	accession	descriptior	score	cover	# pro	# unique p	#pep	#PSM	AA
1	P02994	Elongation factor 1-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TEF1 PE=1 SV=1 - [EF1A_YEAST]	619.19	41.27%	4	14	14	175	458
2	P00549	Pyruvate kinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC19 PE=1 SV=2 - [KPYK1_YEAST]	592.11	81.00%	5	35	35	173	500

3	P10664	60S ribosomal protein L4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL4A PE=1 SV=4 - [RL4A_YEAST]	434.66	50.55%	2	15	15	119	362
4	P00359	Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TDH3 PE=1 SV=3 - [G3P3_YEAST]	382.47	74.70%	2	9	21	111	332

5	P32324	Elongation factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EFT1 PE=1 SV=1 - [EF2_YEAST]	379.72	52.14%	2	35	35	109	842
6	P00358	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TDH2 PE=1 SV=3 - [G3P2_YEAST]	245.53	70.18%	2	3	16	75	332

7	P16521	Elongation factor 3A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YEF3 PE=1 SV=4 - [EF3A_YEAST]	202.41	32.28%	4	27	27	62	1044
8	P05030	Plasma membrane ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMA1 PE=1 SV=2 - [PMA1_YEAST]	210.84	26.80%	2	20	20	56	918

9	P00560	Phosphoglycerate kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PGK1 PE=1 SV=2 - [PGK_YEAST]	196.89	62.74%	2	25	25	55	416
10	P14126	60S ribosomal protein L3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL3 PE=1 SV=4 - [RL3_YEAST]	185.15	38.24%	2	15	15	54	387

11	P0CX50	60S ribosomal protein L18-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL18B PE=1 SV=1 - [RL18B_YEAST]	161.61	42.47%	1	8	8	46	186
12	P05750	40S ribosomal protein S3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS3 PE=1 SV=5 - [RS3_YEAST]	159.94	50.42%	1	12	12	46	240

13	P06169	Pyruvate decarboxylase isozyme 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDC1 PE=1 SV=7 - [PDC1_YEAST]	154.48	37.30%	2	14	15	44	563
14	P0CX39	40S ribosomal protein S8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS8A PE=1 SV=1 - [RS8A_YEAST]	132	41.00%	1	7	7	42	200

15	P0CX37	40S ribosomal protein S6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS6A PE=1 SV=1 - [RS6A_YEAST]	145.24	44.92%	1	14	14	41	236
16	P24000	60S ribosomal protein L24-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL24B PE=1 SV=1 - [RL24B_YEAST]	142.12	23.23%	1	1	4	41	155

17	P0CX23	60S ribosomal protein L20-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL20A PE=1 SV=1 - [RL20A_YEAST]	134.53	37.79%	1	9	9	40	172
18	P25443	40S ribosomal protein S2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS2 PE=1 SV=3 - [RS2_YEAST]	172.86	40.16%	1	7	7	39	254

19	P07259	Protein URA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=URA2 PE=1 SV=5 - [PYR1_YEAST]	124.67	14.81%	2	25	25	39	2214
20	P38720	6-phosphogluconate dehydrogenase, decarboxylating 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GND1 PE=1 SV=1 - [6PGD1_YEAST]	112.19	27.40%	2	12	12	38	489

21	P00950	Phosphoglycerate mutase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPM1 PE=1 SV=3 - [PMG1_YEAST]	113.75	45.75%	1	13	13	37	247
22	P05740	60S ribosomal protein L17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL17A PE=1 SV=4 - [RL17A_YEAST]	132	45.65%	1	1	7	36	184

23	P14120	60S ribosomal protein L30 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL30 PE=1 SV=3 - [RL30_YEAST]	125.09	59.05%	2	6	6	35	105
24	P05737	60S ribosomal protein L7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL7A PE=1 SV=3 - [RL7A_YEAST]	115.46	42.62%	3	10	10	35	244

25	P0CX41	60S ribosomal protein L23-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL23A PE=1 SV=1 - [RL23A_YEAST]	108.48	41.61%	1	7	7	35	137
26	P46990	60S ribosomal protein L17-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL17B PE=1 SV=2 - [RL17B_YEAST]	124.64	45.65%	1	1	7	33	184

27	P0CX35	40S ribosomal protein S4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS4A PE=1 SV=1 - [RS4A_YEAST]	107.14	45.59%	1	12	12	33	261
28	P29453	60S ribosomal protein L8-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL8B PE=1 SV=3 - [RL8B_YEAST]	109.34	44.53%	1	3	11	32	256

29	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]	107.32	56.74%	1	12	12	32	319
30	B3RHV0	40S ribosomal protein S1-A OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RPS1A PE=3 SV=1 - [RS3A1_YEAS1]	99.56	40.39%	1	4	9	32	255

31	P11484	Ribosome-associated molecular chaperone SSB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSB1 PE=1 SV=3 - [SSB1_YEAST]	111.65	49.43%	2	2	19	31	613
32	P02407	40S ribosomal protein S17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS17A PE=1 SV=1 - [RS17A_YEAST]	104.9	51.47%	2	9	9	31	136

33	P0CX45	60S ribosomal protein L2-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL2A PE=1 SV=1 - [RL2A_YEAST]	100.94	45.67%	2	10	10	31	254
34	B3LLJ2	40S ribosomal protein S1-B OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RPS1B PE=3 SV=1 - [RS3A2_YEAS1]	93.4	39.61%	3	3	8	30	255

35	P40150	Ribosome-associated molecular chaperone SSB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSB2 PE=1 SV=2 - [SSB2_YEAST]	105.72	47.31%	1	1	18	29	613
36	P02406	60S ribosomal protein L28 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL28 PE=1 SV=3 - [RL28_YEAST]	86.41	35.57%	1	7	7	29	149

37	P0CX26	60S ribosomal protein L43-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL43B PE=1 SV=1 - [RL43B_YEAST]	110.47	43.48%	1	5	5	28	92
38	P0CX83	60S ribosomal protein L19-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL19B PE=1 SV=1 - [RL19B_YEAST]	101.41	21.16%	1	5	5	28	189

39	P06168	Ketol-acid reductoisomerase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV5 PE=1 SV=1 - [ILV5_YEAST]	96.34	36.20%	1	11	11	28	395
40	Q01855	40S ribosomal protein S15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS15 PE=1 SV=1 - [RS15_YEAST]	86.31	42.25%	1	5	5	28	142

41	P04449	60S ribosomal protein L24-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL24A PE=1 SV=1 - [RL24A_YEAST]	98.39	23.23%	2	2	5	27	155
42	P17076	60S ribosomal protein L8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL8A PE=1 SV=4 - [RL8A_YEAST]	93.15	39.45%	1	2	10	27	256

43	P0CX47	40S ribosomal protein S11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS11A PE=1 SV=1 - [RS11A_YEAST]	89.34	60.90%	1	9	9	27	156
44	Q02326	60S ribosomal protein L6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL6A PE=1 SV=2 - [RL6A_YEAST]	81.21	39.77%	1	6	9	27	176

45	P38219	Obg-like ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OLA1 PE=1 SV=1 - [OLA1_YEAST]	89.96	38.83%	1	13	13	26	394
46	P16861	ATP-dependent 6-phosphofructokinase subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PFK1 PE=1 SV=1 - [PFKA1_YEAST]	88.95	23.20%	1	19	19	26	987

47	P00360	Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TDH1 PE=1 SV=3 - [G3P1_YEAST]	84.49	35.84%	1	2	8	25	332
48	P38701	40S ribosomal protein S20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS20 PE=1 SV=3 - [RS20_YEAST]	84.09	78.51%	1	12	12	25	121

49	P05756	40S ribosomal protein S13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS13 PE=1 SV=3 - [RS13_YEAST]	74.43	53.64%	1	8	8	25	151
50	P05739	60S ribosomal protein L6-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL6B PE=1 SV=4 - [RL6B_YEAST]	73.8	43.18%	1	5	8	25	176

51	Q00955	Acetyl-CoA carboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACC1 PE=1 SV=2 - [ACAC_YEAST]	82.04	12.72%	6	20	20	24	2233
52	P26321	60S ribosomal protein L5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL5 PE=1 SV=4 - [RL5_YEAST]	84.02	38.05%	1	8	8	23	297

53	P41940	Mannose-1-phosphate guanyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PSA1 PE=1 SV=2 - [MPG1_YEAST]	83.29	25.21%	1	6	7	23	361
54	P05755	40S ribosomal protein S9-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS9B PE=1 SV=4 - [RS9B_YEAST]	62.1	45.64%	2	9	9	23	195

55	P0CX43	60S ribosomal protein L1-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL1A PE=1 SV=1 - [RL1A_YEAST]	79.33	22.58%	2	6	6	22	217
56	P23254	Transketolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TKL1 PE=1 SV=4 - [TKT1_YEAST]	70.24	26.47%	2	15	15	22	680

57	P06367	40S ribosomal protein S14-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS14A PE=1 SV=5 - [RS14A_YEAST]	75.9	45.26%	3	9	9	21	137
58	P40024	ABC transporter ATP-binding protein ARB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARB1 PE=1 SV=1 - [ARB1_YEAST]	74.36	26.56%	1	13	13	21	610

59	P05317	60S acidic ribosomal protein P0 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP0 PE=1 SV=2 - [RLA0_YE	71.19	22.12%	1	6	6	21	312
60	P07149	Fatty acid synthase subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAS1 PE=1 SV=2 - [FAS1_YEAST]	69.87	10.97%	1	16	16	21	2051

61	P0CX53	60S ribosomal protein L12-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL12A PE=1 SV=1 - [RL12A_YEAST]	66.78	47.27%	1	6	6	21	165
62	P49167	60S ribosomal protein L38 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL38 PE=1 SV=1 - [RL38_YEAST]	64.65	33.33%	1	3	3	21	78

63	P41805	60S ribosomal protein L10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL10 PE=1 SV=1 - [RL10_YEAST]	63.77	52.04%	1	11	11	21	221
64	P0C2H6	60S ribosomal protein L27-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL27A PE=1 SV=1 - [RL27A_YEAST]	63.3	43.38%	2	7	7	21	136

65	P26785	60S ribosomal protein L16-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL16B PE=1 SV=3 - [RL16B_YEAST]	61.72	24.24%	1	3	6	21	198
66	P39015	Suppressor protein STM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STM1 PE=1 SV=3 - [STM1_YEAST]	78.95	28.94%	1	4	4	20	273

67	P40212	60S ribosomal protein L13-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL13B PE=1 SV=1 - [RL13B_YEAST]	76.01	35.68%	3	7	7	20	199
68	P16862	ATP-dependent 6-phosphofructokinase subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PFK2 PE=1 SV=4 - [PFKA2_YEAST]	74.8	18.35%	1	10	10	20	959

69	P19097	Fatty acid synthase subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAS2 PE=1 SV=2 - [FAS2_YEAST]	69.22	13.78%	2	18	18	20	1887
70	P26783	40S ribosomal protein S5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS5 PE=1 SV=3 - [RS5_YEAST]	58.91	24.44%	1	6	6	20	225

71	P0C0W1	40S ribosomal protein S22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS22A PE=1 SV=2 - [RS22A_YEAST]	75.05	53.08%	3	7	7	19	130
72	P0CX84	60S ribosomal protein L35-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL35A PE=1 SV=1 - [RL35A_YEAST]	70.54	42.50%	1	8	8	19	120

73	P07342	Acetolactate synthase catalytic subunit, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV2 PE=1 SV=1 - [ILVB_YEAST]	70.39	22.85%	1	12	12	19	687
74	P32527	Zuotin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ZUO1 PE=1 SV=1 - [ZUO1_YEAST]	68.67	36.72%	1	11	11	19	433

75	P38625	GMP synthase [glutamine-hydrolyzing] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GUA1 PE=1 SV=4 - [GUAA_YEAST]	68.22	25.33%	2	12	12	19	525
76	P38788	Ribosome-associated complex subunit SSZ1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSZ1 PE=1 SV=2 - [SSZ1_YEAST]	71.34	33.46%	1	12	12	18	538

77	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]	59.17	17.55%	2	14	14	18	1071
78	P07280	40S ribosomal protein S19-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS19A PE=1 SV=2 - [RS19A_YEAST]	58.19	50.69%	2	7	7	18	144

79	P04456	60S ribosomal protein L25 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL25 PE=1 SV=4 - [RL25_YEAST]	61.4	44.37%	1	6	6	17	142
80	P51401	60S ribosomal protein L9-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL9B PE=1 SV=1 - [RL9B_YEAST]	59.25	35.60%	2	6	6	17	191

81	P02400	60S acidic ribosomal protein P2-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP2B PE=1 SV=2 - [RLA4_YEAST]	54.39	34.55%	1	5	5	17	110
82	P37291	Serine hydroxymethyltransferase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SHM2 PE=1 SV=2 - [GLYC_YEAST]	57.51	26.23%	2	11	11	16	469

83	P00925	Enolase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ENO2 PE=1 SV=2 - [ENO2_YEAST]	57.42	44.39%	3	13	13	16	437
84	P15108	ATP-dependent molecular chaperone HSC82 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSC82 PE=1 SV=4 - [HSC82_YEAST]	56.18	22.98%	5	13	13	16	705

85	A6ZRX0	ATP-dependent RNA helicase DBP2 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP2 PE=3 SV=1 - [DBP2_YEAS7]	54.55	20.51%	4	8	9	16	546
86	P10592	Heat shock protein SSA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSA2 PE=1 SV=3 - [HSP72_YEAST]	53.2	27.54%	4	10	11	16	639

87	P0CX32	40S ribosomal protein S24-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS24B PE=1 SV=1 - [RS24B_YEAST]	44.12	27.41%	1	5	5	16	135
88	Q08972	[NU+] prion formation protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NEW1 PE=1 SV=1 - [NEW1_YEAST]	54.58	13.55%	1	13	13	15	1196

89	A6ZP47	ATP-dependent RNA helicase DED1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DED1 PE=3 SV=1 - [DED1_YEAS7]	49.34	22.35%	8	10	11	15	604
90	P48589	40S ribosomal protein S12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS12 PE=1 SV=1 - [RS12_YEAST]	42.28	46.85%	1	7	7	15	143

91	P0C0T4	40S ribosomal protein S25-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS25B PE=1 SV=1 - [RS25B_YEAST]	40.55	33.33%	3	4	4	15	108
92	P06105	Protein SCP160 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCP160 PE=1 SV=3 - [SC160_YEAST]	47.72	14.57%	1	11	12	14	1222

93	P52910	Acetyl-coenzyme A synthetase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACS2 PE=1 SV=1 - [ACS2_YEAST]	47.26	17.28%	1	10	10	14	683
94	B3LT19	40S ribosomal protein S0-B OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RPS0B PE=3 SV=1 - [RSSA2_YEAS1]	46.55	32.14%	4	5	5	14	252

95	O14455	60S ribosomal protein L36-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL36B PE=1 SV=3 - [RL36B_YEAST]	44.68	42.00%	2	7	7	14	100
96	P53221	60S ribosomal protein L26-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL26B PE=1 SV=2 - [RL26B_YEAST]	41.99	44.09%	2	9	9	14	127

97	P0CX55	40S ribosomal protein S18-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS18A PE=1 SV=1 - [RS18A_YEAST]	41.95	49.32%	1	9	9	14	146
98	P0C2H8	60S ribosomal protein L31-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL31A PE=1 SV=1 - [RL31A_YEAST]	54.03	40.71%	2	5	5	13	113

99	P46784	40S ribosomal protein S10-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS10B PE=1 SV=1 - [RS10B_YEAST]	41.81	43.81%	2	3	3	13	105
100	P28274	CTP synthase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=URA7 PE=1 SV=2 - [URA7_YEAST]	41.2	15.54%	1	9	9	13	579

101	P26784	60S ribosomal protein L16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL16A PE=1 SV=3 - [RL16A_YEAST]	38.48	24.12%	1	2	5	13	199
102	P48164	40S ribosomal protein S7-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS7B PE=1 SV=1 - [RS7B_YEAST]	44.48	37.37%	1	3	6	12	190

103	A6ZPE5	Nucleolar protein 58 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NOP58 PE=3 SV=1 - [NOP58_Y	43.86	26.22%	3	10	10	12	511
104	P38934	Nuclear segregation protein BFR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BFR1 PE=1 SV=1 - [BFR1_YE	40.3	24.04%	1	8	8	12	470

105	P07251	ATP synthase subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP1 PE=1 SV=5 - [ATPA_YEAST]	38.84	20.55%	1	9	9	12	545
106	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]	38.68	15.77%	1	11	11	12	964

107	P07245	C-1-tetrahydrofolate synthase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE3 PE=1 SV=1 - [C1TC_YEAST]	37.4	14.90%	1	12	12	12	946
108	P27476	Nuclear localization sequence-binding protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NSR1 PE=1 SV=1 - [NSR1_YEAST]	37.07	28.02%	1	7	7	12	414

109	P38061	60S ribosomal protein L32 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL32 PE=1 SV=1 - [RL32_YEAST]	36.1	36.92%	1	6	6	12	130
110	Q03195	Translation initiation factor RLI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RLI1 PE=1 SV=1 - [RLI1_YEAST]	34.9	17.43%	1	9	9	12	608

111	P26786	40S ribosomal protein S7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS7A PE=1 SV=4 - [RS7A_YEAST]	39.9	49.47%	1	4	7	11	190
112	A6ZY89	Pentafunctional AROM polypeptide OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ARO1 PE=3 SV=1 - [ARO1_YEAS7]	37.65	10.20%	6	10	10	11	1588

113	P0CX51	40S ribosomal protein S16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS16A PE=1 SV=1 - [RS16A_YEAST]	36.65	42.66%	3	5	5	11	143
114	P28777	Chorismate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARO2 PE=1 SV=1 - [AROC_YEAST]	36.58	26.60%	1	7	7	11	376

115	A6ZWL1	Nascent polypeptide-associated complex subunit beta-1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=EGD1 PE=3 SV=1 - [NACB1_YEAS7]	35.21	29.30%	1	3	3	11	157
116	P47079	T-complex protein 1 subunit theta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT8 PE=1 SV=1 - [TCPQ_YEAST]	33.73	21.48%	1	9	9	11	568

117	P00330	Alcohol dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADH1 PE=1 SV=5 - [ADH1_YEAST]	33.41	22.70%	4	7	7	11	348
118	Q12460	Nucleolar protein 56 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP56 PE=1 SV=1 - [NOP56_Y	36.35	15.87%	1	7	7	10	504

119	P19882	Heat shock protein 60, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP60 PE=1 SV=1 - [HSP60_YEAST]	35.55	19.58%	1	8	8	10	572
120	P23301	Eukaryotic translation initiation factor 5A-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HYP2 PE=1 SV=3 - [IF5A1_YEAST]	33.33	16.56%	2	4	4	10	157

121	P14742	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GFA1 PE=1 SV=4 - [GFA1_YEAST]	33.2	11.44%	1	6	6	10	717
122	P05748	60S ribosomal protein L15-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL15A PE=1 SV=3 - [RL15A_YEAST]	32.37	23.04%	1	2	4	10	204

123	P00927	Threonine dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV1 PE=1 SV=2 - [THDH_YEAST]	32.18	21.70%	1	9	9	10	576
124	P05744	60S ribosomal protein L33-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL33A PE=1 SV=3 - [RL33A_YEAST]	29.66	45.79%	1	2	6	10	107

125	P40525	60S ribosomal protein L34-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL34B PE=1 SV=1 - [RL34B_YEAST]	29.12	20.66%	2	2	2	10	121
126	P14540	Fructose-bisphosphate aldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FBA1 PE=1 SV=3 - [ALF_YEAST]	38.76	24.51%	1	6	6	9	359

127	P50095	Inosine-5'-monophosphate dehydrogenase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMD3 PE=1 SV=1 - [IMDH3_YEAST]	35.41	21.99%	3	4	6	9	523
128	P32861	UTP--glucose-1-phosphate uridylyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UGP1 PE=1 SV=1 - [UGPA1_YEAST]	34.26	17.84%	1	7	7	9	499

129	P07262	NADP-specific glutamate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GDH1 PE=1 SV=2 - [DHE4_YEAST]	32.47	22.25%	3	7	7	9	454
130	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]	31.48	19.73%	1	7	7	9	527

131	P16474	Endoplasmic reticulum chaperone BiP OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KAR2 PE=1 SV=1 - [BIP_YEAST]	31.19	10.41%	2	6	7	9	682
132	P10081	ATP-dependent RNA helicase eIF4A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF1 PE=1 SV=3 - [IF4A_YEAST]	31.12	24.56%	3	7	7	9	395

133	P05759	Ubiquitin-40S ribosomal protein S31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS31 PE=1 SV=3 - [RS31_YEAST]	30.46	38.16%	2	4	6	9	152
134	P54780	60S ribosomal protein L15-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL15B PE=1 SV=2 - [RL15B_YEAST]	29.88	19.61%	1	1	3	9	204

135	Q02892	Nucleolar GTP-binding protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOG1 PE=1 SV=1 - [NOG1_YEAST]	28.91	15.15%	2	8	8	9	647
136	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]	28.87	7.45%	1	8	8	9	1664

137	P0C0W9	60S ribosomal protein L11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL11A PE=1 SV=2 - [RL11A_YEAST]	28.67	33.33%	3	5	5	9	174
138	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]	28.09	5.92%	2	7	7	9	1876

139	P36105	60S ribosomal protein L14-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL14A PE=1 SV=1 - [RL14A_YEAST]	26.72	20.29%	2	4	4	9	138
140	P40010	Nuclear GTP-binding protein NUG1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NUG1 PE=1 SV=1 - [NUG1_YEAST]	26.07	18.27%	1	7	7	9	520

141	P04147	Polyadenylate-binding protein, cytoplasmic and nuclear OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PAB1 PE=1 SV=4 - [PABP_YEAST]	25.89	21.14%	3	8	8	9	577
142	P50094	Inosine-5'-monophosphate dehydrogenase 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMD4 PE=1 SV=1 - [IMDH4_YEAST]	33.35	20.61%	1	4	6	8	524

143	P25294	Protein SIS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SIS1 PE=1 SV=1 - [SIS1_YEAST]	29.13	22.44%	1	4	4	8	352
144	Q12680	Glutamate synthase [NADH] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLT1 PE=1 SV=2 - [GLT1_YEAST]	26.94	4.94%	1	8	8	8	2145

145	P39522	Dihydroxy-acid dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV3 PE=1 SV=2 - [ILV3_YEAST]	26.13	11.62%	1	6	6	8	585
146	P39938	40S ribosomal protein S26-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS26A PE=1 SV=1 - [RS26A_YEAST]	25.65	30.25%	2	3	3	8	119

147	P16140	V-type proton ATPase subunit B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA2 PE=1 SV=2 - [VATB_YEAST]	25.46	16.05%	1	6	6	8	517
148	P38891	Branched-chain-amino-acid aminotransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BAT1 PE=1 SV=1 - [BCA1_YEAST]	25.21	27.74%	2	8	8	8	393

149	P39730	Eukaryotic translation initiation factor 5B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FUN12 PE=1 SV=2 - [IF2P_YEAST]	24.67	11.48%	1	7	7	8	1002
150	P10659	S-adenosylmethionine synthase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAM1 PE=1 SV=2 - [METK1_YEAST]	24.57	19.63%	1	2	7	8	382

151	P38879	Nascent polypeptide-associated complex subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EGD2 PE=1 SV=3 - [NACA_YEAST]	27.33	28.74%	1	3	3	7	174
152	P0C0V8	40S ribosomal protein S21-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS21A PE=1 SV=1 - [RS21A_YEAST]	24.65	50.57%	2	4	4	7	87

153	P36013	NAD-dependent malic enzyme, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAE1 PE=1 SV=1 - [MAOM_YEAST]	24.48	14.35%	1	5	5	7	669
154	P25087	Sterol 24-C-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG6 PE=1 SV=4 - [ERG6_YEAST]	24.4	21.67%	1	6	6	7	383

155	P40482	Protein transport protein SEC24 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC24 PE=1 SV=1 - [SEC24_YEAST]	23.64	8.86%	2	6	6	7	926
156	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]	23.54	14.56%	1	7	7	7	618

157	P40069	Importin subunit beta-4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KAP123 PE=1 SV=1 - [IMB4_YEAST]	21.6	8.98%	1	7	7	7	1113
158	Q03690	Clustered mitochondria protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CLU1 PE=1 SV=1 - [CLU_YEAST]	21.44	7.13%	1	7	7	7	1277

159	Q02753	60S ribosomal protein L21-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL21A PE=1 SV=1 - [RL21A_YEAST]	21.26	32.50%	1	2	5	7	160
160	P0CH08	Ubiquitin-60S ribosomal protein L40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL40A PE=1 SV=1 - [RL40A_YEAST]	20.59	27.34%	2	1	3	7	128

161	P19358	S-adenosylmethionine synthase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAM2 PE=1 SV=3 - [METK2_YEAST]	19.97	18.49%	1	2	7	7	384
162	P21954	Isocitrate dehydrogenase [NADP], mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IDP1 PE=1 SV=1 - [IDHP_YEAST]	19.95	8.88%	1	4	4	7	428

163	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]	19.93	8.78%	2	6	6	7	763
164	P41056	60S ribosomal protein L33-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL33B PE=1 SV=2 - [RL33B_YEAST]	19.25	45.79%	1	1	5	7	107

165	P05749	60S ribosomal protein L22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL22A PE=1 SV=3 - [RL22A_YEAST]	27.24	32.23%	1	2	2	6	121
166	P16467	Pyruvate decarboxylase isozyme 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDC5 PE=1 SV=4 - [PDC5_YEAST]	25.81	9.77%	2	3	4	6	563

167	P10622	60S acidic ribosomal protein P1-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP1B PE=1 SV=3 - [RLA3_YEAST]	24.07	15.09%	1	1	1	6	106
168	P15303	Protein transport protein SEC23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC23 PE=1 SV=1 - [SEC23_YEAST]	19.76	6.38%	2	5	5	6	768

169	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]	19.55	7.73%	1	5	5	6	854
170	P37292	Serine hydroxymethyltransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SHM1 PE=1 SV=2 - [GLYM_YEAST]	19.26	13.88%	2	5	5	6	490

171	P04173	3-isopropylmalate dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LEU2 PE=1 SV=4 - [LEU3_YEAST]	19.04	18.96%	3	6	6	6	364
172	P25491	Mitochondrial protein import protein MAS5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YDJ1 PE=1 SV=1 - [MAS5_YEAST]	19	16.14%	1	5	5	6	409

173	A6ZMA9	Ribosome biogenesis protein ERB1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ERB1 PE=3 SV=1 - [ERB1_YEAS7]	18.9	10.66%	4	6	6	6	807
174	P15646	rRNA 2'-O-methyltransferase fibrillarin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP1 PE=1 SV=1 - [FBRL_YEAST]	18.44	14.68%	2	4	4	6	327

175	P13663	Aspartate-semialdehyde dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOM2 PE=1 SV=1 - [DHAS_YEAST]	18.34	17.26%	1	5	5	6	365
176	P18239	ADP,ATP carrier protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PET9 PE=1 SV=2 - [ADT2_YEAST]	18.27	16.98%	3	5	5	6	318

177	Q12672	60S ribosomal protein L21-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL21B PE=1 SV=1 - [RL21B_YEAST]	18.25	33.13%	1	2	5	6	160
178	P41338	Acetyl-CoA acetyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG10 PE=1 SV=3 - [THIL_YEAST]	18.04	15.33%	2	5	5	6	398

179	P06106	Homocysteine/cysteine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET17 PE=1 SV=3 - [CYSD_YEAST]	17.87	16.89%	1	6	6	6	444
180	P12612	T-complex protein 1 subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TCP1 PE=1 SV=2 - [TCPA_YEAST]	17.72	14.49%	1	6	6	6	559

181	P48570	Homocitrate synthase, cytosolic isozyme OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS20 PE=1 SV=1 - [HOSC_YEAST]	17.6	16.59%	2	6	6	6	428
182	Q05022	rRNA biogenesis protein RRP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP5 PE=1 SV=1 - [RRP5_YEAST]	16.4	3.53%	1	5	6	6	1729

183	P39692	Sulfite reductase [NADPH] flavoprotein component OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET10 PE=1 SV=2 - [MET10_YEAST]	16.35	5.80%	1	4	5	6	1035
184	P38805	Ribosome production factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPF1 PE=1 SV=1 - [RPF1_YEAST]	22.21	15.25%	1	3	3	5	295

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]	18.96	9.01%	2	5	5	5	888
186	P02992	Elongation factor Tu, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUF1 PE=1 SV=1 - [EFTU_YEAST]	18.81	13.96%	1	4	4	5	437

187	P38708	Putative proline--tRNA ligase YHR020W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YHR020W PE=1 SV=1 - [YHI0_YEAST]	18.64	11.63%	1	5	5	5	688
188	A6ZN26	Eukaryotic translation initiation factor 3 subunit C OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NIP1 PE=3 SV=1 - [EIF3C_YEAS7]	18.43	7.51%	2	5	5	5	812

189	P19414	Aconitate hydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACO1 PE=1 SV=2 - [ACON_YEAST]	17.78	5.91%	1	3	3	5	778
190	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]	17.64	7.38%	1	5	5	5	840

191	P38861	60S ribosomal export protein NMD3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NMD3 PE=1 SV=3 - [NMD3_YEAST]	17.57	9.85%	1	4	4	5	518
192	P32368	Phosphoinositide phosphatase SAC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAC1 PE=1 SV=1 - [SAC1_YEAST]	17.56	9.47%	1	4	4	5	623

193	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]	17.4	6.90%	1	5	5	5	1203
194	P40185	Protein MMF1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MMF1 PE=1 SV=1 - [MMF1_YEAST]	17.31	52.41%	1	5	5	5	145

195	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]	16.8	14.99%	2	4	4	5	347
196	P17128	Actin OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) OX=284590 GN=ACT PE=3 SV=2 - [ACT_KLULA]	16.46	12.00%	3	3	3	5	375

197	P04801	Threonine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=THS1 PE=1 SV=2 - [SYTC_YEAST]	16.45	9.40%	1	5	5	5	734
198	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]	16.4	10.98%	1	4	4	5	437

199	P15019	Transaldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TAL1 PE=1 SV=4 - [TAL1_YEAST]	16.25	17.61%	1	4	4	5	335
200	P39076	T-complex protein 1 subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT2 PE=1 SV=1 - [TCPB_YEAST]	16.22	12.71%	1	5	5	5	527

201	P54839	Hydroxymethylglutaryl-CoA synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG13 PE=1 SV=1 - [HMCS_YEAST]	16.01	13.65%	1	5	5	5	491
202	P46655	Glutamate--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GUS1 PE=1 SV=3 - [SYEC_YEAST]	15.97	8.47%	1	5	5	5	708

203	P00830	ATP synthase subunit beta, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP2 PE=1 SV=2 - [ATPB_YEAST]	15.83	13.50%	1	5	5	5	511
204	P39078	T-complex protein 1 subunit delta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT4 PE=1 SV=2 - [TCPD_YEAST]	15.58	11.74%	1	4	4	5	528

205	P39729	Ribosome-interacting GTPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RBG1 PE=1 SV=1 - [RBG1_YEAST]	15.35	16.26%	1	4	4	5	369
206	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]	15.31	6.80%	2	4	5	5	1118

207	P32895	Ribose-phosphate pyrophosphokinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRS1 PE=1 SV=1 - [KPR1_YEAST]	14.91	13.58%	1	4	4	5	427
208	P23641	Mitochondrial phosphate carrier protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MIR1 PE=1 SV=1 - [MPCP_YEAST]	14.75	21.86%	1	5	5	5	311

209	A6ZPA9	Ribosome biogenesis protein YTM1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=YTM1 PE=3 SV=1 - [YTM1_YEAS7]	14.72	16.30%	1	5	5	5	460
210	P39079	T-complex protein 1 subunit zeta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT6 PE=1 SV=1 - [TCPZ_YEAST]	14.7	11.54%	1	4	4	5	546

211	P39986	Manganese-transporting ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SPF1 PE=1 SV=1 - [ATC6_YEAST]	14.48	4.86%	1	5	5	5	1215
212	P17064	Purine-cytosine permease FCY2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FCY2 PE=1 SV=2 - [FCY2_YEAST]	14.22	2.44%	1	1	1	5	533

213	P10614	Lanosterol 14-alpha demethylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG11 PE=1 SV=1 - [CP51_YEAST]	13.68	13.77%	3	5	5	5	530
214	P32476	Squalene monooxygenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG1 PE=1 SV=2 - [ERG1_YEAST]	13.57	6.85%	1	3	3	5	496

215	P05747	60S ribosomal protein L29 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL29 PE=1 SV=3 - [RL29_YEAST]	12.4	13.56%	1	1	1	5	59
216	Q9LIK9	ATP sulfurylase 1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=APS1 PE=1 SV=1 - [APS1_ARATH]	11.71	4.10%	1	1	1	5	463

217	P0CX27	60S ribosomal protein L42-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL42A PE=1 SV=1 - [RL44A_YEAST]	10.99	7.55%	2	1	1	5	106
218	P00942	Triosephosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPI1 PE=1 SV=2 - [TPIS_YEAST]	18.01	20.16%	1	3	3	4	248

219	P00931	Tryptophan synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRP5 PE=1 SV=1 - [TRP_YEAST]	15.96	6.65%	1	3	3	4	707
220	P07213	Mitochondrial import receptor subunit TOM70 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOM70 PE=1 SV=2 - [TOM70_YEAST]	15.78	8.59%	1	4	4	4	617

221	P49367	Homoaconitase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS4 PE=1 SV=1 - [LYS4_YEAST]	15.02	7.65%	1	4	4	4	693
222	O14467	Multiprotein-bridging factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MBF1 PE=1 SV=2 - [MBF1_YEAST]	14.38	19.21%	1	3	3	4	151

223	P07260	Eukaryotic translation initiation factor 4E OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC33 PE=1 SV=1 - [IF4E_YEAST]	14.29	18.78%	1	3	3	4	213
224	P25694	Cell division control protein 48 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC48 PE=1 SV=3 - [CDC48_Y	14.28	5.15%	1	3	3	4	835

225	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]	14.11	7.49%	1	4	4	4	694
226	P42943	T-complex protein 1 subunit eta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT7 PE=1 SV=1 - [TCPH_YEAST]	13.98	10.91%	1	4	4	4	550

227	P33322	H/ACA ribonucleoprotein complex subunit CBF5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CBF5 PE=1 SV=1 - [CBF5_YEAST]	13.97	7.25%	1	2	2	4	483
228	P38009	Bifunctional purine biosynthesis protein ADE17 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE17 PE=1 SV=2 - [PUR92_YEAST]	13.93	12.16%	2	4	4	4	592

229	P38264	SRP-independent targeting protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PHO88 PE=1 SV=1 - [PHO88_YEAST]	13.64	18.62%	1	3	3	4	188
230	P27809	Glycolipid 2-alpha-mannosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRE2 PE=1 SV=1 - [KRE2_YEAST]	13.47	10.41%	1	3	3	4	442

231	P53742	Nucleolar GTP-binding protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOG2 PE=1 SV=1 - [NOG2_YEAST]	13.47	9.67%	1	4	4	4	486
232	Q03940	RuvB-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RVB1 PE=1 SV=1 - [RUVB1_YEAST]	13.47	13.61%	2	4	4	4	463

233	Q03532	ATP-dependent RNA helicase HAS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HAS1 PE=1 SV=1 - [HAS1_YEAST]	13.35	7.72%	2	3	3	4	505
234	P54115	Magnesium-activated aldehyde dehydrogenase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALD6 PE=1 SV=4 - [ALDH6_YEAST]	13.2	11.20%	1	4	4	4	500

235	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]	13.04	3.57%	5	4	4	4	1511
236	P07560	Ras-related protein SEC4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC4 PE=1 SV=1 - [SEC4_YEAST]	12.94	18.60%	5	3	3	4	215

237	P10869	Aspartokinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOM3 PE=1 SV=2 - [AK_YEAST]	12.9	10.25%	1	4	4	4	527
238	P38910	10 kDa heat shock protein, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP10 PE=1 SV=1 - [CH10_YEAST]	12.79	57.55%	1	4	4	4	106

239	P32565	26S proteasome regulatory subunit RPN2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN2 PE=1 SV=4 - [RPN2_YEAST]	12.62	5.19%	1	4	4	4	945
240	P33892	eIF-2-alpha kinase activator GCN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCN1 PE=1 SV=1 - [GCN1_YEAST]	12.02	1.91%	1	4	4	4	2672

241	Q06205	FK506-binding protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FPR4 PE=1 SV=1 - [FKBP4_YEAST]	11.77	9.69%	2	1	2	4	392
242	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]	11.45	6.52%	1	4	4	4	767

243	P29704	Squalene synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG9 PE=1 SV=2 - [FDFT_YEAST]	11.33	9.46%	1	4	4	4	444
244	P41810	Coatomer subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC26 PE=1 SV=2 - [COPB_YEAST]	11.15	5.65%	1	4	4	4	973

245	A6ZT02	Low-affinity glucose transporter HXT4 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=HXT4 PE=3 SV=1 - [HXT4_YEAS7]	10.94	6.77%	4	3	3	4	576
246	Q08962	60S ribosome subunit biogenesis protein NIP7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NIP7 PE=1 SV=1 - [NIP7_YEAST]	9.63	16.57%	1	3	3	4	181

247	P20107	Zinc/cadmium resistance protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ZRC1 PE=1 SV=2 - [ZRC1_YEAST]	13.57	12.67%	1	3	3	3	442
248	P07991	Ornithine aminotransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CAR2 PE=1 SV=2 - [OAT_YEAST]	13.36	12.26%	1	3	3	3	424

249	P32602	Alpha-soluble NSF attachment protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC17 PE=1 SV=4 - [SEC17_YEAST]	13.35	16.10%	1	3	3	3	292
250	P40462	Protein TMA108 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA108 PE=1 SV=1 - [TM108_YEAST]	12.18	5.29%	1	3	3	3	946

251	P46985	Probable alpha-1,6-mannosyltransferase MNN11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MNN11 PE=1 SV=2 - [MNN11_YEAST]	11.93	7.35%	1	2	2	3	422
252	P07284	Serine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SES1 PE=1 SV=2 - [SYSC_YEAST]	11.59	6.28%	1	2	2	3	462

253	P40531	Protein GVP36 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GVP36 PE=1 SV=1 - [GVP36_YEAST]	11.55	11.04%	1	3	3	3	326
254	P56628	60S ribosomal protein L22-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL22B PE=1 SV=2 - [RL22B_YEAST]	11.45	32.79%	1	2	2	3	122

255	P36049	rRNA-processing protein EBP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EBP2 PE=1 SV=1 - [EBP2_YEAST]	11.32	7.96%	1	3	3	3	427
256	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]	11.17	15.16%	1	3	3	3	244

257	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]	11.11	19.31%	1	2	2	3	145
258	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]	11.06	8.26%	1	2	2	3	339

259	A6ZUA1	ATP-dependent RNA helicase DBP3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP3 PE=3 SV=1 - [DBP3_YEAS7]	10.81	7.84%	2	3	3	3	523
260	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]	10.63	7.14%	1	2	2	3	420

261	P05319	60S acidic ribosomal protein P2-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP2A PE=1 SV=1 - [RLA2_YEAST]	10.59	65.09%	1	3	3	3	106
262	P0C0X0	40S ribosomal protein S28-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS28B PE=1 SV=1 - [RS28B_YEAST]	10.56	31.34%	3	2	2	3	67

263	P38911	FK506-binding nuclear protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FPR3 PE=1 SV=2 - [FKBP3_YEAST]	10.5	9.25%	2	1	2	3	411
264	P32466	Low-affinity glucose transporter HXT3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HXT3 PE=1 SV=1 - [HXT3_YEAST]	10.41	8.82%	1	3	3	3	567

265	P32327	Pyruvate carboxylase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PYC2 PE=1 SV=2 - [PYC2_YEAST]	10.12	3.22%	2	3	3	3	1180
266	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]	10.05	5.24%	1	3	3	3	802

267	P38779	Proteasome-interacting protein CIC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CIC1 PE=1 SV=1 - [CIC1_YEAST]	10.04	11.70%	1	3	3	3	376
268	P22137	Clathrin heavy chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CHC1 PE=1 SV=1 - [CLH_YEAST]	9.83	2.24%	1	3	3	3	1653

269	P00899	Anthranilate synthase component 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRP2 PE=1 SV=4 - [TRPE_YEAST]	9.8	8.68%	1	3	3	3	507
270	Q12176	Ribosome biogenesis protein MAK21 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAK21 PE=1 SV=1 - [MAK21_YEAST]	9.7	4.39%	1	3	3	3	1025

271	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]	9.62	11.08%	1	3	3	3	370
272	P26637	Leucine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC60 PE=1 SV=1 - [SYLC_YEAST]	9.46	3.94%	1	3	3	3	1090

273	P32386	ATP-dependent bile acid permease OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YBT1 PE=1 SV=2 - [YBT1_YEAST]	9.4	2.41%	1	3	3	3	1661
274	P32911	Eukaryotic translation initiation factor eIF-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUI1 PE=1 SV=1 - [SUI1_YEAST]	9.38	14.81%	1	2	2	3	108

275	P14906	Protein translocation protein SEC63 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC63 PE=1 SV=2 - [SEC63_YEAST]	9.34	4.98%	1	3	3	3	663
276	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]	9.29	7.47%	1	3	3	3	482

277	P41921	Glutathione reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLR1 PE=1 SV=2 - [GSHR_YEAST]	9.29	8.07%	2	3	3	3	483
278	P21264	Phosphoribosylaminoimidazole carboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE2 PE=1 SV=1 - [PUR6_YEAST]	9.18	4.90%	1	2	3	3	571

279	Q04947	Reticulon-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RTN1 PE=1 SV=1 - [RTN1_YEAST]	9.14	10.85%	1	3	3	3	295
280	P40413	T-complex protein 1 subunit epsilon OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT5 PE=1 SV=3 - [TCPE_YEAST]	9	6.58%	1	3	3	3	562

281	P23542	Aspartate aminotransferase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AAT2 PE=1 SV=3 - [AATC_YEAST]	8.88	10.29%	1	3	3	3	418
282	P54783	D-arabinono-1,4-lactone oxidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALO1 PE=1 SV=1 - [ALO_YEAST]	8.81	7.41%	1	3	3	3	526

283	P40850	Protein MKT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MKT1 PE=1 SV=2 - [MKT1_YEAST]	8.61	3.73%	1	3	3	3	830
284	P32074	Coatomer subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC21 PE=1 SV=2 - [COPG_YEAST]	8.61	3.64%	1	3	3	3	935

285	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]	8.59	4.82%	2	3	3	3	685
286	A6ZRM0	Adenylosuccinate synthetase OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ADE12 PE=3 SV=1 - [PURA_YEAS7]	8.59	8.78%	4	3	3	3	433

287	P34167	Eukaryotic translation initiation factor 4B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF3 PE=1 SV=1 - [IF4B_YEAST]	8.53	2.98%	1	1	1	3	436
288	P15705	Heat shock protein STI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STI1 PE=1 SV=1 - [STI1_YEAST]	8.5	7.47%	1	3	3	3	589

289	P40825	Alanine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALA1 PE=1 SV=3 - [SYA_YEAST]	8.49	3.66%	1	3	3	3	983
290	Q12449	Hsp90 co-chaperone AHA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AHA1 PE=1 SV=1 - [AHA1_YEAST]	8.46	9.43%	1	3	3	3	350

291	P20424	Signal recognition particle subunit SRP54 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRP54 PE=1 SV=2 - [SRP54_YEAST]	8.17	2.22%	1	1	1	3	541
292	P49090	Asparagine synthetase [glutamine-hydrolyzing] 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ASN2 PE=1 SV=2 - [ASNS2_YEAST]	8.12	6.64%	1	2	3	3	572

293	P04802	Aspartate--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DPS1 PE=1 SV=3 - [SYDC_YEAST]	8.06	5.75%	1	3	3	3	557
294	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]	7.94	6.56%	1	2	2	3	366

295	P11076	ADP-ribosylation factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARF1 PE=1 SV=3 - [ARF1_YEAST]	7.92	10.50%	3	2	2	3	181
296	Q07362	Protein PBP4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PBP4 PE=1 SV=1 - [PBP4_YEAST]	7.87	23.24%	1	3	3	3	185

297	Q01662	Methionine aminopeptidase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAP1 PE=1 SV=2 - [MAP1_YEAST]	7.87	4.91%	1	2	2	3	387
298	A6ZVM6	NADH-cytochrome b5 reductase 1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=CBR1 PE=3 SV=2 - [NCB5R_YEAS7]	7.87	11.27%	2	3	3	3	284

299	P05694	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET6 PE=1 SV=4 - [METE_YEAST]	7.66	4.82%	1	3	3	3	767
300	P41057	40S ribosomal protein S29-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS29A PE=1 SV=3 - [RS29A_YEAST]	7.16	35.71%	2	3	3	3	56

301	Q03862	Probable metalloprotease ARX1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARX1 PE=1 SV=1 - [ARX1_YEAST]	6.56	4.72%	1	2	2	3	593
302	P47019	Ribosome biogenesis protein ALB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALB1 PE=1 SV=1 - [ALB1_YEAST]	10.13	14.29%	1	1	1	2	175

303	Q06705	Phosphatidylinositol transfer protein CSR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CSR1 PE=1 SV=1 - [CSR1_YEAST]	9.54	8.33%	1	2	2	2	408
304	P35725	Uncharacterized protein YKL063C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YKL063C PE=1 SV=1 - [YKG3_YEAST]	9.48	21.56%	1	1	1	2	167

305	P53883	Nucleolar protein 13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP13 PE=1 SV=2 - [NOP13_Y	8.93	10.92%	1	2	2	2	403
306	P39990	13 kDa ribonucleoprotein-associated protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SNU13 PE=1 SV=1 - [SNU13_YEAST]	8.79	17.46%	2	1	1	2	126

307	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]	8.68	2.59%	1	2	2	2	1237
308	P38998	Saccharopine dehydrogenase [NAD(+), L-lysine-forming] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS1 PE=1 SV=3 - [LYS1_YEAST]	8.62	8.04%	1	2	2	2	373

309	Q07824	Polyamine transporter 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPO1 PE=1 SV=1 - [TPO1_YEAST]	8.48	5.63%	1	2	2	2	586
310	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]	8.43	4.29%	1	2	2	2	700

311	P12709	Glucose-6-phosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PGI1 PE=1 SV=3 - [G6PI_YEAST]	8.25	5.23%	2	2	2	2	554
312	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]	8.17	6.26%	1	2	2	2	431

313	Q05359	Protein ERP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERP1 PE=1 SV=1 - [ERP1_YEAST]	8.16	13.70%	1	2	2	2	219
314	P32352	C-8 sterol isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG2 PE=1 SV=1 - [ERG2_YEAST]	8.02	13.06%	1	2	2	2	222

315	P32468	Cell division control protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC12 PE=1 SV=1 - [CDC12_Y	7.89	7.37%	1	2	2	2	407
316	P35180	Mitochondrial import receptor subunit TOM20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOM20 PE=1 SV=1 - [TOM20_YEAST]	7.76	18.03%	1	2	2	2	183

317	A6ZV85	Pescadillo homolog OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NOP7 PE=3 SV=1 - [PESC_YEAS7]	7.7	5.29%	1	2	2	2	605
318	A6ZPB3	Cap-associated protein CAF20 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=CAF20 PE=3 SV=1 - [CAF20_YEAS7]	7.69	24.84%	2	2	2	2	161

319	P53235	Eukaryotic translation initiation factor 2A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YGR054W PE=1 SV=1 - [EIF2A_YEAST]	7.63	4.67%	1	2	2	2	642
320	O74302	Transposon Ty1-DR4 Gag polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TY1A-DR4 PE=2 SV=1 - [YD13A_YEAST]	7.34	3.41%	50	1	1	2	440

321	P36008	Elongation factor 1-gamma 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TEF4 PE=1 SV=1 - [EF1G2_YEAST]	7.33	7.77%	1	2	2	2	412
322	P07263	Histidine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HTS1 PE=1 SV=2 - [SYH_YEAST]	7.23	2.56%	1	1	1	2	546

323	Q12265	Ribose-phosphate pyrophosphokinase 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRS5 PE=1 SV=1 - [KPR5_YEAST]	7.21	6.05%	1	2	2	2	496
324	P53723	UPF0674 endoplasmic reticulum membrane protein YNR021W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YNR021W PE=1 SV=3 - [YN8B_YEAST]	7.2	6.44%	1	2	2	2	404

325	P20606	Small COPII coat GTPase SAR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAR1 PE=1 SV=1 - [SAR1_YEAST]	7.14	13.68%	1	2	2	2	190
326	P14832	Peptidyl-prolyl cis-trans isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CPR1 PE=1 SV=3 - [CYPH_YEAST]	7.12	17.90%	1	2	2	2	162

327	P25567	RNA-binding protein SRO9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRO9 PE=1 SV=2 - [SRO9_YEAST]	7.12	8.29%	1	2	2	2	434
328	P39676	Flavohemoprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YHB1 PE=1 SV=2 - [FHP_YEAST]	7.11	8.02%	1	2	2	2	399

329	P51996	GTP-binding protein YPT32/YPT11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPT32 PE=1 SV=3 - [YPT32_YEAST]	7.05	11.71%	2	2	2	2	222
330	Q05911	Adenylosuccinate lyase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE13 PE=1 SV=1 - [PUR8_YEAST]	6.97	4.56%	1	2	2	2	482

331	P32263	Pyrroline-5-carboxylate reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRO3 PE=1 SV=1 - [P5CR_YEAST]	6.91	8.74%	1	2	2	2	286
332	P53845	Protein transport protein YIF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YIF1 PE=1 SV=1 - [YIF1_YEAST]	6.82	4.46%	1	1	1	2	314

333	P04037	Cytochrome c oxidase subunit 4, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COX4 PE=1 SV=1 - [COX4_YEAST]	6.76	23.23%	1	2	2	2	155
334	P40517	Ran-specific GTPase-activating protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YRB2 PE=1 SV=1 - [YRB2_YEAST]	6.76	9.48%	1	2	2	2	327

335	P38817	ADP-ribosylation factor-binding protein GGA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GGA2 PE=1 SV=1 - [GGA2_YEAST]	6.75	5.81%	1	2	2	2	585
336	P07806	Valine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VAS1 PE=1 SV=2 - [SYV_YEAST]	6.75	2.36%	1	2	2	2	1104

337	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]	6.68	5.45%	1	2	2	2	440
338	P38333	Essential nuclear protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ENP1 PE=1 SV=1 - [ENP1_YEAST]	6.56	4.97%	1	2	2	2	483

339	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]	6.52	12.98%	1	2	2	2	285
340	Q04697	Glucose-signaling factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GSF2 PE=1 SV=1 - [GSF2_YEAST]	6.44	6.95%	1	2	2	2	403

341	P31353	Phosphomannomutase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PMM1 PE=1 SV=1 - [PMM_CANAL]	6.43	4.37%	2	1	1	2	252
342	P40495	Homoisocitrate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS12 PE=1 SV=1 - [LYS12_YEAST]	6.41	5.93%	1	2	2	2	371

343	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]	6.41	12.25%	1	2	2	2	204
344	A6ZNQ1	ATP-dependent RNA helicase DBP5 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP5 PE=3 SV=1 - [DBP5_YEAS7]	6.4	6.22%	1	2	2	2	482

345	P40581	Glutathione peroxidase-like peroxiredoxin HYR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HYR1 PE=1 SV=1 - [GPX3_YEAST]	6.39	8.59%	1	2	2	2	163
346	P39940	E3 ubiquitin-protein ligase RSP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RSP5 PE=1 SV=1 - [RSP5_YEAST]	6.28	4.45%	1	2	2	2	809

347	A6ZL22	Cell wall protein ECM33 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ECM33 PE=3 SV=2 - [ECM33_YEAS7]	6.27	5.83%	4	2	2	2	429
348	Q00245	GTP-binding protein RHO3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RHO3 PE=1 SV=2 - [RHO3_YEAST]	6.22	10.39%	2	2	2	2	231

349	P32332	Mitochondrial oxaloacetate transport protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OAC1 PE=1 SV=1 - [OAC1_YEAST]	6.17	7.41%	1	2	2	2	324
350	P09440	C-1-tetrahydrofolate synthase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MIS1 PE=1 SV=1 - [C1TM_YEAST]	6.11	2.46%	1	2	2	2	975

351	P40302	Proteasome subunit alpha type-6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE5 PE=1 SV=1 - [PSA6_YEAST]	6.09	12.39%	1	2	2	2	234
352	P41807	V-type proton ATPase subunit H OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA13 PE=1 SV=1 - [VATH_YEAST]	6.01	5.02%	1	2	2	2	478

353	P41277	Glycerol-1-phosphate phosphohydrolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPP1 PE=1 SV=3 - [GPP1_YEAST]	6.01	11.20%	2	2	2	2	250
354	Q12166	2-isopropylmalate synthase 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LEU9 PE=1 SV=1 - [LEU9_YEAST]	5.99	4.80%	2	2	2	2	604

355	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]	5.98	16.37%	1	2	2	2	171
356	P40078	Ribosome biogenesis protein NSA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NSA2 PE=1 SV=1 - [NSA2_YEAST]	5.92	13.79%	3	2	2	2	261

357	P39744	Nucleolar complex protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOC2 PE=1 SV=2 - [NOC2_YEAST]	5.92	3.52%	1	2	2	2	710
358	P40693	Ribosome biogenesis protein RLP7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RLP7 PE=1 SV=1 - [RLP7_YEAST]	5.91	8.70%	1	2	2	2	322

359	P38431	Eukaryotic translation initiation factor 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF5 PE=1 SV=1 - [IF5_YEAST]	5.88	5.93%	1	2	2	2	405
360	P32598	Serine/threonine-protein phosphatase PP1-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLC7 PE=1 SV=1 - [PP12_YEAST]	5.83	5.13%	1	1	1	2	312

361	P16603	NADPH--cytochrome P450 reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NCP1 PE=1 SV=3 - [NCPR_YEAST]	5.79	3.47%	2	2	2	2	691
362	P09624	Dihydrolipoyl dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LPD1 PE=1 SV=1 - [DLDH_YEAST]	5.78	5.41%	1	2	2	2	499

363	P31373	Cystathionine gamma-lyase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYS3 PE=1 SV=2 - [CYS3_YEAST]	5.77	7.11%	1	2	2	2	394
364	Q04013	Citrate/oxoglutarate carrier protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YHM2 PE=1 SV=1 - [YHM2_YEAST]	5.73	3.82%	1	1	1	2	314

365	P35844	Oxysterol-binding protein homolog 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KES1 PE=1 SV=1 - [KES1_YEAST]	5.66	4.61%	1	2	2	2	434
366	P14020	Dolichol-phosphate mannosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DPM1 PE=1 SV=3 - [DPM1_YEAST]	5.56	7.49%	1	2	2	2	267

367	P43588	Ubiquitin carboxyl-terminal hydrolase RPN11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN11 PE=1 SV=1 - [RPN11_YEAST]	5.55	8.82%	2	2	2	2	306
368	P39077	T-complex protein 1 subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT3 PE=1 SV=2 - [TCPG_YEAST]	5.52	4.31%	1	2	2	2	534

369	P53337	ER-derived vesicles protein ERV29 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERV29 PE=1 SV=1 - [ERV29_YEAST]	5.49	7.74%	1	2	2	2	310
370	P41058	40S ribosomal protein S29-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS29B PE=1 SV=3 - [RS29B_YEAST]	5.44	14.29%	1	1	1	2	56

371	P39976	D-2-hydroxyglutarate--pyruvate transhydrogenase DLD3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DLD3 PE=1 SV=1 - [DLD3_YEAST]	5.41	5.44%	1	2	2	2	496
372	P32803	Endosomal protein P24B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMP24 PE=1 SV=1 - [EMP24_YEAST]	5.4	5.91%	1	1	1	2	203

373	P00958	Methionine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MES1 PE=1 SV=4 - [SYMC_YEAST]	5.32	3.60%	1	2	2	2	751
374	P09734	Tubulin alpha-3 chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUB3 PE=1 SV=1 - [TBA3_YEAST]	5.28	4.72%	1	1	1	2	445

375	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]	5.28	11.04%	1	2	2	2	335
376	P21576	Vacuolar protein sorting-associated protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VPS1 PE=1 SV=2 - [VPS1_YEAST]	5.22	3.41%	1	2	2	2	704

377	P38221	Phosphatidate cytidylyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDS1 PE=1 SV=1 - [CDS1_YEAST]	5.16	4.16%	1	2	2	2	457
378	P31382	Dolichyl-phosphate-mannose--protein mannosyltransferase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMT2 PE=1 SV=2 - [PMT2_YEAST]	5.11	3.29%	1	2	2	2	759

379	Q752H4	Mannose-1-phosphate guanyltransferase OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=MPG1 PE=3 SV=1 - [MPG1_ASHGO]	5.09	9.97%	1	1	2	2	361
380	P36160	Ribosome biogenesis protein RPF2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPF2 PE=1 SV=1 - [RPF2_YEAST]	5.09	6.10%	1	2	2	2	344

381	P35691	Translationally-controlled tumor protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA19 PE=1 SV=1 - [TCTP_YEAST]	5.06	11.98%	1	2	2	2	167
382	P18759	Vesicular-fusion protein SEC18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC18 PE=1 SV=2 - [SEC18_YEAST]	5.05	3.56%	2	2	2	2	758

383	P20484	Protein MAK11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAK11 PE=1 SV=2 - [MAK11_YEAST]	5.04	5.56%	1	2	2	2	414
384	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]	5.02	9.81%	4	2	2	2	214

385	P07246	Alcohol dehydrogenase 3, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADH3 PE=1 SV=2 - [ADH3_YEAST]	5.01	5.33%	1	2	2	2	375
386	P39533	Homocitrate dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACO2 PE=1 SV=1 - [ACON2_YEAST]	4.89	3.17%	1	2	2	2	789

387	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]	4.88	9.54%	1	2	2	2	304
388	P33201	Ribosome assembly factor MRT4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MRT4 PE=1 SV=1 - [MRT4_YEAST]	4.82	6.78%	2	2	2	2	236

389	Q12159	RNA annealing protein YRA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YRA1 PE=1 SV=2 - [YRA1_YEAST]	4.67	8.85%	1	2	2	2	226
390	Q04225	Ribosome assembly protein RRB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRB1 PE=1 SV=1 - [RRB1_YEAST]	4.66	6.07%	1	2	2	2	511

391	P53145	Large subunit GTPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LSG1 PE=1 SV=1 - [LSG1_YEAST]	4.5	3.13%	1	2	2	2	640
392	P49089	Asparagine synthetase [glutamine-hydrolyzing] 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ASN1 PE=1 SV=2 - [ASNS1_YEAST]	4.45	3.67%	1	1	2	2	572

393	P39960	GTPase-activating protein BEM2/IPL2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BEM2 PE=1 SV=1 - [BEM2_YEAST]	5.97	1.38%	1	1	1	1	2167
394	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]	5.72	28.57%	1	1	1	1	70

395	A6ZTA3	Pre-rRNA-processing protein RIX1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=RIX1 PE=3 SV=1 - [RIX1_YEAS7]	5.33	2.49%	2	1	1	1	763
396	P47089	Translation machinery-associated protein 22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA22 PE=1 SV=1 - [DENR_YEAST]	5.12	8.59%	1	1	1	1	198

397	P38736	Golgi SNAP receptor complex member 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GOS1 PE=1 SV=1 - [GOSR1_YEAST]	5.02	7.62%	1	1	1	1	223
398	P22214	Protein transport protein SEC22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC22 PE=1 SV=1 - [SEC22_YEAST]	4.98	7.48%	1	1	1	1	214

399	Q04201	CUE domain-containing protein CUE4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CUE4 PE=1 SV=1 - [CUE4_YEAST]	4.97	23.93%	1	1	1	1	117
400	P32582	Cystathionine beta-synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYS4 PE=1 SV=1 - [CBS_YEAST]	4.94	3.35%	1	1	1	1	507

401	Q06338	Protein BCP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BCP1 PE=1 SV=1 - [BCP1_YEAST]	4.93	6.01%	1	1	1	1	283
402	P15180	Lysine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRS1 PE=1 SV=2 - [SYKC_YEAST]	4.86	2.71%	1	1	1	1	591

403	P09733	Tubulin alpha-1 chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUB1 PE=1 SV=2 - [TBA1_YEAST]	4.78	4.70%	1	1	1	1	447
404	P38426	Trehalose synthase complex regulatory subunit TPS3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPS3 PE=1 SV=3 - [TPS3_YEAST]	4.77	1.80%	1	1	1	1	1054

405	P38789	Ribosome biogenesis protein SSF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSF1 PE=1 SV=1 - [SSF1_YEAST]	4.76	3.53%	2	1	1	1	453
406	P05318	60S acidic ribosomal protein P1-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP1A PE=1 SV=4 - [RLA1_YEAST]	4.62	20.75%	1	1	1	1	106

407	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]	4.51	1.04%	1	1	1	1	1733
408	P32802	Transmembrane 9 superfamily member 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMP70 PE=1 SV=2 - [TMN1_YEAST]	4.49	2.55%	1	1	1	1	667

409	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]	4.47	1.29%	1	1	1	1	1319
410	P53045	Methylsterol monooxygenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG25 PE=1 SV=1 - [MSMO_YEAST]	4.47	4.85%	1	1	1	1	309

411	P38707	Asparagine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DED81 PE=1 SV=1 - [SYNC_YEAST]	4.45	2.53%	1	1	1	1	554
412	P39007	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STT3 PE=1 SV=2 - [STT3_YEAST]	4.42	2.51%	1	1	1	1	718

413	P39727	ER-derived vesicles protein ERV46 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERV46 PE=1 SV=2 - [ERV46_YEAST]	4.3	3.37%	1	1	1	1	415
414	Q3E834	Protein transport protein YOS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YOS1 PE=1 SV=1 - [YOS1_YEAST]	4.3	18.82%	1	1	1	1	85

415	P53297	PAB1-binding protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PBP1 PE=1 SV=1 - [PBP1_YEAST]	4.28	2.08%	1	1	1	1	722
416	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]	4.22	1.59%	1	1	1	1	817

417	Q05016	NADP-dependent 3-hydroxy acid dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YMR226C PE=1 SV=1 - [YM71_YEAST]	4.19	5.24%	1	1	1	1	267
418	P17505	Malate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MDH1 PE=1 SV=2 - [MDHM_YEAST]	4.14	4.19%	1	1	1	1	334

419	P43555	Protein EMP47 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMP47 PE=1 SV=1 - [EMP47_YEAST]	4.12	2.70%	1	1	1	1	445
420	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]	4.11	16.09%	1	1	1	1	87

421	P25342	Cell division control protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC10 PE=1 SV=1 - [CDC10_Y	4.08	4.04%	1	1	1	1	322
422	P29311	Protein BMH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BMH1 PE=1 SV=4 - [BMH1_YEAST]	4.06	5.24%	1	1	1	1	267

423	P37303	Low specificity L-threonine aldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLY1 PE=1 SV=2 - [GLY1_YEAST]	4.02	3.62%	1	1	1	1	387
424	Q99207	Nucleolar complex protein 14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP14 PE=1 SV=1 - [NOP14_Y	4.02	1.60%	1	1	1	1	810

425	Q12136	Something about silencing protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAS10 PE=1 SV=1 - [SAS10_Y	4.01	2.62%	1	1	1	1	610
426	P32791	Ferric/cupric reductase transmembrane component 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FRE1 PE=1 SV=1 - [FRE1_YEAST]	3.99	2.04%	1	1	1	1	686

427	P53889	Uncharacterized mitochondrial hydrolase FMP41 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FMP41 PE=1 SV=1 - [FMP41_YEAST]	3.98	10.04%	1	1	1	1	259
428	P04840	Mitochondrial outer membrane protein porin 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=POR1 PE=1 SV=4 - [VDAC1_YEAST]	3.98	4.24%	1	1	1	1	283

429	P38013	Peroxiredoxin AHP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AHP1 PE=1 SV=4 - [AHP1_YEAST]	3.96	11.36%	1	1	1	1	176
430	Q12754	Ribosomal RNA-processing protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP12 PE=1 SV=1 - [RRP12_YEAST]	3.94	2.28%	1	1	1	1	1228

431	A6ZZR2	RNA polymerase II degradation factor 1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DEF1 PE=3 SV=1 - [DEF1_YEAS7]	3.86	3.00%	3	1	1	1	733
432	P08417	Fumarate hydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FUM1 PE=1 SV=2 - [FUMH_YEAST]	3.84	3.07%	1	1	1	1	488

433	Q06287	Ribosomal RNA small subunit methyltransferase NEP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMG1 PE=1 SV=1 - [NEP1_YEAST]	3.81	5.16%	1	1	1	1	252
434	P53914	RNA cytidine acetyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRE33 PE=1 SV=1 - [NAT10_YEAST]	3.75	1.42%	1	1	1	1	1056

435	P25367	[PIN+] prion protein RNQ1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RNQ1 PE=1 SV=2 - [RNQ1_YEAST]	3.74	4.20%	1	1	1	1	405
436	P38077	ATP synthase subunit gamma, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP3 PE=1 SV=1 - [ATPG_YEAST]	3.73	4.18%	1	1	1	1	311

437	Q02895	Putative aryl-alcohol dehydrogenase AAD16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AAD16 PE=1 SV=1 - [AAD16_YEAST]	3.71	4.39%	1	1	1	1	342
438	P49095	Glycine dehydrogenase (decarboxylating), mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCV2 PE=1 SV=1 - [GCSP_YEAST]	3.7	1.26%	1	1	1	1	1034

439	P21243	Proteasome subunit alpha type-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCL1 PE=1 SV=1 - [PSA1_YEAST]	3.69	5.16%	1	1	1	1	252
440	Q12117	Protein MRH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MRH1 PE=1 SV=1 - [MRH1_YEAST]	3.67	5.31%	1	1	1	1	320

441	P41819	Dimethyladenosine transferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DIM1 PE=3 SV=1 - [DIM1_YEAST]	3.67	4.72%	2	1	1	1	318
442	Q08689	N-alpha-acetyltransferase NAT5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NAT5 PE=1 SV=1 - [NAT5_YEAST]	3.66	7.95%	1	1	1	1	176

443	Q02931	NET1-associated nuclear protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NAN1 PE=1 SV=1 - [UTP17_YEAST]	3.66	2.34%	1	1	1	1	896
444	P38972	Phosphoribosylformylglycinamidine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE6 PE=1 SV=2 - [PUR4_YEAST]	3.65	1.18%	1	1	1	1	1358

445	P22147	5'-3' exoribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=XRN1 PE=1 SV=1 - [XRN1_YEAST]	3.63	0.92%	1	1	1	1	1528
446	P00424	Cytochrome c oxidase polypeptide 5A, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COX5A PE=1 SV=1 - [COX5A_YEAST]	3.6	9.80%	1	1	1	1	153

447	Q01939	26S proteasome regulatory subunit 8 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT6 PE=1 SV=4 - [PRS8_YEAST]	3.58	3.95%	1	1	1	1	405
448	P25045	Serine palmitoyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LCB1 PE=1 SV=2 - [LCB1_YEAST]	3.56	2.33%	1	1	1	1	558

449	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]	3.55	1.58%	1	1	1	1	887
450	Q07915	Ribosome biogenesis protein RLP24 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RLP24 PE=1 SV=1 - [RLP24_YEAST]	3.54	5.03%	1	1	1	1	199

451	A6ZRK4	Cysteine proteinase 1, mitochondrial OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=LAP3 PE=3 SV=2 - [BLH1_YEAS7]	3.53	3.52%	3	1	1	1	483
452	Q06218	ATP-dependent RNA helicase DBP9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DBP9 PE=1 SV=1 - [DBP9_YEAST]	3.51	2.53%	1	1	1	1	594

453	P07172	Histidinol-phosphate aminotransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HIS5 PE=3 SV=2 - [HIS8_YEAST]	3.44	3.64%	1	1	1	1	385
454	P38689	Ribose-phosphate pyrophosphokinase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRS3 PE=1 SV=1 - [KPR3_YEAST]	3.41	3.75%	1	1	1	1	320

455	P25574	ER membrane protein complex subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMC1 PE=1 SV=1 - [EMC1_YEAST]	3.41	1.97%	1	1	1	1	760
456	P40348	Replication factor C subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RFC2 PE=1 SV=1 - [RFC2_YEAST]	3.38	4.25%	1	1	1	1	353

457	P0CX33	40S ribosomal protein S30-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS30A PE=1 SV=1 - [RS30A_YEAST]	3.38	15.87%	1	1	1	1	63
458	P12684	3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HMG2 PE=1 SV=1 - [HMDH2_YEAST]	3.37	1.34%	2	1	1	1	1045

459	P38968	Protein transport protein SEC31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC31 PE=1 SV=3 - [SEC31_YEAST]	3.36	1.26%	1	1	1	1	1273
460	P33775	Dolichyl-phosphate-mannose--protein mannosyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMT1 PE=1 SV=1 - [PMT1_YEAST]	3.36	1.71%	1	1	1	1	817

461	P43593	Ubiquitin carboxyl-terminal hydrolase 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UBP6 PE=1 SV=1 - [UBP6_YEAST]	3.35	3.21%	1	1	1	1	499
462	Q07451	Endoplasmic reticulum transmembrane protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YET3 PE=1 SV=1 - [YET3_YEAST]	3.32	6.40%	1	1	1	1	203

463	A6ZUT6	Protein PXR1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=PXR1 PE=3 SV=1 - [PXR1_YEAS7]	3.31	4.80%	2	1	1	1	271
464	Q99297	Mitochondrial 2-oxodicarboxylate carrier 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ODC2 PE=1 SV=1 - [ODC2_YEAST]	3.31	4.89%	1	1	1	1	307

465	P25043	Proteasome subunit beta type-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PUP1 PE=1 SV=1 - [PSB2_YEAST]	3.3	4.60%	1	1	1	1	261
466	P06780	GTP-binding protein RHO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RHO1 PE=1 SV=3 - [RHO1_YEAST]	3.3	4.78%	1	1	1	1	209

467	P38166	Protein transport protein SFT2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SFT2 PE=1 SV=1 - [SFT2_YEAST]	3.29	5.58%	1	1	1	1	215
468	P34232	mRNA transport regulator MTR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MTR2 PE=1 SV=1 - [MTR2_YEAST]	3.29	9.24%	1	1	1	1	184

469	Q00764	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 56 kDa subunit OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPS1 PE=1 SV=2 - [TPS1_YEAST]	3.28	3.23%	1	1	1	1	495
470	P25293	Nucleosome assembly protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NAP1 PE=1 SV=2 - [NAP1_YEAST]	3.28	4.08%	1	1	1	1	417

471	P02309	Histone H4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HHF1 PE=1 SV=2 - [H4_YEAST]	3.26	11.65%	2	1	1	1	103
472	P23585	High-affinity glucose transporter HXT2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HXT2 PE=1 SV=1 - [HXT2_YEAST]	3.25	2.03%	1	1	1	1	541

473	P0CS90	Heat shock protein SSC1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSC1 PE=1 SV=1 - [HSP77_YEAST]	3.25	1.83%	2	1	1	1	654
474	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]	3.23	4.32%	2	1	1	1	301

475	P02557	Tubulin beta chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUB2 PE=1 SV=2 - [TBB_YEA	3.23	3.28%	1	1	1	1	457
476	P53326	Uncharacterized protein YGR266W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YGR266W PE=1 SV=1 - [YG5L_YEAST]	3.22	2.14%	1	1	1	1	701

477	Q06103	26S proteasome regulatory subunit RPN7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN7 PE=1 SV=3 - [RPN7_YEAST]	3.19	5.13%	1	1	1	1	429
478	P35179	Protein transport protein SSS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSS1 PE=1 SV=2 - [SC61G_YEAST]	3.19	12.50%	1	1	1	1	80

479	P32288	Glutamine synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLN1 PE=1 SV=4 - [GLNA_YE	3.17	4.86%	1	1	1	1	370
480	P53011	Nucleoporin SEH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEH1 PE=1 SV=1 - [SEH1_YEAST]	3.17	3.15%	1	1	1	1	349

481	O13563	26S proteasome regulatory subunit RPN13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN13 PE=1 SV=1 - [RPN13_YEAST]	3.15	8.33%	1	1	1	1	156
482	P04046	Amidophosphoribosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE4 PE=1 SV=2 - [PUR1_YEAST]	3.14	2.16%	2	1	1	1	510

483	Q12377	26S proteasome regulatory subunit RPN6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN6 PE=1 SV=3 - [RPN6_YEAST]	3.13	2.76%	1	1	1	1	434
484	P38256	Uncharacterized protein YBR096W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YBR096W PE=1 SV=1 - [YBU6_YEAST]	3.13	5.22%	1	1	1	1	230

485	P14743	Glycylpeptide N-tetradecanoyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NMT1 PE=1 SV=1 - [NMT_YEAST]	3.12	3.74%	1	1	1	1	455
486	Q04991	Protein FMP42 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FMP42 PE=1 SV=1 - [FMP42_YEAST]	3.11	3.37%	1	1	1	1	504

487	P31688	Trehalose-phosphatase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPS2 PE=1 SV=3 - [TPS2_YEAST]	3.11	1.23%	1	1	1	1	896
488	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]	3.1	3.68%	1	1	1	1	326

489	P38206	Oligosaccharide translocation protein RFT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RFT1 PE=1 SV=1 - [RFT1_YEAST]	3.09	2.44%	1	1	1	1	574
490	P47154	CAAX prenyl protease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STE24 PE=1 SV=1 - [STE24_YEAST]	3.09	2.21%	1	1	1	1	453

491	Q12522	Eukaryotic translation initiation factor 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF6 PE=1 SV=1 - [IF6_YEAST]	3.06	5.71%	1	1	1	1	245
492	P31539	Heat shock protein 104 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP104 PE=1 SV=2 - [HS104_YEAST]	3.05	1.54%	1	1	1	1	908

493	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]	3.05	3.00%	1	1	1	1	367
494	P32471	Elongation factor 1-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EFB1 PE=1 SV=4 - [EF1B_YEAST]	3.05	5.34%	1	1	1	1	206

495	P13586	Calcium-transporting ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMR1 PE=1 SV=1 - [ATC1_YEAST]	3.05	1.68%	1	1	1	1	950
496	P00410	Cytochrome c oxidase subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COX2 PE=1 SV=1 - [COX2_YEAST]	3.05	6.77%	1	1	1	1	251

497	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]	3.04	0.68%	1	1	1	1	1769
498	A6ZQE9	Alpha-1,2-mannosyltransferase MNN5 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=MNN5 PE=3 SV=1 - [MNN5_YEAS7]	3.04	2.39%	2	1	1	1	586

499	P39935	Eukaryotic initiation factor 4F subunit p150 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF4631 PE=1 SV=2 - [IF4F1_YEAST]	3.01	1.47%	1	1	1	1	952
500	Q99288	Broad-range acid phosphatase DET1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DET1 PE=1 SV=1 - [DET1_YEAST]	3	6.89%	1	1	1	1	334

501	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
502	P41920	Ran-specific GTPase-activating protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YRB1 PE=1 SV=1 - [YRB1_YEAST]	2.99	5.47%	1	1	1	1	201

503	A6ZR73	High osmolarity signaling protein SHO1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=SHO1 PE=3 SV=1 - [SHO1_YEAS7]	2.98	4.09%	6	1	1	1	367
504	P40312	Cytochrome b5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYB5 PE=1 SV=2 - [CYB5_YEAST]	2.95	10.83%	1	1	1	1	120

505	P40007	Nucleolar protein 16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP16 PE=1 SV=1 - [NOP16_Y	2.95	5.19%	1	1	1	1	231
506	P38954	Inositolphosphotransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IPT1 PE=1 SV=2 - [IPT1_YEAST]	2.94	2.85%	1	1	1	1	527

507	P25358	Elongation of fatty acids protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ELO2 PE=1 SV=1 - [ELO2_YEAST]	2.93	2.88%	1	1	1	1	347
508	P23644	Mitochondrial import receptor subunit TOM40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOM40 PE=1 SV=1 - [TOM40_YEAST]	2.92	4.13%	1	1	1	1	387

509	Q12000	Translation machinery-associated protein 46 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA46 PE=1 SV=2 - [TMA46_YEAST]	2.91	2.90%	1	1	1	1	345
510	P19073	Cell division control protein 42 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC42 PE=1 SV=2 - [CDC42_Y	2.91	5.24%	2	1	1	1	191

511	P00546	Cyclin-dependent kinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC28 PE=1 SV=1 - [CDK1_YEAST]	2.89	3.69%	1	1	1	1	298
512	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]	2.88	4.49%	1	1	1	1	312

513	P32892	ATP-dependent RNA helicase DRS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DRS1 PE=1 SV=2 - [DRS1_YEAST]	2.88	1.60%	2	1	1	1	752
514	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]	2.87	4.15%	1	1	1	1	265

515	P40327	26S proteasome regulatory subunit 4 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT2 PE=1 SV=3 - [PRS4_YEAST]	2.86	2.75%	1	1	1	1	437
516	P23639	Proteasome subunit alpha type-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE8 PE=1 SV=1 - [PSA2_YEAST]	2.86	4.80%	1	1	1	1	250

517	P00937	Multifunctional tryptophan biosynthesis protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRP3 PE=1 SV=2 - [TRPG_YEAST]	2.85	2.69%	1	1	1	1	484
518	Q12207	Non-classical export protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NCE102 PE=1 SV=1 - [NCE2_YEAST]	2.85	7.51%	1	1	1	1	173

519	Q08965	Ribosome biogenesis protein BMS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BMS1 PE=1 SV=1 - [BMS1_YEAST]	2.84	1.10%	1	1	1	1	1183
520	A6ZU71	Ribosome biogenesis protein NSA1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NSA1 PE=3 SV=1 - [NSA1_YEAS7]	2.84	2.59%	2	1	1	1	463

521	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]	2.83	2.95%	1	1	1	1	713
522	P53756	ABC transporter ATP-binding protein/permease PDR18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDR18 PE=1 SV=1 - [PDR18_YEAST]	2.83	0.75%	2	1	1	1	1333

523	P38353	Sec sixty-one protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSH1 PE=1 SV=1 - [SSH1_YEAST]	2.83	2.86%	1	1	1	1	490
524	P31116	Homoserine dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOM6 PE=1 SV=1 - [DHOM_YEAST]	2.83	3.34%	1	1	1	1	359

525	P25605	Acetolactate synthase small subunit, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV6 PE=1 SV=2 - [ILV6_YEAST]	2.79	4.53%	1	1	1	1	309
526	P53903	Processing of GAS1 and ALP protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PGA2 PE=1 SV=3 - [PGA2_YEAST]	2.78	10.08%	1	1	1	1	129

527	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]	2.77	0.90%	1	1	1	1	1224
528	Q08237	RNA exonuclease 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=REX4 PE=1 SV=1 - [REXO4_YEAST]	2.76	4.50%	1	1	1	1	289

529	P36015	Synaptobrevin homolog YKT6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YKT6 PE=1 SV=1 - [YKT6_YEAST]	2.76	9.50%	1	1	1	1	200
530	Q755G5	RuvB-like helicase 2 OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=RVB2 PE=3 SV=2 - [RUVB2_ASHGO]	2.76	2.35%	3	1	1	1	469

531	P38767	Ethionine resistance-conferring protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERC1 PE=1 SV=1 - [ERC1_YEAST]	2.74	2.75%	1	1	1	1	581
532	P43535	Protein GCN20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCN20 PE=1 SV=1 - [GCN20_YEAST]	2.73	1.86%	1	1	1	1	752

533	P49723	Ribonucleoside-diphosphate reductase small chain 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RNR4 PE=1 SV=1 - [RIR4_YEAST]	2.71	3.48%	1	1	1	1	345
534	P00044	Cytochrome c iso-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYC1 PE=1 SV=2 - [CYC1_YEAST]	2.71	15.60%	1	1	1	1	109

535	P21147	Acyl-CoA desaturase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OLE1 PE=1 SV=2 - [ACO1_YEAST]	2.68	2.35%	1	1	1	1	510
536	P32486	Beta-glucan synthesis-associated protein KRE6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRE6 PE=1 SV=2 - [KRE6_YEAST]	2.67	2.08%	1	1	1	1	720

537	Q12220	U3 small nucleolar RNA-associated protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DIP2 PE=1 SV=1 - [UTP12_YEAST]	2.65	1.48%	1	1	1	1	943
538	P39985	rDNA transcriptional regulator POL5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=POL5 PE=1 SV=1 - [DPO5_YEAST]	2.64	1.08%	1	1	1	1	1022

539	Q12019	Midasin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MDN1 PE=1 SV=1 - [MDN1_YEAST]	2.64	0.24%	1	1	1	1	4910
540	P34222	Peptidyl-tRNA hydrolase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PTH2 PE=1 SV=2 - [PTH2_YEAST]	2.63	5.29%	1	1	1	1	208

541	P16120	Threonine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=THR4 PE=1 SV=1 - [THRC_YEAST]	2.63	2.53%	1	1	1	1	514
542	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]	2.62	1.81%	1	1	1	1	554

543	P38836	Putative metallocarboxypeptidase ECM14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ECM14 PE=1 SV=1 - [ECM14_YEAST]	2.62	2.56%	1	1	1	1	430
544	P40215	External NADH-ubiquinone oxidoreductase 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NDE1 PE=1 SV=1 - [NDH1_YEAST]	2.61	1.96%	1	1	1	1	560

545	P16550	Protein APA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=APA1 PE=1 SV=4 - [APA1_YEAST]	2.61	4.05%	1	1	1	1	321
546	P53721	Respiratory supercomplex factor 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RCF2 PE=1 SV=1 - [RCF2_YEAST]	2.6	4.91%	1	1	1	1	224

547	Q12743	DER1-like family member protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DFM1 PE=1 SV=1 - [DFM1_YEAST]	2.6	3.52%	1	1	1	1	341
548	P32353	Delta(7)-sterol 5(6)-desaturase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG3 PE=1 SV=1 - [ERG3_YEAST]	2.59	3.01%	1	1	1	1	365

549	P53927	Ribosome biogenesis protein 15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP15 PE=1 SV=1 - [NOP15_Y	2.58	4.09%	1	1	1	1	220
550	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]	2.57	7.87%	6	1	1	1	127

551	P38069	Alpha-1,2-mannosyltransferase MNN2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MNN2 PE=1 SV=1 - [MNN2_YEAST]	2.57	1.68%	1	1	1	1	597
552	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]	2.56	12.00%	1	1	1	1	125

553	P32899	U3 small nucleolar ribonucleoprotein protein IMP3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMP3 PE=1 SV=1 - [IMP3_YEAST]	2.55	8.20%	1	1	1	1	183
554	Q02256	Tyrosine-protein phosphatase YVH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YVH1 PE=1 SV=1 - [PVH1_YEAST]	2.53	3.85%	1	1	1	1	364

555	P35207	Antiviral helicase SKI2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SKI2 PE=1 SV=2 - [SKI2_YEAST]	2.52	0.93%	1	1	1	1	1287
556	P09457	ATP synthase subunit 5, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP5 PE=1 SV=1 - [ATPO_YEAST]	2.52	5.66%	1	1	1	1	212

557	P06197	CDP-diacylglycerol--inositol 3-phosphatidyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PIS1 PE=1 SV=1 - [PIS_YEAST]	2.51	5.00%	1	1	1	1	220
558	P32495	H/ACA ribonucleoprotein complex subunit NHP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NHP2 PE=1 SV=2 - [NHP2_YEAST]	2.51	9.62%	1	1	1	1	156

559	P14741	Translation initiation factor eIF-2B subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCN3 PE=1 SV=1 - [EI2BA_YEAST]	2.5	3.61%	1	1	1	1	305
560	A6ZQU8	Nucleolar protein 16 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NOP16 PE=3 SV=1 - [NOP16_Y	2.5	5.19%	1	1	1	1	231

561	P40506	Phosphopantothenate--cysteine ligase CAB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CAB2 PE=1 SV=2 - [PPCS_YEAST]	2.49	2.74%	1	1	1	1	365
562	P28273	5-oxoprolinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OXP1 PE=1 SV=2 - [OPLA_YEAST]	2.48	1.01%	1	1	1	1	1286

563	P35997	40S ribosomal protein S27-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS27A PE=1 SV=1 - [RS27A_YEAST]	2.48	8.54%	2	1	1	1	82
564	P07143	Cytochrome c1, heme protein, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYT1 PE=1 SV=1 - [CY1_YEAST]	2.47	5.18%	1	1	1	1	309

565	P38088	Glycine--tRNA ligase 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GRS1 PE=1 SV=3 - [SYG_YEAST]	2.45	2.17%	1	1	1	1	690
566	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]	2.44	2.27%	2	1	1	1	484

567	Q3E772	Protein LSO2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LSO2 PE=2 SV=1 - [LSO2_YEAST]	2.43	14.13%	1	1	1	1	92
568	P87185	Cysteine desulfurase, mitochondrial OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=NFS1 PE=2 SV=1 - [NFS1_CANAL]	2.43	3.48%	2	1	1	1	488

569	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]	2.43	1.30%	1	1	1	1	694
570	Q12244	Uncharacterized transcriptional regulatory protein YLL054C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YLL054C PE=1 SV=2 - [YL054_YEAST]	2.43	1.19%	1	1	1	1	843

571	P32794	ATPase family gene 2 protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AFG2 PE=1 SV=1 - [AFG2_YEAST]	2.43	1.79%	1	1	1	1	780
572	P53073	ER membrane protein complex subunit 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMC4 PE=1 SV=1 - [EMC4_YEAST]	2.42	5.26%	1	1	1	1	190

573	Q02821	Importin subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRP1 PE=1 SV=1 - [IMA1_YEAST]	2.42	2.77%	1	1	1	1	542
574	Q01560	Nucleolar protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NPL3 PE=1 SV=1 - [NOP3_YEAST]	2.42	2.90%	1	1	1	1	414

575	P51601	GTP cyclohydrolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FOL2 PE=1 SV=1 - [GCH1_YEAST]	2.41	4.94%	1	1	1	1	243
576	P29547	Elongation factor 1-gamma 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CAM1 PE=1 SV=2 - [EF1G1_YEAST]	2.41	3.13%	1	1	1	1	415

577	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]	2.4	1.84%	1	1	1	1	651
578	Q04373	Pumilio homology domain family member 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PUF6 PE=1 SV=1 - [PUF6_YEAST]	2.4	1.83%	1	1	1	1	656

579	P31412	V-type proton ATPase subunit C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA5 PE=1 SV=4 - [VATC_YEAST]	2.38	2.55%	1	1	1	1	392
580	Q12074	Spermidine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SPE3 PE=3 SV=1 - [SPEE_YEAST]	2.38	4.10%	1	1	1	1	293

581	P39109	Metal resistance protein YCF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YCF1 PE=1 SV=2 - [YCFI_YEAST]	2.36	0.99%	1	1	1	1	1515
582	P27810	Alpha-1,2	2.36	2.54%	1	1	1	1	393
583	P32558	FACT com	2.36	1.64%	1	1	1	1	1035
584	P36022	Dynein hea	2.35	0.37%	1	1	1	1	4092
585	P33333	Probable 1	2.34	3.96%	1	1	1	1	303
586	P22276	DNA-direc	2.34	0.87%	1	1	1	1	1149
587	Q07896	Nucleolar	2.33	1.66%	1	1	1	1	663
588	P22768	Argininosu	2.31	2.38%	1	1	1	1	420
589	Q08746	Regulator	2.31	6.40%	1	1	1	1	203
590	P04650	60S riboso	2.31	19.61%	1	1	1	1	51
591	P07347	N-terminal	2.3	5.88%	1	1	1	1	238
592	P39954	Adenosylh	2.3	3.34%	1	1	1	1	449
593	A6ZZ25	Eukaryotic	2.29	2.92%	2	1	1	1	274
594	P32589	Heat shock	2.25	1.15%	4	1	1	1	693
595	P36009	Probable A	2.25	1.36%	1	1	1	1	735
596	Q751T2	MICOS con	2.25	12.20%	2	1	1	1	82
597	P29496	Minichrom	2.24	1.03%	1	1	1	1	775
598	P09032	Translatio	2.24	2.60%	1	1	1	1	578
599	Q06107	Uncharact	2.24	3.17%	1	1	1	1	315
600	A5DXC6	Histone H2	2.23	6.77%	3	1	1	1	133
601	P32501	Translatio	2.22	1.83%	1	1	1	1	712
602	Q753N1	Probable k	2.21	1.66%	1	1	1	1	661
603	P48362	Protein HG	2.21	2.79%	1	1	1	1	394
604	A5DXS8	Histone H2	2.21	6.98%	6	1	1	1	129
605	P53142	Vacuolar p	2.19	4.12%	1	1	1	1	486
606	P33750	Protein SO	2.18	2.45%	1	1	1	1	489
607	P49166	60S riboso	2.17	7.95%	2	1	1	1	88
608	Q04305	U3 small n	2.16	2.14%	1	1	1	1	513
609	P48439	Dolichyl-di	2.16	3.43%	1	1	1	1	350
610	P34077	Nucleopor	2.14	1.19%	1	1	1	1	839

611	P08536	Sulfate ade	2.13	1.96%	1	1	1	1	511
612	P38130	Probable n	2.13	3.47%	1	1	1	1	404
613	P47117	Actin-relat	2.13	2.45%	1	1	1	1	449
614	P38853	Kelch repe	2.12	1.03%	1	1	1	1	1164
615	P49954	Omega-am	2.12	5.50%	1	1	1	1	291
616	Q08235	Ribosome	2.11	3.09%	1	1	1	1	291
617	Q08742	Thiosulfate	2.11	5.37%	1	1	1	1	149
618	P32419	Malate del	2.1	2.62%	1	1	1	1	343