

Supplementary Table S2, Lin et al.

Number	RSC core protein	Identified Proteins (1636)	Accession Number	Molecular Weight	TEV Eluate				TEV Eluate				TEV Eluate			
					Streptactin 2	Streptactin 3	Peak grad.	Total spectrum count	Streptactin 2	Streptactin 3	Peak grad.	Exclusive unique peptide count	Streptactin 2	Streptactin 3	Peak grad.	Sequence coverage
1	Yes	Sth1p [Saccharomyces cerevisiae S288c]	gi 6322065	157 kDa	584	1117	1536	1025	80	87	92	80	48.1%	50.1%	51.3%	47.8%
2	Yes	Rsc8p [Saccharomyces cerevisiae S288c]	gi 14318562 (+1)	63 kDa	283	657	906	949	40	45	49	44	58.5%	63.9%	74.1%	62.7%
3	Yes	Rsc4p [Saccharomyces cerevisiae S288c]	gi 398364889 (+2)	72 kDa	558	492	632	654	42	46	43	38	59.2%	58.6%	64.0%	52.5%
4	Yes	Rsc2p [Saccharomyces cerevisiae S288c]	gi 6323389	102 kDa	235	500	612	483	44	60	66	60	55.0%	62.4%	70.5%	62.4%
5	Yes	Rsc58p [Saccharomyces cerevisiae S288c]	gi 6323061 (+1)	58 kDa	172	466	608	586	32	40	43	39	59.8%	75.3%	75.3%	73.1%
6	Yes	Npl6p [Saccharomyces cerevisiae S288c]	gi 6323738	50 kDa	216	497	630	557	27	29	29	30	61.8%	63.7%	69.7%	65.1%
7	Yes	Rsc9p [Saccharomyces cerevisiae S288c]	gi 6323508	65 kDa	107	347	457	385	22	28	38	28	32.5%	37.7%	56.3%	41.8%
8	Yes	Arp9p [Saccharomyces cerevisiae S288c]	gi 6323676	53 kDa	140	375	501	399	21	26	29	27	37.7%	35.8%	48.8%	42.0%
9	Yes	Rsc3p [Saccharomyces cerevisiae S288c]	gi 398366459	102 kDa	169	268	293	153	54	46	50	36	52.3%	49.4%	50.3%	42.9%
10	Yes	Arp7p [Saccharomyces cerevisiae S288c]	gi 6325291	54 kDa	53	211	293	244	17	25	32	28	34.4%	41.1%	57.0%	52.0%
11	Yes	Rsc6p [Saccharomyces cerevisiae S288c]	gi 6319900 (+1)	54 kDa	74	242	334	245	20	24	31	26	42.7%	52.8%	56.5%	55.3%
12	Yes	Rsc1p [Saccharomyces cerevisiae S288c]	gi 6321493 (+1)	107 kDa	126	172	274	286	31	34	40	39	39.7%	45.6%	52.6%	50.8%
13	No	Eno2p [Saccharomyces cerevisiae S288c]	gi 6321968	47 kDa	471	166	44	10	31	21	17	5	60.6%	41.2%	39.8%	13.3%
14	Yes	Sfh1p [Saccharomyces cerevisiae S288c]	gi 6323354 (+1)	49 kDa	47	153	199	158	13	16	20	15	33.1%	39.7%	62.0%	43.2%
15	No	Pgk1p [Saccharomyces cerevisiae S288c]	gi 10383781	45 kDa	423	136	40	3	34	28	22	3	71.9%	66.3%	57.5%	9.62%
16	Yes	Rsc30p [Saccharomyces cerevisiae S288c]	gi 41629685	101 kDa	79	124	128	63	22	21	21	14	26.8%	23.4%	26.2%	18.5%
17	No	Chain C, Structure Of The Ribosomal 80s-Eef2-Si	gi 49258841 (+1)	44 kDa	218	114	86	28	16	14	14	8	38.1%	33.7%	33.9%	19.9%
18	No	YGR192C [Saccharomyces cerevisiae]	gi 45269553 (+1)	36 kDa	224	59	20	4	23	13	10	2	56.9%	34.6%	32.5%	7.23%
19	Yes	Rtt102p [Saccharomyces cerevisiae S288c]	gi 37362657	18 kDa	31	109	127	114	9	10	13	10	69.4%	75.2%	84.1%	70.7%
20	No	Ssb1p [Saccharomyces cerevisiae S288c]	gi 6319972	67 kDa	138	81	92	22	28	30	18	41.3%	41.4%	52.2%	35.1%	
21	No	Tef2p [Saccharomyces cerevisiae S288c]	gi 6319594	50 kDa	161	24	31	9	20	6	11	2	46.9%	19.0%	32.5%	4.37%
22	No	Cdc19p [Saccharomyces cerevisiae S288c]	gi 6319279	55 kDa	171	49	10	0	33	19	9	0	72.0%	50.8%	26.0%	0.0
23	No	Fas2p [Saccharomyces cerevisiae S288c]	gi 6325025	207 kDa	192	0	41	0	81	0	37	0	43.4%	0.0	22.4%	0.0
24	No	ribosomal protein L19 [Saccharomyces cerevisiae]	gi 602897 (+1)	22 kDa	161	29	31	9	13	8	10	5	41.3%	38.1%	40.2%	24.3%
25	No	stress-seventy subfamily A protein [Saccharomyces cerevisiae]	gi 151941387	70 kDa	144	42	40	4	36	24	24	3	51.1%	37.2%	39.4%	6.54%
26	No	ribosomal protein L16B [Saccharomyces cerevisiae]	gi 151944465 (+1)	22 kDa	99	40	32	5	12	9	10	5	44.4%	37.4%	36.9%	23.7%
27	No	Chain D, Structure Of The Ribosomal 80s-Eef2-Si	gi 49258842 (+1)	39 kDa	96	68	67	15	14	13	7	42.7%	39.6%	39.6%	24.9%	
28	No	Rps1bp [Saccharomyces cerevisiae S288c]	gi 6323577	29 kDa	86	51	68	3	19	15	17	3	65.9%	52.2%	62.0%	11.0%
29	No	ribosomal protein L4 [Saccharomyces cerevisiae]	gi 172444 (+1)	28 kDa	53	55	54	9	21	16	14	6	58.0%	45.9%	45.9%	24.3%
30	No	Rps3p [Saccharomyces cerevisiae S288c]	gi 6324151	27 kDa	88	45	41	7	19	14	14	7	54.6%	45.4%	45.4%	34.6%
31	No	Chain A, Yeast Alcohol Dehydrogenase I, Saccha	gi 112491285 (+2)	37 kDa	134	33	13	0	17	9	8	0	49.9%	31.4%	29.1%	0.000%
32	No	ribosomal protein L13B [Saccharomyces cerevisiae]	gi 190408368 (+2)	23 kDa	91	33	39	13	11	7	9	4	51.8%	42.7%	51.3%	20.6%
33	Yes	Ldb7p [Saccharomyces cerevisiae S288c]	gi 41629675	20 kDa	14	37	67	69	5	4	5	5	33.3%	28.3%	33.3%	33.3%
34	No	Rpl18bp [Saccharomyces cerevisiae S288c]	gi 6324028	21 kDa	80	18	27	12	5	4	5	3	31.2%	24.2%	31.2%	19.9%
35	No	Chain A, Crystal Structure Of Adp-Ribosylated Ri	gi 55670150 (+1)	93 kDa	129	20	9	0	53	14	9	0	53.2%	18.4%	14.4%	0.0
36	Yes	Htl1p [Saccharomyces cerevisiae S288c]	gi 6319868	9 kDa	15	43	58	44	5	5	6	5	64.1%	64.1%	65.4%	64.1%
37	No	Fas1p [Saccharomyces cerevisiae S288c]	gi 6322666	229 kDa	119	0	27	0	69	0	25	0	37.8%	0.0	14.5%	0.0
38	No	Rpl10p [Saccharomyces cerevisiae S288c]	gi 6323104	25 kDa	42	22	37	1	16	10	13	1	49.3%	34.4%	41.6%	5.88%
39	No	Rpl7bp [Saccharomyces cerevisiae S288c]	gi 6325058	28 kDa	51	33	27	5	16	13	12	4	56.1%	39.8%	34.8%	17.2%
40	No	ribosomal protein L27A [Saccharomyces cerevisiae]	gi 190405795 (+1)	19 kDa	63	25	29	19	9	6	6	6	43.2%	37.7%	37.7%	34.6%
41	No	protein SLA2 [Saccharomyces cerevisiae RM11-; gi]	gi 190409212 (+1)	109 kDa	18	5	5	2	2	1	1	1	18.2%	0.826%	0.826%	0.826%
42	No	Chain B, Structure Of The Ribosomal 80s-Eef2-Si	gi 49258840 (+1)	27 kDa	53	32	38	7	9	8	9	4	34.0%	30.8%	34.0%	15.8%
43	No	Rps6ap [Saccharomyces cerevisiae EC1118]	gi 259150068 (+1)	27 kDa	72	24	38	3	15	6	9	3	42.4%	26.3%	37.3%	18.2%
44	No	carbamyl phosphate synthetase [Saccharomyces cerevisiae]	gi 173146	245 kDa	118	0	7	0	59	0	7	0	28.3%	0.000%	3.30%	0.0
45	No	Pdc1p [Saccharomyces cerevisiae S288c]	gi 6323073	61 kDa	102	12	7	0	19	6	6	0	39.6%	12.6%	13.3%	0.0
46	No	Rpl15ap [Saccharomyces cerevisiae EC1118]	gi 259148018 (+2)	24 kDa	71	16	22	0	5	3	5	0	29.4%	20.6%	29.4%	0.000%
47	No	Rpl20ap [Saccharomyces cerevisiae S288c]	gi 154199621	20 kDa	48	30	32	28	8	10	9	4	53.5%	48.3%	53.5%	30.2%
48	No	Chain G, 12-Subunit Rna Polymerase Ii	gi 110590860	24 kDa	38	32	34	41	3	2	4	2	10.7%	5.12%	6.05%	5.12%
49	No	elongation factor 3 [Saccharomyces cerevisiae]	gi 173214 (+2)	116 kDa	100	8	7	0	33	8	7	0	33.2%	8.52%	7.57%	0.0
50	No	Rps8ap [Saccharomyces cerevisiae S288c]	gi 6319399	22 kDa	53	35	42	5	8	7	7	4	46.5%	41.5%	41.5%	27.5%
51	No	Acc1p [Saccharomyces cerevisiae S288c]	gi 6324343	250 kDa	50	0	61	0	41	0	51	0	21.6%	0.000%	28.2%	0.000%
52	No	aldolase [Saccharomyces cerevisiae RM11-1a]	gi 190409769 (+1)	40 kDa	81	26	9	0	14	10	8	0	38.7%	37.6%	35.1%	0.0
53	No	hsc82 protein [Saccharomyces cerevisiae]	gi 171723 (+1)	81 kDa	92	8	10	0	36	8	10	0	39.7%	13.9%	17.3%	0.0
54	No	Gus1p [Saccharomyces cerevisiae S288c]	gi 37362649	81 kDa	38	43	30	0	21	22	23	0	32.6%	32.2%	35.2%	0.000%
55	No	RNA polymerase A(l) large subunit [Saccharomyces cerevisiae]	gi 172215 (+1)	186 kDa	44	9	41	13	34	9	29	9	25.4%	7.15%	22.1%	7.09%

56	No	Rpl6ap [Saccharomyces cerevisiae S288c]	gi 6323567	20 kDa	27	20	23	4	6	8	9	3	33.5%	45.5%	46.0%	18.2%
57	No	Rpl25p [Saccharomyces cerevisiae S288c]	gi 6324445	16 kDa	60	29	28	6	9	7	7	4	53.5%	43.0%	43.0%	28.9%
58	No	ribosomal protein rp59 [Saccharomyces cerevisiae S288c]	gi 547604	15 kDa	54	34	32	6	13	12	10	4	67.4%	67.4%	52.2%	26.1%
59	No	Rps11bp [Saccharomyces cerevisiae S288c]	gi 6319522	18 kDa	27	30	32	2	9	9	9	2	50.0%	50.0%	50.0%	17.3%
60	No	Chain M, Structure Of The Ribosomal 80s-Eef2-5 [Saccharomyces cerevisiae S288c] (+1)	gi 49258832	15 kDa	39	25	22	1	10	8	8	1	63.6%	54.5%	54.5%	8.33%
61	No	Rpl16ap [Saccharomyces cerevisiae S288c]	gi 6322058	22 kDa	51	27	20	3	8	8	6	3	43.7%	42.7%	45.2%	18.1%
62	No	Rpp0p [Saccharomyces cerevisiae S288c]	gi 6323371	34 kDa	40	19	28	1	11	7	10	1	33.0%	26.0%	32.1%	3.21%
63	No	Rrp5p [Saccharomyces cerevisiae S288c]	gi 6323885	193 kDa	78	0	0	0	45	0	0	0	25.5%	0.0	0.0	0.0
64	No	ribosomal protein S9B [Saccharomyces cerevisiae S288c]	gi 151946577	22 kDa	33	21	15	3	10	11	9	3	43.1%	46.7%	39.0%	16.9%
65	No	Chain G, Structure Of Ribosome-Bound Cricket F [Saccharomyces cerevisiae S288c] (+1)	gi 119390529	24 kDa	23	30	31	11	8	10	11	7	29.6%	33.8%	38.0%	32.9%
66	No	Kar2p [Saccharomyces cerevisiae S288c]	gi 6322426	74 kDa	43	13	25	18	22	12	19	13	33.1%	23.8%	31.4%	26.1%
67	No	Rpl26bp [Saccharomyces cerevisiae S288c]	gi 116006491	14 kDa	43	10	17	1	14	8	11	1	61.4%	46.5%	55.1%	7.09%
68	No	Rps24ap [Saccharomyces cerevisiae S288c]	gi 6320918	15 kDa	39	15	17	2	11	7	8	2	48.9%	40.7%	42.2%	17.8%
69	No	Rps4bp [Saccharomyces cerevisiae S288c]	gi 6321997	29 kDa	32	12	14	1	12	9	10	1	45.6%	33.3%	35.6%	4.21%
70	No	Rps2p [Saccharomyces cerevisiae S288c]	gi 6321315	27 kDa	41	3	6	0	4	2	4	0	17.7%	11.0%	17.7%	0.000%
71	No	Rpl21ap [Saccharomyces cerevisiae S288c]	gi 6319668	18 kDa	41	12	14	0	7	5	6	0	34.4%	28.7%	29.4%	0.000%
72	No	Gpm1p [Saccharomyces cerevisiae S288c]	gi 6322697	28 kDa	57	13	9	0	11	7	7	0	45.7%	30.4%	34.4%	0.0
73	No	ribosomal protein L14A [Saccharomyces cerevisiae S288c]	gi 151941540	15 kDa	24	22	21	0	7	8	6	0	27.5%	33.3%	27.5%	0.000%
74	No	Chain A, Crystal Structure Analysis Of Gnd1 In S [Saccharomyces cerevisiae S288c] (+1)	gi 157835612	55 kDa	59	16	3	0	24	11	3	0	51.3%	29.0%	8.25%	0.0
75	No	Ade3p [Saccharomyces cerevisiae S288c]	gi 6321643	102 kDa	58	18	4	0	34	11	4	0	37.2%	15.6%	6.03%	0.0
76	No	Rpa135p [Saccharomyces cerevisiae S288c]	gi 6325267	136 kDa	29	6	24	13	25	5	21	13	26.6%	6.15%	26.3%	13.3%
77	No	Rrm3p [Saccharomyces cerevisiae S288c]	gi 6321820	82 kDa	11	9	4	4	1	1	1	1	1.38%	1.38%	1.38%	1.38%
78	No	YFL039Cp-like protein [Saccharomyces cerevisiae S288c]	gi 207345741	40 kDa	44	18	12	1	14	9	7	1	43.3%	30.8%	23.3%	2.78%
79	No	His4p [Saccharomyces cerevisiae S288c]	gi 10383761	88 kDa	86	1	4	0	33	1	4	0	40.9%	1.38%	5.51%	0.0
80	No	Chain Q, Localization Of The Large Subunit Ribosome [Saccharomyces cerevisiae S288c] (+1)	gi 315113347	34 kDa	34	7	18	7	8	3	6	3	30.3%	11.4%	18.9%	11.4%
81	No	Rpl30p [Saccharomyces cerevisiae S288c]	gi 6321408	11 kDa	47	15	20	4	10	6	8	4	64.8%	42.9%	42.9%	40.0%
82	No	Rps5p [Saccharomyces cerevisiae S288c]	gi 6322583	25 kDa	50	9	10	0	11	7	7	0	36.9%	28.9%	28.9%	0.0
83	No	Rpl33ap [Saccharomyces cerevisiae JAY291]	gi 256274177	12 kDa	22	15	15	6	5	5	5	5	33.3%	33.3%	33.3%	33.3%
84	No	YGL008Cp-like protein [Saccharomyces cerevisiae S288c]	gi 207345258	100 kDa	74	1	2	0	22	1	1	0	25.9%	1.09%	1.09%	0.000%
85	No	lsw1p [Saccharomyces cerevisiae S288c]	gi 6319722	131 kDa	38	19	18	0	32	15	16	0	31.4%	18.4%	17.4%	0.0
86	No	Chain A, Nmr Structure Of Chaperone Chz1 Com [Saccharomyces cerevisiae S288c]	gi 188595808	21 kDa	9	13	19	0	5	6	6	0	19.8%	25.5%	25.5%	0.000%
87	No	mitochondrial chaperones [Saccharomyces cerevisiae S288c]	gi 151945113	71 kDa	69	3	4	0	22	3	4	0	33.8%	5.78%	7.15%	0.0
88	No	Rps25bp [Saccharomyces cerevisiae S288c]	gi 6323365	12 kDa	29	17	21	3	9	6	7	3	46.3%	42.6%	44.4%	21.3%
89	No	Rpl17ap [Saccharomyces cerevisiae S288c]	gi 6322668	21 kDa	37	18	18	2	9	7	7	2	48.4%	43.5%	43.5%	15.8%
90	No	Chain I, Structure Of The Ribosomal 80s-Eef2-So [Saccharomyces cerevisiae S288c] (+1)	gi 49258828	16 kDa	37	14	15	0	10	6	6	0	66.2%	48.6%	48.6%	0.000%
91	No	valyl-tRNA synthetase [Saccharomyces cerevisiae S288c]	gi 173164	126 kDa	65	1	0	0	35	1	0	0	35.7%	0.996%	0.0	0.0
92	No	Scp160p [Saccharomyces cerevisiae S288c]	gi 6322381	135 kDa	76	0	0	0	50	0	0	0	40.5%	0.0	0.0	0.0
93	No	97 kDa protein [Saccharomyces cerevisiae RM1:gi 190406684] (+4)	gi 190406684	112 kDa	67	0	0	0	22	0	0	0	21.5%	0.000%	0.000%	0.0
94	No	Chain J, Structure Of The Ribosomal 80s-Eef2-Sc [Saccharomyces cerevisiae S288c] (+2)	gi 49258848	20 kDa	23	9	16	0	9	5	7	0	38.2%	24.9%	26.6%	0.0
95	No	Rpl12bp [Saccharomyces cerevisiae S288c]	gi 6320625	18 kDa	57	8	11	0	7	4	2	0	57.6%	37.0%	16.4%	0.0
96	No	hypothetical protein YER138C [Saccharomyces cerevisiae S288c] (+1)	gi 6320985	199 kDa	58	0	0	0	22	0	0	0	16.5%	0.0	0.000%	0.0
97	No	lIs1p [Saccharomyces cerevisiae S288c]	gi 6319395	123 kDa	54	0	0	0	32	0	0	0	33.1%	0.0	0.0	0.0
98	No	Rps7ap [Saccharomyces cerevisiae JAY291]	gi 256272964	22 kDa	31	2	6	0	10	2	5	0	40.8%	11.0%	23.6%	0.0
99	No	Chc1p [Saccharomyces cerevisiae S288c]	gi 6321232	187 kDa	67	2	1	0	46	1	1	0	28.7%	0.665%	0.665%	0.0
100	No	AdoMet-homocysteine methyltransferase [Saccharomyces cerevisiae S288c]	gi 151942529	37 kDa	7	8	5	9	6	1	1	1	15.7%	3.38%	3.38%	3.38%
101	No	Stm1p [Saccharomyces cerevisiae S288c]	gi 6323179	30 kDa	37	4	8	0	12	3	5	0	46.2%	17.6%	22.3%	0.000%
102	No	Mdn1p [Saccharomyces cerevisiae S288c]	gi 6323135	559 kDa	55	0	1	0	51	0	1	0	13.3%	0.0	0.224%	0.000%
103	No	SSE1 protein [Saccharomyces cerevisiae S288c]	gi 533365	77 kDa	47	7	6	0	27	7	6	0	44.4%	13.3%	11.0%	0.0
104	No	Pgi1p [Saccharomyces cerevisiae S288c]	gi 6319673	61 kDa	45	16	2	0	16	11	2	0	38.8%	28.5%	4.33%	0.0
105	No	Kem1p [Saccharomyces cerevisiae S288c]	gi 6321265	175 kDa	48	0	1	0	32	0	1	0	22.3%	0.000%	0.785%	0.000%
106	No	polyadenylate-binding protein [Saccharomyces cerevisiae S288c]	gi 172092	64 kDa	67	0	0	0	26	0	0	0	48.4%	0.0	0.0	0.0
107	No	Rpl24ap [Saccharomyces cerevisiae S288c]	gi 6321407	18 kDa	29	14	19	1	7	4	6	1	29.7%	27.1%	27.7%	9.03%
108	No	Rpl28p [Saccharomyces cerevisiae JAY291]	gi 256273217	17 kDa	30	9	13	0	9	4	7	0	51.3%	23.3%	41.3%	0.000%
109	No	ribosomal protein S13 [Saccharomyces cerevisiae S288c]	gi 190404968	19 kDa	24	14	13	0	6	6	5	0	34.5%	34.5%	27.9%	0.0
110	No	Chain B, Crystal Structure Of The Yeast Nucleoside [Saccharomyces cerevisiae S288c] (+1)	gi 15988133	11 kDa	33	11	18	2	10	7	8	1	57.3%	45.6%	46.6%	9.71%
111	No	Rpl35bp [Saccharomyces cerevisiae S288c]	gi 6320010	14 kDa	31	13	11	0	10	8	8	0	48.3%	45.0%	38.3%	0.0
112	No	TOP2 [Saccharomyces cerevisiae S288c]	gi 19880873	164 kDa	22	0	1	0	17	0	1	0	12.6%	0.000%	0.910%	0.000%
113	No	Bmh1p [Saccharomyces cerevisiae S288c]	gi 6321025	30 kDa	41	7	3	0	16	4	3	0	51.3%	16.9%	13.1%	0.0
114	No	Rps17bp [Saccharomyces cerevisiae S288c]	gi 6320655	16 kDa	43	5	11	0	10	5	7	0	58.1%	46.3%	53.7%	0.0

115	No	Clu1p [Saccharomyces cerevisiae S288c]	gi 6323654	145 kDa	48	0	0	0	29	0	0	0	25.8%	0.0	0.0	0.0
116	No	Tal1p [Saccharomyces cerevisiae S288c]	gi 6323386	37 kDa	41	9	3	0	21	7	2	0	63.0%	24.5%	6.87%	0.0
117	No	transmembrane ATPase-like protein [Saccharon gi 172907 (+1)		114 kDa	46	4	0	0	28	3	0	0	27.8%	3.30%	0.0	0.0
118	No	5'-phosphoribosylformyl glycinamide synthetase gi 151943341 (+1)		149 kDa	53	0	0	0	33	0	0	0	30.8%	0.0	0.0	0.0
119	No	Chain A, Saicar-Synthase Complexed With Atp gi 157879484 (+1)		34 kDa	36	8	5	0	16	8	5	0	58.7%	36.4%	18.7%	0.0
120	No	Chain A, Structure Of Yeast Triosephosphate Iso gi 230405 (+1)		27 kDa	31	15	6	0	10	8	6	0	34.8%	36.8%	29.1%	0.0
121	No	Chain C, Mechanism Of Eif6s Anti-Association A gi 292659544 (+1)		14 kDa	24	11	9	0	9	6	4	0	49.2%	47.0%	34.8%	0.0
122	No	Dps1p [Saccharomyces cerevisiae S288c]	gi 6323011	64 kDa	53	0	1	0	29	0	1	0	50.6%	0.0	1.97%	0.0
123	No	glycyl-tRNA synthetase [Saccharomyces cerevisi gi 151946513 (+2)		75 kDa	47	0	0	0	21	0	0	0	36.6%	0.000%	0.0	0.0
124	No	Hsp60p [Saccharomyces cerevisiae S288c]	gi 6323288	61 kDa	52	6	4	0	25	5	4	0	44.6%	12.4%	9.97%	0.0
125	No	Tif2p [Saccharomyces cerevisiae S288c]	gi 6322323	45 kDa	38	11	4	0	18	9	4	0	52.9%	30.1%	12.2%	0.0
126	No	Rpg1p [Saccharomyces cerevisiae S288c]	gi 6319553	110 kDa	34	1	2	0	26	1	2	0	30.6%	1.24%	2.90%	0.0
127	No	Rps7bp [Saccharomyces cerevisiae]	gi 71064104	22 kDa	27	7	15	0	5	3	3	0	49.7%	27.2%	27.2%	0.0
128	No	Chain B, Structure Of Split Monoubiquitinated P gi 291463616		19 kDa	26	0	2	0	6	0	1	0	36.1%	0.000%	5.33%	0.0
129	No	RecName: Full=ATP-dependent RNA helicase DE gi 160380641 (+1)		66 kDa	50	2	1	0	19	2	1	0	34.1%	4.47%	2.32%	0.0
130	No	Acs2p [Saccharomyces cerevisiae S288c]	gi 6323182	75 kDa	46	0	1	0	21	0	1	0	31.0%	0.000%	1.61%	0.0
131	No	Sah1p [Saccharomyces cerevisiae S288c]	gi 6320882	49 kDa	38	9	0	0	18	9	0	0	32.1%	19.6%	0.000%	0.0
132	No	karyopherin beta 4 [Saccharomyces cerevisiae Y gi 151944826 (+1)		123 kDa	44	0	0	0	18	0	0	0	19.5%	0.0	0.0	0.0
133	No	Pfk1p [Saccharomyces cerevisiae JAY291]	gi 256272639 (+1)	108 kDa	38	2	3	0	29	2	3	0	31.7%	2.74%	3.44%	0.0
134	No	glutamate synthase (NADPH) [Saccharomyces c gi 1370295 (+3)		238 kDa	36	0	0	0	26	0	0	0	14.8%	0.000%	0.000%	0.0
135	No	alanyl-tRNA synthetase [Saccharomyces cerevis gi 190407630 (+1)		107 kDa	40	0	0	0	27	0	0	0	35.1%	0.0	0.0	0.0
136	No	Rps20p [Saccharomyces cerevisiae S288c]	gi 6321772	14 kDa	28	10	14	0	8	6	5	0	41.3%	38.8%	32.2%	0.0
137	No	Rps26ap [Saccharomyces cerevisiae S288c]	gi 6321249	14 kDa	19	8	13	1	4	3	4	1	33.6%	30.3%	33.6%	12.6%
138	No	Hsp104p [Saccharomyces cerevisiae S288c]	gi 6323002	102 kDa	34	2	0	0	30	2	0	0	36.1%	2.64%	0.0	0.0
139	No	leucyl-tRNA synthetase [Saccharomyces cerevis gi 151942639 (+1)		124 kDa	45	0	0	0	29	0	0	0	32.9%	0.0	0.0	0.0
140	No	Ssz1p [Saccharomyces cerevisiae S288c]	gi 37362658 (+1)	58 kDa	35	0	1	0	13	0	1	0	30.5%	0.0	1.67%	0.0
141	No	Gcn1p [Saccharomyces cerevisiae S288c]	gi 6321243	297 kDa	26	1	0	0	19	1	0	0	7.71%	0.374%	0.0	0.0
142	No	Mdr1p [Saccharomyces cerevisiae EC1118]	gi 259146602 (+1)	109 kDa	2	2	3	3	1	1	1	1	0.842%	0.842%	0.842%	0.842%
143	No	serine hydroxymethyltransferase [Saccharomyc gi 151941227		52 kDa	34	3	0	0	20	3	0	0	43.9%	7.25%	0.0	0.0
144	No	Bfr1p [Saccharomyces cerevisiae S288c]	gi 6324772	55 kDa	45	0	0	0	22	0	0	0	38.3%	0.0	0.000%	0.0
145	No	Rpl43bp [Saccharomyces cerevisiae S288c]	gi 6322554	10 kDa	14	12	9	2	4	2	5	1	51.1%	28.3%	52.2%	19.6%
146	No	nuclear localization sequence binding protein [S gi 151943436 (+3)		45 kDa	16	13	11	0	6	5	7	0	17.9%	12.7%	18.2%	0.000%
147	No	YDL160Cp-like protein [Saccharomyces cerevisi gi 207347082 (+1)		58 kDa	13	14	16	0	9	14	13	0	20.4%	30.8%	28.9%	0.0
148	No	lmd3p [Saccharomyces cerevisiae JAY291]	gi 256271116 (+1)	57 kDa	33	5	6	1	14	4	4	1	32.3%	11.7%	12.8%	3.44%
149	No	Sec53p [Saccharomyces cerevisiae S288c]	gi 14318474 (+1)	29 kDa	25	1	0	0	13	1	0	0	45.3%	5.91%	0.000%	0.000%
150	No	Rps1ap [Saccharomyces cerevisiae S288c]	gi 6323474	29 kDa	13	10	14	1	5	4	5	1	65.9%	48.6%	58.8%	8.24%
151	No	YHR020W-like protein [Saccharomyces cerevisi gi 256269239 (+1)		77 kDa	39	0	0	0	25	0	0	0	46.2%	0.0	0.0	0.0
152	No	Krs1p [Saccharomyces cerevisiae S288c]	gi 6320242	68 kDa	36	0	0	0	20	0	0	0	33.2%	0.0	0.0	0.0
153	No	Rpl36bp [Saccharomyces cerevisiae S288c]	gi 6325006	11 kDa	16	6	3	1	5	4	2	1	42.0%	33.0%	21.0%	12.0%
154	No	Rpl6bp [Saccharomyces cerevisiae S288c]	gi 6323481	20 kDa	14	7	7	0	4	5	5	0	40.3%	51.7%	51.7%	10.2%
155	No	Rvb2p [Saccharomyces cerevisiae S288c]	gi 6325021	52 kDa	14	11	16	1	11	9	13	1	24.8%	19.1%	30.1%	2.55%
156	No	Rpl32p [Saccharomyces cerevisiae S288c]	gi 6319378	15 kDa	21	3	5	0	5	2	3	0	36.9%	17.7%	23.8%	0.0
157	No	Thr4p [Saccharomyces cerevisiae S288c]	gi 6319901	57 kDa	29	7	0	0	22	7	0	0	45.3%	17.3%	0.0	0.0
158	No	Chain A, Crystal Structure Of The Uba1-Ubiquiti gi 262118833 (+2)		113 kDa	34	1	0	0	27	1	0	0	29.6%	1.38%	0.0	0.0
159	No	Gln4p [Saccharomyces cerevisiae S288c]	gi 6324742	93 kDa	41	0	0	0	33	0	0	0	41.4%	0.0	0.0	0.0
160	No	actin binding protein [Saccharomyces cerevisi gi 151943898		66 kDa	42	0	0	0	19	0	0	0	40.7%	0.0	0.0	0.0
161	No	tRNA synthetase [Saccharomyces cerevisiae]	gi 3924 (+1)	86 kDa	20	10	8	0	19	10	7	0	31.3%	16.5%	12.4%	0.0
162	No	flavo-hemoglobin [Saccharomyces cerevisiae YJ gi 151943508 (+2)		45 kDa	34	8	2	0	14	4	1	0	49.6%	13.3%	3.01%	0.0
163	No	Ade13p [Saccharomyces cerevisiae S288c]	gi 6323391	55 kDa	33	5	0	0	16	5	0	0	25.9%	10.4%	0.0	0.0
164	No	Ade17p [Saccharomyces cerevisiae EC1118]	gi 259148695 (+1)	65 kDa	34	1	0	0	20	1	0	0	37.7%	2.03%	0.0	0.0
165	No	Tkl1p [Saccharomyces cerevisiae S288c]	gi 6325331	74 kDa	25	3	1	0	18	3	1	0	29.1%	5.44%	1.76%	0.0
166	No	cytosolic aldehyde dehydrogenase [Saccharomy gi 1336076 (+2)		55 kDa	32	1	0	0	20	1	0	0	37.7%	2.99%	0.000%	0.000%
167	No	Hxk2p [Saccharomyces cerevisiae S288c]	gi 6321184	54 kDa	29	14	0	0	14	10	0	0	34.4%	27.0%	0.0	0.0
168	No	Rpl9bp [Saccharomyces cerevisiae S288c]	gi 6324262	22 kDa	19	7	8	1	6	3	4	1	26.2%	12.0%	19.9%	6.28%
169	No	SPT6 [Saccharomyces cerevisiae]	gi 1945326 (+1)	159 kDa	7	5	15	0	7	5	15	0	6.07%	5.19%	12.4%	0.0
170	No	Nop1p [Saccharomyces cerevisiae S288c]	gi 6320190	34 kDa	14	12	9	0	8	7	7	0	26.3%	27.5%	26.0%	0.0
171	No	Chain A, Crystal Structure Of The Full Length E gi 215794766 (+1)		18 kDa	31	4	2	0	7	4	2	0	34.1%	28.7%	21.6%	0.0
172	No	Chain B, Crystal Structure Analysis Of Enolase M gi 88192082		47 kDa	31	5	2	0	9	3	2	0	49.5%	34.9%	29.1%	0.0
173	No	HDF2 protein [Saccharomyces cerevisiae]	gi 112362657 (+2)	71 kDa	2	7	5	0	2	7	5	0	4.45%	12.6%	10.0%	0.000%

174	No	beta COP [Saccharomyces cerevisiae]	gi 595413 (+1)	109 kDa	19	7	9	0	16	6	7	0	19.9%	7.30%	8.53%	0.0
175	No	phosphofruktokinase, beta subunit [Saccharomyces cerevisiae S288c]	gi 172140	105 kDa	27	0	4	0	17	0	4	0	25.5%	0.0	5.11%	0.0
176	No	Cpr1p [Saccharomyces cerevisiae S288c]	gi 6320359	17 kDa	32	3	0	0	12	2	0	0	63.0%	12.3%	0.0	0.0
177	No	New1p [Saccharomyces cerevisiae S288c]	gi 6325030	134 kDa	30	0	0	0	26	0	0	0	24.7%	0.0	0.0	0.0
178	No	Ipp1p [Saccharomyces cerevisiae S288c]	gi 6319483	32 kDa	23	6	2	0	11	5	2	0	38.3%	20.6%	8.71%	0.0
179	No	Gik1p [Saccharomyces cerevisiae S288c]	gi 6319809	55 kDa	27	2	0	0	13	2	0	0	31.2%	4.40%	0.0	0.0
180	No	cell division cycle-related protein [Saccharomyces cerevisiae S288c]	gi 151941877 (+1)	92 kDa	32	3	0	0	18	3	0	0	27.8%	4.19%	0.0	0.0
181	No	Vma2p [Saccharomyces cerevisiae S288c]	gi 6319603	58 kDa	20	11	5	0	17	11	5	0	40.8%	25.9%	12.0%	0.0
182	No	Ade5,7p [Saccharomyces cerevisiae S288c]	gi 6321203	86 kDa	34	0	2	0	20	0	2	0	33.2%	0.0	2.87%	0.0
183	No	Ydj1p [Saccharomyces cerevisiae S288c]	gi 6324265	45 kDa	30	1	5	0	15	1	4	0	44.0%	3.42%	14.2%	0.0
184	No	glyceraldehyde-3-phosphate dehydrogenase [Saccharomyces cerevisiae S288c]	gi 151945032 (+1)	36 kDa	28	7	1	0	14	6	1	0	60.8%	35.5%	12.7%	0.0
185	No	Rpn1p [Saccharomyces cerevisiae S288c]	gi 6321816	109 kDa	35	1	1	0	25	1	1	0	29.6%	1.51%	1.51%	0.0
186	No	Gcd11p [Saccharomyces cerevisiae S288c]	gi 6320863	58 kDa	29	4	0	0	18	4	0	0	39.7%	10.8%	0.000%	0.0
187	No	Met6p [Saccharomyces cerevisiae JAY291]	gi 256271451	86 kDa	35	2	0	0	24	2	0	0	34.2%	2.74%	0.0	0.0
188	No	RecName: Full=Pentafunctional AROM polypept [Saccharomyces cerevisiae S288c]	gi 327507677 (+1)	175 kDa	25	0	0	0	22	0	0	0	16.5%	0.0	0.0	0.0
189	No	DNA-directed RNA polymerases I and III 40 kDa [Saccharomyces cerevisiae S288c]	gi 190408037 (+1)	38 kDa	9	7	13	4	9	5	9	4	32.2%	16.7%	32.8%	13.7%
190	No	Prt1p [Saccharomyces cerevisiae JAY291]	gi 256272564 (+1)	88 kDa	23	2	1	0	17	2	1	0	28.6%	3.14%	1.83%	0.0
191	No	Ola1p [Saccharomyces cerevisiae S288c]	gi 6319499	44 kDa	29	4	0	0	18	4	0	0	47.2%	11.9%	0.000%	0.0
192	No	Rhr2p [Saccharomyces cerevisiae S288c]	gi 86558907	28 kDa	31	1	1	0	12	1	1	0	47.6%	6.00%	6.00%	0.0
193	No	Myo1p [Saccharomyces cerevisiae S288c]	gi 6321812	224 kDa	23	0	1	0	23	0	1	0	14.4%	0.0	0.415%	0.0
194	No	RNA polymerase II core subunit [Saccharomyces cerevisiae S288c]	gi 190405143 (+3)	192 kDa	23	1	2	0	15	1	2	0	11.1%	0.635%	1.27%	0.000%
195	No	Fks1p [Saccharomyces cerevisiae S288c]	gi 6323374	215 kDa	22	0	0	0	15	0	0	0	9.75%	0.0	0.0	0.0
196	No	Rpl34bp [Saccharomyces cerevisiae S288c]	gi 6322137 (+1)	14 kDa	12	0	3	3	2	0	2	2	20.7%	0.000%	20.7%	20.7%
197	No	YLR355Cp-like protein [Saccharomyces cerevisiae S288c]	gi 207342795 (+3)	44 kDa	27	2	0	0	15	1	0	0	38.5%	2.53%	0.000%	0.0
198	No	protein disulfide isomerase [Saccharomyces cerevisiae S288c]	gi 151943788 (+4)	58 kDa	33	0	0	0	17	0	0	0	35.2%	0.0	0.0	0.0
199	No	tryptophan synthase [Saccharomyces cerevisiae S288c]	gi 190406993 (+1)	77 kDa	33	0	0	0	23	0	0	0	38.5%	0.0	0.0	0.0
200	No	Tsa1p [Saccharomyces cerevisiae S288c]	gi 6323613	22 kDa	30	2	1	0	12	2	1	0	47.4%	11.7%	5.61%	0.0
201	No	RecName: Full=Aminopeptidase 2, mitochondrial [Saccharomyces cerevisiae S288c]	gi 115502354 (+5)	106 kDa	30	0	0	0	27	0	0	0	32.0%	0.0	0.0	0.0
202	No	Ssa2p [Saccharomyces cerevisiae S288c]	gi 6323004	69 kDa	17	9	7	1	5	5	4	1	49.9%	37.4%	39.6%	8.61%
203	No	killer toxin resistant protein [Saccharomyces cerevisiae S288c]	gi 151944405 (+1)	119 kDa	13	3	4	0	12	3	4	0	14.1%	3.69%	4.64%	0.0
204	No	Rpl31bp [Saccharomyces cerevisiae S288c]	gi 6323438	13 kDa	17	1	2	0	6	1	2	0	48.7%	9.73%	19.5%	0.0
205	No	Aap1p [Saccharomyces cerevisiae S288c]	gi 6321837	98 kDa	29	0	0	0	25	0	0	0	34.3%	0.0	0.0	0.0
206	No	Sam1p [Saccharomyces cerevisiae S288c]	gi 6323209	42 kDa	27	3	3	0	12	3	2	0	39.0%	8.90%	6.81%	0.0
207	No	YHR179W [Saccharomyces cerevisiae S288c]	gi 45270462 (+1)	45 kDa	23	6	1	0	16	5	1	0	44.5%	14.2%	3.00%	0.0
208	No	Erg10p [Saccharomyces cerevisiae S288c]	gi 6325229	42 kDa	22	11	0	0	11	7	0	0	38.2%	21.4%	0.0	0.0
209	No	Ecm29p [Saccharomyces cerevisiae S288c]	gi 6321757	210 kDa	18	0	0	0	18	0	0	0	11.7%	0.0	0.0	0.0
210	No	Spt16p [Saccharomyces cerevisiae S288c]	gi 6321231	119 kDa	18	9	3	0	17	9	3	0	18.9%	10.1%	2.80%	0.0
211	No	Chain A, Solution Structure Of Myristoylated Yei1 [Saccharomyces cerevisiae S288c]	gi 222142955	21 kDa	26	0	2	0	7	0	2	0	44.8%	0.0	15.5%	0.000%
212	No	Cop1p [Saccharomyces cerevisiae S288c]	gi 6320056	136 kDa	21	0	9	0	18	0	6	0	18.7%	0.0	7.24%	0.0
213	No	Ded81p [Saccharomyces cerevisiae S288c]	gi 6321807	62 kDa	26	0	1	0	18	0	1	0	33.0%	0.0	2.89%	0.0
214	No	Sti1p [Saccharomyces cerevisiae S288c]	gi 6324601	66 kDa	23	0	0	0	18	0	0	0	29.7%	0.000%	0.0	0.0
215	No	Chain A, Crystal Structure Of The Yeast Nucleoside [Saccharomyces cerevisiae S288c]	gi 15988132 (+2)	15 kDa	1	0	0	0	1	0	0	0	6.67%	0.000%	0.000%	0.0
216	No	Mis1p [Saccharomyces cerevisiae S288c]	gi 6319558	106 kDa	26	0	0	0	21	0	0	0	25.9%	0.0	0.0	0.0
217	No	Tup1p [Saccharomyces cerevisiae S288c]	gi 6319926	78 kDa	25	0	0	0	15	0	0	0	26.8%	0.0	0.0	0.0
218	No	acyl-RNA-complex subunit [Saccharomyces cerevisiae S288c]	gi 151943704 (+1)	42 kDa	16	3	4	0	9	3	4	0	34.0%	9.84%	13.3%	0.0
219	No	DNA-directed RNA polymerase III largest subunit [Saccharomyces cerevisiae S288c]	gi 190407445 (+2)	162 kDa	12	8	4	0	12	8	4	0	10.1%	7.81%	4.38%	0.0
220	No	Yra1p [Saccharomyces cerevisiae EC1118]	gi 259145620	25 kDa	24	3	5	0	7	3	5	0	32.3%	13.3%	23.5%	0.0
221	No	YOL058Wp-like protein [Saccharomyces cerevisiae S288c]	gi 207341374 (+1)	47 kDa	22	5	0	0	14	5	0	0	32.9%	12.9%	0.0	0.0
222	No	Gcv1p [Saccharomyces cerevisiae S288c]	gi 6320222	44 kDa	8	2	0	0	6	2	0	0	18.5%	4.50%	0.0	0.0
223	No	Asn1p [Saccharomyces cerevisiae S288c]	gi 6325403	64 kDa	28	1	0	0	19	1	0	0	33.6%	1.75%	0.0	0.0
224	No	RNA elicase [Saccharomyces cerevisiae S288c]	gi 1183961 (+3)	61 kDa	25	0	0	0	15	0	0	0	31.1%	0.0	0.0	0.0
225	No	Gsp1p [Saccharomyces cerevisiae S288c]	gi 6323324	25 kDa	12	3	4	0	5	3	3	0	24.2%	15.5%	15.5%	0.0
226	No	Tdh2p [Saccharomyces cerevisiae S288c]	gi 6322468	36 kDa	12	2	1	0	2	2	1	0	54.8%	41.9%	32.8%	0.0
227	No	conserved protein [Saccharomyces cerevisiae S288c]	gi 151944165 (+1)	33 kDa	22	3	0	0	11	3	0	0	37.1%	11.6%	0.0	0.0
228	No	pyruvate carboxylase [Saccharomyces cerevisiae S288c]	gi 190408630 (+2)	130 kDa	24	0	0	0	21	0	0	0	20.6%	0.0	0.000%	0.0
229	No	Syp1p [Saccharomyces cerevisiae S288c]	gi 10383792 (+1)	96 kDa	31	0	0	0	14	0	0	0	22.2%	0.0	0.0	0.0
230	No	Rps15p [Saccharomyces cerevisiae S288c]	gi 6324533	16 kDa	19	4	5	1	3	2	2	1	30.3%	16.9%	16.9%	7.75%
231	No	Rps0bp [Saccharomyces cerevisiae S288c]	gi 6323077	28 kDa	19	3	2	0	5	3	2	0	29.8%	13.1%	9.92%	0.0
232	No	Asc1p [Saccharomyces cerevisiae JAY291]	gi 256269640 (+1)	35 kDa	20	7	2	0	9	6	2	0	28.1%	21.3%	8.44%	0.0

233	No	Chain H, Structure Of The Ribosomal 80s-Eef2-S	gi 49258827 (+2)	14 kDa	19	3	1	0	0	8	3	1	0	57.4%	24.0%	6.20%	0.0
234	No	adenosine kinase [Saccharomyces cerevisiae YJH]	gi 151945170 (+1)	36 kDa	25	5	0	0	0	9	4	0	0	33.9%	15.9%	0.000%	0.0
235	No	YJR139Cp-like protein [Saccharomyces cerevisiae gi]	gi 207343753 (+2)	39 kDa	19	3	0	0	0	15	3	0	0	35.7%	8.36%	0.0	0.0
236	No	Aco1p [Saccharomyces cerevisiae S288c]	gi 6323335	85 kDa	21	0	0	0	0	17	0	0	0	28.0%	0.000%	0.0	0.0
237	No	Rvb1p [Saccharomyces cerevisiae S288c]	gi 6320396	50 kDa	12	7	8	2	9	7	8	2	2	24.4%	20.3%	21.4%	5.62%
238	No	Rpl38p [Saccharomyces cerevisiae S288c]	gi 6323357	9 kDa	7	2	4	0	4	1	3	0	0	35.9%	19.2%	35.9%	0.0
239	No	Erg20p [Saccharomyces cerevisiae S288c]	gi 6322294	40 kDa	18	6	1	0	0	11	6	1	0	34.1%	17.9%	2.84%	0.0
240	No	O-acetylhomoserine (thio)-lyase [Saccharomyces cerevisiae gi]	gi 190405358 (+1)	49 kDa	21	7	0	0	0	10	5	0	0	28.8%	13.3%	0.000%	0.0
241	No	YHR146Wp-like protein [Saccharomyces cerevisiae gi]	gi 207344559 (+4)	49 kDa	30	0	0	0	0	13	0	0	0	33.1%	0.0	0.0	0.0
242	No	Rpl4ap [Saccharomyces cerevisiae S288c]	gi 6319505	39 kDa	12	7	8	1	2	2	2	1	1	42.5%	39.5%	39.5%	28.7%
243	No	Rps12p [Saccharomyces cerevisiae S288c]	gi 6324945	15 kDa	17	6	5	0	5	5	4	0	0	33.6%	33.6%	25.9%	0.0
244	No	Puf6p [Saccharomyces cerevisiae S288c]	gi 6320704	75 kDa	5	3	3	0	4	2	3	0	0	7.01%	3.66%	5.18%	0.0
245	No	Rps19ap [Saccharomyces cerevisiae S288c]	gi 6324451	16 kDa	20	1	2	0	9	1	1	0	0	46.5%	6.25%	6.25%	0.0
246	No	Tef4p [Saccharomyces cerevisiae JAY291]	gi 256269880	47 kDa	23	1	1	0	11	1	1	0	0	26.4%	2.66%	2.66%	0.0
247	No	Hom2p [Saccharomyces cerevisiae S288c]	gi 6320362	40 kDa	19	3	0	0	0	13	3	0	0	46.3%	10.4%	0.0	0.0
248	No	Hxk1p [Saccharomyces cerevisiae S288c]	gi 14318578 (+1)	54 kDa	26	2	0	0	0	17	2	0	0	39.4%	4.33%	0.0	0.0
249	No	Arb1p [Saccharomyces cerevisiae EC1118]	gi 259145944 (+1)	68 kDa	20	0	1	0	13	0	1	0	0	26.7%	0.0	2.30%	0.0
250	No	arginyl-tRNA synthetase [Saccharomyces cerevisiae gi]	gi 151942316 (+1)	70 kDa	17	1	0	0	0	14	1	0	0	27.0%	1.65%	0.0	0.0
251	No	Ede1p [Saccharomyces cerevisiae S288c]	gi 6319424	151 kDa	21	0	0	0	0	16	0	0	0	14.8%	0.0	0.000%	0.0
252	No	unnamed protein product [Saccharomyces cerevisiae gi]	gi 4619	84 kDa	24	0	0	0	0	19	0	0	0	29.0%	0.0	0.0	0.0
253	No	Spb1p [Saccharomyces cerevisiae JAY291]	gi 256270950 (+1)	97 kDa	2	0	0	0	2	0	0	0	0	2.97%	0.000%	0.000%	0.000%
254	No	translation machinery associated protein [Saccharomyces cerevisiae gi]	gi 151941490 (+1)	19 kDa	11	4	3	0	8	4	3	0	0	40.7%	22.8%	18.0%	0.0
255	No	L3167 [Saccharomyces cerevisiae]	gi 995712	14 kDa	1	1	1	0	1	1	1	0	0	6.45%	6.45%	6.45%	0.000%
256	No	Erg13p [Saccharomyces cerevisiae S288c]	gi 6323509	55 kDa	16	2	0	0	11	2	0	0	0	24.8%	5.09%	0.0	0.0
257	No	coatomer beta'-subunit [Saccharomyces cerevisiae gi]	gi 151943674 (+2)	99 kDa	16	0	8	0	13	0	8	0	0	18.3%	0.0	11.1%	0.0
258	No	Gre3p [Saccharomyces cerevisiae EC1118]	gi 259146857 (+1)	37 kDa	21	2	0	0	0	17	2	0	0	44.0%	7.95%	0.0	0.0
259	No	GTP-binding protein (VPS1) [Saccharomyces cerevisiae gi]	gi 173183 (+1)	79 kDa	14	0	0	0	0	13	0	0	0	22.0%	0.0	0.000%	0.0
260	No	Mtd1p [Saccharomyces cerevisiae S288c]	gi 6322933	36 kDa	22	0	0	0	13	0	0	0	0	48.4%	0.000%	0.0	0.0
261	No	NuA4 histone acetyltransferase subunit [Saccharomyces cerevisiae gi]	gi 151944045 (+3)	433 kDa	17	0	0	0	13	0	0	0	0	4.11%	0.0	0.000%	0.0
262	No	cystathionine beta-synthase [Saccharomyces cerevisiae gi]	gi 415317 (+2)	56 kDa	25	0	0	0	0	21	0	0	0	45.0%	0.0	0.0	0.0
263	No	Nat1p [Saccharomyces cerevisiae S288c]	gi 6320164	99 kDa	21	0	0	0	0	20	0	0	0	26.3%	0.0	0.0	0.0
264	No	Dbp8p [Saccharomyces cerevisiae S288c]	gi 6321963	48 kDa	6	3	5	0	5	3	5	0	0	16.0%	9.51%	12.8%	0.000%
265	No	glutamine synthetase [Saccharomyces cerevisiae gi]	gi 171598 (+1)	39 kDa	13	2	3	0	8	2	3	0	0	29.8%	9.83%	12.1%	0.0
266	No	Dys1p [Saccharomyces cerevisiae S288c]	gi 6321859	43 kDa	26	0	1	0	0	15	0	1	0	43.7%	0.0	2.84%	0.0
267	No	Utp20p [Saccharomyces cerevisiae S288c]	gi 14270688	288 kDa	12	0	1	0	9	0	1	0	0	4.25%	0.0	0.481%	0.0
268	No	mitochondrial phenylalanyl-tRNA synthetase beta	gi 151941229 (+4)	67 kDa	20	0	0	0	0	15	0	0	0	32.4%	0.0	0.0	0.0
269	No	zuotin [Saccharomyces cerevisiae RM11-1a]	gi 190406714 (+1)	49 kDa	18	0	0	0	0	11	0	0	0	22.9%	0.0	0.0	0.0
270	No	Psa1p [Saccharomyces cerevisiae S288c]	gi 6320148 (+1)	40 kDa	20	2	3	0	11	2	3	0	0	32.4%	8.03%	10.8%	0.0
271	No	Ade12p [Saccharomyces cerevisiae S288c]	gi 6324109	48 kDa	17	0	0	0	14	0	0	0	0	37.9%	0.000%	0.000%	0.0
272	No	inositol pyrophosphate synthase [Saccharomyces cerevisiae gi]	gi 151940929 (+3)	130 kDa	16	0	0	0	13	0	0	0	0	14.0%	0.0	0.0	0.0
273	No	Lys2p [Saccharomyces cerevisiae S288c]	gi 6319591	155 kDa	20	0	0	0	0	16	0	0	0	14.4%	0.0	0.0	0.0
274	No	Ahp1p [Saccharomyces cerevisiae S288c]	gi 6323138	19 kDa	12	2	1	0	5	2	1	0	0	34.1%	11.4%	9.66%	0.0
275	No	Leu2p [Saccharomyces cerevisiae S288c]	gi 10383772 (+1)	39 kDa	20	0	3	0	13	0	2	0	0	45.3%	0.000%	6.59%	0.0
276	No	ribosomal RNA processing protein [Saccharomyces cerevisiae gi]	gi 151942780 (+2)	137 kDa	16	0	1	0	13	0	1	0	0	12.1%	0.0	0.814%	0.0
277	No	Kgd1p [Saccharomyces cerevisiae S288c]	gi 6322066	114 kDa	17	0	2	0	0	12	0	2	0	15.1%	0.0	2.37%	0.0
278	No	YCL057W [Saccharomyces cerevisiae]	gi 51830208 (+1)	82 kDa	18	1	0	0	16	1	0	0	0	25.8%	1.40%	0.0	0.0
279	No	Mdh1p [Saccharomyces cerevisiae S288c]	gi 6322765	36 kDa	22	0	0	0	14	0	0	0	0	57.5%	0.000%	0.0	0.0
280	No	DNA-dependent RNA polymerase I subunit A43	gi 1019425 (+1)	36 kDa	7	1	8	5	6	1	7	5	1	15.3%	3.68%	26.1%	12.3%
281	No	Chain A, High-Resolution Structures Of Adenylat	gi 157829936 (+4)	24 kDa	18	4	0	0	11	4	0	0	0	51.4%	17.3%	0.000%	0.0
282	No	Sec7p [Saccharomyces cerevisiae]	gi 1326010 (+6)	205 kDa	10	0	3	0	10	0	3	0	0	6.42%	0.0	1.94%	0.0
283	No	RecName: Full=Eukaryotic translation initiation	gi 238686679 (+2)	93 kDa	16	0	3	0	0	15	0	3	0	20.6%	0.0	5.30%	0.0
284	No	uracil phosphoribosyl transferase [Saccharomyces cerevisiae gi]	gi 7546185	29 kDa	20	1	0	0	12	1	0	0	0	48.8%	5.20%	0.0	0.0
285	No	Uso1p [Saccharomyces cerevisiae EC1118]	gi 259145186	206 kDa	19	0	0	0	0	19	0	0	0	12.1%	0.000%	0.000%	0.0
286	No	Tcp1p [Saccharomyces cerevisiae S288c]	gi 6320418	60 kDa	16	0	0	1	12	0	0	1	0	20.9%	0.0	0.0	1.97%
287	No	Cpa2p [Saccharomyces cerevisiae S288c]	gi 6322569	124 kDa	12	0	0	0	10	0	0	0	0	13.4%	0.0	0.0	0.0
288	No	helicase [Saccharomyces cerevisiae RM11-1a]	gi 190407873 (+2)	210 kDa	6	2	3	1	6	2	3	1	1	3.91%	1.29%	2.09%	0.964%
289	No	hypothetical protein SCRG_02385 [Saccharomyces cerevisiae gi]	gi 190407846 (+3)	138 kDa	10	0	1	0	10	0	1	0	0	11.4%	0.000%	0.736%	0.000%
290	No	Faa1p [Saccharomyces cerevisiae S288c]	gi 6324893	78 kDa	11	1	0	0	10	1	0	0	0	18.1%	2.00%	0.000%	0.0
291	No	RecName: Full=ATP-dependent RNA helicase DEgi	gi 160380616 (+3)	59 kDa	20	0	1	0	13	0	1	0	0	23.7%	0.0	2.29%	0.0

292	No	YDR214Wp-like protein [Saccharomyces cerevis gi 207346583 (+1)	39 kDa	16	1	0	0	9	1	0	0	28.9%	2.57%	0.0	0.0	
293	No	Trr1p [Saccharomyces cerevisiae S288c]	gi 6320560	34 kDa	23	0	0	0	11	0	0	48.6%	0.000%	0.0	0.0	
294	No	gamma chaperonin subunit [Saccharomyces cer gi 151945064	59 kDa	10	0	0	0	10	0	0	0	19.7%	0.000%	0.0	0.000%	
295	No	translation initiation factor eIF-2 beta subunit [S gi 151942564 (+1)	32 kDa	15	0	0	0	9	0	0	0	22.8%	0.0	0.000%	0.0	
296	No	YDR023Wp-like protein [Saccharomyces cerevis gi 207346845 (+1)	51 kDa	21	0	0	0	14	0	0	0	32.0%	0.0	0.0	0.0	
297	No	Lia1p [Saccharomyces cerevisiae S288c]	gi 6322531	36 kDa	18	0	0	12	0	0	0	51.1%	0.0	0.0	0.0	
298	No	Cdc33p [Saccharomyces cerevisiae S288c]	gi 6324433	24 kDa	15	3	3	7	3	3	0	29.6%	16.4%	16.4%	0.0	
299	No	RF-A [Saccharomyces cerevisiae RM11-1a]	gi 190406650 (+2)	70 kDa	8	3	5	7	2	5	0	13.8%	4.03%	9.82%	0.0	
300	No	Cof1p [Saccharomyces cerevisiae S288c]	gi 6322978	16 kDa	18	5	1	6	4	1	0	41.3%	38.5%	11.9%	0.0	
301	No	Slx1p [Saccharomyces cerevisiae S288c]	gi 6319705	36 kDa	0	1	1	0	1	1	0	0.0	5.59%	5.59%	0.000%	
302	No	RNA polymerase II 48 kd subunit [Saccharomyce gi 172211 (+1)	139 kDa	17	0	1	0	16	0	1	0	16.2%	0.0	1.39%	0.0	
303	No	Nog1p [Saccharomyces cerevisiae S288c]	gi 6325164	74 kDa	11	0	5	5	0	5	0	7.42%	0.0	8.81%	0.0	
304	No	RecName: Full=Protein HRI1; AltName: Full=HRF gi 338810331 (+1)	28 kDa	13	2	0	0	10	2	0	0	35.2%	9.84%	0.0	0.0	
305	No	Utp22p [Saccharomyces cerevisiae S288c]	gi 6321527	140 kDa	19	0	0	17	0	0	0	18.4%	0.0	0.000%	0.0	
306	No	Chain A, Structure-Based Functional Annotation gi 112490166	34 kDa	18	0	0	0	13	0	0	0	45.8%	0.000%	0.0	0.0	
307	No	Cdc39p [Saccharomyces cerevisiae S288c]	gi 10383811 (+1)	240 kDa	14	0	0	9	0	0	0	4.55%	0.0	0.0	0.0	
308	No	aminopeptidase yscIII [Saccharomyces cerevisia gi 151946671 (+3)	63 kDa	19	0	0	0	8	0	0	0	17.6%	0.0	0.0	0.0	
309	No	Gdh1p [Saccharomyces cerevisiae S288c]	gi 6324951	50 kDa	15	0	0	13	0	0	0	44.5%	0.0	0.0	0.0	
310	No	Gcv3p: H-protein subunit of the glycine cleavagi 595540	20 kDa	4	5	10	0	4	4	4	0	28.8%	20.3%	21.5%	0.0	
311	No	loc2p [Saccharomyces cerevisiae S288c]	gi 6323124	93 kDa	5	6	7	5	6	7	0	6.90%	8.99%	12.4%	0.0	
312	No	Rrp3p [Saccharomyces cerevisiae S288c]	gi 37362659 (+1)	56 kDa	12	2	2	0	10	2	2	0	21.2%	4.59%	4.59%	0.0
313	No	Chain A, Improved Calcineurin Inhibition By Yea gi 157834293 (+1)	12 kDa	15	3	1	0	6	3	1	0	58.4%	33.6%	10.6%	0.0	
314	No	RNA helicase DEAD box [Saccharomyces cerevis gi 190404852 (+1)	76 kDa	8	1	4	0	6	1	4	0	10.4%	1.81%	6.17%	0.0	
315	No	U3 snoRNP protein [Saccharomyces cerevisiae Y gi 151945015 (+1)	200 kDa	12	0	0	0	11	0	0	0	7.69%	0.0	0.000%	0.0	
316	No	ATP-dependent RNA helicase DOB1 [Saccharom gi 190409449	122 kDa	14	0	0	0	13	0	0	0	15.8%	0.000%	0.000%	0.0	
317	No	SEN3 [Saccharomyces cerevisiae]	gi 172578	104 kDa	11	0	0	10	0	0	0	11.0%	0.0	0.000%	0.0	
318	No	Bat2p [Saccharomyces cerevisiae S288c]	gi 6322608	42 kDa	16	0	0	11	0	0	0	31.4%	0.0	0.0	0.0	
319	No	Rim1p [Saccharomyces cerevisiae EC1118]	gi 259144970	15 kDa	11	3	7	4	3	4	0	28.1%	17.0%	28.1%	0.000%	
320	No	Chain A, Crystal Structure Of Cystathionine Gam gi 27066022 (+1)	42 kDa	13	4	1	0	8	4	1	0	24.9%	12.2%	2.80%	0.0	
321	No	vesicular transport involved protein [Saccharom gi 151940840	105 kDa	10	2	0	0	10	1	0	0	15.8%	0.878%	0.0	0.000%	
322	No	citrate synthase [Saccharomyces cerevisiae YJM gi 151944530 (+2)	53 kDa	14	4	0	0	7	4	0	0	17.5%	10.2%	0.0	0.0	
323	No	Apa1p [Saccharomyces cerevisiae S288c]	gi 10383757 (+1)	36 kDa	15	3	0	0	10	3	0	39.3%	12.1%	0.0	0.0	
324	No	Chain A, Saccharomyces Cerevisiae Nucleoside I gi 209156411 (+1)	18 kDa	16	1	0	0	8	1	0	0	47.2%	10.6%	0.0	0.0	
325	No	Crm1p [Saccharomyces cerevisiae JAY291]	gi 256272669 (+2)	124 kDa	12	0	0	0	12	0	0	12.7%	0.000%	0.000%	0.0	
326	No	CTP synthase [Saccharomyces cerevisiae YJM78 gi 151946355 (+2)	65 kDa	16	0	0	0	12	0	0	0	25.9%	0.000%	0.0	0.0	
327	No	Cym1p [Saccharomyces cerevisiae EC1118]	gi 259145666 (+1)	112 kDa	2	1	1	2	1	1	1	2.12%	1.01%	1.01%	1.01%	
328	No	hypothetical protein YCR016W [Saccharomyces gi 10383784	34 kDa	8	3	4	0	6	3	3	0	25.9%	13.1%	13.1%	0.0	
329	No	Ino80p [Saccharomyces cerevisiae S288c]	gi 6321289	171 kDa	4	6	8	0	3	6	8	2.42%	5.51%	6.72%	0.0	
330	No	aromatic amino acid aminotransferase [Sacchar gi 151943615 (+1)	56 kDa	16	3	0	0	13	3	0	0	28.8%	8.00%	0.0	0.0	
331	No	AAAT2 [Saccharomyces cerevisiae]	gi 1360338 (+1)	48 kDa	14	2	0	0	11	2	0	32.6%	6.02%	0.0	0.0	
332	No	hypothetical protein YDL124W [Saccharomyces gi 6320079	36 kDa	16	2	0	0	13	2	0	0	40.4%	8.97%	0.0	0.0	
333	No	YGR180C [Saccharomyces cerevisiae]	gi 51830370 (+1)	40 kDa	11	1	0	9	1	0	0	29.3%	3.48%	0.0	0.0	
334	No	heat shock protein 78 [Saccharomyces cerevisia gi 190404794	91 kDa	13	1	0	0	11	1	0	0	16.6%	1.23%	0.0	0.0	
335	No	Frs2p [Saccharomyces cerevisiae S288c]	gi 14318497	58 kDa	14	0	0	12	0	0	0	26.4%	0.000%	0.000%	0.000%	
336	No	vesicle coat component [Saccharomyces cerevis gi 190406320 (+2)	104 kDa	15	0	0	0	13	0	0	0	17.9%	0.0	0.0	0.0	
337	No	Cct2p [Saccharomyces cerevisiae EC1118]	gi 259147112 (+1)	57 kDa	16	0	0	11	0	0	0	24.9%	0.0	0.0	0.0	
338	No	mRNA cap binding protein eIF-4F [Saccharomyc gi 151943439 (+2)	107 kDa	19	0	0	0	9	0	0	0	12.2%	0.0	0.0	0.0	
339	No	protein involved in the nonsense-mediated mRt gi 151944022 (+5)	126 kDa	12	0	0	0	10	0	0	0	10.9%	0.0	0.0	0.0	
340	No	YDL182Wp-like protein [Saccharomyces cerevisi gi 207347106 (+1)	47 kDa	17	0	0	0	10	0	0	0	29.4%	0.0	0.0	0.0	
341	No	Lhp1p [Saccharomyces cerevisiae S288c]	gi 6320152	32 kDa	14	0	0	10	0	0	0	36.7%	0.0	0.0	0.0	
342	No	Pck1p [Saccharomyces cerevisiae S288c]	gi 6322950	61 kDa	17	0	0	11	0	0	0	25.1%	0.0	0.0	0.0	
343	No	Gis2p [Saccharomyces cerevisiae S288c]	gi 6324074	17 kDa	6	3	1	0	2	1	0	52.3%	15.7%	7.84%	0.0	
344	No	conserved protein [Saccharomyces cerevisiae Y gi 151946297 (+2)	118 kDa	5	0	0	1	5	0	0	1	6.26%	0.0	0.000%	0.963%	
345	No	histidine-tRNA synthetase mitochondrial [Sacch gi 171732	60 kDa	15	0	0	0	12	0	0	0	25.3%	0.000%	0.000%	0.0	
346	No	conserved protein [Saccharomyces cerevisiae Y gi 151945962 (+1)	22 kDa	2	0	0	0	1	0	0	0	8.51%	0.0	0.000%	0.000%	
347	No	Chain A, Heterodimer Between H48f-Ysod1 And gi 15826571 (+5)	16 kDa	15	4	0	0	7	4	0	0	64.1%	47.7%	0.0	0.0	
348	No	So13p [Saccharomyces cerevisiae S288c]	gi 82795254	28 kDa	16	0	0	13	0	0	0	55.8%	0.000%	0.0	0.0	
349	No	SAP190 [Saccharomyces cerevisiae]	gi 486457	125 kDa	3	0	0	3	0	0	0	4.37%	0.000%	0.000%	0.000%	
350	No	histone deacetylase complex DNA-binding subu gi 151945626 (+4)	175 kDa	12	0	1	0	12	0	1	0	8.98%	0.0	1.17%	0.0	

351	No	tyrosyl-tRNA synthetase [Saccharomyces cerevisiae]	gi 151943462 (+1)	44 kDa	10	0	0	0	6	0	0	0	16.0%	0.000%	0.0	0.0
352	No	hypothetical protein YLR419W [Saccharomyces cerevisiae]	gi 6323451	163 kDa	12	0	0	0	12	0	0	0	10.2%	0.0	0.0	0.0
353	No	Chain A, Apo Histidine-Tagged Saccharopine De [Saccharomyces cerevisiae]	gi 114793467 (+2)	51 kDa	16	0	0	0	13	0	0	0	33.4%	0.0	0.0	0.0
354	No	ATP phosphoribosyltransferase [Saccharomyces cerevisiae]	gi 151944768 (+2)	32 kDa	12	0	0	0	9	0	0	0	33.0%	0.0	0.0	0.0
355	No	Arc35p [Saccharomyces cerevisiae]	gi 259148986 (+1)	40 kDa	7	0	0	0	6	0	0	0	24.6%	0.0	0.0	0.0
356	No	Sub2p [Saccharomyces cerevisiae]	gi 6320119	50 kDa	19	0	0	0	15	0	0	0	39.5%	0.0	0.0	0.0
357	No	Vma4p [Saccharomyces cerevisiae]	gi 6324907	26 kDa	0	18	0	0	9	0	0	0	39.1%	0.0	0.0	0.0
358	No	Ssb2p [Saccharomyces cerevisiae]	gi 6324120	67 kDa	7	5	6	2	2	2	2	2	44.7%	44.9%	52.2%	35.1%
359	No	Rpa49p [Saccharomyces cerevisiae]	gi 6324081	47 kDa	5	0	2	2	3	0	2	2	9.88%	0.0	5.30%	5.78%
360	No	ribosomal protein L8A [Saccharomyces cerevisiae]	gi 151944166 (+2)	28 kDa	7	4	7	0	2	2	3	0	53.5%	45.7%	49.2%	0.0
361	No	ATPase component of a two subunit chromatin [Saccharomyces cerevisiae]	gi 151945386	130 kDa	12	1	1	0	12	1	1	0	15.4%	0.982%	3.66%	0.0
362	No	mitochondrial matrix factor [Saccharomyces cerevisiae]	gi 151943108 (+2)	16 kDa	12	3	0	0	5	2	0	0	40.0%	20.0%	0.0	0.0
363	No	sit4 suppressor [Saccharomyces cerevisiae]	gi 151944523 (+4)	38 kDa	16	0	1	0	12	0	1	0	34.5%	0.0	3.34%	0.0
364	No	hypothetical protein YMR226C [Saccharomyces cerevisiae]	gi 6323882	29 kDa	15	1	0	0	9	1	0	0	37.8%	5.24%	0.0	0.0
365	No	Erg6p [Saccharomyces cerevisiae]	gi 6323635	43 kDa	14	0	0	0	10	0	0	0	34.2%	0.000%	0.0	0.0
366	No	glycogen phosphorylase [Saccharomyces cerevisiae]	gi 151942932 (+1)	103 kDa	13	0	0	0	13	0	0	0	21.0%	0.0	0.000%	0.0
367	No	antiviral protein [Saccharomyces cerevisiae]	gi 558147 (+1)	164 kDa	10	0	0	0	10	0	0	0	8.10%	0.000%	0.0	0.0
368	No	prion protein [Saccharomyces cerevisiae]	gi 19567958 (+7)	77 kDa	13	0	0	0	12	0	0	0	22.0%	0.0	0.000%	0.0
369	No	unknown [Saccharomyces cerevisiae]	gi 1279685 (+2)	113 kDa	1	0	0	0	1	0	0	0	0.905%	0.0	0.0	0.0
370	No	phosphoglucosyltransferase [Saccharomyces cerevisiae]	gi 151946260 (+1)	63 kDa	15	0	0	0	13	0	0	0	28.8%	0.0	0.0	0.0
371	No	Chain A, Crystal Structure Of Imidazole Glycerol [Saccharomyces cerevisiae]	gi 16975311 (+4)	61 kDa	14	0	0	0	13	0	0	0	26.5%	0.0	0.0	0.0
372	No	sec21p [Saccharomyces cerevisiae]	gi 171483 (+1)	105 kDa	17	0	0	0	12	0	0	0	16.8%	0.0	0.0	0.0
373	No	Has1p [Saccharomyces cerevisiae]	gi 6323947	57 kDa	16	0	0	0	15	0	0	0	31.3%	0.0	0.0	0.0
374	No	Ret1p [Saccharomyces cerevisiae]	gi 6324781	129 kDa	8	1	2	1	8	1	2	1	6.88%	0.870%	1.91%	0.870%
375	No	Rpl33bp [Saccharomyces cerevisiae]	gi 6324808	12 kDa	7	5	5	0	2	2	2	0	33.6%	33.6%	33.6%	0.0
376	No	Mak5p [Saccharomyces cerevisiae]	gi 6319618	87 kDa	5	3	2	0	5	3	2	0	8.80%	4.14%	2.72%	0.0
377	No	Rpp2bp [Saccharomyces cerevisiae]	gi 6320590	11 kDa	9	1	4	0	4	1	3	0	34.5%	12.7%	33.6%	0.0
378	No	URA5 [Saccharomyces cerevisiae]	gi 671639	23 kDa	14	3	1	0	10	3	1	0	50.0%	22.9%	7.48%	0.0
379	No	Tif11p [Saccharomyces cerevisiae]	gi 6323916	17 kDa	12	0	1	0	6	0	1	0	34.6%	0.000%	10.5%	0.0
380	No	Dug1p [Saccharomyces cerevisiae]	gi 14318569 (+2)	53 kDa	14	1	0	0	7	1	0	0	19.5%	2.29%	0.0	0.0
381	No	ubiquitin-specific protease [Saccharomyces cerevisiae]	gi 15194869 (+2)	102 kDa	10	0	1	0	7	0	1	0	9.32%	0.0	1.21%	0.0
382	No	Myo2p [Saccharomyces cerevisiae]	gi 6324902	181 kDa	11	0	0	0	9	0	0	0	7.24%	0.0	0.000%	0.000%
383	No	Tho2p [Saccharomyces cerevisiae]	gi 6324190	184 kDa	11	0	0	0	10	0	0	0	6.64%	0.000%	0.0	0.0
384	No	YLL040Cp-like protein [Saccharomyces cerevisiae]	gi 207343275 (+2)	358 kDa	10	0	0	0	10	0	0	0	4.10%	0.0	0.000%	0.0
385	No	Lpd1p [Saccharomyces cerevisiae]	gi 14318501 (+3)	54 kDa	17	0	0	0	14	0	0	0	33.1%	0.0	0.0	0.0
386	No	conserved protein [Saccharomyces cerevisiae]	gi 151944300 (+1)	88 kDa	12	0	0	0	12	0	0	0	17.7%	0.0	0.0	0.0
387	No	myosin-like protein [Saccharomyces cerevisiae]	gi 171959 (+1)	218 kDa	7	0	0	0	7	0	0	0	5.07%	0.0	0.0	0.0
388	No	ATP-dependent RNA helicase DDX25 [Saccharomyces cerevisiae]	gi 190407384 (+1)	54 kDa	19	0	0	0	14	0	0	0	34.6%	0.0	0.0	0.0
389	No	phosphoribosylamino-imidazole-carboxylase [Saccharomyces cerevisiae]	gi 190407456 (+1)	62 kDa	15	0	0	0	15	0	0	0	32.2%	0.0	0.0	0.0
390	No	Dld3p [Saccharomyces cerevisiae]	gi 6320764	55 kDa	15	0	0	0	11	0	0	0	26.8%	0.0	0.0	0.0
391	No	Sgt2p [Saccharomyces cerevisiae]	gi 6324580	37 kDa	19	0	0	0	10	0	0	0	44.8%	0.0	0.0	0.0
392	No	Pdr5p [Saccharomyces cerevisiae]	gi 6324727	170 kDa	14	0	0	0	10	0	0	0	8.54%	0.0	0.0	0.0
393	No	ribosomal protein L24B [Saccharomyces cerevisiae]	gi 151943426 (+1)	18 kDa	4	5	5	0	1	2	2	0	29.7%	27.1%	27.7%	0.0
394	No	Tom1p [Saccharomyces cerevisiae]	gi 6320665	374 kDa	5	2	1	0	5	1	1	0	1.68%	0.275%	0.275%	0.0
395	No	Tif34p [Saccharomyces cerevisiae]	gi 6323795	39 kDa	9	0	3	0	9	0	3	0	32.6%	0.000%	9.80%	0.0
396	No	transcription factor SKN7 [Saccharomyces cerevisiae]	gi 190405981 (+4)	69 kDa	5	1	2	0	3	1	2	0	6.11%	3.38%	4.66%	0.0
397	No	Egd2p [Saccharomyces cerevisiae]	gi 172043 (+1)	18 kDa	11	1	4	0	6	1	4	0	39.4%	7.65%	38.2%	0.0
398	No	EC1118_1111_0133p [Saccharomyces cerevisiae]	gi 290771021 (+1)	22 kDa	9	1	0	1	7	1	0	1	39.4%	6.57%	0.0	12.6%
399	No	alcohol dehydrogenase III [Saccharomyces cerevisiae]	gi 171023 (+1)	40 kDa	11	0	0	0	8	1	0	0	23.7%	2.13%	0.0	0.0
400	No	YLR276C [Saccharomyces cerevisiae]	gi 51830470 (+1)	68 kDa	2	0	0	0	2	0	0	0	3.37%	0.0	0.000%	0.000%
401	No	Chd1p [Saccharomyces cerevisiae]	gi 256271313 (+2)	168 kDa	9	0	0	0	9	0	0	0	5.93%	0.000%	0.0	0.0
402	No	chaperonin containing T-complex subunit seven [Saccharomyces cerevisiae]	gi 151945013 (+1)	60 kDa	12	0	0	0	11	0	0	0	25.3%	0.0	0.0	0.000%
403	No	Sui2p [Saccharomyces cerevisiae]	gi 6322466	35 kDa	11	0	0	0	8	0	0	0	25.7%	0.0	0.0	0.0
404	No	alpha-isopropylmalate synthase [EC 4.1.3.12] [Saccharomyces cerevisiae]	gi 171842 (+2)	65 kDa	4	0	0	0	3	0	0	0	6.62%	0.0	0.0	0.0
405	No	D1229 [Saccharomyces cerevisiae]	gi 1004300	139 kDa	14	0	0	0	9	0	0	0	8.80%	0.0	0.0	0.0
406	No	trehalose-6-phosphate phosphatase [Saccharomyces cerevisiae]	gi 151942063 (+3)	103 kDa	13	0	0	0	12	0	0	0	17.2%	0.0	0.0	0.0
407	No	RNA1-1 allele rna1-1 [Saccharomyces cerevisiae]	gi 172436 (+2)	46 kDa	12	0	0	0	9	0	0	0	26.5%	0.0	0.0	0.0
408	No	conserved hypothetical protein [Saccharomyces cerevisiae]	gi 190406923 (+2)	71 kDa	15	0	0	0	10	0	0	0	21.2%	0.0	0.0	0.0
409	No	glycine cleavage system P subunit [Saccharomyces cerevisiae]	gi 190408414	114 kDa	10	0	0	0	9	0	0	0	8.70%	0.0	0.0	0.0

410	No	YOR374Wp-like protein [Saccharomyces cerevisi gi 207340808 (+1)	57 kDa	17	0	0	0	16	0	0	0	35.3%	0.0	0.0	0.0
411	No	GMP synthase [Saccharomyces cerevisiae] gi 460064 (+1)	59 kDa	14	0	0	0	11	0	0	0	23.4%	0.0	0.0	0.0
412	No	Spe3p [Saccharomyces cerevisiae S288c] gi 6325326	33 kDa	15	0	0	0	10	0	0	0	35.2%	0.0	0.0	0.0
413	No	Nop13p [Saccharomyces cerevisiae JAY291] gi 256270769 (+1)	46 kDa	8	2	1	0	7	2	1	0	19.6%	5.21%	2.98%	0.0
414	No	RecName: Full=Eisosome protein 1 gi 338818127 (+1)	93 kDa	0	0	1	0	0	0	1	0	0.000%	0.000%	2.02%	0.0
415	No	YPL126Wp-like protein [Saccharomyces cerevisi gi 207340618	100 kDa	10	0	0	0	10	0	0	0	14.5%	0.000%	0.000%	0.000%
416	No	Rps29ap [Saccharomyces cerevisiae S288c] gi 6323420	7 kDa	5	0	5	0	3	0	3	0	51.8%	0.000%	51.8%	0.0
417	No	unnamed protein product [Saccharomyces cere gi 296561 (+1)	63 kDa	10	1	0	0	9	1	0	0	18.9%	1.95%	0.0	0.0
418	No	Ugp1p [Saccharomyces cerevisiae S288c] gi 6322815	56 kDa	11	1	0	0	9	1	0	0	23.2%	2.20%	0.0	0.0
419	No	Adh6p [Saccharomyces cerevisiae S288c] gi 6323980	40 kDa	11	0	0	0	8	0	0	0	29.7%	0.0	0.000%	0.000%
420	No	conserved protein [Saccharomyces cerevisiae YJ gi 151946446 (+2)	58 kDa	13	0	0	0	9	0	0	0	19.4%	0.000%	0.0	0.0
421	No	alpha-alpha-trehalase [Saccharomyces cerevisia gi 498787	86 kDa	12	0	0	0	9	0	0	0	12.6%	0.000%	0.0	0.000%
422	No	Chain A, Crystal Structure Of Yeast Mitochondri gi 119389904 (+5)	55 kDa	11	0	0	0	10	0	0	0	21.4%	0.0	0.0	0.0
423	No	insensitive to killer toxin [Saccharomyces cerevi gi 151940905 (+3)	153 kDa	12	0	0	0	9	0	0	0	7.19%	0.0	0.0	0.0
424	No	conserved protein [Saccharomyces cerevisiae YJ gi 151941531 (+1)	203 kDa	9	0	0	0	9	0	0	0	5.56%	0.0	0.0	0.0
425	No	isopropylmalate isomerase [Saccharomyces cere gi 151943279 (+3)	86 kDa	13	0	0	0	12	0	0	0	21.1%	0.0	0.0	0.0
426	No	ORF1 [Saccharomyces cerevisiae] gi 172584 (+1)	39 kDa	16	0	0	0	14	0	0	0	45.2%	0.0	0.0	0.0
427	No	cyclophilin 40 [Saccharomyces cerevisiae RM11 gi 190405282 (+1)	42 kDa	12	0	0	0	9	0	0	0	25.6%	0.0	0.0	0.0
428	No	DNA topoisomerase I [Saccharomyces cerevisiae gi 190407336 (+2)	90 kDa	11	0	0	0	10	0	0	0	11.3%	0.0	0.0	0.0
429	No	YGR103Wp-like protein [Saccharomyces cerevis gi 207345119 (+1)	70 kDa	9	0	0	0	4	0	0	0	9.75%	0.0	0.0	0.0
430	No	Gvp36p [Saccharomyces cerevisiae JAY291] gi 256269794 (+1)	37 kDa	14	0	0	0	10	0	0	0	36.2%	0.0	0.0	0.0
431	No	Tpd3p [Saccharomyces cerevisiae JAY291] gi 256272273	71 kDa	13	0	0	0	10	0	0	0	19.7%	0.0	0.0	0.0
432	No	Cct4p [Saccharomyces cerevisiae JAY291] gi 256273573 (+2)	58 kDa	15	0	0	0	9	0	0	0	20.8%	0.0	0.0	0.0
433	No	Vtc3p [Saccharomyces cerevisiae EC1118] gi 259150137 (+1)	97 kDa	9	0	0	0	9	0	0	0	14.1%	0.0	0.0	0.0
434	No	transcriptional regulator [Saccharomyces cerevi gi 151945372 (+2)	194 kDa	4	1	2	0	4	1	1	0	5.04%	2.34%	2.34%	0.0
435	No	Wtm1p [Saccharomyces cerevisiae S288c] gi 6324804	48 kDa	11	2	0	0	8	2	0	0	22.9%	5.03%	0.0	0.0
436	No	Arp2p [Saccharomyces cerevisiae JAY291] gi 256269683 (+1)	44 kDa	10	0	1	0	6	0	1	0	19.4%	0.0	3.83%	0.0
437	No	phosphomannose isomerase [Saccharomyces cere gi 172166 (+1)	48 kDa	12	1	0	0	9	1	0	0	25.2%	2.33%	0.0	0.0
438	No	Rps23ap [Saccharomyces cerevisiae JAY291] gi 256273384 (+1)	16 kDa	3	0	0	0	3	0	0	0	20.5%	0.0	0.000%	0.0
439	No	Taf1p [Saccharomyces cerevisiae S288c] gi 6321713	121 kDa	1	0	0	0	1	0	0	0	0.844%	0.0	0.000%	0.000%
440	No	Pwp2p [Saccharomyces cerevisiae EC1118] gi 259144998 (+1)	104 kDa	5	0	0	0	5	0	0	0	6.18%	0.0	0.000%	0.0
441	No	Idi1p [Saccharomyces cerevisiae S288c] gi 6325140	33 kDa	10	0	0	0	5	0	0	0	26.0%	0.0	0.000%	0.0
442	No	3-deoxy-D-arabino-heptulosonate 7-phosphate gi 151946635 (+2)	40 kDa	14	0	0	0	6	0	0	0	16.5%	0.0	0.000%	0.0
443	No	dihydroxyacid dehydratase [Saccharomyces cere gi 151945093 (+2)	63 kDa	12	0	0	0	10	0	0	0	22.4%	0.0	0.0	0.0
444	No	conserved protein [Saccharomyces cerevisiae YJ gi 151945535 (+1)	118 kDa	4	0	0	0	4	0	0	0	4.82%	0.0	0.0	0.0
445	No	alpha,alpha-trehalose-phosphate synthase 123 gi 190408146 (+3)	123 kDa	14	0	0	0	9	0	0	0	10.9%	0.0	0.0	0.0
446	No	YHR158C [Saccharomyces cerevisiae] gi 51013057 (+1)	131 kDa	12	0	0	0	12	0	0	0	12.7%	0.0	0.0	0.0
447	No	Dim1p [Saccharomyces cerevisiae S288c] gi 6324989	36 kDa	3	2	3	0	3	2	3	0	13.2%	8.18%	11.3%	0.0
448	No	YJL081Cp-like protein [Saccharomyces cerevisia gi 207344021 (+1)	40 kDa	3	4	2	0	2	4	2	0	7.54%	14.5%	7.26%	0.0
449	No	Rps10ap [Saccharomyces cerevisiae S288c] gi 6324867	13 kDa	7	1	1	0	2	1	1	0	21.0%	13.3%	13.3%	0.0
450	No	hypothetical protein SCY_3068 [Saccharomyces gi 151945216 (+1)	26 kDa	2	5	5	0	1	1	1	0	3.75%	3.75%	3.75%	0.0
451	No	chorismate synthase [Saccharomyces cerevisiae gi 151943663 (+2)	41 kDa	10	1	1	0	6	1	1	0	19.7%	2.93%	3.72%	0.0
452	No	Rps27bp [Saccharomyces cerevisiae S288c] gi 6321809 (+1)	9 kDa	9	0	1	0	4	0	1	0	32.9%	0.0	19.5%	0.000%
453	No	Chain A, Ribonucleotide Reductase Y2y4 Hetero gi 15826569 (+2)	48 kDa	7	0	1	0	6	0	1	0	15.3%	0.000%	2.63%	0.0
454	No	beta-adaptin [Saccharomyces cerevisiae YJM78 gi 151941672 (+2)	82 kDa	5	0	3	0	4	0	3	0	6.34%	0.000%	4.82%	0.0
455	No	Hpt1p [Saccharomyces cerevisiae EC1118] gi 259145638	25 kDa	12	2	0	0	8	2	0	0	40.3%	10.4%	0.0	0.0
456	No	Cka1p [Saccharomyces cerevisiae S288c] gi 6322154	45 kDa	4	0	2	0	3	0	2	0	8.87%	0.0	4.84%	0.0
457	No	Yrb1p [Saccharomyces cerevisiae EC1118] gi 259145246	23 kDa	9	1	0	0	6	1	0	0	42.3%	9.45%	0.0	0.0
458	No	Smc3p [Saccharomyces cerevisiae S288c] gi 6322387	141 kDa	7	0	0	0	7	0	0	0	6.99%	0.000%	0.000%	0.0
459	No	V-ATPase [Saccharomyces cerevisiae] gi 171099 (+1)	42 kDa	10	1	0	0	10	1	0	0	32.7%	2.68%	0.0	0.0
460	No	unnamed protein product [Saccharomyces cere gi 4140 (+1)	134 kDa	8	0	0	0	8	0	0	0	7.90%	0.0	0.000%	0.0
461	No	hypothetical protein YER156C [Saccharomyces gi 6321004	38 kDa	12	0	0	0	9	0	0	0	29.0%	0.000%	0.0	0.0
462	No	Rli1p [Saccharomyces cerevisiae S288c] gi 6320296	68 kDa	10	0	0	0	9	0	0	0	17.3%	0.0	0.0	0.0
463	No	YNR051Cp-like protein [Saccharomyces cerevisi gi 207341545 (+2)	58 kDa	11	0	0	0	11	0	0	0	32.2%	0.0	0.0	0.0
464	No	Sec14p [Saccharomyces cerevisiae JAY291] gi 256273448 (+1)	35 kDa	13	0	0	0	11	0	0	0	39.0%	0.0	0.0	0.0
465	No	metalloprotease [Saccharomyces cerevisiae YJM gi 151940910 (+2)	118 kDa	7	0	0	0	7	0	0	0	8.76%	0.0	0.0	0.0
466	No	RNA polymerase II elongation factor [Saccharon gi 151946151 (+4)	116 kDa	8	0	0	0	6	0	0	0	8.00%	0.0	0.0	0.0
467	No	RecName: Full=ATP-dependent RNA helicase DR gi 160380652 (+2)	85 kDa	14	0	0	0	7	0	0	0	11.0%	0.0	0.0	0.0
468	No	40 kDa ubiquinol cytochrome-c reductase core gi 190408113 (+1)	40 kDa	12	0	0	0	11	0	0	0	33.7%	0.0	0.0	0.0

469	No	Sac6p [Saccharomyces cerevisiae JAY291]	gi 256274418	72 kDa	14	0	0	0	10	0	0	0	22.4%	0.0	0.0	0.0
470	No	Cct8p [Saccharomyces cerevisiae EC1118]	gi 290771197 (+1)	62 kDa	14	0	0	0	14	0	0	0	31.3%	0.0	0.0	0.0
471	No	Ypr1p [Saccharomyces cerevisiae S288c]	gi 6320576	35 kDa	11	0	0	0	9	0	0	0	37.2%	0.0	0.0	0.0
472	No	Aro9p [Saccharomyces cerevisiae S288c]	gi 6321929	59 kDa	11	0	0	0	11	0	0	0	21.2%	0.0	0.0	0.0
473	No	hypothetical protein YPL225W [Saccharomyces gi 6325031		17 kDa	10	0	0	0	6	0	0	0	37.0%	0.0	0.0	0.0
474	No	Cka2p [Saccharomyces cerevisiae S288c]	gi 6324635	39 kDa	6	1	2	0	6	1	2	0	18.0%	2.65%	7.08%	0.0
475	No	Nop4p [Saccharomyces cerevisiae S288c]	gi 6325213	78 kDa	6	2	1	0	4	2	1	0	5.84%	3.07%	1.46%	0.0
476	No	Pda1p: alpha subunit of pyruvate dehydrogenas gi 603419		49 kDa	7	1	1	0	7	1	1	0	16.9%	2.48%	2.48%	0.0
477	No	IMP dehydrogenase [Saccharomyces cerevisiae gi 151946109 (+2)		56 kDa	7	1	0	0	5	1	0	0	25.8%	7.25%	5.92%	0.0
478	No	pre-spliceosome component [Saccharomyces ce gi 151946117		154 kDa	10	2	0	0	10	2	0	0	8.89%	1.62%	0.000%	0.0
479	No	Cct5p [Saccharomyces cerevisiae JAY291]	gi 256273116 (+1)	62 kDa	6	0	0	0	6	0	0	0	13.3%	0.000%	0.000%	0.000%
480	No	mevalonate pyrophosphate decarboxylase [Sac gi 190408959 (+2)		44 kDa	12	1	0	0	11	1	0	0	33.6%	3.28%	0.0	0.0
481	No	Aro3p [Saccharomyces cerevisiae S288c]	gi 6320240	41 kDa	6	1	0	0	5	1	0	0	17.3%	4.32%	0.0	0.0
482	No	Pms1p [Saccharomyces cerevisiae JAY291]	gi 256270259	100 kDa	0	0	1	0	0	0	0	1	0.000%	0.0	0.000%	0.912%
483	No	homoserine kinase [Saccharomyces cerevisiae Y gi 151943969		39 kDa	10	0	0	0	7	0	0	0	23.5%	0.0	0.0	0.000%
484	No	Chain B, Yeast Isocitrate Dehydrogenase With C gi 167013431 (+2)		38 kDa	13	0	0	0	9	0	0	0	34.7%	0.000%	0.0	0.0
485	No	Rpt2p [Saccharomyces cerevisiae S288c]	gi 6320197	49 kDa	7	0	0	0	6	0	0	0	14.9%	0.000%	0.0	0.000%
486	No	Chain D, Crystal Structure Of Yeast Mitochondri gi 119389907		51 kDa	12	0	0	0	11	0	0	0	30.5%	0.000%	0.0	0.0
487	No	HPR1 protein [Saccharomyces cerevisiae]	gi 171702 (+1)	88 kDa	10	0	0	0	10	0	0	0	18.1%	0.0	0.000%	0.0
488	No	Hsp82p [Saccharomyces cerevisiae EC1118]	gi 259149917 (+2)	81 kDa	13	0	0	0	6	0	0	0	39.2%	0.0	0.0	0.0
489	No	Rpt1p [Saccharomyces cerevisiae EC1118]	gi 259147695 (+1)	52 kDa	11	0	0	0	9	0	0	0	22.1%	0.0	0.0	0.0
490	No	Bbc1p [Saccharomyces cerevisiae S288c]	gi 14627173 (+2)	128 kDa	12	0	0	0	7	0	0	0	6.66%	0.0	0.0	0.0
491	No	Chain A, Crystal Structure Of The Regulatory Sul gi 14719648 (+3)		55 kDa	11	0	0	0	10	0	0	0	21.0%	0.0	0.0	0.0
492	No	conserved protein [Saccharomyces cerevisiae Y gi 151942783 (+2)		119 kDa	10	0	0	0	7	0	0	0	8.37%	0.0	0.0	0.0
493	No	ARF-binding protein [Saccharomyces cerevisiae gi 151944054 (+2)		64 kDa	6	0	0	0	6	0	0	0	13.3%	0.0	0.0	0.0
494	No	D-fructose-6-phosphate amidotransferase (EC 2 gi 171596 (+1)		80 kDa	8	0	0	0	8	0	0	0	13.8%	0.0	0.0	0.0
495	No	Asn2p [Saccharomyces cerevisiae S288c]	gi 6321563	65 kDa	13	0	0	0	10	0	0	0	27.3%	0.0	0.0	0.0
496	No	Mrt4p [Saccharomyces cerevisiae S288c]	gi 6322843	27 kDa	10	0	0	0	7	0	0	0	36.9%	0.0	0.0	0.0
497	No	Zwf1p [Saccharomyces cerevisiae S288c]	gi 6324088	58 kDa	10	0	0	0	10	0	0	0	27.3%	0.0	0.0	0.0
498	No	YLR357Wp-like protein [Saccharomyces cerevisi gi 207342792		69 kDa	1	2	3	4	1	1	1	1	49.0%	59.6%	66.9%	58.8%
499	No	Chain B, Crystal Structure Of The Exportin Cse1 gi 58177142 (+1)		59 kDa	4	0	2	1	3	0	1	1	5.66%	0.000%	1.51%	1.51%
500	No	putative RNA polymerase [Saccharomyces cerev gi 555371		92 kDa	2	3	2	0	2	3	2	0	2.42%	4.96%	3.03%	0.0
501	No	transcription factor [Saccharomyces cerevisiae gi 151944508 (+4)		76 kDa	1	3	2	0	1	3	2	0	3.85%	7.84%	3.85%	0.0
502	No	Rpc82p [Saccharomyces cerevisiae EC1118]	gi 259150347	74 kDa	3	3	0	1	3	3	0	1	6.12%	5.81%	0.0	1.99%
503	No	ATP-dependent permease [Saccharomyces cere gi 151943831 (+1)		117 kDa	1	0	0	1	1	0	0	1	0.953%	0.0	0.000%	1.05%
504	No	Mbf1p [Saccharomyces cerevisiae S288c]	gi 42742310	16 kDa	9	0	3	0	4	0	3	0	31.8%	0.0	22.5%	0.0
505	No	Chain A, Crystal Structure Of Unliganded Form gi 13787040 (+1)		21 kDa	7	2	0	0	7	2	0	0	36.0%	15.6%	0.0	0.0
506	No	pre-mRNA splicing factor ATP-dependent RNA h gi 190407071 (+2)		88 kDa	7	0	0	1	7	0	0	1	11.2%	0.0	0.0	1.69%
507	No	periodic tryptophan protein [Saccharomyces ce gi 151941039 (+1)		64 kDa	9	0	1	0	8	0	1	0	16.0%	0.0	1.56%	0.0
508	No	Krr1p [Saccharomyces cerevisiae S288c]	gi 6319791	37 kDa	5	0	0	0	4	0	0	0	14.2%	0.000%	0.0	0.0
509	No	long-chain fatty acid transporter [Saccharomyce gi 151946432 (+2)		77 kDa	1	0	0	0	1	0	0	0	1.64%	0.000%	0.000%	0.000%
510	No	YLR274Wp-like protein [Saccharomyces cerevisi gi 207342873 (+1)		86 kDa	7	0	0	0	7	0	0	0	11.5%	0.000%	0.0	0.000%
511	No	Rps28bp [Saccharomyces cerevisiae S288c]	gi 6323294 (+1)	8 kDa	7	0	0	0	4	0	0	0	41.8%	0.0	0.000%	0.0
512	No	Phb2p [Saccharomyces cerevisiae JAY291]	gi 256272643	34 kDa	2	0	0	0	1	0	0	0	3.55%	0.0	0.000%	0.0
513	No	voltage-dependent anion-selective channel (VD gi 173166 (+1)		31 kDa	9	0	0	0	9	0	0	0	36.0%	0.0	0.0	0.000%
514	No	Ade4p [Saccharomyces cerevisiae S288c]	gi 6323958	57 kDa	7	0	0	0	7	0	0	0	16.5%	0.0	0.0	0.000%
515	No	Taf12p [Saccharomyces cerevisiae S288c]	gi 6320349	61 kDa	7	0	0	0	6	0	0	0	17.6%	0.000%	0.0	0.0
516	No	p-nitrophenyl phosphatase [Saccharomyces cer gi 190405224 (+2)		35 kDa	10	0	0	0	8	0	0	0	28.2%	0.0	0.0	0.0
517	No	aconitate hydratase, mitochondrial precursor [S gi 190409317 (+2)		87 kDa	9	0	0	0	8	0	0	0	11.8%	0.0	0.0	0.0
518	No	POL2 [Saccharomyces cerevisiae]	gi 1045247 (+1)	256 kDa	4	0	0	0	3	0	0	0	1.53%	0.0	0.0	0.0
519	No	Chain A, Crystal Structure Of Oxidized Form Fro gi 122920148 (+1)		12 kDa	10	0	0	0	5	0	0	0	55.0%	0.0	0.0	0.0
520	No	dihydroorotase [Saccharomyces cerevisiae YJM gi 151940937 (+2)		40 kDa	8	0	0	0	7	0	0	0	22.0%	0.0	0.0	0.0
521	No	malic enzyme [Saccharomyces cerevisiae YJM78 gi 151941514 (+2)		74 kDa	10	0	0	0	8	0	0	0	14.9%	0.0	0.0	0.0
522	No	UDP-N-acetylglucosamine pyrophosphorylase [S gi 151941900 (+2)		53 kDa	10	0	0	0	10	0	0	0	24.5%	0.0	0.0	0.0
523	No	1,4-glucan-6-(1,4-glucano)-transferase [Saccha gi 151944699 (+5)		81 kDa	8	0	0	0	6	0	0	0	8.81%	0.0	0.0	0.0
524	No	conserved protein [Saccharomyces cerevisiae Y gi 151946024 (+1)		38 kDa	13	0	0	0	6	0	0	0	26.4%	0.0	0.0	0.0
525	No	dihydroxyacetone kinase [Saccharomyces cerev gi 151946094 (+2)		62 kDa	8	0	0	0	8	0	0	0	18.3%	0.0	0.0	0.0
526	No	MAP2 [Saccharomyces cerevisiae]	gi 1870087 (+1)	48 kDa	5	0	0	0	4	0	0	0	12.8%	0.0	0.0	0.0
527	No	Cic1p [Saccharomyces cerevisiae JAY291]	gi 256270839 (+1)	42 kDa	12	0	0	0	7	0	0	0	25.0%	0.0	0.0	0.0

528	No	Aip1p [Saccharomyces cerevisiae JAY291]	gi 256273500 (+2)	67 kDa	11	0	0	0	0	7	0	0	0	14.6%	0.0	0.0	0.0
529	No	Chain A, Crystal Structure Of Gamma-Glutamyl I	gi 52696231	51 kDa	10	0	0	0	0	8	0	0	0	22.6%	0.0	0.0	0.0
530	No	Gdh2p [Saccharomyces cerevisiae S288c]	gi 6319986	124 kDa	7	0	0	0	0	5	0	0	0	6.32%	0.0	0.0	0.0
531	No	Nop6p [Saccharomyces cerevisiae S288c]	gi 6319988	25 kDa	6	0	0	0	0	3	0	0	0	16.0%	0.0	0.0	0.0
532	No	Rpn3p [Saccharomyces cerevisiae S288c]	gi 6320859	60 kDa	10	0	0	0	0	10	0	0	0	22.8%	0.0	0.0	0.0
533	No	Pre9p [Saccharomyces cerevisiae S288c]	gi 6321574	29 kDa	13	0	0	0	0	9	0	0	0	36.8%	0.0	0.0	0.0
534	No	Ubr1p [Saccharomyces cerevisiae S288c]	gi 6321623	225 kDa	9	0	0	0	0	9	0	0	0	5.18%	0.0	0.0	0.0
535	No	Rrb1p [Saccharomyces cerevisiae S288c]	gi 6323779	57 kDa	12	0	0	0	0	9	0	0	0	21.7%	0.0	0.0	0.0
536	No	Dis3p [Saccharomyces cerevisiae S288c]	gi 6324552	114 kDa	11	0	0	0	0	11	0	0	0	15.1%	0.0	0.0	0.0
537	No	Rpb8p [Saccharomyces cerevisiae S288c]	gi 6324798	17 kDa	6	2	3	0	0	3	2	3	0	17.1%	10.3%	17.1%	0.0
538	No	Rfc1p [Saccharomyces cerevisiae S288c]	gi 6324791	95 kDa	1	0	1	0	0	1	0	1	0	1.51%	0.000%	1.51%	0.0
539	No	Ser1p [Saccharomyces cerevisiae S288c]	gi 6324758 (+1)	43 kDa	10	1	0	0	0	10	1	0	0	24.1%	2.53%	0.000%	0.0
540	No	Pob3p [Saccharomyces cerevisiae S288c]	gi 6323571	63 kDa	6	0	1	0	0	6	0	1	0	10.1%	0.0	1.81%	0.0
541	No	clathrin associated protein complex large subunit	gi 151942818 (+3)	94 kDa	2	0	1	0	0	2	0	1	0	2.76%	0.0	1.32%	0.0
542	No	RPL41A [Saccharomyces cerevisiae]	gi 1302130 (+2)	14 kDa	4	0	1	0	0	1	0	1	0	6.90%	0.0	8.62%	0.0
543	No	Msc7p [Saccharomyces cerevisiae JAY291]	gi 256270595 (+2)	71 kDa	9	0	0	0	0	7	0	0	0	13.0%	0.0	0.000%	0.0
544	No	dihydroorotate dehydrogenase [Saccharomyces cerevisiae]	gi 151941448 (+4)	35 kDa	4	1	0	0	0	3	1	0	0	12.1%	2.87%	0.0	0.0
545	No	U5 snRNP-specific protein [Saccharomyces cerevisiae]	gi 151941746 (+1)	114 kDa	5	0	0	0	0	5	0	0	0	6.35%	0.0	0.000%	0.000%
546	No	Ecm14p [Saccharomyces cerevisiae S288c]	gi 6321924	50 kDa	8	1	0	0	0	4	1	0	0	10.2%	3.72%	0.0	0.0
547	No	Rpn11p [Saccharomyces cerevisiae S288c]	gi 14318526	34 kDa	7	0	1	0	0	7	0	1	0	28.8%	0.0	4.25%	0.0
548	No	unnamed protein product [Saccharomyces cerevisiae]	gi 3788 (+1)	43 kDa	7	0	0	0	0	6	0	0	0	18.0%	0.000%	0.000%	0.0
549	No	vesicle coat component [Saccharomyces cerevisiae]	gi 151942712 (+2)	242 kDa	6	0	0	0	0	4	0	0	0	2.96%	0.000%	0.000%	0.000%
550	No	Chain A, Engineering The Enolase Active Site	Po gi 304445683	48 kDa	1	0	0	0	0	1	0	0	0	41.1%	26.4%	0.0	0.0
551	No	Myo5p [Saccharomyces cerevisiae S288c]	gi 6323756	137 kDa	7	0	0	0	0	5	0	0	0	4.84%	0.0	0.000%	0.0
552	No	conserved hypothetical protein [Saccharomyces cerevisiae]	gi 190409861 (+2)	31 kDa	6	0	0	0	0	5	0	0	0	19.6%	0.000%	0.0	0.0
553	No	sulfite reductase beta subunit [Saccharomyces cerevisiae]	gi 117958157 (+4)	161 kDa	1	0	0	0	0	1	0	0	0	1.04%	0.000%	0.000%	0.0
554	No	conserved protein [Saccharomyces cerevisiae YJM]	gi 151944665	51 kDa	8	0	0	0	0	7	0	0	0	17.4%	0.000%	0.0	0.0
555	No	unnamed protein product [Saccharomyces cerevisiae]	gi 1322832 (+4)	113 kDa	5	0	0	0	0	4	0	0	0	4.92%	0.0	0.0	0.0
556	No	serine/threonine MAP kinase [Saccharomyces cerevisiae]	gi 151943974 (+3)	55 kDa	9	0	0	0	0	8	0	0	0	18.9%	0.0	0.0	0.0
557	No	nuclear GTPase [Saccharomyces cerevisiae YJM]	gi 151944713 (+2)	58 kDa	10	0	0	0	0	10	0	0	0	22.9%	0.0	0.0	0.0
558	No	Hypothetical protein YCL011c [Saccharomyces cerevisiae]	gi 190406428 (+2)	49 kDa	11	0	0	0	0	6	0	0	0	16.9%	0.0	0.0	0.0
559	No	YJL088Wp-like protein [Saccharomyces cerevisiae]	gi 207344036 (+1)	50 kDa	11	0	0	0	0	8	0	0	0	22.5%	0.0	0.0	0.0
560	No	Slh1p [Saccharomyces cerevisiae JAY291]	gi 256272657 (+2)	225 kDa	7	0	0	0	0	7	0	0	0	4.58%	0.0	0.0	0.0
561	No	Dop1p [Saccharomyces cerevisiae EC1118]	gi 259145382 (+1)	195 kDa	6	0	0	0	0	6	0	0	0	4.00%	0.0	0.0	0.0
562	No	Pil1p [Saccharomyces cerevisiae EC1118]	gi 259146589 (+1)	38 kDa	9	0	0	0	0	5	0	0	0	24.2%	0.0	0.0	0.0
563	No	Rvs161p [Saccharomyces cerevisiae EC1118]	gi 290770661	30 kDa	4	0	0	0	0	4	0	0	0	16.6%	0.0	0.0	0.0
564	No	Ncl1p [Saccharomyces cerevisiae S288c]	gi 6319447	78 kDa	8	0	0	0	0	7	0	0	0	15.9%	0.0	0.0	0.0
565	No	Grx1p [Saccharomyces cerevisiae S288c]	gi 6319814	12 kDa	11	0	0	0	0	4	0	0	0	46.4%	0.0	0.0	0.0
566	No	Rtn1p [Saccharomyces cerevisiae S288c]	gi 6320439	33 kDa	10	0	0	0	0	7	0	0	0	24.4%	0.0	0.0	0.0
567	No	Rnr1p [Saccharomyces cerevisiae S288c]	gi 6320914	100 kDa	8	0	0	0	0	4	0	0	0	6.08%	0.0	0.0	0.0
568	No	Bgl2p [Saccharomyces cerevisiae S288c]	gi 6321721	34 kDa	10	0	0	0	0	5	0	0	0	16.0%	0.0	0.0	0.0
569	No	Sec13p [Saccharomyces cerevisiae S288c]	gi 6323237	33 kDa	8	0	0	0	0	7	0	0	0	28.6%	0.0	0.0	0.0
570	No	Erb1p [Saccharomyces cerevisiae S288c]	gi 6323693	92 kDa	7	0	0	0	0	6	0	0	0	8.80%	0.0	0.0	0.0
571	No	Pdr16p [Saccharomyces cerevisiae S288c]	gi 6324098	41 kDa	10	0	0	0	0	7	0	0	0	19.9%	0.0	0.0	0.0
572	No	Mpd2p [Saccharomyces cerevisiae S288c]	gi 6324484	32 kDa	6	0	0	0	0	4	0	0	0	14.1%	0.0	0.0	0.0
573	No	Tuf1p [Saccharomyces cerevisiae S288c]	gi 6324761	48 kDa	11	0	0	0	0	9	0	0	0	25.2%	0.0	0.0	0.0
574	No	Itc1p [Saccharomyces cerevisiae S288c]	gi 6321305	146 kDa	4	1	1	0	0	3	1	1	0	2.69%	0.870%	0.712%	0.000%
575	No	RNA polymerase I enhancer binding protein [Saccharomyces cerevisiae]	gi 151946440 (+2)	92 kDa	4	1	4	0	0	3	1	4	0	5.06%	2.22%	6.67%	0.0
576	No	L-A protein [Saccharomyces cerevisiae]	gi 553134	3 kDa	9	2	1	0	0	1	1	1	0	40.7%	40.7%	40.7%	0.0
577	No	pyruvate dehydrogenase beta subunit (E1 beta)	gi 151946607 (+2)	40 kDa	9	1	1	0	0	5	1	1	0	16.9%	3.28%	3.28%	0.0
578	No	Gpt2p [Saccharomyces cerevisiae S288c]	gi 6322920	84 kDa	0	0	0	1	0	0	0	1	0	0.000%	0.0	0.000%	1.21%
579	No	Glc7p [Saccharomyces cerevisiae JAY291]	gi 256273613 (+1)	36 kDa	9	0	2	0	0	8	0	2	0	26.8%	0.0	9.27%	0.0
580	No	Sec4p [Saccharomyces cerevisiae S288c]	gi 14318517 (+1)	24 kDa	9	0	1	0	0	7	0	1	0	43.3%	0.0	5.58%	0.0
581	No	TSM1 gene [Saccharomyces cerevisiae]	gi 228348	162 kDa	3	0	0	0	0	3	0	0	0	2.27%	0.000%	0.0	0.0
582	No	clin three (clin3) requiring protein [Saccharomyces cerevisiae]	gi 151945491 (+2)	125 kDa	4	0	0	0	0	4	0	0	0	3.99%	0.0	0.000%	0.000%
583	No	unnamed protein product [Saccharomyces cerevisiae]	gi 4593 (+2)	49 kDa	7	0	0	0	0	7	0	0	0	17.8%	0.0	0.000%	0.0
584	No	Chain A, Crystal Structure Of Coproporphyrinogen III	gi 56966162	38 kDa	6	0	0	0	0	5	0	0	0	18.0%	0.000%	0.000%	0.0
585	No	ornithine aminotransferase [Saccharomyces cerevisiae]	gi 190405473 (+2)	46 kDa	8	0	0	0	0	8	0	0	0	24.1%	0.0	0.0	0.000%
586	No	RNA-binding protein [Saccharomyces cerevisiae]	gi 172438 (+3)	48 kDa	5	0	0	0	0	4	0	0	0	8.86%	0.0	0.000%	0.0

587	No	NADPH-cytochrome P450 reductase precursor [gi 218453 (+1)	77 kDa	8	0	0	0	8	0	0	0	13.9%	0.0	0.000%	0.0
588	No	Chain A, Structure Of Sec23-Sar1 Complexed Wlgi 165761044 (+1)	86 kDa	8	0	0	0	8	0	0	0	11.8%	0.0	0.000%	0.0
589	No	Sui1p [Saccharomyces cerevisiae S288c]	12 kDa	10	0	0	0	6	0	0	0	62.0%	0.0	0.000%	0.0
590	No	Lmd2p [Saccharomyces cerevisiae S288c]	57 kDa	7	0	0	0	6	0	0	0	28.5%	0.0	0.0	0.0
591	No	NMA111 [Saccharomyces cerevisiae]	111 kDa	6	0	0	0	6	0	0	0	6.02%	0.0	0.0	0.0
592	No	Smc1p [Saccharomyces cerevisiae S288c]	141 kDa	6	0	0	0	6	0	0	0	5.55%	0.0	0.0	0.0
593	No	septin [Saccharomyces cerevisiae YJM789]	60 kDa	7	0	0	0	7	0	0	0	18.7%	0.0	0.0	0.0
594	No	conserved protein [Saccharomyces cerevisiae YJgi 151941449 (+1)	140 kDa	8	0	0	0	8	0	0	0	8.48%	0.0	0.0	0.0
595	No	chaperonin containing tcp-1 [Saccharomyces ce gi 151942171 (+1)	60 kDa	6	0	0	0	5	0	0	0	9.34%	0.0	0.0	0.0
596	No	translation initiation factor eIF4B [Saccharomyc gi 151942935 (+1)	49 kDa	7	0	0	0	5	0	0	0	14.2%	0.0	0.0	0.0
597	No	nucleolar protein [Saccharomyces cerevisiae YJt gi 151944473 (+4)	70 kDa	8	0	0	0	7	0	0	0	16.0%	0.0	0.0	0.0
598	No	PPIase [Saccharomyces cerevisiae YJM789]	46 kDa	9	0	0	0	5	0	0	0	16.7%	0.0	0.0	0.0
599	No	TafII90 [Saccharomyces cerevisiae YJM789]	89 kDa	7	0	0	0	7	0	0	0	12.2%	0.0	0.0	0.0
600	No	Chain A, Yeast Isocitrate Dehydrogenase With C gi 167013438	38 kDa	9	0	0	0	8	0	0	0	27.2%	0.0	0.0	0.0
601	No	glucosidase I [Saccharomyces cerevisiae RM11-1: gi 190406994 (+3)	96 kDa	8	0	0	0	8	0	0	0	11.5%	0.0	0.0	0.0
602	No	RNA polymerase II mediator complex subunit 5 gi 190407096 (+2)	129 kDa	7	0	0	0	7	0	0	0	7.60%	0.0	0.0	0.0
603	No	YHR049Wp-like protein [Saccharomyces cerevis gi 207344712 (+2)	27 kDa	7	0	0	0	5	0	0	0	25.4%	0.0	0.0	0.0
604	No	glutathione synthase [Saccharomyces cerevisiae gi 229473701 (+1)	56 kDa	6	0	0	0	6	0	0	0	15.7%	0.0	0.0	0.0
605	No	Chain A, Crystal Structure Of S. Cerevisiae Trypt gi 288965772 (+2)	50 kDa	11	0	0	0	11	0	0	0	28.5%	0.0	0.0	0.0
606	No	YBL036C [Saccharomyces cerevisiae]	29 kDa	11	0	0	0	7	0	0	0	38.1%	0.0	0.0	0.0
607	No	Pet9p [Saccharomyces cerevisiae S288c]	34 kDa	6	0	0	0	4	0	0	0	14.8%	0.0	0.0	0.0
608	No	Fpr2p [Saccharomyces cerevisiae S288c]	14 kDa	9	0	0	0	7	0	0	0	51.1%	0.0	0.0	0.0
609	No	Bem2p [Saccharomyces cerevisiae S288c]	245 kDa	4	0	0	0	3	0	0	0	1.62%	0.0	0.0	0.0
610	No	Vma10p [Saccharomyces cerevisiae S288c]	13 kDa	6	0	0	0	3	0	0	0	21.9%	0.0	0.0	0.0
611	No	Car1p [Saccharomyces cerevisiae S288c]	36 kDa	7	0	0	0	6	0	0	0	16.8%	0.0	0.0	0.0
612	No	Tif5p [Saccharomyces cerevisiae S288c]	45 kDa	6	0	0	0	6	0	0	0	19.8%	0.0	0.0	0.0
613	No	alpha-ketoglutarate dehydrogenase complex dil gi 151942132 (+2)	50 kDa	3	1	1	1	3	1	1	1	10.6%	3.46%	3.46%	3.46%
614	No	Hta2p [Saccharomyces cerevisiae S288c]	14 kDa	0	1	2	1	0	1	1	1	0.000%	6.82%	6.82%	6.82%
615	No	conserved protein [Saccharomyces cerevisiae YJ gi 151941620 (+2)	40 kDa	4	1	3	1	1	1	1	1	2.62%	2.62%	2.62%	2.62%
616	No	ribosomal protein L8B [Saccharomyces cerevisia gi 151941127	28 kDa	3	1	1	1	2	1	1	1	57.8%	45.7%	45.7%	24.2%
617	No	Mge1p [Saccharomyces cerevisiae JAY291]	26 kDa	3	2	2	0	3	2	2	0	12.7%	12.7%	12.7%	0.0
618	No	Brx1p [Saccharomyces cerevisiae EC1118]	34 kDa	4	1	2	0	4	1	2	0	19.2%	5.50%	9.97%	0.0
619	No	Ckb1p [Saccharomyces cerevisiae S288c]	32 kDa	3	1	4	0	3	1	3	0	11.5%	2.88%	10.4%	0.0
620	No	Rpl7ap [Saccharomyces cerevisiae S288c]	28 kDa	4	4	3	0	1	1	1	0	56.1%	39.8%	34.8%	0.0
621	No	Rps31p [Saccharomyces cerevisiae S288c]	17 kDa	2	1	0	0	2	1	0	0	38.2%	5.26%	5.92%	0.0
622	No	catabolic serine (threonine) dehydratase [Sacch gi 151943772 (+2)	39 kDa	4	0	3	0	4	0	3	0	13.6%	0.000%	8.61%	0.0
623	No	family of serine hydrolases 3 [Saccharomyces ce gi 190407581 (+1)	30 kDa	6	0	1	0	3	0	1	0	13.9%	0.0	3.38%	0.000%
624	No	HDF1 protein [Saccharomyces cerevisiae]	71 kDa	0	5	6	0	0	5	6	0	0.0	8.31%	11.8%	0.0
625	No	nicotinamidase [Saccharomyces cerevisiae RM1 gi 190407002 (+1)	25 kDa	8	2	0	0	4	1	0	0	27.3%	5.56%	0.0	0.0
626	No	RecName: Full=Nucleolar protein 9; AltName: F gi 332319756	78 kDa	3	0	1	0	3	0	1	0	6.91%	0.0	1.35%	0.0
627	No	branched-chain amino acid transaminase [Sacch gi 151944153 (+1)	44 kDa	6	1	0	0	6	1	0	0	27.7%	2.54%	0.0	0.0
628	No	Msn5 protein [Saccharomyces cerevisiae]	142 kDa	3	0	0	0	3	0	0	0	3.59%	0.000%	0.000%	0.000%
629	No	hypothetical protein SCRG_03913 [Saccharomyc gi 190409726 (+2)	35 kDa	0	2	0	0	0	1	0	0	0.000%	2.91%	0.0	0.0
630	No	protoplasts-secreted [Saccharomyces cerevisiae gi 151942018 (+1)	21 kDa	7	0	0	0	5	0	0	0	29.3%	0.000%	0.0	0.0
631	No	hypothetical protein YNL010W [Saccharomyces gi 6324318	27 kDa	5	0	0	0	3	0	0	0	18.7%	0.000%	0.0	0.0
632	No	conserved protein [Saccharomyces cerevisiae YJ gi 151944044 (+2)	104 kDa	8	0	0	0	6	0	0	0	8.07%	0.000%	0.0	0.0
633	No	RecName: Full=Eukaryotic translation initiation gi 238686682 (+1)	30 kDa	7	0	0	0	6	0	0	0	21.9%	0.000%	0.0	0.0
634	No	co-chaperone [Saccharomyces cerevisiae YJM78 gi 151941687 (+1)	24 kDa	8	0	0	0	3	0	0	0	16.7%	0.000%	0.0	0.0
635	No	Fpr4p [Saccharomyces cerevisiae S288c]	44 kDa	4	0	0	0	4	0	0	0	14.3%	0.0	0.000%	0.0
636	No	serine/threonine protein kinase [Saccharomyc gi 151941680 (+4)	76 kDa	6	0	0	0	4	0	0	0	8.68%	0.0	0.000%	0.0
637	No	conserved protein [Saccharomyces cerevisiae YJ gi 151945005 (+3)	54 kDa	8	0	0	0	7	0	0	0	13.9%	0.0	0.000%	0.0
638	No	Lsg1p [Saccharomyces cerevisiae S288c]	73 kDa	9	0	0	0	6	0	0	0	11.1%	0.0	0.000%	0.0
639	No	early meiotic induction protein [Saccharomyces gi 151942477 (+2)	56 kDa	6	0	0	0	4	0	0	0	8.00%	0.0	0.000%	0.0
640	No	nitrilase superfamily [Saccharomyces cerevisiae gi 151940875 (+1)	33 kDa	8	0	0	0	7	0	0	0	28.9%	0.0	0.0	0.0
641	No	Aro10p [Saccharomyces cerevisiae JAY291]	71 kDa	6	0	0	0	6	0	0	0	10.1%	0.0	0.0	0.0
642	No	Gcn2Op [Saccharomyces cerevisiae S288c]	85 kDa	6	0	0	0	4	0	0	0	5.85%	0.0	0.0	0.0
643	No	superkiller [Saccharomyces cerevisiae YJM789 gi 151940919 (+4)	146 kDa	4	0	0	0	4	0	0	0	4.35%	0.0	0.0	0.0
644	No	uridylyate kinase [Saccharomyces cerevisiae YJM gi 151941519 (+4)	23 kDa	7	0	0	0	5	0	0	0	27.5%	0.0	0.0	0.0
645	No	protein associated with ribosomal export compl gi 151942089 (+2)	65 kDa	9	0	0	0	8	0	0	0	15.7%	0.0	0.0	0.0

646	No	proteasome regulatory particle subunit [Sacchaigi]	151942397 (+1)	46 kDa	6	0	0	0	4	0	0	0	14.5%	0.0	0.0	0.0
647	No	multiple RNA-binding domain containing protein gi	151942889 (+1)	101 kDa	7	0	0	0	5	0	0	0	6.99%	0.0	0.0	0.0
648	No	squalene monooxygenase [Saccharomyces cere gi]	151943454 (+3)	55 kDa	7	0	0	0	6	0	0	0	13.7%	0.0	0.0	0.0
649	No	oxysterol-binding family protein [Saccharomyce gi]	151943940 (+3)	50 kDa	6	0	0	0	5	0	0	0	14.2%	0.0	0.0	0.0
650	No	conserved protein [Saccharomyces cerevisiae Yj gi]	151944116 (+3)	59 kDa	10	0	0	0	10	0	0	0	21.6%	0.0	0.0	0.0
651	No	replication factor C subunit 3 [Saccharomyces c gi]	151944257 (+1)	38 kDa	9	0	0	0	9	0	0	0	32.6%	0.0	0.0	0.0
652	No	mediator complex subunit [Saccharomyces cere gi]	151944311 (+3)	111 kDa	5	0	0	0	5	0	0	0	6.06%	0.0	0.0	0.0
653	No	ligase of succinyl-coa [Saccharomyces cerevisiae gi]	151945761 (+2)	35 kDa	7	0	0	0	7	0	0	0	28.0%	0.0	0.0	0.0
654	No	hypothetical protein SCRG_00135 [Saccharomy gi]	190404667 (+1)	108 kDa	7	0	0	0	7	0	0	0	8.16%	0.0	0.0	0.0
655	No	threonine aldolase [Saccharomyces cerevisiae R gi]	190405520 (+2)	43 kDa	9	0	0	0	7	0	0	0	23.0%	0.0	0.0	0.0
656	No	protein phosphatase 2A B-type regulatory subu gi]	190407355	85 kDa	7	0	0	0	4	0	0	0	6.21%	0.0	0.0	0.0
657	No	Chain A, Crystal Structure Of Saccharomyces Ce gi]	193506511 (+1)	48 kDa	6	0	0	0	6	0	0	0	17.3%	0.0	0.0	0.0
658	No	Chs5p [Saccharomyces cerevisiae JAY291]	gi 256270398	70 kDa	8	0	0	0	8	0	0	0	20.7%	0.0	0.0	0.0
659	No	Chain A, Saccharomyces Cerevisiae (Yeast) Profi gi]	2780895 (+1)	14 kDa	9	0	0	0	3	0	0	0	24.8%	0.0	0.0	0.0
660	No	Vtc4p [Saccharomyces cerevisiae S288c]	gi 42742256	83 kDa	7	0	0	0	6	0	0	0	8.88%	0.0	0.0	0.0
661	No	unnamed protein product [Saccharomyces cere gi]	4303 (+1)	47 kDa	7	0	0	0	4	0	0	0	11.3%	0.0	0.0	0.0
662	No	YLR270W [Saccharomyces cerevisiae]	gi 45269802 (+1)	41 kDa	9	0	0	0	9	0	0	0	30.6%	0.0	0.0	0.0
663	No	Pdx3p [Saccharomyces cerevisiae S288c]	gi 6319509	27 kDa	8	0	0	0	6	0	0	0	36.4%	0.0	0.0	0.0
664	No	Trp2p [Saccharomyces cerevisiae S288c]	gi 6320935	57 kDa	10	0	0	0	8	0	0	0	17.6%	0.0	0.0	0.0
665	No	Rsp5p [Saccharomyces cerevisiae S288c]	gi 6320972	92 kDa	7	0	0	0	6	0	0	0	12.0%	0.0	0.0	0.0
666	No	Rpn10p [Saccharomyces cerevisiae S288c]	gi 6321994	30 kDa	8	0	0	0	8	0	0	0	38.8%	0.0	0.0	0.0
667	No	Lys12p [Saccharomyces cerevisiae S288c]	gi 6322097	40 kDa	8	0	0	0	8	0	0	0	29.4%	0.0	0.0	0.0
668	No	Irc24p [Saccharomyces cerevisiae S288c]	gi 6322227	29 kDa	9	0	0	0	5	0	0	0	21.7%	0.0	0.0	0.0
669	No	Ykt6p [Saccharomyces cerevisiae S288c]	gi 6322652	23 kDa	6	0	0	0	5	0	0	0	31.0%	0.0	0.0	0.0
670	No	Ade16p [Saccharomyces cerevisiae S288c]	gi 6323056	65 kDa	8	0	0	0	7	0	0	0	17.9%	0.0	0.0	0.0
671	No	Rat1p [Saccharomyces cerevisiae S288c]	gi 6324622	116 kDa	6	0	0	0	6	0	0	0	7.36%	0.0	0.0	0.0
672	No	Utp9p [Saccharomyces cerevisiae S288c]	gi 6321990	65 kDa	5	0	0	0	2	0	0	0	5.57%	0.0	0.0	0.0
673	No	YIL043Cp-like protein [Saccharomyces cerevisia gi]	207344301 (+1)	26 kDa	2	2	1	0	2	1	1	0	6.72%	3.36%	3.36%	0.000%
674	No	Tif6p [Saccharomyces cerevisiae S288c]	gi 6325273	26 kDa	4	1	1	0	3	1	1	0	18.4%	5.71%	5.71%	0.0
675	No	14-3-3 protein [Saccharomyces cerevisiae YJM7 gi]	151942087 (+3)	31 kDa	8	1	1	0	4	1	1	0	48.5%	12.9%	12.9%	0.0
676	No	Rpl14ap [Saccharomyces cerevisiae S288c]	gi 6322847	15 kDa	1	3	1	0	1	2	1	0	27.5%	33.3%	27.5%	0.0
677	No	iron-sulfur protein biogenesis, desulfurase-inter gi]	151944760 (+1)	11 kDa	4	1	0	0	4	1	0	0	41.5%	9.57%	0.000%	0.000%
678	No	Ysp1p [Saccharomyces cerevisiae EC1118]	gi 259146912	144 kDa	2	0	0	0	1	0	0	0	0.814%	0.000%	0.000%	0.000%
679	No	Prs3p [Saccharomyces cerevisiae S288c]	gi 6321776	35 kDa	6	0	1	0	6	0	1	0	21.6%	0.000%	2.81%	0.0
680	No	Tub2p [Saccharomyces cerevisiae S288c]	gi 14318481 (+1)	51 kDa	8	0	1	0	6	0	1	0	13.1%	0.0	2.19%	0.000%
681	No	YDR432Wp-like protein [Saccharomyces cerevis gi]	207346289 (+2)	35 kDa	5	2	0	0	3	2	0	0	13.4%	8.39%	0.0	0.0
682	No	YGR270Wp-like protein [Saccharomyces cerevis gi]	207344897 (+2)	158 kDa	2	0	3	0	2	0	3	0	1.60%	0.0	3.34%	0.0
683	No	Chain A, Solution Nmr Structure Of Protein YnrG gi]	109157991 (+2)	13 kDa	3	1	0	0	1	1	0	0	9.17%	9.17%	0.0	0.0
684	No	Abf2p [Saccharomyces cerevisiae S288c]	gi 6323717	22 kDa	0	4	1	0	0	4	1	0	0.0	24.0%	7.65%	0.0
685	No	Faa4p [Saccharomyces cerevisiae S288c]	gi 6323903 (+1)	77 kDa	5	0	1	0	4	0	1	0	7.06%	0.0	1.44%	0.0
686	No	conserved protein [Saccharomyces cerevisiae Yj gi]	151943900 (+1)	21 kDa	4	1	0	0	2	1	0	0	13.7%	5.49%	0.0	0.0
687	No	Hsp10p [Saccharomyces cerevisiae S288c]	gi 6324594	11 kDa	8	0	1	0	4	0	1	0	53.8%	0.0	10.4%	0.0
688	No	Sse2p [Saccharomyces cerevisiae S288c]	gi 6319646	78 kDa	2	0	0	0	2	0	0	0	9.67%	0.0	1.73%	0.0
689	No	transcription factor [Saccharomyces cerevisiae \ gi]	151942776 (+4)	150 kDa	3	0	0	0	3	0	0	0	2.33%	0.000%	0.000%	0.000%
690	No	hypothetical protein SCRG_00140 [Saccharomy gi]	190404672 (+2)	71 kDa	2	0	0	0	2	0	0	0	3.77%	0.000%	0.0	0.0
691	No	RecName: Full=Spindle pole body component 1 gi]	334351093 (+2)	112 kDa	1	0	0	0	1	0	0	0	1.27%	0.0	0.0	0.000%
692	No	RecName: Full=RNA polymerase II degradation f gi]	325530069 (+1)	84 kDa	7	0	0	0	3	0	0	0	6.64%	0.0	0.000%	0.0
693	No	hypothetical protein YFR016C [Saccharomyces c gi]	14318538	138 kDa	5	0	0	0	5	0	0	0	4.87%	0.0	0.000%	0.0
694	No	Ssa4p [Saccharomyces cerevisiae S288c]	gi 6320950	70 kDa	3	0	0	0	3	0	0	0	15.0%	0.0	0.0	1.87%
695	No	Tma108p [Saccharomyces cerevisiae JAY291]	gi 256270234 (+1)	108 kDa	7	0	0	0	7	0	0	0	8.99%	0.0	0.0	0.0
696	No	Pus7p [Saccharomyces cerevisiae S288c]	gi 6324817	77 kDa	7	0	0	0	7	0	0	0	14.6%	0.0	0.0	0.0
697	No	Chain A, Structure Of The Yeast U-Box-Containir gi]	158430229	112 kDa	5	0	0	0	5	0	0	0	6.01%	0.0	0.0	0.0
698	No	3-phosphoglycerate dehydrogenase [Saccharom gi]	117958129 (+1)	51 kDa	10	0	0	0	9	0	0	0	25.4%	0.0	0.0	0.0
699	No	ubiquitin ligase e3 [Saccharomyces cerevisiae Yj gi]	151941535 (+4)	168 kDa	2	0	0	0	2	0	0	0	1.69%	0.0	0.0	0.0
700	No	ARF GTP/GDP exchange factor [Saccharomyces gi]	151944687 (+3)	166 kDa	8	0	0	0	8	0	0	0	6.72%	0.0	0.0	0.0
701	No	transcription factor [Saccharomyces cerevisiae \ gi]	151944955 (+1)	93 kDa	8	0	0	0	8	0	0	0	12.4%	0.0	0.0	0.0
702	No	conserved protein [Saccharomyces cerevisiae Yj gi]	151945109 (+2)	135 kDa	7	0	0	0	7	0	0	0	6.30%	0.0	0.0	0.0
703	No	actin filament binding protein [Saccharomyces c gi]	151945326 (+2)	71 kDa	4	0	0	0	4	0	0	0	8.44%	0.0	0.0	0.0
704	No	trehalose-6-phosphate synthase/phosphatase c gi]	151945968 (+4)	119 kDa	7	0	0	0	5	0	0	0	6.64%	0.0	0.0	0.0

705	No	conserved protein [Saccharomyces cerevisiae YJgi 151946188 (+2)	54 kDa	5	0	0	0	5	0	0	0	12.3%	0.0	0.0	0.0
706	No	CYC8 protein [Saccharomyces cerevisiae] gi 171350 (+4)	107 kDa	6	0	0	0	6	0	0	0	8.39%	0.0	0.0	0.0
707	No	lanosterol 14-demethylase cytochrome P450 [Si:gi 171354 (+2)	61 kDa	5	0	0	0	5	0	0	0	11.9%	0.0	0.0	0.0
708	No	Chain A, Crystal Structure Of Adenine Phosphor gi 17943167 (+2)	21 kDa	8	0	0	0	5	0	0	0	25.1%	0.0	0.0	0.0
709	No	RecName: Full=Myosin-3; AltName: Full=Actin-c gi 190358924 (+2)	143 kDa	6	0	0	0	3	0	0	0	3.62%	0.0	0.0	0.0
710	No	conserved hypothetical protein [Saccharomyces gi 190407555 (+3)	34 kDa	6	0	0	0	6	0	0	0	21.1%	0.0	0.0	0.0
711	No	inorganic phosphate transporter [Saccharomyces gi 190408125 (+2)	64 kDa	7	0	0	0	6	0	0	0	11.4%	0.0	0.0	0.0
712	No	Qns1p [Saccharomyces cerevisiae JAY291] gi 256269444 (+2)	81 kDa	7	0	0	0	7	0	0	0	13.2%	0.0	0.0	0.0
713	No	Get3p [Saccharomyces cerevisiae JAY291] gi 256274115 (+2)	39 kDa	8	0	0	0	7	0	0	0	22.9%	0.0	0.0	0.0
714	No	Scs2p [Saccharomyces cerevisiae S288c] gi 6320966	27 kDa	6	0	0	0	4	0	0	0	20.9%	0.0	0.0	0.0
715	No	Rp1p [Saccharomyces cerevisiae S288c] gi 6321880	35 kDa	8	0	0	0	6	0	0	0	27.1%	0.0	0.0	0.0
716	No	Rps21bp [Saccharomyces cerevisiae S288c] gi 6322325 (+1)	10 kDa	8	0	0	0	3	0	0	0	36.8%	0.0	0.0	0.0
717	No	Mrp8p [Saccharomyces cerevisiae S288c] gi 6322707	25 kDa	5	0	0	0	5	0	0	0	28.8%	0.0	0.0	0.0
718	No	Nup2p [Saccharomyces cerevisiae S288c] gi 6323367	78 kDa	6	0	0	0	5	0	0	0	13.1%	0.0	0.0	0.0
719	No	hypothetical protein YOR021C [Saccharomyces gi 6324595	25 kDa	5	0	0	0	5	0	0	0	25.4%	0.0	0.0	0.0
720	No	Cam1p [Saccharomyces cerevisiae S288c] gi 6325209	47 kDa	7	0	0	0	5	0	0	0	15.9%	0.0	0.0	0.0
721	No	Unknown [Saccharomyces cerevisiae] gi 7706833	121 kDa	8	0	0	0	8	0	0	0	8.00%	0.0	0.0	0.0
722	No	RecName: Full=Pre-rRNA-processing protein RIX gi 160165464 (+5)	87 kDa	2	0	0	0	2	0	0	0	2.88%	0.0	0.0	0.0
723	No	Mck1p [Saccharomyces cerevisiae S288c] gi 6324022	43 kDa	4	0	0	0	3	0	0	0	9.33%	0.0	0.0	0.0
724	No	RNA polymerase C [Saccharomyces cerevisiae Y.gi 151944532 (+1)	36 kDa	4	1	1	0	4	1	1	0	18.6%	3.47%	3.47%	0.0
725	No	tata-box factor protein [Saccharomyces cerevisi gi 172899 (+2)	27 kDa	2	1	1	0	1	1	1	0	7.08%	7.08%	7.08%	0.0
726	No	les1p [Saccharomyces cerevisiae S288c] gi 14318508 (+3)	79 kDa	1	1	1	0	1	1	1	0	1.88%	1.88%	1.88%	0.0
727	No	Cns1p [Saccharomyces cerevisiae JAY291] gi 256270196	44 kDa	2	1	2	0	2	1	1	0	5.45%	2.86%	2.86%	0.0
728	No	Rep 1 protein [Saccharomyces cerevisiae A364A gi 11466069	43 kDa	2	0	2	0	2	2	0	0	5.09%	0.000%	5.09%	0.0
729	No	Arp8p [Saccharomyces cerevisiae S288c] gi 6324715	100 kDa	2	0	3	0	2	0	3	0	3.41%	0.000%	4.20%	0.0
730	No	MLS1 [Saccharomyces cerevisiae] gi 125863518 (+4)	63 kDa	4	0	0	0	4	0	0	0	7.76%	0.000%	0.0	0.000%
731	No	Ycf1p [Saccharomyces cerevisiae S288c] gi 6320339	171 kDa	4	0	1	0	4	0	1	0	3.37%	0.0	0.660%	0.0
732	No	Rps30ap [Saccharomyces cerevisiae S288c] gi 6323318	7 kDa	2	0	1	0	2	0	1	0	17.5%	0.0	15.9%	0.0
733	No	Chain C, Structure Of A Sumo-Binding-Motif Mir gi 149241626 (+2)	12 kDa	3	0	1	0	2	0	1	0	31.1%	0.0	10.4%	0.0
734	No	Hxt6p [Saccharomyces cerevisiae EC1118] gi 259145579 (+1)	63 kDa	4	0	1	0	2	0	1	0	5.96%	0.0	2.81%	0.0
735	No	Hsp26p [Saccharomyces cerevisiae S288c] gi 6319546	24 kDa	7	1	0	0	7	1	0	0	41.1%	7.48%	0.0	0.0
736	No	dismutase,Mn superoxide gi 223570	23 kDa	7	1	0	0	5	1	0	0	27.1%	4.43%	0.0	0.0
737	No	Mrc1p [Saccharomyces cerevisiae S288c] gi 10383754 (+2)	124 kDa	0	0	3	0	0	0	1	0	0.0	0.000%	0.000%	1.37%
738	No	U3 snoRNP protein [Saccharomyces cerevisiae Y gi 151943408 (+1)	80 kDa	4	0	0	0	4	0	0	0	8.70%	0.0	0.0	0.000%
739	No	exocyst complex component [Saccharomyces ce gi 151944716 (+4)	155 kDa	2	0	0	0	2	0	0	0	2.02%	0.000%	0.0	0.0
740	No	uroporphyrinogen III synthase [Saccharomyces gi 151945361 (+2)	31 kDa	0	1	0	0	0	1	0	0	0.000%	2.91%	0.0	0.000%
741	No	NUM1 protein gi 228467 (+2)	313 kDa	7	0	0	0	4	0	0	0	2.40%	0.0	0.0	0.000%
742	No	delta 1-pyrroline-5-carboxylate reductase [Sac gi 151944733 (+1)	30 kDa	6	0	0	0	4	0	0	0	17.1%	0.0	0.0	0.000%
743	No	Sar1p [Saccharomyces cerevisiae JAY291] gi 256272801	22 kDa	4	0	0	0	3	0	0	0	19.4%	0.0	0.000%	0.0
744	No	conserved protein [Saccharomyces cerevisiae YJ gi 151946092 (+4)	171 kDa	5	0	0	0	4	0	0	0	3.95%	0.0	0.0	0.000%
745	No	alpha tubulin [Saccharomyces cerevisiae] gi 173058 (+2)	50 kDa	7	0	0	0	7	0	0	0	21.5%	0.0	0.000%	0.0
746	No	actin-related protein [Saccharomyces cerevisiae gi 151945133 (+1)	50 kDa	6	0	0	0	5	0	0	0	11.8%	0.000%	0.0	0.0
747	No	Ltp1p [Saccharomyces cerevisiae JAY291] gi 256268979	19 kDa	2	0	0	0	1	0	0	0	11.2%	0.000%	0.0	0.0
748	No	Ubx5p [Saccharomyces cerevisiae S288c] gi 6320537	57 kDa	1	0	0	0	1	0	0	0	2.40%	0.0	0.000%	0.0
749	No	Skp1p [Saccharomyces cerevisiae] gi 1438746 (+1)	22 kDa	4	0	0	0	3	0	0	0	23.2%	0.0	0.0	0.0
750	No	conserved protein [Saccharomyces cerevisiae YJ gi 151944447 (+3)	132 kDa	2	0	0	0	2	0	0	0	1.95%	0.0	0.0	0.0
751	No	S-adenosylmethionine synthetase 2 [Saccharom gi 190404577 (+2)	42 kDa	6	0	0	0	5	0	0	0	21.9%	0.0	0.0	0.0
752	No	ATP-dependent protease [Saccharomyces cerev gi 151946373 (+2)	127 kDa	4	0	0	0	4	0	0	0	3.71%	0.0	0.0	0.0
753	No	argininosuccinate lyase [Saccharomyces cerevis gi 151943960 (+2)	52 kDa	6	0	0	0	6	0	0	0	16.2%	0.0	0.0	0.0
754	No	Chain A, The Crystal Structure Of Allosteric Chor gi 1127167 (+1)	30 kDa	6	0	0	0	5	0	0	0	22.3%	0.0	0.0	0.0
755	No	Vtc2p [Saccharomyces cerevisiae S288c] gi 14318518 (+4)	95 kDa	8	0	0	0	8	0	0	0	11.0%	0.0	0.0	0.0
756	No	N-myristoyl transferase [Saccharomyces cerevis gi 151941038 (+3)	53 kDa	5	0	0	0	4	0	0	0	11.2%	0.0	0.0	0.0
757	No	conserved protein [Saccharomyces cerevisiae YJ gi 151942541 (+2)	63 kDa	6	0	0	0	6	0	0	0	12.0%	0.0	0.0	0.0
758	No	pheromone response pathway suppressor [Sacc gi 151943711 (+1)	53 kDa	6	0	0	0	4	0	0	0	7.05%	0.0	0.0	0.0
759	No	phosphoacetylglucosamine mutase [Saccharom gi 151944654 (+5)	62 kDa	8	0	0	0	8	0	0	0	17.2%	0.0	0.0	0.0
760	No	aspartate kinase [Saccharomyces cerevisiae YJM gi 151944764 (+1)	58 kDa	5	0	0	0	5	0	0	0	14.0%	0.0	0.0	0.0
761	No	nicotinate phosphoribosyltransferase [Saccharo gi 151945299 (+3)	49 kDa	6	0	0	0	6	0	0	0	19.1%	0.0	0.0	0.0
762	No	karyopherin [Saccharomyces cerevisiae YJM789 gi 151946017 (+1)	121 kDa	4	0	0	0	4	0	0	0	5.05%	0.0	0.0	0.0
763	No	Chain A, Yeast 5-Aminolaevulinic Acid Dehydrat gi 15825885 (+3)	37 kDa	9	0	0	0	7	0	0	0	25.0%	0.0	0.0	0.0

764	No	Chain C, Crystal Structure Of A Novel Chaperone	gi 166007290 (+2)	29 kDa	6	0	0	0	6	0	0	0	23.7%	0.0	0.0	0.0
765	No	threonine deaminase [Saccharomyces cerevisiae]	gi 190405649 (+3)	64 kDa	7	0	0	0	7	0	0	0	17.7%	0.0	0.0	0.0
766	No	hypothetical protein SCR_G_01604 [Saccharomyces]	gi 190407526 (+2)	56 kDa	4	0	0	0	4	0	0	0	10.5%	0.0	0.0	0.0
767	No	mitochondrial phosphate carrier protein [Saccharomyces]	gi 190409551 (+1)	33 kDa	6	0	0	0	6	0	0	0	21.2%	0.0	0.0	0.0
768	No	YDR117Cp-like protein [Saccharomyces cerevisiae]	gi 207346718 (+1)	64 kDa	7	0	0	0	6	0	0	0	13.1%	0.0	0.0	0.0
769	No	YNL045W-like protein [Saccharomyces cerevisiae]	gi 256273273 (+2)	77 kDa	4	0	0	0	4	0	0	0	6.11%	0.0	0.0	0.0
770	No	Bdh1p [Saccharomyces cerevisiae S288c]	gi 330443362 (+1)	42 kDa	6	0	0	0	6	0	0	0	19.6%	0.0	0.0	0.0
771	No	Tsr1p [Saccharomyces cerevisiae S288c]	gi 6320143	91 kDa	5	0	0	0	5	0	0	0	6.85%	0.0	0.0	0.0
772	No	Cdc12p [Saccharomyces cerevisiae S288c]	gi 6321899	47 kDa	6	0	0	0	5	0	0	0	20.1%	0.0	0.0	0.0
773	No	Spt8p [Saccharomyces cerevisiae S288c]	gi 6323084	66 kDa	5	0	0	0	4	0	0	0	8.64%	0.0	0.0	0.0
774	No	Rgr1p [Saccharomyces cerevisiae S288c]	gi 6323100	123 kDa	6	0	0	0	6	0	0	0	6.47%	0.0	0.0	0.0
775	No	Erg27p [Saccharomyces cerevisiae S288c]	gi 6323129	40 kDa	5	0	0	0	5	0	0	0	15.9%	0.0	0.0	0.0
776	No	Cpr3p [Saccharomyces cerevisiae S288c]	gi 6323562	20 kDa	6	0	0	0	5	0	0	0	29.1%	0.0	0.0	0.0
777	No	llv2p [Saccharomyces cerevisiae S288c]	gi 6323755	75 kDa	9	0	0	0	8	0	0	0	16.4%	0.0	0.0	0.0
778	No	Hch1p [Saccharomyces cerevisiae S288c]	gi 6324048	17 kDa	5	0	0	0	4	0	0	0	34.6%	0.0	0.0	0.0
779	No	Rpt5p [Saccharomyces cerevisiae S288c]	gi 6324691	48 kDa	5	0	0	0	4	0	0	0	11.8%	0.0	0.0	0.0
780	No	Get4p [Saccharomyces cerevisiae S288c]	gi 6324738	36 kDa	7	0	0	0	7	0	0	0	23.7%	0.0	0.0	0.0
781	No	Fcy1p [Saccharomyces cerevisiae S288c]	gi 6325319	18 kDa	9	0	0	0	5	0	0	0	41.8%	0.0	0.0	0.0
782	No	Dpm1p [Saccharomyces cerevisiae S288c]	gi 6325441	30 kDa	6	0	0	0	6	0	0	0	22.1%	0.0	0.0	0.0
783	No	SET domain-containing protein [Saccharomyces]	gi 151944961 (+1)	85 kDa	1	0	0	0	1	0	0	0	2.05%	0.0	0.0	0.0
784	No	replication factor-A subunit 3 [Saccharomyces]	gi 151944957 (+2)	14 kDa	3	3	2	0	2	2	2	0	27.0%	27.0%	27.0%	0.0
785	No	Rpp1bp [Saccharomyces cerevisiae S288c]	gi 6320073	11 kDa	6	1	1	0	1	1	1	0	15.1%	15.1%	15.1%	0.0
786	No	Rpa12p [Saccharomyces cerevisiae S288c]	gi 6322523	14 kDa	3	0	3	1	2	0	2	1	26.4%	0.000%	26.4%	12.0%
787	No	actin-related protein [Saccharomyces cerevisiae]	gi 151944074 (+2)	43 kDa	0	2	3	0	0	2	3	0	0.000%	5.99%	10.7%	0.0
788	No	loc3p [Saccharomyces cerevisiae S288c]	gi 14318535 (+3)	91 kDa	4	0	1	0	3	0	1	0	5.08%	0.000%	1.78%	0.0
789	No	Rpc10p [Saccharomyces cerevisiae S288c]	gi 6321937	8 kDa	3	0	2	0	1	0	1	0	28.6%	0.0	28.6%	0.0
790	No	bmh sensitive protein [Saccharomyces cerevisiae]	gi 151942584 (+1)	136 kDa	2	1	0	0	2	1	0	0	2.11%	1.69%	0.0	0.0
791	No	Arf2p [Saccharomyces cerevisiae S288c]	gi 6320064	21 kDa	6	0	1	0	2	0	1	0	44.8%	0.0	15.5%	0.0
792	No	U5 snRNP and spliceosome component [Saccharomyces]	gi 151944111 (+5)	280 kDa	2	0	0	0	2	0	0	0	0.746%	0.0	0.000%	0.000%
793	No	3'(2')5'-biphosphate nucleotidase [Saccharomyces]	gi 151945570 (+4)	39 kDa	5	1	0	0	5	1	0	0	18.8%	2.80%	0.0	0.0
794	No	delta-1-pyrroline-5-carboxylate dehydrogenase	gi 151943981 (+2)	64 kDa	4	0	1	0	4	0	1	0	7.83%	0.0	2.26%	0.0
795	No	Snu13p [Saccharomyces cerevisiae S288c]	gi 6320809	14 kDa	3	0	0	0	3	0	0	0	31.7%	0.0	0.000%	0.0
796	No	conserved hypothetical protein [Saccharomyces]	gi 190405447	105 kDa	1	0	0	0	1	0	0	0	1.17%	0.0	0.0	0.000%
797	No	hypothetical protein YLR179C [Saccharomyces]	gi 6323208	22 kDa	5	0	0	0	4	0	0	0	23.9%	0.000%	0.0	0.0
798	No	histone deacetylase [Saccharomyces cerevisiae]	gi 190409024 (+1)	80 kDa	2	0	0	0	2	0	0	0	3.68%	0.000%	0.0	0.0
799	No	Sdo1p [Saccharomyces cerevisiae S288c]	gi 6323050	28 kDa	2	0	0	0	2	0	0	0	9.20%	0.0	0.000%	0.0
800	No	conserved protein [Saccharomyces cerevisiae YJ]	gi 151942617 (+4)	115 kDa	2	0	0	0	2	0	0	0	3.16%	0.0	0.000%	0.0
801	No	conserved hypothetical protein [Saccharomyces]	gi 190404671 (+1)	26 kDa	4	0	0	0	4	0	0	0	22.0%	0.0	0.000%	0.0
802	No	Mrh1p [Saccharomyces cerevisiae S288c]	gi 6320236	36 kDa	3	0	0	0	2	0	0	0	10.3%	0.0	0.000%	0.0
803	No	ebna1-binding protein [Saccharomyces cerevisiae]	gi 151941747 (+3)	50 kDa	4	0	0	0	3	0	0	0	9.74%	0.0	0.0	0.0
804	No	Srh1p [Saccharomyces cerevisiae]	gi 4538 (+1)	60 kDa	5	0	0	0	4	0	0	0	10.2%	0.0	0.0	0.0
805	No	TOM70 [Saccharomyces cerevisiae]	gi 125863515 (+6)	70 kDa	4	0	0	0	4	0	0	0	10.9%	0.0	0.0	0.0
806	No	conserved hypothetical protein [Saccharomyces]	gi 190408357 (+1)	145 kDa	6	0	0	0	5	0	0	0	4.10%	0.0	0.0	0.0
807	No	Sol2p [Saccharomyces cerevisiae S288c]	gi 10383806 (+1)	35 kDa	7	0	0	0	4	0	0	0	17.8%	0.0	0.0	0.0
808	No	processing/termination factor [Saccharomyces]	gi 1097162 (+4)	19 kDa	5	0	0	0	4	0	0	0	30.0%	0.0	0.0	0.0
809	No	Ubp6p [Saccharomyces cerevisiae S288c]	gi 14318532	57 kDa	6	0	0	0	6	0	0	0	14.4%	0.0	0.0	0.0
810	No	Rpn12p [Saccharomyces cerevisiae S288c]	gi 14318577	32 kDa	7	0	0	0	6	0	0	0	24.5%	0.0	0.0	0.0
811	No	coronin [Saccharomyces cerevisiae YJM789]	gi 151940945 (+3)	73 kDa	6	0	0	0	5	0	0	0	9.22%	0.0	0.0	0.0
812	No	U3 snoRNP protein [Saccharomyces cerevisiae Y]	gi 151941291 (+1)	106 kDa	3	0	0	0	3	0	0	0	4.77%	0.0	0.0	0.0
813	No	luminal Hsp70 protein [Saccharomyces cerevisiae]	gi 151941472 (+1)	100 kDa	5	0	0	0	5	0	0	0	6.24%	0.0	0.0	0.0
814	No	phosphoglucomutase minor isoform [Saccharomyces]	gi 151941679 (+2)	63 kDa	6	0	0	0	5	0	0	0	14.2%	0.0	0.0	0.0
815	No	maintenance of killer [Saccharomyces cerevisiae]	gi 151942049	117 kDa	6	0	0	0	6	0	0	0	6.44%	0.0	0.0	0.0
816	No	actin-associated protein [Saccharomyces cerevisiae]	gi 151942363 (+2)	53 kDa	4	0	0	0	4	0	0	0	10.4%	0.0	0.0	0.0
817	No	TATA-binding protein-associated-factor [Saccharomyces]	gi 151943698 (+2)	58 kDa	7	0	0	0	5	0	0	0	11.2%	0.0	0.0	0.0
818	No	trehalose-6-phosphate synthase [Saccharomyces]	gi 156068996 (+5)	56 kDa	7	0	0	0	6	0	0	0	16.0%	0.0	0.0	0.0
819	No	Chain A, Solution Nmr Structure Of A Yeast Iso-1	gi 157834304	12 kDa	7	0	0	0	3	0	0	0	25.9%	0.0	0.0	0.0
820	No	Chain A, Structure Of Isoniazid (Inh) Bound To C	gi 161761100 (+2)	34 kDa	6	0	0	0	6	0	0	0	26.2%	0.0	0.0	0.0
821	No	scl1+ suppressor protein [Saccharomyces cerevisiae]	gi 172546 (+2)	30 kDa	7	0	0	0	6	0	0	0	24.1%	0.0	0.0	0.0
822	No	DNA polymerase phi [Saccharomyces cerevisiae]	gi 190405512	116 kDa	5	0	0	0	5	0	0	0	5.19%	0.0	0.0	0.0

823	No	N alpha-acetyltransferase major subunit [Sacchi] gi 190405798 (+2)	28 kDa	5	0	0	0	5	0	0	0	20.2%	0.0	0.0	0.0
824	No	26S proteasome regulatory subunit RPN8 [Saccl] gi 190407565 (+1)	38 kDa	6	0	0	0	6	0	0	0	24.3%	0.0	0.0	0.0
825	No	hypothetical protein SCRG_02257 [Saccharomygi] 190407722 (+2)	69 kDa	6	0	0	0	5	0	0	0	12.0%	0.0	0.0	0.0
826	No	hypothetical protein SCRG_02352 [Saccharomygi] 190407816 (+5)	49 kDa	7	0	0	0	7	0	0	0	24.2%	0.0	0.0	0.0
827	No	4-amino-4-deoxychorismate lyase [Saccharomygi] 190408515 (+1)	43 kDa	4	0	0	0	4	0	0	0	12.3%	0.0	0.0	0.0
828	No	YKR002Wp-like protein [Saccharomyces cerevisi] gi 207343429 (+1)	65 kDa	4	0	0	0	4	0	0	0	9.51%	0.0	0.0	0.0
829	No	YER080Wp-like protein [Saccharomyces cerevisi] gi 207345926 (+4)	65 kDa	6	0	0	0	6	0	0	0	11.9%	0.0	0.0	0.0
830	No	YER073Wp-like protein [Saccharomyces cerevisi] gi 207345937 (+2)	57 kDa	6	0	0	0	6	0	0	0	15.0%	0.0	0.0	0.0
831	No	gamma-glutamylcysteine synthetase [Saccharor] gi 229473703	78 kDa	4	0	0	0	4	0	0	0	6.78%	0.0	0.0	0.0
832	No	Lsm2p [Saccharomyces cerevisiae JAY291] gi 256269256 (+1)	11 kDa	4	0	0	0	3	0	0	0	33.3%	0.0	0.0	0.0
833	No	Srv2p [Saccharomyces cerevisiae JAY291] gi 256273824 (+1)	58 kDa	7	0	0	0	7	0	0	0	18.1%	0.0	0.0	0.0
834	No	Cor1p [Saccharomyces cerevisiae EC1118] gi 259144801 (+1)	50 kDa	5	0	0	0	4	0	0	0	11.4%	0.0	0.0	0.0
835	No	Rad23p [Saccharomyces cerevisiae EC1118] gi 259145863 (+2)	43 kDa	7	0	0	0	6	0	0	0	15.4%	0.0	0.0	0.0
836	No	Arg5,6p [Saccharomyces cerevisiae EC1118] gi 259145983 (+1)	95 kDa	5	0	0	0	5	0	0	0	7.07%	0.0	0.0	0.0
837	No	Kri1p [Saccharomyces cerevisiae EC1118] gi 259149064 (+1)	69 kDa	4	0	0	0	4	0	0	0	8.12%	0.0	0.0	0.0
838	No	RecName: Full=Heterogeneous nuclear rmp K-like gi 332319675 (+2)	42 kDa	4	0	0	0	3	0	0	0	9.45%	0.0	0.0	0.0
839	No	Chain A, Crystal Structure Of Exo-1,3-Beta Gluca gi 37926403 (+1)	47 kDa	6	0	0	0	6	0	0	0	19.9%	0.0	0.0	0.0
840	No	YDR272W [Saccharomyces cerevisiae] gi 45269369 (+1)	31 kDa	6	0	0	0	5	0	0	0	21.9%	0.0	0.0	0.0
841	No	Gpx2p [Saccharomyces cerevisiae S288c] gi 6319721	18 kDa	5	0	0	0	4	0	0	0	27.2%	0.0	0.0	0.0
842	No	Inm1p [Saccharomyces cerevisiae S288c] gi 6321836	33 kDa	5	0	0	0	5	0	0	0	20.0%	0.0	0.0	0.0
843	No	Cox6p [Saccharomyces cerevisiae S288c] gi 6321842	17 kDa	5	0	0	0	4	0	0	0	22.3%	0.0	0.0	0.0
844	No	Nap1p [Saccharomyces cerevisiae S288c] gi 6322901	48 kDa	7	0	0	0	7	0	0	0	26.1%	0.0	0.0	0.0
845	No	Yar1p [Saccharomyces cerevisiae S288c] gi 6325017	22 kDa	6	0	0	0	6	0	0	0	38.0%	0.0	0.0	0.0
846	No	Sto1p [Saccharomyces cerevisiae S288c] gi 6579194	100 kDa	3	0	0	0	3	0	0	0	4.41%	0.0	0.0	0.0
847	No	Chain A, The Exportin Cse1 In Its Cargo-Free, Cy gi 67464500	110 kDa	6	0	0	0	4	0	0	0	4.44%	0.0	0.0	0.0
848	No	soluble cell wall protein [Saccharomyces cerevisi] gi 151943551 (+2)	40 kDa	7	0	0	0	3	0	0	0	10.1%	0.0	0.0	0.0
849	No	YPL211Wp-like protein [Saccharomyces cerevisi] gi 207340712 (+1)	20 kDa	3	0	0	0	3	0	0	0	16.6%	0.0	0.0	0.0
850	No	Esf1p [Saccharomyces cerevisiae EC1118] gi 259145602 (+1)	72 kDa	5	0	0	0	3	0	0	0	5.57%	0.0	0.0	0.0
851	No	Pan1p [Saccharomyces cerevisiae JAY291] gi 256274128 (+2)	160 kDa	2	0	0	0	2	0	0	0	1.97%	0.0	0.0	0.0
852	No	Chain E, A Gated Channel Into The Proteasome gi 11513996 (+2)	26 kDa	4	0	0	0	2	0	0	0	12.4%	0.0	0.0	0.0
853	No	Pgm3p [Saccharomyces cerevisiae S288c] gi 6323934	71 kDa	2	0	0	0	2	0	0	0	2.89%	0.0	0.0	0.0
854	No	Cis3p [Saccharomyces cerevisiae S288c] gi 6322303	23 kDa	6	0	0	0	2	0	0	0	7.93%	0.0	0.0	0.0
855	No	Nhp10p [Saccharomyces cerevisiae JAY291] gi 256268985 (+2)	24 kDa	1	2	3	0	1	2	3	0	7.88%	12.3%	19.2%	0.0
856	No	Ssa1p [Saccharomyces cerevisiae S288c] gi 144228166	70 kDa	4	1	1	0	1	1	1	0	50.3%	37.2%	39.4%	0.0
857	No	Ret2p [Saccharomyces cerevisiae S288c] gi 14318576	61 kDa	3	1	1	0	3	1	1	0	6.23%	1.65%	1.65%	0.0
858	No	Rpl26ap [Saccharomyces cerevisiae S288c] gi 6323376	14 kDa	2	1	0	0	1	1	0	0	61.4%	55.1%	46.5%	0.0
859	No	unnamed protein product [Saccharomyces cere] gi 1256510 (+1)	26 kDa	3	0	1	0	1	0	1	0	6.81%	0.000%	6.81%	0.0
860	No	3'-5'-exonuclease complex component [Sacchar] gi 151945995 (+2)	111 kDa	2	0	1	0	2	0	1	0	2.48%	0.000%	1.14%	0.0
861	No	CCR4-NOT transcriptional complex subunit [Sac] gi 151941371 (+3)	94 kDa	2	0	1	0	2	0	1	0	3.35%	0.0	2.51%	0.000%
862	No	CCR4-NOT transcriptional complex subunit [Sac] gi 151943121 (+4)	94 kDa	2	0	0	0	2	0	0	0	4.31%	0.0	0.000%	0.000%
863	No	RNA polymerase A [Saccharomyces cerevisiae Y.gi] 151944979 (+3)	27 kDa	2	0	2	0	2	0	2	0	7.73%	0.0	7.73%	0.0
864	No	septin [Saccharomyces cerevisiae YJM789] gi 151943823 (+1)	37 kDa	2	0	1	0	2	0	1	0	6.83%	0.0	4.04%	0.0
865	No	Tao3p [Saccharomyces cerevisiae] gi 71064089	270 kDa	2	0	1	0	2	0	1	0	0.884%	0.0	0.505%	0.0
866	No	karyopherin [Saccharomyces cerevisiae YJM789] gi 151940872 (+2)	95 kDa	5	0	1	0	5	0	1	0	5.92%	0.0	1.86%	0.0
867	No	translation elongation factor EF-1 beta [Sacchar] gi 151941388 (+2)	23 kDa	4	1	0	0	2	1	0	0	9.66%	5.31%	0.0	0.0
868	No	Smc2p [Saccharomyces cerevisiae EC1118] gi 259146222	134 kDa	1	1	0	0	1	1	0	0	1.03%	0.769%	0.0	0.0
869	No	histone acetyltransferase SAGA complex memb gi 151946472	152 kDa	1	0	0	0	1	0	0	0	0.901%	0.0	0.000%	0.0
870	No	tau 95 subunit of transcription factor TFIIC [Sac] gi 151946515 (+2)	74 kDa	1	0	0	0	1	0	0	0	1.85%	0.0	0.000%	0.000%
871	No	Mdh3p [Saccharomyces cerevisiae S288c] gi 6320125	37 kDa	6	0	1	0	6	0	0	1	19.0%	0.0	0.0	2.92%
872	No	loc4p [Saccharomyces cerevisiae YJM789] gi 151946205 (+3)	55 kDa	2	0	0	0	2	0	0	0	4.64%	0.000%	0.000%	0.0
873	No	ribosome biogenesis [Saccharomyces cerevisiae] gi 190405562 (+1)	27 kDa	2	0	0	0	2	0	0	0	9.52%	0.000%	0.000%	0.000%
874	No	potassium transporter [Saccharomyces cerevisi] gi 151941590 (+2)	101 kDa	0	1	0	0	0	1	0	0	0.0	1.24%	0.000%	0.000%
875	No	Arg7p [Saccharomyces cerevisiae S288c] gi 6323707	48 kDa	2	0	0	0	2	0	0	0	6.12%	0.0	0.0	0.000%
876	No	EC1118_1M3_0012p [Saccharomyces cerevisiae] gi 259148442 (+2)	40 kDa	1	0	0	0	1	0	0	0	3.56%	0.000%	0.0	0.0
877	No	Gad1p [Saccharomyces cerevisiae EC1118] gi 259148836	66 kDa	5	0	0	0	5	0	0	0	10.3%	0.000%	0.0	0.0
878	No	Img1p [Saccharomyces cerevisiae S288c] gi 6319894	19 kDa	3	0	0	0	3	0	0	0	18.9%	0.0	0.000%	0.0
879	No	RecName: Full=Bud site selection protein 4 gi 187470649 (+2)	164 kDa	0	0	0	1	0	0	0	1	0.0	0.0	0.000%	0.968%
880	No	Nop14p [Saccharomyces cerevisiae JAY291] gi 256273589	94 kDa	2	0	0	0	2	0	0	0	2.84%	0.000%	0.0	0.0
881	No	Ssf1p [Saccharomyces cerevisiae S288c] gi 6321857	52 kDa	2	0	0	0	2	0	0	0	4.64%	0.0	0.0	0.000%

882	No	conserved hypothetical protein [Saccharomyces gi 190409886 (+3)	18 kDa	3	0	0	0	2	0	0	0	11.6%	0.000%	0.0	0.0
883	No	conserved protein [Saccharomyces cerevisiae YJ gi 151945370 (+3)	36 kDa	5	0	0	0	4	0	0	0	14.5%	0.0	0.000%	0.0
884	No	Trm5p [Saccharomyces cerevisiae S288c] gi 6321861	57 kDa	1	0	0	0	1	0	0	0	3.01%	0.0	0.000%	0.0
885	No	Chain C, A Gated Channel Into The Proteasome gi 11513994 (+3)	27 kDa	4	0	0	0	4	0	0	0	18.5%	0.0	0.000%	0.0
886	No	homoacnitase [Saccharomyces cerevisiae RM1 gi 190404816 (+2)	75 kDa	5	0	0	0	5	0	0	0	10.5%	0.0	0.000%	0.0
887	No	Etr1p [Saccharomyces cerevisiae JAY291] gi 256273170 (+2)	42 kDa	6	0	0	0	6	0	0	0	17.4%	0.0	0.000%	0.0
888	No	mitochondrial distribution and morphology [Sac gi 151945559 (+4)	93 kDa	4	0	0	0	4	0	0	0	4.65%	0.000%	0.0	0.0
889	No	GCN2 [Saccharomyces cerevisiae] gi 171578 (+1)	182 kDa	2	0	0	0	2	0	0	0	1.19%	0.0	0.0	0.0
890	No	replication factor C subunit 4 [Saccharomyces c gi 190407255 (+1)	36 kDa	5	0	0	0	5	0	0	0	17.3%	0.0	0.0	0.0
891	No	MCM2 [Saccharomyces cerevisiae] gi 3912	101 kDa	4	0	0	0	4	0	0	0	6.74%	0.0	0.0	0.0
892	No	RecName: Full=Cysteine proteinase 1, mitochond gi 150421522 (+12)	55 kDa	7	0	0	0	5	0	0	0	13.7%	0.0	0.0	0.0
893	No	conserved protein [Saccharomyces cerevisiae YJ gi 151942902 (+2)	39 kDa	4	0	0	0	4	0	0	0	12.5%	0.0	0.0	0.0
894	No	arginyl-tRNA-protein transferase [Saccharomyce gi 151943271 (+3)	58 kDa	4	0	0	0	4	0	0	0	10.9%	0.0	0.0	0.0
895	No	DEIH-box ATPase [Saccharomyces cerevisiae YJ gi 151944889 (+2)	246 kDa	4	0	0	0	4	0	0	0	2.04%	0.0	0.0	0.0
896	No	replication factor C subunit 2 [Saccharomyces c gi 151945136 (+3)	40 kDa	4	0	0	0	4	0	0	0	12.5%	0.0	0.0	0.0
897	No	nucleolar complex associated [Saccharomyces c gi 151945296 (+1)	82 kDa	5	0	0	0	5	0	0	0	6.61%	0.0	0.0	0.0
898	No	MutS-like protein [Saccharomyces cerevisiae YJ gi 151945544 (+4)	109 kDa	4	0	0	0	4	0	0	0	4.67%	0.0	0.0	0.0
899	No	mediator complex subunit [Saccharomyces cere gi 151945584 (+3)	122 kDa	3	0	0	0	3	0	0	0	3.28%	0.0	0.0	0.0
900	No	inositol polyphosphate 5-phosphatase [Sacchar gi 151945731 (+4)	125 kDa	6	0	0	0	5	0	0	0	5.69%	0.0	0.0	0.0
901	No	calcineurin subunit A [Saccharomyces cerevisiae gi 151946108 (+2)	69 kDa	7	0	0	0	4	0	0	0	9.11%	0.0	0.0	0.0
902	No	nuclear accommodation of mitochondria [Sacch gi 151946238 (+2)	109 kDa	4	0	0	0	4	0	0	0	5.36%	0.0	0.0	0.0
903	No	DST1 [Saccharomyces cerevisiae] gi 171424 (+4)	35 kDa	5	0	0	0	5	0	0	0	19.1%	0.0	0.0	0.0
904	No	squalene synthetase [Saccharomyces cerevisiae gi 171481 (+2)	52 kDa	5	0	0	0	5	0	0	0	13.3%	0.0	0.0	0.0
905	No	RecName: Full=NADH-cytochrome b5 reductase gi 187609654 (+1)	34 kDa	4	0	0	0	4	0	0	0	15.9%	0.0	0.0	0.0
906	No	cation-transporting ATPase 4 [Saccharomyces c gi 190405534 (+2)	135 kDa	3	0	0	0	3	0	0	0	3.13%	0.0	0.0	0.0
907	No	pre-mRNA splicing factor PRP19 [Saccharomyce gi 190406012 (+3)	57 kDa	3	0	0	0	3	0	0	0	6.96%	0.0	0.0	0.0
908	No	phosphoserine phosphatase [Saccharomyces ce gi 190406782 (+2)	34 kDa	6	0	0	0	6	0	0	0	16.5%	0.0	0.0	0.0
909	No	nucleolar protein 12 [Saccharomyces cerevisiae gi 190407303 (+1)	52 kDa	6	0	0	0	5	0	0	0	13.7%	0.0	0.0	0.0
910	No	YHL021Cp-like protein [Saccharomyces cerevisi gi 207344827	53 kDa	5	0	0	0	4	0	0	0	10.8%	0.0	0.0	0.0
911	No	Rbg1p [Saccharomyces cerevisiae JAY291] gi 256270522 (+1)	41 kDa	5	0	0	0	5	0	0	0	19.5%	0.0	0.0	0.0
912	No	Rpt6p [Saccharomyces cerevisiae JAY291] gi 256271329 (+2)	45 kDa	5	0	0	0	4	0	0	0	12.3%	0.0	0.0	0.0
913	No	Paa1p [Saccharomyces cerevisiae EC1118] gi 259145314 (+1)	22 kDa	5	0	0	0	5	0	0	0	29.8%	0.0	0.0	0.0
914	No	Cdc37p [Saccharomyces cerevisiae EC1118] gi 259145406 (+1)	58 kDa	3	0	0	0	3	0	0	0	10.5%	0.0	0.0	0.0
915	No	Efg1p [Saccharomyces cerevisiae EC1118] gi 259146774	27 kDa	3	0	0	0	3	0	0	0	19.3%	0.0	0.0	0.0
916	No	Ycp4p [Saccharomyces cerevisiae EC1118] gi 290770654 (+1)	26 kDa	5	0	0	0	3	0	0	0	19.4%	0.0	0.0	0.0
917	No	hypothetical protein YKL033W-A [Saccharomyce gi 42759861	26 kDa	6	0	0	0	5	0	0	0	20.3%	0.0	0.0	0.0
918	No	YOR051C [Saccharomyces cerevisiae] gi 45269980 (+1)	47 kDa	4	0	0	0	3	0	0	0	8.50%	0.0	0.0	0.0
919	No	hypothetical protein YCR051W [Saccharomyces gi 6319899	25 kDa	7	0	0	0	5	0	0	0	38.7%	0.0	0.0	0.0
920	No	Cpr5p [Saccharomyces cerevisiae S288c] gi 6320510	25 kDa	5	0	0	0	4	0	0	0	22.2%	0.0	0.0	0.0
921	No	Tpa1p [Saccharomyces cerevisiae S288c] gi 6320890	74 kDa	3	0	0	0	3	0	0	0	5.28%	0.0	0.0	0.0
922	No	Pet10p [Saccharomyces cerevisiae S288c] gi 6322899	31 kDa	5	0	0	0	5	0	0	0	25.4%	0.0	0.0	0.0
923	No	Emw1p [Saccharomyces cerevisiae S288c] gi 6324016	102 kDa	5	0	0	0	5	0	0	0	6.53%	0.0	0.0	0.0
924	No	Ipi3p [Saccharomyces cerevisiae S288c] gi 6324147	62 kDa	2	0	0	0	2	0	0	0	3.60%	0.0	0.0	0.0
925	No	Tpm1p [Saccharomyces cerevisiae S288c] gi 6324250	24 kDa	3	0	0	0	3	0	0	0	20.6%	0.0	0.0	0.0
926	No	Trm3p [Saccharomyces cerevisiae S288c] gi 6320091	165 kDa	3	0	0	0	3	0	0	0	2.44%	0.0	0.0	0.0
927	No	RecName: Full=CTP synthase 2; AltName: Full=C gi 239977666 (+2)	64 kDa	3	0	0	0	3	0	0	0	6.92%	0.0	0.0	0.0
928	No	Ras2p [Saccharomyces cerevisiae EC1118] gi 259149262	35 kDa	3	0	0	0	2	0	0	0	8.39%	0.0	0.0	0.0
929	No	ubiquitin-specific protease [Saccharomyces cere gi 151946012 (+3)	144 kDa	2	0	0	0	2	0	0	0	1.87%	0.0	0.0	0.0
930	No	regulatory component of the proteasome pathv gi 190409634 (+2)	79 kDa	2	0	0	0	2	0	0	0	3.92%	0.0	0.0	0.0
931	No	cell division control protein 54 [Saccharomyces gi 190407963 (+1)	105 kDa	2	0	0	0	2	0	0	0	2.79%	0.0	0.0	0.0
932	No	repressible alkaline phosphatase (EC 3.1.3.1) [S gi 172164	63 kDa	3	0	0	0	2	0	0	0	4.24%	0.0	0.0	0.0
933	No	Rpl22ap [Saccharomyces cerevisiae S288c] gi 6323090	14 kDa	4	0	0	0	2	0	0	0	32.2%	0.0	0.0	0.0
934	No	acid phosphatase [Saccharomyces cerevisiae YJ gi 151941431 (+7)	52 kDa	2	0	0	0	1	0	0	0	2.61%	0.0	0.0	0.0
935	No	Vph1p [Saccharomyces cerevisiae S288c] gi 6324844	96 kDa	2	0	0	0	1	0	0	0	1.43%	0.0	0.0	0.0
936	No	Vps74p [Saccharomyces cerevisiae S288c] gi 6320580	39 kDa	2	0	0	0	2	0	0	0	7.54%	0.0	0.0	0.0
937	No	RecName: Full=Nonsense-mediated mRNA deca gi 1171739 (+4)	120 kDa	1	0	0	0	1	0	0	0	1.24%	0.0	0.0	0.0
938	No	Rps9ap [Saccharomyces cerevisiae S288c] gi 6325176	22 kDa	2	1	2	0	1	1	2	0	43.7%	47.2%	39.6%	8.63%
939	No	RecName: Full=Nucleolar protein 58; AltName: gi 206558283 (+2)	57 kDa	2	2	1	0	2	2	1	0	5.28%	3.91%	1.96%	0.0
940	No	Arp5p [Saccharomyces cerevisiae S288c] gi 6324269	88 kDa	2	1	1	0	2	1	1	0	2.52%	1.32%	1.32%	0.0

941	No	Rpl17bp [Saccharomyces cerevisiae S288c]	gi 6322284	21 kDa	2	2	1	0	1	1	1	0	48.4%	43.5%	43.5%	0.0
942	No	Rfa2p [Saccharomyces cerevisiae JAY291]	gi 256269456 (+1)	30 kDa	1	1	2	0	1	1	2	0	5.11%	5.11%	12.0%	0.0
943	No	unnamed protein product [Saccharomyces cerevisiae]	gi 3497 (+1)	21 kDa	3	1	0	0	2	1	0	0	11.0%	5.76%	0.0	0.0
944	No	conserved protein [Saccharomyces cerevisiae YJgi]	151944383 (+2)	32 kDa	1	0	0	0	1	0	0	0	4.38%	0.0	0.0	0.000%
945	No	YBL007Cp-like protein [Saccharomyces cerevisiae gi]	207347817	92 kDa	1	0	0	0	1	0	0	0	2.12%	0.000%	0.000%	0.000%
946	No	Rpn7p [Saccharomyces cerevisiae EC1118]	gi 259150257 (+1)	49 kDa	5	0	1	0	4	0	1	0	9.56%	0.0	2.10%	0.0
947	No	Ckb2p [Saccharomyces cerevisiae S288c]	gi 6324613	30 kDa	1	0	0	0	1	0	0	0	3.49%	0.000%	0.000%	0.0
948	No	class E vacuolar-protein sorting and endocytosis gi]	151941544 (+2)	26 kDa	1	0	0	0	1	0	0	0	3.88%	0.0	0.000%	0.000%
949	No	Chain F, A Gated Channel Into The Proteasome i	gi 11513997 (+3)	27 kDa	4	0	0	0	4	0	0	0	18.1%	0.000%	0.000%	0.0
950	No	Tho1p [Saccharomyces cerevisiae JAY291]	gi 256270787 (+1)	24 kDa	2	0	0	0	2	0	0	0	12.4%	0.0	0.0	0.000%
951	No	cell division cycle-related protein [Saccharomyces cerevisiae gi]	151941870 (+2)	94 kDa	2	0	0	0	2	0	0	0	3.44%	0.0	0.000%	0.000%
952	No	Bre1p [Saccharomyces cerevisiae EC1118]	gi 259145171 (+1)	81 kDa	2	0	0	0	2	0	0	0	3.71%	0.000%	0.0	0.0
953	No	hypothetical protein YHR113W [Saccharomyces cerevisiae gi]	6321905	54 kDa	2	0	0	0	2	0	0	0	4.29%	0.000%	0.0	0.0
954	No	Atg11p [Saccharomyces cerevisiae EC1118]	gi 259150202 (+1)	135 kDa	0	1	0	0	0	1	0	0	0.000%	0.849%	0.000%	0.0
955	No	pantothenate synthase [Saccharomyces cerevisiae gi]	190406356 (+1)	35 kDa	1	0	0	0	1	0	0	0	3.24%	0.000%	0.0	0.0
956	No	ATP synthase [Saccharomyces cerevisiae YJM78 gi]	151944234 (+1)	37 kDa	1	0	0	0	3	0	0	0	10.7%	0.0	0.000%	0.0
957	No	hypothetical protein YPR148C [Saccharomyces cerevisiae gi]	6325406	49 kDa	5	0	0	0	5	0	0	0	14.3%	0.0	0.000%	0.0
958	No	aspartate aminotransferase [Saccharomyces cerevisiae gi]	190409728 (+5)	52 kDa	1	0	0	0	1	0	0	0	2.22%	0.0	0.000%	0.0
959	No	Utp13p [Saccharomyces cerevisiae EC1118]	gi 259148205	91 kDa	5	0	0	0	5	0	0	0	8.20%	0.0	0.000%	0.0
960	No	actin patches distal [Saccharomyces cerevisiae YJgi]	151946540 (+1)	36 kDa	3	0	0	0	3	0	0	0	10.8%	0.0	0.000%	0.0
961	No	conserved protein [Saccharomyces cerevisiae YJgi]	151943059 (+3)	78 kDa	4	0	0	0	4	0	0	0	6.32%	0.0	0.000%	0.0
962	No	YLR151Cp-like protein [Saccharomyces cerevisiae gi]	207343028 (+1)	40 kDa	4	0	0	0	3	0	0	0	9.71%	0.0	0.000%	0.0
963	No	bud site selection protein BUD3 [Saccharomyces cerevisiae gi]	190406426 (+2)	185 kDa	3	0	0	0	3	0	0	0	2.93%	0.000%	0.0	0.0
964	No	Caj1p [Saccharomyces cerevisiae EC1118]	gi 259145957 (+1)	45 kDa	2	0	0	0	2	0	0	0	5.88%	0.0	0.000%	0.0
965	No	Niemann Pick type C-like protein [Saccharomyces cerevisiae gi]	151941952 (+1)	19 kDa	4	0	0	0	3	0	0	0	16.8%	0.0	0.0	0.0
966	No	serine/threonine protein kinase [Saccharomyces cerevisiae gi]	151945588 (+3)	124 kDa	0	1	0	0	0	1	0	0	0.0	0.999%	0.0	0.0
967	No	Cwp1p [Saccharomyces cerevisiae JAY291]	gi 256269915 (+3)	24 kDa	4	0	0	0	4	0	0	0	26.8%	0.0	0.0	0.0
968	No	Rcl1p [Saccharomyces cerevisiae S288c]	gi 6324564	40 kDa	2	0	0	0	2	0	0	0	5.99%	0.0	0.0	0.0
969	No	conserved protein [Saccharomyces cerevisiae YJgi]	151944483 (+2)	99 kDa	3	0	0	0	3	0	0	0	7.19%	0.0	0.0	0.0
970	No	YLR380Wp-like protein [Saccharomyces cerevisiae gi]	207342769 (+3)	47 kDa	3	0	0	0	2	0	0	0	5.88%	0.0	0.0	0.0
971	No	RecName: Full=Mitochondrial outer membrane gi]	189041600 (+2)	82 kDa	4	0	0	0	4	0	0	0	6.34%	0.0	0.0	0.0
972	No	hypothetical protein YFR006W [Saccharomyces cerevisiae gi]	14318528 (+3)	62 kDa	4	0	0	0	4	0	0	0	9.72%	0.0	0.0	0.0
973	No	topoisomerase II-associated protein [Saccharomyces cerevisiae gi]	14588957 (+4)	88 kDa	3	0	0	0	3	0	0	0	4.27%	0.0	0.0	0.0
974	No	Chain A, Crystal Structure Of Glutathione Reduc gi]	149242065 (+5)	53 kDa	4	0	0	0	4	0	0	0	12.1%	0.0	0.0	0.0
975	No	conserved protein [Saccharomyces cerevisiae YJgi]	151942271 (+2)	62 kDa	4	0	0	0	3	0	0	0	6.88%	0.0	0.0	0.0
976	No	integral membrane protein that along with Pil1 gi]	151942788 (+1)	38 kDa	6	0	0	0	4	0	0	0	19.6%	0.0	0.0	0.0
977	No	regulator of Ty1 transposition [Saccharomyces cerevisiae gi]	151944100 (+1)	123 kDa	4	0	0	0	4	0	0	0	4.95%	0.0	0.0	0.0
978	No	conserved protein [Saccharomyces cerevisiae YJgi]	151944146 (+2)	45 kDa	4	0	0	0	4	0	0	0	11.6%	0.0	0.0	0.0
979	No	glyoxylate reductase [Saccharomyces cerevisiae gi]	151944274 (+1)	39 kDa	5	0	0	0	5	0	0	0	17.4%	0.0	0.0	0.0
980	No	vacuolar import and degradation protein [Saccharomyces cerevisiae gi]	151944332 (+2)	89 kDa	4	0	0	0	4	0	0	0	6.27%	0.0	0.0	0.0
981	No	part of a pre-60S complex [Saccharomyces cerevisiae gi]	151944581 (+2)	56 kDa	5	0	0	0	5	0	0	0	12.6%	0.0	0.0	0.0
982	No	ribosomal RNA processing protein [Saccharomyces cerevisiae gi]	151945630 (+2)	84 kDa	3	0	0	0	3	0	0	0	5.05%	0.0	0.0	0.0
983	No	bud7 and chs6-like protein [Saccharomyces cerevisiae gi]	151945942 (+2)	82 kDa	6	0	0	0	6	0	0	0	8.56%	0.0	0.0	0.0
984	No	conserved protein [Saccharomyces cerevisiae YJgi]	151945966	164 kDa	3	0	0	0	3	0	0	0	2.61%	0.0	0.0	0.0
985	No	Chain A, The Yeast Ribosome Synthesis Factor E gi]	152149541	29 kDa	5	0	0	0	4	0	0	0	20.5%	0.0	0.0	0.0
986	No	Chain A, Recombinant Yeast Fumarase gi]	157834306 (+3)	53 kDa	5	0	0	0	5	0	0	0	10.9%	0.0	0.0	0.0
987	No	RecName: Full=ATP-dependent RNA helicase DE gi]	160380619 (+5)	87 kDa	5	0	0	0	4	0	0	0	5.97%	0.0	0.0	0.0
988	No	2-dehydropanoate 2-reductase [Saccharomyces cerevisiae gi]	190405846 (+3)	43 kDa	5	0	0	0	5	0	0	0	16.1%	0.0	0.0	0.0
989	No	NADPH-dependent methylglyoxal reductase GR gi]	190407101 (+4)	38 kDa	4	0	0	0	4	0	0	0	17.0%	0.0	0.0	0.0
990	No	vacuolar protein sorting-associated protein VPS gi]	190409355	109 kDa	3	0	0	0	3	0	0	0	3.60%	0.0	0.0	0.0
991	No	YML086Cp-like protein [Saccharomyces cerevisiae gi]	207342570 (+2)	60 kDa	5	0	0	0	5	0	0	0	11.6%	0.0	0.0	0.0
992	No	YER089Cp-like protein [Saccharomyces cerevisiae gi]	207345913 (+2)	50 kDa	4	0	0	0	4	0	0	0	9.48%	0.0	0.0	0.0
993	No	YCL017Cp-like protein [Saccharomyces cerevisiae gi]	207347362	54 kDa	5	0	0	0	5	0	0	0	11.9%	0.0	0.0	0.0
994	No	RecName: Full=tRNA (guanine-N(7)-)-methyltra gi]	229891707 (+1)	33 kDa	5	0	0	0	4	0	0	0	15.4%	0.0	0.0	0.0
995	No	Apl5p [Saccharomyces cerevisiae JAY291]	gi 256270625 (+2)	107 kDa	5	0	0	0	4	0	0	0	4.72%	0.0	0.0	0.0
996	No	Ypt32p [Saccharomyces cerevisiae EC1118]	gi 259146304 (+1)	25 kDa	6	0	0	0	5	0	0	0	24.8%	0.0	0.0	0.0
997	No	Chain G, Structure Of Rabgdp-Dissociation Inhib gi]	55670316 (+1)	51 kDa	5	0	0	0	5	0	0	0	12.4%	0.0	0.0	0.0
998	No	Pep1p [Saccharomyces cerevisiae S288c]	gi 6319454	178 kDa	4	0	0	0	4	0	0	0	3.29%	0.0	0.0	0.0
999	No	Fes1p [Saccharomyces cerevisiae S288c]	gi 6319577	33 kDa	6	0	0	0	5	0	0	0	22.1%	0.0	0.0	0.0

1000	No	Trm1p [Saccharomyces cerevisiae S288c]	gi 6320325	64 kDa	4	0	0	0	4	0	0	0	8.07%	0.0	0.0	0.0
1001	No	Utp4p [Saccharomyces cerevisiae S288c]	gi 6320531	88 kDa	6	0	0	0	6	0	0	0	7.99%	0.0	0.0	0.0
1002	No	Ade8p [Saccharomyces cerevisiae S288c]	gi 6320616	24 kDa	4	0	0	0	3	0	0	0	15.0%	0.0	0.0	0.0
1003	No	Trs31p [Saccharomyces cerevisiae S288c]	gi 6320680	32 kDa	4	0	0	0	4	0	0	0	16.3%	0.0	0.0	0.0
1004	No	Rib3p [Saccharomyces cerevisiae S288c]	gi 6320695	23 kDa	4	0	0	0	4	0	0	0	21.2%	0.0	0.0	0.0
1005	No	Tma20p [Saccharomyces cerevisiae S288c]	gi 6320844	20 kDa	6	0	0	0	5	0	0	0	26.0%	0.0	0.0	0.0
1006	No	Hor2p [Saccharomyces cerevisiae S288c]	gi 6320905	28 kDa	5	0	0	0	5	0	0	0	40.4%	0.0	0.0	0.0
1007	No	Zpr1p [Saccharomyces cerevisiae S288c]	gi 6321650	55 kDa	5	0	0	0	5	0	0	0	11.9%	0.0	0.0	0.0
1008	No	Otu2p [Saccharomyces cerevisiae S288c]	gi 6321774	36 kDa	4	0	0	0	4	0	0	0	15.3%	0.0	0.0	0.0
1009	No	Asg1p [Saccharomyces cerevisiae S288c]	gi 6322061	109 kDa	3	0	0	0	3	0	0	0	4.25%	0.0	0.0	0.0
1010	No	Ypt52p [Saccharomyces cerevisiae S288c]	gi 6322866	26 kDa	6	0	0	0	6	0	0	0	32.1%	0.0	0.0	0.0
1011	No	Mrp13p [Saccharomyces cerevisiae S288c]	gi 6323666	44 kDa	3	0	0	0	3	0	0	0	8.46%	0.0	0.0	0.0
1012	No	Ccs1p [Saccharomyces cerevisiae S288c]	gi 6323681	27 kDa	4	0	0	0	4	0	0	0	22.5%	0.0	0.0	0.0
1013	No	Zeo1p [Saccharomyces cerevisiae S288c]	gi 6324463	13 kDa	6	0	0	0	5	0	0	0	31.0%	0.0	0.0	0.0
1014	No	Rki1p [Saccharomyces cerevisiae S288c]	gi 6324669 (+1)	28 kDa	5	0	0	0	5	0	0	0	19.8%	0.0	0.0	0.0
1015	No	Nce102p [Saccharomyces cerevisiae S288c]	gi 6325407	19 kDa	5	0	0	0	3	0	0	0	13.3%	0.0	0.0	0.0
1016	No	conserved protein [Saccharomyces cerevisiae YJgi 151944161 (+1)		67 kDa	3	0	0	0	3	0	0	0	6.15%	0.0	0.0	0.0
1017	No	ribosomal-like protein [Saccharomyces cerevisiae gi 151944528 (+3)		37 kDa	4	0	0	0	3	0	0	0	13.0%	0.0	0.0	0.0
1018	No	conserved protein [Saccharomyces cerevisiae YJgi 151945028 (+3)		27 kDa	3	0	0	0	3	0	0	0	17.1%	0.0	0.0	0.0
1019	No	Ptc7p [Saccharomyces cerevisiae S288c]	gi 154199605	38 kDa	2	0	0	0	2	0	0	0	6.12%	0.0	0.0	0.0
1020	No	26S proteasome regulatory subunit RPN5 [Saccl gi 190405150 (+2)		52 kDa	2	0	0	0	2	0	0	0	6.07%	0.0	0.0	0.0
1021	No	Cms1p [Saccharomyces cerevisiae S288c]	gi 6323031	33 kDa	5	0	0	0	3	0	0	0	11.7%	0.0	0.0	0.0
1022	No	Rkr1p [Saccharomyces cerevisiae S288c]	gi 6323904	180 kDa	2	0	0	0	2	0	0	0	2.11%	0.0	0.0	0.0
1023	No	Pmt2p [Saccharomyces cerevisiae S288c]	gi 27469358	87 kDa	2	0	0	0	2	0	0	0	3.03%	0.0	0.0	0.0
1024	No	Chain A, N77y Point Mutant Of S.Cerevisiae Ntf; gi 21730277 (+2)		15 kDa	6	0	0	0	3	0	0	0	25.6%	0.0	0.0	0.0
1025	No	Sik1p [Saccharomyces cerevisiae EC1118]	gi 259148182 (+1)	57 kDa	5	0	0	0	3	0	0	0	5.75%	0.0	0.0	0.0
1026	No	splicing endonuclease [Saccharomyces cerevisiae gi 151940946 (+3)		253 kDa	1	0	0	0	1	0	0	0	0.672%	0.0	0.0	0.0
1027	No	ATPase [Saccharomyces cerevisiae YJM789]	gi 151946471 (+2)	84 kDa	3	0	0	0	3	0	0	0	5.94%	0.0	0.0	0.0
1028	No	Grx3p [Saccharomyces cerevisiae S288c]	gi 6320303	32 kDa	3	0	0	0	2	0	0	0	7.72%	0.0	0.0	0.0
1029	No	Chain A, Crystal Structure Of Mlc1p Bound To Iq gi 27065557 (+1)		16 kDa	1	0	0	0	1	0	0	0	5.41%	0.0	0.0	0.0
1030	No	Gcs1p [Saccharomyces cerevisiae S288c]	gi 6319975	39 kDa	1	0	0	0	1	0	0	0	3.12%	0.0	0.0	0.0
1031	No	carboxypeptidase yscY [Saccharomyces cerevisi gi 151946005 (+4)		60 kDa	4	0	0	0	2	0	0	0	3.57%	0.0	0.0	0.0
1032	No	Rpn6p [Saccharomyces cerevisiae S288c]	gi 6320106	50 kDa	2	0	0	0	2	0	0	0	5.07%	0.0	0.0	0.0
1033	No	cyclophilin-related protein [Saccharomyces cere gi 1326035 (+1)		23 kDa	3	0	0	0	3	0	0	0	20.9%	0.0	0.0	0.0
1034	No	tRNA ligase [Saccharomyces cerevisiae YJM789 gi 151945242 (+3)		95 kDa	2	0	0	0	2	0	0	0	3.26%	0.0	0.0	0.0
1035	No	Arc19p [Saccharomyces cerevisiae S288c]	gi 6322839	20 kDa	4	0	0	0	2	0	0	0	16.4%	0.0	0.0	0.0
1036	No	Rep 2 protein [Saccharomyces cerevisiae A364A gi 11466071		33 kDa	5	0	0	0	2	0	0	0	8.78%	0.0	0.0	0.0
1037	No	MSH6 gene	gi 1588283	140 kDa	2	0	0	0	2	0	0	0	1.77%	0.0	0.0	0.0
1038	No	Uga1p [Saccharomyces cerevisiae EC1118]	gi 259146522 (+2)	53 kDa	1	0	0	0	1	0	0	0	2.76%	0.0	0.0	0.0
1039	No	Rpo41p [Saccharomyces cerevisiae S288c]	gi 14318482 (+5)	153 kDa	1	0	0	0	1	0	0	0	0.888%	0.0	0.0	0.0
1040	No	conserved hypothetical protein [Saccharomyces gi 190405905 (+1)		27 kDa	1	0	0	0	1	0	0	0	4.94%	0.0	0.0	0.0
1041	No	Rpp2ap [Saccharomyces cerevisiae EC1118]	gi 259149446 (+1)	11 kDa	2	1	2	0	2	1	2	0	21.7%	10.4%	21.7%	0.0
1042	No	RNA polymerase C [Saccharomyces cerevisiae Y. gi 151941569 (+2)		33 kDa	1	1	1	0	1	1	1	0	4.14%	3.10%	3.10%	0.0
1043	No	les3p [Saccharomyces cerevisiae S288c]	gi 6323081	28 kDa	1	1	1	0	1	1	1	0	4.40%	4.40%	4.00%	0.0
1044	No	RecName: Full-Histone chaperone RTT106; AltN gi 193806658 (+1)		52 kDa	1	1	1	0	1	1	1	0	2.64%	2.20%	2.64%	0.0
1045	No	HIR2 [Saccharomyces cerevisiae RM11-1a]	gi 190407377 (+1)	98 kDa	0	1	1	0	0	1	1	0	0.000%	1.03%	1.26%	0.0
1046	No	Rpc19p [Saccharomyces cerevisiae S288c]	gi 6324215	16 kDa	2	0	2	0	2	0	2	0	18.3%	0.0	0.0	0.000%
1047	No	Chain A, Structure Of The Pho85-Pho80 Cdk-Cyc gi 162329961 (+3)		36 kDa	2	0	0	1	2	0	0	1	5.99%	0.0	0.000%	3.79%
1048	No	RNA polymerase subunit [Saccharomyces cerevi gi 1680605 (+2)		25 kDa	3	0	2	0	3	0	2	0	16.3%	0.0	12.1%	0.0
1049	No	Lsm12p [Saccharomyces cerevisiae S288c]	gi 6321913	21 kDa	2	0	1	0	2	0	1	0	13.9%	0.0	8.02%	0.0
1050	No	Tfg1p [Saccharomyces cerevisiae EC1118]	gi 259146688 (+2)	82 kDa	3	1	0	0	2	1	0	0	3.13%	1.09%	0.0	0.0
1051	No	Tri1p [Saccharomyces cerevisiae S288c]	gi 6323889	26 kDa	1	0	0	0	1	0	0	0	3.98%	0.000%	0.000%	0.0
1052	No	conserved protein [Saccharomyces cerevisiae YJ gi 151941915 (+2)		31 kDa	4	1	0	0	1	1	0	0	4.76%	4.76%	0.0	0.0
1053	No	YHR209W [Saccharomyces cerevisiae]	gi 45269425 (+1)	34 kDa	2	1	0	0	4	1	0	0	18.6%	2.75%	0.0	0.0
1054	No	glyceroldehyde-3-phosphate dehydrogenase [Sc gi 151943468		36 kDa	3	1	0	0	1	1	0	0	48.5%	26.2%	0.0	0.0
1055	No	xylulokinase [Saccharomyces cerevisiae]	gi 14253006 (+5)	67 kDa	2	0	0	0	2	0	0	0	4.40%	0.000%	0.0	0.0
1056	No	small nucleolar RNP protein [Saccharomyces cer gi 190405871 (+1)		21 kDa	1	0	1	0	1	0	1	0	6.34%	0.0	6.34%	0.0
1057	No	eukaryotic initiation factor 4F subunit p130 [Sac gi 190407012		104 kDa	1	0	0	0	1	0	0	0	2.41%	0.000%	0.0	0.0
1058	No	histone deacetylase [Saccharomyces cerevisiae gi 151944221 (+2)		49 kDa	0	0	1	0	0	0	1	0	0.000%	0.0	3.70%	0.0

1059	No	RecName: Full=Required for respiratory growth	gi 313471448 (+3)	43 kDa	0	1	0	0	0	1	0	0	0.000%	3.29%	0.0	0.000%
1060	No	protein kinase 1 [Saccharomyces cerevisiae]	gi 171787 (+2)	120 kDa	0	0	3	0	0	0	3	0	0.0	0.000%	3.20%	0.0
1061	No	3-hydroxyanthranilic acid dioxygenase [Sacchari	gi 151945099 (+1)	20 kDa	4	0	0	0	0	4	0	0	31.1%	0.000%	0.0	0.0
1062	No	histone H1 [Saccharomyces cerevisiae YJM789]	gi 151942671 (+2)	28 kDa	4	0	0	0	0	2	0	0	8.53%	0.0	0.000%	0.0
1063	No	triacylglycerol lipase [Saccharomyces cerevisiae	gi 151941628 (+2)	103 kDa	0	0	1	0	0	0	1	0	0.000%	0.000%	1.32%	0.0
1064	No	translation initiation factor eIF2B subunit [Sacch	gi 151943360 (+3)	71 kDa	3	0	0	0	3	0	0	0	6.14%	0.0	0.000%	0.0
1065	No	Pti1p [Saccharomyces cerevisiae EC1118]	gi 259146659 (+2)	47 kDa	1	0	0	0	1	0	0	0	2.35%	0.0	0.000%	0.000%
1066	No	carboxypeptidase Y-deficient [Saccharomyces c	gi 151945936 (+2)	118 kDa	1	0	0	0	1	0	0	0	0.875%	0.0	0.000%	0.0
1067	No	END3 [Saccharomyces cerevisiae]	gi 19880903	40 kDa	1	0	0	0	1	0	0	0	4.01%	0.000%	0.000%	0.0
1068	No	YMR093Wp-like protein [Saccharomyces cerevis	gi 207342335 (+3)	58 kDa	2	0	0	0	2	0	0	0	4.68%	0.0	0.000%	0.000%
1069	No	Chain B, Crystal Structure Of A-Cop In Complex	gi 298508679 (+2)	35 kDa	1	0	0	0	1	0	0	0	2.90%	0.0	0.000%	0.0
1070	No	protein kinase [Saccharomyces cerevisiae]	gi 467608 (+1)	64 kDa	2	0	0	0	2	0	0	0	5.36%	0.000%	0.0	0.0
1071	No	GTPase-activating protein [Saccharomyces cere	gi 151941711 (+5)	127 kDa	2	0	0	0	2	0	0	0	1.81%	0.0	0.000%	0.0
1072	No	Ach1p [Saccharomyces cerevisiae EC1118]	gi 259144831 (+1)	59 kDa	2	0	0	0	2	0	0	0	4.37%	0.0	0.0	0.0
1073	No	YLR192Cp-like protein [Saccharomyces cerevisia	gi 207342975 (+1)	28 kDa	3	0	0	0	2	0	0	0	8.94%	0.0	0.0	0.0
1074	No	pre-mRNA splicing factor ATP-dependent RNA h	gi 190405574 (+2)	130 kDa	1	0	0	0	1	0	0	0	0.873%	0.0	0.0	0.0
1075	No	pyruvate decarboxylase isozyme [Saccharomyce	gi 190406893	62 kDa	1	0	0	0	1	0	0	0	10.3%	0.0	0.0	0.0
1076	No	EC1118_104_2993p [Saccharomyces cerevisiae	gi 259149575	187 kDa	1	0	0	0	1	0	0	0	0.850%	0.0	0.0	0.0
1077	No	Pho88p [Saccharomyces cerevisiae S288c]	gi 6319582	21 kDa	3	0	0	0	3	0	0	0	18.6%	0.0	0.0	0.0
1078	No	Chain N, Crystal Structure Of Epoxomicin:20s Pr	gi 11513426 (+5)	21 kDa	5	0	0	0	3	0	0	0	16.3%	0.0	0.0	0.0
1079	No	Mdh2p [Saccharomyces cerevisiae S288c]	gi 116006499 (+3)	41 kDa	4	0	0	0	3	0	0	0	8.22%	0.0	0.0	0.0
1080	No	Hog1p: Mitogen-activated and osmosensing prc	gi 1256876 (+2)	49 kDa	3	0	0	0	3	0	0	0	11.5%	0.0	0.0	0.0
1081	No	conserved protein [Saccharomyces cerevisiae Y	gi 151941712 (+2)	36 kDa	4	0	0	0	4	0	0	0	18.7%	0.0	0.0	0.0
1082	No	nonhistone chromosomal protein [Saccharomyc	gi 151942838 (+1)	11 kDa	4	0	0	0	3	0	0	0	41.9%	0.0	0.0	0.0
1083	No	twinfilin A, an actin monomer sequestering prot	gi 151943357 (+1)	37 kDa	4	0	0	0	4	0	0	0	17.8%	0.0	0.0	0.0
1084	No	protein kinase activator [Saccharomyces cerevis	gi 151943694 (+2)	36 kDa	4	0	0	0	4	0	0	0	14.6%	0.0	0.0	0.0
1085	No	monensin sensitivity protein [Saccharomyces ce	gi 151944251 (+2)	187 kDa	3	0	0	0	3	0	0	0	2.44%	0.0	0.0	0.0
1086	No	pyruvate dehydrogenase complex dihydrolipoar	gi 151944463 (+3)	52 kDa	3	0	0	0	3	0	0	0	7.68%	0.0	0.0	0.0
1087	No	proteasome component Y7 [Saccharomyces cer	gi 151946074 (+1)	27 kDa	4	0	0	0	4	0	0	0	20.4%	0.0	0.0	0.0
1088	No	capping protein beta subunit [Saccharomyces c	gi 190406254 (+2)	33 kDa	4	0	0	0	4	0	0	0	20.2%	0.0	0.0	0.0
1089	No	succinyl-CoA ligase beta-chain, mitochondrial	gi 190406750 (+3)	47 kDa	3	0	0	0	3	0	0	0	9.37%	0.0	0.0	0.0
1090	No	microtubule-associated protein YTM1 [Saccharc	gi 190407574 (+3)	51 kDa	4	0	0	0	4	0	0	0	8.70%	0.0	0.0	0.0
1091	No	XPA-binding protein 1 [Saccharomyces cerevisia	gi 190409546	43 kDa	5	0	0	0	3	0	0	0	10.6%	0.0	0.0	0.0
1092	No	YKL212Wp-like protein [Saccharomyces cerevisi	gi 207343708 (+3)	42 kDa	3	0	0	0	3	0	0	0	12.4%	0.0	0.0	0.0
1093	No	YGL246Cp-like protein [Saccharomyces cerevisi	gi 207345568 (+2)	45 kDa	3	0	0	0	3	0	0	0	9.56%	0.0	0.0	0.0
1094	No	Cgi121p [Saccharomyces cerevisiae JAY291]	gi 256270864	21 kDa	3	0	0	0	3	0	0	0	18.7%	0.0	0.0	0.0
1095	No	Sds22p [Saccharomyces cerevisiae EC1118]	gi 259147649 (+1)	39 kDa	3	0	0	0	3	0	0	0	8.58%	0.0	0.0	0.0
1096	No	Cdc21p [Saccharomyces cerevisiae EC1118]	gi 259149556 (+1)	35 kDa	4	0	0	0	4	0	0	0	16.4%	0.0	0.0	0.0
1097	No	Chain A, Crystal Structure Of The Oxidised Form	gi 261824811 (+2)	12 kDa	5	0	0	0	4	0	0	0	55.0%	0.0	0.0	0.0
1098	No	Unknown [Saccharomyces cerevisiae]	gi 4261673 (+3)	18 kDa	4	0	0	0	4	0	0	0	20.9%	0.0	0.0	0.0
1099	No	Prx1p [Saccharomyces cerevisiae S288c]	gi 6319407	29 kDa	3	0	0	0	3	0	0	0	14.6%	0.0	0.0	0.0
1100	No	Dut1p [Saccharomyces cerevisiae S288c]	gi 6319729	15 kDa	4	0	0	0	4	0	0	0	32.0%	0.0	0.0	0.0
1101	No	Mrp1p [Saccharomyces cerevisiae S288c]	gi 6320554	37 kDa	4	0	0	0	3	0	0	0	13.1%	0.0	0.0	0.0
1102	No	hypothetical protein YHR112C [Saccharomyces	gi 6321904	42 kDa	3	0	0	0	3	0	0	0	11.6%	0.0	0.0	0.0
1103	No	Rnt1p [Saccharomyces cerevisiae S288c]	gi 6323895	54 kDa	4	0	0	0	4	0	0	0	9.55%	0.0	0.0	0.0
1104	No	Csl4p [Saccharomyces cerevisiae S288c]	gi 6324097	32 kDa	4	0	0	0	4	0	0	0	14.0%	0.0	0.0	0.0
1105	No	translation initiation factor eIF2B subunit [Sacch	gi 151942191 (+1)	81 kDa	3	0	0	0	3	0	0	0	4.49%	0.0	0.0	0.0
1106	No	Chain A, The Structure Of A Class Ii Ubiquitin-Co	gi 52695852 (+1)	24 kDa	2	0	0	0	2	0	0	0	11.6%	0.0	0.0	0.0
1107	No	Aim2p [Saccharomyces cerevisiae S288c]	gi 6319267	27 kDa	3	0	0	0	3	0	0	0	11.0%	0.0	0.0	0.0
1108	No	Asp1p [Saccharomyces cerevisiae S288c]	gi 6320527	41 kDa	3	0	0	0	3	0	0	0	9.71%	0.0	0.0	0.0
1109	No	YDL022Wp-like protein [Saccharomyces cerevisi	gi 207346895 (+2)	43 kDa	5	0	0	0	3	0	0	0	8.25%	0.0	0.0	0.0
1110	No	YGL221C [Saccharomyces cerevisiae]	gi 51013883 (+1)	32 kDa	3	0	0	0	3	0	0	0	10.8%	0.0	0.0	0.0
1111	No	Rbk1p [Saccharomyces cerevisiae S288c]	gi 10383797 (+3)	37 kDa	3	0	0	0	3	0	0	0	9.61%	0.0	0.0	0.0
1112	No	Yhr009cp [Saccharomyces cerevisiae]	gi 500703 (+1)	57 kDa	3	0	0	0	3	0	0	0	8.88%	0.0	0.0	0.0
1113	No	Ham1p [Saccharomyces cerevisiae S288c]	gi 6322529	22 kDa	3	0	0	0	3	0	0	0	19.3%	0.0	0.0	0.0
1114	No	Chain A, Crystal Structure At 1.9a Of The Apo Q	gi 170785208 (+2)	32 kDa	3	0	0	0	3	0	0	0	12.6%	0.0	0.0	0.0
1115	No	Chain A, Crystal Structure Of A Mutant Prolifera	gi 218766882 (+3)	29 kDa	2	0	0	0	2	0	0	0	19.8%	0.0	0.0	0.0
1116	No	YNL134C-like protein [Saccharomyces cerevisiae	gi 256273814 (+1)	41 kDa	2	0	0	0	2	0	0	0	7.18%	0.0	0.0	0.0
1117	No	hypothetical protein SCY_2143 [Saccharomyces	gi 151943526 (+1)	41 kDa	3	0	0	0	2	0	0	0	6.20%	0.0	0.0	0.0

1118	No	Adi1p [Saccharomyces cerevisiae S288c]	gi 6323651	21 kDa	4	0	0	0	2	0	0	0	15.1%	0.0	0.0	0.0
1119	No	hypothetical protein SCRG_02736 [Saccharomyces cerevisiae]	gi 190408616 (+2)	42 kDa	2	0	0	0	2	0	0	0	7.03%	0.0	0.0	0.0
1120	No	Gin4p [Saccharomyces cerevisiae S288c]	gi 6320715	130 kDa	2	0	0	0	2	0	0	0	1.84%	0.0	0.0	0.0
1121	No	YOL059Wp-like protein [Saccharomyces cerevisiae]	gi 207341380 (+3)	47 kDa	2	0	0	0	2	0	0	0	5.04%	0.0	0.0	0.0
1122	No	conserved protein [Saccharomyces cerevisiae YJ]	gi 151945711 (+3)	134 kDa	2	0	0	0	2	0	0	0	4.22%	0.0	0.0	0.0
1123	No	Dtd1p [Saccharomyces cerevisiae JAY291]	gi 256270993 (+1)	17 kDa	3	0	0	0	2	0	0	0	14.6%	0.0	0.0	0.0
1124	No	RecName: Full=Methylthioribose-1-phosphate i	gi 313471358 (+1)	45 kDa	2	0	0	0	2	0	0	0	4.87%	0.0	0.0	0.0
1125	No	Rtg2p [Saccharomyces cerevisiae S288c]	gi 6321185	66 kDa	2	0	0	0	2	0	0	0	4.42%	0.0	0.0	0.0
1126	No	RecName: Full=mRNA-decapping enzyme subun	gi 251764671	109 kDa	2	0	0	0	2	0	0	0	2.16%	0.0	0.0	0.0
1127	No	conserved hypothetical protein [Saccharomyces gi]	gi 190406481 (+2)	65 kDa	2	0	0	0	2	0	0	0	3.91%	0.0	0.0	0.0
1128	No	ATPase family protein [Saccharomyces cerevisia	gi 151940918 (+3)	85 kDa	2	0	0	0	2	0	0	0	2.95%	0.0	0.0	0.0
1129	No	Arc18p [Saccharomyces cerevisiae S288c]	gi 6323402	21 kDa	1	0	0	0	1	0	0	0	7.30%	0.0	0.0	0.0
1130	No	ribosomal protein S30A [Saccharomyces cerevis	gi 151940993	7 kDa	4	0	0	0	2	0	0	0	17.5%	0.0	0.0	0.0
1131	No	conserved protein [Saccharomyces cerevisiae YJ	gi 151946233 (+3)	79 kDa	1	0	0	0	1	0	0	0	1.46%	0.0	0.0	0.0
1132	No	protein phosphatase T [Saccharomyces cerevisia	gi 151943403 (+2)	58 kDa	1	0	0	0	1	0	0	0	1.95%	0.0	0.0	0.0
1133	No	Arl1p [Saccharomyces cerevisiae S288c]	gi 6319641	20 kDa	2	0	0	0	2	0	0	0	11.5%	0.0	0.0	0.0
1134	No	Chain A, Crystal Structure Of Glutathione-Deper	gi 203282397 (+1)	20 kDa	1	0	0	0	1	0	0	0	18.1%	0.0	0.0	0.0
1135	No	Cos6p [Saccharomyces cerevisiae S288c]	gi 6321734	46 kDa	1	0	0	0	1	0	0	0	2.62%	0.0	0.0	0.0
1136	No	tRNA acetylation [Saccharomyces cerevisiae YJN	gi 151943586 (+2)	34 kDa	1	0	0	0	1	0	0	0	4.50%	0.0	0.0	0.0
1137	No	Cit2p [Saccharomyces cerevisiae S288c]	gi 6319850	51 kDa	1	0	0	0	1	0	0	0	2.61%	0.0	0.0	0.0
1138	No	conserved protein [Saccharomyces cerevisiae YJ	gi 151943303 (+2)	35 kDa	1	0	0	0	1	0	0	0	3.37%	0.0	0.0	0.0
1139	No	Cir1p [Saccharomyces cerevisiae S288c]	gi 6321646	29 kDa	1	0	0	0	1	0	0	0	4.60%	0.0	0.0	0.0
1140	No	exocyst complex component [Saccharomyces cere	gi 151942148 (+2)	112 kDa	1	0	0	0	1	0	0	0	1.03%	0.0	0.0	0.0
1141	No	Mdj1p [Saccharomyces cerevisiae JAY291]	gi 256268876	56 kDa	1	0	0	0	1	0	0	0	3.72%	0.0	0.0	0.0
1142	No	YLR401Cp-like protein [Saccharomyces cerevisia	gi 207342739 (+3)	77 kDa	1	0	0	0	1	0	0	0	1.50%	0.0	0.0	0.0
1143	No	conserved protein [Saccharomyces cerevisiae YJ	gi 151945152 (+4)	34 kDa	1	0	0	0	1	0	0	0	3.42%	0.0	0.0	0.0
1144	No	Chain A, Crystal Structure Of The Yeast Ortholog	gi 223674073	35 kDa	0	1	0	0	0	1	0	0	0	0.0	0.0	11.6%
1145	No	Htz1p [Saccharomyces cerevisiae S288c]	gi 6324562	14 kDa	1	1	2	0	1	1	1	0	24.6%	24.6%	24.6%	0.0
1146	No	Chain B, X-Ray Structure Of Rna Polymerase Iii S	gi 112490174 (+2)	25 kDa	1	1	1	0	1	1	1	0	4.13%	4.59%	4.59%	0.0
1147	No	Mrp135p [Saccharomyces cerevisiae S288c]	gi 6320528	43 kDa	2	0	1	0	2	0	1	0	5.99%	0.0	3.00%	0.0
1148	No	radiation sensitive protein [Saccharomyces cere	gi 151946129 (+5)	52 kDa	1	0	2	0	1	0	1	0	2.12%	0.0	2.12%	0.0
1149	No	inhibitor 2 proteinase B	gi 223158 (+1)	8 kDa	1	1	0	0	1	1	0	0	23.0%	23.0%	0.0	0.0
1150	No	Sporulation-specific chitinase [Saccharomyces c	gi 151942343 (+3)	59 kDa	0	1	2	0	0	1	2	0	0.0	2.15%	4.11%	0.0
1151	No	sister chromatid cohesion [Saccharomyces cere	gi 151942163 (+4)	171 kDa	1	0	0	0	1	0	0	0	0.804%	0.0	0.000%	0.0
1152	No	Bro1p [Saccharomyces cerevisiae]	gi 1098953 (+3)	97 kDa	1	0	0	0	1	0	0	0	1.54%	0.0	0.000%	0.000%
1153	No	Chain A, Lumazine Synthase From Saccharomyc	gi 13399523 (+3)	18 kDa	1	0	0	0	1	0	0	0	7.74%	0.000%	0.0	0.0
1154	No	vesicle coat component [Saccharomyces cerevis	gi 190407935 (+1)	22 kDa	1	0	0	0	1	0	0	0	6.88%	0.000%	0.000%	0.0
1155	No	YGL022Wp-like protein [Saccharomyces cerevis	gi 207345276 (+2)	81 kDa	3	0	0	0	3	0	0	0	5.15%	0.000%	0.0	0.0
1156	No	Icl1p [Saccharomyces cerevisiae S288c]	gi 6320908	62 kDa	2	0	0	0	2	0	0	0	5.57%	0.0	0.000%	0.0
1157	No	swr complex subunit [Saccharomyces cerevisiae	gi 151943289 (+2)	55 kDa	1	0	0	0	1	0	0	0	3.78%	0.000%	0.0	0.0
1158	No	GP38 [Saccharomyces cerevisiae]	gi 297485 (+1)	37 kDa	2	0	0	0	2	0	0	0	6.78%	0.000%	0.0	0.0
1159	No	NADH:ubiquinone oxidoreductase [Saccharomy	gi 151946043 (+1)	57 kDa	2	0	0	0	2	0	0	0	4.68%	0.0	0.000%	0.0
1160	No	YGR200Cp-like protein [Saccharomyces cerevisi	gi 207344991 (+3)	89 kDa	3	0	0	0	3	0	0	0	5.84%	0.0	0.000%	0.0
1161	No	unnamed protein product [Saccharomyces cere	gi 3366 (+1)	57 kDa	2	0	0	0	2	0	0	0	4.28%	0.000%	0.0	0.0
1162	No	Chain W, Structure Of Yeast Complex Iii With Isc	gi 188036325	12 kDa	1	0	0	0	1	0	0	0	19.6%	0.0	0.0	0.0
1163	No	Ecm21p [Saccharomyces cerevisiae JAY291]	gi 256271195 (+2)	124 kDa	1	0	0	0	1	0	0	0	1.07%	0.0	0.0	0.0
1164	No	conserved protein [Saccharomyces cerevisiae YJ	gi 151945577	80 kDa	1	0	0	0	1	0	0	0	1.83%	0.0	0.0	0.0
1165	No	1-methyladenosine tRNA methyltransferase sub	gi 151944472 (+2)	54 kDa	1	0	0	0	1	0	0	0	2.09%	0.0	0.0	0.0
1166	No	Hef3p [Saccharomyces cerevisiae JAY291]	gi 256274162 (+1)	116 kDa	2	0	0	0	1	0	0	0	10.1%	0.0	0.0	0.0
1167	No	Hgh1p [Saccharomyces cerevisiae]	gi 1002516 (+2)	33 kDa	3	0	0	0	3	0	0	0	13.7%	0.0	0.0	0.0
1168	No	Gna1p [Saccharomyces cerevisiae S288c]	gi 14318503	18 kDa	3	0	0	0	3	0	0	0	27.7%	0.0	0.0	0.0
1169	No	glutathione-dependent formaldehyde dehydrog	gi 151941836 (+1)	41 kDa	3	0	0	0	3	0	0	0	10.6%	0.0	0.0	0.0
1170	No	ARF-binding protein [Saccharomyces cerevisiae	gi 151942331 (+2)	62 kDa	4	0	0	0	4	0	0	0	9.34%	0.0	0.0	0.0
1171	No	conserved protein [Saccharomyces cerevisiae YJ	gi 151942795 (+1)	37 kDa	4	0	0	0	4	0	0	0	16.5%	0.0	0.0	0.0
1172	No	suppressor of mar inhibitor [Saccharomyces cer	gi 151943503 (+3)	57 kDa	3	0	0	0	3	0	0	0	8.12%	0.0	0.0	0.0
1173	No	conserved protein [Saccharomyces cerevisiae YJ	gi 151943897 (+1)	17 kDa	3	0	0	0	3	0	0	0	23.0%	0.0	0.0	0.0
1174	No	translation initiation factor eIF2B gamma subun	gi 151945345 (+2)	66 kDa	4	0	0	0	4	0	0	0	9.52%	0.0	0.0	0.0
1175	No	conserved protein [Saccharomyces cerevisiae YJ	gi 151945900 (+3)	127 kDa	3	0	0	0	3	0	0	0	4.23%	0.0	0.0	0.0
1176	No	glyoxalase I [Saccharomyces cerevisiae YJM789]	gi 151946158 (+1)	37 kDa	4	0	0	0	4	0	0	0	16.6%	0.0	0.0	0.0

1177	No	conserved protein [Saccharomyces cerevisiae YJgi 151946503 (+1)	26 kDa	3	0	0	0	3	0	0	0	17.3%	0.0	0.0	0.0
1178	No	carbon catabolite derepressing protein kinase [Sgi 190404601 (+1)	72 kDa	3	0	0	0	3	0	0	0	6.46%	0.0	0.0	0.0
1179	No	hit family protein 1 [Saccharomyces cerevisiae Fgi 190405127 (+1)	18 kDa	3	0	0	0	3	0	0	0	28.5%	0.0	0.0	0.0
1180	No	hypothetical protein SCRG_04988 [Saccharomyces gi 190406041 (+2)	85 kDa	3	0	0	0	3	0	0	0	5.02%	0.0	0.0	0.0
1181	No	hypothetical protein SCRG_04099 [Saccharomyces gi 190409896 (+1)	69 kDa	4	0	0	0	4	0	0	0	9.33%	0.0	0.0	0.0
1182	No	YDR518Wp-like protein [Saccharomyces cerevis gi 207346177	61 kDa	3	0	0	0	3	0	0	0	6.94%	0.0	0.0	0.0
1183	No	Yip3p [Saccharomyces cerevisiae JAY291]	20 kDa	3	0	0	0	3	0	0	0	21.5%	0.0	0.0	0.0
1184	No	calmodulin-dependent protein kinase type II [Sagi 3556 (+1)	50 kDa	3	0	0	0	3	0	0	0	8.28%	0.0	0.0	0.0
1185	No	Rrp46p [Saccharomyces cerevisiae S288c]	24 kDa	3	0	0	0	3	0	0	0	16.1%	0.0	0.0	0.0
1186	No	TBF1 protein [Saccharomyces cerevisiae]	gi 4604 (+1)	63 kDa	3	0	0	3	0	0	0	5.69%	0.0	0.0	0.0
1187	No	Cox4p [Saccharomyces cerevisiae S288c]	gi 6321251	17 kDa	4	0	0	4	0	0	0	41.3%	0.0	0.0	0.0
1188	No	Vps29p [Saccharomyces cerevisiae S288c]	gi 6321800	31 kDa	3	0	0	3	0	0	0	13.1%	0.0	0.0	0.0
1189	No	hypothetical protein YJL068C [Saccharomyces c gi 6322393 (+1)	34 kDa	4	0	0	0	4	0	0	0	16.1%	0.0	0.0	0.0
1190	No	Cap1p [Saccharomyces cerevisiae S288c]	gi 6322845	31 kDa	4	0	0	4	0	0	0	17.2%	0.0	0.0	0.0
1191	No	Rpn13p [Saccharomyces cerevisiae S288c]	gi 6323453	18 kDa	3	0	0	3	0	0	0	22.4%	0.0	0.0	0.0
1192	No	hypothetical protein YOR283W [Saccharomyces gi 6324857	26 kDa	3	0	0	0	3	0	0	0	18.3%	0.0	0.0	0.0
1193	No	Chain A, Gppnhp-Bound Ypt51 At 1.48 A Resolu gi 7767071	19 kDa	4	0	0	0	4	0	0	0	32.9%	0.0	0.0	0.0
1194	No	Ypr169wp [Saccharomyces cerevisiae]	gi 786294 (+1)	58 kDa	3	0	0	3	0	0	0	7.00%	0.0	0.0	0.0
1195	No	CCR4-NOT transcriptional complex subunit [Saci gi 151944783 (+3)	65 kDa	3	0	0	0	3	0	0	0	6.47%	0.0	0.0	0.0
1196	No	cleavage and polyadenylation factor CF I compo gi 151945512 (+2)	60 kDa	4	0	0	0	3	0	0	0	7.12%	0.0	0.0	0.0
1197	No	Cdc28 protein kinase subunit [Saccharomyces c gi 190408710 (+1)	17 kDa	4	0	0	0	3	0	0	0	23.2%	0.0	0.0	0.0
1198	No	Map1p [Saccharomyces cerevisiae EC1118]	gi 259148226 (+1)	43 kDa	3	0	0	3	0	0	0	8.27%	0.0	0.0	0.0
1199	No	Ilv6p [Saccharomyces cerevisiae S288c]	gi 6319837	34 kDa	4	0	0	3	0	0	0	13.6%	0.0	0.0	0.0
1200	No	Hmf1p [Saccharomyces cerevisiae S288c]	gi 6320899	14 kDa	4	0	0	3	0	0	0	41.9%	0.0	0.0	0.0
1201	No	Nop8p [Saccharomyces cerevisiae S288c]	gi 6324428	57 kDa	3	0	0	3	0	0	0	11.0%	0.0	0.0	0.0
1202	No	Ddp1p [Saccharomyces cerevisiae S288c]	gi 6324737	22 kDa	4	0	0	3	0	0	0	20.2%	0.0	0.0	0.0
1203	No	Pyk2p [Saccharomyces cerevisiae S288c]	gi 6324923	55 kDa	2	0	0	2	0	0	0	6.32%	0.0	0.0	0.0
1204	No	poly(A)RNA binding protein [Saccharomyces cer gi 151942630 (+2)	67 kDa	3	0	0	0	3	0	0	0	5.84%	0.0	0.0	0.0
1205	No	6-phosphogluconolactonase [Saccharomyces ce gi 151943522	28 kDa	2	0	0	0	2	0	0	0	12.2%	0.0	0.0	0.0
1206	No	2-deoxyglucose-6-phosphate phosphatase [Sacc gi 151943988 (+2)	27 kDa	4	0	0	0	3	0	0	0	11.8%	0.0	0.0	0.0
1207	No	Mas2p [Saccharomyces cerevisiae EC1118]	gi 259147053 (+2)	53 kDa	3	0	0	3	0	0	0	6.02%	0.0	0.0	0.0
1208	No	Ktr1p [Saccharomyces cerevisiae S288c]	gi 6324673	46 kDa	3	0	0	3	0	0	0	8.91%	0.0	0.0	0.0
1209	No	nuclear pore complex subunit [Saccharomyces gi 190409459 (+2)	84 kDa	3	0	0	0	3	0	0	0	5.22%	0.0	0.0	0.0
1210	No	Rrp43p [Saccharomyces cerevisiae S288c]	gi 10383796 (+2)	44 kDa	3	0	0	3	0	0	0	8.88%	0.0	0.0	0.0
1211	No	Rbg2p [Saccharomyces cerevisiae EC1118]	gi 259146678 (+1)	41 kDa	3	0	0	3	0	0	0	9.51%	0.0	0.0	0.0
1212	No	Gcy1p [Saccharomyces cerevisiae JAY291]	gi 256272994 (+1)	35 kDa	2	0	0	2	0	0	0	14.1%	0.0	0.0	0.0
1213	No	Pdr17p [Saccharomyces cerevisiae EC1118]	gi 259149106 (+1)	41 kDa	2	0	0	2	0	0	0	6.57%	0.0	0.0	0.0
1214	No	Cmk1p [Saccharomyces cerevisiae S288c]	gi 14318536 (+1)	50 kDa	2	0	0	2	0	0	0	5.83%	0.0	0.0	0.0
1215	No	Myo4p [Saccharomyces cerevisiae JAY291]	gi 256272305	169 kDa	2	0	0	2	0	0	0	3.33%	0.0	0.0	0.0
1216	No	RecName: Full=Alpha-1,2-mannosyltransferase gi 1353043 (+4)	67 kDa	3	0	0	0	3	0	0	0	6.14%	0.0	0.0	0.0
1217	No	Chain M, Crystal Structure Of The 20s Proteaso gi 3114281 (+1)	25 kDa	2	0	0	0	2	0	0	0	10.4%	0.0	0.0	0.0
1218	No	Gcd7p [Saccharomyces cerevisiae JAY291]	gi 256269819 (+1)	43 kDa	2	0	0	2	0	0	0	6.82%	0.0	0.0	0.0
1219	No	YJL117W [Saccharomyces cerevisiae]	gi 45269645 (+1)	35 kDa	2	0	0	2	0	0	0	8.36%	0.0	0.0	0.0
1220	No	Hmo1p [Saccharomyces cerevisiae JAY291]	gi 256272846 (+2)	28 kDa	2	0	0	2	0	0	0	9.76%	0.0	0.0	0.0
1221	No	Gcn3p [Saccharomyces cerevisiae S288c]	gi 6322878	34 kDa	2	0	0	2	0	0	0	7.87%	0.0	0.0	0.0
1222	No	Chain A, Glutaredoxin 2 Oxidized Structure gi 210060958 (+1)	12 kDa	3	0	0	0	2	0	0	0	21.1%	0.0	0.0	0.0
1223	No	Hmt1p [Saccharomyces cerevisiae S288c]	gi 6319508	40 kDa	2	0	0	2	0	0	0	6.03%	0.0	0.0	0.0
1224	No	serine/threonine protein kinase [Saccharomyces gi 151944150	92 kDa	3	0	0	0	2	0	0	0	3.03%	0.0	0.0	0.0
1225	No	Utp25p [Saccharomyces cerevisiae S288c]	gi 6322100	84 kDa	2	0	0	2	0	0	0	3.74%	0.0	0.0	0.0
1226	No	Yju2p [Saccharomyces cerevisiae S288c]	gi 6322755	32 kDa	2	0	0	2	0	0	0	9.71%	0.0	0.0	0.0
1227	No	ran binder protein [Saccharomyces cerevisiae Y gi 151943100	36 kDa	2	0	0	0	2	0	0	0	10.1%	0.0	0.0	0.0
1228	No	U3 snoRNP protein [Saccharomyces cerevisiae Y gi 151942910 (+1)	65 kDa	3	0	0	0	2	0	0	0	4.01%	0.0	0.0	0.0
1229	No	COMPASS (complex proteins associated with Se gi 151941527 (+1)	37 kDa	2	0	0	0	2	0	0	0	8.51%	0.0	0.0	0.0
1230	No	hypothetical protein YJR084W [Saccharomyces gi 6322543	49 kDa	2	0	0	0	2	0	0	0	4.73%	0.0	0.0	0.0
1231	No	Tma7p [Saccharomyces cerevisiae S288c]	gi 6323292	7 kDa	2	0	0	2	0	0	0	39.1%	0.0	0.0	0.0
1232	No	Vma8p [Saccharomyces cerevisiae S288c]	gi 6320784	29 kDa	3	0	0	2	0	0	0	4.69%	0.0	0.0	0.0
1233	No	YOR241Wp-like protein [Saccharomyces cerevis gi 207340987	52 kDa	2	0	0	0	2	0	0	0	4.10%	0.0	0.0	0.0
1234	No	suppressor of g2 (two) allele of skp1 [Saccharon gi 151945683 (+3)	45 kDa	2	0	0	0	2	0	0	0	5.06%	0.0	0.0	0.0
1235	No	urea amidolyase [Saccharomyces cerevisiae YJM gi 151946596 (+3)	202 kDa	2	0	0	0	2	0	0	0	1.20%	0.0	0.0	0.0

1236	No	Srp14p [Saccharomyces cerevisiae EC1118]	gi 259145152 (+1)	16 kDa	2	0	0	0	2	0	0	0	14.4%	0.0	0.0	0.0
1237	No	epsin-like protein [Saccharomyces cerevisiae YJ]	gi 151941047 (+5)	72 kDa	1	0	0	0	1	0	0	0	2.11%	0.0	0.0	0.0
1238	No	EC1118_1E8_2740p [Saccharomyces cerevisiae gi]	gi 259146060 (+1)	20 kDa	2	0	0	0	2	0	0	0	10.7%	0.0	0.0	0.0
1239	No	Gnp1p [Saccharomyces cerevisiae S288c]	gi 6320717 (+1)	74 kDa	2	0	0	0	2	0	0	0	3.92%	0.0	0.0	0.0
1240	No	Rpt3p [Saccharomyces cerevisiae S288c]	gi 6320602	48 kDa	2	0	0	0	2	0	0	0	9.11%	0.0	0.0	0.0
1241	No	SPX19 [Saccharomyces cerevisiae]	gi 553143 (+2)	28 kDa	2	0	0	0	2	0	0	0	8.37%	0.0	0.0	0.0
1242	No	D protein [Saccharomyces cerevisiae A364A]	gi 11466070 (+1)	21 kDa	2	0	0	0	2	0	0	0	10.5%	0.0	0.0	0.0
1243	No	hypothetical protein YNL108C [Saccharomyces gi]	gi 6324221	31 kDa	1	0	0	0	1	0	0	0	3.33%	0.0	0.0	0.0
1244	No	YPL184Cp-like protein [Saccharomyces cerevisiae gi]	gi 207340676 (+3)	59 kDa	3	0	0	0	2	0	0	0	3.77%	0.0	0.0	0.0
1245	No	EC1118_104_5171p [Saccharomyces cerevisiae gi]	gi 259149760 (+1)	15 kDa	2	0	0	0	2	0	0	0	18.7%	0.0	0.0	0.0
1246	No	RecName: Full=SWI5-dependent HO expression gi	gi 334351057 (+2)	28 kDa	2	0	0	0	2	0	0	0	10.2%	0.0	0.0	0.0
1247	No	Chain B, Mms2UBC13 UBIQUITIN CONJUGATING gi	gi 14719687 (+1)	16 kDa	1	0	0	0	1	0	0	0	7.25%	0.0	0.0	0.0
1248	No	conserved protein [Saccharomyces cerevisiae Yj]	gi 151943786 (+2)	87 kDa	1	0	0	0	1	0	0	0	1.97%	0.0	0.0	0.0
1249	No	hypothetical protein YGL101W [Saccharomyces gi]	gi 6321337	25 kDa	1	0	0	0	1	0	0	0	5.12%	0.0	0.0	0.0
1250	No	nuclear cap binding complex subunit [Saccharor gi]	gi 151942621 (+2)	24 kDa	2	0	0	0	2	0	0	0	9.62%	0.0	0.0	0.0
1251	No	Chain K, Crystal Structure Of Epoxomicin:20s Pr gi	gi 11513423 (+4)	23 kDa	1	0	0	0	1	0	0	0	6.16%	0.0	0.0	0.0
1252	No	Chain A, Crystal Structure Of Saccharopine Deh gi	gi 160285837	42 kDa	2	0	0	0	2	0	0	0	7.87%	0.0	0.0	0.0
1253	No	Chain A, Crystal Structure Of The Yml079w Prot gi	gi 60593991 (+2)	23 kDa	1	0	0	0	1	0	0	0	7.39%	0.0	0.0	0.0
1254	No	mitochondrial intermembrane space import anc gi	gi 151941724 (+2)	45 kDa	1	0	0	0	1	0	0	0	3.47%	0.0	0.0	0.0
1255	No	Rrp45p [Saccharomyces cerevisiae S288c]	gi 6320486	34 kDa	1	0	0	0	1	0	0	0	3.61%	0.0	0.0	0.0
1256	No	conserved protein [Saccharomyces cerevisiae Yj]	gi 151946648 (+1)	26 kDa	1	0	0	0	1	0	0	0	4.74%	0.0	0.0	0.0
1257	No	YJR059Wp-like protein [Saccharomyces cerevisi gi]	gi 207343849 (+3)	91 kDa	1	0	0	0	1	0	0	0	1.10%	0.0	0.0	0.0
1258	No	Mrp13p [Saccharomyces cerevisiae EC1118]	gi 259147838 (+3)	32 kDa	1	0	0	0	1	0	0	0	5.09%	0.0	0.0	0.0
1259	No	Hsh155p [Saccharomyces cerevisiae JAY291]	gi 256270708 (+1)	110 kDa	1	0	0	0	1	0	0	0	1.34%	0.0	0.0	0.0
1260	No	unnamed protein product [Saccharomyces cere gi]	gi 2204269 (+1)	134 kDa	1	0	0	0	1	0	0	0	0.861%	0.0	0.0	0.0
1261	No	SNARE protein [Saccharomyces cerevisiae YJM7 gi]	gi 151944168 (+2)	25 kDa	1	0	0	0	1	0	0	0	4.48%	0.0	0.0	0.0
1262	No	Nsa2p [Saccharomyces cerevisiae S288c]	gi 6320973	30 kDa	2	0	0	0	1	0	0	0	3.83%	0.0	0.0	0.0
1263	No	YJL189Wp-like protein [Saccharomyces cerevisi gi]	gi 207344160 (+1)	5 kDa	1	0	0	0	1	0	0	0	25.6%	0.0	0.0	0.0
1264	No	Rpb1Op [Saccharomyces cerevisiae S288c]	gi 6324784	8 kDa	1	0	0	0	1	0	0	0	15.7%	0.0	0.0	0.0
1265	No	Chain A, Crystal Structure Of Threonine Synthas gi	gi 20664123	57 kDa	2	0	0	0	1	0	0	0	39.5%	0.0	0.0	0.0
1266	No	Pdc1p [Saccharomyces cerevisiae JAY291]	gi 256270485	47 kDa	2	0	0	0	1	0	0	0	39.2%	0.0	0.0	0.0
1267	No	Shm2p [Saccharomyces cerevisiae S288c]	gi 6323087	52 kDa	3	0	0	0	1	0	0	0	43.9%	0.0	0.0	0.0
1268	No	Rgi1p [Saccharomyces cerevisiae S288c]	gi 6320910	19 kDa	2	1	0	0	1	1	0	0	8.07%	8.07%	0.0	0.0
1269	No	Rpo26p [Saccharomyces cerevisiae S288c]	gi 6325445	18 kDa	0	1	2	0	0	1	1	0	0.0	12.3%	12.3%	0.0
1270	No	hypothetical protein YCLO57C-A [Saccharomyce gi]	gi 10383755	10 kDa	2	0	0	0	2	0	0	0	22.7%	0.0	0.000%	0.0
1271	No	les4p [Saccharomyces cerevisiae S288c]	gi 6324763	13 kDa	0	1	0	0	0	1	0	0	0.000%	0.0	10.3%	0.0
1272	No	maintenance of killer [Saccharomyces cerevisi gi]	gi 151944659 (+4)	84 kDa	1	0	0	0	1	0	0	0	1.36%	0.0	0.0	0.000%
1273	No	repressor activator protein [Saccharomyces cer gi]	gi 151944328 (+3)	92 kDa	2	0	0	0	2	0	0	0	3.02%	0.0	0.000%	0.0
1274	No	Sap155p [Saccharomyces cerevisiae]	gi 1345142 (+7)	115 kDa	2	0	0	0	2	0	0	0	2.10%	0.0	0.0	0.000%
1275	No	RecName: Full=ATP-dependent RNA helicase DE gi	gi 160380625 (+4)	70 kDa	2	0	0	0	2	0	0	0	3.66%	0.000%	0.0	0.0
1276	No	Sit4p [Saccharomyces cerevisiae EC1118]	gi 259145197 (+1)	36 kDa	2	0	0	0	2	0	0	0	6.75%	0.0	0.0	0.000%
1277	No	hypothetical protein [Saccharomyces cerevisi gi]	gi 895898	80 kDa	1	0	0	0	1	0	0	0	1.88%	0.0	0.000%	0.0
1278	No	protein serine-threonine kinase [Saccharomyce gi]	gi 151941902 (+3)	59 kDa	1	0	0	0	1	0	0	0	1.75%	0.0	0.000%	0.0
1279	No	conserved protein [Saccharomyces cerevisiae Yj gi]	gi 151944512 (+1)	33 kDa	1	0	0	0	1	0	0	0	4.63%	0.0	0.000%	0.0
1280	No	Tim11p [Saccharomyces cerevisiae S288c]	gi 6320529	11 kDa	1	0	0	0	1	0	0	0	10.4%	0.000%	0.0	0.0
1281	No	Nbp35p [Saccharomyces cerevisiae]	gi 1360147 (+2)	35 kDa	1	0	0	0	1	0	0	0	3.05%	0.0	0.0	0.0
1282	No	5-aminolevulinate synthase [Saccharomyces cer gi]	gi 151942209 (+5)	59 kDa	1	0	0	0	1	0	0	0	2.36%	0.0	0.000%	0.0
1283	No	Rdi1p [Saccharomyces cerevisiae S288c]	gi 6320066	23 kDa	2	0	0	0	2	0	0	0	10.4%	0.0	0.0	0.0
1284	No	pyruvate dehydrogenase complex protein X con gi]	gi 151943469 (+4)	45 kDa	2	0	0	0	2	0	0	0	6.34%	0.0	0.0	0.0
1285	No	maintenance of killer 11 protein [Saccharomyce gi]	gi 190409801 (+1)	54 kDa	2	0	0	0	2	0	0	0	4.49%	0.0	0.0	0.0
1286	No	Msh3p [Saccharomyces cerevisiae S288c]	gi 157285763 (+4)	117 kDa	1	0	0	0	1	0	0	0	0.982%	0.0	0.0	0.0
1287	No	YCR021Cp-like protein [Saccharomyces cerevisi gi]	gi 207347312 (+1)	37 kDa	3	0	0	0	3	0	0	0	16.9%	0.0	0.0	0.0
1288	No	Svf1p [Saccharomyces cerevisiae JAY291]	gi 256269243 (+2)	54 kDa	3	0	0	0	3	0	0	0	7.28%	0.0	0.0	0.0
1289	No	glycerate phosphomutase [Saccharomyces cere gi]	gi 151941972 (+1)	36 kDa	3	0	0	0	3	0	0	0	14.8%	0.0	0.0	0.0
1290	No	conserved protein [Saccharomyces cerevisiae Yj gi]	gi 151943973 (+3)	33 kDa	3	0	0	0	3	0	0	0	12.9%	0.0	0.0	0.0
1291	No	gamma-glutamyl kinase [Saccharomyces cerevis gi]	gi 190404757	47 kDa	3	0	0	0	3	0	0	0	9.81%	0.0	0.0	0.0
1292	No	dipeptidyl aminopeptidase B [Saccharomyces ce gi]	gi 190405813 (+1)	93 kDa	3	0	0	0	3	0	0	0	4.03%	0.0	0.0	0.0
1293	No	conserved hypothetical protein [Saccharomyces gi]	gi 190406295 (+2)	42 kDa	3	0	0	0	3	0	0	0	8.49%	0.0	0.0	0.0
1294	No	casein kinase I isoform gamma-2 [Saccharomyce gi]	gi 190409139 (+3)	62 kDa	3	0	0	0	3	0	0	0	8.24%	0.0	0.0	0.0

1295	No	Pnp1p [Saccharomyces cerevisiae S288c]	gi 6323238	34 kDa	3	0	0	0	3	0	0	13.8%	0.0	0.0	0.0
1296	No	riboflavin synthase [Saccharomyces cerevisiae Y gi 151946643 (+1)		26 kDa	3	0	0	0	3	0	0	15.1%	0.0	0.0	0.0
1297	No	RHO3p [Saccharomyces cerevisiae]	gi 218474 (+2)	25 kDa	3	0	0	0	3	0	0	14.3%	0.0	0.0	0.0
1298	No	Amd1p [Saccharomyces cerevisiae S288c]	gi 6323606	93 kDa	2	0	0	0	2	0	0	3.21%	0.0	0.0	0.0
1299	No	cleavage factor II (CF II) component [Saccharom gi 151941347 (+1)		89 kDa	2	0	0	0	2	0	0	2.93%	0.0	0.0	0.0
1300	No	mitochondrial ribosome recycling factor [Sacch gi 151943982 (+3)		26 kDa	2	0	0	0	2	0	0	10.4%	0.0	0.0	0.0
1301	No	Rsr1p [Saccharomyces cerevisiae EC1118]	gi 259146655 (+1)	30 kDa	3	0	0	0	3	0	0	12.5%	0.0	0.0	0.0
1302	No	Trp4p [Saccharomyces cerevisiae S288c]	gi 6320561	41 kDa	2	0	0	0	2	0	0	5.00%	0.0	0.0	0.0
1303	No	Tma22p [Saccharomyces cerevisiae S288c]	gi 6322474	22 kDa	2	0	0	0	2	0	0	13.6%	0.0	0.0	0.0
1304	No	YKL151Cp-like protein [Saccharomyces cerevisia gi 207343617 (+1)		36 kDa	3	0	0	0	3	0	0	10.9%	0.0	0.0	0.0
1305	No	Chain B, Structure Of Trm8-Trm82, The Yeast Tr gi 163310991 (+4)		51 kDa	2	0	0	0	2	0	0	6.67%	0.0	0.0	0.0
1306	No	Ent3p [Saccharomyces cerevisiae S288c]	gi 6322585	45 kDa	2	0	0	0	2	0	0	6.62%	0.0	0.0	0.0
1307	No	YLR025W [Saccharomyces cerevisiae]	gi 45270294 (+1)	27 kDa	2	0	0	0	2	0	0	10.4%	0.0	0.0	0.0
1308	No	Chain A, Ppm1 In The Absence Of 1,8-Ans (Cf 1j gi 126031470 (+4)		38 kDa	2	0	0	0	2	0	0	7.95%	0.0	0.0	0.0
1309	No	UBP14 [Saccharomyces cerevisiae]	gi 536297	91 kDa	2	0	0	0	2	0	0	2.86%	0.0	0.0	0.0
1310	No	conserved hypothetical protein [Saccharomyces gi 190406721 (+3)		34 kDa	2	0	0	0	2	0	0	7.21%	0.0	0.0	0.0
1311	No	hypothetical protein SCRG_00811 [Saccharomy gi 190406780 (+1)		45 kDa	2	0	0	0	2	0	0	8.52%	0.0	0.0	0.0
1312	No	karyopherin beta 2 [Saccharomyces cerevisiae Y gi 151946410 (+4)		103 kDa	2	0	0	0	2	0	0	2.62%	0.0	0.0	0.0
1313	No	peroxisomal-coenzyme A synthetase [Saccharo gi 190408627 (+1)		60 kDa	2	0	0	0	2	0	0	5.16%	0.0	0.0	0.0
1314	No	acetylmethionine aminotransferase [Saccharom gi 151945496 (+1)		47 kDa	2	0	0	0	2	0	0	7.57%	0.0	0.0	0.0
1315	No	fructose-1,6-bisphosphatase [Saccharomyces ce gi 190405420 (+1)		38 kDa	2	0	0	0	2	0	0	8.33%	0.0	0.0	0.0
1316	No	3'-5' exoribonuclease [Saccharomyces cerevisia gi 190405851 (+2)		39 kDa	2	0	0	0	2	0	0	6.96%	0.0	0.0	0.0
1317	No	transcription regulatory protein SNF12 [Sacchar gi 190408979 (+1)		64 kDa	2	0	0	0	2	0	0	5.30%	0.0	0.0	0.0
1318	No	ubiquitin-specific protease [Saccharomyces cere gi 151945745 (+5)		146 kDa	2	0	0	0	2	0	0	1.65%	0.0	0.0	0.0
1319	No	YLR147C [Saccharomyces cerevisiae]	gi 45270956 (+1)	11 kDa	3	0	0	0	3	0	0	41.6%	0.0	0.0	0.0
1320	No	ubiquitin hydrolase [Saccharomyces cerevisiae gi 151945164 (+2)		26 kDa	2	0	0	0	2	0	0	11.4%	0.0	0.0	0.0
1321	No	cleavage factor II (CF II) component [Saccharom gi 151942273 (+3)		153 kDa	2	0	0	0	2	0	0	2.06%	0.0	0.0	0.0
1322	No	L3177 [Saccharomyces cerevisiae]	gi 995714	79 kDa	2	0	0	0	2	0	0	3.46%	0.0	0.0	0.0
1323	No	non-histone protein [Saccharomyces cerevisiae gi 151941799 (+2)		19 kDa	2	0	0	0	2	0	0	16.2%	0.0	0.0	0.0
1324	No	thioredoxin peroxidase [Saccharomyces cerevisi gi 151943147 (+1)		24 kDa	3	0	0	0	2	0	0	11.6%	0.0	0.0	0.0
1325	No	conserved protein [Saccharomyces cerevisiae Y gi 151944060 (+3)		71 kDa	3	0	0	0	2	0	0	4.58%	0.0	0.0	0.0
1326	No	glyoxalase [Saccharomyces cerevisiae YJM789]	gi 151944837 (+3)	55 kDa	3	0	0	0	2	0	0	4.46%	0.0	0.0	0.0
1327	No	protoplasts-secreted [Saccharomyces cerevisiae gi 151946469 (+7)		34 kDa	2	0	0	0	2	0	0	7.65%	0.0	0.0	0.0
1328	No	NHP6B [Saccharomyces cerevisiae]	gi 1870101 (+2)	7 kDa	3	0	0	0	2	0	0	41.0%	0.0	0.0	0.0
1329	No	U3 snoRNP protein [Saccharomyces cerevisiae Y gi 151942414 (+2)		52 kDa	2	0	0	0	2	0	0	4.55%	0.0	0.0	0.0
1330	No	Did2p [Saccharomyces cerevisiae S288c]	gi 6322887 (+1)	23 kDa	3	0	0	0	2	0	0	11.8%	0.0	0.0	0.0
1331	No	conserved protein [Saccharomyces cerevisiae Y gi 151946481 (+6)		106 kDa	2	0	0	0	2	0	0	2.22%	0.0	0.0	0.0
1332	No	conserved protein [Saccharomyces cerevisiae Y gi 151941091 (+2)		36 kDa	2	0	0	0	2	0	0	9.97%	0.0	0.0	0.0
1333	No	RecName: Full=Ribosome biogenesis protein NS gi 206558288 (+2)		52 kDa	2	0	0	0	2	0	0	4.10%	0.0	0.0	0.0
1334	No	conserved protein [Saccharomyces cerevisiae Y gi 151944385 (+2)		15 kDa	2	0	0	0	2	0	0	14.0%	0.0	0.0	0.0
1335	No	conserved hypothetical protein [Saccharomyces gi 190407967 (+1)		45 kDa	1	0	0	0	1	0	0	3.74%	0.0	0.0	0.0
1336	No	exocyst complex component [Saccharomyces ce gi 151943585 (+3)		105 kDa	2	0	0	0	2	0	0	2.42%	0.0	0.0	0.0
1337	No	Ayr1p [Saccharomyces cerevisiae S288c]	gi 6322067 (+1)	33 kDa	2	0	0	0	2	0	0	7.07%	0.0	0.0	0.0
1338	No	Ufd1p [Saccharomyces cerevisiae S288c]	gi 6321485 (+1)	40 kDa	2	0	0	0	2	0	0	6.37%	0.0	0.0	0.0
1339	No	Smd2p [Saccharomyces cerevisiae S288c]	gi 6323305	13 kDa	2	0	0	0	2	0	0	21.8%	0.0	0.0	0.0
1340	No	Kap114p [Saccharomyces cerevisiae S288c]	gi 6321196	114 kDa	2	0	0	0	2	0	0	1.99%	0.0	0.0	0.0
1341	No	transcription factor [Saccharomyces cerevisiae Y gi 151941026 (+4)		91 kDa	2	0	0	0	2	0	0	3.24%	0.0	0.0	0.0
1342	No	Chain E, Crystal Structure Of The Eukaryotic Cla gi 50513625 (+1)		40 kDa	2	0	0	0	2	0	0	6.78%	0.0	0.0	0.0
1343	No	Lsb5p [Saccharomyces cerevisiae S288c]	gi 10383760 (+1)	40 kDa	3	0	0	0	2	0	0	7.91%	0.0	0.0	0.0
1344	No	Oca1p [Saccharomyces cerevisiae S288c]	gi 6324230	27 kDa	2	0	0	0	2	0	0	9.66%	0.0	0.0	0.0
1345	No	hypothetical protein YBR139W [Saccharomyces gi 6319615		58 kDa	2	0	0	0	2	0	0	4.13%	0.0	0.0	0.0
1346	No	protein IKI1 [Saccharomyces cerevisiae RM11-1: gi 190405962 (+1)		35 kDa	2	0	0	0	2	0	0	8.09%	0.0	0.0	0.0
1347	No	Tub3p [Saccharomyces cerevisiae JAY291]	gi 256270013 (+1)	50 kDa	2	0	0	0	2	0	0	14.1%	0.0	0.0	0.0
1348	No	Pno1p [Saccharomyces cerevisiae S288c]	gi 6324720	30 kDa	1	0	0	0	1	0	0	5.47%	0.0	0.0	0.0
1349	No	conserved protein [Saccharomyces cerevisiae Y gi 151945207 (+1)		40 kDa	1	0	0	0	1	0	0	3.51%	0.0	0.0	0.0
1350	No	clathrin light chain [Saccharomyces cerevisiae Y gi 151943443 (+3)		27 kDa	2	0	0	0	2	0	0	10.3%	0.0	0.0	0.0
1351	No	Dcs2p [Saccharomyces cerevisiae S288c]	gi 116006500 (+1)	41 kDa	2	0	0	0	2	0	0	8.78%	0.0	0.0	0.0
1352	No	target of Sbf [Saccharomyces cerevisiae YJM789 gi 151946551 (+2)		48 kDa	2	0	0	0	2	0	0	7.91%	0.0	0.0	0.0
1353	No	karyopherin [Saccharomyces cerevisiae YJM789 gi 151943272 (+3)		124 kDa	2	0	0	0	2	0	0	1.94%	0.0	0.0	0.0

1354	No	U3 snoRNP protein [Saccharomyces cerevisiae Ygi 151945077 (+3)	67 kDa	1	0	0	0	1	0	0	0	2.19%	0.0	0.0	0.0
1355	No	UBX domain-containing protein 1 [Saccharomyces gi 190408881 (+3)	47 kDa	1	0	0	0	1	0	0	0	4.02%	0.0	0.0	0.0
1356	No	lethal with conditional pap1 [Saccharomyces ce gi 151944842 (+1)	41 kDa	1	0	0	0	1	0	0	0	4.20%	0.0	0.0	0.0
1357	No	RecName: Full=Low-affinity glucose transporter gi 290463322 (+2)	64 kDa	1	0	0	0	1	0	0	0	2.43%	0.0	0.0	0.0
1358	No	unnamed protein product [Saccharomyces cere gi 1420545 (+2)	36 kDa	0	0	0	0	1	0	0	0	4.58%	0.0	0.0	0.0
1359	No	Shs1p [Saccharomyces cerevisiae JAY291] gi 256271003 (+1)	63 kDa	1	0	0	0	1	0	0	0	2.90%	0.0	0.0	0.0
1360	No	arylfornamidase [Saccharomyces cerevisiae YJn gi 151945267 (+3)	50 kDa	1	0	0	0	1	0	0	0	3.60%	0.0	0.0	0.0
1361	No	RecName: Full=Potential protein lysine methyltr gi 171704581 (+2)	61 kDa	1	0	0	0	1	0	0	0	1.90%	0.0	0.0	0.0
1362	No	Snz1p [Saccharomyces cerevisiae S288c] gi 6323743	32 kDa	1	0	0	0	1	0	0	0	5.05%	0.0	0.0	0.0
1363	No	conserved protein [Saccharomyces cerevisiae YJ gi 151941410 (+2)	135 kDa	2	0	0	0	2	0	0	0	1.60%	0.0	0.0	0.0
1364	No	Dap1p [Saccharomyces cerevisiae S288c] gi 6325087	17 kDa	1	0	0	0	1	0	0	0	8.55%	0.0	0.0	0.0
1365	No	MNN1 [Saccharomyces cerevisiae] gi 437726 (+1)	89 kDa	1	0	0	0	1	0	0	0	1.84%	0.0	0.0	0.0
1366	No	vacuole-related protein [Saccharomyces cerevis gi 151944697 (+1)	63 kDa	1	0	0	0	1	0	0	0	2.08%	0.0	0.0	0.0
1367	No	Nop15p [Saccharomyces cerevisiae S288c] gi 6324219	25 kDa	2	0	0	0	2	0	0	0	10.00%	0.0	0.0	0.0
1368	No	hypothetical protein YFR024c-a - yeast [Sacchar gi 1362490 (+2)	49 kDa	2	0	0	0	2	0	0	0	3.77%	0.0	0.0	0.0
1369	No	Pph22p [Saccharomyces cerevisiae S288c] gi 6320013	43 kDa	0	0	0	0	1	0	0	0	2.92%	0.0	0.0	0.0
1370	No	Rpb9p [Saccharomyces cerevisiae S288c] gi 6321368	14 kDa	1	0	0	0	1	0	0	0	8.20%	0.0	0.0	0.0
1371	No	transcription initiation factor TFIID subunit 11 [s gi 190408225 (+1)	41 kDa	1	0	0	0	1	0	0	0	3.18%	0.0	0.0	0.0
1372	No	Xpt1p [Saccharomyces cerevisiae EC1118] gi 259147596 (+1)	24 kDa	2	0	0	0	1	0	0	0	5.26%	0.0	0.0	0.0
1373	No	Pyc1p [Saccharomyces cerevisiae S288c] gi 6321376	130 kDa	1	0	0	0	1	0	0	0	17.3%	0.0	0.0	0.0
1374	No	Tyr1p [Saccharomyces cerevisiae S288c] gi 6319643	51 kDa	1	0	0	0	1	0	0	0	2.21%	0.0	0.0	0.0
1375	No	DNA polymerase alpha binding protein [Sacchar gi 151942909	104 kDa	1	0	0	0	1	0	0	0	1.19%	0.0	0.0	0.0
1376	No	conserved protein [Saccharomyces cerevisiae YJ gi 151942763 (+2)	65 kDa	1	0	0	0	1	0	0	0	2.29%	0.0	0.0	0.0
1377	No	TFIID subunit [Saccharomyces cerevisiae YJM78 gi 151945931 (+4)	67 kDa	3	0	0	0	2	0	0	0	4.07%	0.0	0.0	0.0
1378	No	RecName: Full=Elongation factor G, mitochondr gi 261263163	85 kDa	1	0	0	0	1	0	0	0	1.58%	0.0	0.0	0.0
1379	No	Rps29bp [Saccharomyces cerevisiae S288c] gi 6320142	7 kDa	1	0	0	0	1	0	0	0	33.9%	0.0	0.0	0.0
1380	No	geranylgeranyltransferase type II alpha subunit gi 190409467 (+2)	35 kDa	1	0	0	0	1	0	0	0	4.14%	0.0	0.0	0.0
1381	No	Nob1p [Saccharomyces cerevisiae EC1118] gi 259149538 (+1)	52 kDa	1	0	0	0	1	0	0	0	1.96%	0.0	0.0	0.0
1382	No	adrenodoxin oxidoreductase homolog [Sacchar gi 1055300 (+4)	56 kDa	1	0	0	0	1	0	0	0	2.23%	0.0	0.0	0.0
1383	No	Gir2p [Saccharomyces cerevisiae S288c] gi 6320356	31 kDa	1	0	0	0	1	0	0	0	3.40%	0.0	0.0	0.0
1384	No	Cdc28p [Saccharomyces cerevisiae S288c] gi 6319636	34 kDa	1	0	0	0	1	0	0	0	10.1%	0.0	0.0	0.0
1385	No	Tvp15p [Saccharomyces cerevisiae S288c] gi 6320305	16 kDa	1	0	0	0	1	0	0	0	14.0%	0.0	0.0	0.0
1386	No	Sly1p [Saccharomyces cerevisiae] gi 1289305 (+4)	58 kDa	1	0	0	0	1	0	0	0	1.56%	0.0	0.0	0.0
1387	No	Chain D, Rna Polymerase II-Tfiis Complex gi 34810556 (+3)	25 kDa	1	0	0	0	1	0	0	0	3.62%	0.0	0.0	0.0
1388	No	V-ATPase V0 sector subunit a [Saccharomyces c gi 151946213 (+6)	102 kDa	1	0	0	0	1	0	0	0	1.24%	0.0	0.0	0.0
1389	No	tau 55 subunit of transcription factor TFIIC [Sac gi 151945732 (+4)	49 kDa	1	0	0	0	1	0	0	0	1.84%	0.0	0.0	0.0
1390	No	hypothetical protein SCRG_02755 [Saccharomy: gi 190408634 (+2)	57 kDa	1	0	0	0	1	0	0	0	1.90%	0.0	0.0	0.0
1391	No	polyamine oxidase [Saccharomyces cerevisiae Y gi 151946181 (+4)	58 kDa	1	0	0	0	1	0	0	0	2.17%	0.0	0.0	0.0
1392	No	Rsa4p [Saccharomyces cerevisiae S288c] gi 10383804 (+1)	57 kDa	1	0	0	0	1	0	0	0	2.91%	0.0	0.0	0.0
1393	No	mevalonate kinase [Saccharomyces cerevisiae Y gi 151945912 (+2)	48 kDa	1	0	0	0	1	0	0	0	2.26%	0.0	0.0	0.0
1394	No	elongase [Saccharomyces cerevisiae YJM789] gi 151940895 (+3)	39 kDa	2	0	0	0	1	0	0	0	4.93%	0.0	0.0	0.0
1395	No	RecName: Full=Adenylyltransferase and sulfurtr gi 226713013 (+1)	49 kDa	2	0	0	0	1	0	0	0	2.27%	0.0	0.0	0.0
1396	No	polyadenylated RNA binding protein [Saccharon gi 151943688 (+3)	57 kDa	1	0	0	0	1	0	0	0	1.95%	0.0	0.0	0.0
1397	No	Chain E, Structure Of The Yeast Cytochrome Bc1 gi 14277716 (+2)	20 kDa	2	0	0	0	1	0	0	0	6.49%	0.0	0.0	0.0
1398	No	conserved protein [Saccharomyces cerevisiae YJ gi 151941077 (+1)	89 kDa	1	0	0	0	1	0	0	0	2.05%	0.0	0.0	0.0
1399	No	conserved hypothetical protein [Saccharomyces gi 190405201 (+1)	38 kDa	1	1	0	0	1	1	0	0	7.37%	7.37%	0.0	0.0
1400	No	Sth1p [Saccharomyces cerevisiae JAY291] gi 256269545	157 kDa	0	0	1	1	0	0	1	1	0.0	0.0	48.3%	44.8%
1401	No	mitochondrial acidic matrix protein [Saccharom gi 151943093 (+3)	30 kDa	1	0	0	0	1	0	0	0	3.76%	0.000%	0.0	0.0
1402	No	YDL178Wp-like protein [Saccharomyces cerevisi gi 207347109 (+3)	59 kDa	1	0	0	0	1	0	0	0	4.15%	0.000%	0.0	0.0
1403	No	Hsh49p [Saccharomyces cerevisiae S288c] gi 6324895	25 kDa	0	1	0	0	0	1	0	0	0.0	5.16%	0.000%	0.0
1404	No	Ada2p [Saccharomyces cerevisiae S288c] gi 6320656	51 kDa	1	0	0	0	1	0	0	0	2.30%	0.000%	0.0	0.0
1405	No	radiation sensitive protein [Saccharomyces cere gi 151946150	20 kDa	1	0	0	0	1	0	0	0	6.78%	0.0	0.000%	0.0
1406	No	Fmp41p [Saccharomyces cerevisiae S288c] gi 6324161	29 kDa	1	0	0	0	1	0	0	0	10.0%	0.0	0.000%	0.0
1407	No	YPL015Cp-like protein [Saccharomyces cerevisia gi 207340454	43 kDa	1	0	0	0	1	0	0	0	2.89%	0.000%	0.0	0.0
1408	No	Hmg2p [Saccharomyces cerevisiae EC1118] gi 259148426 (+2)	116 kDa	1	0	0	0	1	0	0	0	1.34%	0.0	0.000%	0.0
1409	No	CDC2 [Saccharomyces cerevisiae] gi 1199547 (+5)	125 kDa	2	0	0	0	2	0	0	0	1.91%	0.0	0.0	0.0
1410	No	conserved protein [Saccharomyces cerevisiae YJ gi 151941476 (+1)	20 kDa	2	0	0	0	2	0	0	0	12.8%	0.0	0.0	0.0
1411	No	carboxypeptidase Y inhibitor [Saccharomyces ce gi 190405247 (+5)	24 kDa	2	0	0	0	2	0	0	0	15.1%	0.0	0.0	0.0
1412	No	Chain A, Crystal Structure Of Saccharomyces Ce gi 241913259 (+1)	18 kDa	2	0	0	0	2	0	0	0	12.5%	0.0	0.0	0.0

1413	No	Atg27p [Saccharomyces cerevisiae S288c]	gi 42742253	30 kDa	2	0	0	0	2	0	0	8.12%	0.0	0.0	0.0
1414	No	Rfs1p [Saccharomyces cerevisiae S288c]	gi 6319526	23 kDa	2	0	0	0	2	0	0	10.5%	0.0	0.0	0.0
1415	No	Cdc34p [Saccharomyces cerevisiae S288c]	gi 6320259	34 kDa	2	0	0	0	2	0	0	9.83%	0.0	0.0	0.0
1416	No	Aah1p [Saccharomyces cerevisiae S288c]	gi 6324188	40 kDa	2	0	0	0	2	0	0	7.20%	0.0	0.0	0.0
1417	No	unknown protein [Saccharomyces cerevisiae]	gi 7537305	17 kDa	2	0	0	0	2	0	0	20.1%	0.0	0.0	0.0
1418	No	RecName: Full=Exosome complex component R	gi 14285754 (+1)	27 kDa	2	0	0	0	2	0	0	11.2%	0.0	0.0	0.0
1419	No	toxin-insensitive protein [Saccharomyces cerevisiae]	gi 151941692 (+4)	35 kDa	2	0	0	0	2	0	0	7.03%	0.0	0.0	0.0
1420	No	zinc metalloprotease [Saccharomyces cerevisiae]	gi 151945182 (+4)	52 kDa	2	0	0	0	2	0	0	5.96%	0.0	0.0	0.0
1421	No	Hfi1p [Saccharomyces cerevisiae]	gi 1145779 (+1)	54 kDa	2	0	0	0	2	0	0	5.94%	0.0	0.0	0.0
1422	No	Hrr25p [Saccharomyces cerevisiae S288c]	gi 6325052	57 kDa	2	0	0	0	2	0	0	6.28%	0.0	0.0	0.0
1423	No	Bcp1p [Saccharomyces cerevisiae S288c]	gi 6320568	33 kDa	2	0	0	0	2	0	0	8.48%	0.0	0.0	0.0
1424	No	adenine phosphoribosyltransferase 2 [Saccharo	gi 190404630 (+2)	20 kDa	2	0	0	0	2	0	0	11.6%	0.0	0.0	0.0
1425	No	Egd1p [Saccharomyces cerevisiae S288c]	gi 6325220	17 kDa	2	0	0	0	2	0	0	16.6%	0.0	0.0	0.0
1426	No	anthranilate synthase Component II:indole-3-gh	gi 173045 (+2)	54 kDa	2	0	0	0	2	0	0	4.75%	0.0	0.0	0.0
1427	No	translocase of the outer membrane [Saccharom	gi 151945907 (+2)	42 kDa	2	0	0	0	2	0	0	8.27%	0.0	0.0	0.0
1428	No	Trx3p [Saccharomyces cerevisiae S288c]	gi 6319925	14 kDa	2	0	0	0	2	0	0	13.4%	0.0	0.0	0.0
1429	No	phorphobilinogen deaminase [Saccharomyces c	gi 151941802 (+1)	37 kDa	2	0	0	0	2	0	0	8.56%	0.0	0.0	0.0
1430	No	YJR144Wp-like protein [Saccharomyces cerevisi	gi 207343744 (+1)	28 kDa	2	0	0	0	2	0	0	9.52%	0.0	0.0	0.0
1431	No	Msl1p [Saccharomyces cerevisiae S288c]	gi 6322199	13 kDa	2	0	0	0	2	0	0	15.3%	0.0	0.0	0.0
1432	No	calcineurin subunit A [Saccharomyces cerevisi	gi 151940949 (+1)	63 kDa	2	0	0	0	2	0	0	4.52%	0.0	0.0	0.0
1433	No	RecName: Full=54S ribosomal protein L22, mito	gi 1730808	35 kDa	2	0	0	0	2	0	0	10.0%	0.0	0.0	0.0
1434	No	Sub1p [Saccharomyces cerevisiae S288c]	gi 6323682	33 kDa	2	0	0	0	2	0	0	7.88%	0.0	0.0	0.0
1435	No	Pfd1p [Saccharomyces cerevisiae S288c]	gi 330443601	13 kDa	2	0	0	0	2	0	0	22.9%	0.0	0.0	0.0
1436	No	Sec61p [Saccharomyces cerevisiae EC1118]	gi 259148357 (+1)	53 kDa	2	0	0	0	2	0	0	3.96%	0.0	0.0	0.0
1437	No	conserved protein [Saccharomyces cerevisiae YJ	gi 151942398 (+4)	30 kDa	2	0	0	0	2	0	0	10.3%	0.0	0.0	0.0
1438	No	protein ERP1 precursor [Saccharomyces cerevisi	gi 190406652 (+1)	25 kDa	2	0	0	0	2	0	0	9.59%	0.0	0.0	0.0
1439	No	unnamed protein product [Saccharomyces cere	gi 4780	8 kDa	2	0	0	0	2	0	0	33.3%	0.0	0.0	0.0
1440	No	Img2p [Saccharomyces cerevisiae S288c]	gi 10383803 (+1)	16 kDa	2	0	0	0	2	0	0	15.8%	0.0	0.0	0.0
1441	No	invertase [Saccharomyces cerevisiae]	gi 296178357	61 kDa	2	0	0	0	2	0	0	3.95%	0.0	0.0	0.0
1442	No	Mnn2p [Saccharomyces cerevisiae EC1118]	gi 259144859 (+2)	68 kDa	2	0	0	0	2	0	0	3.52%	0.0	0.0	0.0
1443	No	Sdh2p [Saccharomyces cerevisiae S288c]	gi 6322987	30 kDa	2	0	0	0	2	0	0	9.02%	0.0	0.0	0.0
1444	No	Caf16p [Saccharomyces cerevisiae EC1118]	gi 259146162	33 kDa	2	0	0	0	2	0	0	6.92%	0.0	0.0	0.0
1445	No	Yhm2p [Saccharomyces cerevisiae S288c]	gi 6323897	34 kDa	2	0	0	0	2	0	0	9.55%	0.0	0.0	0.0
1446	No	Dcc1p [Saccharomyces cerevisiae S288c]	gi 10383774 (+1)	44 kDa	2	0	0	0	2	0	0	5.26%	0.0	0.0	0.0
1447	No	TAF(II) complex component [Saccharomyces cer	gi 151942781 (+1)	40 kDa	2	0	0	0	2	0	0	6.52%	0.0	0.0	0.0
1448	No	Tvp18p [Saccharomyces cerevisiae S288c]	gi 6323716	19 kDa	1	0	0	0	1	0	0	8.38%	0.0	0.0	0.0
1449	No	thiamin pyrophosphokinase [Saccharomyces ce	gi 151945762 (+2)	37 kDa	1	0	0	0	1	0	0	4.70%	0.0	0.0	0.0
1450	No	conserved protein [Saccharomyces cerevisiae YJ	gi 151946443 (+3)	40 kDa	1	0	0	0	1	0	0	4.19%	0.0	0.0	0.0
1451	No	Tma16p [Saccharomyces cerevisiae EC1118]	gi 259149729 (+1)	21 kDa	1	0	0	0	1	0	0	7.30%	0.0	0.0	0.0
1452	No	YLR017W [Saccharomyces cerevisiae]	gi 51013591 (+2)	38 kDa	1	0	0	0	1	0	0	3.26%	0.0	0.0	0.0
1453	No	conserved protein [Saccharomyces cerevisiae YJ	gi 151942498 (+3)	56 kDa	1	0	0	0	1	0	0	2.19%	0.0	0.0	0.0
1454	No	conserved protein [Saccharomyces cerevisiae YJ	gi 151946633 (+2)	55 kDa	1	0	0	0	1	0	0	3.31%	0.0	0.0	0.0
1455	No	transcriptional regulator [Saccharomyces cerevi	gi 151942071 (+3)	104 kDa	1	0	0	0	1	0	0	1.30%	0.0	0.0	0.0
1456	No	conserved hypothetical protein [Saccharomyces	gi 190408762 (+2)	18 kDa	1	0	0	0	1	0	0	8.02%	0.0	0.0	0.0
1457	No	Emp47p [Saccharomyces cerevisiae S288c]	gi 14318471 (+3)	50 kDa	1	0	0	0	1	0	0	2.70%	0.0	0.0	0.0
1458	No	Ubc4p [Saccharomyces cerevisiae S288c]	gi 6319556	16 kDa	1	0	0	0	1	0	0	7.43%	0.0	0.0	0.0
1459	No	unnamed protein product [Saccharomyces cere	gi 1322953 (+3)	22 kDa	1	0	0	0	1	0	0	7.77%	0.0	0.0	0.0
1460	No	hypothetical protein SCRG_01508 [Saccharomy	gi 190407441 (+4)	85 kDa	1	0	0	0	1	0	0	1.31%	0.0	0.0	0.0
1461	No	isoamyl acetate-hydrolyzing esterase [Saccharo	gi 190407454 (+1)	27 kDa	1	0	0	0	1	0	0	4.20%	0.0	0.0	0.0
1462	No	Chain D, Yeast TfiiaBPDNA COMPLEX	gi 1633310 (+1)	13 kDa	1	0	0	0	1	0	0	8.26%	0.0	0.0	0.0
1463	No	Erg2p [Saccharomyces cerevisiae S288c]	gi 6323858	25 kDa	1	0	0	0	1	0	0	7.66%	0.0	0.0	0.0
1464	No	F(1)F(0)-ATPase complex subunit b [Saccharom	gi 190407875	27 kDa	1	0	0	0	1	0	0	3.69%	0.0	0.0	0.0
1465	No	Ypd1p [Saccharomyces cerevisiae EC1118]	gi 259145789 (+5)	19 kDa	2	0	0	0	2	0	0	15.6%	0.0	0.0	0.0
1466	No	conserved protein [Saccharomyces cerevisiae YJ	gi 151945984 (+3)	39 kDa	1	0	0	0	1	0	0	3.22%	0.0	0.0	0.0
1467	No	RecName: Full=Membrane protein PTM1; Flags:	gi 193806410 (+2)	60 kDa	2	0	0	0	2	0	0	3.44%	0.0	0.0	0.0
1468	No	RNase MRP subunit [Saccharomyces cerevisiae	gi 151944006 (+2)	32 kDa	1	0	0	0	1	0	0	4.78%	0.0	0.0	0.0
1469	No	mitochondrial protein [Saccharomyces cerevisi	gi 151943412 (+2)	32 kDa	1	0	0	0	1	0	0	3.03%	0.0	0.0	0.0
1470	No	Spe2p [Saccharomyces cerevisiae S288c]	gi 6324521	46 kDa	1	0	0	0	1	0	0	2.27%	0.0	0.0	0.0
1471	No	36-kDa vacuolar H+-ATPase membrane sector p	gi 173171 (+1)	40 kDa	1	0	0	0	1	0	0	2.90%	0.0	0.0	0.0

1472	No	YCL047C-like protein [Saccharomyces cerevisiae gi 256270949 (+1)	30 kDa	1	0	0	0	1	0	0	0	3.49%	0.0	0.0	0.0
1473	No	Yop1p [Saccharomyces cerevisiae JAY291]	gi 256271982 (+1)	20 kDa	1	0	0	1	0	0	0	4.42%	0.0	0.0	0.0
1474	No	Lys21p [Saccharomyces cerevisiae S288c]	gi 6320071	49 kDa	1	0	0	1	0	0	0	28.6%	0.0	0.0	0.0
1475	No	amino acid transporter [Saccharomyces cerevisiae gi 151942537 (+3)	68 kDa	1	0	0	0	1	0	0	0	1.64%	0.0	0.0	0.0
1476	No	Vma9p [Saccharomyces cerevisiae S288c]	gi 41629681	8 kDa	1	0	0	1	0	0	0	12.3%	0.0	0.0	0.0
1477	No	glycolipid-anchored surface protein 5 precursor gi 190407313 (+3)	52 kDa	1	0	0	0	1	0	0	0	2.48%	0.0	0.0	0.0
1478	No	NADP-dependent isocitrate dehydrogenase [Sac gi 151941018 (+1)	47 kDa	1	0	0	0	1	0	0	0	8.25%	0.0	0.0	0.0
1479	No	YMR183Cp-like protein [Saccharomyces cerevisiae gi 207342204 (+2)	25 kDa	1	0	0	0	1	0	0	0	4.59%	0.0	0.0	0.0
1480	No	Prs5p [Saccharomyces cerevisiae S288c]	gi 6324511	54 kDa	1	0	0	1	0	0	0	3.63%	0.0	0.0	0.0
1481	No	hypothetical protein YGL039W [Saccharomyces gi 6321399	38 kDa	1	0	0	0	1	0	0	0	4.02%	0.0	0.0	0.0
1482	No	hypothetical protein YCR015C [Saccharomyces gi 10383783	36 kDa	1	0	0	0	1	0	0	0	3.79%	0.0	0.0	0.0
1483	No	RNA exonuclease [Saccharomyces cerevisiae YJ gi 151945554 (+2)	33 kDa	1	0	0	0	1	0	0	0	4.50%	0.0	0.0	0.0
1484	No	SmX4 protein [Saccharomyces cerevisiae]	gi 732947	4 kDa	1	0	0	1	0	0	0	27.3%	0.0	0.0	0.0
1485	No	DNA polymerase alpha-primase complex B subunit gi 190408861 (+2)	79 kDa	1	0	0	0	1	0	0	0	1.70%	0.0	0.0	0.0
1486	No	mediator complex subunit [Saccharomyces cere gi 151942853 (+2)	64 kDa	1	0	0	0	1	0	0	0	2.47%	0.0	0.0	0.0
1487	No	Chain D, Structure Of The Yeast Cytochrome Bc gi 14277715 (+6)	27 kDa	1	0	0	0	1	0	0	0	6.53%	0.0	0.0	0.0
1488	No	YPR086W [Saccharomyces cerevisiae]	gi 51013915	38 kDa	1	0	0	1	0	0	0	3.77%	0.0	0.0	0.0
1489	No	Sss1p [Saccharomyces cerevisiae]	gi 414692 (+1)	9 kDa	1	0	0	1	0	0	0	12.5%	0.0	0.0	0.0
1490	No	rho GTPase [Saccharomyces cerevisiae YJM789] gi 151944360 (+3)	37 kDa	1	0	0	0	1	0	0	0	4.23%	0.0	0.0	0.0
1491	No	Orc3p [Saccharomyces cerevisiae EC1118]	gi 259147986 (+1)	72 kDa	1	0	0	1	0	0	0	1.30%	0.0	0.0	0.0
1492	No	Yap1p binding protein [Saccharomyces cerevisiae gi 151946603 (+3)	78 kDa	2	0	0	0	2	0	0	0	3.71%	0.0	0.0	0.0
1493	No	conserved protein [Saccharomyces cerevisiae YJ gi 151941458 (+2)	31 kDa	1	0	0	0	1	0	0	0	3.00%	0.0	0.0	0.0
1494	No	mitochondrial outer membrane (OM45) [Sacch gi 172066 (+3)	45 kDa	1	0	0	0	1	0	0	0	2.80%	0.0	0.0	0.0
1495	No	oligosaccharyl transferase glycoprotein complex gi 151944706 (+2)	49 kDa	1	0	0	0	1	0	0	0	2.09%	0.0	0.0	0.0
1496	No	hypothetical protein YCR061W [Saccharomyces gi 10383800 (+3)	71 kDa	1	0	0	0	1	0	0	0	2.85%	0.0	0.0	0.0
1497	No	NADP-dependent isocitrate dehydrogenase [Sac gi 151944521 (+2)	48 kDa	1	0	0	0	1	0	0	0	7.38%	0.0	0.0	0.0
1498	No	alpha-isopropylmalate synthase [Saccharomyce gi 190407437 (+1)	67 kDa	1	0	0	0	1	0	0	0	5.13%	0.0	0.0	0.0
1499	No	hypothetical protein YNL035C [Saccharomyces gi 6324293	44 kDa	1	0	0	0	1	0	0	0	4.63%	0.0	0.0	0.0
1500	No	YGR130C-like protein [Saccharomyces cerevisiae gi 256270353 (+2)	93 kDa	1	0	0	0	1	0	0	0	2.33%	0.0	0.0	0.0
1501	No	nuclear pore complex subunit [Saccharomyces gi 151943708 (+2)	39 kDa	1	0	0	0	1	0	0	0	2.29%	0.0	0.0	0.0
1502	No	cell division cycle-related protein [Saccharomyce gi 151946591 (+3)	95 kDa	1	0	0	0	1	0	0	0	1.78%	0.0	0.0	0.0
1503	No	daughter-specific expression-related protein [S gi 151944595 (+2)	121 kDa	1	0	0	0	1	0	0	0	1.43%	0.0	0.0	0.0
1504	No	transcriptional regulator [Saccharomyces cerevi gi 151944877 (+1)	15 kDa	1	0	0	0	1	0	0	0	7.75%	0.0	0.0	0.0
1505	No	Gsy1p [Saccharomyces cerevisiae S288c]	gi 14318537 (+2)	81 kDa	1	0	0	1	0	0	0	1.41%	0.0	0.0	0.0
1506	No	Kcc4p [Saccharomyces cerevisiae EC1118]	gi 259144917	117 kDa	1	0	0	1	0	0	0	0.964%	0.0	0.0	0.0
1507	No	Rib1p [Saccharomyces cerevisiae S288c]	gi 6319438	38 kDa	1	0	0	1	0	0	0	5.22%	0.0	0.0	0.0
1508	No	YDR392Wp-like protein [Saccharomyces cerevis gi 207346346 (+2)	32 kDa	1	0	0	0	1	0	0	0	9.06%	0.0	0.0	0.0
1509	No	Nucleolar, serine-rich protein with a role in pr gi 151941631 (+2)	41 kDa	1	0	0	0	1	0	0	0	2.98%	0.0	0.0	0.0
1510	No	beta-adaptin [Saccharomyces cerevisiae YJM78 gi 151945080 (+4)	81 kDa	1	0	0	0	1	0	0	0	1.57%	0.0	0.0	0.0
1511	No	conserved protein [Saccharomyces cerevisiae YJ gi 151945664	90 kDa	1	0	0	0	1	0	0	0	1.39%	0.0	0.0	0.0
1512	No	Gda1p [Saccharomyces cerevisiae S288c]	gi 6320793	57 kDa	1	0	0	1	0	0	0	1.74%	0.0	0.0	0.0
1513	No	mitochondrial RNase P subunit [Saccharomyces gi 151946075 (+3)	139 kDa	0	0	1	0	0	0	1	0	0.0	0.0	0.915%	0.0
1514	No	RNase [Saccharomyces cerevisiae YJM789]	gi 151945993 (+2)	60 kDa	1	0	0	1	0	0	0	3.50%	0.0	0.0	0.0
1515	No	conserved protein [Saccharomyces cerevisiae YJ gi 151941610 (+2)	39 kDa	1	0	0	0	1	0	0	0	3.69%	0.0	0.0	0.0
1516	No	Ypt6p [Saccharomyces cerevisiae JAY291]	gi 256271753 (+1)	24 kDa	1	0	0	1	0	0	0	10.2%	0.0	0.0	0.0
1517	No	Rrp42p [Saccharomyces cerevisiae S288c]	gi 6320092	29 kDa	1	0	0	1	0	0	0	5.28%	0.0	0.0	0.0
1518	No	carboxypeptidase ysc5 [Saccharomyces cerevisi gi 151944958	65 kDa	1	0	0	0	1	0	0	0	2.26%	0.0	0.0	0.0
1519	No	alpha mannosidase [Saccharomyces cerevisiae gi 151943657 (+3)	125 kDa	1	0	0	0	1	0	0	0	0.923%	0.0	0.0	0.0
1520	No	kre2-related protein [Saccharomyces cerevisiae gi 151946587 (+6)	55 kDa	1	0	0	0	1	0	0	0	2.16%	0.0	0.0	0.0
1521	No	Imp3p [Saccharomyces cerevisiae S288c]	gi 6321942	22 kDa	1	0	0	1	0	0	0	8.20%	0.0	0.0	0.0
1522	No	Dot6p [Saccharomyces cerevisiae S288c]	gi 6320933	73 kDa	1	0	0	1	0	0	0	2.09%	0.0	0.0	0.0
1523	No	unnamed protein product [Saccharomyces cere gi 1321952 (+4)	63 kDa	1	0	0	0	1	0	0	0	2.75%	0.0	0.0	0.0
1524	No	Rfm1p [Saccharomyces cerevisiae S288c]	gi 6324853	35 kDa	0	0	1	0	0	0	1	0.0	0.0	6.45%	0.0
1525	No	cleavage and polyadenylation factor CF I compo gi 151943247 (+2)	33 kDa	1	0	0	0	1	0	0	0	5.08%	0.0	0.0	0.0
1526	No	conserved hypothetical protein [Saccharomyces gi 190407013 (+1)	31 kDa	1	0	0	0	1	0	0	0	5.86%	0.0	0.0	0.0
1527	No	YDR083Wp-like protein [Saccharomyces cerevis gi 207346766 (+4)	35 kDa	1	0	0	0	1	0	0	0	4.71%	0.0	0.0	0.0
1528	No	YBL055C [Saccharomyces cerevisiae]	gi 51012703 (+1)	47 kDa	1	0	0	1	0	0	0	2.87%	0.0	0.0	0.0
1529	No	suppressor of erd2 deletion [Saccharomyces cer gi 151943880 (+4)	116 kDa	1	0	0	0	1	0	0	0	1.11%	0.0	0.0	0.0
1530	No	CBP2 protein [Saccharomyces cerevisiae]	gi 171169 (+1)	74 kDa	1	0	0	1	0	0	0	3.17%	0.0	0.0	0.0

1531	No	La motif-containing protein [Saccharomyces cer gi] 5326	52 kDa	1	0	0	0	1	0	0	0	3.22%	0.0	0.0	0.0
1532	No	succinate dehydrogenase flavoprotein subunit [gi] 190409691 (+3)	70 kDa	1	0	0	0	1	0	0	0	1.72%	0.0	0.0	0.0
1533	No	Mpm1p [Saccharomyces cerevisiae JAY291] gi 256271682 (+1)	28 kDa	1	0	0	0	1	0	0	0	6.75%	0.0	0.0	0.0
1534	No	mitochondrial processing protease beta subunit gi 151941009 (+2)	51 kDa	1	0	0	0	1	0	0	0	2.81%	0.0	0.0	0.0
1535	No	sec17p protein [Saccharomyces cerevisiae] gi 172561	33 kDa	1	0	0	0	1	0	0	0	5.50%	0.0	0.0	0.0
1536	No	RNA splicing factor [Saccharomyces cerevisiae Y gi] 151941965 (+1)	63 kDa	1	0	0	0	1	0	0	0	2.08%	0.0	0.0	0.0
1537	No	Chain A, Mms2UBC13~UBIQUITIN gi 116667301 (+3)	17 kDa	1	0	0	0	1	0	0	0	12.5%	0.0	0.0	0.0
1538	No	suppressor of clathrin deficiency [Saccharomyce gi] 151942904 (+3)	39 kDa	2	0	0	0	1	0	0	0	3.15%	0.0	0.0	0.0
1539	No	tubulin folding cofactor A [Saccharomyces cerev gi] 151945349 (+1)	12 kDa	2	0	0	0	1	0	0	0	12.3%	0.0	0.0	0.0
1540	No	nuclear protein required for efficient mating [Sa gi] 151945523 (+3)	24 kDa	2	0	0	0	1	0	0	0	5.19%	0.0	0.0	0.0
1541	No	tyrosine transporter [Saccharomyces cerevisiae gi] 151946460 (+2)	69 kDa	2	0	0	0	1	0	0	0	1.94%	0.0	0.0	0.0
1542	No	nucleolar complex-associated protein 3 [Saccha gi] 190406043	76 kDa	2	0	0	0	1	0	0	0	1.66%	0.0	0.0	0.0
1543	No	DNA topoisomerase 2 [Saccharomyces cerevisia gi] 190409077	164 kDa	1	0	0	0	1	0	0	0	14.1%	0.0	0.0	0.0
1544	No	YNL022Cp-like protein [Saccharomyces cerevisi gi] 207341631	56 kDa	2	0	0	0	1	0	0	0	1.84%	0.0	0.0	0.0
1545	No	YNL173Cp-like protein [Saccharomyces cerevisi gi] 207341822 (+3)	8 kDa	2	0	0	0	1	0	0	0	15.1%	0.0	0.0	0.0
1546	No	YKL060Cp-like protein [Saccharomyces cerevisi gi] 207343503	24 kDa	2	0	0	0	1	0	0	0	31.8%	0.0	0.0	0.0
1547	No	oligo-1,4 - 1,4-glucantransferase / amylo-1,6- gi] 3986291	175 kDa	2	0	0	0	1	0	0	0	0.716%	0.0	0.0	0.0
1548	No	Prb1p [Saccharomyces cerevisiae S288c] gi 6320775	70 kDa	2	0	0	0	1	0	0	0	2.68%	0.0	0.0	0.0
1549	No	hypothetical protein YPR063C [Saccharomyces c gi] 6325320	15 kDa	2	0	0	0	1	0	0	0	8.57%	0.0	0.0	0.0
1550	No	Spn1p [Saccharomyces cerevisiae S288c] gi 6325390	46 kDa	1	0	0	0	1	0	0	0	3.66%	0.0	0.0	0.0
1551	No	YHR045Wp-like protein [Saccharomyces cerevis gi] 207344720	61 kDa	1	0	0	0	1	0	0	0	1.85%	0.0	0.0	0.0
1552	No	suppressor of mar1-1 [Saccharomyces cerevisiae gi] 151942282 (+4)	118 kDa	0	0	1	0	0	0	1	0	0.0	0.0	1.60%	0.0
1553	No	CRE-binding bZIP protein SKO1 [Saccharomyces gi] 190409151 (+2)	70 kDa	0	0	1	0	0	0	1	0	0.0	0.0	1.70%	0.0
1554	No	Mnp1p [Saccharomyces cerevisiae JAY291] gi 256269709 (+1)	21 kDa	0	0	1	0	0	0	1	0	0.0	0.0	5.67%	0.0
1555	No	hypothetical protein SCRG_05458 [Saccharomyce gi] 190406490 (+2)	58 kDa	0	1	0	0	0	1	0	0	0.0	1.92%	0.0	0.0
1556	No	Rpl21bp [Saccharomyces cerevisiae S288c] gi 6325178	18 kDa	0	1	0	0	0	1	0	0	0.0	28.7%	0.0	0.0
1557	No	Chain G, Crystal Structure Of Yeast Mitochondri gi] 119389910 (+2)	31 kDa	1	0	0	0	1	0	0	0	4.68%	0.0	0.0	0.0
1558	No	Activator of Fab1p [Saccharomyces cerevisiae Y. gi] 151940907 (+3)	100 kDa	1	0	0	0	1	0	0	0	1.14%	0.0	0.0	0.0
1559	No	Vps20 associated protein [Saccharomyces cerev gi] 151941025 (+4)	37 kDa	1	0	0	0	1	0	0	0	3.94%	0.0	0.0	0.0
1560	No	ribosome assembly [Saccharomyces cerevisiae Y gi] 151941061 (+2)	25 kDa	1	0	0	0	1	0	0	0	5.91%	0.0	0.0	0.0
1561	No	Kynureninase [Saccharomyces cerevisiae YJM78 gi] 151941070 (+2)	51 kDa	1	0	0	0	1	0	0	0	2.87%	0.0	0.0	0.0
1562	No	oxysterol-binding family protein [Saccharomyce gi] 151941548 (+2)	52 kDa	1	0	0	0	1	0	0	0	6.92%	0.0	0.0	0.0
1563	No	conserved protein [Saccharomyces cerevisiae YJ gi] 151942052 (+2)	17 kDa	1	0	0	0	1	0	0	0	7.38%	0.0	0.0	0.0
1564	No	conserved protein [Saccharomyces cerevisiae YJ gi] 151942239 (+1)	31 kDa	1	0	0	0	1	0	0	0	5.88%	0.0	0.0	0.0
1565	No	mitochondrial homologous DNA recombination gi] 151942268 (+1)	27 kDa	1	0	0	0	1	0	0	0	6.19%	0.0	0.0	0.0
1566	No	U3 snoRNP protein [Saccharomyces cerevisiae Y gi] 151942372 (+3)	72 kDa	1	0	0	0	1	0	0	0	1.40%	0.0	0.0	0.0
1567	No	geranylgeranyltransferase type II beta subunit [gi] 151942947 (+4)	37 kDa	1	0	0	0	1	0	0	0	4.00%	0.0	0.0	0.0
1568	No	activation of smt3p involved protein [Saccharon gi] 151942950 (+2)	39 kDa	1	0	0	0	1	0	0	0	4.61%	0.0	0.0	0.0
1569	No	ER vesicle protein [Saccharomyces cerevisiae YJ gi] 151943556 (+2)	35 kDa	1	0	0	0	1	0	0	0	3.87%	0.0	0.0	0.0
1570	No	protein of the mitochondrial intermembrane sp gi] 151943946 (+2)	10 kDa	1	0	0	0	1	0	0	0	11.8%	0.0	0.0	0.0
1571	No	22.6 kDa proteasome subunit [Saccharomyces c gi] 151944720 (+1)	23 kDa	1	0	0	0	1	0	0	0	7.07%	0.0	0.0	0.0
1572	No	cytochrome C oxidase [Saccharomyces cerevisia gi] 151944859 (+3)	55 kDa	1	0	0	0	1	0	0	0	2.26%	0.0	0.0	0.0
1573	No	large ap-1 accessory protein [Saccharomyces ce gi] 151944929 (+4)	230 kDa	1	0	0	0	1	0	0	0	0.546%	0.0	0.0	0.0
1574	No	histone acetyltransferase SAGA complex membi gi] 151945488 (+4)	68 kDa	1	0	0	0	1	0	0	0	3.81%	0.0	0.0	0.0
1575	No	sphingoid long chain base (LCB) kinase [Sacchar gi] 151945788 (+3)	70 kDa	1	0	0	0	1	0	0	0	1.76%	0.0	0.0	0.0
1576	No	aldehyde dehydrogenase [Saccharomyces cerev gi] 151945871 (+4)	55 kDa	1	0	0	0	1	0	0	0	2.57%	0.0	0.0	0.0
1577	No	mitochondrial targeting protein [Saccharomyces gi] 151946102 (+1)	45 kDa	1	0	0	0	1	0	0	0	2.81%	0.0	0.0	0.0
1578	No	vesicle coat component [Saccharomyces cerevis gi] 151946149 (+1)	24 kDa	1	0	0	0	1	0	0	0	4.27%	0.0	0.0	0.0
1579	No	hexose transporter [Saccharomyces cerevisiae Y gi] 151946171 (+1)	60 kDa	1	0	0	0	1	0	0	0	2.59%	0.0	0.0	0.0
1580	No	conserved protein [Saccharomyces cerevisiae YJ gi] 151946444 (+2)	39 kDa	1	0	0	0	1	0	0	0	5.52%	0.0	0.0	0.0
1581	No	P-body associated protein [Saccharomyces cere gi] 151946488 (+3)	86 kDa	1	0	0	0	1	0	0	0	1.33%	0.0	0.0	0.0
1582	No	hexose transporter 3 [Saccharomyces cerevisiae gi] 158668214 (+4)	63 kDa	1	0	0	0	1	0	0	0	2.12%	0.0	0.0	0.0
1583	No	RecName: Full=ATP-dependent RNA helicase DE gi] 160380607 (+3)	68 kDa	1	0	0	0	1	0	0	0	8.75%	0.0	0.0	0.0
1584	No	CDC8 gene [Saccharomyces cerevisiae] gi 171204 (+3)	25 kDa	1	0	0	0	1	0	0	0	4.17%	0.0	0.0	0.0
1585	No	RecName: Full=Fe-S cluster assembly protein Df gi] 171704587 (+2)	38 kDa	1	0	0	0	1	0	0	0	2.59%	0.0	0.0	0.0
1586	No	growth regulation protein [Saccharomyces cere gi] 173189 (+1)	55 kDa	1	0	0	0	1	0	0	0	2.67%	0.0	0.0	0.0
1587	No	RecName: Full=Cap-associated protein CAF20; A gi] 187470653 (+3)	18 kDa	1	0	0	0	1	0	0	0	8.70%	0.0	0.0	0.0
1588	No	valine transporter [Saccharomyces cerevisiae Rf gi] 190404983 (+2)	67 kDa	1	0	0	0	1	0	0	0	1.99%	0.0	0.0	0.0
1589	No	conserved hypothetical protein [Saccharomyces gi] 190405392 (+2)	58 kDa	1	0	0	0	1	0	0	0	2.55%	0.0	0.0	0.0

1590	No	glutathione transferase [Saccharomyces cerevis gi 190406186 (+2)	27 kDa	1	0	0	0	1	0	0	0	5.13%	0.0	0.0	0.0
1591	No	conserved hypothetical protein [Saccharomyces gi 190407039 (+5)	43 kDa	1	0	0	0	1	0	0	0	2.62%	0.0	0.0	0.0
1592	No	methylenetetrahydrofolate reductase [Saccharc gi 190407923 (+1)	74 kDa	1	0	0	0	1	0	0	0	2.28%	0.0	0.0	0.0
1593	No	hypothetical protein SCRG_02646 [Saccharomy gi 190408095 (+1)	23 kDa	1	0	0	0	1	0	0	0	9.00%	0.0	0.0	0.0
1594	No	protein SFT2 [Saccharomyces cerevisiae RM11-1-gi 190408920 (+1)	24 kDa	1	0	0	0	1	0	0	0	5.58%	0.0	0.0	0.0
1595	No	hypothetical protein SCRG_03524 [Saccharomy gi 190409357 (+2)	15 kDa	1	0	0	0	1	0	0	0	24.8%	0.0	0.0	0.0
1596	No	YOR042Wp-like protein [Saccharomyces cerevis gi 207341248 (+3)	47 kDa	1	0	0	0	1	0	0	0	3.89%	0.0	0.0	0.0
1597	No	YOL023Wp-like protein [Saccharomyces cerevis gi 207341331 (+4)	76 kDa	1	0	0	0	1	0	0	0	1.92%	0.0	0.0	0.0
1598	No	YMR243Cp-like protein [Saccharomyces cerevis gi 207342121 (+4)	46 kDa	1	0	0	0	1	0	0	0	4.02%	0.0	0.0	0.0
1599	No	YML094Wp-like protein [Saccharomyces cerevis gi 207342582 (+2)	14 kDa	1	0	0	0	1	0	0	0	8.00%	0.0	0.0	0.0
1600	No	YER016Wp-like protein [Saccharomyces cerevis gi 207346026 (+1)	39 kDa	1	0	0	0	1	0	0	0	4.91%	0.0	0.0	0.0
1601	No	YBR283Cp-like protein [Saccharomyces cerevis gi 207347456 (+2)	47 kDa	1	0	0	0	1	0	0	0	3.26%	0.0	0.0	0.0
1602	No	Chain A, Crystal Structure Of The Yeast Inter-Me gi 218766671 (+1)	10 kDa	1	0	0	0	1	0	0	0	15.7%	0.0	0.0	0.0
1603	No	YLR414C-like protein [Saccharomyces cerevisiae gi 256269137 (+3)	29 kDa	1	0	0	0	1	0	0	0	6.84%	0.0	0.0	0.0
1604	No	Rio2p [Saccharomyces cerevisiae JAY291] gi 256270760 (+1)	49 kDa	1	0	0	0	1	0	0	0	2.35%	0.0	0.0	0.0
1605	No	Yos1p [Saccharomyces cerevisiae JAY291] gi 256271437 (+1)	10 kDa	1	0	0	0	1	0	0	0	18.4%	0.0	0.0	0.0
1606	No	Dcp1p [Saccharomyces cerevisiae JAY291] gi 256272082 (+1)	26 kDa	1	0	0	0	1	0	0	0	3.90%	0.0	0.0	0.0
1607	No	Kre6p [Saccharomyces cerevisiae JAY291] gi 256272419 (+1)	80 kDa	1	0	0	0	1	0	0	0	1.81%	0.0	0.0	0.0
1608	No	Lsm6p [Saccharomyces cerevisiae JAY291] gi 256273052 (+2)	9 kDa	1	0	0	0	1	0	0	0	14.0%	0.0	0.0	0.0
1609	No	Rrp15p [Saccharomyces cerevisiae JAY291] gi 256273382	30 kDa	1	0	0	0	1	0	0	0	4.18%	0.0	0.0	0.0
1610	No	Chain C, Cryo-Em Structure Of The Active Yeast gi 270346340 (+1)	9 kDa	1	0	0	0	1	0	0	0	14.9%	0.0	0.0	0.0
1611	No	RecName: Full=Probable GDP-mannose transpo gi 290463236 (+2)	38 kDa	1	0	0	0	1	0	0	0	4.40%	0.0	0.0	0.0
1612	No	Pam16p [Saccharomyces cerevisiae EC1118] gi 290771126 (+1)	16 kDa	1	0	0	0	1	0	0	0	18.1%	0.0	0.0	0.0
1613	No	RecName: Full=Restriction of telomere capping gi 334351042 (+1)	64 kDa	1	0	0	0	1	0	0	0	1.94%	0.0	0.0	0.0
1614	No	TFF1 [Saccharomyces cerevisiae] gi 3417405	68 kDa	1	0	0	0	1	0	0	0	30.3%	0.0	0.0	0.0
1615	No	Chain A, X-Ray Structure Of Ybl001c Northeast S gi 34810941 (+1)	11 kDa	1	0	0	0	1	0	0	0	12.5%	0.0	0.0	0.0
1616	No	glycolipid-anchored surface protein [Saccharom gi 3730 (+1)	60 kDa	1	0	0	0	1	0	0	0	2.68%	0.0	0.0	0.0
1617	No	alcohol dehydrogenase 2 [Saccharomyces pasto gi 37787875	37 kDa	1	0	0	0	1	0	0	0	23.9%	0.0	0.0	0.0
1618	No	Chain A, Crystal Structure Of The Yeast Px-Doan gi 40889191 (+1)	19 kDa	1	0	0	0	1	0	0	0	6.79%	0.0	0.0	0.0
1619	No	YGR043C [Saccharomyces cerevisiae] gi 45269555 (+2)	37 kDa	1	0	0	0	1	0	0	0	6.01%	0.0	0.0	0.0
1620	No	YLR172C [Saccharomyces cerevisiae] gi 45269786 (+1)	34 kDa	1	0	0	0	1	0	0	0	4.33%	0.0	0.0	0.0
1621	No	hypothetical protein [Saccharomyces cerevisiae gi 45720124 (+4)	26 kDa	1	0	0	0	1	0	0	0	11.1%	0.0	0.0	0.0
1622	No	YBR287W [Saccharomyces cerevisiae] gi 51012631 (+1)	48 kDa	1	0	0	0	1	0	0	0	2.11%	0.0	0.0	0.0
1623	No	Pop5p [Saccharomyces cerevisiae S288c] gi 6319286	20 kDa	1	0	0	0	1	0	0	0	7.51%	0.0	0.0	0.0
1624	No	Pin4p [Saccharomyces cerevisiae S288c] gi 6319420	74 kDa	1	0	0	0	1	0	0	0	2.84%	0.0	0.0	0.0
1625	No	Uga2p [Saccharomyces cerevisiae S288c] gi 6319478	54 kDa	1	0	0	0	1	0	0	0	3.82%	0.0	0.0	0.0
1626	No	Sna2p [Saccharomyces cerevisiae S288c] gi 6320734	9 kDa	1	0	0	0	1	0	0	0	19.0%	0.0	0.0	0.0
1627	No	Erg28p [Saccharomyces cerevisiae S288c] gi 6320883	17 kDa	1	0	0	0	1	0	0	0	8.11%	0.0	0.0	0.0
1628	No	Erv14p [Saccharomyces cerevisiae S288c] gi 6321384	16 kDa	1	0	0	0	1	0	0	0	0.000%	0.0	0.0	0.0
1629	No	Get1p [Saccharomyces cerevisiae S288c] gi 6321418	27 kDa	1	0	0	0	1	0	0	0	5.53%	0.0	0.0	0.0
1630	No	Ssp120p [Saccharomyces cerevisiae S288c] gi 6323279	27 kDa	1	0	0	0	1	0	0	0	5.13%	0.0	0.0	0.0
1631	No	Sas2p [Saccharomyces cerevisiae S288c] gi 6323775	39 kDa	1	0	0	0	1	0	0	0	3.55%	0.0	0.0	0.0
1632	No	Taf9p [Saccharomyces cerevisiae S288c] gi 6323892	17 kDa	1	0	0	0	1	0	0	0	12.7%	0.0	0.0	0.0
1633	No	Chain A, Nmr Structural Analysis Of Nop10p Fro gi 83754026	7 kDa	1	0	0	0	1	0	0	0	14.3%	0.0	0.0	0.0
1634	No	ORF YJR83.16 [Saccharomyces cerevisiae] gi 854596	15 kDa	1	0	0	0	1	0	0	0	9.38%	0.0	0.0	0.0
1635	No	conserved hypothetical protein [Saccharomyces gi 190406307 (+3)	39 kDa	1	0	0	0	1	0	0	0	4.46%	0.0	0.0	0.0
1636	No	ribosome export [Saccharomyces cerevisiae YJM gi 151941136 (+3)	93 kDa	1	0	0	0	1	0	0	0	2.51%	0.0	0.0	0.0