	accession	descriptior	score	cover	# pro	# unique p	#pep	#PSM	AA
1	P00549	Pyruvate kinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC19 PE=1 SV=2 - [KPYK1_YEAST]	619.82	82.80%	5	36	36	192	500
2	P32324	Elongation factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EFT1 PE=1 SV=1 - [EF2_YEAST]	444.26	43.94%	4	27	27	128	842

3	P00359	Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TDH3 PE=1 SV=3 - [G3P3_YEAST]	414.85	65.66%	2	6	17	126	332
4	P02994	Elongation factor 1-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TEF1 PE=1 SV=1 - [EF1A_YEAST]	421.11	41.70%	4	13	13	125	458

5	P10664	60S ribosomal protein L4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL4A PE=1 SV=4 - [RL4A_YEAST]	390.92	50.55%	2	15	15	110	362
6	P00358	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TDH2 PE=1 SV=3 - [G3P2_YEAST]	349.36	54.22%	3	2	13	108	332

7	P0CX37	40S ribosomal protein S6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS6A PE=1 SV=1 - [RS6A_YEAST]	262.54	30.08%	2	8	8	79	236
8	P00560	Phosphoglycerate kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PGK1 PE=1 SV=2 - [PGK_YEAST]	248.73	52.88%	2	17	17	73	416

9	P05750	40S ribosomal protein S3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS3 PE=1 SV=5 - [RS3_YEAST]	230.55	56.25%	1	12	12	71	240
10	P05030	Plasma membrane ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMA1 PE=1 SV=2 - [PMA1_YEAST]	237.14	21.90%	2	15	15	69	918

11	P16521	Elongation factor 3A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YEF3 PE=1 SV=4 - [EF3A_YEAST]	196.03	28.54%	3	19	21	60	1044
12	P0CX53	60S ribosomal protein L12-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL12A PE=1 SV=1 - [RL12A_YEAST]	196.36	35.76%	1	5	5	58	165

13	P00950	Phosphoglycerate mutase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPM1 PE=1 SV=3 - [PMG1_YEAST]	150.29	47.37%	1	13	13	51	247
14	P0CX23	60S ribosomal protein L20-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL20A PE=1 SV=1 - [RL20A_YEAST]	162.97	36.05%	1	8	8	50	172

15	P02400	60S acidic ribosomal protein P2-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP2B PE=1 SV=2 - [RLA4_YEAST]	156.53	34.55%	1	4	4	47	110
16	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]	155.24	41.07%	1	11	11	45	319

17	P06168	Ketol-acid reductoisomerase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV5 PE=1 SV=1 - [ILV5_YEAST]	145.51	38.73%	1	10	10	44	395
18	P06169	Pyruvate decarboxylase isozyme 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDC1 PE=1 SV=7 - [PDC1_YEAST]	157.02	31.44%	2	12	13	44	563

19	P02407	40S ribosomal protein S17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS17A PE=1 SV=1 - [RS17A_YEAST]	151.16	50.74%	2	8	8	43	136
20	P11484	Ribosome-associated molecular chaperone SSB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSB1 PE=1 SV=3 - [SSB1_YEAST]	150.35	39.48%	2	2	15	43	613

21	P0CX39	40S ribosomal protein S8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS8A PE=1 SV=1 - [RS8A_YEAST]	132.73	33.00%	1	6	6	39	200
22	O14455	60S ribosomal protein L36-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL36B PE=1 SV=3 - [RL36B_YEAST]	118.48	43.00%	2	5	5	38	100

23	P14126	60S ribosomal protein L3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL3 PE=1 SV=4 - [RL3_YEAST]	132.25	34.11%	2	13	13	37	387
24	P17076	60S ribosomal protein L8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL8A PE=1 SV=4 - [RL8A_YEAST]	121.54	32.03%	1	2	9	37	256

25	P38701	40S ribosomal protein S20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS20 PE=1 SV=3 - [RS20_YEAST]	127.73	62.81%	1	7	7	37	121
26	P05748	60S ribosomal protein L15-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL15A PE=1 SV=3 - [RL15A_YEAST]	109.17	23.04%	1	2	4	36	204

27	P29453	60S ribosomal protein L8-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL8B PE=1 SV=3 - [RL8B_YEAST]	118.96	33.59%	1	2	9	36	256
28	P40212	60S ribosomal protein L13-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL13B PE=1 SV=1 - [RL13B_YEAST]	125.4	29.65%	2	1	5	36	199

29	P05317	60S acidic ribosomal protein P0 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP0 PE=1 SV=2 - [RLA0_YE	101.9	14.10%	1	4	4	34	312
30	P0CX50	60S ribosomal protein L18-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL18B PE=1 SV=1 - [RL18B_YEAST]	114.09	24.19%	1	4	4	34	186

31	P40150	Ribosome-associated molecular chaperone SSB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSB2 PE=1 SV=2 - [SSB2_YEAST]	121.35	37.36%	1	1	14	34	613
32	P48164	40S ribosomal protein S7-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS7B PE=1 SV=1 - [RS7B_YEAST]	105.42	33.16%	1	4	5	34	190

33	P00330	Alcohol dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADH1 PE=1 SV=5 - [ADH1_YEAST]	99.38	24.14%	3	6	6	32	348
34	P07280	40S ribosomal protein S19-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS19A PE=1 SV=2 - [RS19A_YEAST]	99.5	52.78%	2	8	8	32	144

35	P14120	60S ribosomal protein L30 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL30 PE=1 SV=3 - [RL30_YEAST]	117.32	45.71%	2	4	4	32	105
36	P37291	Serine hydroxymethyltransferase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SHM2 PE=1 SV=2 - [GLYC_YEAST]	106.89	24.09%	2	12	12	31	469

37	P05740	60S ribosomal protein L17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL17A PE=1 SV=4 - [RL17A_YEAST]	113.96	41.30%	1	1	5	30	184
38	P26786	40S ribosomal protein S7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS7A PE=1 SV=4 - [RS7A_YEAST]	90.31	46.32%	1	5	6	30	190

39	Q01855	40S ribosomal protein S15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS15 PE=1 SV=1 - [RS15_YEAST]	87.05	38.03%	1	4	4	30	142
40	P46990	60S ribosomal protein L17-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL17B PE=1 SV=2 - [RL17B_YEAST]	110.18	41.30%	1	1	5	29	184

41	P00925	Enolase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ENO2 PE=1 SV=2 - [ENO2_YEAST]	83.27	37.07%	3	10	10	28	437
42	P07259	Protein URA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=URA2 PE=1 SV=5 - [PYR1_YEAST]	84.95	10.30%	2	19	19	28	2214

43	Q12690	60S ribosomal protein L13-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL13A PE=1 SV=1 - [RL13A_YEAST]	91.17	29.65%	2	1	5	28	199
44	P0CX83	60S ribosomal protein L19-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL19B PE=1 SV=1 - [RL19B_YEAST]	108.11	20.63%	1	5	5	27	189

45	P26783	40S ribosomal protein S5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS5 PE=1 SV=3 - [RS5_YEAST]	76.82	28.44%	1	6	6	27	225
46	P05739	60S ribosomal protein L6-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL6B PE=1 SV=4 - [RL6B_YEAST]	67.02	35.23%	1	5	8	26	176

47	P0C0W9	60S ribosomal protein L11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL11A PE=1 SV=2 - [RL11A_YEAST]	77.21	25.86%	3	6	6	26	174
48	P0CX55	40S ribosomal protein S18-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS18A PE=1 SV=1 - [RS18A_YEAST]	74.36	28.77%	1	4	4	26	146

49	P53221	60S ribosomal protein L26-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL26B PE=1 SV=2 - [RL26B_YEAST]	70.83	44.09%	2	8	8	26	127
50	P54780	60S ribosomal protein L15-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL15B PE=1 SV=2 - [RL15B_YEAST]	84.77	19.61%	1	1	3	26	204

51	P04456	60S ribosomal protein L25 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL25 PE=1 SV=4 - [RL25_YEAST]	84.86	26.76%	1	4	4	24	142
52	P39938	40S ribosomal protein S26-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS26A PE=1 SV=1 - [RS26A_YEAST]	72.32	20.17%	2	2	2	24	119

53	P05756	40S ribosomal protein S13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS13 PE=1 SV=3 - [RS13_YEAST]	59.54	29.14%	1	4	4	23	151
54	P06367	40S ribosomal protein S14-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS14A PE=1 SV=5 - [RS14A_YEAST]	77.34	52.55%	3	8	8	23	137

55	P32527	Zuotin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ZUO1 PE=1 SV=1 - [ZUO1_YEAST]	79.74	30.48%	1	9	9	23	433
56	P39015	Suppressor protein STM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STM1 PE=1 SV=3 - [STM1_YEAST]	92.83	42.49%	1	8	8	23	273

57	P0CX32	40S ribosomal protein S24-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS24B PE=1 SV=1 - [RS24B_YEAST]	59.96	37.04%	1	6	6	22	135
58	P10592	Heat shock protein SSA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSA2 PE=1 SV=3 - [HSP72_YEAST]	68.4	25.98%	2	6	11	21	639

59	P0CX26	60S ribosomal protein L43-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL43B PE=1 SV=1 - [RL43B_YEAST]	75.15	42.39%	1	3	3	20	92
60	P0CX35	40S ribosomal protein S4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS4A PE=1 SV=1 - [RS4A_YEAST]	58.91	29.12%	1	7	7	20	261

61	P0CX41	60S ribosomal protein L23-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL23A PE=1 SV=1 - [RL23A_YEAST]	56.97	35.77%	1	6	6	20	137
62	P38625	GMP synthase [glutamine-hydrolyzing] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GUA1 PE=1 SV=4 - [GUAA_YEAST]	67.08	14.67%	2	6	6	20	525

63	P38788	Ribosome-associated complex subunit SSZ1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSZ1 PE=1 SV=2 - [SSZ1_YEAST]	68.63	31.41%	1	11	11	20	538
64	Q02326	60S ribosomal protein L6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL6A PE=1 SV=2 - [RL6A_YEAST]	53.94	28.98%	1	2	6	20	176

65	B3LT19	40S ribosomal protein S0-B OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RPS0B PE=3 SV=1 - [RSSA2_YEAS1]	54.87	32.14%	4	5	5	19	252
66	P04449	60S ribosomal protein L24-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL24A PE=1 SV=1 - [RL24A_YEAST]	65.84	21.94%	2	2	4	19	155

67	P05737	60S ribosomal protein L7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL7A PE=1 SV=3 - [RL7A_YEAST]	69.6	28.28%	3	6	6	19	244
68	P05744	60S ribosomal protein L33-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL33A PE=1 SV=3 - [RL33A_YEAST]	51.43	26.17%	1	2	4	19	107

69	P15019	Transaldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TAL1 PE=1 SV=4 - [TAL1_YEAST]	62.11	30.75%	1	8	8	19	335
70	P41805	60S ribosomal protein L10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL10 PE=1 SV=1 - [RL10_YEAST]	55.42	28.51%	1	7	7	19	221

71	A6ZL22	Cell wall protein ECM33 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ECM33 PE=3 SV=2 - [ECM33_YEAS7]	60.41	9.56%	4	4	4	18	429
72	B3RHV0	40S ribosomal protein S1-A OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RPS1A PE=3 SV=1 - [RS3A1_YEAS1]	52.32	30.20%	2	4	7	18	255

73	P0CX45	60S ribosomal protein L2-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL2A PE=1 SV=1 - [RL2A_YEAST]	55.86	39.37%	2	7	7	18	254
74	P0CX84	60S ribosomal protein L35-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL35A PE=1 SV=1 - [RL35A_YEAST]	59.85	34.17%	1	6	6	18	120

75	P10591	Heat shock protein SSA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSA1 PE=1 SV=4 - [HSP71_YEAST]	59.11	18.38%	2	2	8	18	642
76	P26321	60S ribosomal protein L5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL5 PE=1 SV=4 - [RL5_YEAST]	63.28	31.31%	2	7	7	18	297

77	P02406	60S ribosomal protein L28 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL28 PE=1 SV=3 - [RL28_YEAST]	48.07	17.45%	1	3	3	17	149
78	P0C0V8	40S ribosomal protein S21-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS21A PE=1 SV=1 - [RS21A_YEAST]	54.26	45.98%	1	1	3	17	87

79	P0C2H6	60S ribosomal protein L27-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL27A PE=1 SV=1 - [RL27A_YEAST]	59.05	36.76%	2	5	5	17	136
80	P0CX47	40S ribosomal protein S11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS11A PE=1 SV=1 - [RS11A_YEAST]	48.89	42.95%	1	7	7	17	156

81	P16861	ATP-dependent 6-phosphofructokinase subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PFK1 PE=1 SV=1 - [PFKA1_YEAST]	59.94	16.41%	1	11	11	17	987
82	P38061	60S ribosomal protein L32 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL32 PE=1 SV=1 - [RL32_YEAST]	46.01	36.92%	1	5	5	17	130

83	Q3E754	40S ribosomal protein S21-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS21B PE=1 SV=1 - [RS21B_YEAST]	54.3	45.98%	1	1	3	17	87
84	B3LLJ2	40S ribosomal protein S1-B OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RPS1B PE=3 SV=1 - [RS3A2_YEAS1]	50.3	29.41%	4	3	6	16	255

85	P07342	Acetolactate synthase catalytic subunit, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV2 PE=1 SV=1 - [ILVB_YEAST]	54.24	19.94%	1	8	8	16	687
86	P0CX43	60S ribosomal protein L1-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL1A PE=1 SV=1 - [RL1A_YEAST]	56.5	29.95%	2	7	7	16	217

87	P16862	ATP-dependent 6-phosphofructokinase subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PFK2 PE=1 SV=4 - [PFKA2_YEAST]	63.44	13.66%	1	7	7	16	959
88	P19882	Heat shock protein 60, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP60 PE=1 SV=1 - [HSP60_YEAST]	56.94	19.23%	1	8	8	16	572

89	P23254	Transketolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TKL1 PE=1 SV=4 - [TKT1_YEAST]	50.94	13.82%	1	7	7	16	680
90	P26785	60S ribosomal protein L16-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL16B PE=1 SV=3 - [RL16B_YEAST]	44.61	32.32%	1	4	8	16	198

91	P38219	Obg-like ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OLA1 PE=1 SV=1 - [OLA1_YEAST]	54.67	24.87%	1	7	7	16	394
92	P48589	40S ribosomal protein S12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS12 PE=1 SV=1 - [RS12_YEAST]	47.97	39.86%	1	6	6	16	143

93	P0C0W1	40S ribosomal protein S22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS22A PE=1 SV=2 - [RS22A_YEAST]	49.13	25.38%	3	3	3	15	130
94	P41056	60S ribosomal protein L33-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL33B PE=1 SV=2 - [RL33B_YEAST]	43.67	25.23%	1	1	3	15	107

95	P10622	60S acidic ribosomal protein P1-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP1B PE=1 SV=3 - [RLA3_YEAST]	52.97	15.09%	1	1	1	14	106
96	P38934	Nuclear segregation protein BFR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BFR1 PE=1 SV=1 - [BFR1_YE	45.09	25.96%	1	11	11	14	470

97	A6ZP47	ATP-dependent RNA helicase DED1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DED1 PE=3 SV=1 - [DED1_YEAS7]	43.65	21.36%	8	9	10	13	604
98	P05319	60S acidic ribosomal protein P2-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP2A PE=1 SV=1 - [RLA2_YEAST]	37.47	65.09%	1	3	3	13	106

99	P23301	Eukaryotic translation initiation factor 5A-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HYP2 PE=1 SV=3 - [IF5A1_YEAST]	37.95	16.56%	2	4	4	13	157
100	P26784	60S ribosomal protein L16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL16A PE=1 SV=3 - [RL16A_YEAST]	36.04	26.13%	1	2	6	13	199

101	P05759	Ubiquitin-40S ribosomal protein S31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS31 PE=1 SV=3 - [RS31_YEAST]	40.74	36.18%	3	4	4	12	152
102	P15108	ATP-dependent molecular chaperone HSC82 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSC82 PE=1 SV=4 - [HSC82_YEAST]	37.96	15.89%	5	9	9	12	705

103	P19097	Fatty acid synthase subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAS2 PE=1 SV=2 - [FAS2_YEAST]	37.82	7.31%	2	11	11	12	1887
104	P19358	S-adenosylmethionine synthase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAM2 PE=1 SV=3 - [METK2_YEAST]	37.68	17.97%	2	6	6	12	384

105	P24000	60S ribosomal protein L24-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL24B PE=1 SV=1 - [RL24B_YEAST]	44.52	20.65%	1	1	3	12	155
106	P25443	40S ribosomal protein S2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS2 PE=1 SV=3 - [RS2_YEAST]	50.06	21.65%	1	4	4	12	254

107	P41940	Mannose-1-phosphate guanyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PSA1 PE=1 SV=2 - [MPG1_YEAST]	43.51	26.32%	2	7	7	12	361
108	P07149	Fatty acid synthase subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAS1 PE=1 SV=2 - [FAS1_YEAST]	34.63	5.80%	1	9	9	11	2051

109	P0C0X0	40S ribosomal protein S28-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS28B PE=1 SV=1 - [RS28B_YEAST]	31.4	31.34%	3	2	2	11	67
110	Q00955	Acetyl-CoA carboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACC1 PE=1 SV=2 - [ACAC_YEAST]	34.48	5.46%	6	9	9	11	2233

111	P06105	Protein SCP160 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCP160 PE=1 SV=3 - [SC160_YEAST]	30.37	7.69%	1	7	7	10	1222
112	P0C2H9	60S ribosomal protein L31-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL31B PE=1 SV=1 - [RL31B_YEAST]	36.84	47.79%	3	5	5	10	113

113	P15646	rRNA 2'-O-methyltransferase fibrillarin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP1 PE=1 SV=1 - [FBRL_YEAST]	31.33	18.35%	2	5	5	10	327
114	P25087	Sterol 24-C-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG6 PE=1 SV=4 - [ERG6_YEAST]	34.2	21.41%	1	6	6	10	383

115	P49167	60S ribosomal protein L38 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL38 PE=1 SV=1 - [RL38_YEAST]	28.5	33.33%	1	3	3	10	78
116	A6ZPE5	Nucleolar protein 58 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NOP58 PE=3 SV=1 - [NOP58_Y	26.57	8.22%	2	3	3	9	511

117	P05755	40S ribosomal protein S9-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS9B PE=1 SV=4 - [RS9B_YEAST]	25.72	26.15%	2	5	5	9	195
118	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]	27.51	10.48%	2	7	7	9	763

119	P0CX33	40S ribosomal protein S30-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS30A PE=1 SV=1 - [RS30A_YEAST]	26.84	15.87%	1	1	1	9	63
120	P16474	Endoplasmic reticulum chaperone BiP OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KAR2 PE=1 SV=1 - [BIP_YEAST]	29.13	10.70%	3	4	5	9	682

121	P27476	Nuclear localization sequence-binding protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NSR1 PE=1 SV=1 - [NSR1_YEAST]	27.48	8.94%	1	4	4	9	414
122	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]	26.93	9.02%	1	8	8	9	964

123	P38879	Nascent polypeptide-associated complex subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EGD2 PE=1 SV=3 - [NACA_YEAST]	35.41	29.31%	1	3	3	9	174
124	P38910	10 kDa heat shock protein, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP10 PE=1 SV=1 - [CH10_YEAST]	33.71	47.17%	1	3	3	9	106

125	P40024	ABC transporter ATP-binding protein ARB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARB1 PE=1 SV=1 - [ARB1_YEAST]	31.58	18.52%	1	8	8	9	610
126	P40482	Protein transport protein SEC24 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC24 PE=1 SV=1 - [SEC24_YEAST]	26.71	10.04%	4	7	7	9	926

127	A6ZRX0	ATP-dependent RNA helicase DBP2 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP2 PE=3 SV=1 - [DBP2_YEAS7]	26.48	17.22%	4	6	7	8	546
128	P05749	60S ribosomal protein L22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL22A PE=1 SV=3 - [RL22A_YEAST]	33.49	32.23%	1	2	2	8	121

129	P07262	NADP-specific glutamate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GDH1 PE=1 SV=2 - [DHE4_YEAST]	31.02	15.42%	2	4	4	8	454
130	P0CX51	40S ribosomal protein S16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS16A PE=1 SV=1 - [RS16A_YEAST]	25.38	32.87%	3	5	5	8	143

131	P16467	Pyruvate decarboxylase isozyme 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDC5 PE=1 SV=4 - [PDC5_YEAST]	32.6	6.04%	1	1	2	8	563
132	P20107	Zinc/cadmium resistance protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ZRC1 PE=1 SV=2 - [ZRC1_YEAST]	25.6	6.33%	1	2	2	8	442

133	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]	26.25	9.49%	1	3	3	8	527
134	P36105	60S ribosomal protein L14-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL14A PE=1 SV=1 - [RL14A_YEAST]	20.19	20.29%	2	4	4	8	138

135	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]	19.44	3.09%	2	4	5	8	1876
136	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]	24.69	17.21%	1	3	3	8	244

137	P40525	60S ribosomal protein L34-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL34B PE=1 SV=1 - [RL34B_YEAST]	21.1	20.66%	2	2	2	8	121
138	P40531	Protein GVP36 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GVP36 PE=1 SV=1 - [GVP36_YEAST]	25	20.86%	1	6	6	8	326

139	P47079	T-complex protein 1 subunit theta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT8 PE=1 SV=1 - [TCPQ_YEAST]	24.1	13.20%	2	6	6	8	568
140	P50094	Inosine-5'-monophosphate dehydrogenase 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMD4 PE=1 SV=1 - [IMDH4_YEAST]	24.61	7.06%	1	2	3	8	524

141	P51401	60S ribosomal protein L9-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL9B PE=1 SV=1 - [RL9B_YEAST]	25.74	27.23%	2	4	4	8	191
142	A6ZWL1	Nascent polypeptide-associated complex subunit beta-1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=EGD1 PE=3 SV=1 - [NACB1_YEAS7]	23.6	29.94%	1	3	3	7	157

143	P00830	ATP synthase subunit beta, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP2 PE=1 SV=2 - [ATPB_YEAST]	19.6	9.78%	1	4	4	7	511
144	P02557	Tubulin beta chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUB2 PE=1 SV=2 - [TBB_YEA	19.74	8.10%	1	3	3	7	457

145	P04147	Polyadenylate-binding protein, cytoplasmic and nuclear OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PAB1 PE=1 SV=4 - [PABP_YEAST]	24.07	12.48%	1	5	5	7	577
146	P10081	ATP-dependent RNA helicase eIF4A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF1 PE=1 SV=3 - [IF4A_YEAST]	23.23	21.27%	2	6	6	7	395

147	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]	19.39	12.00%	3	3	3	7	375
148	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]	18.65	7.66%	2	7	7	7	1071

149	P28777	Chorismate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARO2 PE=1 SV=1 - [AROC_YEAST]	20.23	22.61%	1	5	5	7	376
150	P38720	6-phosphogluconate dehydrogenase, decarboxylating 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GND1 PE=1 SV=1 - [6PGD1_YEAST]	20.83	17.59%	2	6	6	7	489

151	P39567	Putative inosine-5'-monophosphate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMD1 PE=5 SV=1 - [IMDH1_YEAST]	22.41	8.44%	3	1	2	7	403
152	Q02753	60S ribosomal protein L21-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL21A PE=1 SV=1 - [RL21A_YEAST]	19.41	35.00%	2	5	5	7	160

153	Q05022	rRNA biogenesis protein RRP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP5 PE=1 SV=1 - [RRP5_YEAST]	18.74	3.82%	1	6	7	7	1729
154	Q08972	[NU+] prion formation protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NEW1 PE=1 SV=1 - [NEW1_YEAST]	24.57	6.69%	1	6	6	7	1196

155	Q12159	RNA annealing protein YRA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YRA1 PE=1 SV=2 - [YRA1_YEAST]	20.27	15.04%	1	3	3	7	226
156	P07251	ATP synthase subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP1 PE=1 SV=5 - [ATPA_YEAST]	19.25	11.19%	1	5	5	6	545

157	P07260	Eukaryotic translation initiation factor 4E OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC33 PE=1 SV=1 - [IF4E_YEAST]	20.44	13.62%	1	2	2	6	213
158	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]	18.08	31.03%	1	3	3	6	145

159	P12612	T-complex protein 1 subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TCP1 PE=1 SV=2 - [TCPA_YEAST]	17.67	7.69%	1	4	4	6	559
160	P18239	ADP,ATP carrier protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PET9 PE=1 SV=2 - [ADT2_YEAST]	16.66	12.26%	3	4	4	6	318

161	P25567	RNA-binding protein SRO9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRO9 PE=1 SV=2 - [SRO9_YEAST]	18.54	14.75%	1	4	4	6	434
162	P39078	T-complex protein 1 subunit delta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT4 PE=1 SV=2 - [TCPD_YEAST]	18.31	8.90%	1	3	3	6	528

163	P39522	Dihydroxy-acid dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV3 PE=1 SV=2 - [ILV3_YEAST]	19.2	11.62%	1	5	5	6	585
164	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]	19.69	12.46%	1	6	6	6	618

165	P41277	Glycerol-1-phosphate phosphohydrolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPP1 PE=1 SV=3 - [GPP1_YEAST]	17.81	22.00%	2	4	4	6	250
166	P48570	Homocitrate synthase, cytosolic isozyme OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS20 PE=1 SV=1 - [HOSC_YEAST]	17.76	17.29%	2	5	5	6	428

167	Q01560	Nucleolar protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NPL3 PE=1 SV=1 - [NOP3_YEAST]	18.87	6.28%	1	2	2	6	414
168	Q12522	Eukaryotic translation initiation factor 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF6 PE=1 SV=1 - [IF6_YEAST]	18.46	11.43%	1	2	2	6	245

169	O14467	Multiprotein-bridging factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MBF1 PE=1 SV=2 - [MBF1_YEAST]	15.16	17.88%	1	2	2	5	151
170	P07283	Phosphomannomutase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC53 PE=1 SV=1 - [PMM_YEAST]	16.38	18.11%	2	4	4	5	254

171	P07991	Ornithine aminotransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CAR2 PE=1 SV=2 - [OAT_YEAST]	17.36	18.40%	1	5	5	5	424
172	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]	13.45	2.76%	1	4	4	5	1664

173	P14540	Fructose-bisphosphate aldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FBA1 PE=1 SV=3 - [ALF_YEAST]	24.37	15.60%	1	3	3	5	359
174	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]	17.97	4.32%	1	4	4	5	1203

175	P25294	Protein SIS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SIS1 PE=1 SV=1 - [SIS1_YEAST]	18.73	17.61%	1	3	3	5	352
176	P27809	Glycolipid 2-alpha-mannosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRE2 PE=1 SV=1 - [KRE2_YEAST]	16.98	13.12%	1	4	4	5	442

177	P28274	CTP synthase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=URA7 PE=1 SV=2 - [URA7_YEAST]	19.45	10.54%	1	5	5	5	579
178	P32476	Squalene monooxygenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG1 PE=1 SV=2 - [ERG1_YEAST]	14.35	6.85%	1	3	3	5	496

179	P39730	Eukaryotic translation initiation factor 5B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FUN12 PE=1 SV=2 - [IF2P_YEAST]	15.03	4.29%	1	3	3	5	1002
180	P39986	Manganese-transporting ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SPF1 PE=1 SV=1 - [ATC6_YEAST]	14.9	3.79%	1	4	4	5	1215

181	P52910	Acetyl-coenzyme A synthetase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACS2 PE=1 SV=1 - [ACS2_YEAST]	12.73	3.51%	1	2	2	5	683
182	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]	15.35	19.47%	1	4	5	5	339

183	Q02892	Nucleolar GTP-binding protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOG1 PE=1 SV=1 - [NOG1_YEAST]	17.48	11.13%	1	5	5	5	647
184	Q03690	Clustered mitochondria protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CLU1 PE=1 SV=1 - [CLU_YEAST]	17.31	3.84%	1	4	4	5	1277

185	A6ZNQ1	ATP-dependent RNA helicase DBP5 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP5 PE=3 SV=1 - [DBP5_YEAS7]	12.45	11.41%	1	4	4	4	482
186	A6ZPA9	Ribosome biogenesis protein YTM1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=YTM1 PE=3 SV=1 - [YTM1_YEAS7]	17.38	10.43%	1	3	3	4	460

187	P00899	Anthranilate synthase component 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRP2 PE=1 SV=4 - [TRPE_YEAST]	14.47	8.48%	1	3	3	4	507
188	P00927	Threonine dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV1 PE=1 SV=2 - [THDH_YEAST]	10.95	8.85%	1	4	4	4	576

189	P06106	Homocysteine/cysteine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET17 PE=1 SV=3 - [CYSD_YEAST]	12.58	10.59%	1	4	4	4	444
190	P07245	C-1-tetrahydrofolate synthase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE3 PE=1 SV=1 - [C1TC_YEAST]	10.79	5.18%	1	4	4	4	946

191	P07806	Valine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VAS1 PE=1 SV=2 - [SYV_YEAST]	12.25	4.71%	1	4	4	4	1104
192	P09624	Dihydrolipoyl dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LPD1 PE=1 SV=1 - [DLDH_YEAST]	10.42	9.02%	1	4	4	4	499

193	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]	10.72	6.64%	1	3	3	4	482
194	P16140	V-type proton ATPase subunit B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA2 PE=1 SV=2 - [VATB_YEAST]	12.59	10.44%	1	4	4	4	517

195	P17967	Protein disulfide-isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDI1 PE=1 SV=2 - [PDI_YEAST]	14.83	9.20%	1	4	4	4	522
196	P23542	Aspartate aminotransferase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AAT2 PE=1 SV=3 - [AATC_YEAST]	13.84	6.70%	1	2	2	4	418

197	P25491	Mitochondrial protein import protein MAS5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YDJ1 PE=1 SV=1 - [MAS5_YEAST]	11.97	11.25%	1	3	3	4	409
198	P32368	Phosphoinositide phosphatase SAC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAC1 PE=1 SV=1 - [SAC1_YEAST]	11.4	7.54%	1	4	4	4	623

199	P32602	Alpha-soluble NSF attachment protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC17 PE=1 SV=4 - [SEC17_YEAST]	15.01	16.10%	1	3	3	4	292
200	P38891	Branched-chain-amino-acid aminotransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BAT1 PE=1 SV=1 - [BCA1_YEAST]	9.9	10.94%	2	4	4	4	393

201	P39676	Flavohemoprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YHB1 PE=1 SV=2 - [FHP_YEAST]	11.2	6.77%	1	2	2	4	399
202	P42943	T-complex protein 1 subunit eta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT7 PE=1 SV=1 - [TCPH_YEAST]	13.88	11.82%	1	4	4	4	550

203	P51996	GTP-binding protein YPT32/YPT11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPT32 PE=1 SV=3 - [YPT32_YEAST]	11.69	16.67%	2	3	3	4	222
204	P53978	Elongation factor 3B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HEF3 PE=1 SV=2 - [EF3B_YEAST]	10.21	2.78%	1	1	3	4	1044

205	Q04947	Reticulon-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RTN1 PE=1 SV=1 - [RTN1_YEAST]	11.68	14.58%	1	4	4	4	295
206	Q12230	Sphingolipid long chain base-responsive protein LSP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LSP1 PE=1 SV=1 - [LSP1_YEAST]	14.39	13.78%	1	2	3	4	341

207	Q12363	Transcriptional modulator WTM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=WTM1 PE=1 SV=1 - [WTM1_YEAST]	11.7	12.59%	1	4	4	4	437
208	Q12460	Nucleolar protein 56 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP56 PE=1 SV=1 - [NOP56_Y	14.79	12.30%	1	4	4	4	504

209	A5DXS8	Histone H2A.2 OS=Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) OX=379508 GN=HTA2 PE=3 SV=1 - [H2A2_LODEL]	7.36	6.98%	6	1	1	3	129
210	A6ZN26	Eukaryotic translation initiation factor 3 subunit C OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NIP1 PE=3 SV=1 - [EIF3C_YEAS7]	9.98	4.56%	2	3	3	3	812

211	A6ZUA1	ATP-dependent RNA helicase DBP3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP3 PE=3 SV=1 - [DBP3_YEAS7]	9.19	6.88%	2	3	3	3	523
212	B3LNF5	Vacuolar protein sorting/targeting protein PEP1 OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=PEP1 PE=3 SV=1 - [VPS10_YEAS1]	8.43	2.28%	9	3	3	3	1577

213	P00942	Triosephosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPI1 PE=1 SV=2 - [TPIS_YEAST]	9.32	18.15%	1	3	3	3	248
214	P04801	Threonine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=THS1 PE=1 SV=2 - [SYTC_YEAST]	10.12	6.27%	1	3	3	3	734

215	P05747	60S ribosomal protein L29 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL29 PE=1 SV=3 - [RL29_YEAST]	7.42	13.56%	1	1	1	3	59
216	P06780	GTP-binding protein RHO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RHO1 PE=1 SV=3 - [RHO1_YEAST]	12.57	19.14%	1	2	2	3	209

217	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]	10.94	5.24%	1	3	3	3	802
218	P07278	cAMP-dependent protein kinase regulatory subunit OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BCY1 PE=1 SV=4 - [KAPR_YEAST]	8.01	7.69%	1	3	3	3	416

219	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]	7.6	2.78%	1	3	3	3	1224
220	P09733	Tubulin alpha-1 chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUB1 PE=1 SV=2 - [TBA1_YEAST]	12.26	4.70%	1	1	1	3	447

221	P0CS90	Heat shock protein SSC1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSC1 PE=1 SV=1 - [HSP77_YEAST]	7.33	4.43%	2	1	2	3	654
222	P11632	Non-histone chromosomal protein 6A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NHP6A PE=1 SV=1 - [NHP6A_YEAST]	8.84	29.03%	1	3	3	3	93

223	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]	8.94	5.95%	1	2	2	3	437
224	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]	9.67	4.92%	1	3	3	3	854

225	P14742	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GFA1 PE=1 SV=4 - [GFA1_YEAST]	9.59	3.49%	1	2	2	3	717
226	P15303	Protein transport protein SEC23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC23 PE=1 SV=1 - [SEC23_YEAST]	10.71	4.95%	2	3	3	3	768

227	P21524	Ribonucleoside-diphosphate reductase large chain 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RNR1 PE=1 SV=2 - [RIR1_YEAST]	13.44	3.72%	1	2	2	3	888
228	P21965	Protein kinase MCK1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MCK1 PE=1 SV=1 - [MCK1_YEAST]	8.48	8.00%	1	3	3	3	375

229	P23641	Mitochondrial phosphate carrier protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MIR1 PE=1 SV=1 - [MPCP_YEAST]	8.36	13.83%	1	3	3	3	311
230	P23644	Mitochondrial import receptor subunit TOM40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOM40 PE=1 SV=1 - [TOM40_YEAST]	10.57	17.31%	1	3	3	3	387

231	P25694	Cell division control protein 48 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC48 PE=1 SV=3 - [CDC48_Y	10.55	4.91%	1	3	3	3	835
232	P28834	Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IDH1 PE=1 SV=2 - [IDH1_YEAST]	9.46	7.78%	1	2	2	3	360

233	P29311	Protein BMH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BMH1 PE=1 SV=4 - [BMH1_YEAST]	9.72	9.36%	2	2	2	3	267
234	P32486	Beta-glucan synthesis-associated protein KRE6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRE6 PE=1 SV=2 - [KRE6_YEAST]	10.61	5.83%	1	3	3	3	720

235	P32582	Cystathionine beta-synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYS4 PE=1 SV=1 - [CBS_YEAST]	10.65	8.28%	1	3	3	3	507
236	P32861	UTP--glucose-1-phosphate uridylyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UGP1 PE=1 SV=1 - [UGPA1_YEAST]	9.32	7.21%	1	3	3	3	499

237	P33201	Ribosome assembly factor MRT4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MRT4 PE=1 SV=1 - [MRT4_YEAST]	8.54	16.10%	2	3	3	3	236
238	P33297	26S proteasome regulatory subunit 6A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT5 PE=1 SV=3 - [PRS6A_YEAST]	8.74	9.91%	1	3	3	3	434

239	P33322	H/ACA ribonucleoprotein complex subunit CBF5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CBF5 PE=1 SV=1 - [CBF5_YEAST]	11.45	6.42%	1	2	2	3	483
240	P33750	Protein SOF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SOF1 PE=1 SV=1 - [DCA13_YEAST]	9.4	7.57%	1	3	3	3	489

241	P34167	Eukaryotic translation initiation factor 4B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF3 PE=1 SV=1 - [IF4B_YEAST]	8.16	7.80%	1	3	3	3	436
242	P36013	NAD-dependent malic enzyme, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAE1 PE=1 SV=1 - [MAOM_YEAST]	9.64	7.77%	1	3	3	3	669

243	P36049	rRNA-processing protein EBP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EBP2 PE=1 SV=1 - [EBP2_YEAST]	13.24	10.30%	1	3	3	3	427
244	P37263	UPF0743 protein YCR087C-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YCR087C-A PE=1 SV=1 - [YC16_YEAST]	10.09	21.57%	1	3	3	3	153

245	P38911	FK506-binding nuclear protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FPR3 PE=1 SV=2 - [FKBP3_YEAST]	8.47	6.81%	3	2	2	3	411
246	P38968	Protein transport protein SEC31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC31 PE=1 SV=3 - [SEC31_YEAST]	10.69	2.20%	1	2	2	3	1273

247	P39077	T-complex protein 1 subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT3 PE=1 SV=2 - [TCPG_YEAST]	9.41	6.37%	1	3	3	3	534
248	P39079	T-complex protein 1 subunit zeta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT6 PE=1 SV=1 - [TCPZ_YEAST]	10.77	7.14%	1	3	3	3	546

249	P39935	Eukaryotic initiation factor 4F subunit p150 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF4631 PE=1 SV=2 - [IF4F1_YEAST]	8.6	3.99%	1	3	3	3	952
250	P39954	Adenosylhomocysteinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAH1 PE=1 SV=1 - [SAHH_YEAST]	9.06	7.35%	1	3	3	3	449

251	P40047	Aldehyde dehydrogenase 5, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALD5 PE=1 SV=4 - [ALDH5_YEAST]	7.57	5.00%	1	2	2	3	520
252	P40185	Protein MMF1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MMF1 PE=1 SV=1 - [MMF1_YEAST]	8.73	24.14%	1	3	3	3	145

253	P40327	26S proteasome regulatory subunit 4 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT2 PE=1 SV=3 - [PRS4_YEAST]	7.08	4.12%	1	2	2	3	437
254	P40413	T-complex protein 1 subunit epsilon OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT5 PE=1 SV=3 - [TCPE_YEAST]	10.4	6.94%	1	3	3	3	562

255	P40693	Ribosome biogenesis protein RLP7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RLP7 PE=1 SV=1 - [RLP7_YEAST]	8.92	13.66%	1	3	3	3	322
256	P40825	Alanine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALA1 PE=1 SV=3 - [SYA_YEAST]	11.72	3.87%	1	3	3	3	983

257	P41338	Acetyl-CoA acetyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG10 PE=1 SV=3 - [THIL_YEAST]	9.28	9.30%	2	3	3	3	398
258	P46784	40S ribosomal protein S10-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS10B PE=1 SV=1 - [RS10B_YEAST]	9.82	17.14%	2	1	1	3	105

259	P47117	Actin-related protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARP3 PE=1 SV=1 - [ARP3_YEAST]	7.11	6.68%	1	3	3	3	449
260	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]	10.46	3.75%	1	2	2	3	694

261	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]	12.35	10.21%	1	3	3	3	431
262	Q03532	ATP-dependent RNA helicase HAS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HAS1 PE=1 SV=1 - [HAS1_YEAST]	8.79	6.53%	2	3	3	3	505

263	Q03940	RuvB-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RVB1 PE=1 SV=1 - [RUVB1_YEAST]	8.1	7.34%	2	3	3	3	463
264	Q05911	Adenylosuccinate lyase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE13 PE=1 SV=1 - [PUR8_YEAST]	9.86	6.85%	1	3	3	3	482

265	Q07362	Protein PBP4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PBP4 PE=1 SV=1 - [PBP4_YEAST]	8.68	24.86%	1	3	3	3	185
266	Q12265	Ribose-phosphate pyrophosphokinase 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRS5 PE=1 SV=1 - [KPR5_YEAST]	9.73	7.66%	1	3	3	3	496

267	A5DZE1	Ribosome biogenesis protein NSA2 OS=Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) OX=379508 GN=NSA2 PE=3 SV=1 - [NSA2_LODEL]	5.05	3.45%	3	1	1	2	261
268	A6ZMA9	Ribosome biogenesis protein ERB1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ERB1 PE=3 SV=1 - [ERB1_YEAS7]	5.75	2.85%	2	2	2	2	807

269	A6ZPB3	Cap-associated protein CAF20 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=CAF20 PE=3 SV=1 - [CAF20_YEAS7]	7.32	8.70%	2	1	1	2	161
270	A6ZQE9	Alpha-1,2-mannosyltransferase MNN5 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=MNN5 PE=3 SV=1 - [MNN5_YEAS7]	6.45	4.27%	2	2	2	2	586

271	A6ZRK4	Cysteine proteinase 1, mitochondrial OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=LAP3 PE=3 SV=2 - [BLH1_YEAS7]	6.72	5.80%	3	2	2	2	483
272	A6ZV85	Pescadillo homolog OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NOP7 PE=3 SV=1 - [PESC_YEAS7]	7.8	4.96%	1	2	2	2	605

273	A6ZXD2	tRNA (guanine-N(7)-)-methyltransferase OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=TRM8 PE=3 SV=1 - [TRMB_YEAS7]	5.72	7.69%	3	2	2	2	286
274	A6ZYI0	Adenylate kinase OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ADK1 PE=3 SV=1 - [KAD2_YEAS7]	5.44	9.01%	3	2	2	2	222

275	A6ZZ25	Eukaryotic translation initiation factor 3 subunit G OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=TIF35 PE=3 SV=1 - [EIF3G_YEAS7]	5.45	9.85%	2	2	2	2	274
276	B3LRA0	MICOS complex subunit MIC60 OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=MIC60 PE=3 SV=1 - [MIC60_YEAS1]	6.37	5.75%	4	2	2	2	539

277	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]	6.57	25.29%	2	2	2	2	87
278	P00546	Cyclin-dependent kinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC28 PE=1 SV=1 - [CDK1_YEAST]	6.84	8.39%	1	2	2	2	298

279	P00931	Tryptophan synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRP5 PE=1 SV=1 - [TRP_YEAST]	6.74	3.68%	1	2	2	2	707
280	P04046	Amidophosphoribosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE4 PE=1 SV=2 - [PUR1_YEAST]	5.53	3.53%	2	2	2	2	510

281	P04173	3-isopropylmalate dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LEU2 PE=1 SV=4 - [LEU3_YEAST]	5.9	9.07%	1	2	2	2	364
282	P04802	Aspartate--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DPS1 PE=1 SV=3 - [SYDC_YEAST]	6.7	4.49%	1	2	2	2	557

283	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]	5.42	1.46%	2	1	1	2	685
284	P05694	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET6 PE=1 SV=4 - [METE_YEAST]	4.75	2.48%	1	2	2	2	767

285	P07257	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=QCR2 PE=1 SV=1 - [QCR2_YEAST]	5.78	5.71%	1	2	2	2	368
286	P07273	Transcription elongation factor S-II OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DST1 PE=1 SV=4 - [TFS2_YEAST]	5.26	7.12%	1	2	2	2	309

287	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]	7.17	7.16%	1	2	2	2	335
288	P0C0T4	40S ribosomal protein S25-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS25B PE=1 SV=1 - [RS25B_YEAST]	6.07	12.96%	2	1	1	2	108

289	P11154	Pyruvate carboxylase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PYC1 PE=1 SV=2 - [PYC1_YEAST]	6.83	2.12%	2	2	2	2	1178
290	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]	6.26	2.11%	2	2	2	2	1045

291	P14020	Dolichol-phosphate mannosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DPM1 PE=1 SV=3 - [DPM1_YEAST]	5.22	4.12%	1	1	1	2	267
292	P14832	Peptidyl-prolyl cis-trans isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CPR1 PE=1 SV=3 - [CYPH_YEAST]	7.76	17.90%	1	2	2	2	162

293	P15703	Glucan 1,3-beta-glucosidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BGL2 PE=1 SV=1 - [BGL2_YEAST]	7.31	7.99%	1	2	2	2	313
294	P15705	Heat shock protein STI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STI1 PE=1 SV=1 - [STI1_YEAST]	6.34	3.57%	1	2	2	2	589

295	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]	4.69	2.14%	1	1	1	2	420
296	P16603	NADPH--cytochrome P450 reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NCP1 PE=1 SV=3 - [NCPR_YEAST]	6.14	3.33%	2	2	2	2	691

297	P18759	Vesicular-fusion protein SEC18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC18 PE=1 SV=2 - [SEC18_YEAST]	5.91	3.69%	1	2	2	2	758
298	P19073	Cell division control protein 42 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC42 PE=1 SV=2 - [CDC42_Y	6.39	5.24%	2	1	1	2	191

299	P19414	Aconitate hydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACO1 PE=1 SV=2 - [ACON_YEAST]	7.62	3.47%	1	2	2	2	778
300	P21243	Proteasome subunit alpha type-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCL1 PE=1 SV=1 - [PSA1_YEAST]	6.1	9.52%	1	2	2	2	252

301	P21264	Phosphoribosylaminoimidazole carboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE2 PE=1 SV=1 - [PUR6_YEAST]	6.13	4.20%	1	2	2	2	571
302	P21304	Periodic tryptophan protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PWP1 PE=1 SV=1 - [PWP1_YEAST]	10.64	6.25%	1	2	2	2	576

303	P21954	Isocitrate dehydrogenase [NADP], mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IDP1 PE=1 SV=1 - [IDHP_YEAST]	6.06	4.67%	1	2	2	2	428
304	P22203	V-type proton ATPase subunit E OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA4 PE=1 SV=4 - [VATE_YEAST]	4.86	8.15%	1	2	2	2	233

305	P22217	Thioredoxin-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRX1 PE=1 SV=3 - [TRX1_YEAST]	6.19	20.39%	2	2	2	2	103
306	P23639	Proteasome subunit alpha type-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE8 PE=1 SV=1 - [PSA2_YEAST]	5.3	8.80%	1	2	2	2	250

307	P25342	Cell division control protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC10 PE=1 SV=1 - [CDC10_Y	4.42	4.35%	1	1	2	2	322
308	P25605	Acetolactate synthase small subunit, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV6 PE=1 SV=2 - [ILV6_YEAST]	4.87	6.47%	1	2	2	2	309

309	P29704	Squalene synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG9 PE=1 SV=2 - [FDFT_YEAST]	5.32	4.50%	1	2	2	2	444
310	P31116	Homoserine dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOM6 PE=1 SV=1 - [DHOM_YEAST]	5.27	6.41%	1	1	2	2	359

311	P32263	Pyrroline-5-carboxylate reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRO3 PE=1 SV=1 - [P5CR_YEAST]	6.75	8.74%	1	2	2	2	286
312	P32379	Proteasome subunit alpha type-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PUP2 PE=1 SV=2 - [PSA5_YEAST]	7.3	10.00%	1	2	2	2	260

313	P32468	Cell division control protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC12 PE=1 SV=1 - [CDC12_Y	6.26	5.90%	1	2	2	2	407
314	P32565	26S proteasome regulatory subunit RPN2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN2 PE=1 SV=4 - [RPN2_YEAST]	6.88	2.22%	1	2	2	2	945

315	P32583	Suppressor protein SRP40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRP40 PE=1 SV=2 - [SRP40_YEAST]	5.79	5.67%	1	1	2	2	406
316	P32598	Serine/threonine-protein phosphatase PP1-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLC7 PE=1 SV=1 - [PP12_YEAST]	6.35	5.13%	1	1	1	2	312

317	P32621	Guanosine-diphosphatase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GDA1 PE=1 SV=1 - [GDA1_YEAST]	4.89	4.25%	1	2	2	2	518
318	P32803	Endosomal protein P24B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMP24 PE=1 SV=1 - [EMP24_YEAST]	6.77	6.90%	1	1	1	2	203

319	P33775	Dolichyl-phosphate-mannose--protein mannosyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMT1 PE=1 SV=1 - [PMT1_YEAST]	4.65	1.35%	1	1	1	2	817
320	P33892	eIF-2-alpha kinase activator GCN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCN1 PE=1 SV=1 - [GCN1_YEAST]	5.4	0.79%	1	2	2	2	2672

321	P35725	Uncharacterized protein YKL063C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YKL063C PE=1 SV=1 - [YKG3_YEAST]	7.46	21.56%	1	1	1	2	167
322	P38013	Peroxiredoxin AHP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AHP1 PE=1 SV=4 - [AHP1_YEAST]	7.02	15.91%	1	2	2	2	176

323	P38431	Eukaryotic translation initiation factor 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF5 PE=1 SV=1 - [IF5_YEAST]	6.88	5.93%	1	2	2	2	405
324	P38629	Replication factor C subunit 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RFC3 PE=1 SV=1 - [RFC3_YEAST]	8.49	8.53%	1	2	2	2	340

325	P38694	Putative aldehyde dehydrogenase-like protein YHR039C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MSC7 PE=1 SV=1 - [MSC7_YEAST]	6	4.19%	1	2	2	2	644
326	P38817	ADP-ribosylation factor-binding protein GGA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GGA2 PE=1 SV=1 - [GGA2_YEAST]	6.79	5.47%	1	2	2	2	585

327	P38861	60S ribosomal export protein NMD3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NMD3 PE=1 SV=3 - [NMD3_YEAST]	5.01	3.67%	1	2	2	2	518
328	P39007	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STT3 PE=1 SV=2 - [STT3_YEAST]	7.42	3.90%	1	2	2	2	718

329	P39076	T-complex protein 1 subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT2 PE=1 SV=1 - [TCPB_YEAST]	6.6	4.17%	1	2	2	2	527
330	P39109	Metal resistance protein YCF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YCF1 PE=1 SV=2 - [YCFI_YEAST]	5.83	1.65%	1	2	2	2	1515

331	P39729	Ribosome-interacting GTPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RBG1 PE=1 SV=1 - [RBG1_YEAST]	5.16	5.15%	1	2	2	2	369
332	P39744	Nucleolar complex protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOC2 PE=1 SV=2 - [NOC2_YEAST]	5.27	1.41%	1	1	1	2	710

333	P40010	Nuclear GTP-binding protein NUG1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NUG1 PE=1 SV=1 - [NUG1_YEAST]	6.6	4.42%	1	2	2	2	520
334	P40040	Protein THO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=THO1 PE=1 SV=1 - [THO1_YEAST]	5.71	9.63%	1	2	2	2	218

335	P40215	External NADH-ubiquinone oxidoreductase 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NDE1 PE=1 SV=1 - [NDH1_YEAST]	4.74	2.86%	1	2	2	2	560
336	P40302	Proteasome subunit alpha type-6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE5 PE=1 SV=1 - [PSA6_YEAST]	7.63	12.39%	1	2	2	2	234

337	P40303	Proteasome subunit alpha type-4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE6 PE=1 SV=1 - [PSA4_YEAST]	4.47	3.54%	1	1	1	2	254
338	P40581	Glutathione peroxidase-like peroxiredoxin HYR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HYR1 PE=1 SV=1 - [GPX3_YEAST]	5.89	12.88%	2	2	2	2	163

339	P41807	V-type proton ATPase subunit H OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA13 PE=1 SV=1 - [VATH_YEAST]	4.91	1.46%	1	1	1	2	478
340	P41811	Coatomer subunit beta' OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC27 PE=1 SV=1 - [COPB2_YEAST]	4.57	2.02%	1	2	2	2	889

341	P43535	Protein GCN20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCN20 PE=1 SV=1 - [GCN20_YEAST]	5.93	3.32%	1	2	2	2	752
342	P46682	AP-3 complex subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=APL6 PE=1 SV=2 - [AP3B_YEAST]	6.7	1.85%	1	1	1	2	809

343	P47047	ATP-dependent RNA helicase DOB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MTR4 PE=1 SV=1 - [MTR4_YEAST]	5.95	2.42%	1	2	2	2	1073
344	P47075	Vacuolar transporter chaperone 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VTC4 PE=1 SV=2 - [VTC4_YEAST]	4.43	2.50%	1	1	2	2	721

345	P47083	U3 small nucleolar RNA-associated protein MPP10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MPP10 PE=1 SV=1 - [MPP10_YEAST]	6.23	3.54%	1	2	2	2	593
346	P47154	CAAX prenyl protease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STE24 PE=1 SV=1 - [STE24_YEAST]	5.63	4.86%	1	2	2	2	453

347	P49090	Asparagine synthetase [glutamine-hydrolyzing] 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ASN2 PE=1 SV=2 - [ASNS2_YEAST]	5.84	4.02%	2	2	2	2	572
348	P49166	60S ribosomal protein L37-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL37A PE=1 SV=2 - [RL37A_YEAST]	4.44	7.95%	1	1	1	2	88

349	P49367	Homoaconitase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS4 PE=1 SV=1 - [LYS4_YEAST]	7.06	3.90%	1	2	2	2	693
350	P53235	Eukaryotic translation initiation factor 2A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YGR054W PE=1 SV=1 - [EIF2A_YEAST]	6.78	4.67%	1	2	2	2	642

351	P53598	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LSC1 PE=1 SV=1 - [SUCA_YEAST]	6.22	8.81%	1	2	2	2	329
352	P53834	Hsp90 co-chaperone HCH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HCH1 PE=1 SV=1 - [HCH1_YEAST]	4.7	12.42%	1	2	2	2	153

353	P54000	RNA polymerase II transcriptional coactivator SUB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUB1 PE=1 SV=1 - [SUB1_YEAST]	6.12	9.93%	1	2	2	2	292
354	P54115	Magnesium-activated aldehyde dehydrogenase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALD6 PE=1 SV=4 - [ALDH6_YEAST]	5.02	4.40%	1	2	2	2	500

355	P54839	Hydroxymethylglutaryl-CoA synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG13 PE=1 SV=1 - [HMCS_YEAST]	7.27	5.91%	1	2	2	2	491
356	P56628	60S ribosomal protein L22-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL22B PE=1 SV=2 - [RL22B_YEAST]	5.94	32.79%	1	2	2	2	122

357	P87108	Mitochondrial import inner membrane translocase subunit TIM10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIM10 PE=1 SV=1 - [TIM10_YEAST]	7.16	34.41%	1	2	2	2	93
358	Q00245	GTP-binding protein RHO3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RHO3 PE=1 SV=2 - [RHO3_YEAST]	6.92	10.39%	2	2	2	2	231

359	Q04225	Ribosome assembly protein RRB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRB1 PE=1 SV=1 - [RRB1_YEAST]	6.57	4.89%	1	2	2	2	511
360	Q04697	Glucose-signaling factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GSF2 PE=1 SV=1 - [GSF2_YEAST]	5.4	4.96%	1	2	2	2	403

361	Q06103	26S proteasome regulatory subunit RPN7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN7 PE=1 SV=3 - [RPN7_YEAST]	4.77	6.99%	1	2	2	2	429
362	Q06505	Transcription factor SPN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SPN1 PE=1 SV=1 - [IWS1_YEAST]	6.22	7.07%	1	2	2	2	410

363	Q06705	Phosphatidylinositol transfer protein CSR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CSR1 PE=1 SV=1 - [CSR1_YEAST]	4.98	5.64%	1	2	2	2	408
364	Q06892	NADH kinase POS5, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=POS5 PE=1 SV=2 - [POS5_YEAST]	6.5	3.38%	1	1	1	2	414

365	Q08746	Regulator of ribosome biosynthesis OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRS1 PE=1 SV=1 - [RRS1_YEAST]	5.13	11.33%	1	2	2	2	203
366	Q08965	Ribosome biogenesis protein BMS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BMS1 PE=1 SV=1 - [BMS1_YEAST]	4.51	1.78%	1	2	2	2	1183

367	Q12019	Midasin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MDN1 PE=1 SV=1 - [MDN1_YEAST]	7.15	0.65%	1	2	2	2	4910
368	Q12464	RuvB-like protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RVB2 PE=1 SV=1 - [RUVB2_YEAST]	5.54	5.10%	3	2	2	2	471

369	Q12680	Glutamate synthase [NADH] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLT1 PE=1 SV=2 - [GLT1_YEAST]	7.25	1.45%	1	2	2	2	2145
370	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]	6.47	10.75%	4	2	2	2	214

371	Q99207	Nucleolar complex protein 14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP14 PE=1 SV=1 - [NOP14_Y	6.81	2.84%	1	2	2	2	810
372	A5DUP0	UPF0507 protein LELG_01076 OS=Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) OX=379508 GN=LELG_01076 PE=3 SV=1 - [U507_LODEL]	2.14	0.56%	1	1	1	1	1260

373	A6ZPU3	ATP-dependent RNA helicase DBP4 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP4 PE=3 SV=1 - [DBP4_YEAS7]	3.46	1.95%	2	1	1	1	770
374	A6ZR36	Altered inheritance of mitochondria protein 9, mitochondrial OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=AIM9 PE=3 SV=1 - [AIM9_YEAS7]	3	1.75%	5	1	1	1	627

375	A6ZR39	Golgi to ER traffic protein 2 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=GET2 PE=3 SV=1 - [GET2_YEAS7]	3.59	7.72%	2	1	1	1	285
376	A6ZR73	High osmolarity signaling protein SHO1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=SHO1 PE=3 SV=1 - [SHO1_YEAS7]	3.14	4.09%	6	1	1	1	367

377	A6ZRM0	Adenylosuccinate synthetase OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ADE12 PE=3 SV=1 - [PURA_YEAS7]	4.09	3.93%	4	1	1	1	433
378	A6ZSX1	ATP-dependent rRNA helicase RRP3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=RRP3 PE=3 SV=1 - [RRP3_YEAS7]	3.02	2.20%	2	1	1	1	501

379	A6ZT02	Low-affinity glucose transporter HXT4 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=HXT4 PE=3 SV=1 - [HXT4_YEAS7]	2.98	1.56%	3	1	1	1	576
380	A6ZTA3	Pre-rRNA-processing protein RIX1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=RIX1 PE=3 SV=1 - [RIX1_YEAS7]	5.01	2.49%	2	1	1	1	763

381	A6ZU71	Ribosome biogenesis protein NSA1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NSA1 PE=3 SV=1 - [NSA1_YEAS7]	2.13	2.59%	2	1	1	1	463
382	A6ZUG2	Mitochondrial group I intron splicing factor CCM1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=CCM1 PE=3 SV=1 - [CCM1_YEAS7]	2.24	1.50%	5	1	1	1	864

383	A6ZUS8	rRNA-processing protein EFG1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=EFG1 PE=3 SV=1 - [EFG1P_YEAS7]	3.67	6.44%	1	1	1	1	233
384	A6ZUT6	Protein PXR1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=PXR1 PE=3 SV=1 - [PXR1_YEAS7]	2.87	5.54%	2	1	1	1	271
385	A6ZV63	Ribosome biogenesis protein SLX9 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=SLX9 PE=3 SV=1 - [SLX9_YEAS7]	2.96	5.71%	2	1	1	1	210

386	A6ZVM6	NADH-cytochrome b5 reductase 1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=CBR1 PE=3 SV=2 - [NCB5R_YEAS7]	2.22	2.82%	2	1	1	1	284
387	A6ZXM9	ATPase GET3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=GET3 PE=3 SV=1 - [GET3_YEAS7]	2.66	2.54%	1	1	1	1	354

388	A6ZXP4	ATP-dependent RNA helicase SUB2 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=SUB2 PE=3 SV=1 - [SUB2_YEAS7]	3.54	2.69%	2	1	1	1	446
389	A6ZY89	Pentafunctional AROM polypeptide OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ARO1 PE=3 SV=1 - [ARO1_YEAS7]	3.26	0.76%	5	1	1	1	1588

390	A6ZZS6	Membrane protein PTM1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=PTM1 PE=3 SV=1 - [PTM1_YEAS7]	2.66	2.10%	2	1	1	1	523
391	A7A261	LAS seventeen-binding protein 3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=LSB3 PE=3 SV=2 - [LSB3_YEAS7]	4.87	3.92%	1	1	1	1	459
392	B3LIN5	Golgi to ER traffic protein 1 OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=GET1 PE=3 SV=1 - [GET1_YEAS1]	3.42	5.96%	1	1	1	1	235

393	B3LNM2	Methionine aminopeptidase 2 OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=MAP2 PE=3 SV=1 - [MAP2_YEAS1]	4.94	3.80%	1	1	1	1	421
394	B3LQY3	Flap endonuclease 1 OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RAD27 PE=3 SV=1 - [FEN1_YEAS1]	3.53	3.66%	2	1	1	1	382

395	B3LRE5	Fe-S cluster assembly protein DRE2 OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=DRE2 PE=3 SV=1 - [DRE2_YEAS1]	2.53	3.45%	2	1	1	1	348
396	B3LU25	KRR1 small subunit processome component OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=KRR1 PE=3 SV=1 - [KRR1_YEAS1]	4.4	5.38%	1	1	1	1	316

397	O13563	26S proteasome regulatory subunit RPN13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN13 PE=1 SV=1 - [RPN13_YEAST]	3.11	8.33%	1	1	1	1	156
398	O74302	Transposon Ty1-DR4 Gag polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TY1A-DR4 PE=2 SV=1 - [YD13A_YEAST]	2.36	2.50%	48	1	1	1	440

399	P00128	Cytochrome b-c1 complex subunit 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=QCR7 PE=1 SV=2 - [QCR7_YEAST]	2.61	15.75%	1	1	1	1	127
400	P00425	Cytochrome c oxidase polypeptide 5B, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COX5B PE=1 SV=3 - [COX5B_YEAST]	3.82	9.27%	2	1	1	1	151

401	P00445	Superoxide dismutase [Cu-Zn] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SOD1 PE=1 SV=2 - [SODC_YEAST]	2.37	11.04%	1	1	1	1	154
402	P00958	Methionine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MES1 PE=1 SV=4 - [SYMC_YEAST]	3.08	1.73%	1	1	1	1	751

403	P01119	Ras-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RAS1 PE=1 SV=2 - [RAS1_YEAST]	2.15	3.88%	1	1	1	1	309
404	P02309	Histone H4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HHF1 PE=1 SV=2 - [H4_YEAST]	3.03	11.65%	2	1	1	1	103

405	P02992	Elongation factor Tu, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUF1 PE=1 SV=1 - [EFTU_YEAST]	2.37	2.06%	1	1	1	1	437
406	P04037	Cytochrome c oxidase subunit 4, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COX4 PE=1 SV=1 - [COX4_YEAST]	3.56	10.32%	1	1	1	1	155

407	P04806	Hexokinase-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HXK1 PE=1 SV=2 - [HXKA_YEAST]	2.49	1.65%	2	1	1	1	485
408	P04840	Mitochondrial outer membrane protein porin 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=POR1 PE=1 SV=4 - [VDAC1_YEAST]	3.35	4.24%	1	1	1	1	283

409	P05318	60S acidic ribosomal protein P1-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP1A PE=1 SV=4 - [RLA1_YEAST]	4.11	20.75%	1	1	1	1	106
410	P05626	ATP synthase subunit 4, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP4 PE=1 SV=2 - [ATPF_YEAST]	3.32	6.15%	1	1	1	1	244

411	P06102	General negative regulator of transcription subunit 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOT3 PE=1 SV=2 - [NOT3_YEAST]	3.48	1.56%	1	1	1	1	836
412	P06785	Thymidylate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC21 PE=1 SV=1 - [TYSY_YEAST]	4.63	4.93%	1	1	1	1	304

413	P06787	Calmodulin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CMD1 PE=1 SV=1 - [CALM_YEAST]	3.06	7.48%	1	1	1	1	147
414	P07143	Cytochrome c1, heme protein, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYT1 PE=1 SV=1 - [CY1_YEAST]	2.64	5.18%	1	1	1	1	309

415	P07213	Mitochondrial import receptor subunit TOM70 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOM70 PE=1 SV=2 - [TOM70_YEAST]	5.55	3.24%	1	1	1	1	617
416	P07246	Alcohol dehydrogenase 3, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADH3 PE=1 SV=2 - [ADH3_YEAST]	2.83	3.20%	1	1	1	1	375

417	P07263	Histidine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HTS1 PE=1 SV=2 - [SYH_YEAST]	3.46	2.56%	1	1	1	1	546
418	P07264	3-isopropylmalate dehydratase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LEU1 PE=1 SV=3 - [LEUC_YEAST]	2.19	1.28%	1	1	1	1	779

419	P07347	N-terminal acetyltransferase A complex catalytic subunit ARD1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARD1 PE=1 SV=2 - [ARD1_YEAST]	2.76	4.62%	1	1	1	1	238
420	P08417	Fumarate hydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FUM1 PE=1 SV=2 - [FUMH_YEAST]	4.1	3.07%	1	1	1	1	488

421	P08524	Farnesyl pyrophosphate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG20 PE=1 SV=2 - [FPPS_YEAST]	3.27	3.41%	1	1	1	1	352
422	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]	2.64	9.12%	1	1	1	1	285

423	P09436	Isoleucine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILS1 PE=1 SV=1 - [SYIC_YEAST]	2.91	1.31%	1	1	1	1	1072
424	P09440	C-1-tetrahydrofolate synthase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MIS1 PE=1 SV=1 - [C1TM_YEAST]	2.48	1.23%	1	1	1	1	975

425	P09457	ATP synthase subunit 5, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP5 PE=1 SV=1 - [ATPO_YEAST]	2.13	5.66%	1	1	1	1	212
426	P09620	Pheromone-processing carboxypeptidase KEX1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KEX1 PE=1 SV=1 - [KEX1_YEAST]	2.55	1.37%	4	1	1	1	729

427	P09734	Tubulin alpha-3 chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUB3 PE=1 SV=1 - [TBA3_YEAST]	2.52	2.02%	1	1	1	1	445
428	P09938	Ribonucleoside-diphosphate reductase small chain 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RNR2 PE=1 SV=2 - [RIR2_YEAST]	3.34	2.76%	1	1	1	1	399

429	P0CX27	60S ribosomal protein L42-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL42A PE=1 SV=1 - [RL44A_YEAST]	2.59	8.49%	2	1	1	1	106
430	P10363	DNA primase small subunit OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRI1 PE=1 SV=2 - [PRI1_YEAST]	2.25	3.18%	1	1	1	1	409

431	P10869	Aspartokinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOM3 PE=1 SV=2 - [AK_YEAST]	3.18	2.09%	1	1	1	1	527
432	P10962	Protein MAK16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAK16 PE=1 SV=2 - [MAK16_YEAST]	2.6	3.59%	1	1	1	1	306

433	P11076	ADP-ribosylation factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARF1 PE=1 SV=3 - [ARF1_YEAST]	2.51	4.42%	3	1	1	1	181
434	P11633	Non-histone chromosomal protein 6B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NHP6B PE=1 SV=3 - [NHP6B_YEAST]	3.36	13.13%	1	1	1	1	99

435	P11792	Serine/threonine-protein kinase SCH9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCH9 PE=1 SV=3 - [SCH9_YEAST]	2.79	2.43%	1	1	1	1	824
436	P12688	Serine/threonine-protein kinase YPK1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPK1 PE=1 SV=2 - [YPK1_YEAST]	4.54	2.50%	1	1	1	1	680

437	P12709	Glucose-6-phosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PGI1 PE=1 SV=3 - [G6PI_YEAST]	4.78	2.71%	1	1	1	1	554
438	P14906	Protein translocation protein SEC63 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC63 PE=1 SV=2 - [SEC63_YEAST]	4.15	1.81%	1	1	1	1	663

439	P16120	Threonine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=THR4 PE=1 SV=1 - [THRC_YEAST]	2.19	2.72%	1	1	1	1	514
440	P16370	DNA-directed RNA polymerase II subunit RPB3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPB3 PE=1 SV=2 - [RPB3_YEAST]	4.23	5.35%	1	1	1	1	318

441	P17423	Homoserine kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=THR1 PE=1 SV=4 - [KHSE_YEAST]	3.8	3.92%	1	1	1	1	357
442	P17505	Malate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MDH1 PE=1 SV=2 - [MDHM_YEAST]	4.52	4.19%	1	1	1	1	334

443	P17883	Superkiller protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SKI3 PE=1 SV=2 - [SKI3_YEAST]	2.76	1.05%	1	1	1	1	1432
444	P19454	Casein kinase II subunit alpha' OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CKA2 PE=1 SV=2 - [CSK22_YEAST]	2.82	2.65%	1	1	1	1	339

445	P19659	Mediator of RNA polymerase II transcription subunit 15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GAL11 PE=1 SV=3 - [MED15_YEAST]	2.33	1.30%	1	1	1	1	1081
446	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]	3.89	4.28%	1	1	1	1	304

447	P20606	Small COPII coat GTPase SAR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAR1 PE=1 SV=1 - [SAR1_YEAST]	4.03	6.84%	1	1	1	1	190
448	P21242	Probable proteasome subunit alpha type-7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE10 PE=1 SV=2 - [PSA7_YEAST]	2.64	4.17%	1	1	1	1	288

449	P21306	ATP synthase subunit epsilon, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP15 PE=1 SV=2 - [ATP5E_YEAST]	2.81	17.74%	1	1	1	1	62
450	P21576	Vacuolar protein sorting-associated protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VPS1 PE=1 SV=2 - [VPS1_YEAST]	2.63	1.70%	1	1	1	1	704

451	P21734	Ubiquitin-conjugating enzyme E2 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UBC1 PE=1 SV=1 - [UBC1_YEAST]	2.46	6.98%	1	1	1	1	215
452	P22141	Proteasome subunit beta type-4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE1 PE=1 SV=2 - [PSB4_YEAST]	3.41	5.56%	1	1	1	1	198

453	P22146	1,3-beta-glucanosyltransferase GAS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GAS1 PE=1 SV=2 - [GAS1_YEAST]	2.37	1.79%	1	1	1	1	559
454	P22506	Beta-glucosidase 1 OS=Saccharomycopsis fibuligera OX=4944 GN=BGL1 PE=3 SV=1 - [BGL1_SACFI]	2.23	1.14%	1	1	1	1	876

455	P22768	Argininosuccinate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARG1 PE=1 SV=3 - [ASSY_YEAST]	2.41	2.14%	1	1	1	1	420
456	P23291	Casein kinase I homolog 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YCK1 PE=1 SV=1 - [KC11_YEAST]	6.11	4.09%	1	1	1	1	538

457	P23585	High-affinity glucose transporter HXT2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HXT2 PE=1 SV=1 - [HXT2_YEAST]	3.24	2.03%	1	1	1	1	541
458	P23638	Proteasome subunit alpha type-3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE9 PE=1 SV=1 - [PSA3_YEAST]	2.81	5.43%	1	1	1	1	258

459	P23724	Proteasome subunit beta type-6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE7 PE=1 SV=1 - [PSB6_YEAST]	2.55	4.15%	1	1	1	1	241
460	P24280	SEC14 cytosolic factor OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC14 PE=1 SV=3 - [SEC14_YEAST]	3.85	4.28%	1	1	1	1	304

461	P25043	Proteasome subunit beta type-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PUP1 PE=1 SV=1 - [PSB2_YEAST]	2.42	4.60%	1	1	1	1	261
462	P25045	Serine palmitoyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LCB1 PE=1 SV=2 - [LCB1_YEAST]	4.27	2.51%	1	1	1	1	558

463	P25339	Pumilio homology domain family member 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PUF4 PE=1 SV=2 - [PUF4_YEAST]	3.17	1.13%	1	1	1	1	888
464	P25343	Reduced viability upon starvation protein 161 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RVS161 PE=1 SV=1 - [RV161_YEAST]	3.63	4.15%	1	1	1	1	265

465	P25623	Suppressor of yeast profilin deletion OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SYP1 PE=1 SV=3 - [SYP1_YEAST]	3.56	1.61%	1	1	1	1	870
466	P25644	DNA topoisomerase 2-associated protein PAT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PAT1 PE=1 SV=4 - [PAT1_YEAST]	4.15	2.01%	1	1	1	1	796

467	P26637	Leucine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC60 PE=1 SV=1 - [SYLC_YEAST]	4.14	1.83%	1	1	1	1	1090
468	P27614	Carboxypeptidase S OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CPS1 PE=1 SV=2 - [CBPS_YEAST]	4.05	2.26%	1	1	1	1	576

469	P27692	Transcription elongation factor SPT5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SPT5 PE=1 SV=1 - [SPT5_YEAST]	3.38	1.88%	1	1	1	1	1063
470	P27810	Alpha-1,2 mannosyltransferase KTR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KTR1 PE=1 SV=1 - [KTR1_YEAST]	2.62	3.05%	1	1	1	1	393

471	P28000	DNA-directed RNA polymerases I and III subunit RPAC2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPC19 PE=1 SV=1 - [RPAC2_YEAST]	4.55	10.56%	1	1	1	1	142
472	P28273	5-oxoprolinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OXP1 PE=1 SV=2 - [OPLA_YEAST]	2.97	1.01%	1	1	1	1	1286

473	P29055	Transcription initiation factor IIB OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUA7 PE=1 SV=1 - [TF2B_YEAST]	2.41	3.77%	1	1	1	1	345
474	P29496	Minichromosome maintenance protein 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MCM5 PE=1 SV=1 - [MCM5_YEAST]	2.12	1.03%	1	1	1	1	775

475	P29547	Elongation factor 1-gamma 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CAM1 PE=1 SV=2 - [EF1G1_YEAST]	2.33	3.13%	1	1	1	1	415
476	P30605	Myo-inositol transporter 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ITR1 PE=1 SV=2 - [ITR1_YEAST]	3.41	2.05%	1	1	1	1	584

477	P30656	Proteasome subunit beta type-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE2 PE=1 SV=3 - [PSB5_YEAST]	3.36	4.53%	1	1	1	1	287
478	P30822	Exportin-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CRM1 PE=1 SV=1 - [XPO1_YEAST]	2.48	0.92%	1	1	1	1	1084

479	P31373	Cystathionine gamma-lyase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYS3 PE=1 SV=2 - [CYS3_YEAST]	3.03	3.81%	1	1	1	1	394
480	P31382	Dolichyl-phosphate-mannose--protein mannosyltransferase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMT2 PE=1 SV=2 - [PMT2_YEAST]	2.46	1.32%	1	1	1	1	759

481	P31412	V-type proton ATPase subunit C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA5 PE=1 SV=4 - [VATC_YEAST]	2.62	2.55%	1	1	1	1	392
482	P32288	Glutamine synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLN1 PE=1 SV=4 - [GLNA_YE	4	4.86%	1	1	1	1	370

483	P32332	Mitochondrial oxaloacetate transport protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OAC1 PE=1 SV=1 - [OAC1_YEAST]	3.19	4.94%	1	1	1	1	324
484	P32333	TATA-binding protein-associated factor MOT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MOT1 PE=1 SV=1 - [MOT1_YEAST]	2.25	0.80%	1	1	1	1	1867

485	P32352	C-8 sterol isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG2 PE=1 SV=1 - [ERG2_YEAST]	3.06	5.41%	1	1	1	1	222
486	P32386	ATP-dependent bile acid permease OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YBT1 PE=1 SV=2 - [YBT1_YEAST]	2.56	0.72%	1	1	1	1	1661

487	P32445	Single-stranded DNA-binding protein RIM1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RIM1 PE=1 SV=1 - [RIM1_YEAST]	2.53	6.67%	1	1	1	1	135
488	P32457	Cell division control protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC3 PE=1 SV=3 - [CDC3_YEAST]	3.32	1.92%	1	1	1	1	520

489	P32463	Acyl carrier protein, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACP1 PE=1 SV=1 - [ACPM_YEAST]	3.74	12.80%	1	1	1	1	125
490	P32466	Low-affinity glucose transporter HXT3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HXT3 PE=1 SV=1 - [HXT3_YEAST]	2.11	1.76%	1	1	1	1	567

491	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]	2.95	3.28%	1	1	1	1	366
492	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]	4.1	12.00%	1	1	1	1	125

493	P32561	Histone deacetylase RPD3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPD3 PE=1 SV=1 - [RPD3_YEAST]	4.32	3.70%	1	1	1	1	433
494	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]	3.53	1.43%	1	1	1	1	840

495	P32564	Protein SCM4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCM4 PE=1 SV=1 - [SCM4_YEAST]	2.57	5.35%	1	1	1	1	187
496	P32588	Nuclear and cytoplasmic polyadenylated RNA-binding protein PUB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PUB1 PE=1 SV=4 - [PUB1_YEAST]	2.17	1.99%	1	1	1	1	453

497	P32608	Retrograde regulation protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RTG2 PE=1 SV=2 - [RTG2_YEAST]	2.4	1.87%	1	1	1	1	588
498	P32791	Ferric/cupric reductase transmembrane component 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FRE1 PE=1 SV=1 - [FRE1_YEAST]	3.22	2.04%	1	1	1	1	686

499	P32892	ATP-dependent RNA helicase DRS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DRS1 PE=1 SV=2 - [DRS1_YEAST]	3.19	1.60%	2	1	1	1	752
500	P32899	U3 small nucleolar ribonucleoprotein protein IMP3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMP3 PE=1 SV=1 - [IMP3_YEAST]	3.1	5.46%	1	1	1	1	183

501	P32901	Peptide transporter PTR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PTR2 PE=1 SV=2 - [PTR2_YEAST]	4.35	2.33%	1	1	1	1	601
502	P32911	Eukaryotic translation initiation factor eIF-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUI1 PE=1 SV=1 - [SUI1_YEAST]	3.62	13.89%	1	1	1	1	108

503	P32916	Signal recognition particle receptor subunit alpha homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRP101 PE=1 SV=2 - [SRPR_YEAST]	3.06	1.93%	1	1	1	1	621
504	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]	2.78	9.36%	1	1	1	1	171

505	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]	2.22	0.99%	1	1	1	1	1511
506	P33313	Hsp70/Hsp90 co-chaperone CNS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CNS1 PE=1 SV=1 - [CNS1_YEAST]	3.75	4.68%	1	1	1	1	385

507	P33328	Synaptobrevin homolog 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SNC2 PE=1 SV=2 - [SNC2_YEAST]	2.3	10.43%	1	1	1	1	115
508	P33399	La protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LHP1 PE=1 SV=2 - [LHP1_YEAST]	5.61	6.18%	1	1	1	1	275

509	P35180	Mitochondrial import receptor subunit TOM20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOM20 PE=1 SV=1 - [TOM20_YEAST]	3.41	7.10%	1	1	1	1	183
510	P35691	Translationally-controlled tumor protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA19 PE=1 SV=1 - [TCTP_YEAST]	4.32	9.58%	1	1	1	1	167

511	P36008	Elongation factor 1-gamma 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TEF4 PE=1 SV=1 - [EF1G2_YEAST]	2.16	1.70%	1	1	1	1	412
512	P36015	Synaptobrevin homolog YKT6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YKT6 PE=1 SV=1 - [YKT6_YEAST]	3.37	6.00%	1	1	1	1	200

513	P36057	Signal recognition particle receptor subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRP102 PE=1 SV=1 - [SRPB_YEAST]	3.02	6.56%	1	1	1	1	244
514	P36081	Uncharacterized protein YKL077W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YKL077W PE=1 SV=1 - [YKH7_YEAST]	2.26	3.06%	1	1	1	1	392

515	P36144	Ribosome biogenesis protein UTP30 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP30 PE=1 SV=1 - [RL1D1_YEAST]	2.25	5.47%	1	1	1	1	274
516	P36149	Trafficking protein particle complex subunit BET3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BET3 PE=1 SV=1 - [BET3_YEAST]	2.81	5.70%	1	1	1	1	193

517	P36160	Ribosome biogenesis protein RPF2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPF2 PE=1 SV=1 - [RPF2_YEAST]	2.48	3.49%	1	1	1	1	344
518	P36161	Nucleoporin NUP133 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NUP133 PE=1 SV=1 - [NU133_YEAST]	3.04	1.04%	1	1	1	1	1157

519	P36521	54S ribosomal protein L11, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MRPL11 PE=1 SV=2 - [RM11_YEAST]	2.74	4.02%	1	1	1	1	249
520	P36528	54S ribosomal protein L17, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MRPL17 PE=1 SV=2 - [RM17_YEAST]	4.59	4.98%	1	1	1	1	281

521	P37303	Low specificity L-threonine aldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLY1 PE=1 SV=2 - [GLY1_YEAST]	3.43	3.62%	1	1	1	1	387
522	P37838	Nucleolar protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP4 PE=1 SV=1 - [NOP4_YEAST]	5	2.92%	1	1	1	1	685

523	P38077	ATP synthase subunit gamma, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP3 PE=1 SV=1 - [ATPG_YEAST]	3.98	4.18%	1	1	1	1	311
524	P38088	Glycine--tRNA ligase 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GRS1 PE=1 SV=3 - [SYG_YEAST]	3.89	2.32%	1	1	1	1	690

525	P38137	Peroxisomal-coenzyme A synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PCS60 PE=1 SV=1 - [FAT2_YEAST]	4.11	2.39%	1	1	1	1	543
526	P38152	Tricarboxylate transport protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CTP1 PE=2 SV=3 - [TXTP_YEAST]	2.4	3.68%	1	1	1	1	299

527	P38153	AP-3 complex subunit mu OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=APM3 PE=1 SV=2 - [AP3M_YEAST]	3.86	2.90%	1	1	1	1	483
528	P38205	Multisite-specific tRNA:(cytosine-C(5))-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NCL1 PE=1 SV=1 - [NCL1_YEAST]	3.86	2.34%	1	1	1	1	684

529	P38221	Phosphatidate cytidylyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDS1 PE=1 SV=1 - [CDS1_YEAST]	2.97	2.63%	1	1	1	1	457
530	P38256	Uncharacterized protein YBR096W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YBR096W PE=1 SV=1 - [YBU6_YEAST]	3.45	5.22%	1	1	1	1	230

531	P38264	SRP-independent targeting protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PHO88 PE=1 SV=1 - [PHO88_YEAST]	2.64	11.17%	1	1	1	1	188
532	P38288	Protein TOS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOS1 PE=1 SV=1 - [TOS1_YEAST]	2.15	2.20%	1	1	1	1	455

533	P38323	ATP-dependent clpX-like chaperone, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MCX1 PE=1 SV=1 - [CLPX_YEAST]	3.79	2.50%	1	1	1	1	520
534	P38333	Essential nuclear protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ENP1 PE=1 SV=1 - [ENP1_YEAST]	3.05	3.31%	1	1	1	1	483

535	P38342	3-ketodihydrosphingosine reductase TSC10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TSC10 PE=1 SV=2 - [TSC10_YEAST]	2.45	2.81%	1	1	1	1	320
536	P38604	Lanosterol synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG7 PE=1 SV=6 - [ERG7_YEAST]	3.89	2.05%	1	1	1	1	731

537	P38682	ADP-ribosylation factor GTPase-activating protein GLO3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLO3 PE=1 SV=1 - [GLO3_YEAST]	3.15	2.23%	1	1	1	1	493
538	P38689	Ribose-phosphate pyrophosphokinase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRS3 PE=1 SV=1 - [KPR3_YEAST]	3.51	3.75%	1	1	1	1	320

539	P38691	Serine/threonine-protein kinase KSP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KSP1 PE=1 SV=1 - [KSP1_YEAST]	2.34	1.07%	1	1	1	1	1029
540	P38707	Asparagine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DED81 PE=1 SV=1 - [SYNC_YEAST]	4.13	2.53%	1	1	1	1	554

541	P38708	Putative proline--tRNA ligase YHR020W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YHR020W PE=1 SV=1 - [YHI0_YEAST]	2.43	2.33%	1	1	1	1	688
542	P38787	2-dehydropantoate 2-reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PAN5 PE=1 SV=1 - [PANE_YEAST]	3.66	3.69%	1	1	1	1	379

543	P38795	Glutamine-dependent NAD(+) synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=QNS1 PE=1 SV=1 - [NADE_YE	4.42	2.10%	1	1	1	1	714
544	P38805	Ribosome production factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPF1 PE=1 SV=1 - [RPF1_YEAST]	2.7	4.41%	1	1	1	1	295

545	P38810	SED5-binding protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SFB3 PE=1 SV=1 - [SFB3_YEAST]	3.21	1.08%	1	1	1	1	929
546	P38836	Putative metallocarboxypeptidase ECM14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ECM14 PE=1 SV=1 - [ECM14_YEAST]	2.14	2.09%	1	1	1	1	430

547	P38882	U3 small nucleolar RNA-associated protein 9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP9 PE=1 SV=1 - [UTP9_YEAST]	2.34	2.09%	1	1	1	1	575
548	P38886	26S proteasome regulatory subunit RPN10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN10 PE=1 SV=3 - [RPN10_YEAST]	2.87	7.09%	1	1	1	1	268

549	P38972	Phosphoribosylformylglycinamidine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE6 PE=1 SV=2 - [PUR4_YEAST]	3.18	1.10%	1	1	1	1	1358
550	P38998	Saccharopine dehydrogenase [NAD(+), L-lysine-forming] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS1 PE=1 SV=3 - [LYS1_YEAST]	3.95	5.09%	1	1	1	1	373

551	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]	2.62	1.30%	1	1	1	1	694
552	P39533	Homocitrate dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACO2 PE=1 SV=1 - [ACON2_YEAST]	2.8	1.65%	1	1	1	1	789

553	P39692	Sulfite reductase [NADPH] flavoprotein component OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET10 PE=1 SV=2 - [MET10_YEAST]	2.47	1.16%	1	1	1	1	1035
554	P39925	Mitochondrial respiratory chain complexes assembly protein AFG3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AFG3 PE=1 SV=1 - [AFG3_YEAST]	2.59	1.58%	2	1	1	1	761

555	P39926	Protein SSO2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSO2 PE=1 SV=2 - [SSO2_YEAST]	2.65	3.39%	1	1	1	1	295
556	P39931	Protein SSP120 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSP120 PE=1 SV=1 - [SS120_YEAST]	3.6	5.13%	1	1	1	1	234

557	P39968	Vacuolar protein 8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VAC8 PE=1 SV=3 - [VAC8_YEAST]	2.47	1.90%	1	1	1	1	578
558	P39985	rDNA transcriptional regulator POL5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=POL5 PE=1 SV=1 - [DPO5_YEAST]	2.54	1.08%	1	1	1	1	1022

559	P40007	Nucleolar protein 16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP16 PE=1 SV=1 - [NOP16_Y	3.38	5.19%	1	1	1	1	231
560	P40016	26S proteasome regulatory subunit RPN3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN3 PE=1 SV=5 - [RPN3_YEAST]	4.06	2.87%	1	1	1	1	523

561	P40032	Prolyl 3,4-dihydroxylase TPA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPA1 PE=1 SV=1 - [TPA1_YEAST]	2.25	1.86%	1	1	1	1	644
562	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]	3.54	2.17%	1	1	1	1	554

563	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]	2.62	2.31%	2	1	1	1	347
564	P40348	Replication factor C subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RFC2 PE=1 SV=1 - [RFC2_YEAST]	4.01	4.25%	1	1	1	1	353

565	P40462	Protein TMA108 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA108 PE=1 SV=1 - [TM108_YEAST]	2.22	0.85%	1	1	1	1	946
566	P40478	Mitochondrial outer membrane protein porin 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=POR2 PE=1 SV=1 - [VDAC2_YEAST]	2.94	5.34%	1	1	1	1	281

567	P40495	Homoisocitrate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS12 PE=1 SV=1 - [LYS12_YEAST]	3.12	3.23%	1	1	1	1	371
568	P40533	Protein TED1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TED1 PE=1 SV=1 - [TED1_YEAST]	2.73	2.33%	1	1	1	1	473

569	P40557	ER-retained PMA1-suppressing protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EPS1 PE=1 SV=1 - [EPS1_YEAST]	2.26	1.57%	1	1	1	1	701
570	P40580	Benzil reductase ((S)-benzoin forming) IRC24 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IRC24 PE=1 SV=1 - [BZRD_YEAST]	2.58	3.80%	1	1	1	1	263

571	P40850	Protein MKT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MKT1 PE=1 SV=2 - [MKT1_YEAST]	2.74	1.20%	1	1	1	1	830
572	P41057	40S ribosomal protein S29-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS29A PE=1 SV=3 - [RS29A_YEAST]	2.34	17.86%	1	1	1	1	56

573	P41058	40S ribosomal protein S29-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS29B PE=1 SV=3 - [RS29B_YEAST]	2.18	12.50%	1	1	1	1	56
574	P41810	Coatomer subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC26 PE=1 SV=2 - [COPB_YEAST]	2.93	1.03%	1	1	1	1	973

575	P41819	Dimethyladenosine transferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DIM1 PE=3 SV=1 - [DIM1_YEAST]	2.84	3.46%	2	1	1	1	318
576	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]	2.53	2.95%	1	1	1	1	440

577	P41920	Ran-specific GTPase-activating protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YRB1 PE=1 SV=1 - [YRB1_YEAST]	3.74	5.47%	1	1	1	1	201
578	P42842	Essential for maintenance of the cell wall protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMW1 PE=1 SV=1 - [EMW1_YEAST]	2.4	1.11%	1	1	1	1	904

579	P42846	Protein KRI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRI1 PE=1 SV=1 - [KRI1_YEAST]	2.53	1.86%	1	1	1	1	591
580	P43123	UDP-N-acetylglucosamine pyrophosphorylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=QRI1 PE=1 SV=1 - [UAP1_YEAST]	3.22	2.10%	1	1	1	1	477

581	P43556	Rho-GTPase-activating protein RGD2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RGD2 PE=1 SV=1 - [RGD2_YEAST]	2.2	1.40%	1	1	1	1	714
582	P43585	Vacuolar transporter chaperone 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VTC2 PE=1 SV=1 - [VTC2_YEAST]	2.72	1.45%	1	1	1	1	828

583	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]	3.89	6.37%	1	1	1	1	204
584	P43636	Alpha-1,3/1,6-mannosyltransferase ALG2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALG2 PE=1 SV=2 - [ALG2_YEAST]	2.75	2.58%	1	1	1	1	503

585	P46655	Glutamate--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GUS1 PE=1 SV=3 - [SYEC_YEAST]	2.33	1.41%	1	1	1	1	708
586	P46985	Probable alpha-1,6-mannosyltransferase MNN11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MNN11 PE=1 SV=2 - [MNN11_YEAST]	2.34	1.66%	1	1	1	1	422

587	P46992	Cell wall protein YJL171C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YJL171C PE=1 SV=2 - [YJR1_YEAST]	3.19	3.54%	1	1	1	1	396
588	P47006	DNA-directed RNA polymerase I subunit RPA34 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPA34 PE=1 SV=1 - [RPA34_YEAST]	2.25	3.43%	1	1	1	1	233

589	P47018	Maintenance of telomere capping protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MTC1 PE=1 SV=1 - [MTC1_YEAST]	2.45	2.30%	1	1	1	1	478
590	P47019	Ribosome biogenesis protein ALB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALB1 PE=1 SV=1 - [ALB1_YEAST]	6.18	14.29%	1	1	1	1	175

591	P47068	Myosin tail region-interacting protein MTI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BBC1 PE=1 SV=2 - [BBC1_YEAST]	2.72	0.95%	1	1	1	1	1157
592	P47089	Translation machinery-associated protein 22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA22 PE=1 SV=1 - [DENR_YEAST]	5.38	8.59%	1	1	1	1	198

593	P48234	Ribosome biogenesis protein ENP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ENP2 PE=1 SV=2 - [NOL10_YEAST]	4.03	2.69%	1	1	1	1	707
594	P48239	Glutathione S-transferase omega-like 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GTO1 PE=1 SV=1 - [GTO1_YEAST]	4.29	4.49%	1	1	1	1	356

595	P48361	Activator of SKN7 protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ASK10 PE=1 SV=2 - [ASK10_Y	2.98	1.48%	1	1	1	1	1146
596	P48362	Protein HGH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HGH1 PE=1 SV=2 - [HGH1_YEAST]	3.28	3.30%	1	1	1	1	394

597	P48415	COPII coat assembly protein SEC16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC16 PE=1 SV=2 - [SEC16_YEAST]	3.7	0.73%	1	1	1	1	2195
598	P49095	Glycine dehydrogenase (decarboxylating), mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCV2 PE=1 SV=1 - [GCSP_YEAST]	3.34	1.26%	1	1	1	1	1034

599	P49573	Copper transport protein CTR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CTR1 PE=1 SV=1 - [CTR1_YEAST]	4.66	4.19%	1	1	1	1	406
600	P49723	Ribonucleoside-diphosphate reductase small chain 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RNR4 PE=1 SV=1 - [RIR4_YEAST]	2.15	2.61%	1	1	1	1	345

601	P51601	GTP cyclohydrolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FOL2 PE=1 SV=1 - [GCH1_YEAST]	2.35	3.70%	1	1	1	1	243
602	P52871	Protein transport protein SBH2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SBH2 PE=1 SV=1 - [SC6B2_YEAST]	3.21	14.77%	1	1	1	1	88

603	P53073	ER membrane protein complex subunit 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMC4 PE=1 SV=1 - [EMC4_YEAST]	2.44	5.26%	1	1	1	1	190
604	P53081	NGG1-interacting factor 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NIF3 PE=1 SV=1 - [NIF3_YEAST]	2.6	4.51%	1	1	1	1	288

605	P53090	Aromatic/aminoadipate aminotransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARO8 PE=1 SV=1 - [ARO8_YEAST]	2.24	2.40%	1	1	1	1	500
606	P53111	NADPH-dependent aldehyde reductase ARI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARI1 PE=1 SV=1 - [ARI1_YEAST]	3.24	4.32%	1	1	1	1	347

607	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]	2.63	1.17%	1	1	1	1	767
608	P53145	Large subunit GTPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LSG1 PE=1 SV=1 - [LSG1_YEAST]	4.26	2.19%	1	1	1	1	640

609	P53183	Putative uncharacterized oxidoreductase YGL039W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YGL039W PE=1 SV=1 - [YGD9_YEAST]	3.43	4.31%	1	1	1	1	348
610	P53184	Nicotinamidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PNC1 PE=1 SV=1 - [PNC1_YEAST]	2.64	5.56%	1	1	1	1	216

611	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]	3.76	1.05%	1	1	1	1	1237
612	P53278	Uncharacterized protein YGR130C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YGR130C PE=1 SV=1 - [YG3A_YEAST]	3.67	2.33%	1	1	1	1	816

613	P53297	PAB1-binding protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PBP1 PE=1 SV=1 - [PBP1_YEAST]	4.55	2.08%	1	1	1	1	722
614	P53299	Mitochondrial import inner membrane translocase subunit TIM13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIM13 PE=1 SV=1 - [TIM13_YEAST]	3.07	10.48%	1	1	1	1	105

615	P53549	26S proteasome subunit RPT4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT4 PE=1 SV=4 - [PRS10_YEAST]	3.1	2.52%	1	1	1	1	437
616	P53723	UPF0674 endoplasmic reticulum membrane protein YNR021W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YNR021W PE=1 SV=3 - [YN8B_YEAST]	3.74	4.21%	1	1	1	1	404

617	P53742	Nucleolar GTP-binding protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOG2 PE=1 SV=1 - [NOG2_YEAST]	3.23	2.67%	1	1	1	1	486
618	P53849	Zinc finger protein GIS2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GIS2 PE=1 SV=1 - [GIS2_YEA	2.74	7.84%	1	1	1	1	153

619	P53868	Alpha-1,2-mannosyltransferase ALG9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALG9 PE=1 SV=1 - [ALG9_YEAST]	4.03	2.34%	1	1	1	1	555
620	P53874	Ubiquitin carboxyl-terminal hydrolase 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UBP10 PE=1 SV=2 - [UBP10_YEAST]	2.15	0.88%	1	1	1	1	792

621	P53881	54S ribosomal protein L22, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MRPL22 PE=1 SV=2 - [RM22_YEAST]	3.38	5.18%	1	1	1	1	309
622	P53914	RNA cytidine acetyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRE33 PE=1 SV=1 - [NAT10_YEAST]	3.69	1.42%	1	1	1	1	1056

623	P54783	D-arabinono-1,4-lactone oxidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALO1 PE=1 SV=1 - [ALO_YEAST]	2.89	3.04%	1	1	1	1	526
624	P54885	Gamma-glutamyl phosphate reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRO2 PE=1 SV=1 - [PROA_YEAST]	4.4	3.51%	1	1	1	1	456

625	P89102	Exocyst complex component SEC5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC5 PE=1 SV=1 - [SEC5_YEAST]	2.44	1.34%	1	1	1	1	971
626	Q01477	Ubiquitin carboxyl-terminal hydrolase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UBP3 PE=1 SV=1 - [UBP3_YEAST]	4.28	1.75%	1	1	1	1	912

627	Q01649	Spindle pole body-associated protein CIK1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CIK1 PE=1 SV=1 - [CIK1_YEAST]	2.53	1.52%	1	1	1	1	594
628	Q01662	Methionine aminopeptidase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAP1 PE=1 SV=2 - [MAP1_YEAST]	2.58	2.07%	1	1	1	1	387

629	Q01939	26S proteasome regulatory subunit 8 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT6 PE=1 SV=4 - [PRS8_YEAST]	2.45	3.46%	1	1	1	1	405
630	Q02196	Adenylyl-sulfate kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET14 PE=1 SV=1 - [KAPS_YEAST]	3.08	6.44%	3	1	1	1	202

631	Q02256	Tyrosine-protein phosphatase YVH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YVH1 PE=1 SV=1 - [PVH1_YEAST]	3.35	4.40%	1	1	1	1	364
632	Q02354	U3 small nucleolar RNA-associated protein 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP6 PE=1 SV=2 - [UTP6_YEAST]	2.38	2.05%	1	1	1	1	440

633	Q02793	Antiviral protein SKI8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SKI8 PE=1 SV=1 - [SKI8_YEAST]	2.36	2.52%	1	1	1	1	397
634	Q02931	NET1-associated nuclear protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NAN1 PE=1 SV=1 - [UTP17_YEAST]	2.44	1.12%	1	1	1	1	896

635	Q03102	Uncharacterized membrane protein YML131W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YML131W PE=1 SV=1 - [YMN1_YEAST]	2.38	2.74%	1	1	1	1	365
636	Q03195	Translation initiation factor RLI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RLI1 PE=1 SV=1 - [RLI1_YEAST]	2.6	1.81%	1	1	1	1	608

637	Q03264	RNA exonuclease NGL2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NGL2 PE=1 SV=1 - [NGL2_YEAST]	3.15	3.11%	1	1	1	1	515
638	Q03655	Probable 1,3-beta-glucanosyltransferase GAS3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GAS3 PE=1 SV=1 - [GAS3_YEAST]	2.32	2.10%	1	1	1	1	524

639	Q03769	Epsin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ENT5 PE=1 SV=1 - [ENT5_YEAST]	2.82	2.92%	1	1	1	1	411
640	Q03862	Probable metalloprotease ARX1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARX1 PE=1 SV=1 - [ARX1_YEAST]	3.29	2.19%	1	1	1	1	593

641	Q03973	High mobility group protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HMO1 PE=1 SV=1 - [HMO1_YEAST]	2.88	4.88%	1	1	1	1	246
642	Q04062	26S proteasome regulatory subunit RPN9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN9 PE=1 SV=1 - [RPN9_YEAST]	2.55	2.54%	1	1	1	1	393

643	Q04177	U3 small nucleolar RNA-associated protein 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP5 PE=1 SV=1 - [UTP5_YEAST]	4.41	2.18%	1	1	1	1	643
644	Q04201	CUE domain-containing protein CUE4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CUE4 PE=1 SV=1 - [CUE4_YEAST]	5.84	23.93%	1	1	1	1	117

645	Q04305	U3 small nucleolar RNA-associated protein 15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP15 PE=1 SV=1 - [UTP15_YEAST]	3.19	2.53%	1	1	1	1	513
646	Q04338	t-SNARE VTI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VTI1 PE=1 SV=3 - [VTI1_YEAST]	3.98	6.45%	1	1	1	1	217

647	Q04344	Hit family protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HNT1 PE=1 SV=2 - [HNT1_YEAST]	3.25	7.59%	1	1	1	1	158
648	Q04602	Vacuolar basic amino acid transporter 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VBA4 PE=1 SV=1 - [VBA4_YEAST]	4.25	2.21%	1	1	1	1	768

649	Q04869	Uncharacterized protein YMR315W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YMR315W PE=1 SV=1 - [YM94_YEAST]	3.07	6.30%	1	1	1	1	349
650	Q04991	Protein FMP42 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FMP42 PE=1 SV=1 - [FMP42_YEAST]	2.76	2.18%	1	1	1	1	504

651	Q05016	NADP-dependent 3-hydroxy acid dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YMR226C PE=1 SV=1 - [YM71_YEAST]	2.2	4.87%	1	1	1	1	267
652	Q05027	Transcription initiation factor TFIID subunit 9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TAF9 PE=1 SV=1 - [TAF9_YEAST]	2.81	12.74%	1	1	1	1	157

653	Q05359	Protein ERP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERP1 PE=1 SV=1 - [ERP1_YEAST]	3.79	5.48%	1	1	1	1	219
654	Q05543	Regulator of Ty1 transposition protein 103 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RTT103 PE=1 SV=1 - [RT103_YEAST]	3.15	3.91%	1	1	1	1	409

655	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]	2.52	4.15%	1	1	1	1	265
656	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]	3.33	1.35%	1	1	1	1	817

657	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]	2.75	1.58%	1	1	1	1	887
658	Q06142	Importin subunit beta-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KAP95 PE=1 SV=1 - [IMB1_YEAST]	2.27	1.16%	1	1	1	1	861

659	Q06287	Ribosomal RNA small subunit methyltransferase NEP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMG1 PE=1 SV=1 - [NEP1_YEAST]	4.29	5.16%	1	1	1	1	252
660	Q06344	Pre-rRNA-processing protein ESF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ESF1 PE=1 SV=1 - [ESF1_YEAST]	3.25	2.23%	1	1	1	1	628

661	Q07457	E3 ubiquitin-protein ligase BRE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BRE1 PE=1 SV=1 - [BRE1_YEAST]	2.44	1.86%	1	1	1	1	700
662	Q07657	Seventh homolog of septin 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SHS1 PE=1 SV=1 - [SHS1_YEAST]	3.04	2.18%	1	1	1	1	551

663	Q07824	Polyamine transporter 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPO1 PE=1 SV=1 - [TPO1_YEAST]	4.26	2.90%	1	1	1	1	586
664	Q07896	Nucleolar complex-associated protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOC3 PE=1 SV=1 - [NOC3_YEAST]	3.07	2.11%	1	1	1	1	663

665	Q07915	Ribosome biogenesis protein RLP24 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RLP24 PE=1 SV=1 - [RLP24_YEAST]	3.27	5.03%	1	1	1	1	199
666	Q07953	Ribosome maturation protein SDO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SDO1 PE=1 SV=1 - [SDO1_YEAST]	2.44	3.20%	1	1	1	1	250

667	Q08208	Nucleolar protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP12 PE=1 SV=1 - [NOP12_Y	3.24	2.83%	1	1	1	1	459
668	Q08237	RNA exonuclease 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=REX4 PE=1 SV=1 - [REXO4_YEAST]	2.57	4.50%	1	1	1	1	289

669	Q08287	60S ribosome subunit biogenesis protein NOP8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP8 PE=1 SV=1 - [NOP8_YEAST]	3.51	2.89%	1	1	1	1	484
670	Q08444	20S-pre-rRNA D-site endonuclease NOB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOB1 PE=1 SV=1 - [NOB1_YEAST]	2.93	2.61%	1	1	1	1	459

671	Q08492	Bud site selection protein 21 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BUD21 PE=1 SV=1 - [BUD21_Y	2.52	5.14%	1	1	1	1	214
672	Q08742	Thiosulfate sulfurtransferase RDL2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RDL2 PE=1 SV=1 - [RDL2_YEAST]	2.47	5.37%	1	1	1	1	149

673	Q08962	60S ribosome subunit biogenesis protein NIP7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NIP7 PE=1 SV=1 - [NIP7_YEAST]	2.62	6.08%	1	1	1	1	181
674	Q12000	Translation machinery-associated protein 46 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA46 PE=1 SV=2 - [TMA46_YEAST]	2.83	2.90%	1	1	1	1	345

675	Q12034	Protein SLF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SLF1 PE=1 SV=1 - [SLF1_YEAST]	2.82	3.58%	1	1	1	1	447
676	Q12055	Adenylate kinase isoenzyme 6 homolog FAP7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAP7 PE=1 SV=1 - [KAD6_YEAST]	3.37	6.09%	1	1	1	1	197

677	Q12080	Ribosome biogenesis protein NOP53 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP53 PE=1 SV=1 - [NOP53_YEAST]	3.38	3.08%	1	1	1	1	455
678	Q12118	Small glutamine-rich tetratricopeptide repeat-containing protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SGT2 PE=1 SV=1 - [SGT2_YEAST]	2.15	2.60%	1	1	1	1	346

679	Q12136	Something about silencing protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAS10 PE=1 SV=1 - [SAS10_Y	4.34	2.62%	1	1	1	1	610
680	Q12176	Ribosome biogenesis protein MAK21 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAK21 PE=1 SV=1 - [MAK21_YEAST]	3.68	1.27%	1	1	1	1	1025

681	Q12233	ATP synthase subunit g, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP20 PE=1 SV=1 - [ATPN_YEAST]	3	9.57%	1	1	1	1	115
682	Q12246	Sphingoid long chain base kinase 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LCB4 PE=1 SV=1 - [LCB4_YEAST]	3.52	2.56%	1	1	1	1	624

683	Q12263	Serine/threonine-protein kinase GIN4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GIN4 PE=1 SV=1 - [GIN4_YEAST]	2.76	1.31%	1	1	1	1	1142
684	Q12305	Thiosulfate:glutathione sulfurtransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RDL1 PE=1 SV=1 - [RDL1_YEAST]	3.72	10.07%	1	1	1	1	139

685	Q12402	Protein YOP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YOP1 PE=1 SV=3 - [YOP1_YEAST]	2.9	4.44%	1	1	1	1	180
686	Q12434	Rho GDP-dissociation inhibitor OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RDI1 PE=1 SV=1 - [GDIR_YEAST]	2.23	5.45%	1	1	1	1	202

687	Q12449	Hsp90 co-chaperone AHA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AHA1 PE=1 SV=1 - [AHA1_YEAST]	2.51	2.86%	1	1	1	1	350
688	Q12466	Tricalbin-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TCB1 PE=1 SV=1 - [TCB1_YEAST]	3.48	1.01%	1	1	1	1	1186

689	Q12480	Probable electron transfer flavoprotein subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AIM45 PE=1 SV=1 - [ETFA_YEAST]	4.61	5.52%	1	1	1	1	344
690	Q12675	Phospholipid-transporting ATPase DNF2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DNF2 PE=1 SV=1 - [ATC4_YEAST]	2.18	0.62%	1	1	1	1	1612

691	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]	3.14	4.49%	1	1	1	1	312
692	Q3E764	Translation machinery-associated protein 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA7 PE=1 SV=1 - [TMA7_YEAST]	2.52	20.31%	1	1	1	1	64

693	Q3E772	Protein LSO2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LSO2 PE=2 SV=1 - [LSO2_YEAST]	3.44	14.13%	1	1	1	1	92
694	Q3E834	Protein transport protein YOS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YOS1 PE=1 SV=1 - [YOS1_YEAST]	3.64	18.82%	1	1	1	1	85

695	Q74ZK4	Glutathione reductase OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=GLR1 PE=3 SV=1 - [GSHR_ASHGO]	3.76	2.92%	2	1	1	1	480
696	Q753C6	Pre-rRNA-processing protein PNO1 OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=PNO1 PE=3 SV=3 - [PNO1_ASHGO]	2.18	3.00%	2	1	1	1	267

697	Q75EB3	Mediator of RNA polymerase II transcription subunit 31 OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=SOH1 PE=3 SV=1 - [MED31_ASHGO]	2.13	6.30%	1	1	1	1	127
698	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]	2.27	7.87%	6	1	1	1	127

699	Q8NJR6	Protein URE2 OS=Saccharomyces bayanus OX=4931 GN=URE2 PE=3 SV=1 - [URE2_SACBA]	2.93	3.48%	3	1	1	1	345
700	Q99297	Mitochondrial 2-oxodicarboxylate carrier 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ODC2 PE=1 SV=1 - [ODC2_YEAST]	2.65	3.91%	1	1	1	1	307
701	Q9LIK9	ATP sulfurylase 1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=APS1 PE=1 SV=1 - [APS1_ARATH]	2.35	4.10%	1	1	1	1	463