401  997      VQIDRLITGRLQSLQ  RLITGRLQS  4        0.2459
3497.0    29.00  0.41     Sequence
 HLA-DPA10201-DPB11401  998      QIDRLITGRLQSLQT  RLITGRLQS  3        0.2442
3559.7    29.00  0.43     Sequence
 HLA-DPA10201-DPB11401  999      IDRLITGRLQSLQTY  RLITGRLQS  2        0.2296
4170.7    33.00  0.50     Sequence
 HLA-DPA10201-DPB11401 1000      DRLITGRLQSLQTYV  RLITGRLQS  1        0.2359
3894.8    32.00  0.31     Sequence
 HLA-DPA10201-DPB11401 1001      RLITGRLQSLQTYVT  RLQSLQTYV  5        0.2333
4005.7    32.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1002      LITGRLQSLQTYVTQ  RLQSLQTYV  4        0.2057
5399.0    41.00  0.40     Sequence
 HLA-DPA10201-DPB11401 1003      ITGRLQSLQTYVTQQ  RLQSLQTYV  3        0.2048
5454.2    41.00  0.42     Sequence
 HLA-DPA10201-DPB11401 1004      TGRLQSLQTYVTQQL  RLQSLQTYV  2        0.2285
4218.3    34.00  0.35     Sequence
 HLA-DPA10201-DPB11401 1005      GRLQSLQTYVTQQLI  RLQSLQTYV  1        0.2532
3231.4    27.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1006      RLQSLQTYVTQQLIR  QTYVTQQLI  5        0.2670
2782.3    24.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1007      LQSLQTYVTQQLIRA  QTYVTQQLI  4        0.2759
2527.7    22.00  0.44     Sequence
 HLA-DPA10201-DPB11401 1008      QSLQTYVTQQLIRAA  QTYVTQQLI  3        0.3160
1637.5    15.00  0.39     Sequence
 HLA-DPA10201-DPB11401 1009      SLQTYVTQQLIRAAE  QTYVTQQLI  2        0.3185
1592.7    15.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1010      LQTYVTQQLIRAAEI  QTYVTQQLI  1        0.3176
1609.4    15.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1011      QTYVTQQLIRAAEIR  QQLIRAAEI  5        0.3325
1370.0    13.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1012      TYVTQQLIRAAEIRA  QQLIRAAEI  4        0.3739
875.3     8.00  0.36     Sequence          WB
 HLA-DPA10201-DPB11401 1013      YVTQQLIRAAEIRAS  QQLIRAAEI  3        0.4044
629.3     5.50  0.33     Sequence          WB
 HLA-DPA10201-DPB11401 1014      VTQQLIRAAEIRASA  QQLIRAAEI  2        0.4261
497.6     4.50  0.28     Sequence          WB
 HLA-DPA10201-DPB11401 1015      TQQLIRAAEIRASAN  RAAEIRASA  5        0.4233
512.7     4.50  0.24     Sequence          WB
 HLA-DPA10201-DPB11401 1016      QQLIRAAEIRASANL  RAAEIRASA  4        0.4327
463.0     4.00  0.31     Sequence          WB
 HLA-DPA10201-DPB11401 1017      QLIRAAEIRASANLA  RAAEIRASA  3        0.4199
531.7     4.50  0.38     Sequence          WB
 HLA-DPA10201-DPB11401 1018      LIRAAEIRASANLAA  RAAEIRASA  2        0.4200
531.5     4.50  0.34     Sequence          WB
 HLA-DPA10201-DPB11401 1019      IRAAEIRASANLAAI  RASANLAAI  6        0.4524
374.2     3.00  0.32     Sequence          WB
```

```
 HLA-DPA10201-DPB11401 1020      RAAEIRASANLAAIK  RASANLAAI  5        0.4757
290.9     2.50  0.48     Sequence         WB
 HLA-DPA10201-DPB11401 1021      AAEIRASANLAAIKM  RASANLAAI  4        0.4875
256.0     1.70  0.53     Sequence         SB
 HLA-DPA10201-DPB11401 1022      AEIRASANLAAIKMS  RASANLAAI  3        0.4962
233.1     1.50  0.52     Sequence         SB
 HLA-DPA10201-DPB11401 1023      EIRASANLAAIKMSE  RASANLAAI  2        0.4791
280.3     2.00  0.54     Sequence         WB
 HLA-DPA10201-DPB11401 1024      IRASANLAAIKMSEC  RASANLAAI  1        0.4058
619.7     5.50  0.44     Sequence         WB
 HLA-DPA10201-DPB11401 1025      RASANLAAIKMSECV  RASANLAAI  0        0.3285
1429.7    13.00  0.42     Sequence
 HLA-DPA10201-DPB11401 1026      ASANLAAIKMSECVL  SANLAAIKM  1        0.2632
2899.7    25.00  0.19     Sequence
 HLA-DPA10201-DPB11401 1027      SANLAAIKMSECVLG  LAAIKMSEC  3        0.2875
2227.6    20.00  0.16     Sequence
 HLA-DPA10201-DPB11401 1028      ANLAAIKMSECVLGQ  KMSECVLGQ  6        0.3623
992.0     9.00  0.40     Sequence         WB
 HLA-DPA10201-DPB11401 1029      NLAAIKMSECVLGQS  KMSECVLGQ  5        0.3888
744.8     6.50  0.52     Sequence         WB
 HLA-DPA10201-DPB11401 1030      LAAIKMSECVLGQSK  KMSECVLGQ  4        0.4074
609.2     5.50  0.55     Sequence         WB
 HLA-DPA10201-DPB11401 1031      AAIKMSECVLGQSKR  KMSECVLGQ  3        0.4237
510.7     4.50  0.56     Sequence         WB
 HLA-DPA10201-DPB11401 1032      AIKMSECVLGQSKRV  KMSECVLGQ  2        0.4267
494.4     4.00  0.56     Sequence         WB
 HLA-DPA10201-DPB11401 1033      IKMSECVLGQSKRVD  KMSECVLGQ  1        0.3008
1930.4    17.00  0.50     Sequence
 HLA-DPA10201-DPB11401 1034      KMSECVLGQSKRVDF  KMSECVLGQ  0        0.2110
5098.4    39.00  0.42     Sequence
 HLA-DPA10201-DPB11401 1035      MSECVLGQSKRVDFC  CVLGQSKRV  3        0.1055
15963.6    80.00  0.48     Sequence
 HLA-DPA10201-DPB11401 1036      SECVLGQSKRVDFCG  CVLGQSKRV  2        0.0960
17699.8    85.00  0.58     Sequence
 HLA-DPA10201-DPB11401 1037      ECVLGQSKRVDFCGK  CVLGQSKRV  1        0.0997
16996.9    80.00  0.50     Sequence
 HLA-DPA10201-DPB11401 1038      CVLGQSKRVDFCGKG  CVLGQSKRV  0        0.0907
18737.9    85.00  0.37     Sequence
 HLA-DPA10201-DPB11401 1039      VLGQSKRVDFCGKGY  KRVDFCGKG  5        0.0906
18762.9    85.00  0.36     Sequence
 HLA-DPA10201-DPB11401 1040      LGQSKRVDFCGKGYH  KRVDFCGKG  4        0.0959
17708.0    85.00  0.35     Sequence
 HLA-DPA10201-DPB11401 1041      GQSKRVDFCGKGYHL  KRVDFCGKG  3        0.1147
14454.3    75.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1042      QSKRVDFCGKGYHLM  KRVDFCGKG  2        0.1509
9766.8    60.00  0.28     Sequence
 HLA-DPA10201-DPB11401 1043      SKRVDFCGKGYHLMS  KRVDFCGKG  1        0.1529
9564.7    60.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1044      KRVDFCGKGYHLMSF  DFCGKGYHL  3        0.1416
10808.8    65.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1045      RVDFCGKGYHLMSFP  DFCGKGYHL  2        0.1308
12140.8    70.00  0.23     Sequence
 HLA-DPA10201-DPB11401 1046      VDFCGKGYHLMSFPQ  KGYHLMSFP  5        0.1266
12713.3    70.00  0.23     Sequence
 HLA-DPA10201-DPB11401 1047      DFCGKGYHLMSFPQS  KGYHLMSFP  4        0.1379
11246.4    70.00  0.23     Sequence
 HLA-DPA10201-DPB11401 1048      FCGKGYHLMSFPQSA  HLMSFPQSA  6        0.1744
7572.7    55.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1049      CGKGYHLMSFPQSAP  HLMSFPQSA  5        0.1833
6882.6    48.00  0.37     Sequence
 HLA-DPA10201-DPB11401 1050      GKGYHLMSFPQSAPH  HLMSFPQSA  4        0.1868
6624.7    47.00  0.38     Sequence
 HLA-DPA10201-DPB11401 1051      KGYHLMSFPQSAPHG  HLMSFPQSA  3        0.1750
7524.6    55.00  0.40     Sequence
 HLA-DPA10201-DPB11401 1052      GYHLMSFPQSAPHGV  HLMSFPQSA  2        0.1543
9418.4    60.00  0.40     Sequence
```

```
 HLA-DPA10201-DPB11401 1053      YHLMSFPQSAPHGVV  HLMSFPQSA  1        0.1588
8967.5    60.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1054      HLMSFPQSAPHGVVF  HLMSFPQSA  0        0.1523
9623.8    60.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1055      LMSFPQSAPHGVVFL  QSAPHGVVF  5        0.1533
9520.4    60.00  0.33     Sequence
 HLA-DPA10201-DPB11401 1056      MSFPQSAPHGVVFLH  QSAPHGVVF  4        0.1652
8372.6    55.00  0.35     Sequence
 HLA-DPA10201-DPB11401 1057      SFPQSAPHGVVFLHV  PHGVVFLHV  6        0.2128
4998.3    38.00  0.30     Sequence
 HLA-DPA10201-DPB11401 1058      FPQSAPHGVVFLHVT  PHGVVFLHV  5        0.2358
3897.7    32.00  0.38     Sequence
 HLA-DPA10201-DPB11401 1059      PQSAPHGVVFLHVTY  PHGVVFLHV  4        0.2209
4581.3    36.00  0.41     Sequence
 HLA-DPA10201-DPB11401 1060      QSAPHGVVFLHVTYV  PHGVVFLHV  3        0.2051
5437.3    41.00  0.48     Sequence
 HLA-DPA10201-DPB11401 1061      SAPHGVVFLHVTYVP  PHGVVFLHV  2        0.2097
5173.9    39.00  0.47     Sequence
 HLA-DPA10201-DPB11401 1062      APHGVVFLHVTYVPA  PHGVVFLHV  1        0.2405
3704.4    30.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1063      PHGVVFLHVTYVPAQ  FLHVTYVPA  5        0.2630
2905.8    25.00  0.39     Sequence
 HLA-DPA10201-DPB11401 1064      HGVVFLHVTYVPAQE  FLHVTYVPA  4        0.2613
2958.7    25.00  0.41     Sequence
 HLA-DPA10201-DPB11401 1065      GVVFLHVTYVPAQEK  FLHVTYVPA  3        0.2833
2332.3    21.00  0.37     Sequence
 HLA-DPA10201-DPB11401 1066      VVFLHVTYVPAQEKN  FLHVTYVPA  2        0.2931
2098.1    19.00  0.38     Sequence
 HLA-DPA10201-DPB11401 1067      VFLHVTYVPAQEKNF  VTYVPAQEK  4        0.2889
2195.8    19.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1068      FLHVTYVPAQEKNFT  VTYVPAQEK  3        0.2594
3018.8    26.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1069      LHVTYVPAQEKNFTT  VTYVPAQEK  2        0.1990
5803.8    43.00  0.46     Sequence
 HLA-DPA10201-DPB11401 1070      HVTYVPAQEKNFTTA  VTYVPAQEK  1        0.1499
9873.0    65.00  0.57     Sequence
 HLA-DPA10201-DPB11401 1071      VTYVPAQEKNFTTAP  VTYVPAQEK  0        0.1048
16082.3    80.00  0.44     Sequence
 HLA-DPA10201-DPB11401 1072      TYVPAQEKNFTTAPA  KNFTTAPAX  7        0.0802
20984.2    90.00  0.19     Sequence
 HLA-DPA10201-DPB11401 1073      YVPAQEKNFTTAPAI  KNFTTAPAI  6        0.3192
1581.4    14.00  0.70     Sequence
 HLA-DPA10201-DPB11401 1074      VPAQEKNFTTAPAIC  KNFTTAPAI  5        0.3977
676.1     6.00  0.68     Sequence         WB
 HLA-DPA10201-DPB11401 1075      PAQEKNFTTAPAICH  KNFTTAPAI  4        0.4459
401.6     3.50  0.62     Sequence         WB
 HLA-DPA10201-DPB11401 1076      AQEKNFTTAPAICHD  KNFTTAPAI  3        0.4466
398.7     3.50  0.62     Sequence         WB
 HLA-DPA10201-DPB11401 1077      QEKNFTTAPAICHDG  KNFTTAPAI  2        0.4419
419.3     3.50  0.63     Sequence         WB
 HLA-DPA10201-DPB11401 1078      EKNFTTAPAICHDGK  KNFTTAPAI  1        0.4246
505.4     4.50  0.60     Sequence         WB
 HLA-DPA10201-DPB11401 1079      KNFTTAPAICHDGKA  KNFTTAPAI  0        0.3972
680.4     6.00  0.51     Sequence         WB
 HLA-DPA10201-DPB11401 1080      NFTTAPAICHDGKAH  NFTTAPAIC  0        0.1395
11057.1    65.00  0.32     Sequence
 HLA-DPA10201-DPB11401 1081      FTTAPAICHDGKAHF  FTTAPAICH  0        0.0774
21638.7    90.00  0.28     Sequence
 HLA-DPA10201-DPB11401 1082      TTAPAICHDGKAHFP  ICHDGKAHF  5        0.0423
31623.6   100.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1083      TAPAICHDGKAHFPR  CHDGKAHFP  5        0.0485
29590.0   100.00  0.23     Sequence
 HLA-DPA10201-DPB11401 1084      APAICHDGKAHFPRE  CHDGKAHFP  4        0.0528
28242.1    95.00  0.23     Sequence
 HLA-DPA10201-DPB11401 1085      PAICHDGKAHFPREG  CHDGKAHFP  3        0.0510
28802.5    95.00  0.23     Sequence
```

```
 HLA-DPA10201-DPB11401 1086      AICHDGKAHFPREGV  KAHFPREGV  6        0.0927
18344.3    85.00  0.36     Sequence
 HLA-DPA10201-DPB11401 1087      ICHDGKAHFPREGVF  KAHFPREGV  5        0.0955
17790.4    85.00  0.47     Sequence
 HLA-DPA10201-DPB11401 1088      CHDGKAHFPREGVFV  KAHFPREGV  4        0.1317
12023.1    70.00  0.46     Sequence
 HLA-DPA10201-DPB11401 1089      HDGKAHFPREGVFVS  KAHFPREGV  3        0.1654
8350.6    55.00  0.38     Sequence
 HLA-DPA10201-DPB11401 1090      DGKAHFPREGVFVSN  KAHFPREGV  2        0.1821
6968.3    49.00  0.30     Sequence
 HLA-DPA10201-DPB11401 1091      GKAHFPREGVFVSNG  KAHFPREGV  1        0.1974
5910.2    43.00  0.27     Sequence
 HLA-DPA10201-DPB11401 1092      KAHFPREGVFVSNGT  PREGVFVSN  4        0.1963
5975.4    44.00  0.19     Sequence
 HLA-DPA10201-DPB11401 1093      AHFPREGVFVSNGTH  REGVFVSNG  4        0.1572
9128.6    60.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1094      HFPREGVFVSNGTHW  REGVFVSNG  3        0.1544
9409.6    60.00  0.36     Sequence
 HLA-DPA10201-DPB11401 1095      FPREGVFVSNGTHWF  REGVFVSNG  2        0.1395
11054.7    65.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1096      PREGVFVSNGTHWFV  REGVFVSNG  1        0.1117
14934.3    80.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1097      REGVFVSNGTHWFVT  VFVSNGTHW  3        0.1060
15876.2    80.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1098      EGVFVSNGTHWFVTQ  FVSNGTHWF  3        0.0869
19536.0    85.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1099      GVFVSNGTHWFVTQR  FVSNGTHWF  2        0.0892
19049.1    85.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1100      VFVSNGTHWFVTQRN  FVSNGTHWF  1        0.0772
21699.2    90.00  0.21     Sequence
 HLA-DPA10201-DPB11401 1101      FVSNGTHWFVTQRNF  SNGTHWFVT  2        0.0686
23806.8    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1102      VSNGTHWFVTQRNFY  HWFVTQRNF  5        0.0641
24991.3    95.00  0.30     Sequence
 HLA-DPA10201-DPB11401 1103      SNGTHWFVTQRNFYE  HWFVTQRNF  4        0.0755
22097.0    90.00  0.29     Sequence
 HLA-DPA10201-DPB11401 1104      NGTHWFVTQRNFYEP  FVTQRNFYE  5        0.0807
20885.2    90.00  0.21     Sequence
 HLA-DPA10201-DPB11401 1105      GTHWFVTQRNFYEPQ  FVTQRNFYE  4        0.0851
19916.6    85.00  0.21     Sequence
 HLA-DPA10201-DPB11401 1106      THWFVTQRNFYEPQI  FVTQRNFYE  3        0.1024
16508.6    80.00  0.20     Sequence
 HLA-DPA10201-DPB11401 1107      HWFVTQRNFYEPQII  RNFYEPQII  6        0.2020
5620.5    42.00  0.50     Sequence
 HLA-DPA10201-DPB11401 1108      WFVTQRNFYEPQIIT  RNFYEPQII  5        0.2456
3508.6    29.00  0.55     Sequence
 HLA-DPA10201-DPB11401 1109      FVTQRNFYEPQIITT  RNFYEPQII  4        0.2794
2432.6    21.00  0.50     Sequence
 HLA-DPA10201-DPB11401 1110      VTQRNFYEPQIITTD  RNFYEPQII  3        0.2725
2622.1    23.00  0.50     Sequence
 HLA-DPA10201-DPB11401 1111      TQRNFYEPQIITTDN  RNFYEPQII  2        0.2707
2671.9    23.00  0.46     Sequence
 HLA-DPA10201-DPB11401 1112      QRNFYEPQIITTDNT  RNFYEPQII  1        0.2626
2919.0    25.00  0.44     Sequence
 HLA-DPA10201-DPB11401 1113      RNFYEPQIITTDNTF  RNFYEPQII  0        0.2314
4088.1    33.00  0.40     Sequence
 HLA-DPA10201-DPB11401 1114      NFYEPQIITTDNTFV  FYEPQIITT  1        0.1186
13855.7    75.00  0.35     Sequence
 HLA-DPA10201-DPB11401 1115      FYEPQIITTDNTFVS  FYEPQIITT  0        0.0938
18122.8    85.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1116      YEPQIITTDNTFVSG  ITTDNTFVS  5        0.0677
24028.0    95.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1117      EPQIITTDNTFVSGN  ITTDNTFVS  4        0.0674
24108.5    95.00  0.28     Sequence
 HLA-DPA10201-DPB11401 1118      PQIITTDNTFVSGNC  ITTDNTFVS  3        0.0664
24370.5    95.00  0.29     Sequence
```

```
 HLA-DPA10201-DPB11401 1119      QIITTDNTFVSGNCD  ITTDNTFVS  2        0.0595
26277.7    95.00  0.35     Sequence
 HLA-DPA10201-DPB11401 1120      IITTDNTFVSGNCDV  ITTDNTFVS  1        0.0443
30948.9   100.00  0.30     Sequence
 HLA-DPA10201-DPB11401 1121      ITTDNTFVSGNCDVV  TFVSGNCDV  5        0.0424
31600.0   100.00  0.21     Sequence
 HLA-DPA10201-DPB11401 1122      TTDNTFVSGNCDVVI  FVSGNCDVV  5        0.0481
29704.2   100.00  0.31     Sequence
 HLA-DPA10201-DPB11401 1123      TDNTFVSGNCDVVIG  FVSGNCDVV  4        0.0469
30108.7   100.00  0.31     Sequence
 HLA-DPA10201-DPB11401 1124      DNTFVSGNCDVVIGI  FVSGNCDVV  3        0.0592
26356.9    95.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1125      NTFVSGNCDVVIGIV  GNCDVVIGI  5        0.1043
16182.3    80.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1126      TFVSGNCDVVIGIVN  NCDVVIGIV  5        0.1094
15308.4    80.00  0.20     Sequence
 HLA-DPA10201-DPB11401 1127      FVSGNCDVVIGIVNN  NCDVVIGIV  4        0.1065
15796.2    80.00  0.23     Sequence
 HLA-DPA10201-DPB11401 1128      VSGNCDVVIGIVNNT  NCDVVIGIV  3        0.1122
14845.5    80.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1129      SGNCDVVIGIVNNTV  NCDVVIGIV  2        0.1253
12890.5    75.00  0.20     Sequence
 HLA-DPA10201-DPB11401 1130      GNCDVVIGIVNNTVY  DVVIGIVNN  3        0.1278
12542.4    70.00  0.17     Sequence
 HLA-DPA10201-DPB11401 1131      NCDVVIGIVNNTVYD  DVVIGIVNN  2        0.1174
14044.9    75.00  0.20     Sequence
 HLA-DPA10201-DPB11401 1132      CDVVIGIVNNTVYDP  VVIGIVNNT  2        0.0898
18916.8    85.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1133      DVVIGIVNNTVYDPL  VIGIVNNTV  2        0.0912
18644.1    85.00  0.19     Sequence
 HLA-DPA10201-DPB11401 1134      VVIGIVNNTVYDPLQ  VNNTVYDPL  5        0.0940
18074.6    85.00  0.28     Sequence
 HLA-DPA10201-DPB11401 1135      VIGIVNNTVYDPLQP  VNNTVYDPL  4        0.0931
18262.8    85.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1136      IGIVNNTVYDPLQPE  VNNTVYDPL  3        0.0881
19281.7    85.00  0.37     Sequence
 HLA-DPA10201-DPB11401 1137      GIVNNTVYDPLQPEL  TVYDPLQPE  5        0.1062
15844.0    80.00  0.31     Sequence
 HLA-DPA10201-DPB11401 1138      IVNNTVYDPLQPELD  TVYDPLQPE  4        0.1025
16496.1    80.00  0.32     Sequence
 HLA-DPA10201-DPB11401 1139      VNNTVYDPLQPELDS  TVYDPLQPE  3        0.0973
17454.6    85.00  0.37     Sequence
 HLA-DPA10201-DPB11401 1140      NNTVYDPLQPELDSF  TVYDPLQPE  2        0.0861
19701.0    85.00  0.40     Sequence
 HLA-DPA10201-DPB11401 1141      NTVYDPLQPELDSFK  TVYDPLQPE  1        0.0737
22516.0    90.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1142      TVYDPLQPELDSFKE  VYDPLQPEL  1        0.0617
25641.0    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1143      VYDPLQPELDSFKEE  VYDPLQPEL  0        0.0477
29846.6   100.00  0.19     Sequence
 HLA-DPA10201-DPB11401 1144      YDPLQPELDSFKEEL  PELDSFKEE  5        0.0417
31834.7   100.00  0.20     Sequence
 HLA-DPA10201-DPB11401 1145      DPLQPELDSFKEELD  ELDSFKEEL  5        0.0398
32506.1   100.00  0.28     Sequence
 HLA-DPA10201-DPB11401 1146      PLQPELDSFKEELDK  ELDSFKEEL  4        0.0421
31720.6   100.00  0.30     Sequence
 HLA-DPA10201-DPB11401 1147      LQPELDSFKEELDKY  ELDSFKEEL  3        0.0440
31052.9   100.00  0.31     Sequence
 HLA-DPA10201-DPB11401 1148      QPELDSFKEELDKYF  ELDSFKEEL  2        0.0438
31121.2   100.00  0.28     Sequence
 HLA-DPA10201-DPB11401 1149      PELDSFKEELDKYFK  KEELDKYFK  6        0.0597
26217.5    95.00  0.29     Sequence
 HLA-DPA10201-DPB11401 1150      ELDSFKEELDKYFKN  KEELDKYFK  5        0.0615
25698.2    95.00  0.31     Sequence
 HLA-DPA10201-DPB11401 1151      LDSFKEELDKYFKNH  KEELDKYFK  4        0.0692
23644.5    90.00  0.34     Sequence
```

```
 HLA-DPA10201-DPB11401 1152      DSFKEELDKYFKNHT  KEELDKYFK  3        0.0769
21748.4    90.00  0.32     Sequence
 HLA-DPA10201-DPB11401 1153      SFKEELDKYFKNHTS  KEELDKYFK  2        0.0830
20375.2    90.00  0.33     Sequence
 HLA-DPA10201-DPB11401 1154      FKEELDKYFKNHTSP  KYFKNHTSP  6        0.0853
19857.0    85.00  0.24     Sequence
 HLA-DPA10201-DPB11401 1155      KEELDKYFKNHTSPD  KYFKNHTSP  5        0.0846
20028.1    90.00  0.31     Sequence
 HLA-DPA10201-DPB11401 1156      EELDKYFKNHTSPDV  KYFKNHTSP  4        0.1011
16741.0    80.00  0.31     Sequence
 HLA-DPA10201-DPB11401 1157      ELDKYFKNHTSPDVD  KYFKNHTSP  3        0.1107
15101.8    80.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1158      LDKYFKNHTSPDVDL  KNHTSPDVD  5        0.1315
12048.9    70.00  0.29     Sequence
 HLA-DPA10201-DPB11401 1159      DKYFKNHTSPDVDLG  KNHTSPDVD  4        0.1264
12730.3    70.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1160      KYFKNHTSPDVDLGD  KNHTSPDVD  3        0.1280
12521.7    70.00  0.27     Sequence
 HLA-DPA10201-DPB11401 1161      YFKNHTSPDVDLGDI  KNHTSPDVD  2        0.1053
15995.9    80.00  0.35     Sequence
 HLA-DPA10201-DPB11401 1162      FKNHTSPDVDLGDIS  KNHTSPDVD  1        0.0737
22513.1    90.00  0.35     Sequence
 HLA-DPA10201-DPB11401 1163      KNHTSPDVDLGDISG  KNHTSPDVD  0        0.0409
32133.0    100.00  0.30    Sequence
 HLA-DPA10201-DPB11401 1164      NHTSPDVDLGDISGI  HTSPDVDLG  1        0.0322
35296.3    100.00  0.22    Sequence
 HLA-DPA10201-DPB11401 1165      HTSPDVDLGDISGIN  VDLGDISGI  5        0.0309
35797.4    100.00  0.31    Sequence
 HLA-DPA10201-DPB11401 1166      TSPDVDLGDISGINA  VDLGDISGI  4        0.0392
32722.4    100.00  0.35    Sequence
 HLA-DPA10201-DPB11401 1167      SPDVDLGDISGINAS  VDLGDISGI  3        0.0431
31377.2    100.00  0.34    Sequence
 HLA-DPA10201-DPB11401 1168      PDVDLGDISGINASF  VDLGDISGI  2        0.0455
30551.0    100.00  0.30    Sequence
 HLA-DPA10201-DPB11401 1169      DVDLGDISGINASFV  ISGINASFV  6        0.0882
19256.9    85.00  0.31     Sequence
 HLA-DPA10201-DPB11401 1170      VDLGDISGINASFVN  ISGINASFV  5        0.1244
13014.9    75.00  0.44     Sequence
 HLA-DPA10201-DPB11401 1171      DLGDISGINASFVNI  ISGINASFV  4        0.1470
10193.8    65.00  0.44     Sequence
 HLA-DPA10201-DPB11401 1172      LGDISGINASFVNIQ  ISGINASFV  3        0.1826
6936.5    49.00  0.32     Sequence
 HLA-DPA10201-DPB11401 1173      GDISGINASFVNIQK  ISGINASFV  2        0.2015
5648.2    42.00  0.27     Sequence
 HLA-DPA10201-DPB11401 1174      DISGINASFVNIQKE  ISGINASFV  1        0.2098
5168.2    39.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1175      ISGINASFVNIQKEI  ASFVNIQKE  5        0.2440
3566.4    29.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1176      SGINASFVNIQKEID  ASFVNIQKE  4        0.2289
4199.0    34.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1177      GINASFVNIQKEIDR  ASFVNIQKE  3        0.2269
4295.2    34.00  0.30     Sequence
 HLA-DPA10201-DPB11401 1178      INASFVNIQKEIDRL  ASFVNIQKE  2        0.2353
3922.1    32.00  0.31     Sequence
 HLA-DPA10201-DPB11401 1179      NASFVNIQKEIDRLN  SFVNIQKEI  2        0.2069
5330.5    40.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1180      ASFVNIQKEIDRLNE  SFVNIQKEI  1        0.1988
5817.6    43.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1181      SFVNIQKEIDRLNEV  KEIDRLNEV  6        0.1982
5858.0    43.00  0.31     Sequence
 HLA-DPA10201-DPB11401 1182      FVNIQKEIDRLNEVA  KEIDRLNEV  5        0.1682
8099.5    55.00  0.54     Sequence
 HLA-DPA10201-DPB11401 1183      VNIQKEIDRLNEVAK  KEIDRLNEV  4        0.1846
6782.9    48.00  0.56     Sequence
 HLA-DPA10201-DPB11401 1184      NIQKEIDRLNEVAKN  KEIDRLNEV  3        0.1947
6085.4    44.00  0.54     Sequence
```

```
 HLA-DPA10201-DPB11401 1185      IQKEIDRLNEVAKNL  RLNEVAKNL  6        0.3154
1647.7    15.00  0.50      Sequence
 HLA-DPA10201-DPB11401 1186      QKEIDRLNEVAKNLN  RLNEVAKNL  5        0.3313
1388.0    13.00  0.63      Sequence
 HLA-DPA10201-DPB11401 1187      KEIDRLNEVAKNLNE  RLNEVAKNL  4        0.3227
1522.3    14.00  0.66      Sequence
 HLA-DPA10201-DPB11401 1188      EIDRLNEVAKNLNES  RLNEVAKNL  3        0.3163
1631.9    15.00  0.69      Sequence
 HLA-DPA10201-DPB11401 1189      IDRLNEVAKNLNESL  RLNEVAKNL  2        0.3237
1506.7    14.00  0.68      Sequence
 HLA-DPA10201-DPB11401 1190      DRLNEVAKNLNESLI  RLNEVAKNL  1        0.3164
1630.2    15.00  0.57      Sequence
 HLA-DPA10201-DPB11401 1191      RLNEVAKNLNESLID  RLNEVAKNL  0        0.2979
1990.6    18.00  0.44      Sequence
 HLA-DPA10201-DPB11401 1192      LNEVAKNLNESLIDL  KNLNESLID  5        0.2333
4005.3    32.00  0.41      Sequence
 HLA-DPA10201-DPB11401 1193      NEVAKNLNESLIDLQ  KNLNESLID  4        0.2402
3717.9    30.00  0.40      Sequence
 HLA-DPA10201-DPB11401 1194      EVAKNLNESLIDLQE  KNLNESLID  3        0.2405
3706.5    30.00  0.40      Sequence
 HLA-DPA10201-DPB11401 1195      VAKNLNESLIDLQEL  KNLNESLID  2        0.2456
3508.1    29.00  0.37      Sequence
 HLA-DPA10201-DPB11401 1196      AKNLNESLIDLQELG  KNLNESLID  1        0.2043
5479.8    41.00  0.35      Sequence
 HLA-DPA10201-DPB11401 1197      KNLNESLIDLQELGK  KNLNESLID  0        0.1676
8158.5    55.00  0.23      Sequence
 HLA-DPA10201-DPB11401 1198      NLNESLIDLQELGKY  ESLIDLQEL  3        0.1308
12140.6    70.00  0.34      Sequence
 HLA-DPA10201-DPB11401 1199      LNESLIDLQELGKYE  ESLIDLQEL  2        0.1137
14619.2    75.00  0.40      Sequence
 HLA-DPA10201-DPB11401 1200      NESLIDLQELGKYEQ  ESLIDLQEL  1        0.0982
17284.2    85.00  0.41      Sequence
 HLA-DPA10201-DPB11401 1201      ESLIDLQELGKYEQY  ESLIDLQEL  0        0.0922
18435.7    85.00  0.35      Sequence
 HLA-DPA10201-DPB11401 1202      SLIDLQELGKYEQYI  LIDLQELGK  1        0.0636
25121.2    95.00  0.22      Sequence
 HLA-DPA10201-DPB11401 1203      LIDLQELGKYEQYIK  DLQELGKYE  2        0.0639
25031.7    95.00  0.14      Sequence
 HLA-DPA10201-DPB11401 1204      IDLQELGKYEQYIKW  GKYEQYIKW  6        0.0635
25147.3    95.00  0.28      Sequence
 HLA-DPA10201-DPB11401 1205      DLQELGKYEQYIKWP  GKYEQYIKW  5        0.1030
16408.7    80.00  0.35      Sequence
 HLA-DPA10201-DPB11401 1206      LQELGKYEQYIKWPW  KYEQYIKWP  5        0.1190
13791.0    75.00  0.29      Sequence
 HLA-DPA10201-DPB11401 1207      QELGKYEQYIKWPWY  KYEQYIKWP  4        0.1253
12893.7    75.00  0.32      Sequence
 HLA-DPA10201-DPB11401 1208      ELGKYEQYIKWPWYI  KYEQYIKWP  3        0.1593
8920.6    60.00  0.28      Sequence
 HLA-DPA10201-DPB11401 1209      LGKYEQYIKWPWYIW  QYIKWPWYI  5        0.1741
7602.2    55.00  0.23      Sequence
 HLA-DPA10201-DPB11401 1210      GKYEQYIKWPWYIWL  QYIKWPWYI  4        0.2025
5591.5    42.00  0.22      Sequence
 HLA-DPA10201-DPB11401 1211      KYEQYIKWPWYIWLG  IKWPWYIWL  5        0.2201
4621.7    36.00  0.29      Sequence
 HLA-DPA10201-DPB11401 1212      YEQYIKWPWYIWLGF  IKWPWYIWL  4        0.1907
6350.4    46.00  0.34      Sequence
 HLA-DPA10201-DPB11401 1213      EQYIKWPWYIWLGFI  IKWPWYIWL  3        0.1991
5799.8    43.00  0.32      Sequence
 HLA-DPA10201-DPB11401 1214      QYIKWPWYIWLGFIA  IKWPWYIWL  2        0.2097
5170.8    39.00  0.28      Sequence
 HLA-DPA10201-DPB11401 1215      YIKWPWYIWLGFIAG  IKWPWYIWL  1        0.1969
5939.3    44.00  0.25      Sequence
 HLA-DPA10201-DPB11401 1216      IKWPWYIWLGFIAGL  YIWLGFIAG  5        0.2164
4810.4    37.00  0.19      Sequence
 HLA-DPA10201-DPB11401 1217      KWPWYIWLGFIAGLI  IWLGFIAGL  5        0.2534
3224.2    27.00  0.23      Sequence
```

```
 HLA-DPA10201-DPB11401 1218      WPWYIWLGFIAGLIA  IWLGFIAGL  4        0.2648
2849.3    24.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1219      PWYIWLGFIAGLIAI  IWLGFIAGL  3        0.2856
2275.9    20.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1220      WYIWLGFIAGLIAIV  WLGFIAGLI  3        0.2999
1948.6    17.00  0.23     Sequence
 HLA-DPA10201-DPB11401 1221      YIWLGFIAGLIAIVM  WLGFIAGLI  2        0.3065
1814.2    16.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1222      IWLGFIAGLIAIVMV  GFIAGLIAI  3        0.2871
2237.9    20.00  0.20     Sequence
 HLA-DPA10201-DPB11401 1223      WLGFIAGLIAIVMVT  GFIAGLIAI  2        0.2448
3536.2    29.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1224      LGFIAGLIAIVMVTI  FIAGLIAIV  2        0.2172
4766.4    37.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1225      GFIAGLIAIVMVTIM  IAGLIAIVM  2        0.2025
5591.1    42.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1226      FIAGLIAIVMVTIML  GLIAIVMVT  3        0.1736
7642.6    55.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1227      IAGLIAIVMVTIMLC  GLIAIVMVT  2        0.1319
12001.4    70.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1228      AGLIAIVMVTIMLCC  GLIAIVMVT  1        0.1059
15895.1    80.00  0.30     Sequence
 HLA-DPA10201-DPB11401 1229      GLIAIVMVTIMLCCM  GLIAIVMVT  0        0.0928
18315.8    85.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1230      LIAIVMVTIMLCCMT  IAIVMVTIM  1        0.0556
27407.0    95.00  0.28     Sequence
 HLA-DPA10201-DPB11401 1231      IAIVMVTIMLCCMTS  IAIVMVTIM  0        0.0520
28500.6    95.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1232      AIVMVTIMLCCMTSC  IVMVTIMLC  1        0.0418
31800.6   100.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1233      IVMVTIMLCCMTSCC  MVTIMLCCM  2        0.0330
35000.8   100.00  0.20     Sequence
 HLA-DPA10201-DPB11401 1234      VMVTIMLCCMTSCCS  TIMLCCMTS  3        0.0253
38016.2   100.00  0.23     Sequence
 HLA-DPA10201-DPB11401 1235      MVTIMLCCMTSCCSC  TIMLCCMTS  2        0.0234
38832.3   100.00  0.28     Sequence
 HLA-DPA10201-DPB11401 1236      VTIMLCCMTSCCSCL  TIMLCCMTS  1        0.0251
38114.2   100.00  0.20     Sequence
 HLA-DPA10201-DPB11401 1237      TIMLCCMTSCCSCLK  CMTSCCSCL  5        0.0319
35402.2   100.00  0.24     Sequence
 HLA-DPA10201-DPB11401 1238      IMLCCMTSCCSCLKG  CMTSCCSCL  4        0.0311
35703.0   100.00  0.30     Sequence
 HLA-DPA10201-DPB11401 1239      MLCCMTSCCSCLKGC  CMTSCCSCL  3        0.0318
35427.1   100.00  0.31     Sequence
 HLA-DPA10201-DPB11401 1240      LCCMTSCCSCLKGCC  CMTSCCSCL  2        0.0318
35425.6   100.00  0.32     Sequence
 HLA-DPA10201-DPB11401 1241      CCMTSCCSCLKGCCS  MTSCCSCLK  2        0.0306
35914.6   100.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1242      CMTSCCSCLKGCCSC  CMTSCCSCL  0        0.0262
37649.4   100.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1243      MTSCCSCLKGCCSCG  SCCSCLKGC  2        0.0191
40680.3   100.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1244      TSCCSCLKGCCSCGS  SCCSCLKGC  1        0.0173
41463.3   100.00  0.18     Sequence
 HLA-DPA10201-DPB11401 1245      SCCSCLKGCCSCGSC  LKGCCSCGS  5        0.0185
40951.0   100.00  0.17     Sequence
 HLA-DPA10201-DPB11401 1246      CCSCLKGCCSCGSCC  LKGCCSCGS  4        0.0182
41054.8   100.00  0.20     Sequence
 HLA-DPA10201-DPB11401 1247      CSCLKGCCSCGSCCK  LKGCCSCGS  3        0.0202
40162.5   100.00  0.19     Sequence
 HLA-DPA10201-DPB11401 1248      SCLKGCCSCGSCCKF  LKGCCSCGS  2        0.0231
38952.6   100.00  0.17     Sequence
 HLA-DPA10201-DPB11401 1249      CLKGCCSCGSCCKFD  KGCCSCGSC  2        0.0205
40054.8   100.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1250      LKGCCSCGSCCKFDE  LKGCCSCGS  0        0.0168
41694.1   100.00  0.17     Sequence
```

```
 HLA-DPA10201-DPB11401 1251      KGCCSCGSCCKFDED  CCSCGSCCK  2        0.0109
44450.6   100.00  0.16     Sequence
 HLA-DPA10201-DPB11401 1252      GCCSCGSCCKFDEDD  CSCGSCCKF  2        0.0082
45769.8   100.00  0.33     Sequence
 HLA-DPA10201-DPB11401 1253      CCSCGSCCKFDEDDS  CSCGSCCKF  1        0.0096
45090.0   100.00  0.26     Sequence
 HLA-DPA10201-DPB11401 1254      CSCGSCCKFDEDDSE  CKFDEDDSE  6        0.0141
42923.1   100.00  0.25     Sequence
 HLA-DPA10201-DPB11401 1255      SCGSCCKFDEDDSEP  KFDEDDSEP  6        0.0281
36896.5   100.00  0.49     Sequence
 HLA-DPA10201-DPB11401 1256      CGSCCKFDEDDSEPV  KFDEDDSEP  5        0.0461
30366.5   100.00  0.47     Sequence
 HLA-DPA10201-DPB11401 1257      GSCCKFDEDDSEPVL  KFDEDDSEP  4        0.0644
24896.9    95.00  0.38     Sequence
 HLA-DPA10201-DPB11401 1258      SCCKFDEDDSEPVLK  KFDEDDSEP  3        0.0812
20759.0    90.00  0.33     Sequence
 HLA-DPA10201-DPB11401 1259      CCKFDEDDSEPVLKG  KFDEDDSEP  2        0.0791
21254.7    90.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1260      CKFDEDDSEPVLKGV  FDEDDSEPV  2        0.0836
20235.9    90.00  0.19     Sequence
 HLA-DPA10201-DPB11401 1261      KFDEDDSEPVLKGVK  FDEDDSEPV  1        0.0867
19564.6    85.00  0.20     Sequence
 HLA-DPA10201-DPB11401 1262      FDEDDSEPVLKGVKL  EPVLKGVKL  6        0.0828
20419.5    90.00  0.22     Sequence
 HLA-DPA10201-DPB11401 1263      DEDDSEPVLKGVKLH  PVLKGVKLH  6        0.1386
11162.1    65.00  0.37     Sequence
 HLA-DPA10201-DPB11401 1264      EDDSEPVLKGVKLHY  PVLKGVKLH  5        0.1727
7721.1    55.00  0.34     Sequence
 HLA-DPA10201-DPB11401 1265      DDSEPVLKGVKLHYT  PVLKGVKLH  4        0.1911
6321.5    46.00  0.31     Sequence
```