	accession	descriptior	score	cover	# pro	# unique p	#pep	#PSM	AA
1	P00549	Pyruvate kinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC19 PE=1 SV=2 - [KPYK1_YEAST]	669.76	74.00%	5	31	31	180	500
2	P02994	Elongation factor 1-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TEF1 PE=1 SV=1 - [EF1A_YEAST]	444.25	46.29%	4	8	14	128	458

3	P00359	Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TDH3 PE=1 SV=3 - [G3P3_YEAST]	389.03	59.94%	2	5	14	110	332
4	P32324	Elongation factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EFT1 PE=1 SV=1 - [EF2_YEAST]	305.99	44.77%	2	17	30	91	842

5	P10664	60S ribosomal protein L4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL4A PE=1 SV=4 - [RL4A_YEAST]	350.47	43.92%	2	13	13	91	362
6	P41752	Elongation factor 1-alpha OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=TEF PE=3 SV=1 - [EF1A_ASHGO]	225.74	36.24%	4	1	10	76	458

7	P00358	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TDH2 PE=1 SV=3 - [G3P2_YEAST]	237.67	43.67%	2	1	11	68	332
8	P16521	Elongation factor 3A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YEF3 PE=1 SV=4 - [EF3A_YEAST]	191.66	38.79%	3	30	32	56	1044

9	P05030	Plasma membrane ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMA1 PE=1 SV=2 - [PMA1_YEAST]	202.33	30.07%	2	23	23	53	918
10	P00360	Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TDH1 PE=1 SV=3 - [G3P1_YEAST]	184.28	30.42%	1	4	8	53	332

11	P39015	Suppressor protein STM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STM1 PE=1 SV=3 - [STM1_YEAST]	193.71	37.36%	1	9	9	52	273
12	P05750	40S ribosomal protein S3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS3 PE=1 SV=5 - [RS3_YEAST]	156.47	55.00%	1	14	14	51	240

13	Q875S0	Elongation factor 2 OS=Lachancea kluyveri (strain ATCC 58438 / CBS 3082 / CCRC 21498 / NBRC 1685 / JCM 7257 / NCYC 543 / NRRL Y-12651) OX=226302 GN=EFT2 PE=3 SV=1 - [EF2_LACK1]	155.75	16.75%	1	1	14	49	842
14	P14126	60S ribosomal protein L3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL3 PE=1 SV=4 - [RL3_YEAST]	159.15	33.07%	2	14	14	49	387

15	P00560	Phosphoglycerate kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PGK1 PE=1 SV=2 - [PGK_YEAST]	176.25	64.90%	2	23	23	47	416
16	P07259	Protein URA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=URA2 PE=1 SV=5 - [PYR1_YEAST]	137.58	20.78%	2	34	34	42	2214

17	P11484	Ribosome-associated molecular chaperone SSB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSB1 PE=1 SV=3 - [SSB1_YEAST]	156.73	54.98%	2	2	22	41	613
18	P06169	Pyruvate decarboxylase isozyme 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDC1 PE=1 SV=7 - [PDC1_YEAST]	150.97	35.88%	2	12	13	38	563

19	P14120	60S ribosomal protein L30 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL30 PE=1 SV=3 - [RL30_YEAST]	135.29	64.76%	2	7	7	38	105
20	P40150	Ribosome-associated molecular chaperone SSB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSB2 PE=1 SV=2 - [SSB2_YEAST]	142.07	52.85%	1	1	21	37	613

21	P26321	60S ribosomal protein L5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL5 PE=1 SV=4 - [RL5_YEAST]	116.12	34.01%	1	6	6	35	297
22	P38934	Nuclear segregation protein BFR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BFR1 PE=1 SV=1 - [BFR1_YE	109.21	27.45%	1	13	13	34	470

23	P00950	Phosphoglycerate mutase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPM1 PE=1 SV=3 - [PMG1_YEAST]	117.47	61.13%	1	12	12	34	247
24	P0CX35	40S ribosomal protein S4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS4A PE=1 SV=1 - [RS4A_YEAST]	111.62	35.25%	1	7	7	31	261

25	Q01855	40S ribosomal protein S15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS15 PE=1 SV=1 - [RS15_YEAST]	93.89	38.03%	1	4	4	31	142
26	P16861	ATP-dependent 6-phosphofructokinase subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PFK1 PE=1 SV=1 - [PFKA1_YEAST]	107.02	24.62%	1	18	18	30	987

27	P00925	Enolase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ENO2 PE=1 SV=2 - [ENO2_YEAST]	110.9	47.60%	3	14	14	29	437
28	P0CX45	60S ribosomal protein L2-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL2A PE=1 SV=1 - [RL2A_YEAST]	91.06	41.73%	2	8	8	29	254

29	P0CX53	60S ribosomal protein L12-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL12A PE=1 SV=1 - [RL12A_YEAST]	97.11	58.79%	1	8	8	29	165
30	P02400	60S acidic ribosomal protein P2-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP2B PE=1 SV=2 - [RLA4_YEAST]	94.54	78.18%	1	5	5	29	110

31	P07149	Fatty acid synthase subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAS1 PE=1 SV=2 - [FAS1_YEAST]	91.99	18.82%	1	24	24	28	2051
32	P25443	40S ribosomal protein S2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS2 PE=1 SV=3 - [RS2_YEAST]	110.81	35.43%	1	6	6	28	254

33	P0CX41	60S ribosomal protein L23-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL23A PE=1 SV=1 - [RL23A_YEAST]	96.73	35.04%	1	5	5	28	137
34	Q00955	Acetyl-CoA carboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACC1 PE=1 SV=2 - [ACAC_YEAST]	95.62	16.79%	6	24	24	27	2233

35	P26783	40S ribosomal protein S5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS5 PE=1 SV=3 - [RS5_YEAST]	76.94	30.22%	1	6	6	26	225
36	P06168	Ketol-acid reductoisomerase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV5 PE=1 SV=1 - [ILV5_YEAST]	86.17	37.22%	1	12	12	25	395

37	P0CX39	40S ribosomal protein S8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS8A PE=1 SV=1 - [RS8A_YEAST]	76.37	35.00%	1	6	6	25	200
38	P40212	60S ribosomal protein L13-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL13B PE=1 SV=1 - [RL13B_YEAST]	99.51	29.65%	2	1	5	25	199

39	P07342	Acetolactate synthase catalytic subunit, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV2 PE=1 SV=1 - [ILVB_YEAST]	82.61	29.84%	1	13	13	24	687
40	P10592	Heat shock protein SSA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSA2 PE=1 SV=3 - [HSP72_YEAST]	81.77	37.25%	3	5	16	24	639

41	P38788	Ribosome-associated complex subunit SSZ1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSZ1 PE=1 SV=2 - [SSZ1_YEAST]	97.1	40.15%	1	14	14	24	538
42	P0C2H8	60S ribosomal protein L31-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL31A PE=1 SV=1 - [RL31A_YEAST]	89.9	62.83%	1	1	8	24	113

43	P38720	6-phosphogluconate dehydrogenase, decarboxylating 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GND1 PE=1 SV=1 - [6PGD1_YEAST]	73.23	42.54%	2	17	17	23	489
44	P0C2H9	60S ribosomal protein L31-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL31B PE=1 SV=1 - [RL31B_YEAST]	87.91	62.83%	2	1	8	23	113

45	P17255	V-type proton ATPase catalytic subunit A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA1 PE=1 SV=3 - [VATA_YEAST]	67.91	15.50%	2	13	13	22	1071
46	P32589	Heat shock protein homolog SSE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSE1 PE=1 SV=4 - [HSP7F_YEAST]	65.43	7.22%	3	4	4	22	693

47	P10591	Heat shock protein SSA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSA1 PE=1 SV=4 - [HSP71_YEAST]	76.95	30.84%	3	2	14	22	642
48	A6ZP47	ATP-dependent RNA helicase DED1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DED1 PE=3 SV=1 - [DED1_YEAS7]	76.65	40.56%	8	16	17	22	604

49	P32527	Zuotin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ZUO1 PE=1 SV=1 - [ZUO1_YEAST]	73.39	39.72%	1	14	14	22	433
50	P0CX23	60S ribosomal protein L20-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL20A PE=1 SV=1 - [RL20A_YEAST]	75.62	37.79%	1	8	8	22	172

51	P04449	60S ribosomal protein L24-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL24A PE=1 SV=1 - [RL24A_YEAST]	83.23	16.77%	2	2	3	22	155
52	P19097	Fatty acid synthase subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAS2 PE=1 SV=2 - [FAS2_YEAST]	78.21	15.53%	2	20	20	21	1887

53	P06105	Protein SCP160 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCP160 PE=1 SV=3 - [SC160_YEAST]	68.06	22.26%	1	21	21	21	1222
54	P16862	ATP-dependent 6-phosphofructokinase subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PFK2 PE=1 SV=4 - [PFKA2_YEAST]	77.15	29.09%	1	14	14	21	959

55	P40024	ABC transporter ATP-binding protein ARB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARB1 PE=1 SV=1 - [ARB1_YEAST]	75.96	25.25%	1	12	12	21	610
56	P38011	Guanine nucleotide-binding protein subunit beta-like protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ASC1 PE=1 SV=4 - [GBLP_YEAST]	66.32	30.72%	1	9	9	21	319

57	P05317	60S acidic ribosomal protein P0 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP0 PE=1 SV=2 - [RLA0_YE	68.87	25.64%	1	7	7	21	312
58	P0CX43	60S ribosomal protein L1-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL1A PE=1 SV=1 - [RL1A_YEAST]	72.7	35.94%	2	7	7	21	217

59	P0CX50	60S ribosomal protein L18-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL18B PE=1 SV=1 - [RL18B_YEAST]	66.71	24.19%	1	4	4	21	186
60	P24000	60S ribosomal protein L24-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL24B PE=1 SV=1 - [RL24B_YEAST]	79.81	16.77%	1	2	3	21	155

61	P0C0W9	60S ribosomal protein L11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL11A PE=1 SV=2 - [RL11A_YEAST]	60.99	37.93%	3	6	6	20	174
62	P02407	40S ribosomal protein S17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS17A PE=1 SV=1 - [RS17A_YEAST]	65.9	58.09%	2	10	10	20	136

63	P06367	40S ribosomal protein S14-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS14A PE=1 SV=5 - [RS14A_YEAST]	75.34	36.50%	3	7	7	20	137
64	P0CX37	40S ribosomal protein S6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS6A PE=1 SV=1 - [RS6A_YEAST]	65.75	30.51%	2	9	9	19	236

65	P05739	60S ribosomal protein L6-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL6B PE=1 SV=4 - [RL6B_YEAST]	57.4	40.91%	1	6	8	19	176
66	P05756	40S ribosomal protein S13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS13 PE=1 SV=3 - [RS13_YEAST]	55.51	46.36%	1	7	7	18	151

67	P0CX51	40S ribosomal protein S16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS16A PE=1 SV=1 - [RS16A_YEAST]	63.05	34.27%	3	4	4	18	143
68	P38625	GMP synthase [glutamine-hydrolyzing] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GUA1 PE=1 SV=4 - [GUAA_YEAST]	69.05	24.19%	2	10	10	17	525

69	P38219	Obg-like ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OLA1 PE=1 SV=1 - [OLA1_YEAST]	53.32	37.06%	1	13	13	17	394
70	P29453	60S ribosomal protein L8-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL8B PE=1 SV=3 - [RL8B_YEAST]	63.2	33.98%	1	2	10	17	256

71	P38631	1,3-beta-glucan synthase component FKS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FKS1 PE=1 SV=2 - [FKS1_YEAST]	58.02	9.86%	2	11	11	16	1876
72	P19882	Heat shock protein 60, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP60 PE=1 SV=1 - [HSP60_YEAST]	51.38	32.69%	1	15	15	16	572

73	P41940	Mannose-1-phosphate guanyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PSA1 PE=1 SV=2 - [MPG1_YEAST]	60.69	32.41%	2	9	9	16	361
74	B3LT19	40S ribosomal protein S0-B OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RPS0B PE=3 SV=1 - [RSSA2_YEAS1]	51.84	42.06%	4	6	6	16	252

75	P05737	60S ribosomal protein L7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL7A PE=1 SV=3 - [RL7A_YEAST]	55.57	38.11%	3	9	9	16	244
76	Q02326	60S ribosomal protein L6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL6A PE=1 SV=2 - [RL6A_YEAST]	47.83	23.30%	1	2	5	16	176

77	P38879	Nascent polypeptide-associated complex subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EGD2 PE=1 SV=3 - [NACA_YEAST]	66.33	37.93%	1	5	5	16	174
78	Q12680	Glutamate synthase [NADH] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLT1 PE=1 SV=2 - [GLT1_YEAST]	53.06	10.30%	1	14	14	15	2145

79	P15108	ATP-dependent molecular chaperone HSC82 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSC82 PE=1 SV=4 - [HSC82_YEAST]	48.52	21.70%	5	13	13	15	705
80	P04147	Polyadenylate-binding protein, cytoplasmic and nuclear OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PAB1 PE=1 SV=4 - [PABP_YEAST]	56.23	35.01%	3	13	13	15	577

81	P12612	T-complex protein 1 subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TCP1 PE=1 SV=2 - [TCPA_YEAST]	51.29	25.58%	1	11	11	15	559
82	A6ZPE5	Nucleolar protein 58 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NOP58 PE=3 SV=1 - [NOP58_Y	54.16	27.98%	3	11	11	15	511

83	Q12460	Nucleolar protein 56 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP56 PE=1 SV=1 - [NOP56_Y	60.35	25.40%	1	11	11	15	504
84	P48570	Homocitrate synthase, cytosolic isozyme OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS20 PE=1 SV=1 - [HOSC_YEAST]	51.15	36.92%	1	2	11	15	428

85	P10081	ATP-dependent RNA helicase eIF4A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF1 PE=1 SV=3 - [IF4A_YEAST]	51.97	31.90%	3	9	9	15	395
86	P27476	Nuclear localization sequence-binding protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NSR1 PE=1 SV=1 - [NSR1_YEAST]	48.27	22.46%	1	8	8	15	414

87	B3LLJ2	40S ribosomal protein S1-B OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RPS1B PE=3 SV=1 - [RS3A2_YEAS1]	45.55	38.04%	3	4	8	15	255
88	Q12690	60S ribosomal protein L13-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL13A PE=1 SV=1 - [RL13A_YEAST]	54.93	29.65%	2	1	5	15	199

89	P05755	40S ribosomal protein S9-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS9B PE=1 SV=4 - [RS9B_YEAST]	40.56	39.49%	2	8	8	15	195
90	P53221	60S ribosomal protein L26-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL26B PE=1 SV=2 - [RL26B_YEAST]	44.98	44.09%	2	9	9	15	127

91	P05319	60S acidic ribosomal protein P2-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP2A PE=1 SV=1 - [RLA2_YEAST]	49.06	98.11%	1	6	6	15	106
92	Q08972	[NU+] prion formation protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NEW1 PE=1 SV=1 - [NEW1_YEAST]	46.03	15.38%	1	14	14	14	1196

93	P07262	NADP-specific glutamate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GDH1 PE=1 SV=2 - [DHE4_YEAST]	51.55	35.02%	3	10	10	14	454
94	Q12122	Homocitrate synthase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS21 PE=1 SV=1 - [HOSM_YEAST]	47.94	33.18%	1	1	10	14	440

95	B3RHV0	40S ribosomal protein S1-A OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RPS1A PE=3 SV=1 - [RS3A1_YEAS1]	43.7	41.18%	1	5	9	14	255
96	P41805	60S ribosomal protein L10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL10 PE=1 SV=1 - [RL10_YEAST]	40.65	38.46%	1	8	8	14	221

97	P26785	60S ribosomal protein L16-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL16B PE=1 SV=3 - [RL16B_YEAST]	45.41	16.67%	1	3	4	14	198
98	Q02753	60S ribosomal protein L21-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL21A PE=1 SV=1 - [RL21A_YEAST]	40.54	32.50%	1	2	5	14	160

99	A6ZWL1	Nascent polypeptide-associated complex subunit beta-1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=EGD1 PE=3 SV=1 - [NACB1_YEAS7]	49.49	42.68%	1	5	5	14	157
100	P02406	60S ribosomal protein L28 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL28 PE=1 SV=3 - [RL28_YEAST]	39.31	42.28%	1	8	8	14	149

101	P07280	40S ribosomal protein S19-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS19A PE=1 SV=2 - [RS19A_YEAST]	54.41	47.92%	2	6	6	14	144
102	P04456	60S ribosomal protein L25 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL25 PE=1 SV=4 - [RL25_YEAST]	48.8	28.87%	1	4	4	14	142

103	P48589	40S ribosomal protein S12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS12 PE=1 SV=1 - [RS12_YEAST]	46.84	32.87%	1	5	5	14	143
104	A6ZY89	Pentafunctional AROM polypeptide OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ARO1 PE=3 SV=1 - [ARO1_YEAS7]	44.66	12.09%	5	11	11	13	1588

105	P23254	Transketolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TKL1 PE=1 SV=4 - [TKT1_YEAST]	42.1	22.21%	1	12	12	13	680
106	P37291	Serine hydroxymethyltransferase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SHM2 PE=1 SV=2 - [GLYC_YEAST]	44.35	25.80%	2	9	9	13	469

107	P19358	S-adenosylmethionine synthase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAM2 PE=1 SV=3 - [METK2_YEAST]	41.95	29.17%	1	3	9	13	384
108	P10659	S-adenosylmethionine synthase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAM1 PE=1 SV=2 - [METK1_YEAST]	44.53	31.94%	1	3	9	13	382

109	P26786	40S ribosomal protein S7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS7A PE=1 SV=4 - [RS7A_YEAST]	51.1	37.89%	1	4	5	13	190
110	P0CX32	40S ribosomal protein S24-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS24B PE=1 SV=1 - [RS24B_YEAST]	38.5	27.41%	1	4	4	13	135

111	P0CX84	60S ribosomal protein L35-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL35A PE=1 SV=1 - [RL35A_YEAST]	50.1	34.17%	1	6	6	13	120
112	P38701	40S ribosomal protein S20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS20 PE=1 SV=3 - [RS20_YEAST]	47.96	55.37%	1	6	6	13	121

113	P0CX26	60S ribosomal protein L43-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL43B PE=1 SV=1 - [RL43B_YEAST]	48.85	43.48%	1	4	4	13	92
114	P14742	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GFA1 PE=1 SV=4 - [GFA1_YEAST]	36.33	20.50%	1	11	11	12	717

115	P0CX83	60S ribosomal protein L19-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL19B PE=1 SV=1 - [RL19B_YEAST]	42.49	25.40%	1	6	6	12	189
116	P05740	60S ribosomal protein L17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL17A PE=1 SV=4 - [RL17A_YEAST]	46	41.30%	1	1	6	12	184

117	P46990	60S ribosomal protein L17-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL17B PE=1 SV=2 - [RL17B_YEAST]	45.96	41.30%	1	1	6	12	184
118	P0CX55	40S ribosomal protein S18-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS18A PE=1 SV=1 - [RS18A_YEAST]	39.52	49.32%	1	8	8	12	146

119	P0C0W1	40S ribosomal protein S22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS22A PE=1 SV=2 - [RS22A_YEAST]	51.92	30.77%	3	4	4	12	130
120	P05749	60S ribosomal protein L22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL22A PE=1 SV=3 - [RL22A_YEAST]	47.74	32.23%	1	2	2	12	121

121	P0C0V8	40S ribosomal protein S21-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS21A PE=1 SV=1 - [RS21A_YEAST]	37.36	62.07%	2	1	5	12	87
122	Q03690	Clustered mitochondria protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CLU1 PE=1 SV=1 - [CLU_YEAST]	34.1	10.34%	1	10	10	11	1277

123	P07245	C-1-tetrahydrofolate synthase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE3 PE=1 SV=1 - [C1TC_YEAST]	33.76	16.38%	1	10	10	11	946
124	P16474	Endoplasmic reticulum chaperone BiP OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KAR2 PE=1 SV=1 - [BIP_YEAST]	39.97	17.60%	2	8	9	11	682

125	P39522	Dihydroxy-acid dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV3 PE=1 SV=2 - [ILV3_YEAST]	34.72	22.56%	1	9	9	11	585
126	A6ZRX0	ATP-dependent RNA helicase DBP2 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP2 PE=3 SV=1 - [DBP2_YEAS7]	35.78	16.85%	4	7	8	11	546

127	P50095	Inosine-5'-monophosphate dehydrogenase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMD3 PE=1 SV=1 - [IMDH3_YEAST]	43.79	26.77%	3	1	8	11	523
128	P28777	Chorismate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARO2 PE=1 SV=1 - [AROC_YEAST]	37.9	32.71%	1	9	9	11	376

129	P00330	Alcohol dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADH1 PE=1 SV=5 - [ADH1_YEAST]	34.65	31.90%	3	9	9	11	348
130	P40531	Protein GVP36 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GVP36 PE=1 SV=1 - [GVP36_YEAST]	40.31	44.79%	1	8	8	11	326

131	P17076	60S ribosomal protein L8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL8A PE=1 SV=4 - [RL8A_YEAST]	38.63	32.81%	1	1	9	11	256
132	Q12672	60S ribosomal protein L21-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL21B PE=1 SV=1 - [RL21B_YEAST]	30.51	31.25%	1	2	5	11	160

133	P49167	60S ribosomal protein L38 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL38 PE=1 SV=1 - [RL38_YEAST]	31.91	33.33%	1	3	3	11	78
134	P04801	Threonine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=THS1 PE=1 SV=2 - [SYTC_YEAST]	26.1	9.26%	1	5	5	10	734

135	P00927	Threonine dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV1 PE=1 SV=2 - [THDH_YEAST]	34.96	19.10%	1	8	8	10	576
136	P39079	T-complex protein 1 subunit zeta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT6 PE=1 SV=1 - [TCPZ_YEAST]	38.74	26.37%	1	8	8	10	546

137	P39076	T-complex protein 1 subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT2 PE=1 SV=1 - [TCPB_YEAST]	38.61	23.91%	1	8	8	10	527
138	P26784	60S ribosomal protein L16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL16A PE=1 SV=3 - [RL16A_YEAST]	30.39	16.58%	1	2	3	10	199

139	P0CX47	40S ribosomal protein S11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS11A PE=1 SV=1 - [RS11A_YEAST]	25.8	37.18%	1	7	7	10	156
140	P05759	Ubiquitin-40S ribosomal protein S31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS31 PE=1 SV=3 - [RS31_YEAST]	32.51	39.47%	3	6	6	10	152

141	P38754	60S ribosomal protein L14-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL14B PE=1 SV=1 - [RL14B_YEAST]	30.58	21.01%	2	4	4	10	138
142	Q05022	rRNA biogenesis protein RRP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP5 PE=1 SV=1 - [RRP5_YEAST]	28.52	8.39%	1	9	9	9	1729

143	P06103	Eukaryotic translation initiation factor 3 subunit B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRT1 PE=1 SV=1 - [EIF3B_YEAST]	28.81	13.76%	2	7	7	9	763
144	P46655	Glutamate--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GUS1 PE=1 SV=3 - [SYEC_YEAST]	25.81	14.97%	1	9	9	9	708

145	Q03195	Translation initiation factor RLI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RLI1 PE=1 SV=1 - [RLI1_YEAST]	26.06	17.43%	1	9	9	9	608
146	P38009	Bifunctional purine biosynthesis protein ADE17 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE17 PE=1 SV=2 - [PUR92_YEAST]	25.96	10.14%	1	3	4	9	592

147	P47079	T-complex protein 1 subunit theta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT8 PE=1 SV=1 - [TCPQ_YEAST]	25.6	22.89%	2	8	8	9	568
148	P10614	Lanosterol 14-alpha demethylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG11 PE=1 SV=1 - [CP51_YEAST]	27.31	22.45%	3	8	8	9	530

149	P42943	T-complex protein 1 subunit eta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT7 PE=1 SV=1 - [TCPH_YEAST]	33.63	19.82%	1	7	7	9	550
150	P39077	T-complex protein 1 subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT3 PE=1 SV=2 - [TCPG_YEAST]	29.98	22.28%	1	9	9	9	534

151	P17967	Protein disulfide-isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDI1 PE=1 SV=2 - [PDI_YEAST]	31.14	18.20%	1	6	6	9	522
152	P16140	V-type proton ATPase subunit B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA2 PE=1 SV=2 - [VATB_YEAST]	27.52	26.69%	1	9	9	9	517

153	P50094	Inosine-5'-monophosphate dehydrogenase 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMD4 PE=1 SV=1 - [IMDH4_YEAST]	35.28	21.76%	2	4	7	9	524
154	P54115	Magnesium-activated aldehyde dehydrogenase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALD6 PE=1 SV=4 - [ALDH6_YEAST]	32.11	32.60%	1	8	8	9	500

155	P02557	Tubulin beta chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUB2 PE=1 SV=2 - [TBB_YEA	32.06	26.48%	1	7	7	9	457
156	Q03940	RuvB-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RVB1 PE=1 SV=1 - [RUVB1_YEAST]	28.15	26.57%	2	9	9	9	463

157	P07991	Ornithine aminotransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CAR2 PE=1 SV=2 - [OAT_YEAST]	31.16	22.88%	1	7	7	9	424
158	P25087	Sterol 24-C-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG6 PE=1 SV=4 - [ERG6_YEAST]	32.13	22.72%	1	6	6	9	383

159	P25294	Protein SIS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SIS1 PE=1 SV=1 - [SIS1_YEAST]	30.75	30.40%	1	6	6	9	352
160	P18239	ADP,ATP carrier protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PET9 PE=1 SV=2 - [ADT2_YEAST]	24.7	25.16%	3	7	7	9	318

161	P25605	Acetolactate synthase small subunit, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV6 PE=1 SV=2 - [ILV6_YEAST]	22.51	19.42%	1	4	4	9	309
162	Q04947	Reticulon-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RTN1 PE=1 SV=1 - [RTN1_YEAST]	25.82	29.49%	1	7	7	9	295

163	P51401	60S ribosomal protein L9-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL9B PE=1 SV=1 - [RL9B_YEAST]	29.98	29.32%	2	4	4	9	191
164	P23301	Eukaryotic translation initiation factor 5A-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HYP2 PE=1 SV=3 - [IF5A1_YEAST]	33.17	28.66%	2	5	5	9	157

165	P10964	DNA-directed RNA polymerase I subunit RPA190 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPA190 PE=1 SV=2 - [RPA1_YEAST]	28.89	7.99%	1	8	8	8	1664
166	P40069	Importin subunit beta-4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KAP123 PE=1 SV=1 - [IMB4_YEAST]	26.14	10.33%	1	8	8	8	1113

167	P32563	V-type proton ATPase subunit a, vacuolar isoform OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VPH1 PE=1 SV=3 - [VPH1_YEAST]	29.04	15.83%	1	8	8	8	840
168	Q02892	Nucleolar GTP-binding protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOG1 PE=1 SV=1 - [NOG1_YEAST]	24.77	16.23%	2	8	8	8	647

169	P36013	NAD-dependent malic enzyme, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAE1 PE=1 SV=1 - [MAOM_YEAST]	29.44	19.88%	1	8	8	8	669
170	P0CS90	Heat shock protein SSC1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSC1 PE=1 SV=1 - [HSP77_YEAST]	25.06	16.67%	3	7	7	8	654

171	P40991	25S rRNA (cytosine(2870)-C(5))-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP2 PE=1 SV=1 - [NOP2_YEAST]	28.82	20.39%	1	7	7	8	618
172	P32481	Eukaryotic translation initiation factor 2 subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCD11 PE=1 SV=1 - [IF2G_YEAST]	28.74	23.53%	1	8	8	8	527

173	P38697	Inosine-5'-monophosphate dehydrogenase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMD2 PE=1 SV=1 - [IMDH2_YEAST]	32.42	21.99%	3	1	6	8	523
174	P54839	Hydroxymethylglutaryl-CoA synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG13 PE=1 SV=1 - [HMCS_YEAST]	26.14	16.50%	1	6	6	8	491

175	P37292	Serine hydroxymethyltransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SHM1 PE=1 SV=2 - [GLYM_YEAST]	26.61	17.76%	1	6	6	8	490
176	P25491	Mitochondrial protein import protein MAS5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YDJ1 PE=1 SV=1 - [MAS5_YEAST]	23.95	22.49%	1	7	7	8	409

177	P60010	Actin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACT1 PE=1 SV=1 - [ACT_YEAST]	25.7	28.00%	3	6	6	8	375
178	P14540	Fructose-bisphosphate aldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FBA1 PE=1 SV=3 - [ALF_YEAST]	33.11	25.63%	1	5	5	8	359

179	P40217	Eukaryotic translation initiation factor 3 subunit I OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF34 PE=1 SV=1 - [EIF3I_YEAST]	28.81	31.12%	3	8	8	8	347
180	P15019	Transaldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TAL1 PE=1 SV=4 - [TAL1_YEAST]	26.29	28.36%	1	7	7	8	335

181	Q08745	40S ribosomal protein S10-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS10A PE=1 SV=1 - [RS10A_YEAST]	24.87	38.10%	2	3	3	8	105
182	O14455	60S ribosomal protein L36-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL36B PE=1 SV=3 - [RL36B_YEAST]	27.24	39.00%	2	5	5	8	100

183	Q3E754	40S ribosomal protein S21-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS21B PE=1 SV=1 - [RS21B_YEAST]	26.28	62.07%	2	1	5	8	87
184	P22138	DNA-directed RNA polymerase I subunit RPA135 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPA135 PE=1 SV=1 - [RPA2_YEAST]	24.4	8.73%	1	7	7	7	1203

185	P21524	Ribonucleoside-diphosphate reductase large chain 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RNR1 PE=1 SV=2 - [RIR1_YEAST]	32.33	14.30%	2	6	6	7	888
186	P49367	Homoaconitase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS4 PE=1 SV=1 - [LYS4_YEAST]	28.68	15.87%	1	6	6	7	693

187	P54113	Bifunctional purine biosynthesis protein ADE16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE16 PE=1 SV=1 - [PUR91_YEAST]	19.22	5.92%	1	1	2	7	591
188	P28274	CTP synthase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=URA7 PE=1 SV=2 - [URA7_YEAST]	21.26	14.85%	1	6	6	7	579

189	P07251	ATP synthase subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP1 PE=1 SV=5 - [ATPA_YEAST]	20.6	13.76%	1	7	7	7	545
190	P40010	Nuclear GTP-binding protein NUG1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NUG1 PE=1 SV=1 - [NUG1_YEAST]	22.58	14.62%	1	7	7	7	520

191	P32861	UTP--glucose-1-phosphate uridylyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UGP1 PE=1 SV=1 - [UGPA1_YEAST]	22.78	19.84%	1	7	7	7	499
192	P00830	ATP synthase subunit beta, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP2 PE=1 SV=2 - [ATPB_YEAST]	27.13	20.94%	1	7	7	7	511

193	P27809	Glycolipid 2-alpha-mannosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRE2 PE=1 SV=1 - [KRE2_YEAST]	23.88	19.46%	1	6	6	7	442
194	P12385	Eukaryotic peptide chain release factor subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUP45 PE=1 SV=2 - [ERF1_YEAST]	23.81	23.11%	1	7	7	7	437

195	A6ZL22	Cell wall protein ECM33 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ECM33 PE=3 SV=2 - [ECM33_YEAS7]	25.79	9.56%	4	4	4	7	429
196	P38891	Branched-chain-amino-acid aminotransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BAT1 PE=1 SV=1 - [BCA1_YEAST]	21.08	22.65%	2	6	6	7	393

197	Q01662	Methionine aminopeptidase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAP1 PE=1 SV=2 - [MAP1_YEAST]	20.61	17.05%	1	6	6	7	387
198	P53252	Sphingolipid long chain base-responsive protein PIL1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PIL1 PE=1 SV=1 - [PIL1_YEAST]	22.78	27.43%	1	5	6	7	339

199	P15646	rRNA 2'-O-methyltransferase fibrillarin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP1 PE=1 SV=1 - [FBRL_YEAST]	25	18.04%	2	4	4	7	327
200	P33201	Ribosome assembly factor MRT4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MRT4 PE=1 SV=1 - [MRT4_YEAST]	20.39	33.90%	2	6	6	7	236

201	P38736	Golgi SNAP receptor complex member 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GOS1 PE=1 SV=1 - [GOSR1_YEAST]	24.2	13.90%	1	2	2	7	223
202	P38910	10 kDa heat shock protein, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP10 PE=1 SV=1 - [CH10_YEAST]	23.71	57.55%	1	5	5	7	106

203	P0C0X0	40S ribosomal protein S28-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS28B PE=1 SV=1 - [RS28B_YEAST]	23.49	31.34%	3	2	2	7	67
204	P32386	ATP-dependent bile acid permease OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YBT1 PE=1 SV=2 - [YBT1_YEAST]	19.88	5.36%	1	6	6	6	1661

205	P39692	Sulfite reductase [NADPH] flavoprotein component OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET10 PE=1 SV=2 - [MET10_YEAST]	15.9	6.47%	1	6	6	6	1035
206	P09440	C-1-tetrahydrofolate synthase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MIS1 PE=1 SV=1 - [C1TM_YEAST]	21.85	9.74%	1	6	6	6	975

207	A6ZN26	Eukaryotic translation initiation factor 3 subunit C OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NIP1 PE=3 SV=1 - [EIF3C_YEAS7]	25.27	8.62%	2	5	5	6	812
208	P21576	Vacuolar protein sorting-associated protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VPS1 PE=1 SV=2 - [VPS1_YEAST]	15.65	8.38%	1	5	5	6	704

209	P38708	Putative proline--tRNA ligase YHR020W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YHR020W PE=1 SV=1 - [YHI0_YEAST]	21.11	15.70%	1	6	6	6	688
210	P05453	Eukaryotic peptide chain release factor GTP-binding subunit OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUP35 PE=1 SV=1 - [ERF3_YEAST]	23.42	11.68%	1	5	5	6	685

211	P52910	Acetyl-coenzyme A synthetase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACS2 PE=1 SV=1 - [ACS2_YEAST]	20.77	10.83%	1	5	5	6	683
212	P32368	Phosphoinositide phosphatase SAC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAC1 PE=1 SV=1 - [SAC1_YEAST]	21.32	12.68%	1	5	5	6	623

213	A6ZV85	Pescadillo homolog OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NOP7 PE=3 SV=1 - [PESC_YEAS7]	17.47	12.73%	1	6	6	6	605
214	P39078	T-complex protein 1 subunit delta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT4 PE=1 SV=2 - [TCPD_YEAST]	21.33	14.77%	1	5	5	6	528

215	P32476	Squalene monooxygenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG1 PE=1 SV=2 - [ERG1_YEAST]	17.52	11.09%	1	4	4	6	496
216	P38431	Eukaryotic translation initiation factor 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF5 PE=1 SV=1 - [IF5_YEAST]	16.4	19.75%	1	6	6	6	405

217	P38779	Proteasome-interacting protein CIC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CIC1 PE=1 SV=1 - [CIC1_YEAST]	20.73	17.29%	1	4	4	6	376
218	P07246	Alcohol dehydrogenase 3, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADH3 PE=1 SV=2 - [ADH3_YEAST]	17.45	16.53%	1	5	5	6	375

219	P32449	Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARO4 PE=1 SV=2 - [AROG_YEAST]	19.36	25.68%	1	5	5	6	370
220	P07260	Eukaryotic translation initiation factor 4E OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC33 PE=1 SV=1 - [IF4E_YEAST]	21.74	24.41%	1	4	4	6	213

221	P48164	40S ribosomal protein S7-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS7B PE=1 SV=1 - [RS7B_YEAST]	20.98	33.16%	1	4	5	6	190
222	P40185	Protein MMF1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MMF1 PE=1 SV=1 - [MMF1_YEAST]	19.98	65.52%	1	6	6	6	145

223	P0C2H6	60S ribosomal protein L27-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL27A PE=1 SV=1 - [RL27A_YEAST]	20.12	27.94%	2	4	4	6	136
224	P39109	Metal resistance protein YCF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YCF1 PE=1 SV=2 - [YCFI_YEAST]	16.76	5.68%	1	5	5	5	1515

225	P39730	Eukaryotic translation initiation factor 5B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FUN12 PE=1 SV=2 - [IF2P_YEAST]	17.62	5.99%	1	4	4	5	1002
226	P32565	26S proteasome regulatory subunit RPN2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN2 PE=1 SV=4 - [RPN2_YEAST]	14.98	6.67%	1	5	5	5	945

227	P25694	Cell division control protein 48 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC48 PE=1 SV=3 - [CDC48_Y	12.74	7.43%	1	5	5	5	835
228	A6ZMA9	Ribosome biogenesis protein ERB1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ERB1 PE=3 SV=1 - [ERB1_YEAS7]	17.56	7.68%	4	5	5	5	807

229	P19414	Aconitate hydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACO1 PE=1 SV=2 - [ACON_YEAST]	15.1	8.48%	1	5	5	5	778
230	P16603	NADPH--cytochrome P450 reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NCP1 PE=1 SV=3 - [NCPR_YEAST]	14.7	11.72%	2	5	5	5	691

231	P07213	Mitochondrial import receptor subunit TOM70 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOM70 PE=1 SV=2 - [TOM70_YEAST]	19.99	11.18%	1	5	5	5	617
232	P22146	1,3-beta-glucanosyltransferase GAS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GAS1 PE=1 SV=2 - [GAS1_YEAST]	15.59	6.80%	1	4	4	5	559

233	P38861	60S ribosomal export protein NMD3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NMD3 PE=1 SV=3 - [NMD3_YEAST]	15.4	11.78%	1	5	5	5	518
234	Q05911	Adenylosuccinate lyase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE13 PE=1 SV=1 - [PUR8_YEAST]	17.5	14.94%	1	5	5	5	482

235	P09624	Dihydrolipoyl dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LPD1 PE=1 SV=1 - [DLDH_YEAST]	14.44	13.63%	1	5	5	5	499
236	P12695	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LAT1 PE=1 SV=1 - [ODP2_YEAST]	15.27	11.41%	1	5	5	5	482

237	Q08193	1,3-beta-glucanosyltransferase GAS5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GAS5 PE=1 SV=1 - [GAS5_YEAST]	15.31	15.70%	1	5	5	5	484
238	P09734	Tubulin alpha-3 chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUB3 PE=1 SV=1 - [TBA3_YEAST]	15.16	17.30%	2	3	5	5	445

239	P06106	Homocysteine/cysteine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET17 PE=1 SV=3 - [CYSD_YEAST]	13.48	13.29%	1	5	5	5	444
240	P21954	Isocitrate dehydrogenase [NADP], mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IDP1 PE=1 SV=1 - [IDHP_YEAST]	15.74	14.02%	3	4	4	5	428

241	P33297	26S proteasome regulatory subunit 6A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT5 PE=1 SV=3 - [PRS6A_YEAST]	14.25	14.98%	1	5	5	5	434
242	P36008	Elongation factor 1-gamma 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TEF4 PE=1 SV=1 - [EF1G2_YEAST]	15.38	12.38%	1	4	4	5	412

243	P23542	Aspartate aminotransferase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AAT2 PE=1 SV=3 - [AATC_YEAST]	15.91	12.68%	1	4	4	5	418
244	P41338	Acetyl-CoA acetyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG10 PE=1 SV=3 - [THIL_YEAST]	18.11	18.84%	2	5	5	5	398

245	P32602	Alpha-soluble NSF attachment protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC17 PE=1 SV=4 - [SEC17_YEAST]	19.42	25.00%	1	5	5	5	292
246	P09064	Eukaryotic translation initiation factor 2 subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUI3 PE=1 SV=2 - [IF2B_YEAST]	21.59	25.26%	1	5	5	5	285

247	P14020	Dolichol-phosphate mannosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DPM1 PE=1 SV=3 - [DPM1_YEAST]	12.86	19.48%	1	4	4	5	267
248	P07283	Phosphomannomutase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC53 PE=1 SV=1 - [PMM_YEAST]	16.62	15.35%	2	3	3	5	254

249	Q12159	RNA annealing protein YRA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YRA1 PE=1 SV=2 - [YRA1_YEAST]	13.68	19.03%	1	4	4	5	226
250	O14467	Multiprotein-bridging factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MBF1 PE=1 SV=2 - [MBF1_YEAST]	17.75	19.21%	1	3	3	5	151

251	P04911	Histone H2A.1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HTA1 PE=1 SV=2 - [H2A1_YEAST]	14.71	29.55%	9	3	3	5	132
252	P32911	Eukaryotic translation initiation factor eIF-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUI1 PE=1 SV=1 - [SUI1_YEAST]	17.97	50.93%	1	5	5	5	108

253	P05747	60S ribosomal protein L29 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL29 PE=1 SV=3 - [RL29_YEAST]	11.9	13.56%	1	1	1	5	59
254	P33892	eIF-2-alpha kinase activator GCN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCN1 PE=1 SV=1 - [GCN1_YEAST]	10.56	1.87%	1	4	4	4	2672

255	P38968	Protein transport protein SEC31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC31 PE=1 SV=3 - [SEC31_YEAST]	16.39	6.91%	1	4	4	4	1273
256	P39986	Manganese-transporting ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SPF1 PE=1 SV=1 - [ATC6_YEAST]	12.05	5.43%	1	4	4	4	1215

257	P26637	Leucine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC60 PE=1 SV=1 - [SYLC_YEAST]	13.78	5.69%	1	4	4	4	1090
258	P40825	Alanine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALA1 PE=1 SV=3 - [SYA_YEAST]	10.27	3.87%	1	3	3	4	983

259	P41810	Coatomer subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC26 PE=1 SV=2 - [COPB_YEAST]	9.85	7.30%	1	4	4	4	973
260	P32074	Coatomer subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC21 PE=1 SV=2 - [COPG_YEAST]	14.93	7.17%	1	4	4	4	935

261	P40482	Protein transport protein SEC24 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC24 PE=1 SV=1 - [SEC24_YEAST]	13.8	5.72%	4	4	4	4	926
262	P53131	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRP43 PE=1 SV=1 - [PRP43_YEAST]	11.85	8.60%	1	4	4	4	767

263	P07264	3-isopropylmalate dehydratase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LEU1 PE=1 SV=3 - [LEUC_YEAST]	13.27	7.06%	1	4	4	4	779
264	P15303	Protein transport protein SEC23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC23 PE=1 SV=1 - [SEC23_YEAST]	12.39	8.98%	2	3	3	4	768

265	P47912	Long-chain-fatty-acid--CoA ligase 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAA4 PE=1 SV=1 - [LCF4_YEAST]	13.94	7.20%	1	4	4	4	694
266	P00931	Tryptophan synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRP5 PE=1 SV=1 - [TRP_YEAST]	15.69	8.77%	1	4	4	4	707

267	P15705	Heat shock protein STI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STI1 PE=1 SV=1 - [STI1_YEAST]	14.31	11.38%	1	4	4	4	589
268	Q03862	Probable metalloprotease ARX1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARX1 PE=1 SV=1 - [ARX1_YEAST]	13.94	9.11%	1	4	4	4	593

269	P38817	ADP-ribosylation factor-binding protein GGA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GGA2 PE=1 SV=1 - [GGA2_YEAST]	17.76	9.57%	1	3	3	4	585
270	P16467	Pyruvate decarboxylase isozyme 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDC5 PE=1 SV=4 - [PDC5_YEAST]	14.89	7.82%	2	2	3	4	563

271	P12709	Glucose-6-phosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PGI1 PE=1 SV=3 - [G6PI_YEAST]	13.89	13.18%	2	4	4	4	554
272	P07263	Histidine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HTS1 PE=1 SV=2 - [SYH_YEAST]	14.25	12.64%	1	4	4	4	546

273	P21147	Acyl-CoA desaturase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OLE1 PE=1 SV=2 - [ACO1_YEAST]	11.35	4.31%	1	2	2	4	510
274	P10869	Aspartokinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOM3 PE=1 SV=2 - [AK_YEAST]	13.55	11.95%	1	4	4	4	527

275	P32621	Guanosine-diphosphatase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GDA1 PE=1 SV=1 - [GDA1_YEAST]	14.66	12.93%	1	4	4	4	518
276	P00899	Anthranilate synthase component 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRP2 PE=1 SV=4 - [TRPE_YEAST]	13.82	10.45%	1	4	4	4	507

277	Q03532	ATP-dependent RNA helicase HAS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HAS1 PE=1 SV=1 - [HAS1_YEAST]	12.66	7.13%	2	3	3	4	505
278	P53742	Nucleolar GTP-binding protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOG2 PE=1 SV=1 - [NOG2_YEAST]	12.1	9.88%	1	4	4	4	486

279	A6ZNQ1	ATP-dependent RNA helicase DBP5 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP5 PE=3 SV=1 - [DBP5_YEAS7]	13.29	13.49%	1	4	4	4	482
280	Q12265	Ribose-phosphate pyrophosphokinase 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRS5 PE=1 SV=1 - [KPR5_YEAST]	12.6	10.08%	1	4	4	4	496

281	P41921	Glutathione reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLR1 PE=1 SV=2 - [GSHR_YEAST]	14.38	15.73%	2	4	4	4	483
282	P43123	UDP-N-acetylglucosamine pyrophosphorylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=QRI1 PE=1 SV=1 - [UAP1_YEAST]	10.96	8.81%	1	4	4	4	477

283	P09733	Tubulin alpha-1 chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUB1 PE=1 SV=2 - [TBA1_YEAST]	14.87	15.21%	2	2	4	4	447
284	P0C2J2	Transposon Ty2-GR1 Gag polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TY2A-GR1 PE=5 SV=1 - [YG21A_YEAST]	10.69	8.22%	22	4	4	4	438

285	P41911	Glycerol-3-phosphate dehydrogenase [NAD(+)] 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPD2 PE=1 SV=2 - [GPD2_YEAST]	15.97	10.45%	1	3	3	4	440
286	P39954	Adenosylhomocysteinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAH1 PE=1 SV=1 - [SAHH_YEAST]	12.07	11.14%	1	4	4	4	449

287	P34167	Eukaryotic translation initiation factor 4B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF3 PE=1 SV=1 - [IF4B_YEAST]	13.07	15.14%	1	4	4	4	436
288	P25567	RNA-binding protein SRO9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRO9 PE=1 SV=2 - [SRO9_YEAST]	18.39	9.45%	1	3	3	4	434

289	P02992	Elongation factor Tu, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUF1 PE=1 SV=1 - [EFTU_YEAST]	13.8	17.85%	1	4	4	4	437
290	P16387	Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDA1 PE=1 SV=2 - [ODPA_YEAST]	11.49	11.67%	1	4	4	4	420

291	P21965	Protein kinase MCK1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MCK1 PE=1 SV=1 - [MCK1_YEAST]	11.66	13.60%	1	4	4	4	375
292	P39729	Ribosome-interacting GTPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RBG1 PE=1 SV=1 - [RBG1_YEAST]	15.31	16.80%	1	4	4	4	369

293	P40495	Homoisocitrate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS12 PE=1 SV=1 - [LYS12_YEAST]	12.92	14.82%	1	4	4	4	371
294	P13663	Aspartate-semialdehyde dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOM2 PE=1 SV=1 - [DHAS_YEAST]	13.23	17.53%	1	4	4	4	365

295	P28834	Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IDH1 PE=1 SV=2 - [IDH1_YEAST]	13.65	15.00%	1	3	3	4	360
296	P04173	3-isopropylmalate dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LEU2 PE=1 SV=4 - [LEU3_YEAST]	12.3	17.31%	3	4	4	4	364

297	P32598	Serine/threonine-protein phosphatase PP1-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLC7 PE=1 SV=1 - [PP12_YEAST]	13.12	18.27%	1	4	4	4	312
298	Q12746	Plasma membrane-associated coenzyme Q6 reductase PGA3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PGA3 PE=1 SV=1 - [PGA3_YEAST]	13.77	18.27%	1	4	4	4	312

299	P38805	Ribosome production factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPF1 PE=1 SV=1 - [RPF1_YEAST]	14.79	18.64%	1	4	4	4	295
300	P04840	Mitochondrial outer membrane protein porin 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=POR1 PE=1 SV=4 - [VDAC1_YEAST]	14.87	19.08%	1	4	4	4	283

301	P29311	Protein BMH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BMH1 PE=1 SV=4 - [BMH1_YEAST]	11.24	17.60%	2	3	3	4	267
302	P32263	Pyrroline-5-carboxylate reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRO3 PE=1 SV=1 - [P5CR_YEAST]	12.79	24.13%	1	4	4	4	286

303	P41277	Glycerol-1-phosphate phosphohydrolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPP1 PE=1 SV=3 - [GPP1_YEAST]	12.28	16.80%	2	3	3	4	250
304	P40075	Vesicle-associated membrane protein-associated protein SCS2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCS2 PE=1 SV=3 - [SCS2_YEAST]	13.29	19.26%	1	3	3	4	244

305	P05748	60S ribosomal protein L15-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL15A PE=1 SV=3 - [RL15A_YEAST]	13.83	18.14%	2	3	3	4	204
306	P20606	Small COPII coat GTPase SAR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAR1 PE=1 SV=1 - [SAR1_YEAST]	11.73	24.74%	5	4	4	4	190

307	P38264	SRP-independent targeting protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PHO88 PE=1 SV=1 - [PHO88_YEAST]	11.81	32.98%	1	4	4	4	188
308	P89886	Translation machinery-associated protein 20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA20 PE=1 SV=1 - [TMA20_YEAST]	11.46	30.94%	1	4	4	4	181

309	P14832	Peptidyl-prolyl cis-trans isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CPR1 PE=1 SV=3 - [CYPH_YEAST]	15.24	17.90%	1	2	2	4	162
310	P0CY39	40S ribosomal protein S23-A OS=Naumovozyma castellii (strain ATCC 76901 / CBS 4309 / NBRC 1992 / NRRL Y-12630) OX=1064592 GN=RPS23A PE=1 SV=1 - [RS23A_NAUCC]	14.05	19.31%	1	2	2	4	145

311	Q8J1F8	Histone H2B.2 OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=HTB2 PE=3 SV=3 - [H2B2_ASHGO]	12.55	26.77%	6	3	3	4	127
312	P39938	40S ribosomal protein S26-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS26A PE=1 SV=1 - [RS26A_YEAST]	12.35	30.25%	2	3	3	4	119

313	P41056	60S ribosomal protein L33-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL33B PE=1 SV=2 - [RL33B_YEAST]	12.7	25.23%	1	1	3	4	107
314	P05744	60S ribosomal protein L33-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL33A PE=1 SV=3 - [RL33A_YEAST]	12.26	25.23%	1	1	3	4	107

315	P87108	Mitochondrial import inner membrane translocase subunit TIM10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIM10 PE=1 SV=1 - [TIM10_YEAST]	17.51	55.91%	1	3	3	4	93
316	P25655	General negative regulator of transcription subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC39 PE=1 SV=3 - [NOT1_YEAST]	10.65	2.13%	1	3	3	3	2108

317	P22137	Clathrin heavy chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CHC1 PE=1 SV=1 - [CLH_YEAST]	7.95	2.18%	1	3	3	3	1653
318	Q03640	Tricalbin-3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TCB3 PE=1 SV=1 - [TCB3_YEAST]	8.95	2.85%	1	3	3	3	1545

319	P53254	U3 small nucleolar RNA-associated protein 22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP22 PE=1 SV=1 - [UTP22_YEAST]	9.61	3.88%	1	3	3	3	1237
320	P53622	Coatomer subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COP1 PE=1 SV=2 - [COPA_YEAST]	12.64	6.00%	1	3	3	3	1201

321	P11154	Pyruvate carboxylase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PYC1 PE=1 SV=2 - [PYC1_YEAST]	8.84	3.06%	2	3	3	3	1178
322	P03965	Carbamoyl-phosphate synthase arginine-specific large chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CPA2 PE=1 SV=1 - [CARB_YEAST]	10.6	4.03%	1	3	3	3	1118

323	P47047	ATP-dependent RNA helicase DOB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MTR4 PE=1 SV=1 - [MTR4_YEAST]	9.99	3.82%	1	3	3	3	1073
324	P25997	Elongation factor 3 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CEF3 PE=1 SV=3 - [EF3_CANAL]	7.16	4.67%	1	1	3	3	1050

325	P38249	Eukaryotic translation initiation factor 3 subunit A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPG1 PE=1 SV=1 - [EIF3A_YEAST]	9.4	3.94%	1	3	3	3	964
326	P39935	Eukaryotic initiation factor 4F subunit p150 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF4631 PE=1 SV=2 - [IF4F1_YEAST]	8.88	5.15%	1	3	3	3	952

327	P14907	Nucleoporin NSP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NSP1 PE=1 SV=1 - [NSP1_YEAST]	10.68	9.36%	1	3	3	3	823
328	P05694	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET6 PE=1 SV=4 - [METE_YEAST]	10	5.87%	1	3	3	3	767

329	P53297	PAB1-binding protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PBP1 PE=1 SV=1 - [PBP1_YEAST]	12.71	8.59%	1	3	3	3	722
330	P34237	Protein CASP OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COY1 PE=1 SV=2 - [CASP_YEAST]	10.49	6.48%	1	3	3	3	679

331	P14906	Protein translocation protein SEC63 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC63 PE=1 SV=2 - [SEC63_YEAST]	8.57	6.03%	1	3	3	3	663
332	A6ZR36	Altered inheritance of mitochondria protein 9, mitochondrial OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=AIM9 PE=3 SV=1 - [AIM9_YEAS7]	7.11	6.22%	5	3	3	3	627

333	Q12136	Something about silencing protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAS10 PE=1 SV=1 - [SAS10_Y	10.46	7.21%	1	3	3	3	610
334	P38069	Alpha-1,2-mannosyltransferase MNN2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MNN2 PE=1 SV=1 - [MNN2_YEAST]	10.94	6.87%	1	3	3	3	597

335	Q12166	2-isopropylmalate synthase 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LEU9 PE=1 SV=1 - [LEU9_YEAST]	9.09	7.28%	2	3	3	3	604
336	P32466	Low-affinity glucose transporter HXT3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HXT3 PE=1 SV=1 - [HXT3_YEAST]	12.19	6.88%	1	2	2	3	567

337	P21264	Phosphoribosylaminoimidazole carboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE2 PE=1 SV=1 - [PUR6_YEAST]	11.02	6.65%	1	2	2	3	571
338	P25045	Serine palmitoyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LCB1 PE=1 SV=2 - [LCB1_YEAST]	9.79	7.89%	1	3	3	3	558

339	P38707	Asparagine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DED81 PE=1 SV=1 - [SYNC_YEAST]	10.72	7.40%	1	3	3	3	554
340	P40413	T-complex protein 1 subunit epsilon OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT5 PE=1 SV=3 - [TCPE_YEAST]	10.5	6.58%	1	3	3	3	562

341	P04046	Amidophosphoribosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE4 PE=1 SV=2 - [PUR1_YEAST]	9.27	7.65%	2	3	3	3	510
342	P32582	Cystathionine beta-synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYS4 PE=1 SV=1 - [CBS_YEAST]	10.51	7.10%	1	3	3	3	507

343	P39976	D-2-hydroxyglutarate--pyruvate transhydrogenase DLD3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DLD3 PE=1 SV=1 - [DLD3_YEAST]	9.03	8.47%	1	3	3	3	496
344	Q05518	Protein PAL1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PAL1 PE=1 SV=1 - [PAL1_YEAST]	11.47	10.62%	1	3	3	3	499

345	P07284	Serine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SES1 PE=1 SV=2 - [SYSC_YEAST]	14.47	11.04%	1	3	3	3	462
346	P08417	Fumarate hydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FUM1 PE=1 SV=2 - [FUMH_YEAST]	13.89	11.48%	1	3	3	3	488

347	Q12464	RuvB-like protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RVB2 PE=1 SV=1 - [RUVB2_YEAST]	8.83	9.34%	3	3	3	3	471
348	A6ZPA9	Ribosome biogenesis protein YTM1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=YTM1 PE=3 SV=1 - [YTM1_YEAS7]	10.27	12.17%	1	3	3	3	460

349	P43555	Protein EMP47 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMP47 PE=1 SV=1 - [EMP47_YEAST]	11.88	10.56%	1	3	3	3	445
350	P07256	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COR1 PE=1 SV=1 - [QCR1_YEAST]	9.58	8.75%	1	3	3	3	457

351	O74302	Transposon Ty1-DR4 Gag polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TY1A-DR4 PE=2 SV=1 - [YD13A_YEAST]	11.21	10.45%	50	2	2	3	440
352	P20107	Zinc/cadmium resistance protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ZRC1 PE=1 SV=2 - [ZRC1_YEAST]	12.42	12.67%	1	3	3	3	442

353	P25293	Nucleosome assembly protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NAP1 PE=1 SV=2 - [NAP1_YEAST]	12.94	17.27%	1	3	3	3	417
354	Q06705	Phosphatidylinositol transfer protein CSR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CSR1 PE=1 SV=1 - [CSR1_YEAST]	10.07	10.54%	1	3	3	3	408

355	P38911	FK506-binding nuclear protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FPR3 PE=1 SV=2 - [FKBP3_YEAST]	9.03	11.92%	2	2	3	3	411
356	Q04697	Glucose-signaling factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GSF2 PE=1 SV=1 - [GSF2_YEAST]	11.19	11.91%	1	3	3	3	403

357	Q01560	Nucleolar protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NPL3 PE=1 SV=1 - [NOP3_YEAST]	10.72	11.84%	1	3	3	3	414
358	P31373	Cystathionine gamma-lyase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYS3 PE=1 SV=2 - [CYS3_YEAST]	8.48	10.66%	1	3	3	3	394

359	P23644	Mitochondrial import receptor subunit TOM40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOM40 PE=1 SV=1 - [TOM40_YEAST]	11.74	17.31%	1	3	3	3	387
360	Q02256	Tyrosine-protein phosphatase YVH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YVH1 PE=1 SV=1 - [PVH1_YEAST]	14.1	14.56%	1	3	3	3	364

361	P14843	Phospho-2-dehydro-3-deoxyheptonate aldolase, phenylalanine-inhibited OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARO3 PE=1 SV=1 - [AROF_YEAST]	8.78	13.24%	1	3	3	3	370
362	P53860	Phosphatidylinositol transfer protein PDR16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDR16 PE=1 SV=1 - [PDR16_YEAST]	7.61	8.83%	1	3	3	3	351

363	P07257	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=QCR2 PE=1 SV=1 - [QCR2_YEAST]	10.32	12.77%	1	3	3	3	368
364	P32473	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDB1 PE=1 SV=2 - [ODPB_YEAST]	10.35	10.66%	1	3	3	3	366

365	P32366	V-type proton ATPase subunit d OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA6 PE=1 SV=2 - [VA0D_YEAST]	13.1	17.10%	1	3	3	3	345
366	Q12230	Sphingolipid long chain base-responsive protein LSP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LSP1 PE=1 SV=1 - [LSP1_YEAST]	9.6	13.20%	1	2	3	3	341

367	P07703	DNA-directed RNA polymerases I and III subunit RPAC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPC40 PE=1 SV=1 - [RPAC1_YEAST]	9.99	13.43%	1	3	3	3	335
368	P16550	Protein APA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=APA1 PE=1 SV=4 - [APA1_YEAST]	9.02	16.20%	1	3	3	3	321

369	P41819	Dimethyladenosine transferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DIM1 PE=3 SV=1 - [DIM1_YEAST]	10	10.06%	2	3	3	3	318
370	P10962	Protein MAK16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAK16 PE=1 SV=2 - [MAK16_YEAST]	7.78	13.07%	1	3	3	3	306

371	P32332	Mitochondrial oxaloacetate transport protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OAC1 PE=1 SV=1 - [OAC1_YEAST]	8.45	11.42%	1	3	3	3	324
372	P38689	Ribose-phosphate pyrophosphokinase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRS3 PE=1 SV=1 - [KPR3_YEAST]	8.68	10.00%	1	3	3	3	320

373	P53598	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LSC1 PE=1 SV=1 - [SUCA_YEAST]	8.98	13.68%	1	3	3	3	329
374	P00546	Cyclin-dependent kinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC28 PE=1 SV=1 - [CDK1_YEAST]	9.27	11.07%	2	2	3	3	298

375	P23641	Mitochondrial phosphate carrier protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MIR1 PE=1 SV=1 - [MPCP_YEAST]	8.75	12.54%	1	3	3	3	311
376	P00817	Inorganic pyrophosphatase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IPP1 PE=1 SV=4 - [IPYR_YEAST]	8.87	12.89%	2	3	3	3	287

377	Q04067	Eukaryotic translation initiation factor 3 subunit G OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF35 PE=1 SV=1 - [EIF3G_YEAST]	13.09	12.41%	2	2	2	3	274
378	P25343	Reduced viability upon starvation protein 161 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RVS161 PE=1 SV=1 - [RV161_YEAST]	8.71	12.08%	1	3	3	3	265

379	P40513	Mitochondrial acidic protein MAM33 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAM33 PE=1 SV=1 - [MAM33_YEAST]	11.43	11.65%	1	3	3	3	266
380	Q05775	Eukaryotic translation initiation factor 3 subunit J OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HCR1 PE=1 SV=1 - [EIF3J_YEAST]	10.76	17.74%	1	3	3	3	265

381	Q06287	Ribosomal RNA small subunit methyltransferase NEP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMG1 PE=1 SV=1 - [NEP1_YEAST]	11.41	18.25%	1	3	3	3	252
382	P23639	Proteasome subunit alpha type-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE8 PE=1 SV=1 - [PSA2_YEAST]	7.95	15.20%	1	3	3	3	250

383	P00942	Triosephosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPI1 PE=1 SV=2 - [TPIS_YEAST]	12.65	12.10%	1	2	2	3	248
384	P22203	V-type proton ATPase subunit E OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA4 PE=1 SV=4 - [VATE_YEAST]	7.43	10.73%	1	3	3	3	233

385	Q00245	GTP-binding protein RHO3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RHO3 PE=1 SV=2 - [RHO3_YEAST]	7.59	14.29%	2	3	3	3	231
386	P32352	C-8 sterol isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG2 PE=1 SV=1 - [ERG2_YEAST]	11.63	13.06%	1	2	2	3	222

387	Q74ZA9	GTP-binding nuclear protein GSP1/Ran OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=GSP1 PE=3 SV=1 - [GSP1_ASHGO]	7.73	15.89%	4	3	3	3	214
388	P32939	GTP-binding protein YPT7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPT7 PE=1 SV=1 - [YPT7_YEAST]	8.31	23.56%	1	3	3	3	208

389	P35691	Translationally-controlled tumor protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA19 PE=1 SV=1 - [TCTP_YEAST]	10.84	14.37%	1	2	2	3	167
390	P56628	60S ribosomal protein L22-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL22B PE=1 SV=2 - [RL22B_YEAST]	11.75	32.79%	1	2	2	3	122

391	P39990	13 kDa ribonucleoprotein-associated protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SNU13 PE=1 SV=1 - [SNU13_YEAST]	11	23.81%	2	2	2	3	126
392	P40525	60S ribosomal protein L34-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL34B PE=1 SV=1 - [RL34B_YEAST]	7.92	20.66%	2	2	2	3	121

393	P48836	V-type proton ATPase subunit G OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA10 PE=1 SV=1 - [VATG_YEAST]	11.28	22.81%	1	3	3	3	114
394	P0C0T4	40S ribosomal protein S25-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS25B PE=1 SV=1 - [RS25B_YEAST]	8.84	21.30%	2	2	2	3	108

395	P22217	Thioredoxin-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRX1 PE=1 SV=3 - [TRX1_YEAST]	8.5	48.54%	1	3	3	3	103
396	P41057	40S ribosomal protein S29-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS29A PE=1 SV=3 - [RS29A_YEAST]	7.74	32.14%	2	2	2	3	56

397	P48415	COPII coat assembly protein SEC16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC16 PE=1 SV=2 - [SEC16_YEAST]	6.24	1.73%	1	2	2	2	2195
398	P42945	U3 small nucleolar RNA-associated protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP10 PE=1 SV=1 - [UTP10_YEAST]	6.35	1.53%	1	2	2	2	1769

399	P04050	DNA-directed RNA polymerase II subunit RPB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPO21 PE=1 SV=2 - [RPB1_YEAST]	8.25	2.14%	1	2	2	2	1733
400	P33302	Pleiotropic ABC efflux transporter of multiple drugs OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDR5 PE=1 SV=1 - [PDR5_YEAST]	7.23	1.79%	5	2	2	2	1511

401	P40318	ERAD-associated E3 ubiquitin-protein ligase DOA10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSM4 PE=1 SV=1 - [DOA10_YEAST]	7.03	2.27%	1	2	2	2	1319
402	P08518	DNA-directed RNA polymerase II subunit RPB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPB2 PE=1 SV=2 - [RPB2_YEAST]	10.26	3.59%	1	2	2	2	1224

403	Q12754	Ribosomal RNA-processing protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP12 PE=1 SV=1 - [RRP12_YEAST]	7.12	2.36%	1	2	2	2	1228
404	P22276	DNA-directed RNA polymerase III subunit RPC2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RET1 PE=1 SV=2 - [RPC2_YEAST]	6.7	3.05%	1	2	2	2	1149

405	P07806	Valine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VAS1 PE=1 SV=2 - [SYV_YEAST]	6.03	1.99%	1	2	2	2	1104
406	P09436	Isoleucine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILS1 PE=1 SV=1 - [SYIC_YEAST]	9.55	4.38%	1	2	2	2	1072

407	P53914	RNA cytidine acetyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRE33 PE=1 SV=1 - [NAT10_YEAST]	6.88	3.03%	1	2	2	2	1056
408	Q12176	Ribosome biogenesis protein MAK21 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAK21 PE=1 SV=1 - [MAK21_YEAST]	5.87	2.24%	1	2	2	2	1025

409	P49095	Glycine dehydrogenase (decarboxylating), mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCV2 PE=1 SV=1 - [GCSP_YEAST]	6.31	2.80%	1	2	2	2	1034
410	P33338	Protein SLA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SLA2 PE=1 SV=5 - [SLA2_YEAST]	7.03	4.13%	1	2	2	2	968

411	P40462	Protein TMA108 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA108 PE=1 SV=1 - [TM108_YEAST]	9.02	3.91%	1	2	2	2	946
412	P13586	Calcium-transporting ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMR1 PE=1 SV=1 - [ATC1_YEAST]	7.2	3.37%	1	2	2	2	950

413	Q01477	Ubiquitin carboxyl-terminal hydrolase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UBP3 PE=1 SV=1 - [UBP3_YEAST]	7.62	4.50%	1	2	2	2	912
414	Q06106	Multiple RNA-binding domain-containing protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MRD1 PE=1 SV=1 - [MRD1_YEAST]	6.34	2.93%	1	2	2	2	887

415	P25582	27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SPB1 PE=1 SV=2 - [SPB1_YEAST]	6.09	3.80%	1	2	2	2	841
416	Q01217	Protein ARG5,6, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARG5,6 PE=1 SV=1 - [ARG56_YEAST]	7.09	4.06%	1	2	2	2	863

417	P40850	Protein MKT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MKT1 PE=1 SV=2 - [MKT1_YEAST]	6.46	3.01%	1	2	2	2	830
418	Q99207	Nucleolar complex protein 14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP14 PE=1 SV=1 - [NOP14_Y	6.74	3.58%	1	2	2	2	810

419	Q05946	U3 small nucleolar RNA-associated protein 13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP13 PE=1 SV=1 - [UTP13_YEAST]	6.87	4.28%	1	2	2	2	817
420	P31382	Dolichyl-phosphate-mannose--protein mannosyltransferase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMT2 PE=1 SV=2 - [PMT2_YEAST]	5.41	3.29%	1	2	2	2	759

421	A6ZTA3	Pre-rRNA-processing protein RIX1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=RIX1 PE=3 SV=1 - [RIX1_YEAS7]	7.3	4.06%	2	2	2	2	763
422	P07244	Bifunctional purine biosynthetic protein ADE5,7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE5,7 PE=1 SV=1 - [PUR2_YEAST]	8.17	4.49%	1	2	2	2	802

423	P18759	Vesicular-fusion protein SEC18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC18 PE=1 SV=2 - [SEC18_YEAST]	6.06	4.22%	1	2	2	2	758
424	C7GP20	RNA polymerase II degradation factor 1 OS=Saccharomyces cerevisiae (strain JAY291) OX=574961 GN=DEF1 PE=3 SV=1 - [DEF1_YEAS2]	9.85	6.37%	3	2	2	2	738

425	P39744	Nucleolar complex protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOC2 PE=1 SV=2 - [NOC2_YEAST]	5.44	2.96%	1	2	2	2	710
426	P32501	Translation initiation factor eIF-2B subunit epsilon OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCD6 PE=1 SV=1 - [EI2BE_YEAST]	5.41	3.23%	1	2	2	2	712

427	P38088	Glycine--tRNA ligase 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GRS1 PE=1 SV=3 - [SYG_YEAST]	6.55	4.49%	1	2	2	2	690
428	P30624	Long-chain-fatty-acid--CoA ligase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAA1 PE=1 SV=1 - [LCF1_YEAST]	6.44	5.29%	1	2	2	2	700

429	P38205	Multisite-specific tRNA:(cytosine-C(5))-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NCL1 PE=1 SV=1 - [NCL1_YEAST]	5.45	3.95%	1	2	2	2	684
430	P12688	Serine/threonine-protein kinase YPK1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPK1 PE=1 SV=2 - [YPK1_YEAST]	6.21	4.56%	1	2	2	2	680

431	Q06344	Pre-rRNA-processing protein ESF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ESF1 PE=1 SV=1 - [ESF1_YEAST]	7.43	7.17%	1	2	2	2	628
432	P53235	Eukaryotic translation initiation factor 2A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YGR054W PE=1 SV=1 - [EIF2A_YEAST]	9.32	5.92%	1	2	2	2	642

433	A5DYS6	Pescadillo homolog OS=Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) OX=379508 GN=NOP7 PE=3 SV=1 - [PESC_LODEL]	4.85	2.75%	1	1	1	2	619
434	A6ZSB3	ATP-dependent RNA helicase DBP6 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP6 PE=3 SV=1 - [DBP6_YEAS7]	6.05	4.29%	2	2	2	2	629

435	Q12246	Sphingoid long chain base kinase 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LCB4 PE=1 SV=1 - [LCB4_YEAST]	6.27	4.81%	1	2	2	2	624
436	P42846	Protein KRI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRI1 PE=1 SV=1 - [KRI1_YEAST]	6.17	3.72%	1	2	2	2	591

437	Q06218	ATP-dependent RNA helicase DBP9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DBP9 PE=1 SV=1 - [DBP9_YEAST]	6.83	3.87%	1	2	2	2	594
438	P15180	Lysine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRS1 PE=1 SV=2 - [SYKC_YEAST]	7.03	4.74%	1	2	2	2	591

439	A6ZQE9	Alpha-1,2-mannosyltransferase MNN5 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=MNN5 PE=3 SV=1 - [MNN5_YEAS7]	6.63	6.48%	2	2	2	2	586
440	Q07824	Polyamine transporter 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPO1 PE=1 SV=1 - [TPO1_YEAST]	7.97	5.63%	1	2	2	2	586

441	A6ZT02	Low-affinity glucose transporter HXT4 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=HXT4 PE=3 SV=1 - [HXT4_YEAS7]	7.24	2.95%	3	1	1	2	576
442	P53868	Alpha-1,2-mannosyltransferase ALG9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALG9 PE=1 SV=1 - [ALG9_YEAST]	6.97	5.05%	1	2	2	2	555

443	P04802	Aspartate--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DPS1 PE=1 SV=3 - [SYDC_YEAST]	6.25	4.85%	1	2	2	2	557
444	P43590	Uncharacterized peptidase YFR006W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YFR006W PE=1 SV=1 - [YFH6_YEAST]	6.12	6.54%	1	2	2	2	535

445	P32457	Cell division control protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC3 PE=1 SV=3 - [CDC3_YEAST]	6.73	5.00%	1	2	2	2	520
446	P54783	D-arabinono-1,4-lactone oxidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALO1 PE=1 SV=1 - [ALO_YEAST]	6.49	4.37%	1	2	2	2	526

447	A6ZUA1	ATP-dependent RNA helicase DBP3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP3 PE=3 SV=1 - [DBP3_YEAS7]	6.28	3.06%	2	1	1	2	523
448	Q04305	U3 small nucleolar RNA-associated protein 15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP15 PE=1 SV=1 - [UTP15_YEAST]	5.55	4.68%	1	2	2	2	513

449	Q04225	Ribosome assembly protein RRB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRB1 PE=1 SV=1 - [RRB1_YEAST]	6.85	9.39%	1	2	2	2	511
450	Q03655	Probable 1,3-beta-glucanosyltransferase GAS3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GAS3 PE=1 SV=1 - [GAS3_YEAST]	6.55	5.53%	1	2	2	2	524

451	P38682	ADP-ribosylation factor GTPase-activating protein GLO3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLO3 PE=1 SV=1 - [GLO3_YEAST]	6.49	8.92%	1	2	2	2	493
452	A6ZRW0	H/ACA ribonucleoprotein complex non-core subunit NAF1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NAF1 PE=3 SV=1 - [NAF1_YEAS7]	6	10.16%	2	2	2	2	492

453	P33322	H/ACA ribonucleoprotein complex subunit CBF5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CBF5 PE=1 SV=1 - [CBF5_YEAST]	7.57	6.42%	1	2	2	2	483
454	P41807	V-type proton ATPase subunit H OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA13 PE=1 SV=1 - [VATH_YEAST]	5.88	4.39%	1	2	2	2	478

455	P04807	Hexokinase-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HXK2 PE=1 SV=4 - [HXKB_YEAST]	5.43	5.97%	2	2	2	2	486
456	P00937	Multifunctional tryptophan biosynthesis protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRP3 PE=1 SV=2 - [TRPG_YEAST]	6.26	5.99%	1	2	2	2	484

457	P33299	26S proteasome regulatory subunit 7 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT1 PE=1 SV=1 - [PRS7_YEAST]	5.23	4.93%	1	2	2	2	467
458	P29704	Squalene synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG9 PE=1 SV=2 - [FDFT_YEAST]	5.95	4.50%	1	2	2	2	444

459	A6ZYC3	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit TRM82 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=TRM82 PE=3 SV=1 - [TRM82_YEAS7]	8.82	8.33%	3	2	2	2	444
460	A6ZXP4	ATP-dependent RNA helicase SUB2 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=SUB2 PE=3 SV=1 - [SUB2_YEAS7]	4.78	6.50%	2	2	2	2	446

461	P36049	rRNA-processing protein EBP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EBP2 PE=1 SV=1 - [EBP2_YEAST]	6.49	3.04%	1	1	1	2	427
462	Q12377	26S proteasome regulatory subunit RPN6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN6 PE=1 SV=3 - [RPN6_YEAST]	5.95	5.07%	1	2	2	2	434

463	P40160	Serine/threonine-protein kinase RIO2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RIO2 PE=1 SV=1 - [RIO2_YEAST]	6.49	6.59%	1	2	2	2	425
464	P40327	26S proteasome regulatory subunit 4 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT2 PE=1 SV=3 - [PRS4_YEAST]	4.71	5.49%	1	2	2	2	437

465	Q01852	Mitochondrial import inner membrane translocase subunit TIM44 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIM44 PE=1 SV=1 - [TIM44_YEAST]	7.55	6.96%	1	2	2	2	431
466	A6ZRM0	Adenylosuccinate synthetase OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ADE12 PE=3 SV=1 - [PURA_YEAS7]	5.67	5.77%	5	2	2	2	433

467	P35184	Ribosome assembly protein SQT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SQT1 PE=1 SV=2 - [SQT1_YEAST]	6.27	5.34%	1	2	2	2	431
468	P22768	Argininosuccinate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARG1 PE=1 SV=3 - [ASSY_YEAST]	8.14	6.67%	1	2	2	2	420

469	P39727	ER-derived vesicles protein ERV46 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERV46 PE=1 SV=2 - [ERV46_YEAST]	6.4	6.02%	1	2	2	2	415
470	P27810	Alpha-1,2 mannosyltransferase KTR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KTR1 PE=1 SV=1 - [KTR1_YEAST]	6.34	5.34%	1	2	2	2	393

471	Q03558	NADPH dehydrogenase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OYE2 PE=1 SV=3 - [OYE2_YEAST]	9.17	8.50%	1	2	2	2	400
472	P48362	Protein HGH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HGH1 PE=1 SV=2 - [HGH1_YEAST]	8.39	7.61%	1	2	2	2	394

473	P39676	Flavohemoprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YHB1 PE=1 SV=2 - [FHP_YEAST]	7.18	8.02%	1	2	2	2	399
474	P36046	Mitochondrial intermembrane space import and assembly protein 40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MIA40 PE=1 SV=2 - [MIA40_Y	6.89	6.95%	1	2	2	2	403

475	Q06205	FK506-binding protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FPR4 PE=1 SV=1 - [FKBP4_YEAST]	5.61	9.69%	2	1	2	2	392
476	P47122	GPN-loop GTPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NPA3 PE=1 SV=1 - [GPN1_YEAST]	6.23	12.99%	1	2	2	2	385

477	P46992	Cell wall protein YJL171C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YJL171C PE=1 SV=2 - [YJR1_YEAST]	6.89	7.83%	1	2	2	2	396
478	P25367	[PIN+] prion protein RNQ1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RNQ1 PE=1 SV=2 - [RNQ1_YEAST]	9.55	9.88%	1	2	2	2	405

479	P32502	Translation initiation factor eIF-2B subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCD7 PE=1 SV=1 - [EI2BB_YEAST]	5.13	5.77%	1	2	2	2	381
480	A6ZML0	Protein YIM1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=YIM1 PE=3 SV=1 - [YIM1_YEAS7]	8.12	10.96%	4	2	2	2	365

481	A6ZXM9	ATPase GET3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=GET3 PE=3 SV=1 - [GET3_YEAS7]	4.74	5.08%	2	2	2	2	354
482	A6ZQH3	Cell wall mannoprotein HSP150 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=HSP150 PE=3 SV=1 - [HS150_YEAS7]	7.29	7.46%	7	2	2	2	389
483	B3LRE5	Fe-S cluster assembly protein DRE2 OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=DRE2 PE=3 SV=1 - [DRE2_YEAS1]	5.46	6.03%	2	2	2	2	348

484	P32419	Malate dehydrogenase, peroxisomal OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MDH3 PE=1 SV=3 - [MDHP_YEAST]	5.12	6.71%	1	2	2	2	343
485	P40517	Ran-specific GTPase-activating protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YRB2 PE=1 SV=1 - [YRB2_YEAST]	7.6	9.48%	1	2	2	2	327

486	Q12029	Sideroflexin FSF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FSF1 PE=1 SV=1 - [FSF1_YEAST]	5.92	9.48%	1	2	2	2	327
487	P24280	SEC14 cytosolic factor OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC14 PE=1 SV=3 - [SEC14_YEAST]	6.49	9.21%	1	2	2	2	304

488	P07273	Transcription elongation factor S-II OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DST1 PE=1 SV=4 - [TFS2_YEAST]	7.56	11.33%	1	2	2	2	309
489	P20459	Eukaryotic translation initiation factor 2 subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUI2 PE=1 SV=1 - [IF2A_YEAST]	6.79	7.89%	1	2	2	2	304

490	P43588	Ubiquitin carboxyl-terminal hydrolase RPN11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN11 PE=1 SV=1 - [RPN11_YEAST]	5.72	9.15%	1	2	2	2	306
491	Q751E8	Negative regulator of the PHO system OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=PHO85 PE=3 SV=2 - [PHO85_ASHGO]	6.06	6.98%	3	1	2	2	301

492	P15703	Glucan 1,3-beta-glucosidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BGL2 PE=1 SV=1 - [BGL2_YEAST]	7.25	9.27%	1	2	2	2	313
493	P07143	Cytochrome c1, heme protein, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYT1 PE=1 SV=1 - [CY1_YEAST]	5.93	10.36%	1	2	2	2	309

494	P47133	ER membrane protein complex subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMC2 PE=1 SV=1 - [EMC2_YEAST]	6.72	9.93%	1	2	2	2	292
495	P35178	Ribosomal RNA-processing protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP1 PE=1 SV=2 - [RRP1_YEAST]	6.18	12.95%	1	2	2	2	278

496	P38988	Mitochondrial GTP/GDP carrier protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GGC1 PE=1 SV=1 - [GGC1_YEAST]	5.61	7.33%	1	2	2	2	300
497	Q08237	RNA exonuclease 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=REX4 PE=1 SV=1 - [REXO4_YEAST]	5.1	7.27%	1	2	2	2	289

498	P43639	Casein kinase II subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CKB1 PE=1 SV=1 - [CSK2B_YEAST]	7.12	12.59%	1	2	2	2	278
499	P33399	La protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LHP1 PE=1 SV=2 - [LHP1_YEAST]	7.68	9.82%	1	2	2	2	275

500	P53081	NGG1-interacting factor 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NIF3 PE=1 SV=1 - [NIF3_YEAST]	7.57	11.11%	1	2	2	2	288
501	P40961	Prohibitin-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PHB1 PE=1 SV=2 - [PHB1_YEAST]	6.66	7.67%	1	2	2	2	287

502	P36139	Protein PET10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PET10 PE=1 SV=3 - [PET10_YEAST]	5.81	9.54%	1	2	2	2	283
503	Q05016	NADP-dependent 3-hydroxy acid dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YMR226C PE=1 SV=1 - [YM71_YEAST]	6.24	9.36%	1	2	2	2	267

504	P51601	GTP cyclohydrolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FOL2 PE=1 SV=1 - [GCH1_YEAST]	7.02	11.11%	1	2	2	2	243
505	P05626	ATP synthase subunit 4, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP4 PE=1 SV=2 - [ATPF_YEAST]	5.39	12.70%	1	2	2	2	244

506	Q12522	Eukaryotic translation initiation factor 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF6 PE=1 SV=1 - [IF6_YEAST]	6.38	12.65%	1	2	2	2	245
507	Q04338	t-SNARE VTI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VTI1 PE=1 SV=3 - [VTI1_YEAST]	5.51	13.36%	1	2	2	2	217

508	Q05359	Protein ERP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERP1 PE=1 SV=1 - [ERP1_YEAST]	7.95	13.70%	1	2	2	2	219
509	P51996	GTP-binding protein YPT32/YPT11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPT32 PE=1 SV=3 - [YPT32_YEAST]	6.97	11.71%	2	1	2	2	222

510	P40040	Protein THO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=THO1 PE=1 SV=1 - [THO1_YEAST]	5.22	24.77%	1	2	2	2	218
511	P43586	60S ribosomal subunit assembly/export protein LOC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LOC1 PE=1 SV=1 - [LOC1_YEAST]	6.29	12.25%	1	2	2	2	204

512	Q08746	Regulator of ribosome biosynthesis OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRS1 PE=1 SV=1 - [RRS1_YEAST]	6.76	22.66%	1	2	2	2	203
513	P47089	Translation machinery-associated protein 22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA22 PE=1 SV=1 - [DENR_YEAST]	9.06	18.69%	1	2	2	2	198

514	P34760	Peroxiredoxin TSA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TSA1 PE=1 SV=3 - [TSA1_YEAST]	5.62	12.76%	2	2	2	2	196
515	P40070	U6 snRNA-associated Sm-like protein LSm4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LSM4 PE=1 SV=1 - [LSM4_YEAST]	4.54	10.70%	1	2	2	2	187

516	P53163	54S ribosomal protein L12, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MNP1 PE=1 SV=1 - [MNP1_YEAST]	5.57	16.49%	1	2	2	2	194
517	P11076	ADP-ribosylation factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARF1 PE=1 SV=3 - [ARF1_YEAST]	5.1	10.50%	3	2	2	2	181

518	P35180	Mitochondrial import receptor subunit TOM20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOM20 PE=1 SV=1 - [TOM20_YEAST]	7.17	16.39%	1	2	2	2	183
519	Q08004	Bud site selection protein 20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BUD20 PE=1 SV=1 - [BUD20_Y	7.84	23.49%	1	2	2	2	166

520	P00427	Cytochrome c oxidase subunit 6, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COX6 PE=1 SV=1 - [COX6_YEAST]	7.5	23.65%	1	2	2	2	148
521	P04037	Cytochrome c oxidase subunit 4, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COX4 PE=1 SV=1 - [COX4_YEAST]	8.43	23.23%	1	2	2	2	155

522	P49334	Mitochondrial import receptor subunit TOM22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOM22 PE=1 SV=3 - [TOM22_YEAST]	8.67	15.79%	1	2	2	2	152
523	P06787	Calmodulin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CMD1 PE=1 SV=1 - [CALM_YEAST]	6.68	19.73%	1	2	2	2	147

524	P28000	DNA-directed RNA polymerases I and III subunit RPAC2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPC19 PE=1 SV=1 - [RPAC2_YEAST]	7.83	19.01%	1	2	2	2	142
525	P38061	60S ribosomal protein L32 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL32 PE=1 SV=1 - [RL32_YEAST]	6.48	17.69%	1	2	2	2	130

526	P53299	Mitochondrial import inner membrane translocase subunit TIM13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIM13 PE=1 SV=1 - [TIM13_YEAST]	6.33	27.62%	1	2	2	2	105
527	P11632	Non-histone chromosomal protein 6A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NHP6A PE=1 SV=1 - [NHP6A_YEAST]	4.67	29.03%	1	2	2	2	93

528	P10622	60S acidic ribosomal protein P1-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP1B PE=1 SV=3 - [RLA3_YEAST]	7.23	15.09%	1	1	1	2	106
529	O74700	Mitochondrial import inner membrane translocase subunit TIM9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIM9 PE=1 SV=1 - [TIM9_YEAST]	7.08	25.29%	2	2	2	2	87

530	P0CX33	40S ribosomal protein S30-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS30A PE=1 SV=1 - [RS30A_YEAST]	5.86	17.46%	1	2	2	2	63
531	P41058	40S ribosomal protein S29-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS29B PE=1 SV=3 - [RS29B_YEAST]	6.02	14.29%	1	1	1	2	56

532	Q12019	Midasin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MDN1 PE=1 SV=1 - [MDN1_YEAST]	2.73	0.39%	1	1	1	1	4910
533	Q00402	Nuclear migration protein NUM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NUM1 PE=1 SV=2 - [NUM1_YEAST]	2.31	0.40%	1	1	1	1	2748

534	P19812	E3 ubiquitin-protein ligase UBR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UBR1 PE=1 SV=1 - [UBR1_YEAST]	2.95	1.18%	1	1	1	1	1950
535	P32528	Urea amidolyase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DUR1,2 PE=1 SV=2 - [DUR1_YEAST]	2.43	0.76%	1	1	1	1	1835

536	P48563	Protein MON2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MON2 PE=1 SV=1 - [MON2_YEAST]	4.51	1.16%	1	1	1	1	1636
537	P32660	Phospholipid-transporting ATPase DNF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DNF1 PE=1 SV=2 - [ATC5_YEAST]	2.76	0.64%	2	1	1	1	1571

538	P22147	5'-3' exoribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=XRN1 PE=1 SV=1 - [XRN1_YEAST]	3.6	0.92%	1	1	1	1	1528
539	P32568	Protein SNQ2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SNQ2 PE=1 SV=2 - [SNQ2_YEAST]	2.42	0.73%	1	1	1	1	1501

540	P47169	Sulfite reductase [NADPH] subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET5 PE=1 SV=1 - [MET5_YEAST]	4.29	1.66%	1	1	1	1	1442
541	P07702	L-2-aminoadipate reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS2 PE=1 SV=2 - [LYS2_YEAST]	3.6	1.72%	1	1	1	1	1392

542	P38972	Phosphoribosylformylglycinamidine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE6 PE=1 SV=2 - [PUR4_YEAST]	4.03	1.18%	1	1	1	1	1358
543	Q12451	Oxysterol-binding protein homolog 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OSH2 PE=1 SV=1 - [OSH2_YEAST]	2.21	1.25%	1	1	1	1	1283

544	P28273	5-oxoprolinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OXP1 PE=1 SV=2 - [OPLA_YEAST]	3.02	1.01%	1	1	1	1	1286
545	P24276	Protein SSD1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSD1 PE=1 SV=1 - [SSD1_YEAST]	5.24	2.16%	1	1	1	1	1250

546	A6ZKU1	Actin cytoskeleton-regulatory complex protein SLA1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=SLA1 PE=3 SV=1 - [SLA1_YEAS7]	2.65	1.05%	2	1	1	1	1244
547	Q08965	Ribosome biogenesis protein BMS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BMS1 PE=1 SV=1 - [BMS1_YEAST]	2.37	1.01%	1	1	1	1	1183

548	P47068	Myosin tail region-interacting protein MTI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BBC1 PE=1 SV=2 - [BBC1_YEAST]	4.86	2.42%	1	1	1	1	1157
549	P48361	Activator of SKN7 protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ASK10 PE=1 SV=2 - [ASK10_Y	3.08	1.48%	1	1	1	1	1146

550	P30822	Exportin-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CRM1 PE=1 SV=1 - [XPO1_YEAST]	2.51	0.92%	1	1	1	1	1084
551	P38426	Trehalose synthase complex regulatory subunit TPS3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPS3 PE=1 SV=3 - [TPS3_YEAST]	2.46	1.04%	1	1	1	1	1054

552	P39985	rDNA transcriptional regulator POL5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=POL5 PE=1 SV=1 - [DPO5_YEAST]	2.61	1.47%	1	1	1	1	1022
553	P27692	Transcription elongation factor SPT5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SPT5 PE=1 SV=1 - [SPT5_YEAST]	3.71	1.88%	1	1	1	1	1063

554	A6ZXU0	ATP-dependent RNA helicase DBP10 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP10 PE=3 SV=1 - [DBP10_YEAS7]	3.05	1.11%	2	1	1	1	995
555	P38764	26S proteasome regulatory subunit RPN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN1 PE=1 SV=3 - [RPN1_YEAST]	3.53	1.61%	1	1	1	1	993

556	A6ZRW5	mRNA-decapping enzyme subunit 2 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DCP2 PE=3 SV=1 - [DCP2_YEAS7]	3.29	1.55%	2	1	1	1	970
557	P38250	Increased sodium tolerance protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IST2 PE=1 SV=2 - [IST2_YEAST]	3.2	1.90%	1	1	1	1	946

558	P25635	Periodic tryptophan protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PWP2 PE=1 SV=2 - [PWP2_YEAST]	2.8	1.08%	1	1	1	1	923
559	P38810	SED5-binding protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SFB3 PE=1 SV=1 - [SFB3_YEAST]	2.13	0.97%	1	1	1	1	929

560	P39936	Eukaryotic initiation factor 4F subunit p130 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF4632 PE=1 SV=1 - [IF4F2_YEAST]	4.36	3.83%	1	1	1	1	914
561	Q04500	U3 small nucleolar RNA-associated protein 14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP14 PE=1 SV=1 - [UTP14_YEAST]	2.7	1.11%	1	1	1	1	899

562	P31688	Trehalose-phosphatase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPS2 PE=1 SV=3 - [TPS2_YEAST]	3.16	1.23%	1	1	1	1	896
563	P42842	Essential for maintenance of the cell wall protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMW1 PE=1 SV=1 - [EMW1_YEAST]	2.24	1.00%	1	1	1	1	904

564	P31539	Heat shock protein 104 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP104 PE=1 SV=2 - [HS104_YEAST]	3.03	1.54%	1	1	1	1	908
565	P41811	Coatomer subunit beta' OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC27 PE=1 SV=1 - [COPB2_YEAST]	2.15	1.24%	1	1	1	1	889

566	P12945	N-terminal acetyltransferase A complex subunit NAT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NAT1 PE=1 SV=2 - [NAT1_YEAST]	2.68	1.99%	1	1	1	1	854
567	Q12205	Putative endoplasmic reticulum mannosidase MNL2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MNL2 PE=1 SV=1 - [MNL2_YEAST]	2.11	2.00%	1	1	1	1	849

568	P22506	Beta-glucosidase 1 OS=Saccharomycopsis fibuligera OX=4944 GN=BGL1 PE=3 SV=1 - [BGL1_SACFI]	2.36	1.14%	1	1	1	1	876
569	P31384	Glucose-repressible alcohol dehydrogenase transcriptional effector OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCR4 PE=1 SV=2 - [CCR4_YEAST]	4.53	1.91%	1	1	1	1	837

570	Q12028	AP-1 complex subunit gamma-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=APL4 PE=1 SV=1 - [AP1G1_YEAST]	3.05	2.28%	1	1	1	1	832
571	A6ZM93	Eisosome protein 1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=EIS1 PE=3 SV=1 - [EIS1_YEAS7]	3.55	1.90%	6	1	1	1	843

572	P13188	Glutamine--tRNA ligase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLN4 PE=1 SV=2 - [SYQ_YEAST]	2.97	1.11%	1	1	1	1	809
573	Q07844	Ribosome biogenesis ATPase RIX7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RIX7 PE=1 SV=1 - [RIX7_YEAST]	2.83	2.03%	1	1	1	1	837

574	P33775	Dolichyl-phosphate-mannose--protein mannosyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMT1 PE=1 SV=1 - [PMT1_YEAST]	2.72	1.35%	1	1	1	1	817
575	Q03088	Styryl dye vacuolar localization protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SVL3 PE=1 SV=1 - [SVL3_YEAST]	3.44	2.18%	1	1	1	1	825

576	P39940	E3 ubiquitin-protein ligase RSP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RSP5 PE=1 SV=1 - [RSP5_YEAST]	3.9	3.21%	1	1	1	1	809
577	Q06679	U3 small nucleolar RNA-associated protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP4 PE=1 SV=1 - [UTP4_YEAST]	2.12	1.42%	1	1	1	1	776

578	P39719	Flavin carrier protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FLC2 PE=1 SV=2 - [FLC2_YEAST]	2.19	1.15%	1	1	1	1	783
579	A6ZPU3	ATP-dependent RNA helicase DBP4 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP4 PE=3 SV=1 - [DBP4_YEAS7]	3.61	2.99%	2	1	1	1	770

580	A6ZL85	ATP-dependent RNA helicase MAK5 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=MAK5 PE=3 SV=1 - [MAK5_YEAS7]	2.32	1.43%	2	1	1	1	769
581	P53313	Protein SDA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SDA1 PE=1 SV=1 - [SDA1_YEAST]	2.6	1.83%	1	1	1	1	767

582	P39533	Homocitrate dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACO2 PE=1 SV=1 - [ACON2_YEAST]	3.54	2.79%	1	1	1	1	789
583	P00958	Methionine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MES1 PE=1 SV=4 - [SYMC_YEAST]	2.14	1.46%	1	1	1	1	751

584	P43535	Protein GCN20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCN20 PE=1 SV=1 - [GCN20_YEAST]	2.49	1.06%	1	1	1	1	752
585	P32892	ATP-dependent RNA helicase DRS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DRS1 PE=1 SV=2 - [DRS1_YEAST]	2.82	1.99%	2	1	1	1	752

586	P47075	Vacuolar transporter chaperone 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VTC4 PE=1 SV=2 - [VTC4_YEAST]	2.75	1.25%	1	1	1	1	721
587	P32795	Mitochondrial inner membrane i-AAA protease supercomplex subunit YME1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YME1 PE=1 SV=1 - [YME1_YEAST]	3.57	1.87%	1	1	1	1	747

588	P39007	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STT3 PE=1 SV=2 - [STT3_YEAST]	3.37	2.51%	1	1	1	1	718
589	P40557	ER-retained PMA1-suppressing protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EPS1 PE=1 SV=1 - [EPS1_YEAST]	2.28	1.57%	1	1	1	1	701

590	P53326	Uncharacterized protein YGR266W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YGR266W PE=1 SV=1 - [YG5L_YEAST]	3.04	2.14%	1	1	1	1	701
591	P38795	Glutamine-dependent NAD(+) synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=QNS1 PE=1 SV=1 - [NADE_YE	4.09	2.10%	1	1	1	1	714

592	P32486	Beta-glucan synthesis-associated protein KRE6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRE6 PE=1 SV=2 - [KRE6_YEAST]	3.41	2.08%	1	1	1	1	720
593	P53276	U3 small nucleolar RNA-associated protein 8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP8 PE=1 SV=1 - [UTP8_YEAST]	3.29	2.81%	1	1	1	1	713

594	P39002	Long-chain-fatty-acid--CoA ligase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAA3 PE=1 SV=1 - [LCF3_YEAST]	2.53	1.30%	1	1	1	1	694
595	P35817	Bromodomain-containing factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BDF1 PE=1 SV=3 - [BDF1_YEAST]	2.3	1.90%	1	1	1	1	686

596	Q07896	Nucleolar complex-associated protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOC3 PE=1 SV=1 - [NOC3_YEAST]	3.53	1.96%	1	1	1	1	663
597	Q04373	Pumilio homology domain family member 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PUF6 PE=1 SV=1 - [PUF6_YEAST]	2.73	1.83%	1	1	1	1	656

598	P40032	Prolyl 3,4-dihydroxylase TPA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPA1 PE=1 SV=1 - [TPA1_YEAST]	2.31	1.86%	1	1	1	1	644
599	P53918	Uncharacterized transporter ESBP6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ESBP6 PE=1 SV=1 - [ESBP6_YEAST]	2.5	1.93%	1	1	1	1	673

600	P38688	Signal recognition particle subunit SRP72 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRP72 PE=1 SV=2 - [SRP72_YEAST]	3.33	2.66%	1	1	1	1	640
601	P53145	Large subunit GTPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LSG1 PE=1 SV=1 - [LSG1_YEAST]	2.43	4.53%	1	1	1	1	640

602	Q04177	U3 small nucleolar RNA-associated protein 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP5 PE=1 SV=1 - [UTP5_YEAST]	2.55	2.18%	1	1	1	1	643
603	P32599	Fimbrin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAC6 PE=1 SV=1 - [FIMB_YEAST]	4.66	4.52%	1	1	1	1	642

604	P38694	Putative aldehyde dehydrogenase-like protein YHR039C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MSC7 PE=1 SV=1 - [MSC7_YEAST]	2.77	1.71%	1	1	1	1	644
605	P12754	Translation initiation factor eIF-2B subunit delta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCD2 PE=1 SV=1 - [EI2BD_YEAST]	2.24	1.38%	1	1	1	1	651

606	P43561	Iron transport multicopper oxidase FET5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FET5 PE=1 SV=1 - [FET5_YEAST]	2.56	2.09%	1	1	1	1	622
607	Q05506	Arginine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YDR341C PE=1 SV=1 - [SYRC_YEAST]	2.17	1.48%	1	1	1	1	607

608	P32901	Peptide transporter PTR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PTR2 PE=1 SV=2 - [PTR2_YEAST]	4.33	2.33%	1	1	1	1	601
609	P53283	Polyamine transporter 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPO2 PE=1 SV=1 - [TPO2_YEAST]	4.3	3.75%	1	1	1	1	614

610	Q99257	mRNA export factor MEX67 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MEX67 PE=1 SV=1 - [MEX67_YEAST]	2.47	1.84%	1	1	1	1	599
611	P47083	U3 small nucleolar RNA-associated protein MPP10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MPP10 PE=1 SV=1 - [MPP10_YEAST]	3.72	4.89%	1	1	1	1	593

612	A6ZTW2	Outer spore wall assembly protein SHE10 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=SHE10 PE=3 SV=1 - [SHE10_YEAS7]	2.42	1.73%	5	1	1	1	577
613	Q04228	UBX domain-containing protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UBX2 PE=1 SV=1 - [UBX2_YEAST]	3.02	2.40%	1	1	1	1	584

614	P40362	U3 small nucleolar RNA-associated protein 18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP18 PE=1 SV=1 - [UTP18_YEAST]	4.54	3.03%	1	1	1	1	594
615	P09032	Translation initiation factor eIF-2B subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCD1 PE=1 SV=3 - [EI2BG_YEAST]	4.19	3.29%	1	1	1	1	578

616	P32891	D-lactate dehydrogenase [cytochrome] 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DLD1 PE=1 SV=2 - [DLD1_YEAST]	2.15	2.90%	1	1	1	1	587
617	P38882	U3 small nucleolar RNA-associated protein 9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP9 PE=1 SV=1 - [UTP9_YEAST]	2.37	2.61%	1	1	1	1	575

618	Q03103	Endoplasmic oxidoreductin-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERO1 PE=1 SV=1 - [ERO1_YEAST]	2.59	2.31%	1	1	1	1	563
619	Q08179	Mitochondrial distribution and morphology protein 38 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MDM38 PE=1 SV=1 - [MDM38_YEAST]	3.29	2.79%	1	1	1	1	573

620	P29468	Poly(A) polymerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PAP1 PE=1 SV=1 - [PAP_YEAST]	2.14	1.76%	1	1	1	1	568
621	P49089	Asparagine synthetase [glutamine-hydrolyzing] 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ASN1 PE=1 SV=2 - [ASNS1_YEAST]	2.72	2.10%	1	1	1	1	572

622	P53379	Aspartic proteinase MKC7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MKC7 PE=1 SV=2 - [MKC7_YEAST]	5.08	3.36%	1	1	1	1	596
623	P39968	Vacuolar protein 8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VAC8 PE=1 SV=3 - [VAC8_YEAST]	3.1	2.08%	1	1	1	1	578

624	P39003	High-affinity hexose transporter HXT6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HXT6 PE=1 SV=2 - [HXT6_YEAST]	6.57	4.04%	2	1	1	1	570
625	P40215	External NADH-ubiquinone oxidoreductase 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NDE1 PE=1 SV=1 - [NDH1_YEAST]	3.31	1.96%	1	1	1	1	560

626	P40055	U3 small nucleolar RNA-associated protein 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP7 PE=1 SV=1 - [UTP7_YEAST]	2.56	1.81%	1	1	1	1	554
627	Q12211	tRNA pseudouridine synthase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PUS1 PE=1 SV=1 - [PUS1_YEAST]	2.16	3.13%	1	1	1	1	544

628	A6ZRQ4	Pre-rRNA-processing protein IPI3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=IPI3 PE=3 SV=1 - [IPI3_YEAS7]	2.51	3.78%	2	1	1	1	555
629	P39998	Enhancer of mRNA-decapping protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EDC3 PE=1 SV=1 - [EDC3_YEAST]	3.2	2.36%	1	1	1	1	551

630	P23642	Mannan polymerase I complex VAN1 subunit OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VAN1 PE=1 SV=3 - [VAN1_YEAST]	2.95	2.43%	1	1	1	1	535
631	B3LRA0	MICOS complex subunit MIC60 OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=MIC60 PE=3 SV=1 - [MIC60_YEAS1]	2.96	3.53%	4	1	1	1	539

632	P43621	Coatomer subunit delta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RET2 PE=1 SV=3 - [COPD_YEAST]	3.29	6.59%	1	1	1	1	546
633	P37302	Aminopeptidase Y OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=APE3 PE=1 SV=1 - [APE3_YEAST]	4.97	4.10%	1	1	1	1	537

634	P23585	High-affinity glucose transporter HXT2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HXT2 PE=1 SV=1 - [HXT2_YEAST]	3.11	2.03%	1	1	1	1	541
635	P20424	Signal recognition particle subunit SRP54 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRP54 PE=1 SV=2 - [SRP54_YEAST]	2.78	2.22%	1	1	1	1	541

636	P39705	Nucleoporin NUP60 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NUP60 PE=1 SV=1 - [NUP60_YEAST]	2.8	3.34%	1	1	1	1	539
637	P06101	Hsp90 co-chaperone Cdc37 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC37 PE=1 SV=2 - [CDC37_YEAST]	3.23	3.56%	1	1	1	1	506

638	P53043	Serine/threonine-protein phosphatase T OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PPT1 PE=1 SV=1 - [PPT1_YEAST]	2.17	1.36%	1	1	1	1	513
639	P53040	Transcription initiation factor TFIID subunit 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TAF6 PE=1 SV=1 - [TAF6_YEAST]	4.53	3.49%	1	1	1	1	516

640	P11412	Glucose-6-phosphate 1-dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ZWF1 PE=1 SV=4 - [G6PD_YEAST]	2.7	3.37%	1	1	1	1	505
641	P15625	Phenylalanine--tRNA ligase alpha subunit OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FRS2 PE=1 SV=3 - [SYFA_YEAST]	3.18	2.19%	1	1	1	1	503

642	P16120	Threonine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=THR4 PE=1 SV=1 - [THRC_YEAST]	4.36	2.72%	1	1	1	1	514
643	P43593	Ubiquitin carboxyl-terminal hydrolase 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UBP6 PE=1 SV=1 - [UBP6_YEAST]	3.77	3.21%	1	1	1	1	499

644	P32566	Cell wall assembly regulator SMI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SMI1 PE=1 SV=1 - [SMI1_YEAST]	2.23	2.57%	1	1	1	1	505
645	Q08287	60S ribosome subunit biogenesis protein NOP8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP8 PE=1 SV=1 - [NOP8_YEAST]	3.06	4.13%	1	1	1	1	484

646	P33750	Protein SOF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SOF1 PE=1 SV=1 - [DCA13_YEAST]	3.02	3.27%	1	1	1	1	489
647	Q04991	Protein FMP42 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FMP42 PE=1 SV=1 - [FMP42_YEAST]	3.24	2.98%	1	1	1	1	504

648	Q12234	GRIP domain-containing protein RUD3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RUD3 PE=1 SV=1 - [RUD3_YEAST]	2.58	5.37%	1	1	1	1	484
649	A6ZRK4	Cysteine proteinase 1, mitochondrial OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=LAP3 PE=3 SV=2 - [BLH1_YEAS7]	3.3	3.52%	3	1	1	1	483

650	P17709	Glucokinase-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLK1 PE=1 SV=1 - [HXKG_YEAST]	2.61	2.20%	1	1	1	1	500
651	P38333	Essential nuclear protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ENP1 PE=1 SV=1 - [ENP1_YEAST]	3.38	3.31%	1	1	1	1	483

652	Q02776	Mitochondrial import inner membrane translocase subunit TIM50 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIM50 PE=1 SV=1 - [TIM50_YEAST]	4.27	2.94%	1	1	1	1	476
653	P53303	Zinc finger protein ZPR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ZPR1 PE=1 SV=1 - [ZPR1_YE	2.34	2.67%	1	1	1	1	486

654	Q75BS4	ATP-dependent RNA helicase DHH1 OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=DHH1 PE=3 SV=1 - [DHH1_ASHGO]	3.01	2.07%	2	1	1	1	484
655	Q05515	Survival factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SVF1 PE=1 SV=1 - [SVF1_YEAST]	3.5	2.49%	1	1	1	1	481

656	P41543	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OST1 PE=1 SV=1 - [OST1_YEAST]	3.53	2.94%	1	1	1	1	476
657	P87185	Cysteine desulfurase, mitochondrial OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=NFS1 PE=2 SV=1 - [NFS1_CANAL]	2.7	3.48%	2	1	1	1	488

658	P34078	Protein LTV1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LTV1 PE=1 SV=2 - [LTV1_YEAST]	2.46	2.16%	1	1	1	1	463
659	P47018	Maintenance of telomere capping protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MTC1 PE=1 SV=1 - [MTC1_YEAST]	3.14	2.30%	1	1	1	1	478

660	P38353	Sec sixty-one protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSH1 PE=1 SV=1 - [SSH1_YEAST]	2.92	2.86%	1	1	1	1	490
661	P32915	Protein transport protein SEC61 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC61 PE=1 SV=1 - [SC61A_YEAST]	2.16	2.29%	1	1	1	1	480

662	P14743	Glycylpeptide N-tetradecanoyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NMT1 PE=1 SV=1 - [NMT_YEAST]	2.68	3.74%	1	1	1	1	455
663	Q01159	mRNA-capping enzyme subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CEG1 PE=1 SV=2 - [MCE1_YEAST]	3.46	4.14%	1	1	1	1	459

664	Q02354	U3 small nucleolar RNA-associated protein 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP6 PE=1 SV=2 - [UTP6_YEAST]	3.26	3.64%	1	1	1	1	440
665	P38789	Ribosome biogenesis protein SSF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSF1 PE=1 SV=1 - [SSF1_YEAST]	4.31	3.53%	2	1	1	1	453

666	A6ZT54	Cruciform DNA-recognizing protein 1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=CRP1 PE=3 SV=1 - [CRP1_YEAS7]	3.1	2.58%	8	1	1	1	465
667	Q12034	Protein SLF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SLF1 PE=1 SV=1 - [SLF1_YEAST]	3.11	3.58%	1	1	1	1	447

668	P36080	Ribosomal RNA-processing protein 14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP14 PE=1 SV=1 - [RRP14_YEAST]	3.5	2.76%	1	1	1	1	434
669	P19262	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KGD2 PE=1 SV=2 - [ODO2_YEAST]	3.67	3.67%	1	1	1	1	463

670	P32623	Probable glycosidase CRH2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTR2 PE=1 SV=3 - [CRH2_YEAST]	3.44	3.21%	1	1	1	1	467
671	P38755	Oxysterol-binding protein homolog 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OSH7 PE=1 SV=1 - [OSH7_YEAST]	2.23	3.89%	1	1	1	1	437

672	P35844	Oxysterol-binding protein homolog 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KES1 PE=1 SV=1 - [KES1_YEAST]	3.23	2.07%	1	1	1	1	434
673	P53549	26S proteasome subunit RPT4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT4 PE=1 SV=4 - [PRS10_YEAST]	2.74	3.43%	1	1	1	1	437

674	Q12109	Tryptophan--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=WRS1 PE=1 SV=1 - [SYWC_YEAST]	2.28	2.55%	1	1	1	1	432
675	Q06103	26S proteasome regulatory subunit RPN7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN7 PE=1 SV=3 - [RPN7_YEAST]	3.3	5.13%	1	1	1	1	429

676	Q12363	Transcriptional modulator WTM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=WTM1 PE=1 SV=1 - [WTM1_YEAST]	3	4.58%	1	1	1	1	437
677	P33298	26S proteasome regulatory subunit 6B homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT3 PE=1 SV=2 - [PRS6B_YEAST]	3.67	3.50%	1	1	1	1	428

678	P46985	Probable alpha-1,6-mannosyltransferase MNN11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MNN11 PE=1 SV=2 - [MNN11_YEAST]	3.47	5.21%	1	1	1	1	422
679	P38355	Uncharacterized transporter YBR287W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YBR287W PE=1 SV=1 - [YB8B_YEAST]	4.42	6.09%	1	1	1	1	427

680	P42838	Alkylphosphocholine resistance protein LEM3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LEM3 PE=1 SV=1 - [LEM3_YEAST]	2.92	2.66%	1	1	1	1	414
681	C7GLH8	Enhancer of translation termination 1 OS=Saccharomyces cerevisiae (strain JAY291) OX=574961 GN=ETT1 PE=3 SV=1 - [ETT1_YEAS2]	4.43	5.10%	2	1	1	1	412

682	P40087	DNA damage-inducible protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DDI1 PE=1 SV=1 - [DDI1_YEAST]	4.27	3.50%	1	1	1	1	428
683	P07278	cAMP-dependent protein kinase regulatory subunit OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BCY1 PE=1 SV=4 - [KAPR_YEAST]	2.6	2.16%	1	1	1	1	416

684	P32264	Glutamate 5-kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRO1 PE=1 SV=2 - [PROB_YEAST]	3.57	3.74%	1	1	1	1	428
685	P53723	UPF0674 endoplasmic reticulum membrane protein YNR021W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YNR021W PE=1 SV=3 - [YN8B_YEAST]	3.66	4.21%	1	1	1	1	404

686	P32895	Ribose-phosphate pyrophosphokinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRS1 PE=1 SV=1 - [KPR1_YEAST]	3.92	3.28%	1	1	1	1	427
687	P32468	Cell division control protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC12 PE=1 SV=1 - [CDC12_Y	4.49	4.18%	1	1	1	1	407

688	Q01080	DNA-directed RNA polymerase I subunit RPA49 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPA49 PE=1 SV=2 - [RPA49_YEAST]	2.44	2.65%	1	1	1	1	415
689	P47124	Putative glycosyltransferase HOC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOC1 PE=1 SV=3 - [HOC1_YEAST]	2.76	2.53%	1	1	1	1	396

690	P09938	Ribonucleoside-diphosphate reductase small chain 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RNR2 PE=1 SV=2 - [RIR2_YEAST]	3.33	4.01%	1	1	1	1	399
691	P11745	Ran GTPase-activating protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RNA1 PE=1 SV=2 - [RNA1_YEAST]	4.43	4.42%	1	1	1	1	407

692	P16451	Pyruvate dehydrogenase complex protein X component, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDX1 PE=1 SV=1 - [ODPX_YEAST]	3.63	7.80%	1	1	1	1	410
693	Q01939	26S proteasome regulatory subunit 8 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT6 PE=1 SV=4 - [PRS8_YEAST]	5.05	3.95%	1	1	1	1	405

694	Q03529	Ceramide very long chain fatty acid hydroxylase SCS7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCS7 PE=1 SV=1 - [SCS7_YEAST]	2.36	3.91%	1	1	1	1	384
695	P16622	Ferrochelatase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HEM15 PE=1 SV=1 - [HEMH_YEAST]	3.86	5.34%	1	1	1	1	393

696	P49573	Copper transport protein CTR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CTR1 PE=1 SV=1 - [CTR1_YEAST]	5.08	4.19%	1	1	1	1	406
697	P31412	V-type proton ATPase subunit C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA5 PE=1 SV=4 - [VATC_YEAST]	5.2	4.34%	1	1	1	1	392

698	Q02793	Antiviral protein SKI8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SKI8 PE=1 SV=1 - [SKI8_YEAST]	3.54	4.53%	1	1	1	1	397
699	P32377	Diphosphomevalonate decarboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MVD1 PE=1 SV=2 - [MVD1_YEAST]	5.41	5.30%	1	1	1	1	396

700	P33313	Hsp70/Hsp90 co-chaperone CNS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CNS1 PE=1 SV=1 - [CNS1_YEAST]	3.88	4.68%	1	1	1	1	385
701	P36421	Tyrosine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TYS1 PE=1 SV=3 - [SYYC_YEAST]	3.1	3.05%	1	1	1	1	394

702	P37303	Low specificity L-threonine aldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLY1 PE=1 SV=2 - [GLY1_YEAST]	4.01	3.88%	1	1	1	1	387
703	Q12329	Heat shock protein 42 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP42 PE=1 SV=1 - [HSP42_Y	2.34	6.13%	1	1	1	1	375

704	P46672	tRNA-aminoacylation cofactor ARC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARC1 PE=1 SV=2 - [ARC1_YEAST]	3.64	3.46%	1	1	1	1	376
705	P53691	Peptidyl-prolyl cis-trans isomerase CPR6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CPR6 PE=1 SV=1 - [PPID_YEAST]	4.6	10.24%	1	1	1	1	371

706	P40506	Phosphopantothenate--cysteine ligase CAB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CAB2 PE=1 SV=2 - [PPCS_YEAST]	5.31	5.21%	1	1	1	1	365
707	P32288	Glutamine synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLN1 PE=1 SV=4 - [GLNA_YE	2.7	4.86%	1	1	1	1	370

708	P40507	Protein AIR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AIR1 PE=1 SV=1 - [AIR1_YEAST]	3.11	4.72%	1	1	1	1	360
709	P38998	Saccharopine dehydrogenase [NAD(+), L-lysine-forming] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS1 PE=1 SV=3 - [LYS1_YEAST]	4.32	4.56%	1	1	1	1	373

710	Q757U3	Enoyl-[acyl-carrier-protein] reductase, mitochondrial OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=ETR1 PE=3 SV=2 - [ETR1_ASHGO]	2.24	5.05%	1	1	1	1	376
711	P48239	Glutathione S-transferase omega-like 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GTO1 PE=1 SV=1 - [GTO1_YEAST]	3.15	4.21%	1	1	1	1	356

712	P32583	Suppressor protein SRP40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRP40 PE=1 SV=2 - [SRP40_YEAST]	3.23	2.96%	1	1	1	1	406
713	Q08096	RNA 3'-terminal phosphate cyclase-like protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RCL1 PE=1 SV=1 - [RCL1_YEAST]	2.65	3.00%	1	1	1	1	367

714	P25358	Elongation of fatty acids protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ELO2 PE=1 SV=1 - [ELO2_YEAST]	2.61	2.88%	1	1	1	1	347
715	P49723	Ribonucleoside-diphosphate reductase small chain 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RNR4 PE=1 SV=1 - [RIR4_YEAST]	4.95	5.51%	1	1	1	1	345

716	P28241	Isocitrate dehydrogenase [NAD] subunit 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IDH2 PE=1 SV=1 - [IDH2_YEAST]	3.17	4.61%	1	1	1	1	369
717	P36160	Ribosome biogenesis protein RPF2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPF2 PE=1 SV=1 - [RPF2_YEAST]	2.67	2.62%	1	1	1	1	344

718	Q12000	Translation machinery-associated protein 46 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA46 PE=1 SV=2 - [TMA46_YEAST]	2.39	2.90%	1	1	1	1	345
719	P35197	ADP-ribosylation factor GTPase-activating protein GCS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCS1 PE=1 SV=1 - [GCS1_YEAST]	2.73	3.13%	1	1	1	1	352

720	P45978	Protein SCD6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCD6 PE=1 SV=1 - [SCD6_YEAST]	3.85	5.16%	1	1	1	1	349
721	P21560	Protein CBP3, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CBP3 PE=1 SV=1 - [CBP3_YEAST]	2.27	3.28%	1	1	1	1	335

722	P53011	Nucleoporin SEH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEH1 PE=1 SV=1 - [SEH1_YEAST]	2.6	3.15%	1	1	1	1	349
723	P36047	Protein phosphatase 1 regulatory subunit SDS22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SDS22 PE=1 SV=1 - [SDS22_YEAST]	3.17	4.73%	1	1	1	1	338

724	Q01590	Integral membrane protein SED5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SED5 PE=1 SV=1 - [SED5_YEAST]	2.9	5.00%	1	1	1	1	340
725	Q07938	S-methyl-5'-thioadenosine phosphorylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MEU1 PE=1 SV=1 - [MTAP_YEAST]	2.39	3.26%	1	1	1	1	337

726	P08466	Mitochondrial nuclease OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NUC1 PE=1 SV=1 - [NUC1_YEAST]	2.36	3.95%	1	1	1	1	329
727	P25342	Cell division control protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC10 PE=1 SV=1 - [CDC10_Y	3.85	4.04%	1	1	1	1	322

728	Q12480	Probable electron transfer flavoprotein subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AIM45 PE=1 SV=1 - [ETFA_YEAST]	2.68	4.94%	1	1	1	1	344
729	P40693	Ribosome biogenesis protein RLP7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RLP7 PE=1 SV=1 - [RLP7_YEAST]	3.33	4.04%	1	1	1	1	322

730	P53743	Pre-rRNA-processing protein ESF2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ESF2 PE=1 SV=1 - [ESF2_YEAST]	2.36	3.16%	1	1	1	1	316
731	P47143	Adenosine kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADO1 PE=1 SV=1 - [ADK_YEAST]	2.7	3.82%	1	1	1	1	340

732	Q06497	Peroxisomal adenine nucleotide transporter 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ANT1 PE=1 SV=1 - [ANT1_YEAST]	4.89	5.79%	1	1	1	1	328
733	P46669	DNA-directed RNA polymerase I subunit RPA43 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPA43 PE=1 SV=2 - [RPA43_YEAST]	3.01	3.68%	1	1	1	1	326

734	Q12117	Protein MRH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MRH1 PE=1 SV=1 - [MRH1_YEAST]	5.04	5.31%	1	1	1	1	320
735	A6ZPC2	rRNA biogenesis protein RRP36 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=RRP36 PE=3 SV=1 - [RRP36_YEAS7]	2.62	8.33%	4	1	1	1	300

736	P47120	Deoxyhypusine hydroxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LIA1 PE=1 SV=1 - [DOHH_YEAST]	3.55	6.46%	1	1	1	1	325
737	Q06146	Uncharacterized protein YLR257W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YLR257W PE=1 SV=1 - [YL257_YEAST]	4.52	7.17%	1	1	1	1	321

738	P17505	Malate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MDH1 PE=1 SV=2 - [MDHM_YEAST]	2.9	4.19%	1	1	1	1	334
739	P28321	Monoglyceride lipase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YJU3 PE=1 SV=2 - [MGLL_YEAST]	2.91	5.43%	1	1	1	1	313

740	P34253	Protein KTI12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KTI12 PE=1 SV=2 - [KTI12_YEAST]	2.98	3.51%	1	1	1	1	313
741	P06785	Thymidylate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC21 PE=1 SV=1 - [TYSY_YEAST]	4.33	4.93%	1	1	1	1	304

742	P53337	ER-derived vesicles protein ERV29 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERV29 PE=1 SV=1 - [ERV29_YEAST]	2.29	3.87%	1	1	1	1	310
743	P38077	ATP synthase subunit gamma, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP3 PE=1 SV=1 - [ATPG_YEAST]	3.78	4.18%	1	1	1	1	311

744	P29509	Thioredoxin reductase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRR1 PE=1 SV=3 - [TRXB1_YEAST]	2.58	7.21%	1	1	1	1	319
745	Q08686	Thiosulfate sulfurtransferase TUM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUM1 PE=1 SV=1 - [THTR_YEAST]	3.2	8.22%	1	1	1	1	304

746	P33333	Probable 1-acyl-sn-glycerol-3-phosphate acyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SLC1 PE=1 SV=1 - [PLSC_YEAST]	3.33	5.94%	1	1	1	1	303
747	P40509	Coatomer subunit epsilon OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC28 PE=1 SV=2 - [COPE_YEAST]	2.36	5.41%	1	1	1	1	296

748	Q08235	Ribosome biogenesis protein BRX1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BRX1 PE=1 SV=2 - [BRX1_YEAST]	4.57	5.50%	1	1	1	1	291
749	Q04491	Protein transport protein SEC13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC13 PE=1 SV=1 - [SEC13_YEAST]	2.52	3.37%	1	1	1	1	297

750	Q06104	Uncharacterized membrane protein YPR109W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPR109W PE=1 SV=1 - [YPR09_YEAST]	2.39	5.44%	1	1	1	1	294
751	P49954	Omega-amidase NIT3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NIT3 PE=1 SV=1 - [NIT3_YEAST]	3.01	6.19%	1	1	1	1	291

752	P32496	26S proteasome regulatory subunit RPN12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN12 PE=1 SV=3 - [RPN12_YEAST]	2.57	5.47%	1	1	1	1	274
753	Q02795	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit SWP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SWP1 PE=1 SV=1 - [OSTD_YEAST]	2.33	3.85%	1	1	1	1	286

754	A6ZR39	Golgi to ER traffic protein 2 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=GET2 PE=3 SV=1 - [GET2_YEAS7]	3.48	7.72%	2	1	1	1	285
755	A6ZVM6	NADH-cytochrome b5 reductase 1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=CBR1 PE=3 SV=2 - [NCB5R_YEAS7]	2.17	2.82%	2	1	1	1	284

756	Q03219	Uncharacterized protein YMR178W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YMR178W PE=1 SV=1 - [YM44_YEAST]	4.56	6.20%	1	1	1	1	274
757	P08456	CDP-diacylglycerol--serine O-phosphatidyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CHO1 PE=1 SV=3 - [PSS_YEAST]	3.24	7.97%	1	1	1	1	276

758	Q99216	Pre-rRNA-processing protein PNO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PNO1 PE=1 SV=1 - [PNO1_YEAST]	2.44	5.11%	1	1	1	1	274
759	A6ZQF6	Autophagy-related protein 27 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ATG27 PE=3 SV=1 - [ATG27_Y	3.11	3.69%	2	1	1	1	271

760	Q12359	Ammonia transport outward protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATO3 PE=1 SV=1 - [ATO3_YEAST]	2.67	6.55%	1	1	1	1	275
761	A5DZE1	Ribosome biogenesis protein NSA2 OS=Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) OX=379508 GN=NSA2 PE=3 SV=1 - [NSA2_LODEL]	2.19	3.45%	3	1	1	1	261

762	A6ZZL7	U3 small nucleolar RNA-associated protein 11 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=UTP11 PE=3 SV=1 - [UTP11_YEAS7]	2.51	4.80%	1	1	1	1	250
763	P38886	26S proteasome regulatory subunit RPN10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN10 PE=1 SV=3 - [RPN10_YEAST]	3.11	7.09%	1	1	1	1	268

764	Q12270	Rhomboid protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RBD2 PE=1 SV=1 - [RBD2_YEAST]	2.17	9.92%	1	1	1	1	262
765	P53889	Uncharacterized mitochondrial hydrolase FMP41 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FMP41 PE=1 SV=1 - [FMP41_YEAST]	4.99	10.04%	1	1	1	1	259

766	P23638	Proteasome subunit alpha type-3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE9 PE=1 SV=1 - [PSA3_YEAST]	3.48	5.04%	1	1	1	1	258
767	P40303	Proteasome subunit alpha type-4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE6 PE=1 SV=1 - [PSA4_YEAST]	3.78	5.51%	1	1	1	1	254

768	A5DYI1	Mitochondrial inner membrane protease ATP23 OS=Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) OX=379508 GN=ATP23 PE=3 SV=1 - [ATP23_LODEL]	2.18	5.81%	1	1	1	1	241

769	P07347	N-terminal acetyltransferase A complex catalytic subunit ARD1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARD1 PE=1 SV=2 - [ARD1_YEAST]	3.66	5.46%	1	1	1	1	238
770	P39931	Protein SSP120 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSP120 PE=1 SV=1 - [SS120_YEAST]	2.93	5.13%	1	1	1	1	234

771	A6ZUS8	rRNA-processing protein EFG1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=EFG1 PE=3 SV=1 - [EFG1P_YEAS7]	3.87	6.44%	1	1	1	1	233
772	B3LIN5	Golgi to ER traffic protein 1 OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=GET1 PE=3 SV=1 - [GET1_YEAS1]	3.21	5.96%	1	1	1	1	235
773	P40007	Nucleolar protein 16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP16 PE=1 SV=1 - [NOP16_Y	2.83	5.19%	1	1	1	1	231

774	P38771	Ribosome-recycling factor, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRF1 PE=1 SV=1 - [RRF1_YEAST]	2.13	5.22%	1	1	1	1	230
775	P25349	Flavoprotein-like protein YCP4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YCP4 PE=1 SV=1 - [YCP4_YEAST]	3.71	6.88%	1	1	1	1	247

776	Q12040	Broad-specificity phosphatase YOR283W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YOR283W PE=1 SV=1 - [YO283_YEAST]	2.54	7.83%	1	1	1	1	230
777	P53093	Protein YIP4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YIP4 PE=1 SV=2 - [YIP4_YEAST]	2.14	5.11%	1	1	1	1	235

778	P00447	Superoxide dismutase [Mn], mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SOD2 PE=1 SV=1 - [SODM_YEAST]	3.35	6.01%	1	1	1	1	233
779	P40302	Proteasome subunit alpha type-6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE5 PE=1 SV=1 - [PSA6_YEAST]	3.62	6.41%	1	1	1	1	234

780	P53927	Ribosome biogenesis protein 15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP15 PE=1 SV=1 - [NOP15_Y	2.6	4.09%	1	1	1	1	220
781	P22214	Protein transport protein SEC22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC22 PE=1 SV=1 - [SEC22_YEAST]	3.72	7.48%	1	1	1	1	214

782	P13298	Orotate phosphoribosyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=URA5 PE=1 SV=2 - [PYRE_YEAST]	2.87	7.52%	1	1	1	1	226
783	A6ZYI0	Adenylate kinase OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ADK1 PE=3 SV=1 - [KAD2_YEAS7]	2.88	4.05%	2	1	1	1	222

784	P33754	Translocation protein SEC66 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC66 PE=1 SV=1 - [SEC66_YEAST]	2.12	5.34%	1	1	1	1	206
785	P39704	Protein ERP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERP2 PE=1 SV=1 - [ERP2_YEAST]	4.22	12.09%	1	1	1	1	215

786	Q07915	Ribosome biogenesis protein RLP24 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RLP24 PE=1 SV=1 - [RLP24_YEAST]	2.99	5.03%	1	1	1	1	199
787	P39715	Shuttling pre-60S factor ECM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ECM1 PE=1 SV=2 - [ECM1_YEAST]	2.29	4.72%	1	1	1	1	212

788	P47149	Kinetochore-associated protein NNF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NNF1 PE=1 SV=3 - [NNF1_YEAST]	2.53	8.46%	1	1	1	1	201
789	P35723	Endoplasmic reticulum transmembrane protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YET1 PE=1 SV=2 - [YET1_YEAST]	2.58	12.62%	1	1	1	1	206

790	O13547	Covalently-linked cell wall protein 14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCW14 PE=1 SV=1 - [CCW14_	3.88	7.98%	1	1	1	1	238
791	O94646	Mediator of RNA polymerase II transcription subunit 8 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=med8 PE=1 SV=1 - [MED8_SCHPO]	2.65	13.00%	1	1	1	1	200

792	P08067	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RIP1 PE=1 SV=1 - [UCRI_YEAST]	2.72	4.19%	1	1	1	1	215
793	P32803	Endosomal protein P24B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMP24 PE=1 SV=1 - [EMP24_YEAST]	3.06	6.90%	1	1	1	1	203

794	P01123	GTP-binding protein YPT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPT1 PE=1 SV=2 - [YPT1_YEAST]	2.47	5.34%	1	1	1	1	206
795	P06780	GTP-binding protein RHO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RHO1 PE=1 SV=3 - [RHO1_YEAST]	3.21	4.78%	1	1	1	1	209

796	Q12434	Rho GDP-dissociation inhibitor OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RDI1 PE=1 SV=1 - [GDIR_YEAST]	3.53	10.40%	1	1	1	1	202
797	Q02196	Adenylyl-sulfate kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET14 PE=1 SV=1 - [KAPS_YEAST]	3.2	6.44%	3	1	1	1	202

798	P41920	Ran-specific GTPase-activating protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YRB1 PE=1 SV=1 - [YRB1_YEAST]	3.85	5.47%	1	1	1	1	201
799	P09457	ATP synthase subunit 5, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP5 PE=1 SV=1 - [ATPO_YEAST]	3.6	6.13%	1	1	1	1	212

800	Q08873	Transgelin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCP1 PE=1 SV=1 - [SCP1_YEAST]	3.46	7.00%	1	1	1	1	200
801	P20791	Ras-related protein Rab-8B OS=Dictyostelium discoideum OX=44689 GN=rab8B PE=2 SV=1 - [RAB8B_DICDI]	2.77	5.42%	3	1	1	1	203

802	P25451	Proteasome subunit beta type-3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PUP3 PE=1 SV=1 - [PSB3_YEAST]	2.78	7.80%	1	1	1	1	205
803	P32471	Elongation factor 1-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EFB1 PE=1 SV=4 - [EF1B_YEAST]	2.65	5.34%	1	1	1	1	206

804	P34222	Peptidyl-tRNA hydrolase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PTH2 PE=1 SV=2 - [PTH2_YEAST]	2.32	5.29%	1	1	1	1	208
805	P52286	Suppressor of kinetochore protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SKP1 PE=1 SV=2 - [SKP1_YEAST]	3.05	12.89%	1	1	1	1	194

806	P32899	U3 small nucleolar ribonucleoprotein protein IMP3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMP3 PE=1 SV=1 - [IMP3_YEAST]	2.95	8.20%	1	1	1	1	183
807	Q12447	Polyamine N-acetyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PAA1 PE=1 SV=1 - [PAA1_YEAST]	2.98	4.71%	1	1	1	1	191

808	P53600	Coatomer subunit zeta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RET3 PE=1 SV=1 - [COPZ_YEAST]	2.91	7.41%	1	1	1	1	189
809	P19073	Cell division control protein 42 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC42 PE=1 SV=2 - [CDC42_Y	3.11	5.24%	2	1	1	1	191

810	Q12133	Signal peptidase complex subunit SPC3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SPC3 PE=1 SV=1 - [SPC3_YEAST]	2.26	7.07%	1	1	1	1	184
811	Q12335	Protoplast secreted protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PST2 PE=1 SV=1 - [PST2_YEAST]	2.21	4.55%	1	1	1	1	198

812	Q08687	Translation machinery-associated protein 16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA16 PE=1 SV=2 - [TMA16_YEAST]	2.64	6.74%	1	1	1	1	178
813	Q05933	Actin-related protein 2/3 complex subunit 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARC18 PE=1 SV=1 - [ARPC3_YEAST]	4.13	7.30%	1	1	1	1	178

814	Q08962	60S ribosome subunit biogenesis protein NIP7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NIP7 PE=1 SV=1 - [NIP7_YEAST]	2.14	5.52%	1	1	1	1	181
815	Q06975	H/ACA ribonucleoprotein complex subunit gar1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=gar1 PE=2 SV=1 - [GAR1_SCHPO]	4.01	6.70%	2	1	1	1	194

816	P33204	Actin-related protein 2/3 complex subunit 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARC19 PE=1 SV=2 - [ARPC4_YEAST]	3.87	9.36%	1	1	1	1	171
817	P53633	Prenylated Rab acceptor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YIP3 PE=1 SV=2 - [PRA1_YEAST]	2.28	6.25%	1	1	1	1	176

818	P47019	Ribosome biogenesis protein ALB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALB1 PE=1 SV=1 - [ALB1_YEAST]	5.25	14.29%	1	1	1	1	175
819	P38013	Peroxiredoxin AHP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AHP1 PE=1 SV=4 - [AHP1_YEAST]	4.44	9.66%	1	1	1	1	176

820	Q03083	Uncharacterized protein YPL034W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPL034W PE=4 SV=1 - [YP034_YEAST]	2.13	7.27%	1	1	1	1	165
821	P40581	Glutathione peroxidase-like peroxiredoxin HYR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HYR1 PE=1 SV=1 - [GPX3_YEAST]	4.15	11.66%	1	1	1	1	163

822	P40548	HSP70 co-chaperone SNL1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SNL1 PE=1 SV=1 - [SNL1_YEAST]	3.98	10.69%	1	1	1	1	159
823	A6ZPB3	Cap-associated protein CAF20 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=CAF20 PE=3 SV=1 - [CAF20_YEAS7]	2.57	18.01%	2	1	1	1	161

824	Q07914	Mitochondrial import inner membrane translocase subunit TIM14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PAM18 PE=1 SV=1 - [TIM14_YEAST]	5.53	8.93%	1	1	1	1	168
825	P37263	UPF0743 protein YCR087C-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YCR087C-A PE=1 SV=1 - [YC16_YEAST]	2.39	5.88%	1	1	1	1	153

826	P40515	Mitochondrial fission 1 protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FIS1 PE=1 SV=1 - [FIS1_YEAST]	2.45	9.68%	1	1	1	1	155
827	P32495	H/ACA ribonucleoprotein complex subunit NHP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NHP2 PE=1 SV=2 - [NHP2_YEAST]	2.72	8.97%	1	1	1	1	156

828	P40030	Ergosterol biosynthetic protein 28 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG28 PE=1 SV=1 - [ERG28_YEAST]	3.35	8.11%	1	1	1	1	148
829	P40540	ER membrane protein complex subunit 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMC5 PE=1 SV=1 - [EMC5_YEAST]	3.83	9.22%	1	1	1	1	141

830	Q03048	Cofilin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COF1 PE=1 SV=1 - [COFI_YEAST]	4.73	11.89%	2	1	1	1	143
831	P00445	Superoxide dismutase [Cu-Zn] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SOD1 PE=1 SV=2 - [SODC_YEAST]	3.19	11.04%	1	1	1	1	154

832	A5DWE2	Histone H3.1/H3.2 OS=Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) OX=379508 GN=HHT1 PE=3 SV=1 - [H31_LODEL]	2.16	5.15%	3	1	1	1	136
833	P25361	Uncharacterized protein YCR043C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YCR043C PE=1 SV=1 - [YCT3_YEAST]	2.29	9.45%	1	1	1	1	127

834	P46964	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OST2 PE=1 SV=3 - [OST2_YEAST]	4.43	13.08%	1	1	1	1	130
835	P00128	Cytochrome b-c1 complex subunit 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=QCR7 PE=1 SV=2 - [QCR7_YEAST]	4.96	13.39%	1	1	1	1	127

836	P32463	Acyl carrier protein, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACP1 PE=1 SV=1 - [ACPM_YEAST]	2.23	12.80%	1	1	1	1	125
837	P32529	DNA-directed RNA polymerase I subunit RPA12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPA12 PE=1 SV=1 - [RPA12_YEAST]	3.47	12.00%	1	1	1	1	125

838	P40312	Cytochrome b5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYB5 PE=1 SV=2 - [CYB5_YEAST]	2.48	10.83%	1	1	1	1	120
839	Q04201	CUE domain-containing protein CUE4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CUE4 PE=1 SV=1 - [CUE4_YEAST]	5.68	23.93%	1	1	1	1	117

840	P00044	Cytochrome c iso-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYC1 PE=1 SV=2 - [CYC1_YEAST]	4.98	15.60%	1	1	1	1	109
841	P0CX27	60S ribosomal protein L42-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL42A PE=1 SV=1 - [RL44A_YEAST]	2.38	7.55%	2	1	1	1	106

842	P20081	FK506-binding protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FPR1 PE=1 SV=2 - [FKBP_YEAST]	4.22	13.16%	2	1	1	1	114
843	P02309	Histone H4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HHF1 PE=1 SV=2 - [H4_YEAST]	2.63	11.65%	2	1	1	1	103

844	P38203	U6 snRNA-associated Sm-like protein LSm2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LSM2 PE=1 SV=1 - [LSM2_YEAST]	2.64	13.68%	1	1	1	1	95
845	P52871	Protein transport protein SBH2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SBH2 PE=1 SV=1 - [SC6B2_YEAST]	3	14.77%	1	1	1	1	88

846	Q3E834	Protein transport protein YOS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YOS1 PE=1 SV=1 - [YOS1_YEAST]	4.07	18.82%	1	1	1	1	85
847	P04039	Cytochrome c oxidase polypeptide VIII, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COX8 PE=1 SV=2 - [COX8_YEAST]	2.26	12.82%	1	1	1	1	78

848	P35179	Protein transport protein SSS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSS1 PE=1 SV=2 - [SC61G_YEAST]	2.96	12.50%	1	1	1	1	80
849	P35997	40S ribosomal protein S27-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS27A PE=1 SV=1 - [RS27A_YEAST]	2.35	8.54%	2	1	1	1	82

850	P0CT04	Protease B inhibitor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PBI2 PE=1 SV=1 - [IPB2_YEAST]	5.01	22.67%	2	1	1	1	75
851	A5Z2X5	UPF0495 protein YPR010C-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPR010C-A PE=3 SV=1 - [YP010_YEAST]	3.6	22.22%	1	1	1	1	72

852	P40422	DNA-directed RNA polymerases I, II, and III subunit RPABC4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPC10 PE=1 SV=1 - [RPAB4_YEAST]	5.22	28.57%	1	1	1	1	70
853	Q3E7Z5	Uncharacterized protein YIL002W-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YIL002W-A PE=1 SV=1 - [YI002_YEAST]	2.91	14.49%	1	1	1	1	69