30 printed pages

Supplemental Table 1 Zybailov et al, Quantitative Shotgun Proteomics Using a Protease with Broad Specificity and Normalized Spectral Abundance Factors

TM - number of predicted transmembrane domains
Total Unique Peptides - number of unique peptides identifying protein
Total Sequence Coverage - percent of the sequence covered
Total Spectrum Count - total number of MS/MS spectra identifying protein from all three experiments
YPD SpC- the total number of MS/MS spectra identifying a protein in 14N YPD media
Min SpC- the total number of MS/MS spectra identifying a protein in 15N MIN media
YPD NSAF- the normalized spectrum abundance factor of protein found in 14N-YPD media
MIN NSAF- the normalized spectrum abundance factor of protein found in 15N-minimal media
ttest - p-value of the Student t-Test, null hypothesis being that there was no change in expression between 14N-YPD and 15N-minimal growth conditions

					Combined Datasets							Experiment A							Experiment B							Experiment C							
LocusID	Y_Name	Description	TM	L	Total Unique Peptides	Total Sequence Coverage	Total Spectrum Count	YPD SpC	YPD NSAF	MIN SpC	MIN NSAF	Total Unique Peptides	Total Sequence Coverage	Total Spectrum Count	YPD SpC	YPD NSAF	MIN SpC	MIN NSAF	Total Unique Peptides	Total Sequence Coverage	Total Spectrum Count	YPD SpC	YPD NSAF	MIN SpC	MIN NSAF	Total Unique Peptides	Total Sequence Coverage	Total Spectrum Count	YPD SpC	YPD NSAF	MIN SpC	MIN NSAF	ttest
gi|6319258	YAL060W	NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during fermentation and allows using 2,3-butanediol as a carbon source during aerobic growth; Bdh1p	0	382	7	17.3	15	0	3.19E-05	15	0.0009	4	11.5	5	0	2.91E-05	5	0.000849	3	9.2	5	0	3.01E-05	5	0.00086	2	7.1	5	0	3.77E-05	5	0.001004	4.31E-06
gi|6322381	YJL080C	Essential RNA-binding G protein effector of mating response pathway, predominantly associated with nuclear envelope and ER, interacts in mRNA-dependent manner with translating ribosomes via multiple KH domains, similar to vertebrate vigilins; Scp160p	0	1222	9	6.1	13	13	0.000269	0	9.07E-06	4	3.4	5	5	0.000282	0	8.56E-06	4	4	5	5	0.000292	0	8.68E-06	2	2.5	3	3	0.000224	0	1.01E-05	4.52E-06
gi|6324857	YOR283W	hypothetical protein; Yor283wp	0	230	4	8.3	12	0	5.29E-05	12	0.001205	2	8.3	4	0	4.83E-05	4	0.001138	2	8.3	4	0	5E-05	4	0.001153	1	8.3	4	0	6.25E-05	4	0.001345	5.63E-06
gi|6322765	YKL085W	Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p	0	334	5	12	18	18	0.001348	0	3.32E-05	4	12	8	8	0.001629	0	3.13E-05	2	6.3	5	5	0.001068	0	3.17E-05	3	6.3	5	5	0.001335	0	3.71E-05	1.02E-05
gi|6322852	YKL001C	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine metabolism; Met14p	0	202	8	19.8	27	0	6.03E-05	27	0.003018	4	12.4	8	0	5.5E-05	8	0.002539	4	13.9	12	0	5.7E-05	12	0.003832	3	7.4	7	0	7.12E-05	7	0.002635	1.48E-05
gi|6323333	YLR303W	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis; Met17p	0	444	31	26.6	58	0	2.74E-05	58	0.002921	12	19.4	20	0	2.5E-05	20	0.002852	18	15.8	28	0	2.59E-05	28	0.004036	6	11.9	10	0	3.24E-05	10	0.001701	6.45E-05
gi|6319610	YBR133C	Protein arginine N-methyltransferase that exhibits septin and Hsl1p-dependent bud neck localization and periodic Hsl1p-dependent phosphorylation; required along with Hsl1p for bud neck recruitment, phosphorylation, and degradation of Swe1p; Hsl7p	0	827	4	5.9	10	0	1.47E-05	10	0.000281	1	3.5	4	0	1.34E-05	4	0.000316	3	5.9	4	0	1.39E-05	4	0.000321	1	2.2	2	0	1.74E-05	2	0.000195	9.25E-05
gi|6320893	YER052C	Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p	0	527	28	6.3	124	18	0.000855	106	0.00448	10	3.8	41	6	0.00078	35	0.00419	11	3.8	40	7	0.000939	33	0.004004	11	5.7	43	5	0.000846	38	0.005379	9.84E-05
gi|6319500	YBR026C	2-enoyl thioester reductase, member of the medium chain dehydrogenase/reductase family; localized to in mitochondria, where it has a probable role in fatty acid synthesis; Etr1p	0	380	4	12.1	9	9	0.000609	0	2.92E-05	3	7.9	4	4	0.00073	0	2.75E-05	2	7.9	2	2	0.000394	0	2.79E-05	2	7.9	3	3	0.000719	0	3.26E-05	0.00014
gi|6322922	YKR069W	S-adenosyl-L-methionine uroporphyrinogen III transmethylase, involved in sulfate assimilation, methionine metabolism, and siroheme biosynthesis; Met1p	0	593	3	5.6	7	0	2.05E-05	7	0.00028	1	2.4	2	0	1.87E-05	2	0.000229	2	5.6	2	0	1.94E-05	2	0.000232	2	3.2	3	0	2.43E-05	3	0.000397	0.000195
gi|6319439	YBL032W	RNA binding protein with similarity to hnRNP-K that localizes to the cytoplasm and to subtelomeric DNA; required for the proper localization of ASH1 mRNA; involved in the regulation of telomere position effect and telomere length; Hek2p	0	381	2	7.9	4	4	0.000288	0	2.91E-05	1	4.2	2	2	0.000379	0	2.75E-05	1	3.7	1	1	0.000211	0	2.78E-05	1	4.2	1	1	0.000264	0	3.25E-05	0.000227
gi|6323089	YLR060W	Beta subunit of cytoplasmic phenylalanyl-tRNA synthetase, forms a tetramer with Frs2p to generate the active enzyme; evolutionarily distant from mitochondrial phenylalanyl-tRNA synthetase based on protein sequence, but substrate binding is similar; Frs1p	0	595	5	10.6	16	16	0.000675	0	1.86E-05	2	5.2	4	4	0.000467	0	1.76E-05	4	7.7	9	9	0.001064	0	1.78E-05	2	5.7	3	3	0.000459	0	2.08E-05	0.000248
gi|6319367	YBL101C	Non-essential protein of unknown function; promoter contains several Gcn4p binding elements; Ecm21p	0	1117	7	4.1	13	0	1.09E-05	13	0.000268	2	3.7	3	0	9.94E-06	3	0.000178	6	4.1	7	0	1.03E-05	7	0.000408	2	2.4	3	0	1.29E-05	3	0.000211	0.000302
gi|6321796	YHR008C	Manganese-containing superoxide dismutase; protects cells against oxygen toxicity; Sod2p	0	233	8	9	15	15	0.001619	0	4.76E-05	4	9	7	7	0.002049	0	4.49E-05	3	4.7	6	6	0.001828	0	4.55E-05	1	3.9	2	2	0.000803	0	5.31E-05	0.000342
gi|6321407	YGL031C	Ribosomal protein L30 of the large (60S) ribosomal subunit, nearly identical to Rpl24Bp and has similarity to rat L24 ribosomal protein; not essential for translation but may be required for normal translation rate; Rpl24ap	0	155	3	16.8	4	0	7.85E-05	4	0.000644	1	6.5	2	0	7.16E-05	2	0.000878	1	6.5	1	0	7.43E-05	1	0.000479	1	10.3	1	0	9.28E-05	1	0.000559	0.000496
gi|6323315	YLR285W	Putative nicotinamide N-methyltransferase, has a role in rDNA silencing and in lifespan determination; Nnt1p	0	261	1	6.5	5	0	4.66E-05	5	0.000467	1	6.5	2	0	4.25E-05	2	0.000521	1	6.5	1	0	4.41E-05	1	0.000284	1	6.5	2	0	5.51E-05	2	0.000617	0.00081
gi|6319771	YBR294W	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates; Sul1p	9	859	5	1.3	25	0	1.42E-05	25	0.000658	2	1.3	4	0	1.29E-05	4	0.000305	2	1.3	6	0	1.34E-05	6	0.000457	1	1.3	15	0	1.67E-05	15	0.001311	0.001139
gi|6321369	YGL068W	Protein associated with the mitochondrial nucleoid; putative mitochondrial ribosomal protein with similarity to E. coli L7/L12 ribosomal protein; required for normal respiratory growth; Mnp1p	0	194	1	9.8	9	9	0.001192	0	5.71E-05	1	9.8	5	5	0.001774	0	5.39E-05	1	9.8	3	3	0.001127	0	5.47E-05	1	9.8	1	1	0.000519	0	6.38E-05	0.001379
gi|6320410	YDR204W	Protein with a role in ubiquinone (Coenzyme Q) biosynthesis, possibly functioning in stabilization of Coq7p; located on the matrix face of the mitochondrial inner membrane; component of a mitochondrial ubiquinone-synthesizing complex; Coq4p	0	335	3	10.1	4	4	0.000327	0	3.31E-05	1	6	1	1	0.000232	0	3.12E-05	1	6.6	1	1	0.00024	0	3.17E-05	1	3.6	2	2	0.000558	0	3.69E-05	0.001526
gi|6325147	YPL110C	Glycerophosphocholine (GroPCho) phosphodiesterase; hydrolyzes GroPCho to choline and glycerolphosphate after its uptake by Git1p permease, for use as a phosphate source and as a precursor for phosphocholine synthesis; Gde1p	0	1223	2	1	4	0	9.95E-06	4	8.16E-05	1	0.8	1	0	9.08E-06	1	5.99E-05	1	0.8	1	0	9.41E-06	1	6.07E-05	1	1	2	0	1.18E-05	2	0.000132	0.001655

gi|6320027 YDL174C	D-lactate dehydrogenase, oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane; Dld1p	0	587	4	10.4	4	0	2.07E-05	4	0.00017	1	2.7	1	0	1.89E-05	1	0.000125	1	2.6	1	0	1.96E-05	1	0.000126	2	5.1	2	0	2.45E-05	2	0.000274	0.001655
gi|6320190 YDL014W	Nucleolar protein, component of the small subunit processome complex, which is required for processing of pre-18S rRNA; has similarity to mammalian fibrillarin; Nop1p	0	327	45	30	171	113	0.00845	58	0.003966	26	29.1	66	44	0.008998	22	0.004257	22	24.2	62	43	0.009116	19	0.003729	18	19.6	43	26	0.006907	17	0.003899	0.001692
gi|6323244 YLR215C	Protein involved in nutritional control of the cell cycle; regulates abundance of the translation initiation factor eIF2; ortholog of human D123 protein; Cdc123p	0	360	8	11.1	15	0	3.38E-05	15	0.000954	5	11.1	10	0	3.08E-05	10	0.001773	2	7.5	2	0	3.2E-05	2	0.000383	2	7.5	3	0	4E-05	3	0.000653	0.002427
gi|6322116 YIL074C	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p; Ser33p	0	469	9	9.4	30	0	2.6E-05	30	0.001442	5	8.3	10	0	2.37E-05	10	0.001361	6	9.4	18	0	2.45E-05	18	0.002464	2	8.5	2	0	3.07E-05	2	0.000343	0.003318
gi|6322225 YIR034C	Sa pine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of sa pine to L-lysine, which is the final step in the lysine biosynthesis pathway; Lys1p	0	373	27	32.2	70	1	9.79E-05	69	0.004131	20	28.7	39	1	0.000208	38	0.006425	11	16.9	18	0	3.09E-05	18	0.003099	6	11.8	13	0	3.86E-05	13	0.002622	0.003516
gi|6322946 YKR093W	Integral membrane peptide transporter, mediates transport of di- and tri-peptides; conserved protein that contains 12 transmembrane domains; PTR2 expression is regulated by the N-end rule pathway via repression by Cup9p; Ptr2p	11	601	8	18.8	17	17	0.000709	0	1.84E-05	2	6	2	2	0.00024	0	1.74E-05	2	4.7	4	4	0.000479	0	1.76E-05	5	10	11	11	0.001604	0	2.06E-05	0.003554
gi|6324180 YNL149C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum (ER) and YFP-fusion protein to the nuclear envelope-ER network; null mutants have a cell separation defect; Pga2p	1	129	2	20.9	6	6	0.001227	0	8.59E-05	1	20.9	1	1	0.000603	0	8.11E-05	2	20.9	4	4	0.00223	0	8.22E-05	1	20.2	1	1	0.000781	0	9.6E-05	0.00363
gi|1038375 YCL050C	Diadenosine 5',5''-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; has similarity to Apa2p; Apa1p	0	321	9	26.5	41	3	0.000265	38	0.002659	6	26.5	10	1	0.000242	9	0.001793	3	15.9	9	1	0.000251	8	0.001619	5	16.5	22	1	0.000314	21	0.004897	0.003689
gi|6324548 YOL025W	Protein involved in determination of longevity; LAG2 gene is preferentially expressed in young cells; overexpression extends the mean and maximum life span of cells; Lag2p	0	660	2	3.9	9	0	1.84E-05	9	0.000319	1	2.3	4	0	1.68E-05	4	0.000396	1	3.9	1	0	1.74E-05	1	0.000112	1	2.3	4	0	2.18E-05	4	0.000469	0.004148
gi|6320913 YER069W	Protein that is processed in the mitochondrion to yield acetylglutamate kinase and N-acetyl-gamma-glutamyl-phosphate reductase, which catalyze the 2nd and 3rd steps in arginine biosynthesis; enzymes form a complex with Arg2p; Arg5,6p	0	863	1	1.2	8	0	1.41E-05	8	0.000218	1	1.2	5	0	1.29E-05	5	0.000376	1	1.2	1	0	1.33E-05	1	8.6E-05	1	1.2	2	0	1.67E-05	2	0.000186	0.004171
gi|6323288 YLR259C	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p	0	572	33	30.8	78	66	0.00283	12	0.000484	18	21.3	30	24	0.002815	6	0.000677	10	17.5	18	15	0.001831	3	0.000352	9	11.9	30	27	0.004099	3	0.000411	0.004206
gi|6324006 YNL323W	Membrane protein of the plasma membrane and ER, involved in translocation of phospholipids and alkylphosphocholine drugs across the plasma membrane; Lem3p	2	414	6	3.9	7	0	2.94E-05	7	0.000402	1	3.9	1	0	2.68E-05	1	0.000177	2	3.9	2	0	2.78E-05	2	0.000333	3	3.9	4	0	3.47E-05	4	0.000747	0.004293
gi|6321694 YGR255C	Putative flavin-dependent monooxygenase, involved in ubiquinone (Coenzyme Q) biosynthesis; located on the matrix side of the mitochondrial inner membrane; Coq6p	0	479	3	10.6	5	5	0.00028	0	2.31E-05	1	5	1	1	0.000162	0	2.18E-05	1	3.1	1	1	0.000168	0	2.21E-05	1	2.5	3	3	0.000571	0	2.58E-05	0.004681
gi|6325004 YPL252C	Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur proteins; involved in heme A biosynthesis; homologous to human adrenodoxin; Yah1p	0	172	4	15.1	11	11	0.001628	0	6.44E-05	2	15.1	7	7	0.002776	0	6.08E-05	1	15.1	1	1	0.000468	0	6.16E-05	2	14.5	3	3	0.001589	0	7.2E-05	0.004854
gi|6322676 YKL172W	Essential protein required for the maturation of 25S rRNA and 60S ribosomal subunit assembly, localizes to the nucleolus; constituent of 66S pre-ribosomal particles; Ebp2p	0	427	4	5.4	7	7	0.000428	0	2.6E-05	3	5.4	5	5	0.000806	0	2.45E-05	1	4.7	1	1	0.000189	0	2.48E-05	1	4.7	1	1	0.000236	0	2.9E-05	0.005044
gi|6324916 YOR340C	RNA polymerase I subunit A43; Rpa43p	0	326	5	9.2	7	7	0.00056	0	3.4E-05	3	6.4	5	5	0.001056	0	3.21E-05	1	3.4	1	1	0.000247	0	3.25E-05	1	2.8	1	1	0.000309	0	3.8E-05	0.005044
gi|6322083 YIL108W	Putative metalloprotease; Yil108wp	0	696	5	5.7	6	0	1.75E-05	6	0.000207	1	2.7	1	0	1.6E-05	1	0.000105	3	3	4	0	1.65E-05	4	0.000381	1	2.3	1	0	2.07E-05	1	0.000124	0.005253
gi|6324951 YOR375C	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from Gdh3p; expression regulated by nitrogen and carbon sources; Gdh1p	0	454	3	6.2	33	0	2.68E-05	33	0.001636	1	6.2	3	0	2.45E-05	3	0.000438	2	6.2	5	0	2.53E-05	5	0.000724	2	5.3	25	0	3.17E-05	25	0.004117	0.005638
gi|1431853 YFR009W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn20p	0	752	15	8.5	50	9	0.000308	41	0.001223	8	8.5	17	3	0.000281	14	0.001183	7	6.4	18	2	0.000199	16	0.001368	6	4.5	15	4	0.000478	11	0.001103	0.005972
gi|6323763 YMR116C	WD repeat protein (G-beta like protein) involved in translation regulation; required for repression of Gcn4p activity in the absence of amino-acid starvation; core component of the ribosome; ortholog of mammalian RACK1; Asc1p	0	319	3	5	9	0	3.82E-05	9	0.00066	1	5	1	0	3.48E-05	1	0.00023	2	5	6	0	3.61E-05	6	0.00123	1	5	2	0	4.51E-05	2	0.000504	0.006042
gi|6324981 YPL274W	High-affinity S-adenosylmethionine permease, required for utilization of S-adenosylmethionine as a sulfur source; has similarity to S-methylmethionine permease Mmp1p; Sam3p	11	587	3	3.9	10	0	2.07E-05	10	0.000397	1	3.6	2	0	1.89E-05	2	0.000232	3	3.9	7	0	1.96E-05	7	0.000777	1	3.6	1	0	2.45E-05	1	0.000148	0.006103
gi|6323335 YLR304C	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p	0	778	51	26.9	135	106	0.003332	29	0.000841	16	15.9	32	22	0.001898	10	0.000821	20	20.8	53	43	0.003831	10	0.000831	23	20.1	50	41	0.004567	9	0.000875	0.007591
gi|6323118 YLR089C	Putative alanine transaminase (glutamic pyruvic transaminase); Alt1p	0	592	17	11.3	52	51	0.002118	1	5.62E-05	10	8.3	18	18	0.002044	0	1.77E-05	4	7.9	8	8	0.000953	0	1.79E-05	12	11.3	26	25	0.003669	1	0.000146	0.007734
gi|9755335 YKL157W	Zinc-dependent metallopeptidase yscII, may have a role in obtaining leucine from dipeptide substrates; sequence coordinates have changed since RT-PCR analysis showed that the adjacent ORF YKL158W comprises the 5' exon of APE2/YKL157W; Ape2p	0	935	5	5.3	6	6	0.000169	0	1.19E-05	1	1.3	1	1	8.31E-05	0	1.12E-05	1	1.4	1	1	8.62E-05	0	1.13E-05	3	4	4	4	0.000385	0	1.32E-05	0.008277
gi|6319391 YBL080C	Protein required for mitochondrial translation; mutation is functionally complemented by a Bacillus subtilis ortholog; Pet112p	0	541	4	6.5	6	6	0.000292	0	2.05E-05	1	3.1	1	1	0.000144	0	1.93E-05	1	3.3	1	1	0.000149	0	1.96E-05	2	2.6	4	4	0.000665	0	2.29E-05	0.008277
gi|6322892 YKR039W	General amino acid permease; localization to the plasma membrane is regulated by nitrogen source; Gap1p	12	602	8	11	12	0	2.02E-05	12	0.00046	1	3	2	0	1.84E-05	2	0.000226	6	10.8	9	0	1.91E-05	9	0.000969	1	2.8	1	0	2.39E-05	1	0.000144	0.00917

gi|6322115 YIL075C	Subunit of the 26S proteasome, substrate of the N-acetyltransferase Nat1p; Rpn2p	0	945	6	2.1	11	0	1.29E-05	11	0.00027	1	2	1	0	1.17E-05	1	7.75E-05	1	2.1	2	0	1.22E-05	2	0.000146	4	1.9	8	0	1.52E-05	8	0.000642	0.01284
gi|6319456 YBL015W	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth; Ach1p	0	526	15	9.5	41	33	0.00155	8	0.000358	5	8.6	9	6	0.000781	3	0.000378	6	5.1	16	13	0.001729	3	0.000383	6	4.2	16	14	0.002325	2	0.000306	0.013091
gi|6320003 YDL198C	Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein; Ggc1p	0	300	6	9.3	19	1	0.000122	18	0.001367	3	9.3	6	0	3.7E-05	6	0.001291	2	4.7	5	1	0.000269	4	0.000884	3	4.7	8	0	4.8E-05	8	0.002022	0.01322
gi|6322066 YIL125W	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA; Kgd1p	0	1014	13	9.5	35	34	0.000828	1	3.28E-05	3	2	8	8	0.000537	0	1.03E-05	12	9.5	24	23	0.001578	1	7.32E-05	2	3.5	3	3	0.00027	0	1.22E-05	0.014157
gi|1038376 YCL030C	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; catalyzes the second, third, ninth and tenth steps in histidine biosynthesis; His4p	0	799	10	11.8	36	1	4.57E-05	35	0.000985	8	11.5	23	1	9.73E-05	22	0.001742	4	4.5	10	0	1.44E-05	10	0.00081	1	2.4	3	0	1.8E-05	3	0.000294	0.015082
gi|6324639 YOR065W	Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex; Cyt1p	0	309	6	7.4	18	5	0.000433	13	0.000969	2	7.4	6	2	0.000467	4	0.000847	3	7.4	8	2	0.000484	6	0.00127	3	7.4	4	1	0.000326	3	0.000761	0.01616
gi|6320377 YDR172W	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype; Sup35p	0	685	41	21.5	186	50	0.001795	136	0.004418	17	15.6	66	24	0.00235	42	0.003865	26	21.5	76	17	0.001731	59	0.005495	16	13.9	44	9	0.001155	35	0.003813	0.016293
gi|1431855 YFR028C	Protein phosphatase required for mitotic exit; located in the nucleolus until liberated by the FEAR and Mitotic Exit Network in anaphase, enabling it to act on key substrates to effect a decrease in CDK/B-cyclin activity and mitotic exit; Cdc14p	0	551	4	3.3	21	19	0.000862	2	0.000101	3	3.3	8	7	0.000867	1	0.000133	2	3.3	6	5	0.000648	1	0.000135	2	3.3	7	7	0.001123	0	2.25E-05	0.016372
gi|6323512 YML123C	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to arsenate; exit from the ER during maturation requires Pho86p; Pho84p	9	587	7	7.7	14	13	0.00056	1	5.66E-05	3	4.9	4	4	0.000473	0	1.78E-05	3	7.5	5	5	0.000608	0	1.81E-05	3	4.6	5	4	0.000613	1	0.000148	0.017974
gi|6322097 YIL094C	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p	0	371	40	36.1	109	23	0.001542	86	0.005169	15	28.3	40	7	0.001287	33	0.005614	14	16.4	25	6	0.001148	19	0.003287	21	24.8	44	10	0.002365	34	0.00684	0.018878
gi|6323505 YML130C	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum; Ero1p	0	563	19	7.6	62	40	0.001751	22	0.000886	14	7.6	27	17	0.002031	10	0.001134	9	5.2	20	14	0.001738	6	0.000697	7	5.2	15	9	0.001405	6	0.000813	0.019007
gi|6320568 YDR361C	Essential protein involved in nuclear export of Mss4p, which is a lipid kinase that generates phosphatidylinositol 4,5-biphosphate and plays a role in actin cytoskeleton organization and vesicular transport; Bcp1p	0	283	4	14.5	11	1	0.000129	10	0.000823	2	6.7	4	1	0.000275	3	0.000703	1	6.7	3	0	4.07E-05	3	0.000712	2	7.8	4	0	5.08E-05	4	0.001093	0.020972
gi|6322070 YIL121W	Multidrug transporter required for resistance to quinidine, barban, cisplatin, and bleomycin; member of the major facilitator superfamily of transporters conferring multiple drug resistance (MFS-MDR); Qdr2p	12	542	15	14.2	39	2	0.000112	37	0.001534	4	8.3	5	1	0.000143	4	0.000483	10	9	20	1	0.000149	19	0.00225	5	8.1	14	0	2.65E-05	14	0.001941	0.02174
gi|6320071 YDL131W	Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p; Lys21p	0	440	19	24.8	49	3	0.000194	46	0.002343	8	19.8	18	0	2.52E-05	18	0.002593	11	15.9	19	3	0.000497	16	0.002338	7	11.8	12	0	3.27E-05	12	0.002054	0.022756
gi|1038377 YCL018W	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine biosynthesis pathway; Leu2p	0	364	9	25	28	1	0.0001	27	0.001675	6	18.4	16	0	3.05E-05	16	0.002789	2	9.3	3	0	3.16E-05	3	0.000553	6	12.4	9	1	0.000277	8	0.001666	0.024676
gi|6324513 YOL059W	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria; Gpd2p	0	440	28	19.1	161	33	0.001853	128	0.006474	16	19.1	64	14	0.002145	50	0.00716	14	14.3	71	14	0.002223	57	0.008266	10	11.4	26	5	0.001014	21	0.003573	0.025867
gi|1431850 YFL018C	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme complexes; Lpd1p	0	499	7	7.8	12	11	0.000561	1	6.66E-05	1	3	3	3	0.000423	0	2.1E-05	3	6.4	3	3	0.000438	0	2.12E-05	4	6.2	6	5	0.000894	1	0.000174	0.026343
gi|6323269 YLR240W	Phosphatidylinositol 3-kinase responsible for the synthesis of phosphatidylinositol 3-phosphate; forms membrane-associated signal transduction complex with Vps15p to regulate protein sorting; similar to p110 subunit of mammalian PI 3-kinase; Vps34p	0	875	3	4.3	11	3	9.74E-05	8	0.000215	2	1.9	3	1	8.88E-05	2	0.000155	2	4.3	5	1	9.21E-05	4	0.000303	2	1.9	3	1	0.000115	2	0.000184	0.026673
gi|6319558 YBR084W	Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mis1p	0	975	23	14.2	63	52	0.001311	11	0.000261	13	12.9	20	14	0.000968	6	0.000397	13	11.6	21	20	0.001428	1	7.61E-05	10	8.4	22	18	0.001608	4	0.000317	0.028201
gi|6320019 YDL182W	Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p; Lys20p	0	428	15	32.2	39	3	0.000199	36	0.001891	7	22.4	12	0	2.59E-05	12	0.001785	8	18.2	18	3	0.000511	15	0.002254	4	9.3	9	0	3.36E-05	9	0.001591	0.02915
gi|6325018 YPL237W	Beta subunit of the translation initiation factor eIF2, involved in the identification of the start codon; proposed to be involved in mRNA binding; Sui3p	0	285	4	7	13	1	0.000128	12	0.000972	1	3.2	4	0	3.9E-05	4	0.000918	2	3.5	3	0	4.04E-05	3	0.000707	3	6.7	6	1	0.000353	5	0.001346	0.031097
gi|6325276 YPR019W	Essential helicase component of heterohexameric MCM2-7 complexes which bind pre-replication complexes on DNA and melt the DNA prior to replication; accumulates in the nucleus in G1; homolog of S. pombe Cdc21p; Cdc54p	0	933	5	7.9	10	9	0.000248	1	3.56E-05	2	4.1	4	4	0.000298	0	1.12E-05	2	4.6	2	2	0.00016	0	1.14E-05	3	3.9	4	3	0.000293	1	9.29E-05	0.032148
gi|6322592 YJR132W	Karyopherin, a carrier protein involved in nuclear import of proteins; importin beta homolog; Nmd5p	0	1048	5	4.6	7	6	0.000151	1	3.17E-05	2	4.6	3	2	0.000138	1	6.99E-05	1	3.4	2	2	0.000143	0	1.01E-05	2	3	2	2	0.000178	0	1.18E-05	0.032293

gi|6321265 YGL173C	Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance; Kem1p	0	1528	17	9	37	12	0.000199	25	0.00037	8	6.9	12	3	0.000138	9	0.000377	7	4.8	15	6	0.000279	9	0.000382	8	6.7	10	3	0.000179	7	0.000348	0.033047
gi|6323903 YMR246W	Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in the presence of ethanol, functions to incorporate palmitic acid into phospholipids and neutral lipids; Faa4p	0	694	19	10.4	45	33	0.001175	12	0.000399	12	10.4	22	16	0.001552	6	0.000558	9	10.4	15	12	0.001211	3	0.00029	4	5.5	8	5	0.000643	3	0.000339	0.034907
gi|6324617 YOR043W	Protein required, with binding partner Psr1p, for full activation of the general stress response, possibly through Msn2p dephosphorylation; regulates growth during the diauxic shift; negative regulator of G1 cyclin expression; Whi2p	0	486	3	6.2	8	1	7.51E-05	7	0.000342	1	3.1	2	0	2.28E-05	2	0.00028	2	6.2	4	1	0.000166	3	0.000415	1	3.1	2	0	2.96E-05	2	0.000331	0.037025
gi|4162967 YBR041W	Fatty acid transporter and very long-chain fatty acyl-CoA synthetase, may form a complex with Faa1p or Faa4p that imports and activates exogenous fatty acids; Fat1p	2	669	5	8.1	8	7	0.000273	1	4.97E-05	4	8.1	4	3	0.000315	1	0.00011	1	4.2	3	3	0.000327	0	1.58E-05	1	1.8	1	1	0.000151	0	1.85E-05	0.037057
gi|6319594 YBR118W	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef2p	0	458	359	60.3	2265	819	0.043559	1446	0.070016	181	51.5	707	288	0.041917	419	0.05747	177	45.4	734	270	0.040733	464	0.064475	166	49.8	824	261	0.049219	563	0.091322	0.037235
gi|6321331 YGL107C	Mitochondrial protein required for sporulation; Rmd9p	0	646	6	10.4	19	18	0.000697	1	5.15E-05	3	5	6	5	0.000533	1	0.000113	4	8.4	12	12	0.001301	0	1.64E-05	1	2	1	1	0.000156	0	1.92E-05	0.037678
gi|6322119 YIL070C	Acidic protein of the mitochondrial matrix involved in oxidative phosphorylation; related to the human complement receptor gC1q-R; Mam33p	0	266	3	7.9	14	12	0.001144	2	0.000208	2	7.9	5	4	0.001044	1	0.000275	3	7.9	7	6	0.001601	1	0.000279	1	7.9	2	2	0.000703	0	4.65E-05	0.03935
gi|6323861 YMR205C	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p	0	959	15	14.9	33	29	0.000749	4	0.000104	8	7.9	17	14	0.000984	3	0.000207	7	9.9	11	10	0.000732	1	7.74E-05	4	4.6	5	5	0.000465	0	1.29E-05	0.042945
gi|1553018 YFR024C-	Protein containing a C-terminal SH3 domain; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization; Lsb3p	0	451	4	12.2	13	1	8.1E-05	12	0.000614	1	7.3	2	0	2.46E-05	2	0.000302	1	7.3	7	0	2.55E-05	7	0.001011	3	4.9	4	1	0.000223	3	0.000521	0.044138
gi|6320706 YDR498C	Membrane glycoprotein v-SNARE involved in retrograde transport from the Golgi to the ER; required for N- and O-glycosylation in the Golgi but not in the ER; forms a complex with the cytosolic Tip20p; Sec20p	0	383	6	6.3	10	9	0.000604	1	8.68E-05	4	6.3	7	6	0.001073	1	0.000191	1	6.3	2	2	0.000391	0	2.77E-05	1	4.4	1	1	0.000263	0	3.23E-05	0.044951
gi|6323566 YML074C	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p; Fpr3p	0	411	36	37.7	125	80	0.004768	45	0.002454	19	30.7	32	21	0.003431	11	0.001706	22	22.4	49	31	0.005236	18	0.002812	17	31.1	44	28	0.005915	16	0.002921	0.047727
gi|6321823 YHR034C	Protein of unresolved function; may function in protein folding and/or rRNA processing, interacts with a chaperone (Hsp82p), two chromatin remodeling factors (Rvb1p, Rvb2p) and two rRNA processing factors (Rrp43p, Nop58p); Pih1p	0	344	4	16	8	1	0.000106	7	0.000483	3	11.3	4	1	0.000226	3	0.000578	2	11.6	3	0	3.35E-05	3	0.000586	1	4.7	1	0	4.18E-05	1	0.000252	0.048406
gi|6319676 YBR199W	Putative mannosyltransferase involved in protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr4p	1	464	4	9.7	8	1	7.87E-05	7	0.000358	3	9.7	4	1	0.000168	3	0.000429	3	9.7	3	0	2.48E-05	3	0.000434	1	3.7	1	0	3.1E-05	1	0.000187	0.048406
gi|6323460 YLR429W	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p	0	651	81	36.1	223	160	0.006002	63	0.002162	48	29.8	104	63	0.006464	41	0.003971	32	24.3	74	63	0.0067	11	0.001091	23	17.2	45	34	0.00453	11	0.001274	0.049094
gi|6325343 YPR086W	Transcription factor TFIIB, a general transcription factor required for transcription initiation and start site selection by RNA polymerase II; Sua7p	0	345	2	4.6	14	2	0.000176	12	0.000803	2	4.6	7	1	0.000225	6	0.001122	2	4.6	5	1	0.000234	4	0.000768	1	4.6	2	0	4.17E-05	2	0.000466	0.049321
gi|6325291 YPR034W	Actin-related protein involved in transcriptional regulation; subunit of the chromatin remodeling Snf/Swi complex; Arp7p	0	477	7	9.6	12	10	0.000536	2	0.000116	3	3.6	5	3	0.000442	2	0.000285	2	3.8	4	4	0.000603	0	2.22E-05	3	5.7	3	3	0.000573	0	2.59E-05	0.051941
gi|6321984 YHR190W	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway; Erg9p	1	444	24	23.4	52	38	0.002111	14	0.000724	14	23.4	25	15	0.002276	10	0.001438	7	11.5	13	11	0.001737	2	0.00031	6	10.8	14	12	0.002365	2	0.000362	0.05289
gi|6319529 YBR055C	Splicing factor, component of the U4/U6-U5 snRNP complex; Prp6p	0	899	5	6.2	8	1	4.06E-05	7	0.000185	2	1.1	2	1	8.65E-05	1	8.15E-05	2	3.2	3	0	1.28E-05	3	0.000224	2	3	3	0	1.6E-05	3	0.000262	0.057232
gi|6321782 YHL004W	Mitochondrial ribosomal protein of the small subunit; Mrp4p	0	394	4	8.9	12	10	0.000649	2	0.000141	2	3.8	3	2	0.000366	1	0.000186	2	3.8	4	3	0.000555	1	0.000188	3	8.9	5	5	0.001132	0	3.14E-05	0.05885
gi|1431850 YFL016C	Protein involved in folding of mitochondrially synthesized proteins in the mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the DnaJ family of molecular chaperones; Mdj1p	0	511	8	12.7	20	17	0.000834	3	0.000152	4	11.9	6	3	0.000413	3	0.000389	4	12.5	8	8	0.001104	0	2.07E-05	3	10.4	6	6	0.001042	0	2.42E-05	0.060872
gi|6320764 YEL071W	D-lactate dehydrogenase, part of the retrograde regulon which consists of genes whose expression is stimulated by damage to mitochondria and reduced in cells grown with glutamate as the sole nitrogen source, located in the cytoplasm; Dld3p	0	496	5	9.9	23	3	0.000172	20	0.000916	2	2	8	1	0.000157	7	0.000907	3	7.7	7	0	2.32E-05	7	0.000919	3	4.2	8	2	0.000377	6	0.000923	0.062367
gi|6322823 YKL029C	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids; Mae1p	0	669	12	19.9	23	19	0.00071	4	0.000149	3	8.7	6	5	0.000515	1	0.00011	6	13	11	8	0.000843	3	0.000301	5	12	6	6	0.000796	0	1.85E-05	0.063649
gi|6320969 YER122C	ADP-ribosylation factor GTPase activating protein (ARF GAP), involved in ER-Golgi transport; shares functional similarity with Gcs1p; Glo3p	0	493	6	7.9	16	2	0.000123	14	0.000652	3	7.9	6	0	2.25E-05	6	0.000785	2	7.9	4	2	0.000303	2	0.00028	1	2.6	6	0	2.92E-05	6	0.000929	0.063765
gi|6325030 YPL226W	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation, susceptibility to [PSI+] prion induction and aggregation of a fragment of the human Machado-Joseph Disease protein; New1p	0	1196	12	9.3	33	6	0.000132	27	0.00051	4	4.1	7	2	0.000121	5	0.000271	5	6.1	7	2	0.000125	5	0.000275	4	3.3	19	2	0.000156	17	0.001066	0.063877
gi|6323703 YMR058W	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases; Fet3p	1	636	52	27.7	164	29	0.001129	135	0.004723	16	24.8	27	4	0.000436	23	0.002287	29	25.8	82	9	0.000995	73	0.007319	24	9.1	55	16	0.002194	39	0.004574	0.064006
gi|6321014 YER166W	Non-essential P-type ATPase that is a potential aminophospholipid translocase, localizes to the plasma membrane and late exocytic or early endocytic membranes, likely involved in protein transport; Dnf1p	9	1571	12	5.3	27	7	0.000116	20	0.000289	4	4.3	7	1	4.95E-05	6	0.000246	5	4.3	10	3	0.000139	7	0.00029	8	5.2	10	3	0.000174	7	0.000339	0.065507

gi|6323182	YLR153C	Acetyl-coA synthetase isoform, required for growth on glucose; expressed under anaerobic conditions; Acs2p	0	683	19	21.1	28	4	0.00016	24	0.000795	4	5.9	4	1	0.000114	3	0.000291	12	15.5	17	1	0.000118	16	0.001506	4	5.7	7	2	0.000274	5	0.000562	0.065631
gi|6324353	YNR026C	Guanine nucleotide exchange factor (GEF); glycosylated integral membrane protein of the endoplasmic reticulum, important for the initiation of transport vesicle budding from the endoplasmic reticulum through activation of the GTPase Sar1p; Sec12p	1	471	3	5.9	7	6	0.000336	1	7.06E-05	1	2.5	1	1	0.000165	0	2.22E-05	1	3.4	3	3	0.000464	0	2.25E-05	2	3.4	3	2	0.000397	1	0.000184	0.066587
gi|3736269	YOL096C	O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone (Coenzyme Q) biosynthesis; component of a mitochondrial ubiquinone-synthesizing complex; Coq3p	0	312	6	13.5	15	12	0.000975	3	0.000249	3	9	5	4	0.00089	1	0.000235	3	13.1	6	4	0.000922	2	0.000442	2	4.2	4	4	0.001153	0	3.97E-05	0.067031
gi|6324637	YOR063W	Protein component of the large (60S) ribosomal subunit, has similarity to E. coli L3 and rat L3 ribosomal proteins; involved in the replication and maintenance of killer double stranded RNA virus; Rpl3p	0	387	6	12.9	11	9	0.000598	2	0.000143	3	6.5	5	4	0.000717	1	0.000189	1	3.4	2	2	0.000387	0	2.74E-05	3	6.5	4	3	0.000706	1	0.000224	0.072153
gi|6323928	YMR272C	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth; Scs7p	3	384	12	6.2	24	21	0.001363	3	0.000202	8	3.1	14	12	0.002111	2	0.000354	2	3.1	3	2	0.00039	1	0.000193	3	6	7	7	0.001611	0	3.22E-05	0.074728
gi|6321425	YGL013C	Zinc cluster protein that is a master regulator involved in recruiting other zinc cluster proteins to pleiotropic drug response elements (PDREs) to fine tune the regulation of multidrug resistance genes; Pdr1p	0	1068	3	3.2	10	8	0.000194	2	5.19E-05	3	3.2	6	4	0.00026	2	0.000127	1	1.5	2	2	0.00014	0	9.93E-06	1	1.5	2	2	0.000175	0	1.16E-05	0.07477
gi|6320897	YER056C	Purine-cytosine permease, mediates purine (adenine, guanine, and hypoxanthine) and cytosine accumulation; Fcy2p	12	533	4	8.6	18	1	6.85E-05	17	0.000728	1	3	1	0	2.08E-05	1	0.000137	3	8.6	4	1	0.000151	3	0.000378	2	5.1	13	0	2.7E-05	13	0.001835	0.07477
gi|6323294	YLR264W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp and has similarity to rat S28 ribosomal protein; Rps28bp	0	67	6	22.4	18	13	0.004905	5	0.00182	3	22.4	10	8	0.008121	2	0.002031	3	22.4	5	3	0.003264	2	0.002057	3	20.9	3	2	0.002791	1	0.001293	0.075879
gi|6324709	YOR136W	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p	0	369	19	21.7	61	44	0.002936	17	0.001051	12	21.7	23	13	0.002377	10	0.00173	9	14.4	15	10	0.001903	5	0.000891	9	12.5	23	21	0.004951	2	0.000436	0.076269
gi|6323593	YML048W	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression; Gsf2p	1	403	14	15.6	48	35	0.002144	13	0.000743	6	12.4	24	15	0.002507	9	0.001428	5	6	16	13	0.002256	3	0.0005	4	2.7	8	7	0.001535	1	0.000215	0.076859
gi|6319931	YCR088W	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p	0	592	45	46.5	108	62	0.00257	46	0.001741	20	36.5	36	22	0.002495	14	0.001503	21	34	46	25	0.002936	21	0.002275	17	36.7	26	15	0.002211	11	0.001401	0.077659
gi|6320204	YDR001C	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses; may be phosphorylated by Cdc28p; Nth1p	0	751	4	2.3	11	2	8.1E-05	9	0.00028	1	2.3	4	0	1.48E-05	4	0.000348	2	2.3	5	2	0.000199	3	0.000268	2	2.3	2	0	1.92E-05	2	0.000214	0.079998
gi|6321657	YGR218W	Major karyopherin, involved in export of proteins, RNAs, and ribosomal subunits from the nucleus; Crm1p	0	1084	9	6.3	22	17	0.000393	5	0.000112	5	4.2	10	9	0.000563	1	6.76E-05	4	2.7	7	6	0.000393	1	6.85E-05	3	2.4	5	2	0.000173	3	0.000217	0.080703
gi|6321863	YHR072W	Lanosterol synthase, an essential enzyme that catalyzes the cyclization of squalene 2,3-epoxide, a step in ergosterol biosynthesis; Erg7p	0	731	4	3.8	9	7	0.00025	2	7.58E-05	4	3.8	5	3	0.000289	2	0.000186	1	2.1	2	2	0.000205	0	1.45E-05	1	2.1	2	2	0.000256	0	1.69E-05	0.080818
gi|6320980	YER133W	Catalytic subunit of type 1 serine/threonine protein phosphatase, involved in many processes including glycogen metabolism, sporulation, and mitosis; interacts with multiple regulatory subunits; predominantly isolated with Sds22p; Glc7p	0	312	9	20.2	19	6	0.000507	13	0.000959	3	11.9	5	2	0.000463	3	0.000637	4	9.9	8	3	0.000701	5	0.001054	5	16	6	1	0.000323	5	0.00123	0.082864
gi|6320614	YDR406W	ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element; Pdr15p	12	1529	17	9.5	42	26	0.000422	16	0.000239	4	3.5	11	6	0.000269	5	0.000212	8	6.1	18	11	0.000504	7	0.000298	9	4.8	13	9	0.000517	4	0.000202	0.08311
gi|6322289	YJL172W	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions; Cps1p	1	576	39	21.9	149	28	0.001205	121	0.004676	11	12	21	7	0.000829	14	0.001544	15	15.1	71	17	0.002058	54	0.005983	23	21.2	57	4	0.000624	53	0.006855	0.084487
gi|6324750	YOR176W	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic pathway; Yfh1p mediates the use of iron by Hem15p; Hem15p	0	393	11	19.3	30	25	0.00158	5	0.00031	5	8.9	12	11	0.001893	1	0.000186	4	13.7	9	9	0.001611	0	2.7E-05	4	10.2	9	5	0.001135	4	0.000787	0.084525
gi|6322980	YLL048C	Transporter of the ATP-binding cassette (ABC) family involved in bile acid transport; similar to mammalian bile transporters; Ybt1p	14	1661	7	3.1	12	10	0.000154	2	3.34E-05	4	2	7	6	0.000247	1	4.41E-05	3	1.9	4	3	0.000132	1	4.47E-05	1	0.7	1	1	6.06E-05	0	7.45E-06	0.086
gi|6320030	YDL171C	NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamine and alpha-ketoglutarate; with Gln1p, forms the secondary pathway for glutamate biosynthesis from ammonia; expression regulated by nitrogen source; Glt1p	0	2145	11	3.3	22	4	5.11E-05	18	0.000191	4	2.1	8	2	6.73E-05	6	0.000181	3	2.1	3	1	3.76E-05	2	6.43E-05	7	3.2	11	1	4.69E-05	10	0.000352	0.087161
gi|6323482	YLR449W	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p; Fpr4p	0	392	14	27.3	25	21	0.001335	4	0.000254	9	27.3	11	9	0.001558	2	0.000347	5	13.5	9	9	0.001615	0	2.7E-05	3	4.6	5	3	0.000697	2	0.00041	0.091256
gi|6322271	YJL190C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Bp and has similarity to E. coli S8 and rat S15a ribosomal proteins; Rps22ap	0	130	3	12.3	10	2	0.000468	8	0.00145	3	12.3	4	2	0.00111	2	0.001047	1	10.8	4	0	8.85E-05	4	0.002039	1	10.8	2	0	0.000111	2	0.001238	0.092839
gi|6323209	YLR180W	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p	0	382	28	45	62	16	0.001052	46	0.002699	13	40.1	22	4	0.000727	18	0.002986	14	30.4	27	11	0.002019	16	0.002692	7	8.4	13	1	0.000264	12	0.002365	0.093138
gi|6323562	YML078W	Mitochondrial peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; involved in protein refolding after import into mitochondria; Cpr3p	0	182	4	7.7	9	7	0.001003	2	0.000305	2	7.7	3	2	0.000793	1	0.000403	1	7.7	3	3	0.001201	0	5.83E-05	2	5.5	3	2	0.001028	1	0.000476	0.094984

gi|6320327 YDR122W	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; closely related to Kin2p; Kin1p	0	1064	5	3.2	13	10	0.00024	3	7.29E-05	5	3.2	8	5	0.000324	3	0.000187	2	3.2	3	3	0.000206	0	9.97E-06	2	3.2	2	2	0.000176	0	1.16E-05	0.096664
gi|6322154 YIL035C	Alpha catalytic subunit of casein kinase 2, a Ser/Thr protein kinase with roles in cell growth and proliferation; the holoenzyme also contains CKA2, CKB1 and CKB2, the many substrates include transcription factors and all RNA polymerases; Cka1p	0	372	4	14	5	1	9.82E-05	4	0.000268	2	6.7	2	1	0.000209	1	0.000197	1	3.8	1	0	3.09E-05	1	0.0002	1	3.5	2	0	3.87E-05	2	0.000433	0.098886
gi|1431852 YFR004W	Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; couples the deubiquitination and degradation of proteasome substrates; Rpn11p	0	306	8	10.5	18	2	0.000199	16	0.001195	5	5.9	8	2	0.000472	6	0.001265	1	5.2	1	0	3.76E-05	1	0.000243	4	10.5	9	0	4.7E-05	9	0.002225	0.099528
gi|6324009 YNL320W	hypothetical protein; Ynl320wp	1	284	5	12.7	9	7	0.000643	2	0.000195	2	8.1	3	3	0.000743	0	3.69E-05	2	8.1	2	2	0.000527	0	3.73E-05	2	4.6	4	2	0.000658	2	0.000567	0.101936
gi|6321012 YER164W	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; component of both the SAGA and SILK complexes; Chd1p	0	1468	13	5.7	27	19	0.000323	8	0.000128	8	4.8	15	10	0.000461	5	0.000221	5	4.6	5	4	0.000196	1	5.06E-05	4	3	7	5	0.000304	2	0.00011	0.103055
gi|6325382 YPR125W	Mitochondrial inner membrane protein exposed to the mitochondrial matrix, associates with mitochondrial ribosomes, NOT required for respiratory growth; homolog of human Letm1, a protein implicated in Wolf-Hirschhorn syndrome; Ylh47p	1	454	5	14.8	11	9	0.000509	2	0.000122	4	14.8	8	6	0.000905	2	0.0003	1	4.4	2	2	0.00033	0	2.34E-05	1	3.1	1	1	0.000222	0	2.73E-05	0.103063
gi|6321766 YHL021C	The authentic, non-tagged protein was localized to the mitochondria; Fmp12p	0	465	12	7.7	42	34	0.001806	8	0.000405	7	5.2	15	9	0.001313	6	0.000833	6	7.7	20	18	0.002698	2	0.000296	3	4.7	7	7	0.00133	0	2.66E-05	0.104535
gi|6323726 YMR080C	ATP-dependent RNA helicase of the SFI superfamily, required for nonsense mediated mRNA decay and for efficient translation termination at nonsense codons; involved in telomere maintenance; Nam7p	0	971	4	7.1	5	1	3.76E-05	4	0.000103	1	1.8	1	0	1.14E-05	1	7.54E-05	2	3.5	2	1	8.3E-05	1	7.64E-05	2	3.6	2	0	1.48E-05	2	0.000166	0.105269
gi|6324631 YOR057W	Probable cochaperone, regulates activity of Cyr1p (adenylyl cyclase); involved in assembly of the kinetochore complex, associates with the SCF (Skp1p/Cdc53p/F box protein) ubiquitin ligase complex; Sgt1p	0	395	2	4.3	9	2	0.000154	7	0.000421	1	4.3	3	0	2.81E-05	3	0.000503	2	4.3	4	2	0.000379	2	0.000349	1	4.3	2	0	3.64E-05	2	0.000407	0.105348
gi|6322853 YKR001C	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome biogenesis; Vps1p	0	704	32	15.5	66	49	0.001712	17	0.000551	21	14.1	40	30	0.002855	10	0.000907	8	11.1	13	11	0.001095	2	0.000196	9	9.9	13	8	0.001001	5	0.000545	0.108097
gi|6325199 YPL058C	Plasma membrane weak-acid-inducible ATP-binding cassette (ABC) transporter, required for weak organic acid resistance, strongly induced by sorbate and benzoate, regulated by War1p, mutants exhibit sorbate hypersensitivity; Pdr12p	11	1511	6	4.4	18	14	0.000234	4	6.6E-05	1	1	4	4	0.000184	0	6.93E-06	5	4.4	12	8	0.000373	4	0.000175	2	1.9	2	2	0.000124	0	8.19E-06	0.110084
gi|4162968 YML017W	Asn rich cytoplasmic protein that contains RGG motifs; high-copy suppressor of group II intron-splicing defects of a mutation in MRS2 and of a conditional mutation in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing; Psp2p	0	593	5	6.7	22	19	0.000801	3	0.000131	3	6.7	10	9	0.00103	1	0.000124	2	3.4	11	9	0.001067	2	0.000232	1	3.4	1	1	0.00017	0	2.09E-05	0.112236
gi|6319619 YBR143C	Polypeptide release factor involved in translation termination; mutant form acts as a recessive omnipotent suppressor; Sup45p	0	437	8	10.5	11	4	0.000251	7	0.00038	3	6.6	4	1	0.000178	3	0.000455	2	2.7	4	2	0.000342	2	0.000315	3	10.1	3	1	0.00023	2	0.000368	0.112548
gi|6325038 YPL218W	GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles; required for transport vesicle formation during ER to Golgi protein transport; Sar1p	0	190	14	25.8	38	8	0.001089	30	0.003559	11	25.8	21	7	0.002513	14	0.004682	4	7.9	10	1	0.000424	9	0.003069	4	8.4	7	0	7.57E-05	7	0.002801	0.113031
gi|6319546 YBR072W	Small heat shock protein with chaperone activity that is regulated by a heat induced transition from an inactive oligomeric (24-mer) complex to an active dimer; induced by heat, upon entry into stationary phase, and during sporulation; Hsp26p	0	214	4	15.9	8	6	0.000739	2	0.000259	3	7.5	4	2	0.000675	2	0.000636	3	15.9	3	3	0.001022	0	4.95E-05	1	7.5	1	1	0.000471	0	5.78E-05	0.113746
gi|6324780 YOR206W	Protein that forms a nucleolar complex with Mak21p that binds to 90S and 66S pre-ribosomes, as well as a nuclear complex with Noc3p that binds to 66S pre-ribosomes; both complexes mediate intranuclear transport of ribosomal precursors; Noc2p	0	710	6	8.7	10	2	8.57E-05	8	0.000265	3	4.5	4	1	0.000109	3	0.00028	4	6.6	5	1	0.000113	4	0.000373	1	2	1	0	2.03E-05	1	0.000122	0.118375
gi|6324123 YNL206C	Protein with a role in regulation of Ty1 transposition; Rtt106p	0	455	3	7	4	1	8.03E-05	3	0.000171	2	2.9	2	1	0.000171	1	0.000161	1	4.2	1	0	2.53E-05	1	0.000163	1	2.9	1	0	3.16E-05	1	0.00019	0.11846
gi|6322769 YKL081W	Translation elongation factor EF-1 gamma; Tef4p	0	412	83	45.4	228	79	0.004697	149	0.008044	31	35.7	60	26	0.004231	34	0.005207	34	35.2	76	25	0.004218	51	0.007901	44	40.3	92	28	0.005901	64	0.011567	0.120976
gi|6324211 YNL118C	Catalytic subunit of the Dcp1p-Dcp2p decapping enzyme complex, which removes the 5' cap structure from mRNAs prior to their degradation; member of the Nudix hydrolase family; Dcp2p	0	970	3	3.6	11	8	0.000213	3	8E-05	3	3.6	7	4	0.000286	3	0.000205	1	1.4	2	2	0.000154	0	1.09E-05	1	1.4	2	2	0.000193	0	1.28E-05	0.121756
gi|6324902 YOR326W	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo; reversibly phosphorylated in vivo; Myo2p	0	1574	22	7.6	53	40	0.000626	13	0.00019	15	6.4	33	26	0.001108	7	0.000286	7	6.1	13	10	0.000446	3	0.000128	4	1.5	7	4	0.000228	3	0.000149	0.124004
gi|6320189 YDL015C	Enoyl reductase that catalyzes the last step in each cycle of very long chain fatty acid elongation, localizes to the ER, highly enriched in a structure marking nuclear-vacuolar junctions, coimmunoprecipitates with elongases Fen1p and Sur4p; Tsc13p	4	310	4	8.4	24	21	0.001688	3	0.00025	2	3.5	14	12	0.002615	2	0.000439	3	8.4	8	8	0.001819	0	3.42E-05	2	3.5	2	1	0.000325	1	0.00028	0.124563
gi|6320143 YDL060W	Protein required for processing of 20S pre-rRNA in the cytoplasm, associates with pre-40S ribosomal particles; Tsr1p	0	788	4	5.8	11	2	7.72E-05	9	0.000267	3	5.8	4	2	0.000183	2	0.000173	2	5.8	6	0	1.46E-05	6	0.000498	1	1.4	1	0	1.83E-05	1	0.00011	0.13033
gi|1312917 YJL062W-	Putative protein of unknown function, identified based on comparison to related yeast species; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; Yjl062w-ap	0	85	6	28.2	13	4	0.001289	9	0.002478	4	28.2	5	1	0.000914	4	0.003078	2	27.1	3	1	0.000948	2	0.001622	2	27.1	5	2	0.0022	3	0.002767	0.131341
gi|6324357 YNR030W	Alpha-1,6-mannosyltransferase localized to the ER; responsible for the addition of the alpha-1,6 mannose to dolichol-linked Man7GlcNAc2, acts in the dolichol pathway for N-glycosylation; Alg12p	9	551	3	5.4	12	9	0.00042	3	0.000141	2	3.1	6	4	0.000504	2	0.000247	1	3.1	3	3	0.000397	0	1.92E-05	2	5.4	3	2	0.000339	1	0.000157	0.131545

gi|6322067 YIL124W	NADPH-dependent 1-acyl dihydroxyacetone phosphate reductase found in lipid particles and ER; involved in phosphatidic acid biosynthesis and required for spore germination; capable of metabolizing mammalian steroid hormones; Ayr1p	0	297	4	9.1	10	7	0.000615	3	0.000261	2	4.4	6	3	0.00071	3	0.00067	2	9.1	2	2	0.000504	0	3.57E-05	1	4.4	2	2	0.00063	0	4.17E-05	0.132217
gi|6320801 YEL034W	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Anb1p; undergoes an essential hypusination modification; expressed under aerobic conditions; Hyp2p	0	157	9	26.8	18	5	0.000853	13	0.001906	4	20.4	6	2	0.000919	4	0.001667	5	26.1	8	1	0.000513	7	0.002904	2	14	4	2	0.001191	2	0.001025	0.136614
gi|6325209 YPL048W	Translational cofactor elongation factor-1 gamma, participates in the regulation of GTP-binding protein EF-1 alpha, may play a redundant role in the regulation of protein synthesis or another GTP-dependent process; Cam1p	0	415	29	28	70	17	0.001027	53	0.002858	8	15.9	17	3	0.000508	14	0.002144	8	16.9	14	2	0.000361	12	0.001865	15	17.8	39	12	0.00253	27	0.004862	0.13698
gi|6321880 YHR088W	Nucleolar protein involved in the assembly of the large ribosomal subunit; constituent of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA; Rpf1p	0	295	8	12.2	14	2	0.000206	12	0.000939	3	12.2	4	0	3.76E-05	4	0.000887	4	12.2	8	1	0.000273	7	0.001546	2	6.4	2	1	0.000341	1	0.000294	0.137777
gi|6321563 YGR124W	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine from L-aspartate in the asparagine biosynthetic pathway; Asn2p	0	572	11	12.2	21	4	0.000192	17	0.000678	5	5.9	7	2	0.000252	5	0.000567	2	4.9	4	0	2.01E-05	4	0.000463	7	11.5	10	2	0.000327	8	0.00106	0.138135
gi|6323356 YLR324W	Peroxisomal integral membrane protein, involved in negative regulation of peroxisome number; partially functionally redundant with Pex31p; genetic interactions suggest action at a step downstream of steps mediated by Pex28p and Pex29p; Pex30p	1	523	6	8.2	8	6	0.000303	2	0.000106	1	4	2	2	0.000276	0	2E-05	3	8.2	3	3	0.000418	0	2.03E-05	2	4	3	1	0.000193	2	0.000308	0.138722
gi|6324098 YNL231C	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p; Pdr16p	0	351	12	16.8	26	21	0.001491	5	0.000347	6	16.2	10	8	0.00155	2	0.000388	3	10.3	3	3	0.000623	0	3.02E-05	4	7.4	13	10	0.0025	3	0.00067	0.13973
gi|6323445 YLR413W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; Ylr413wp	3	675	10	7.4	30	20	0.000739	10	0.000345	3	1.8	9	8	0.000806	1	0.000109	6	7.4	15	8	0.000835	7	0.000675	3	1.8	6	4	0.000533	2	0.000238	0.140347
gi|6322180 YIL010W	Nuclear thiol peroxidase which functions as an alkyl-hydroperoxide reductase during post-diauxic growth; Dot5p	0	215	5	9.8	13	3	0.000396	10	0.001083	1	9.8	2	0	5.16E-05	2	0.000633	4	9.8	9	3	0.001017	6	0.001825	1	9.8	2	0	6.69E-05	2	0.000748	0.142886
gi|6319378 YBL092W	Protein component of the large (60S) ribosomal subunit, has similarity to rat L32 ribosomal protein; overexpression disrupts telomeric silencing; Rpl32p	0	130	4	17.7	7	5	0.00103	2	0.000426	2	10	3	2	0.00111	1	0.000564	2	16.2	2	1	0.00062	1	0.000571	1	10	2	2	0.001439	0	9.52E-05	0.146865
gi|6319481 YBR009C	One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity; Hhf1p	0	103	8	12.6	18	5	0.0013	13	0.002906	3	12.6	6	0	0.000108	6	0.00376	4	12.6	9	5	0.003464	4	0.002574	1	12.6	3	0	0.00014	3	0.002283	0.147848
gi|6324151 YNL178W	Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic (AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat S3 ribosomal proteins; Rps3p	0	240	21	15.8	63	34	0.003499	29	0.002725	11	11.7	25	13	0.003655	12	0.003183	9	15.8	21	13	0.003788	8	0.002165	7	9.6	17	8	0.002937	9	0.002837	0.154334
gi|6324208 YNL121C	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p	0	617	18	15.7	89	61	0.002427	28	0.001024	12	15.6	43	33	0.003581	10	0.001035	6	8.3	15	11	0.00125	4	0.00043	11	8.3	31	17	0.002401	14	0.001705	0.155878
gi|6325331 YPR074C	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p	0	680	9	12.2	22	8	0.000304	14	0.000473	4	5.7	8	2	0.000212	6	0.000569	4	9.6	8	3	0.000322	5	0.000483	4	5	6	3	0.000402	3	0.000346	0.156067
gi|6321632 YGR193C	Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p	0	410	9	8	19	14	0.000861	5	0.000297	4	8	5	3	0.000515	2	0.000332	4	7.6	8	5	0.00087	3	0.000491	4	7.6	6	6	0.001298	0	3.02E-05	0.156159
gi|6323074 YLR045C	Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates microtubule dynamics during spindle orientation and metaphase chromosome alignment; interacts with spindle pole body component Spc72p; Stu2p	0	888	6	4.1	9	6	0.000178	3	8.74E-05	2	2.6	2	1	8.75E-05	1	8.25E-05	3	2.6	3	2	0.000168	1	8.36E-05	3	3.9	4	3	0.000308	1	9.76E-05	0.158042
gi|6324049 YNL280C	C-14 sterol reductase, acts in ergosterol biosynthesis; mutants accumulate the abnormal sterol ignosterol (ergosta-8,14 dienol), and are viable under anaerobic growth conditions but inviable on rich medium under aerobic conditions; Erg24p	8	438	5	9.6	15	12	0.000695	3	0.000177	4	9.1	9	7	0.00109	2	0.000311	2	5.5	2	1	0.000184	1	0.000169	2	4.1	4	4	0.000821	0	2.83E-05	0.158725
gi|6323387 YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p	0	395	54	31.9	188	117	0.007242	71	0.004013	26	23	71	35	0.005931	36	0.00575	19	20.3	48	27	0.004749	21	0.003409	25	30.1	69	55	0.012055	14	0.002664	0.15891
gi|6321827 YHR038W	Mitochondrial ribosome recycling factor, essential for mitochondrial protein synthesis and for the maintenance of the respiratory function of mitochondria; Rrf1p	0	230	4	15.7	7	5	0.000582	2	0.000241	1	7.4	3	3	0.000917	0	4.55E-05	3	15.7	3	1	0.00035	2	0.000599	1	7.4	1	1	0.000438	0	5.38E-05	0.159774
gi|6319728 YBR251W	Mitochondrial ribosomal protein of the small subunit; Mrps5p	0	307	9	16	33	24	0.001943	9	0.000686	5	16	7	6	0.001338	1	0.000239	6	16	21	15	0.003411	6	0.001278	3	9.8	5	3	0.00089	2	0.000524	0.160476
gi|6323259 YLR229C	Small rho-like GTPase, essential for establishment and maintenance of cell polarity; mutants have defects in the organization of actin and septins; Cdc42p	0	191	10	17.8	39	29	0.00376	10	0.001219	8	17.8	19	11	0.003895	8	0.002685	3	11	12	12	0.004399	0	5.55E-05	3	11	8	6	0.002787	2	0.000842	0.162317
gi|6320103 YDL100C	ATPase, subunit of the GET complex; required for the retrieval of HDEL proteins from the Golgi to the ER in an ERD2 dependent fashion; involved in resistance to heat and metal stress; Get3p	0	354	5	9.9	17	11	0.000791	6	0.000407	4	4.8	9	6	0.001161	3	0.000562	3	9.9	4	3	0.000618	1	0.00021	2	4	4	2	0.000528	2	0.000455	0.164816
gi|6320041 YDL160C	Cytoplasmic DExD/H-box helicase, stimulates mRNA decapping, coordinates distinct steps in mRNA function and decay, interacts with both the decapping and deadenylase complexes, may have a role in mRNA export and translation; Dhh1p	0	506	4	3.8	27	22	0.001083	5	0.000241	3	3.8	15	13	0.001734	2	0.000269	3	3.8	10	8	0.001114	2	0.000272	2	3.8	2	1	0.000199	1	0.000171	0.167578

gi|6323923 YMR267W	Mitochondrial inorganic pyrophosphatase, required for mitochondrial function and possibly involved in energy generation from inorganic pyrophosphate; Ppa2p	0	310	2	5.2	18	11	0.000903	7	0.000536	2	5.2	5	4	0.000895	1	0.000236	2	5.2	7	4	0.000928	3	0.00065	2	5.2	6	3	0.000882	3	0.000759	0.169339
gi|6322876 YKR024C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp7p	0	742	5	2.8	14	8	0.000279	6	0.000194	3	2.8	6	4	0.000374	2	0.000183	2	2.8	4	2	0.000202	2	0.000186	2	2.8	4	2	0.000252	2	0.000217	0.170034
gi|6322682 YKL166C	Subunit of cytoplasmic cAMP-dependent protein kinase, which contains redundant catalytic subunits Tpk1p, Tpk2p, and Tpk3p and regulatory subunit Bcy1p; promotes vegetative growth in response to nutrients; inhibits filamentous growth; Tpk3p	0	398	3	8.5	7	2	0.000153	5	0.000306	2	8.5	4	2	0.000363	2	0.000342	1	4.8	1	0	2.89E-05	1	0.000186	1	3.8	2	0	3.61E-05	2	0.000404	0.170116
gi|6322777 YKL073W	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway; Lhs1p	0	881	13	8.1	24	19	0.000539	5	0.000138	6	4.3	13	11	0.000844	2	0.000154	8	8.1	9	7	0.000562	2	0.000156	2	4.1	2	1	0.000114	1	9.83E-05	0.172749
gi|6320181 YDL022W	NAD-dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high-osmolarity glycerol response pathway; homolog of Gpd2p; Gpd1p	0	391	6	16.1	17	3	0.000218	14	0.000822	3	15.3	10	1	0.000199	9	0.001472	3	7.9	6	2	0.000383	4	0.000678	1	4.9	1	0	3.68E-05	1	0.000222	0.17631
gi|6324844 YOR270C	Subunit of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); Vph1p is located in V-ATPase complexes of the vacuole while Stv1p is located in V-ATPase complexes of the Golgi and endosomes; Vph1p	7	840	8	4.2	18	6	0.000188	12	0.00033	5	1.8	11	6	0.000489	5	0.000386	3	3.8	4	0	1.37E-05	4	0.000316	2	3.5	3	0	1.71E-05	3	0.00028	0.177111
gi|6321471 YGR034W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Ap and has similarity to E. coli L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA; Rpl26bp	0	129	4	20.2	7	5	0.001038	2	0.00043	1	8.5	1	1	0.000603	0	8.11E-05	2	19.4	3	1	0.000625	2	0.001069	2	18.6	3	3	0.002119	0	9.6E-05	0.177197
gi|6319603 YBR127C	Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the cytoplasm; Vma2p	0	517	20	20.9	44	24	0.001154	20	0.000879	7	10.3	14	9	0.001181	5	0.000628	11	16.2	17	9	0.001224	8	0.001005	6	9.5	13	6	0.00103	7	0.00103	0.178101
gi|6322569 YJR109C	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor; Cpa2p	0	1118	14	10.1	51	3	7.62E-05	48	0.000962	3	3.6	9	0	9.93E-06	9	0.000515	2	4.1	2	1	7.21E-05	1	6.64E-05	11	6	40	2	0.000167	38	0.002535	0.178323
gi|6322842 YKL010C	Ubiquitin-protein ligase (E3) that interacts with Rpt4p and Rpt6p, two subunits of the 19S particle of the 26S proteasome; cytoplasmic E3 involved in the degradation of ubiquitin fusion proteins; Ufd4p	0	1483	5	4	9	6	0.000107	3	5.23E-05	1	0.9	3	3	0.000142	0	7.06E-06	3	3.2	5	2	0.000101	3	0.000136	1	1.1	1	1	6.79E-05	0	8.35E-06	0.178621
gi|6320269 YDR064W	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 and rat S13 ribosomal proteins; Rps13p	0	151	6	20.5	15	5	0.000887	10	0.001542	3	20.5	6	1	0.000515	5	0.002149	4	19.9	6	3	0.001448	3	0.001334	2	11.9	3	1	0.000667	2	0.001066	0.180215
gi|6322935 YKR082W	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p; Nup133p	0	1157	11	9.7	22	18	0.000389	4	8.62E-05	6	5.5	9	8	0.00047	1	6.33E-05	3	4.5	9	9	0.000547	0	9.16E-06	3	2.9	4	1	8.7E-05	3	0.000203	0.180347
gi|6320503 YDR297W	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to phytosphingosine in sphingolipid biosyntheis; Sur2p	4	349	8	16	13	9	0.000663	4	0.000286	4	11.7	6	3	0.000604	3	0.00057	3	9.5	3	3	0.000627	0	3.04E-05	3	4.9	4	3	0.000783	1	0.000248	0.182432
gi|6323000 YLL028W	Polyamine transporter that recognizes spermine, putrescine, and spermidine; catalyzes uptake of polyamines at alkaline pH and excretion at acidic pH; phosphorylation enhances activity and sorting to the plasma membrane; Tpo1p	12	586	4	5.8	14	3	0.000145	11	0.000435	2	1.9	3	1	0.000133	2	0.000232	1	3.9	3	0	1.96E-05	3	0.000344	4	5.8	8	2	0.000319	6	0.000782	0.183983
gi|6323135 YLR106C	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm; Mdn1p	0	4910	19	3.5	47	30	0.000151	17	7.9E-05	13	2.7	21	13	0.000179	8	0.000104	5	0.9	9	7	0.000101	2	2.81E-05	8	1.9	17	10	0.000179	7	0.000108	0.185752
gi|6324659 YOR085W	Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is important for N-glycosylation of a subset of proteins; Ost3p	4	350	8	13.7	20	14	0.001009	6	0.000412	3	8.6	6	5	0.000983	1	0.000209	3	13.1	4	4	0.000822	0	3.03E-05	5	8.3	10	5	0.001274	5	0.001096	0.186006
gi|1431847 YFL039C	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p	0	375	70	48.3	241	152	0.0099	89	0.005291	46	42.1	131	80	0.014242	51	0.008568	22	44.5	47	31	0.005739	16	0.002743	28	20.5	63	41	0.009475	22	0.00439	0.18675
gi|6323606 YML035C	AMP deaminase, tetrameric enzyme that catalyzes the deamination of AMP to form IMP and ammonia; may be involved in regulation of intracellular adenine nucleotide pools; Amd1p	0	810	5	3.2	7	5	0.000165	2	6.84E-05	1	3.2	1	1	9.6E-05	0	1.29E-05	2	3.2	3	2	0.000185	1	9.16E-05	3	3	3	2	0.000231	1	0.000107	0.187468
gi|6323553 YML086C	D-Arabinono-1,4-lactone oxidase, catalyzes the final step in biosynthesis of D-erythroascorbic acid, which is protective against oxidative stress; Alo1p	0	526	4	6.7	10	3	0.000162	7	0.000316	4	6.7	6	3	0.000401	3	0.000378	1	2.7	3	0	2.19E-05	3	0.000383	1	2.1	1	0	2.73E-05	1	0.000165	0.191117
gi|6323177 YLR148W	Vacuolar peripheral membrane protein that promotes vesicular docking/fusion reactions in conjunction with SNARE proteins, required for vacuolar biogenesis, forms complex with Pep5p that mediates protein transport to the vacuole; Pep3p	0	918	5	1.7	13	9	0.000252	4	0.000109	3	1.7	6	4	0.000302	2	0.000148	2	1.7	4	2	0.000163	2	0.00015	2	1.7	3	3	0.000298	0	1.35E-05	0.19185
gi|6322323 YJL138C	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif2p	0	395	26	20.8	63	20	0.001263	43	0.002441	17	20.8	29	11	0.001883	18	0.002888	7	11.6	11	3	0.000554	8	0.001315	11	12.9	23	6	0.001348	17	0.003228	0.192953
gi|6323379 YLR347C	Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore complex; Kap95p	0	861	12	5.1	65	39	0.001117	26	0.000682	6	3.4	17	12	0.000941	5	0.000377	3	1.9	27	18	0.001457	9	0.000677	8	3.6	21	9	0.000919	12	0.001049	0.195323
gi|6320205 YDR002W	Ran GTpase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p	0	201	15	53.7	33	7	0.000908	26	0.002923	3	28.4	5	0	5.52E-05	5	0.001614	11	53.7	18	4	0.001431	14	0.004484	5	29.4	10	3	0.00136	7	0.002648	0.196556

gi|6319314 YAL005C	ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p	0	642	44	26.6	196	103	0.003925	93	0.003229	24	20.2	75	35	0.003649	40	0.003929	23	18.4	61	36	0.00389	25	0.002494	18	15.6	60	32	0.004325	28	0.003258	0.196695
gi|6325245 YPL012W	Protein required for export of the ribosomal subunits; associates with the RNA components of the pre-ribosomes; contains HEAT-repeats; Rrp12p	0	1228	6	2.9	10	3	6.94E-05	7	0.000135	2	1.4	3	0	9.04E-06	3	0.000162	4	2.7	6	3	0.000178	3	0.000164	1	1.4	1	0	1.17E-05	1	7.06E-05	0.197601
gi|6323273 YLR244C	Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal methionine from nascent polypeptides; function is partially redundant with that of Map2p; Map1p	0	387	5	12.9	17	4	0.000283	13	0.000773	3	12.9	6	1	0.000201	5	0.000838	1	7.5	6	0	2.97E-05	6	0.001014	3	7.8	5	3	0.000706	2	0.000416	0.198941
gi|6320449 YDR243C	RNA helicase in the DEAD-box family, involved in RNA isomerization at the 5' splice site; Prp28p	0	588	4	6.1	7	2	0.000104	5	0.000207	3	6.1	5	2	0.000245	3	0.000338	1	3.2	1	0	1.96E-05	1	0.000126	1	2.9	1	0	2.45E-05	1	0.000147	0.199633
gi|3736261 YAR042W	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats; localizes to the Golgi and the nucleus-vacuole junction; Swh1p	0	1188	7	5.7	11	3	7.17E-05	8	0.000159	4	4.7	6	1	6.54E-05	5	0.000273	2	1.3	3	1	6.78E-05	2	0.000116	2	2.4	2	1	8.48E-05	1	7.29E-05	0.200299
gi|6325298 YPR041W	Translation initiation factor eIF-5; N-terminal domain functions as a GTPase-activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; Tif5p	0	405	20	24	55	20	0.001232	35	0.001943	8	13.6	22	8	0.001343	14	0.002197	8	17.8	23	8	0.001392	15	0.002382	8	15.3	10	4	0.000888	6	0.001131	0.200576
gi|6322578 YJR118C	Protein of unknown function; may be involved in mitochondrial DNA maintenance; required for slowed DNA synthesis-induced filamentous growth; Ilm1p	2	203	5	33	11	8	0.001019	3	0.000382	2	25.1	4	2	0.000711	2	0.00067	4	33	6	5	0.001758	1	0.000366	1	6.4	1	1	0.000496	0	6.1E-05	0.200953
gi|6320516 YDR310C	Transcriptional repressor required for mitotic repression of middle sporulation-specific genes; involved in telomere maintenance, regulated by the pachytene checkpoint; Sum1p	0	1062	4	6.4	6	4	0.000103	2	5.22E-05	2	3	2	1	7.32E-05	1	6.9E-05	2	3.4	3	2	0.000141	1	6.99E-05	1	2	1	1	9.48E-05	0	1.17E-05	0.202107
gi|6324806 YOR232W	Protein of the mitochondrial matrix involved in protein import into mitochondria; acts as a cochaperone and a nucleotide release factor for Ssc1p; homolog of E. coli GrpE; Mge1p	0	228	8	22.4	15	11	0.001228	4	0.000438	4	16.2	9	6	0.001802	3	0.000872	4	22.4	5	4	0.001262	1	0.000326	1	7.5	1	1	0.000442	0	5.43E-05	0.203064
gi|6322639 YKL210W	Ubiquitin activating enzyme, involved in ubiquitin-mediated protein degradation and essential for viability; Uba1p	0	1024	4	6.8	6	4	0.000107	2	5.41E-05	1	2.1	2	2	0.000141	0	1.02E-05	1	2.1	1	1	7.87E-05	0	1.04E-05	3	4.7	3	1	9.83E-05	2	0.000157	0.205972
gi|1462717 YJL020C	Protein possibly involved in assembly of actin patches; interacts with an actin assembly factor Las17p and with the SH3 domains of Type I myosins Myo3p and Myo5p; localized predominantly to cortical actin patches; Bbc1p	0	1157	15	15	41	30	0.000642	11	0.00022	11	13.5	26	17	0.000988	9	0.000498	7	8	12	10	0.000607	2	0.000119	2	2.7	3	3	0.000236	0	1.07E-05	0.206312
gi|6321843 YHR052W	Essential protein that interacts with proteasome components and has a potential role in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles; Cic1p	0	376	5	13	10	7	0.000486	3	0.000206	1	3.5	2	2	0.000384	0	2.78E-05	1	4	1	1	0.000214	0	2.82E-05	4	12.5	7	4	0.000956	3	0.000625	0.206336
gi|6324808 YOR234C	Ribosomal protein L37 of the large (60S) ribosomal subunit, nearly identical to Rpl33Ap and has similarity to rat L35a; rpl33b null mutant exhibits normal growth while rpl33a rpl33b double null mutant is inviable; Rpl33bp	0	107	2	9.3	6	4	0.001024	2	0.000518	1	9.3	1	1	0.000726	0	9.78E-05	1	9.3	2	2	0.001398	0	9.91E-05	2	9.3	3	1	0.000941	2	0.001504	0.207556
gi|6324241 YNL088W	Essential type II topoisomerase, relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone of both positively and negatively supercoiled DNA; cleaves complementary strands; localizes to axial cores in meiosis; Top2p	0	1428	7	3.5	17	12	0.000213	5	8.54E-05	4	1.5	8	4	0.000194	4	0.000183	1	1.4	2	2	0.000105	0	7.43E-06	4	3.4	7	6	0.000373	1	6.07E-05	0.209584
gi|6321412 YGL026C	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general control system of amino acid biosynthesis; Trp5p	0	707	24	8.9	60	17	0.000603	43	0.001364	13	6.5	23	5	0.000487	18	0.001614	7	4.7	9	2	0.000212	7	0.000645	14	5.9	28	10	0.001241	18	0.001908	0.209633
gi|6320715 YDR507C	Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes autophosphorylation; similar to Kcc4p and Hsl1p; Gin4p	0	1142	12	5.2	28	6	0.000139	22	0.000437	5	5	10	0	9.72E-06	10	0.000559	4	1.6	5	2	0.000131	3	0.000176	6	3.2	13	4	0.000315	9	0.000596	0.210784
gi|6321764 YHL023C	Protein required for sporulation; Rmd11p	0	1146	3	2.6	13	3	7.43E-05	10	0.000203	2	1	4	1	6.78E-05	3	0.000174	2	1	2	1	7.03E-05	1	6.48E-05	3	2.6	7	1	8.79E-05	6	0.0004	0.21149
gi|6322505 YJR045C	Mitochondrial matrix ATPase that is a subunit of the presequence translocase-associated protein import motor (PAM); involved in protein translocation into the matrix and protein folding; member of the heat shock protein 70 (HSP70) family; Ssc1p	0	654	11	17.6	22	13	0.000503	9	0.000322	7	10.1	11	5	0.000526	6	0.000592	5	13.3	7	5	0.000546	2	0.000211	3	3.8	4	3	0.000418	1	0.000132	0.216201
gi|6320972 YER125W	Ubiquitin-protein ligase involved in ubiquitin-mediated protein degradation; plays a role in heat shock element (HSE)-mediated gene expression and multivesicular body sorting; contains a hect (homologous to E6-AP carboxyl terminus) domain; Rsp5p	0	809	6	6.9	14	9	0.000286	5	0.000151	2	1.9	5	5	0.000425	0	1.29E-05	4	5.4	8	3	0.00027	5	0.000406	1	1.5	1	1	0.000124	0	1.53E-05	0.216483
gi|6322163 YIL026C	Subunit of the cohesin complex, which is required for sister chromatid cohesion during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability; Irr1p	0	1150	8	5.9	13	9	0.000201	4	8.67E-05	2	1.7	3	2	0.000126	1	6.37E-05	2	1.4	3	3	0.00019	0	9.22E-06	5	4	7	4	0.000313	3	0.000205	0.217553
gi|6320966 YER120W	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p	1	244	33	29.1	99	59	0.005936	40	0.00368	21	29.1	48	28	0.007691	20	0.00519	16	27.9	34	21	0.00599	13	0.003433	7	9.4	17	10	0.003596	7	0.002181	0.223334
gi|6323630 YML012W	Protein that forms a heterotrimeric complex with Erp1, Erp2p, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	1	211	19	21.3	157	91	0.010557	66	0.006987	13	21.3	64	37	0.011735	27	0.008085	9	13.3	61	39	0.012818	22	0.006683	5	12.8	32	15	0.006204	17	0.006042	0.224703
gi|6320691 YDR483W	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation; Kre2p	0	442	18	18.1	39	26	0.00146	13	0.000677	12	14	23	15	0.002286	8	0.00116	5	11.1	6	5	0.000807	1	0.000168	6	17.6	10	6	0.001204	4	0.0007	0.22764
gi|6321997 YHR203C	Protein component of the small (40S) ribosomal subunit; identical to Rps4Bp and has similarity to rat S4 ribosomal protein; Rps4bp	0	261	5	18	16	10	0.000979	6	0.000552	2	8.4	4	4	0.001064	0	4.01E-05	4	13.8	11	5	0.001367	6	0.001503	1	4.2	1	1	0.000386	0	4.74E-05	0.229693
gi|6321424 YGL014W	Member of the PUF protein family, which is defined by the presence of Pumilio homology domains that confer RNA binding activity; preferentially binds mRNAs encoding nucleolar ribosomal RNA-processing factors; Puf4p	0	888	2	1.8	16	6	0.000178	10	0.000262	1	1.8	2	0	1.25E-05	2	0.000153	2	1.8	10	6	0.00048	4	0.000299	1	1.8	4	0	1.62E-05	4	0.000348	0.230004

gi|6319464 YBL007C	Cytoskeletal protein binding protein required for assembly of the cortical actin cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin dynamics and with proteins required for endocytosis; Sla1p	0	1244	6	6.5	16	12	0.000245	4	8.02E-05	1	1.4	2	2	0.000116	0	8.41E-06	1	3.2	1	1	6.48E-05	0	8.52E-06	5	3.3	13	9	0.000636	4	0.000249	0.230499
gi|6320924 YER080W	The authentic, non-tagged protein was localized to the mitochondria; Fmp29p	0	627	16	16.4	33	22	0.000874	11	0.000407	7	9.1	11	7	0.000761	4	0.000417	4	4.5	5	4	0.000459	1	0.000118	7	8.8	17	11	0.001537	6	0.00073	0.233643
gi|6323322 YLR291C	Beta subunit of the translation initiation factor eIF2B, the guanine-nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a negative regulator of GCN4 expression; Gcd7p	0	381	4	8.7	15	9	0.000607	6	0.000378	3	8.7	5	2	0.000379	3	0.000522	3	4.7	5	4	0.000755	1	0.000195	2	4.7	5	3	0.000717	2	0.000422	0.234377
gi|4162968 YPL094C	Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-dependent and post-translational SRP-independent protein targeting and import into the ER; Sec62p	2	274	12	8.4	22	7	0.000666	15	0.001254	4	8.4	4	1	0.000284	3	0.000726	4	8.4	8	2	0.000546	6	0.001432	4	8	10	4	0.001313	6	0.001671	0.235383
gi|6321599 YGR159C	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p	0	414	23	18.1	76	46	0.002734	30	0.001633	9	11.8	20	10	0.001636	10	0.001542	9	15	22	15	0.00253	7	0.001101	12	8.9	34	21	0.004413	13	0.002362	0.235493
gi|6321426 YGL012W	C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants are viable, but lack ergosterol; Erg4p	7	473	13	15.4	31	21	0.001107	10	0.000492	3	6.6	6	4	0.000587	2	0.000288	4	10.1	6	5	0.000754	1	0.000157	11	11.8	19	12	0.00222	7	0.001125	0.237353
gi|6320374 YDR170C	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles; Sec7p	0	2009	14	5.6	26	16	0.0002	10	0.000116	10	4.4	17	8	0.000271	9	0.000287	2	0.9	5	4	0.000143	1	3.69E-05	3	2.1	4	4	0.000179	0	6.16E-06	0.238772
gi|6321679 YGR240C	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p	0	987	16	13.3	39	13	0.000333	26	0.000595	5	4.6	9	3	0.000214	6	0.000392	6	6.3	13	7	0.000501	6	0.000397	10	8.7	17	3	0.000277	14	0.001066	0.239774
gi|6325112 YPL145C	Member of the oxysterol binding protein family, which includes seven yeast homologs; involved in negative regulation of Sec14p-dependent Golgi complex secretory functions, peripheral membrane protein that localizes to the Golgi complex; Kes1p	0	434	12	19.4	26	18	0.001038	8	0.000434	4	8.1	11	8	0.001254	3	0.000458	3	11.1	4	4	0.000663	0	2.44E-05	7	8.3	11	6	0.001226	5	0.000884	0.240837
gi|6320276 YDR071C	Polyamine acetyltransferase; acetylates polyamines such as putrescine, spermidine and spermine; may be involved in transcription and/or DNA replication via regulation of levels of polyamines bound to chromosomal DNA; Paa1p	0	191	3	11	10	3	0.000446	7	0.000871	3	11	5	2	0.000756	3	0.001041	1	6.3	2	0	6.03E-05	2	0.000722	2	6.3	3	1	0.000527	2	0.000842	0.242984
gi|6323389 YLR357W	One of 15 subunits of the 'Remodel the Structure of Chromatin' (RSC) complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance; Rsc2p	0	889	16	16.2	43	32	0.00089	11	0.000287	3	5.3	5	4	0.000312	1	8.24E-05	4	4	9	6	0.000479	3	0.000227	13	16.2	29	22	0.002152	7	0.000599	0.243153
gi|6324143 YNL186W	Ubiquitin-specific protease that deubiquitinates ubiquitin-protein moieties; may regulate silencing by acting on Sir4p; involved in posttranscriptionally regulating Gap1p and possibly other transporters; primarily located in the nucleus; Ubp10p	0	792	4	7.7	8	2	7.68E-05	6	0.000182	1	5.1	1	0	1.4E-05	1	9.25E-05	1	2.7	1	0	1.45E-05	1	9.37E-05	3	5.1	6	2	0.000236	4	0.000391	0.248365
gi|6322002 YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p	0	393	15	18.8	33	10	0.00065	23	0.001326	9	18.8	14	4	0.000706	10	0.001624	7	18.6	11	6	0.001084	5	0.000836	3	6.4	8	0	3.66E-05	8	0.001543	0.256024
gi|6323568 YML072C	Contains three calcium and lipid binding domains; localized to the bud; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; mRNA is targeted to the bud via the mRNA transport system involving She2p; C-terminal portion of Tcb1p,	1	1545	28	12.2	103	65	0.001032	38	0.000552	20	10.7	54	28	0.001215	26	0.001064	10	4.7	32	28	0.001259	4	0.000172	11	3.4	17	9	0.000512	8	0.000393	0.257223
gi|6322054 YIL137C	Putative metalloprotease; Tma108p	0	946	5	5.1	11	3	9.01E-05	8	0.000199	2	3.1	4	2	0.000153	2	0.000144	3	5.1	6	1	8.52E-05	5	0.000347	1	2.7	1	0	1.52E-05	1	9.16E-05	0.258179
gi|6322431 YJL029C	Component of the GARP (Golgi-associated retrograde protein) complex, Vps51p-Vps52p-Vps53p-Vps54p, which is required for the recycling of proteins from endosomes to the late Golgi; required for vacuolar protein sorting; Vps53p	0	822	4	3.3	10	3	0.000104	7	0.000202	2	3.3	2	0	1.35E-05	2	0.000166	2	1.6	4	2	0.000182	2	0.000168	2	1.7	4	1	0.000123	3	0.000286	0.258581
gi|6322058 YIL133C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, binds to 5.8 S rRNA; has similarity to Rpl16Bp, E. coli L13 and rat L13a ribosomal proteins; transcriptionally regulated by Rap1p; Rpl16ap	0	199	4	13.1	10	3	0.000428	7	0.000836	3	13.1	3	1	0.000391	2	0.000684	2	13.1	3	0	5.78E-05	3	0.001012	4	13.1	4	2	0.00094	2	0.000809	0.259517
gi|6325103 YPL154C	Vacuolar aspartyl protease (proteinase A), required for the posttranslational precursor maturation of vacuolar proteinases; synthesized as a zymogen, self-activates; Pep4p	0	405	6	14.8	7	4	0.00027	3	0.000192	4	14.6	5	2	0.000356	3	0.000491	1	2.5	1	1	0.000199	0	2.62E-05	1	3.7	1	1	0.000249	0	3.06E-05	0.260173
gi|6322577 YJR117W	Highly conserved zinc metalloprotease that functions in two steps of a-factor maturation, C-terminal CAAX proteolysis and the first step of N-terminal proteolytic processing; contains multiple transmembrane spans; Ste24p	4	453	17	10.2	49	29	0.001585	20	0.001003	10	10.2	24	12	0.001789	12	0.001687	4	4.6	11	9	0.001397	2	0.000304	9	10.2	14	8	0.001556	6	0.001011	0.260272
gi|6323755 YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p	0	687	45	23.9	139	53	0.001896	86	0.002791	24	22.4	52	17	0.001665	35	0.003214	18	9.8	56	20	0.002027	36	0.003349	15	13.5	31	16	0.002031	15	0.00164	0.260461
gi|6321206 YGL231C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; Ygl231cp	2	190	5	10	11	4	0.000577	7	0.000875	4	10	8	4	0.001461	4	0.001377	1	7.4	2	0	6.06E-05	2	0.000725	1	5.3	1	0	7.57E-05	1	0.000456	0.260762
gi|6320593 YDR385W	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft2p	0	842	98	34.6	605	310	0.008977	295	0.00778	39	29.1	205	98	0.007767	107	0.007992	42	21.1	224	109	0.008953	115	0.008702	54	20.3	176	103	0.010576	73	0.006454	0.261264
gi|6324161 YNL168C	The authentic, non-tagged protein was localized to mitochondria; Fmp41p	0	259	7	13.5	17	6	0.000611	11	0.000984	3	13.1	5	0	4.29E-05	5	0.001253	6	13.5	11	6	0.001644	5	0.001269	1	6.2	1	0	5.55E-05	1	0.000335	0.262146

gi|6320432 YDR226W	Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the mitochondria; lacks cleavable signal sequence; Adk1p	0	222	3	8.1	15	4	0.000493	11	0.001148	2	8.1	10	3	0.00095	7	0.002027	2	8.1	2	0	5.18E-05	2	0.000621	2	8.1	3	1	0.000454	2	0.000725	0.262336
gi|6323779 YMR131C	Essential nuclear protein involved in early steps of ribosome biogenesis; physically interacts with the ribosomal protein Rpl3p; Rrb1p	0	511	6	10.6	18	11	0.000548	7	0.000325	3	10.2	4	3	0.000413	1	0.000143	3	10.6	5	3	0.000428	2	0.00027	5	10.2	9	5	0.000873	4	0.000606	0.263248
gi|6324062 YNL267W	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-biphosphate; may control cytokineses through the actin cytoskeleton; Pik1p	0	1066	10	1.9	20	7	0.000171	13	0.000281	3	1.9	6	1	7.29E-05	5	0.000304	5	1.9	6	3	0.000205	3	0.000189	5	1.9	8	3	0.000256	5	0.00036	0.263843
gi|6324081 YNL248C	RNA polymerase I subunit A49; Rpa49p	0	415	12	13.7	38	13	0.000792	25	0.001362	4	8.4	11	5	0.000829	6	0.000933	5	12.5	9	2	0.000361	7	0.001099	9	9.6	18	6	0.001283	12	0.002177	0.265433
gi|6322458 YJL002C	Alpha subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost1p	1	476	4	10.3	8	5	0.000281	3	0.000163	1	6.9	1	1	0.000163	0	2.2E-05	1	3.4	3	3	0.000459	0	2.23E-05	3	3.4	4	1	0.000212	3	0.000494	0.266556
gi|6321790 YHR003C	Putative protein of unknown function, localizes to the mitochondria; Yhr003cp	0	429	6	10.5	11	7	0.000426	4	0.000233	5	10.5	9	5	0.000802	4	0.00061	1	3.5	1	1	0.000188	0	2.47E-05	1	3.5	1	1	0.000235	0	2.89E-05	0.266833
gi|6321748 YHL039W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; Yhl039wp	0	585	6	3.4	15	11	0.000479	4	0.000171	4	3.4	9	7	0.000816	2	0.000233	2	3.4	3	3	0.000374	0	1.81E-05	2	3.4	3	1	0.000172	2	0.000275	0.267691
gi|6319530 YBR056W	hypothetical protein; Ybr056wp	0	501	9	14	28	9	0.000462	19	0.000863	4	7.8	9	4	0.000554	5	0.000648	6	9.6	13	5	0.000712	8	0.001037	2	6.6	6	0	2.87E-05	6	0.000914	0.270081
gi|6322604 YJR144W	Protein involved in mitochondrial genome maintenance; component of the mitochondrial nucleoid, required for the repair of oxidative mtDNA damage; Mgm101p	0	269	13	11.2	25	15	0.001403	10	0.000865	3	11.2	5	5	0.00128	0	3.89E-05	11	11.2	19	9	0.002353	10	0.002404	1	7.1	1	1	0.000374	0	4.6E-05	0.270301
gi|4274230 YNL130C	Cholinephosphotransferase, required for phosphatidylcholine biosynthesis and for inositol-dependent regulation of EPT1 transcription; Cpt1p	8	393	3	7.1	6	2	0.000155	4	0.000254	2	3.1	2	1	0.000198	1	0.000186	2	3.1	3	1	0.000205	2	0.000351	1	4.1	1	0	3.66E-05	1	0.00022	0.274488
gi|6323768 YMR120C	Enzyme of 'de novo' purine biosynthesis containing both 5-aminoimidazole-4-carboxamide ribonucleotide transformylase and inosine monophosphate cyclohydrolase activities, isozyme of Ade16p; ade16 ade17 mutants require adenine and histidine; Ade17p	0	592	8	9.1	24	9	0.000391	15	0.00058	3	3.4	8	2	0.000244	6	0.000654	6	6.6	12	6	0.000719	6	0.000663	3	5.9	4	1	0.00017	3	0.000397	0.277127
gi|6321596 YGR157W	Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the conversion of phosphatidylethanolamine to phosphatidylcholine during the methylation pathway of phosphatidylcholine biosynthesis; Cho2p	8	869	6	4	26	5	0.000154	21	0.000548	6	4	15	3	0.000243	12	0.000879	2	1	2	1	9.27E-05	1	8.54E-05	3	2.1	9	1	0.000116	8	0.000698	0.277681
gi|6320993 YER145C	High affinity iron permease involved in the transport of iron across the plasma membrane; forms complex with Fet3p; expression is regulated by iron; Ftr1p	6	404	19	14.1	61	13	0.000813	48	0.002661	5	9.7	5	0	2.75E-05	5	0.000803	13	10.9	49	11	0.001909	38	0.00601	4	6.2	7	2	0.000463	5	0.00095	0.281144
gi|6324886 YOR310C	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p	0	511	75	21.7	250	144	0.006884	106	0.00462	46	18.4	119	76	0.00993	43	0.005305	23	14.5	60	33	0.004482	27	0.003382	30	14.1	71	35	0.00594	36	0.005256	0.281435
gi|6325105 YPL152W	Activator of the phosphotyrosyl phosphatase activity of PP2A; regulates G1 phase progression, the osmoresponse and microtubule dynamics; implicated in the spindle assembly check; subunit of the Tap42p-Pph21p-Rrd2p complex; Rrd2p	0	358	4	8.7	18	11	0.000782	7	0.000464	4	8.7	10	4	0.000775	6	0.001082	2	8.7	5	5	0.000997	0	2.96E-05	2	8.7	3	2	0.000522	1	0.000242	0.281894
gi|6324660 YOR086C	Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and Tcb3p interact; Tcb1p	2	1186	24	13.7	65	42	0.000872	23	0.000439	18	12.6	35	20	0.001133	15	0.000803	8	8.8	17	16	0.000941	1	6.26E-05	7	5.1	13	6	0.000449	7	0.000449	0.283315
gi|6324321 YNL007C	Type II HSP40 co-chaperone that interacts with the HSP70 protein Ssa1p; not functionally redundant with Ydj1p due to due to substrate specificity; shares similarity with bacterial DnaJ proteins; Sis1p	0	352	4	9.1	23	7	0.000519	16	0.001039	4	9.1	8	2	0.00041	6	0.0011	4	9.1	13	5	0.001014	8	0.001476	1	4.5	2	0	4.09E-05	2	0.000457	0.28406
gi|6325172 YPL085W	COPII vesicle coat protein required for ER transport vesicle budding and autophagosome formation; Sec16p is bound to the periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p	0	2195	17	6	54	31	0.000349	23	0.000237	6	3.3	15	9	0.000278	6	0.000176	3	2	15	11	0.000351	4	0.000121	12	4.3	24	11	0.000439	13	0.000445	0.286657
gi|6322720 YKL129C	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo3p	0	1271	8	3.9	18	10	0.000201	8	0.000148	7	3.2	14	6	0.000323	8	0.000403	2	2.4	3	3	0.000172	0	8.34E-06	1	0.7	1	1	7.92E-05	0	9.74E-06	0.287141
gi|6320454 YDR248C	hypothetical protein; Ydr248cp	0	193	7	14.5	14	3	0.000441	11	0.001321	4	14.5	8	0	5.75E-05	8	0.002657	2	14.5	3	2	0.000775	1	0.000385	3	14.5	3	1	0.000522	2	0.000834	0.289973
gi|6320137 YDL066W	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes; Idp1p	0	428	10	8.6	220	156	0.008902	64	0.003341	9	8.6	40	17	0.002672	23	0.003399	4	4.7	52	39	0.006319	13	0.001957	5	8.2	128	100	0.0202	28	0.004888	0.290406
gi|6321437 YGL001C	C-3 sterol dehydrogenase, catalyzes the second of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; Erg26p	0	349	12	16.6	28	5	0.000384	23	0.001493	8	16.6	22	3	0.000604	19	0.003449	3	12	3	1	0.000231	2	0.000395	3	8	3	1	0.000289	2	0.000461	0.292546
gi|6325194 YPL063W	Constituent of the mitochondrial inner membrane presequence translocase (TIM23 complex); may promote binding of incoming precursor proteins to the intermembrane space domain of Tom22p during translocation; Tim50p	0	476	34	33	138	82	0.004219	56	0.002631	24	29.4	77	44	0.006182	33	0.004375	17	21.6	35	24	0.003506	11	0.001492	7	13.2	26	14	0.002569	12	0.001898	0.294198
gi|6323776 YMR128W	Essential DEAH-box ATP-dependent RNA helicase specific to the U3 snoRNP, predominantly nucleolar in distribution, required for 18S rRNA synthesis; Ecm16p	0	1267	8	4.8	17	4	8.65E-05	13	0.000236	1	1.2	1	0	8.76E-06	1	5.78E-05	5	4.8	7	1	6.36E-05	6	0.00031	3	1.3	9	3	0.000216	6	0.000361	0.294585
gi|6321326 YGL112C	Subunit (60 kDa) of TFIID and SAGA complexes, involved in transcription initiation of RNA polymerase II and in chromatin modification, similar to histone H4; Taf6p	0	516	15	12.8	36	23	0.001109	13	0.00058	12	12.8	21	10	0.001313	11	0.001359	1	5.6	3	3	0.000424	0	2.05E-05	6	8.9	12	10	0.001701	2	0.000312	0.29557
gi|6325220 YPL037C	Subunit beta1 of the nascent polypeptide-associated complex (NAC) involved in protein targeting, associated with cytoplasmic ribosomes; enhances DNA binding of the Gal4p activator; homolog of human BTF3b; Egd1p	0	157	9	25.5	14	9	0.001473	5	0.000777	4	8.9	4	3	0.001344	1	0.000467	5	25.5	9	5	0.002272	4	0.001688	1	11.5	1	1	0.000641	0	7.88E-05	0.297443

gi|6322704 YKL145W	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for optimal CDC20 transcription; interacts with Rpn12p and the E3 ubiquitin-protein ligase Ubr1p; Rpt1p	0	467	6	13.7	18	4	0.000235	14	0.000688	6	13.7	10	2	0.000309	8	0.001098	1	3	1	0	2.46E-05	1	0.000159	3	6.6	7	2	0.0004	5	0.000822	0.298015
gi|6324291 YNL037C	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p	0	360	29	18.6	249	150	0.010177	99	0.006127	15	15	76	36	0.006693	40	0.007006	9	13.6	58	36	0.006937	22	0.003917	11	13.6	115	78	0.018741	37	0.007667	0.299887
gi|6323947 YMR290C	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles; Has1p	0	505	11	11.7	39	14	0.000699	25	0.001119	6	7.3	19	10	0.001341	9	0.00114	3	4.4	13	4	0.00057	9	0.001155	4	8.7	7	0	2.85E-05	7	0.001054	0.301393
gi|6320500 YDR294C	Dihydrosphingosine phosphate lyase, regulates intracellular levels of sphingolipid long-chain base phosphates (LCBPs), degrades phosphorylated long chain bases, prefers C16 dihydrosphingosine-l-phosphate as a substrate; Dpl1p	0	589	9	6.1	16	10	0.000434	6	0.000245	4	6.1	6	4	0.000471	2	0.000231	2	1.7	3	3	0.000371	0	1.8E-05	5	3.4	7	3	0.000464	4	0.000525	0.30228
gi|6322833 YKL019W	Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase that catalyze prenylation of proteins containing a CAAX consensus motif; essential protein required for membrane localization of Ras proteins and a-factor; Ram2p	0	316	6	12.3	12	4	0.000347	8	0.000596	1	5.4	1	0	3.51E-05	1	0.000232	1	5.4	2	0	3.64E-05	2	0.000436	5	10.8	9	4	0.001138	5	0.001214	0.302543
gi|6321724 YGR285C	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain and functions as a J-protein partner for Ssb1p and Ssb2p; Zuo1p	0	433	11	11.5	16	11	0.000647	5	0.000282	4	7.4	5	1	0.00018	4	0.000604	3	7.2	4	3	0.000505	1	0.000171	4	6.7	7	7	0.001429	0	2.86E-05	0.303941
gi|6324511 YOL061W	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p	0	496	17	15.3	33	11	0.000564	22	0.001006	8	9.3	15	6	0.000828	9	0.001161	5	12.1	6	3	0.000441	3	0.000406	5	6.7	12	2	0.000377	10	0.001522	0.305946
gi|6322476 YJR016C	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids; Ilv3p	0	585	15	14	40	12	0.00052	28	0.00108	8	11.6	15	2	0.000247	13	0.001413	9	11.6	17	5	0.00061	12	0.001323	6	9.7	8	5	0.000762	3	0.000402	0.306185
gi|6319675 YBR198C	Subunit (90 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation and in chromatin modification; Taf5p	0	798	7	3.3	21	14	0.000442	7	0.000208	6	3.3	11	7	0.000598	4	0.000328	1	2.8	2	2	0.000187	0	1.33E-05	3	2.8	8	5	0.000559	3	0.000295	0.310259
gi|6320799 YEL036C	Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein; has a role in retention of glycosyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol; Anp1p	0	500	9	9.8	29	9	0.000463	20	0.000909	4	7.4	11	2	0.000289	9	0.001151	1	3	3	0	2.3E-05	3	0.000403	6	9.2	15	7	0.001237	8	0.001213	0.311866
gi|6324512 YOL060C	Protein required for normal mitochondrial morphology, has similarity to hemolysins; Mam3p	3	706	20	10.1	50	17	0.000603	33	0.001052	11	5.1	22	9	0.000865	13	0.001171	11	7.5	21	8	0.000799	13	0.001186	4	5.2	7	0	2.04E-05	7	0.000754	0.312939
gi|6320119 YDL084W	Component of the TREX complex required for nuclear mRNA export; DEAD-box RNA helicase involved in early and late steps of spliceosome assembly; homolog of the human splicing factor hUAP56; Sub2p	0	446	11	16.8	16	9	0.000519	7	0.000373	7	14.6	8	4	0.000622	4	0.000587	3	3.8	4	2	0.000335	2	0.000309	3	7.2	4	3	0.000613	1	0.000194	0.320567
gi|4274228 YLR389C	Metalloprotease involved, with homolog Axl1p, in N-terminal processing of pro-a-factor to the mature form; member of the insulin-degrading enzyme family; Ste23p	0	1027	6	6.1	15	9	0.000225	6	0.00014	1	1.8	3	3	0.000205	0	1.02E-05	2	3.7	3	2	0.000146	1	7.23E-05	5	4.2	9	4	0.00035	5	0.000374	0.320938
gi|6322848 YKL005C	Negative regulator of transcription elongation, contains a TFIIS-like domain and a PHD finger, multicopy suppressor of temperature-sensitive ess1 mutations, probably binds RNA polymerase II large subunit; Bye1p	0	594	4	7.9	14	9	0.000389	5	0.000205	1	3.5	2	2	0.000243	0	1.76E-05	4	7.9	8	5	0.000601	3	0.000339	2	3.5	4	2	0.000315	2	0.000271	0.322048
gi|6322939 YKR086W	RNA helicase in the DEAH-box family involved in the second catalytic step of splicing, exhibits ATP-dependent RNA unwinding activity; Prp16p	0	1071	4	4.7	7	3	7.96E-05	4	9.31E-05	2	1.6	5	3	0.000197	2	0.000127	1	1.7	1	0	1.07E-05	1	6.93E-05	1	1.4	1	0	1.34E-05	1	8.09E-05	0.322521
gi|6324705 YOR131C	hypothetical protein; Yor131cp	0	218	5	23.4	8	5	0.000614	3	0.000356	3	17	3	2	0.000662	1	0.000336	1	7.3	1	1	0.00037	0	4.86E-05	3	16.5	4	2	0.000858	2	0.000738	0.323121
gi|6322156 YIL033C	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation; Bcy1p	0	416	8	12.3	16	5	0.000322	11	0.000613	3	5	4	2	0.000347	2	0.000327	4	8.4	8	1	0.000194	7	0.001096	2	8.9	4	2	0.00045	2	0.000387	0.324796
gi|6321795 YHR007C	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4''-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; Erg11p	2	530	12	16.8	24	15	0.000712	9	0.000397	8	16.8	12	7	0.000901	5	0.000612	1	3.4	4	4	0.000543	0	2E-05	5	6.8	8	4	0.000679	4	0.000584	0.325359
gi|6322901 YKR048C	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histones to the nucleus; Nap1p	0	417	12	19.9	55	34	0.002014	21	0.001143	5	15.8	15	6	0.000985	9	0.00138	5	11.8	14	10	0.001684	4	0.000636	6	12.9	26	18	0.00376	8	0.001454	0.32556
gi|6324937 YOR361C	Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Prt1p	0	763	21	16.9	51	17	0.000558	34	0.001002	8	9.8	10	4	0.000364	6	0.000508	6	9.6	13	2	0.000196	11	0.000931	11	14	28	11	0.001263	17	0.001671	0.32602
gi|6322831 YKL021C	Protein essential for cell growth and replication of M dsRNA virus; contains four beta-transducin repeats; Mak11p	0	468	15	11.5	32	10	0.000546	22	0.001066	1	4.7	1	0	2.37E-05	1	0.000157	4	11.3	5	0	2.46E-05	5	0.000702	12	5.3	26	10	0.001875	16	0.002566	0.327486
gi|6324595 YOR021C	hypothetical protein; Yor021cp	0	213	8	8.5	15	10	0.0012	5	0.000572	3	8.5	7	3	0.00099	4	0.001228	1	7	1	1	0.000378	0	4.98E-05	5	8	7	6	0.002499	1	0.000407	0.328184
gi|6321614 YGR175C	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p	2	496	24	19.8	75	56	0.002773	19	0.000872	18	19.8	52	42	0.005664	10	0.001287	4	8.7	6	4	0.00058	2	0.000278	7	7.7	17	10	0.001769	7	0.001073	0.329409
gi|6323104 YLR075W	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family; Rpl10p	0	221	13	12.7	34	21	0.002368	13	0.001354	10	11.8	19	11	0.003366	8	0.00232	3	11.8	8	7	0.002239	1	0.000336	5	11.8	7	3	0.001237	4	0.0014	0.331531
gi|6323554 YML085C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p	0	447	15	18.3	38	21	0.001171	17	0.000868	11	10.1	19	10	0.001515	9	0.001288	5	14.8	10	5	0.000798	5	0.000735	3	4	9	6	0.001191	3	0.000526	0.332396

gi|6320726	YDR518W	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER; Eug1p	0	517	8	11.4	14	9	0.000447	5	0.000236	4	11	6	3	0.000408	3	0.000385	4	5.8	7	5	0.00069	2	0.000267	1	2.9	1	1	0.000195	0	2.39E-05	0.334766
gi|6321927	YHR135C	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p; Yck1p	0	538	24	13.4	65	20	0.000928	45	0.001875	6	8	8	2	0.000268	6	0.00072	12	10.4	35	10	0.001305	25	0.002976	10	10.6	22	8	0.00131	14	0.001956	0.33625
gi|6320573	YDR365C	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels; Esf1p	0	628	19	16.9	31	10	0.000407	21	0.000759	8	11.3	11	6	0.000654	5	0.000517	2	5.7	5	0	1.83E-05	5	0.000523	11	11.6	15	4	0.000573	11	0.001321	0.337786
gi|6324847	YOR273C	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily; Tpo4p	11	659	21	17.5	56	20	0.000757	36	0.001228	9	12.3	19	11	0.001129	8	0.000778	11	14.1	22	9	0.000961	13	0.001271	6	6.5	15	0	2.18E-05	15	0.001709	0.338291
gi|6323412	YLR380W	Phosphatidylinositol transfer protein with a potential role in lipid turnover; interacts specifically with thioredoxin peroxidase (Tsa2p) and may have a role in oxidative stress resistance; Csr1p	0	408	8	17.2	16	12	0.000746	4	0.000245	8	17.2	13	10	0.00166	3	0.000487	2	6.9	2	1	0.000197	1	0.000182	1	2.5	1	1	0.000247	0	3.03E-05	0.343471
gi|6320056	YDL145C	Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles in the early secretory pathway; Cop1p	0	1201	10	9.6	15	8	0.000172	7	0.000138	5	5.7	6	3	0.000176	3	0.000166	4	3.2	6	3	0.000182	3	0.000168	3	2.9	3	2	0.000156	1	7.21E-05	0.34406
gi|6324795	YOR221C	Predicted malonyl-CoA:ACP transferase, putative component of a type-II mitochondrial fatty acid synthase that produces intermediates for phospholipid remodeling; Mct1p	0	384	3	4.7	23	16	0.001046	7	0.000433	2	4.7	13	10	0.001764	3	0.000518	2	4.7	9	5	0.000929	4	0.00069	1	3.9	1	1	0.000262	0	3.22E-05	0.344397
gi|6321700	YGR261C	Beta3-like subunit of the yeast AP-3 complex; functions in transport of alkaline phosphatase to the vacuole via the alternate pathway; exists in both cytosolic and peripherally associated membrane-bound pools; Apl6p	0	809	5	7.8	10	6	0.000196	4	0.000123	2	3.5	2	1	9.61E-05	1	9.06E-05	3	6.3	5	2	0.000185	3	0.000249	1	2.3	3	3	0.000338	0	1.53E-05	0.346204
gi|6319312	YAL007C	Protein that forms a heterotrimeric complex with Erp1p, Emp24p, and Erv25p; member, along with Emp24p and Erv25p, of the p24 family involved in ER to Golgi transport and localized to COPII-coated vesicles; Erp2p	1	215	2	14.4	5	4	0.00051	1	0.000155	1	7.4	2	2	0.000671	0	4.87E-05	1	7	1	0	5.35E-05	1	0.000345	1	7.4	2	2	0.00087	0	5.76E-05	0.347017
gi|6321335	YGL103W	Ribosomal protein L29 of the large (60S) ribosomal subunit, has similarity to E. coli L15 and rat L27a ribosomal proteins; may have peptidyl transferase activity; can mutate to cycloheximide resistance; Rpl28p	0	149	13	26.2	23	9	0.001552	14	0.002157	7	25.5	11	4	0.001863	7	0.00302	5	18.1	6	2	0.001004	4	0.001779	6	26.2	6	3	0.001834	3	0.001578	0.34945
gi|6324016	YNL313C	Protein required for cell viability; Ynl313cp	0	904	14	12.4	28	11	0.00031	17	0.000429	9	12.3	15	9	0.000676	6	0.000428	4	6.5	7	0	1.27E-05	7	0.000504	5	9.7	6	2	0.000207	4	0.000342	0.352725
gi|6319282	YAL035W	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2; Fun12p	0	1002	35	20.1	111	41	0.001008	70	0.00156	12	14.8	33	18	0.001208	15	0.00095	16	13.5	32	15	0.001045	17	0.00109	15	12.7	46	8	0.000703	38	0.002829	0.353158
gi|6324993	YPL262W	Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and mitochondrial localization determined by the N-terminal mitochondrial targeting sequence and protein conformation; Fum1p	0	488	6	5.9	10	6	0.000324	4	0.000204	3	3.7	4	2	0.000296	2	0.000279	3	5.9	5	3	0.000448	2	0.000282	1	2.9	1	1	0.000206	0	2.54E-05	0.353598
gi|6324480	YOL092W	hypothetical protein; Yol092wp	6	308	18	13	40	15	0.001225	25	0.001835	13	13	21	9	0.001983	12	0.002481	6	13	13	6	0.001383	7	0.00148	5	9.7	6	0	4.67E-05	6	0.001487	0.35824
gi|1431855	YFR031C-	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap	0	254	9	20.9	57	35	0.003402	22	0.001964	8	20.9	37	22	0.005814	15	0.00375	4	6.7	11	8	0.00222	3	0.000793	3	11	9	5	0.001756	4	0.001218	0.359166
gi|6323085	YLR056W	C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into episterol, a precursor in ergosterol biosynthesis; mutants are viable, but cannot grow on non-fermentable carbon sources; Erg3p	3	365	10	13.4	18	11	0.000767	7	0.000456	7	13.4	13	7	0.001308	6	0.001061	3	10.7	4	3	0.000599	1	0.000203	1	3.6	1	1	0.000276	0	3.39E-05	0.359319
gi|6323922	YMR266W	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant; Rsn1p	11	953	25	10.4	39	23	0.0006	16	0.000384	3	4.1	4	4	0.000291	0	1.1E-05	18	8.7	26	13	0.000954	13	0.000879	5	4.7	9	6	0.000559	3	0.000247	0.359483
gi|6322637	YKL212W	Lipid phosphoinositide phosphatase of the ER and Golgi, involved in protein trafficking and secretion; Sac1p	2	623	5	8	28	10	0.00041	18	0.000658	3	5.9	10	2	0.000232	8	0.000823	3	5.5	7	4	0.000462	3	0.000323	2	2.6	11	4	0.000577	7	0.000854	0.359522
gi|6323531	YML105C	Subunit of the signal recognition particle (SRP), involved in protein targeting to the ER; interacts with Srp54p; homolog of mammalian SRP19; Sec65p	0	273	12	17.6	55	18	0.00165	37	0.003045	7	17.6	14	8	0.001993	6	0.001418	4	13.6	14	0	4.22E-05	14	0.003301	10	17.6	27	10	0.003214	17	0.00467	0.359638
gi|6319702	YBR225W	hypothetical protein; Ybr225wp	0	900	3	2	7	1	4.06E-05	6	0.00016	1	1.8	3	0	1.23E-05	3	0.000221	1	1.8	1	1	8.95E-05	0	1.18E-05	1	2	3	0	1.6E-05	3	0.000261	0.361658
gi|6321595	YGR156W	Pta1p Interacting protein; Pti1p	0	425	11	4	39	26	0.001518	13	0.000704	8	4	22	15	0.002377	7	0.001059	4	3.5	12	9	0.001489	3	0.000474	2	2.8	5	2	0.00044	3	0.000553	0.362585
gi|6324496	YOL077C	Nucleolar protein, constituent of 66S pre-ribosomal particles; depletion leads to defects in rRNA processing and a block in the assembly of large ribosomal subunits; possesses a sigma(70)-like RNA-binding motif; Brx1p	0	291	5	7.6	9	3	0.000293	6	0.000495	1	7.6	1	0	3.82E-05	1	0.000252	2	7.6	5	2	0.000514	3	0.000692	2	7.6	3	1	0.000346	2	0.000553	0.364524
gi|2746935	YAL023C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals; Pmt2p	10	759	17	16.3	34	21	0.00069	13	0.000394	9	9.4	18	10	0.000892	8	0.000676	5	10.5	8	8	0.000743	0	1.4E-05	5	5.7	8	3	0.00036	5	0.000506	0.365106
gi|6323751	YMR104C	Protein kinase with similarityto serine/threonine protein kinase Ypk1p; functionally redundant with YPK1 at the genetic level; participates in a signaling pathway required for optimal cell wall integrity; homolog of mammalian kinase SGK; Ypk2p	0	677	2	3.2	5	4	0.000162	1	4.91E-05	1	3.2	1	1	0.000115	0	1.55E-05	1	3.2	3	3	0.000323	0	1.57E-05	1	2.8	1	0	2.12E-05	1	0.000128	0.366185
gi|6320291	YDR086C	Subunit of the Sec61p translocation complex (Sec61p-Sss1p-Sbh1p) that forms a channel for passage of secretory proteins through the endoplasmic reticulum membrane, and of the Ssh1p complex (Ssh1p-Sbh2p-Sss1p); interacts with Ost4p and Wbp1p; Sss1p	1	80	4	18.8	19	10	0.003195	9	0.002633	3	18.8	5	4	0.00347	1	0.000916	1	17.5	3	3	0.002733	0	0.000133	3	18.8	11	3	0.003417	8	0.007582	0.36805
gi|6320997	YER149C	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca2+ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth; Pea2p	0	420	12	4.8	31	10	0.000609	21	0.001135	7	4.8	16	5	0.00082	11	0.00167	7	4.8	13	5	0.000849	8	0.001237	1	4.8	2	0	3.43E-05	2	0.000383	0.36942

gi|6320128 YDL075W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Bp and has similarity to rat L31 ribosomal protein; associates with the karyopherin Sxm1p; Rpl31ap	0	113	5	14.2	31	14	0.003124	17	0.003433	4	14.2	8	1	0.000688	7	0.003983	3	14.2	5	0	0.000102	5	0.002909	4	14.2	18	13	0.010057	5	0.003396	0.372066
gi|6324510 YOL062C	Mu2-like subunit of the clathrin associated protein complex (AP-2); involved in vesicle transport; Apm4p	0	491	4	6.5	14	5	0.000273	9	0.000429	1	3.7	3	0	2.26E-05	3	0.000405	4	6.5	7	3	0.000445	4	0.00054	2	3.7	4	2	0.000381	2	0.000328	0.375369
gi|6320417 YDR211W	Catalytic epsilon subunit of the translation initiation factor eIF2B, the guanine-nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a negative regulator of GCN4 expression; Gcd6p	0	712	8	9.6	28	9	0.000325	19	0.000607	6	8.1	14	2	0.000203	12	0.001073	3	4.6	4	1	0.000113	3	0.000283	3	2.7	10	6	0.000748	4	0.000435	0.375389
gi|6320058 YDL143W	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo; Cct4p	0	528	10	11.9	35	14	0.000669	21	0.000903	7	11.9	10	3	0.0004	7	0.000852	5	6.2	11	3	0.000414	8	0.000984	5	9.5	14	8	0.001335	6	0.000867	0.375601
gi|6322159 YIL030C	Ubiquitin-protein ligase of the ER/nuclear envelope, required for degradation of Alpha2p and other proteins containing a Deg1 degradation signal; ssm4 mutation suppresses mRNA instability caused by an rna14 mutation; Ssm4p	14	1319	8	7.4	17	11	0.000212	6	0.000109	3	5.2	6	4	0.00021	2	0.000103	3	3.7	6	6	0.000323	0	8.04E-06	4	3.5	5	1	7.63E-05	4	0.000235	0.37686
gi|6319764 YBR287W	Protein of unknown function; mutation results in a zinc sensitive phenotype; Zsp1p	5	427	9	11	35	22	0.001283	13	0.000701	7	8.2	13	10	0.001586	3	0.000466	8	11	18	10	0.001644	8	0.001217	2	7.7	4	2	0.000438	2	0.000377	0.378596
gi|6320624 YDR416W	Component of the spliceosome complex involved in pre-mRNA splicing; involved in regulation of cell cycle progression; similar to Drosophila crooked neck protein; Syf1p	0	859	3	2.1	7	3	9.92E-05	4	0.000116	1	2.1	1	0	1.29E-05	1	8.53E-05	1	2.1	1	0	1.34E-05	1	8.64E-05	3	2.1	5	3	0.000318	2	0.000187	0.381682
gi|2780870 YBR086C	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process; Ist2p	8	946	9	9.7	24	14	0.000373	10	0.000246	6	7.4	10	5	0.000364	5	0.000343	4	7.1	9	7	0.000523	2	0.000146	2	3.5	5	2	0.000198	3	0.000249	0.383852
gi|6322395 YJL066C	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches; Mpm1p	0	252	12	17.5	28	10	0.001014	18	0.001627	10	17.5	17	7	0.001895	10	0.002533	3	8.3	9	3	0.000868	6	0.001557	1	6.3	2	0	5.71E-05	2	0.000639	0.388907
gi|6320839 YER003C	Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and mannose-6-P; required for early steps in protein mannosylation; Pmi40p	0	429	3	8.6	4	3	0.000199	1	7.75E-05	2	8.4	2	2	0.000336	0	2.44E-05	1	4.4	1	1	0.000188	0	2.47E-05	1	3.5	1	0	3.35E-05	1	0.000202	0.388992
gi|6322815 YKL035W	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p	0	499	31	24.4	106	69	0.003391	37	0.001666	22	24.4	65	40	0.005363	25	0.003167	10	14.6	33	24	0.003344	9	0.001169	4	8.6	8	5	0.000894	3	0.000471	0.390369
gi|6324778 YOR204W	ATP-dependent DEAD (Asp-Glu-Ala-Asp)-box RNA helicase, required for translation initiation of all yeast mRNAs; mutations in human DEAD-box DBY are a frequent cause of male infertility; Ded1p	0	604	3	4.6	29	16	0.000665	13	0.000495	2	2.8	13	6	0.00068	7	0.000745	2	2.8	11	5	0.000591	6	0.00065	2	4.6	5	5	0.000738	0	2.05E-05	0.390497
gi|6323324 YLR293C	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p, Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p	0	219	18	19.6	64	21	0.00239	43	0.004403	10	19.6	24	11	0.003397	13	0.003775	5	13.7	7	1	0.000368	6	0.001791	7	5	33	9	0.003613	24	0.008195	0.391193
gi|6323225 YLR196W	Protein with WD-40 repeats involved in rRNA processing; associates with trans-acting ribosome biogenesis factors; similar to beta-transducin superfamily; Pwp1p	0	576	3	9.4	6	1	6.34E-05	5	0.000212	2	4.5	3	0	1.93E-05	3	0.000345	1	2.8	2	0	2E-05	2	0.000239	1	4.9	1	1	0.000175	0	2.15E-05	0.39129
gi|6323583 YML057W	Calcineurin A; one isoform (the other is CNA1) of the catalytic subunit of calcineurin, a Ca++/calmodulin-regulated protein phosphatase which regulates Crz1p (a stress-response transcription factor), the other calcineurin subunit is CNB1; Cmp2p	0	604	8	8.8	25	8	0.000343	17	0.000642	7	6.1	14	4	0.00046	10	0.001057	1	4.1	5	0	1.91E-05	5	0.000544	3	6.8	6	4	0.000595	2	0.000266	0.392232
gi|6321784 YHL003C	Ceramide synthase component, involved in synthesis of ceramide from C26(acyl)-coenzyme A and dihydrosphingosine or phytosphingosine, functionally equivalent to Lac1p; Lag1p	7	411	2	3.4	6	1	8.88E-05	5	0.000297	1	3.2	2	0	2.7E-05	2	0.000331	1	3.4	1	1	0.000196	0	2.58E-05	1	3.2	3	0	3.5E-05	3	0.000572	0.392754
gi|6319582 YBR106W	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations; Pho88p	1	188	17	31.4	26	16	0.002137	10	0.001238	11	30.3	17	10	0.003603	7	0.002394	2	12.8	4	4	0.00153	0	5.64E-05	4	7.4	5	2	0.000995	3	0.001251	0.394345
gi|6323757 YMR110C	Putative fatty aldehyde dehydrogenase, located in the mitochondrial outer membrane and also in lipid particles; has similarity to human fatty aldehyde dehydrogenase (FALDH) which is implicated in Sjogren-Larsson syndrome; Hfd1p	1	532	9	6.2	29	18	0.000847	11	0.000479	5	6.2	8	4	0.000522	4	0.000492	3	6.2	3	3	0.000411	0	1.99E-05	3	4.3	18	11	0.001812	7	0.001	0.395356
gi|6320444 YDR238C	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence identity with mammalian beta-coat protein (beta-COP); Sec26p	0	973	15	8.2	30	16	0.000413	14	0.00033	9	6.5	16	6	0.000422	10	0.000656	6	8.2	10	6	0.000438	4	0.000272	2	1.5	4	4	0.00037	0	1.27E-05	0.396765
gi|6322671 YKL178C	Receptor for a factor receptor, transcribed in alpha cells and required for mating by alpha cells, couples to MAP kinase cascade to mediate pheromone response; ligand bound receptors are endocytosed and recycled to the plasma membrane; GPCR; Ste3p	6	470	7	3.6	15	10	0.000544	5	0.000259	1	3.6	2	2	0.000307	0	2.23E-05	3	3.2	9	7	0.001053	2	0.000293	3	3.6	4	1	0.000214	3	0.0005	0.39725
gi|6324197 YNL132W	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance; Kre33p	0	1056	18	10.2	45	15	0.000357	30	0.00064	6	5.8	14	1	7.36E-05	13	0.000783	7	6	10	6	0.000403	4	0.000251	10	6.5	21	8	0.000668	13	0.000926	0.398551
gi|6324761 YOR187W	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p	0	437	35	15.6	75	43	0.002423	32	0.001649	22	11.7	40	20	0.003074	20	0.002898	5	6.6	10	9	0.001448	1	0.00017	14	10.1	25	14	0.002798	11	0.001898	0.39857
gi|6324932 YOR356W	hypothetical protein; Yor356wp	0	631	11	9.8	35	23	0.000907	12	0.000439	6	9.8	9	2	0.000229	7	0.000713	5	9.8	13	11	0.001222	2	0.000218	6	8.4	13	10	0.001391	3	0.000373	0.400589
gi|6324268 YNL061W	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles; Nop2p	0	618	19	17.8	62	26	0.001044	36	0.001309	8	11.3	18	6	0.000665	12	0.001236	9	11.8	20	8	0.000913	12	0.001252	9	14.4	24	12	0.001699	12	0.001462	0.403307

gi|6319420 YBL051C	Protein involved in G2/M phase progression and response to DNA damage, interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage; Pin4p	0	668	10	2.8	75	30	0.001112	45	0.00151	5	2.8	16	6	0.000615	10	0.000956	6	2.8	42	19	0.001981	23	0.002206	2	2.5	17	5	0.000668	12	0.001353	0.40379
gi|6323521 YML115C	Component of the mannan polymerase I; forms a complex with Mnn9p, which is involved in mannan synthesis; mutants are vanadate-resistant; Van1p	1	535	10	14.4	21	14	0.00066	7	0.000311	3	7.7	5	2	0.00027	3	0.000372	6	14.4	11	10	0.001312	1	0.000139	2	4.5	5	2	0.00035	3	0.00044	0.40456
gi|6323480 YLR447C	Subunit D of the five-subunit V0 integral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system; stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane; Vma6p	0	345	21	20.6	71	44	0.00314	27	0.001767	16	20.6	46	27	0.005246	19	0.003489	5	13.9	7	5	0.001034	2	0.0004	11	13.6	18	12	0.003044	6	0.001327	0.406769
gi|6319279 YAL038W	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p	0	500	71	31.2	381	207	0.010103	174	0.007737	35	24.8	91	48	0.006418	43	0.005421	34	24	179	97	0.013419	82	0.010455	33	20.2	111	62	0.010732	49	0.007303	0.407138
gi|6319491 YBR017C	Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression; Kap104p	0	918	11	8.1	28	7	0.000199	21	0.000519	7	6.3	11	4	0.000302	7	0.00049	1	1.7	1	0	1.25E-05	1	8.09E-05	5	4.5	16	3	0.000298	13	0.001065	0.407329
gi|6320255 YDR050C	Triose phosphate isomerase, abundant glycolytic enzyme; mRNA half-life is regulated by iron availability; transcription is controlled by activators Reb1p, Gcr1p, and Rap1p through binding sites in the 5' non-coding region; Tpi1p	0	248	3	10.1	4	3	0.000344	1	0.000134	1	5.2	1	1	0.000313	0	4.22E-05	1	4.8	1	0	4.64E-05	1	0.000299	1	4	2	2	0.000754	0	4.99E-05	0.409494
gi|6319791 YCL059C	Essential nucleolar protein required for the synthesis of 18S rRNA and for the assembly of 40S ribosomal subunit; Krr1p	0	316	6	15.8	10	6	0.000501	4	0.000316	2	6.6	4	2	0.000457	2	0.000431	1	4.4	1	1	0.000255	0	3.36E-05	4	14.9	5	3	0.000865	2	0.000509	0.409588
gi|6323843 YMR189W	P subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm; Gcv2p	0	1034	8	4.9	13	7	0.000177	6	0.000139	4	1.9	6	2	0.00014	4	0.000253	3	4.9	5	3	0.000211	2	0.000133	2	1.9	2	2	0.000181	0	1.2E-05	0.41018
gi|6322000 YHR206W	Nuclear response regulator and transcription factor, part of a branched two-component signaling system; required for optimal induction of heat-shock genes in response to oxidative stress; involved in osmoregulation; Skn7p	0	622	2	1.9	8	6	0.000254	2	8.91E-05	1	1.9	4	4	0.000446	0	1.68E-05	1	1.9	2	2	0.000241	0	1.7E-05	1	1.9	2	0	2.31E-05	2	0.000259	0.41237
gi|6322762 YKL088W	Predicted phosphopantothenoylcysteine decarboxylase, may be involved in coenzyme A biosynthesis; interacts with Sis2p and Vhs3p; Ykl088wp	0	571	8	11	19	8	0.000362	11	0.000446	5	8.8	9	4	0.000486	5	0.000568	4	8.1	6	3	0.000383	3	0.000353	3	6	4	1	0.000176	3	0.000412	0.412932
gi|6321772 YHL015W	Protein component of the small (40S) ribosomal subunit; overproduction suppresses mutations affecting RNA polymerase III-dependent transcription; has similarity to E. coli S10 and rat S20 ribosomal proteins; Rps20p	0	121	6	10.7	15	8	0.00171	7	0.001374	4	10.7	10	4	0.002294	6	0.0032	2	10.7	4	3	0.001807	1	0.000613	1	10.7	1	1	0.000832	0	0.000102	0.413711
gi|1431851 YFL008W	Subunit of the multiprotein cohesin complex, essential protein involved in chromosome segregation and in double-strand DNA break repair; SMC chromosomal ATPase family member, binds DNA with a preference for DNA with secondary structure; Smc1p	0	1225	5	2.5	11	6	0.000129	5	9.95E-05	3	1.3	5	1	6.34E-05	4	0.000214	2	1.3	3	2	0.000122	1	6.06E-05	1	1.2	3	3	0.000223	0	1.01E-05	0.419233
gi|6321747 YHL040C	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores; Arn1p	13	627	6	4.3	33	21	0.000835	12	0.000442	5	4.3	8	3	0.000336	5	0.000517	2	4.3	10	3	0.000349	7	0.000727	1	2.6	15	15	0.002088	0	1.97E-05	0.420049
gi|6325164 YPL093W	Putative GTPase that associates with free 60S ribosomal subunits in the nucleolus and is required for 60S ribosomal subunit biogenesis; constituent of 66S pre-ribosomal particles; member of the ODN family of nucleolar G-proteins; Nog1p	0	647	7	12.8	14	8	0.00032	6	0.000223	4	11.3	6	4	0.000429	2	0.00021	4	9.9	7	3	0.000338	4	0.00041	1	2.6	1	1	0.000156	0	1.91E-05	0.423464
gi|6320824 YEL013W	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions; Vac8p	0	578	10	5.5	16	11	0.000484	5	0.000211	10	5.5	13	9	0.001057	4	0.000453	1	1.9	1	1	0.000139	0	1.83E-05	2	1.9	2	1	0.000174	1	0.00015	0.425555
gi|3736265 YHR064C	Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome-associated complex that binds the ribosome via the Zuo1p subunit; also involved in pleiotropic drug resistance via sequential activation of PDR1 and PDR5; binds ATP; Ssz1p	0	538	11	14.7	45	19	0.000882	26	0.001092	8	14.3	17	8	0.001011	9	0.00107	8	11.7	20	9	0.001177	11	0.00132	4	6.7	8	2	0.000348	6	0.000851	0.42831
gi|6322331 YJL130C	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p	0	2214	30	7.8	61	21	0.000236	40	0.000406	12	3	27	12	0.000366	15	0.00043	4	2	4	0	5.2E-06	4	0.00012	16	6.4	30	9	0.000357	21	0.00071	0.4288
gi|6323693 YMR049C	Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of 66S pre-ribosomal particles; homologous to mammalian Bop1; Erb1p	0	807	15	10.5	58	33	0.001011	25	0.000701	11	8.6	20	11	0.000922	9	0.000713	7	6.1	15	6	0.000528	9	0.000723	6	4.1	23	16	0.001729	7	0.00066	0.429644
gi|3736268 YNL256W	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities; Fol1p	0	824	12	10.9	21	12	0.000369	9	0.000256	4	4.9	7	2	0.000175	5	0.000394	4	7.3	8	6	0.000517	2	0.000167	5	6.2	6	4	0.000436	2	0.000195	0.430354
gi|6319449 YBL022C	Mitochondrial ATP-dependent protease involved in intramitochondrial proteolysis; involved in degradation of misfolded proteins in mitochondria; required for bigenesis and maintenance of mitochondria; Pim1p	0	1133	10	10.5	28	16	0.000355	12	0.000245	5	8.2	8	7	0.000421	1	6.47E-05	1	3.2	1	1	7.11E-05	0	9.36E-06	5	2.3	19	8	0.000622	11	0.000732	0.431651
gi|6320362 YDR158W	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom2p	0	365	13	10.4	33	12	0.000834	21	0.001306	11	10.4	23	9	0.001673	14	0.002437	4	6.8	8	3	0.000599	5	0.000901	2	5.8	2	0	3.94E-05	2	0.000441	0.432653

gi|6319591 YBR115C	Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine; activation requires posttranslational phosphopantetheinylation by Lys5p; Lys2p	0	1392	5	2.5	7	1	2.62E-05	6	0.000104	1	1.4	1	1	5.58E-05	0	7.52E-06	1	1	1	0	8.27E-06	1	5.33E-05	3	2.4	5	0	1.03E-05	5	0.000276	0.433055
gi|6322699 YKL150W	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis; Mcr1p	0	302	11	21.9	24	16	0.00133	8	0.000624	10	21.9	17	12	0.002684	5	0.001074	2	4.6	3	2	0.000495	1	0.000246	3	8.9	4	2	0.000619	2	0.000533	0.435237
gi|6320332 YDR127W	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a precursor to aromatic amino acids; Aro1p	0	1588	11	5.3	24	9	0.000146	15	0.000216	2	1.8	3	0	6.99E-06	3	0.000125	5	2.8	9	5	0.000225	4	0.000167	6	3.3	12	4	0.000226	8	0.000382	0.438097
gi|6320265 YDR060W	Constituent of 66S pre-ribosomal particles, required for large (60S) ribosomal subunit biogenesis; involved in nuclear export of pre-ribosomes; required for maintenance of dsRNA virus; homolog of human CAATT-binding protein; Mak21p	0	1025	6	3.7	13	4	0.000107	9	0.000205	1	2.4	1	0	1.08E-05	1	7.15E-05	2	1.3	4	2	0.000146	2	0.000134	3	2.1	8	2	0.000182	6	0.000447	0.441135
gi|6322706 YKL143W	Protein required for growth at low temperature; Ltv1p	0	463	7	13.2	14	6	0.000342	8	0.000407	3	3	7	4	0.0006	3	0.000429	3	13.2	3	1	0.000174	2	0.000298	2	3	4	1	0.000217	3	0.000508	0.442832
gi|6323138 YLR109W	Thiol-specific peroxiredoxin, reduces hydroperoxides to protect against oxidative damage; function in vivo requires covalent conjugation to Urm1p; Ahp1p	0	176	3	10.2	14	8	0.001176	6	0.000819	1	9.7	2	0	6.31E-05	2	0.000773	1	9.7	2	0	6.54E-05	2	0.000783	3	10.2	10	8	0.004005	2	0.000914	0.443702
gi|6320011 YDL190C	Ubiquitin chain assembly factor (E4) that cooperates with a ubiquitin-activating enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a ubiquitin protein ligase (E3) to conjugate ubiquitin to substrates; also functions as an E3; Ufd2p	0	961	10	4	22	9	0.000241	13	0.000311	4	3.6	9	4	0.000289	5	0.000338	3	4	4	0	1.2E-05	4	0.000276	5	3.6	9	5	0.000464	4	0.000322	0.443871
gi|6319993 YDL208W	Nuclear protein related to mammalian high mobility group (HMG) proteins, essential for function of H/ACA-type snoRNPs, which are involved in 18S rRNA processing; Nhp2p	0	173	7	39.9	24	10	0.001478	14	0.001858	3	27.2	7	4	0.001605	3	0.001149	2	9.8	9	3	0.001264	6	0.002268	5	30.1	8	3	0.00158	5	0.002218	0.451149
gi|6321552 YGR116W	Essential protein that interacts with histones and is involved in nucleosome disassembly and reassembly during transcription elongation; Spt6p	0	1451	16	11.7	44	23	0.000394	21	0.000328	6	6.5	20	11	0.000513	9	0.000397	8	6.5	14	7	0.000341	7	0.000314	8	6.1	10	5	0.000307	5	0.000264	0.451334
gi|6323619 YML022W	Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine and 5-phosphoribosylpyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis; Apt1p	0	187	5	20.9	21	11	0.001497	10	0.001245	2	7.5	4	2	0.000772	2	0.000728	2	13.4	4	4	0.001539	0	5.67E-05	4	15	13	5	0.002385	8	0.003243	0.453287
gi|6323837 YMR183C	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p; Sso2p	1	295	9	9.2	23	11	0.000949	12	0.000939	1	9.2	2	0	3.76E-05	2	0.000461	1	7.8	1	0	3.9E-05	1	0.000252	8	8.5	20	11	0.003267	9	0.002308	0.455141
gi|6324033 YNL297C	Peripheral membrane protein with a role in endocytosis and vacuole integrity, interacts with Arl1p and localizes to the endosome; member of the Sec7p family of proteins; Mon2p	0	1636	7	2.3	23	9	0.000141	14	0.000196	3	1.2	6	2	8.82E-05	4	0.00016	4	1.2	7	4	0.000176	3	0.000123	6	2.3	10	3	0.000167	7	0.000325	0.455448
gi|6322228 YIR037W	Thiol peroxidase that functions as a hydroperoxide receptor to sense intracellular hydroperoxide levels and transduce a redox signal to the Yap1p transcription factor; Hyr1p	0	163	2	9.2	3	2	0.000373	1	0.000204	1	9.2	1	1	0.000477	0	6.42E-05	1	9.2	1	1	0.000494	0	6.5E-05	1	9.2	1	0	8.83E-05	1	0.000532	0.455544
gi|6324366 YNR038W	Essential protein involved in ribosome biogenesis; putative ATP-dependent RNA helicase of the DEAD-box protein family; Dbp6p	0	629	2	3.3	3	2	9.68E-05	1	5.29E-05	1	3.3	1	1	0.000124	0	1.66E-05	1	3.3	1	1	0.000128	0	1.69E-05	1	3	1	0	2.29E-05	1	0.000138	0.455544
gi|6320197 YDL007W	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for normal peptide hydrolysis by the core 20S particle; Rpt2p	0	437	6	13	17	9	0.000529	8	0.000431	2	4.3	6	2	0.00033	4	0.000599	4	13	8	4	0.000658	4	0.000607	2	4.3	3	3	0.000625	0	2.83E-05	0.455674
gi|6325041 YPL215W	Mitochondrial protein required for assembly of ubiquinol cytochrome-c reductase complex (cytochrome bc1 complex); interacts with Cbp4p and function is partially redundant with that of Cbp4p; Cbp3p	0	335	6	7.2	16	9	0.00069	7	0.000496	3	7.2	9	4	0.000829	5	0.000968	2	7.2	3	1	0.00024	2	0.000411	3	7.2	4	4	0.001074	0	3.69E-05	0.455736
gi|6321303 YGL135W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1bp	0	217	7	9.2	32	12	0.001402	20	0.002094	3	8.3	6	0	5.12E-05	6	0.001784	7	9.2	21	9	0.002917	12	0.003567	3	8.3	5	3	0.00126	2	0.000742	0.459157
gi|6321333 YGL105W	Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization to the cytoplasm; also binds quadruplex nucleic acids; Arc1p	0	376	8	19.1	16	6	0.000421	10	0.000619	5	16	8	3	0.000561	5	0.000863	4	9.6	7	3	0.000582	4	0.000705	1	5.9	1	0	3.83E-05	1	0.00023	0.461305
gi|6321672 YGR233C	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p-Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p; Pho81p	0	1178	11	8.7	21	11	0.000238	10	0.000198	6	6.2	10	2	0.000123	8	0.000435	2	2.6	3	3	0.000186	0	9E-06	4	3.7	8	6	0.000452	2	0.000137	0.46208
gi|3736264 YGL245W	Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm; Gus1p	0	708	38	21.9	140	52	0.001805	88	0.002771	9	10.3	24	7	0.000674	17	0.001523	6	9.6	14	2	0.000211	12	0.001093	25	15.1	102	43	0.005263	59	0.006206	0.463693
gi|6324850 YOR276W	Phosphoprotein of the mRNA cap-binding complex involved in translational control, repressor of cap-dependent translation initiation, competes with eIF4G for binding to eIF4E; Caf20p	0	161	2	11.8	5	1	0.000227	4	0.00062	1	11.8	1	0	6.9E-05	1	0.000455	1	11.8	3	0	7.15E-05	3	0.001251	1	11.8	1	1	0.000625	0	7.69E-05	0.464138
gi|6323048 YLR020C	Steryl ester hydrolase, catalyzes steryl ester hydrolysis at the plasma membrane; involved in sterol metabolism; Yeh2p	1	538	7	8.7	21	8	0.000385	13	0.000556	3	5.8	5	2	0.000268	3	0.00037	1	3	2	0	2.14E-05	2	0.000256	5	5.4	14	6	0.000989	8	0.001127	0.464422
gi|6319589 YBR112C	General transcriptional co-repressor, acts together with Tup1p; also acts as part of a transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters; Cyc8p	0	966	12	5.2	70	39	0.000995	31	0.000723	11	5.2	35	16	0.001115	19	0.001246	5	2.3	29	18	0.001299	11	0.000735	3	2	6	5	0.000462	1	8.97E-05	0.465034
gi|6321906 YHR114W	SH3 domain protein implicated in the regulation of actin polymerization, able to recruit actin polymerization machinery through its SH3 domains, colocalizes with cortical actin patches and Las17p, interacts with type I myosins; Bzz1p	0	633	5	6	9	5	0.000212	4	0.000158	2	6	4	1	0.000123	3	0.000314	1	2.5	3	3	0.000345	0	1.68E-05	2	2.8	2	1	0.000159	1	0.000137	0.465749

gi|6319497 YBR023C	Chitin synthase III, catalyzes the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for synthesis of the majority of cell wall chitin, the chitin ring during bud emergence, and spore wall chitosan; Chs3p	6	1165	2	1.5	19	9	0.000199	10	0.0002	1	1.5	2	0	9.53E-06	2	0.000117	2	1.5	13	8	0.000484	5	0.000282	2	1.5	4	1	8.64E-05	3	0.000202	0.465968
gi|6324042 YNL287W	Gamma subunit of coatomer, a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo; Sec21p	0	935	8	7.9	17	6	0.000169	11	0.000273	4	4.5	5	4	0.000297	1	7.84E-05	2	3.4	5	2	0.00016	3	0.000215	3	3.5	7	0	1.54E-05	7	0.000569	0.466374
gi|6321339 YGL099W	Putative GTPase involved in 60S ribosomal subunit biogenesis; required for the release of Nmd3p from 60S subunits in the cytoplasm; Lsg1p	0	640	11	10.9	33	12	0.000475	21	0.000745	6	6.2	11	8	0.00085	3	0.000311	5	8.8	14	1	0.000126	13	0.001309	6	5.5	8	3	0.000427	5	0.0006	0.467679
gi|6324146 YNL183C	Protein kinase that stabilizes several plasma membrane amino acid transporters by antagonizing their ubiquitin-mediated degradation; Npr1p	0	790	4	2.5	41	12	0.000385	29	0.000828	3	2.5	17	6	0.00052	11	0.000888	4	2.5	23	6	0.000539	17	0.001382	1	2	1	0	1.82E-05	1	0.00011	0.470045
gi|6321650 YGR211W	Essential protein with two zinc fingers, present in the nucleus of growing cells but relocates to the cytoplasm in starved cells via a process mediated by Cpr1p; binds to translation elongation factor eEF-1 (Tef1p); Zpr1p	0	486	2	5.1	3	2	0.000125	1	6.84E-05	1	2.9	1	0	2.28E-05	1	0.000151	1	2.3	1	1	0.000166	0	2.18E-05	1	2.3	1	1	0.000207	0	2.55E-05	0.470075
gi|6323857 YMR201C	Protein that recognizes and binds damaged DNA during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 1 (NEF1); contains zinc finger motif; homolog of human XPA protein; Rad14p	0	371	2	5.7	3	2	0.000164	1	8.96E-05	1	5.7	1	0	2.99E-05	1	0.000197	1	5.7	1	1	0.000217	0	2.86E-05	1	5.7	1	1	0.000271	0	3.34E-05	0.470075
gi|6323278 YLR249W	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p	0	1044	315	43.9	1956	757	0.017664	1199	0.025471	146	38.5	423	174	0.011114	249	0.014987	124	34.7	545	198	0.013107	347	0.021155	151	33.9	988	385	0.031844	603	0.042908	0.470302
gi|6321612 YGR173W	Protein with similarity to mammalian developmentally regulated GTP-binding protein; Rbg2p	0	368	17	14.4	53	26	0.001753	27	0.001657	10	13.9	23	9	0.00166	14	0.002417	10	14.4	23	10	0.001908	13	0.002276	2	4.9	7	7	0.001681	0	3.36E-05	0.473299
gi|6321198 YGL238W	Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), homolog of metazoan CAS protein, required for accurate chromosome segregation; Cse1p	0	960	9	10.4	21	11	0.000292	10	0.000242	4	7.4	12	5	0.000359	7	0.000469	3	4.6	6	4	0.0003	2	0.000144	2	2.8	3	2	0.000195	1	9.03E-05	0.47434
gi|6324568 YOL006C	Topoisomerase I, nuclear enzyme that relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone; relaxes both positively and negatively supercoiled DNA; functions in replication, transcription, and recombination; Top1p	0	769	7	6.9	15	6	0.000206	9	0.000274	2	4	2	1	0.000101	1	9.53E-05	2	4	4	0	1.5E-05	4	0.000345	5	4.9	9	5	0.00058	4	0.000402	0.475921
gi|6323712 YMR067C	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p; Ubx4p	0	416	8	12.7	17	6	0.00038	11	0.000613	4	9.6	8	0	2.67E-05	8	0.001233	2	6.2	6	5	0.000858	1	0.000178	2	9.1	3	1	0.000242	2	0.000387	0.476055
gi|6321720 YGR281W	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates export of many different organic anions including oligomycin; Yor1p	11	1477	26	8.5	103	57	0.000948	46	0.000698	6	2.4	13	9	0.000413	4	0.000177	20	7	74	37	0.001738	37	0.001601	8	4.2	16	11	0.000653	5	0.00026	0.483817
gi|6324833 YOR259C	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle; Rpt4p	0	437	10	20.4	34	15	0.000863	19	0.000989	8	20.1	16	9	0.001397	7	0.00103	5	10.3	10	5	0.000816	5	0.000752	3	6.9	8	1	0.00023	7	0.001218	0.483879
gi|6321020 YER172C	RNA-dependent ATPase RNA helicase involved in the facilitation and disruption of snRNA interactions, required for disruption of U4/U6 base-pairing in native snRNPs to activate the spliceosome for catalysis; Brr2p	0	2163	4	1.8	7	3	3.94E-05	4	4.61E-05	2	0.8	4	2	6.67E-05	2	6.29E-05	2	1	2	1	3.72E-05	1	3.43E-05	1	0.8	1	0	6.65E-06	1	4.01E-05	0.483962
gi|6324775 YOR201C	Ribose methyltransferase that modifies a functionally critical, conserved nucleotide in mitochondrial 21S rRNA; Mrm1p	0	412	3	5.8	7	3	0.000207	4	0.000242	2	5.8	4	2	0.00035	2	0.00033	2	5.8	2	1	0.000196	1	0.00018	1	5.8	1	0	3.49E-05	1	0.00021	0.483962
gi|1427068 YBL004W	Component of the small-subunit (SSU) processome, which is involved in the biogenesis of the 18S rRNA; Utp20p	0	2493	9	3	16	7	7.32E-05	9	8.45E-05	6	2.6	9	5	0.000138	4	0.000105	2	1.1	2	0	4.62E-06	2	5.53E-05	3	1.4	5	2	7.5E-05	3	9.43E-05	0.487804
gi|6323360 YLR328W	Nicotinic acid mononucleotide adenylyltransferase, involved in NAD(+) salvage pathway; Nma1p	0	401	2	6.5	4	1	9.11E-05	3	0.000193	1	6.5	1	1	0.000194	0	2.61E-05	1	6.5	2	0	2.87E-05	2	0.000344	1	6.5	1	0	3.59E-05	1	0.000216	0.489304
gi|6321196 YGL241W	Karyopherin, responsible for nuclear import of Spt15p, histones H2A and H2B, and Nap1p; amino terminus shows similarity to those of other importins, particularly Cse1p; localization is primarily nuclear; Kap114p	0	1004	2	1.7	4	1	3.64E-05	3	7.73E-05	1	1.7	2	0	1.11E-05	2	0.000136	1	1.7	1	1	8.02E-05	0	1.06E-05	1	1.7	1	0	1.43E-05	1	8.63E-05	0.491767
gi|6319602 YBR126C	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p	0	495	14	8.7	37	16	0.000811	21	0.000963	4	7.7	6	1	0.000157	5	0.000655	6	8.3	13	2	0.000302	11	0.001435	7	6.9	18	13	0.002296	5	0.000775	0.493526
gi|6321706 YGR267C	GTP-cyclohydrolase I, catalyzes the first step in the folic acid biosynthetic pathway; Fol2p	0	243	3	14.8	4	1	0.00015	3	0.000319	1	5.8	1	1	0.00032	0	4.31E-05	1	7.8	1	0	4.74E-05	1	0.000305	1	7.4	2	0	5.92E-05	2	0.000662	0.495726
gi|6324489 YOL083W	hypothetical protein; Yol083wp	0	412	3	7.5	4	1	8.86E-05	3	0.000188	1	3.9	1	1	0.000189	0	2.54E-05	1	3.9	1	0	2.79E-05	1	0.00018	1	3.6	2	0	3.49E-05	2	0.000391	0.495726
gi|6323873 YMR217W	GMP synthase, an enzyme that catalyzes the second step in the biosynthesis of GMP from inosine 5'-phosphate (IMP); transcription is not subject to regulation by guanine but is negatively regulated by nutrient starvation; Gua1p	0	525	4	3.4	14	7	0.000348	7	0.000317	4	3.4	7	3	0.000402	4	0.000498	2	3.4	5	2	0.000285	3	0.000384	1	3.4	2	2	0.000356	0	2.36E-05	0.496068
gi|6320016 YDL185W	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-SceI), which is a site-specific endonuclease; Tfp1p	0	1071	35	17.2	86	33	0.000761	53	0.001107	17	11	38	14	0.000881	24	0.001417	12	10.2	17	9	0.000591	8	0.000485	11	10.6	31	10	0.000819	21	0.001468	0.49611
gi|6319392 YBL079W	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p; Nup170p	0	1502	27	7.5	95	51	0.000835	44	0.000657	25	7.5	72	32	0.001427	40	0.001679	9	6.5	17	16	0.000743	1	4.94E-05	2	1.1	6	3	0.000182	3	0.000157	0.496151
gi|6323002 YLL026W	Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold and reactivate previously denatured, aggregated proteins; responsive to stresses including: heat, ethanol, and sodium arsenite; involved in [PSI+] propagation; Hsp104p	0	908	16	15.9	61	30	0.000818	31	0.000769	11	13.1	24	11	0.000819	13	0.000911	5	5.9	32	14	0.001077	18	0.001273	3	4.7	5	5	0.000491	0	1.36E-05	0.496505

gi|6319432	YBL039C	Major CTP synthase isozyme (see also URA8), catalyzes the ATP-dependent transfer of the amide nitrogen from glutamine to UTP, forming CTP, the final step in de novo biosynthesis of pyrimidines; involved in phospholipid biosynthesis; Ura7p	0	579	5	5.9	16	9	0.000399	7	0.000287	2	3.1	7	3	0.000364	4	0.000452	3	5.7	4	1	0.000139	3	0.000348	3	3.3	5	5	0.00077	0	2.14E-05	0.496747
gi|6321611	YGR172C	Integral membrane protein required for the biogenesis of ER-derived COPII transport vesicles; interacts with Yif1p and Yos1p; localizes to the Golgi, the ER, and COPII vesicles; Yip1p	5	248	10	13.3	52	23	0.002307	29	0.002637	7	7.7	14	7	0.001925	7	0.001815	2	7.7	6	0	4.64E-05	6	0.001582	8	13.3	32	16	0.005627	16	0.004841	0.500558
gi|6323894	YMR238W	Putative mannosidase, essential glycosylphosphatidylinositol (GPI)-anchored membrane protein required for cell wall biogenesis in bud formation, involved in filamentous growth, homologous to Dcw1p; Dfg5p	1	458	3	3.9	32	13	0.000718	19	0.000944	2	3.9	13	7	0.001042	6	0.000845	3	3.9	17	6	0.00093	11	0.001551	1	3.9	2	0	3.14E-05	2	0.000351	0.501411
gi|6324787	YOR213C	Subunit of the SAS complex (Sas2p, Sas4p, Sas5p), which acetylates free histones and nucleosomes and regulates transcriptional silencing; stimulates Sas2p HAT activity; Sas5p	0	248	4	7.7	14	6	0.000638	8	0.00076	3	7.7	6	3	0.000851	3	0.000802	1	7.7	2	0	4.64E-05	2	0.000556	2	7.7	6	3	0.001102	3	0.000948	0.501758
gi|6321832	YHR042W	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p; Ncp1p	0	691	56	26.2	252	139	0.004915	113	0.003641	38	26.2	144	75	0.007247	69	0.006286	11	15.6	52	41	0.004114	11	0.001028	23	12.2	56	23	0.002894	33	0.003565	0.502409
gi|6320890	YER049W	hypothetical protein; Tpa1p	0	644	22	21.1	55	30	0.001153	25	0.000878	6	9.3	11	6	0.000638	5	0.000504	8	11.8	17	12	0.001305	5	0.00051	14	12.9	27	12	0.001631	15	0.001749	0.502792
gi|6320505	YDR299W	Essential protein possibly involved in secretion; multicopy suppressor of sensitivity to Brefeldin A; Bfr2p	0	534	5	10.9	10	8	0.000388	2	0.000104	3	9.2	4	3	0.000395	1	0.000137	1	5.2	1	0	2.16E-05	1	0.000139	2	3.6	5	5	0.000835	0	2.32E-05	0.504459
gi|6324785	YOR211C	Mitochondrial GTPase related to dynamin, present in a complex containing Ugo1p and Fzo1p; required for normal morphology of cristae and for stability of Tim11p; homolog of human OPA1 involved in autosomal dominant optic atrophy; Mgm1p	0	902	5	3.2	22	10	0.000283	12	0.000307	2	1.9	7	5	0.000382	2	0.000151	4	1.9	13	3	0.000242	10	0.000717	2	3.2	2	2	0.000207	0	1.37E-05	0.504646
gi|6324588	YOR014W	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the mammalian B' subunit of PP2A; Rts1p	0	757	25	12.2	105	53	0.00172	52	0.001537	13	9.6	41	23	0.002039	18	0.001507	13	11.9	33	17	0.001566	16	0.001359	10	9	31	13	0.001501	18	0.001782	0.504855
gi|6319849	YCR004C	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ycp4p	0	247	12	21.1	39	22	0.002218	17	0.001571	7	21.1	10	6	0.001663	4	0.001059	7	17.8	24	13	0.003681	11	0.002876	4	11.3	5	3	0.001107	2	0.000651	0.506689
gi|6321360	YGL078C	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; Dbp3p	0	523	39	28.3	94	51	0.002397	43	0.001844	12	17.4	18	10	0.001295	8	0.000981	15	18	30	22	0.002927	8	0.000993	19	15.3	46	19	0.003163	27	0.003858	0.511053
gi|6324484	YOL088C	Member of the protein disulfide isomerase (PDI) family, exhibits chaperone activity; overexpression suppresses the lethality of a pdi1 deletion but does not complement all Pdi1p functions; undergoes oxidation by Ero1p; Mpd2p	0	277	4	20.9	6	4	0.000395	2	0.0002	1	5.8	2	0	4.01E-05	2	0.000491	2	11.2	3	3	0.000789	0	3.83E-05	1	4	1	1	0.000364	0	4.47E-05	0.512915
gi|6324574	YOR001W	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus; Rrp6p	0	733	34	11.5	86	39	0.001312	47	0.001437	19	7.4	39	19	0.001742	20	0.001728	13	6.7	35	19	0.001806	16	0.001403	5	4	12	1	0.000137	11	0.001131	0.514076
gi|6321318	YGL120C	RNA helicase in the DEAH-box family, involved in release of the lariat-intron from the spliceosome; Prp43p	0	767	17	12.1	45	22	0.000714	23	0.000679	7	6.5	17	10	0.000883	7	0.000587	10	7.8	19	12	0.001095	7	0.000594	5	9.1	9	0	1.88E-05	9	0.000888	0.51583
gi|6323112	YLR083C	Protein whose 24kDa cleavage product is found in endosome-enriched membrane fractions, predicted to be a transmembrane protein; Emp70p	9	667	3	4.8	6	4	0.000164	2	8.31E-05	1	2.4	2	0	1.66E-05	2	0.000204	1	2.4	1	1	0.000121	0	1.59E-05	1	2.4	3	3	0.00041	0	1.86E-05	0.522598
gi|6320793	YEL042W	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate; Gda1p	1	518	18	11.6	51	27	0.001292	24	0.001049	11	9.1	26	14	0.001822	12	0.001475	2	4.1	3	3	0.000422	0	2.05E-05	8	6.9	22	10	0.001694	12	0.001744	0.523162
gi|6321626	YGR187C	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm; Hgh1p	0	394	14	9.1	60	34	0.002132	26	0.001491	4	9.1	11	7	0.001212	4	0.000664	5	9.1	9	6	0.001081	3	0.000511	12	8.9	40	21	0.004637	19	0.003613	0.5272
gi|6321477	YGR040W	Mitogen-activated protein kinase (MAPK) involved in signal transduction pathways that control filamentous growth and pheromone response; Kss1p	0	368	12	11.1	33	17	0.001158	16	0.000994	2	6	6	4	0.000754	2	0.00037	5	10.6	7	5	0.000969	2	0.000375	8	10.3	20	8	0.001915	12	0.002455	0.530342
gi|6321301	YGL137W	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p	0	889	12	10.7	33	17	0.000479	16	0.000411	5	6.4	12	5	0.000387	7	0.000506	4	6.2	9	5	0.000401	4	0.000298	6	3.1	12	7	0.000696	5	0.000432	0.530349
gi|6321527	YGR090W	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data; Utp22p	0	1237	13	5.4	27	12	0.000246	15	0.000278	2	2.1	7	0	8.98E-06	7	0.000364	7	2	9	6	0.000344	3	0.000163	6	3.2	11	6	0.00043	5	0.00031	0.531045
gi|6322086	YIL105C	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; subunit of and phosphorylated by the TORC2 complex; Slm1p	0	686	10	4.1	20	11	0.000408	9	0.000307	4	4.1	6	5	0.000502	1	0.000107	6	4.1	12	5	0.00052	7	0.000665	2	2.9	2	1	0.000147	1	0.000126	0.53631
gi|6321909	YHR117W	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins; Tom71p	0	639	11	3.1	28	10	0.0004	18	0.000642	6	3.1	11	5	0.000539	6	0.000606	2	1.9	3	1	0.000126	2	0.000216	5	2.5	14	4	0.000563	10	0.001182	0.540985
gi|6320956	YER110C	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1; Kap123p	0	1113	23	7.4	86	49	0.001083	37	0.000747	15	4.2	45	27	0.001626	18	0.001025	14	6	36	18	0.001127	18	0.001038	4	3.1	5	4	0.000323	1	7.78E-05	0.54426
gi|6324343	YNR016C	Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p	0	2233	52	12.9	159	82	0.000899	77	0.000769	33	10.2	84	39	0.001169	45	0.00127	20	8.2	35	20	0.000624	15	0.000432	12	4.7	40	23	0.000895	17	0.000571	0.545699
gi|6322434	YJL026W	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr2p	0	399	10	13.3	21	11	0.000702	10	0.000583	3	6.5	4	3	0.000529	1	0.000184	5	13.3	10	5	0.000894	5	0.000824	5	6.5	7	3	0.000685	4	0.000776	0.545803
gi|6319483	YBR011C	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p	0	287	12	23	20	8	0.000721	12	0.000966	7	13.9	12	5	0.001199	7	0.001568	3	17.1	4	1	0.000281	3	0.000702	3	9.1	4	2	0.000652	2	0.000561	0.546587

gi|6324327 YNL001W	Probable RNA-binding protein, functions in protein translation to promote G1 progression and differentiation, required for meiotic cell division; Dom34p	0	386	7	11.9	19	10	0.000662	9	0.000546	2	7.8	5	4	0.000719	1	0.00019	2	4.1	4	2	0.000388	2	0.000357	4	4.1	10	4	0.000932	6	0.001186	0.548571
gi|6322923 YKR070W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondrion; Ykr070wp	0	352	3	13.4	5	3	0.000242	2	0.000157	1	4	1	1	0.000221	0	2.97E-05	1	5.4	2	2	0.000425	0	3.01E-05	1	4	2	0	4.09E-05	2	0.000457	0.550562
gi|6320983 YER136W	GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by regulating the dissociation of GDP from the Sec4/Ypt/rab family of GTP binding proteins; Gdi1p	0	451	5	12.6	11	4	0.000243	7	0.000369	2	6	3	1	0.000172	2	0.000302	2	6.7	2	1	0.000179	1	0.000165	2	3.3	6	2	0.000415	4	0.000686	0.551206
gi|6323021 YLL008W	Nucleolar DEAD-box protein required for ribosome assembly and function, including synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles; Drs1p	0	752	7	12.1	11	2	8.09E-05	9	0.00028	4	8.4	6	1	0.000103	5	0.000431	1	2.4	1	1	0.000107	0	1.41E-05	3	6.1	4	0	1.91E-05	4	0.000412	0.551337
gi|6323411 YLR378C	Essential subunit of Sec61 complex (Sec61p, Sbh1p, and Sss1p); forms a channel for SRP-dependent protein import and retrograde transport of misfolded proteins out of the ER; with Sec63 complex allows SRP-independent protein import into ER; Sec61p	5	480	8	6	35	9	0.000482	26	0.001224	4	4.2	15	2	0.000301	13	0.001722	2	4.2	3	2	0.000312	1	0.000155	6	6	17	5	0.000929	12	0.001882	0.551475
gi|6323967 YMR307W	Beta-1,3-glucanosyltransferase, required for cell wall assembly; localizes to the cell surface via a glycosylphosphatidylinositol (GPI) anchor; Gas1p	0	559	13	5.7	47	24	0.001067	23	0.000932	4	3.4	4	3	0.000377	1	0.000131	4	2.3	8	6	0.000762	2	0.000247	7	4.7	35	15	0.002342	20	0.002679	0.554627
gi|6325175 YPL082C	Essential abundant protein involved in regulation of transcription, removes Spt15p (TBP) from DNA via its C-terminal ATPase activity, forms a complex with TBP that binds TATA DNA with high affinity but with altered specificity; Mot1p	0	1867	5	2.2	7	3	4.56E-05	4	5.34E-05	1	1	2	0	5.95E-06	2	7.29E-05	2	1	2	1	4.32E-05	1	3.98E-05	3	2	3	2	0.0001	1	4.64E-05	0.554722
gi|6321231 YGL207W	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure; Spt16p	0	1035	15	9.5	67	46	0.001094	21	0.000461	1	1.1	1	1	7.51E-05	0	1.01E-05	2	1.5	3	2	0.000145	1	7.17E-05	12	6.9	63	43	0.0036	20	0.001447	0.555062
gi|6320439 YDR233C	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily; Rtn1p	2	295	31	27.8	81	42	0.003507	39	0.002968	14	27.8	29	11	0.002522	18	0.003867	13	13.9	38	21	0.004955	17	0.003702	9	11.9	14	10	0.002975	4	0.001049	0.558301
gi|6320053 YDL148C	Nucleolar protein, forms a complex with Noc4p that mediates maturation and nuclear export of 40S ribosomal subunits; also present in the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop14p	0	810	10	8.3	26	11	0.000346	15	0.000424	5	6	6	3	0.00026	3	0.000245	4	6	11	6	0.000526	5	0.000406	4	4.9	9	2	0.000231	7	0.000657	0.560731
gi|6323216 YLR187W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate; similar to Caf120p and Skg4p; Skg3p	0	1026	4	2.9	11	5	0.000131	6	0.00014	1	1.8	1	0	1.08E-05	1	7.14E-05	2	2.9	4	1	7.85E-05	3	0.000196	2	1.8	6	4	0.000351	2	0.000157	0.561176
gi|6321808 YHR020W	Putative protein of unknown function, has similarity to proline-tRNA ligase; YHR020W is an essential gene; Yhr020wp	0	688	4	6.2	19	9	0.000336	10	0.000338	4	6.2	6	4	0.000403	2	0.000198	4	6.2	10	5	0.000519	5	0.000478	1	1.9	3	0	2.09E-05	3	0.000342	0.5646
gi|6323954 YMR296C	Component of serine palmitoyltransferase, responsible along with Lcb2p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb1p	0	558	8	3.4	16	7	0.000327	9	0.000377	4	3.4	10	2	0.000259	8	0.000919	2	3.4	4	4	0.000516	0	1.9E-05	2	3.2	2	1	0.00018	1	0.000155	0.565233
gi|6325423 YPR165W	GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p); Rho1p	0	209	7	21.1	9	7	0.000874	2	0.000265	2	5.7	2	2	0.000691	0	5.01E-05	1	6.7	1	0	5.51E-05	1	0.000355	4	14.4	6	5	0.002134	1	0.000415	0.565332
gi|6324825 YOR251C	catalyzes transfer of the sulfane atom of thiosulfate to cyanide to form sulfite and thiocyanate; Yor251cp	0	304	6	9.9	10	5	0.00044	5	0.000401	1	9.9	2	2	0.000475	0	3.44E-05	2	9.9	3	1	0.000265	2	0.000453	3	8.9	5	2	0.000615	3	0.000774	0.566504
gi|6323840 YMR186W	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10-fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p	0	705	45	28.7	100	51	0.001778	49	0.001557	26	20.1	48	22	0.002095	26	0.002331	13	11.6	22	15	0.001486	7	0.000647	17	14.6	30	14	0.001734	16	0.001703	0.5678
gi|6323777 YMR129W	Nuclear pore membrane glycoprotein; may be involved in duplication of nuclear pores and nuclear pore complexes during S-phase; Pom152p	3	1337	9	7.3	22	14	0.000264	8	0.000141	6	5.4	13	9	0.000457	4	0.000196	2	2.2	2	1	6.03E-05	1	5.55E-05	3	1.8	7	4	0.000269	3	0.000176	0.568976
gi|6323885 YMR229C	Protein required for the synthesis of both 18S and 5.8S rRNA; C-terminal region is crucial for the formation of 18S rRNA and N-terminal region is required for the 5.8S rRNA; component of small ribosomal subunit (SSU) processosome; Rrp5p	0	1729	12	5.7	29	16	0.000232	13	0.000173	6	3.5	7	3	0.000122	4	0.000151	5	3	8	5	0.000206	3	0.000117	5	2.9	14	8	0.000408	6	0.000265	0.570262
gi|6323788 YMR139W	Protein kinase required for signal transduction during entry into meiosis; promotes the formation of the Ime1p-Ume6p complex by phosphorylating Ime1p and Ume6p; shares similarity with mammalian glycogen synthase kinase 3-beta; Rim11p	0	370	2	10.8	3	1	9.87E-05	2	0.00015	1	5.4	1	1	0.00021	0	2.83E-05	1	5.4	1	0	3.11E-05	1	0.000201	1	5.4	1	0	3.89E-05	1	0.000234	0.576798
gi|6323371 YLR340W	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p	0	312	48	32.1	161	85	0.006671	76	0.005436	27	24	65	34	0.007296	31	0.006273	35	27.2	88	44	0.009775	44	0.009006	3	12.2	8	7	0.001983	1	0.000278	0.57691
gi|6322082 YIL109C	Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the binding of the Sec13 complex to ER membranes; homologous to Lst1p and Lss1p; Sec24p	0	926	11	7.2	26	12	0.000329	14	0.000347	5	5.9	8	4	0.0003	4	0.000283	7	6.4	12	7	0.000534	5	0.000355	4	4.6	6	1	0.000109	5	0.000414	0.577368
gi|6325267 YPR010C	RNA polymerase I subunit A135; Rpa135p	0	1203	32	12.9	97	52	0.001062	45	0.000838	14	9.8	32	25	0.001394	7	0.000374	13	8	30	10	0.000584	20	0.001066	14	6.8	35	17	0.001232	18	0.001122	0.582235
gi|6320353 YDR150W	Protein required for nuclear migration, localizes to the mother cell cortex and the bud tip; may mediate interactions of dynein and cytoplasmic microtubules with the cell cortex; Num1p	0	2748	10	3.5	31	17	0.000155	14	0.000117	6	2.5	18	14	0.000343	4	9.52E-05	1	0.6	4	0	4.19E-06	4	9.65E-05	3	1.5	9	3	9.95E-05	6	0.000167	0.583105
gi|6325253 YPL004C	Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Pil1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Lsp1p	0	341	13	26.1	29	12	0.000892	17	0.001138	6	13.2	10	4	0.000814	6	0.001136	11	26.1	18	8	0.001654	10	0.001897	1	5.3	1	0	4.22E-05	1	0.000254	0.585549
gi|6323969 YMR309C	Subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the assembly of preinitiation complex and start codon selection; Nip1p	0	812	28	13.5	58	25	0.000765	33	0.000915	18	11.2	28	15	0.001244	13	0.001018	6	8.4	8	2	0.000184	6	0.000483	12	8.7	22	8	0.000868	14	0.001296	0.586526

gi|6319698 YBR221C	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p	0	366	30	33.1	140	77	0.005155	63	0.003846	19	26	42	29	0.005309	13	0.002259	6	3.3	25	12	0.002295	13	0.002289	17	20.5	73	36	0.008529	37	0.007542	0.586991
gi|6320061 YDL140C	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p	0	1733	16	5.5	130	72	0.001018	58	0.000748	14	4.8	40	24	0.000929	16	0.000586	6	1.3	24	12	0.000485	12	0.000447	7	3.3	66	36	0.001801	30	0.001293	0.587587
gi|6322582 YJR122W	Mitochondrial protein that interacts with Ccr4p in the two-hybrid system; 3'-untranslated region contains a putative mRNA localization element common to genes encoding mitochondrial proteins; Caf17p	0	497	2	3.2	11	6	0.000318	5	0.000245	1	3.2	4	4	0.000559	0	2.11E-05	1	3.2	2	2	0.000301	0	2.13E-05	1	3.2	5	0	2.89E-05	5	0.000772	0.588679
gi|6324491 YOL081W	GTPase-activating protein that negatively regulates RAS by converting it from the GTP- to the GDP-bound inactive form, required for reducing cAMP levels under nutrient limiting conditions, has similarity to Ira1p and human neurofibromin; Ira2p	0	3079	3	0.9	3	1	1.19E-05	2	1.8E-05	1	0.4	1	0	3.61E-06	1	2.38E-05	1	0.6	1	0	3.74E-06	1	2.41E-05	1	0.4	1	1	3.27E-05	0	4.02E-06	0.589287
gi|6323368 YLR336C	Essential nuclear protein with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia; Sgd1p	0	899	13	5.7	52	24	0.000663	28	0.000703	5	3.9	17	6	0.000457	11	0.00078	3	4	4	4	0.00032	0	1.18E-05	8	3.9	31	14	0.00136	17	0.001418	0.593608
gi|6320306 YDR101C	Protein associated with the ribosomal export complex; Arx1p	0	593	4	6.6	7	4	0.000185	3	0.000131	2	6.6	3	3	0.000356	0	1.76E-05	1	2.7	1	1	0.000136	0	1.79E-05	2	6.2	3	0	2.43E-05	3	0.000397	0.596774
gi|6320510 YDR304C	Peptidyl-prolyl cis-trans isomerase (cyclophilin) of the endoplasmic reticulum, catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; transcriptionally induced in response to unfolded proteins in the ER; Cpr5p	0	225	5	8.9	7	4	0.000487	3	0.000345	2	8.4	3	0	4.93E-05	3	0.000884	2	8.4	3	3	0.000972	0	4.71E-05	1	5.8	1	1	0.000448	0	5.5E-05	0.598353
gi|6323224 YLR195C	N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction; Nmt1p	0	455	7	13.8	39	17	0.000936	22	0.001096	5	10.5	14	8	0.001196	6	0.000851	4	10.5	10	4	0.000632	6	0.000862	5	13.8	15	5	0.00098	10	0.001659	0.598487
gi|6322870 YKR018C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; Ykr018cp	0	725	8	12.3	18	8	0.000285	10	0.000321	4	5.2	9	5	0.000475	4	0.000361	4	10.1	5	1	0.000111	4	0.000366	2	3	4	2	0.000258	2	0.000222	0.602055
gi|6321870 YHR079C	Serine-threonine kinase and endoribonuclease; transmembrane protein that initiates the unfolded protein response signal by regulating synthesis of Hac1p through HAC1 mRNA splicing; Ire1p	0	1115	6	2.8	15	3	7.64E-05	12	0.000249	5	2.8	7	2	0.000129	5	0.000291	1	1.3	1	1	7.23E-05	0	9.51E-06	1	1.3	7	0	1.29E-05	7	0.000477	0.602423
gi|6319972 YDL229W	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p	0	613	30	32.6	144	62	0.002482	82	0.002984	15	21.5	84	40	0.004365	44	0.004524	13	17.9	25	10	0.001145	15	0.001574	11	16.2	35	12	0.001713	23	0.002807	0.60244
gi|6319319 YAR002C-	Protein that forms a heterotrimeric complex with Erp2p, Emp24p, and Erv25p; member, along with Emp24p and Erv25p, of the p24 family involved in ER to Golgi transport and localized to COPII-coated vesicles; Erp1p	1	219	5	15.5	29	14	0.001612	15	0.001569	4	8.2	22	10	0.003093	12	0.003489	1	8.2	2	2	0.000683	0	4.84E-05	3	14.2	5	2	0.000854	3	0.001074	0.603368
gi|6320214 YDR011W	ABC transporter protein involved in multidrug resistance and resistance to singlet oxygen species; Snq2p	12	1501	15	6.4	27	12	0.000203	15	0.000229	1	0.5	2	0	7.4E-06	2	9.06E-05	11	5.7	18	8	0.000376	10	0.000431	5	2.3	7	4	0.00024	3	0.000157	0.605904
gi|1431843 YIL078W	Threonyl-tRNA synthetase, essential cytoplasmic protein; Ths1p	0	734	3	2.3	17	8	0.000282	9	0.000287	2	2.3	7	4	0.000378	3	0.000271	2	2.3	9	3	0.000298	6	0.000534	1	1.9	1	1	0.000137	0	1.69E-05	0.606047
gi|6323526 YML110C	2-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase, involved in ubiquinone (Coenzyme Q) biosynthesis; located in mitochondria; Coq5p	0	307	3	9.8	7	5	0.000436	2	0.000181	1	5.9	1	0	3.62E-05	1	0.000239	2	5.9	3	2	0.000487	1	0.000242	1	3.9	3	3	0.00089	0	4.03E-05	0.609173
gi|6321534 YGR097W	Component of the RNA polymerase II holoenzyme, phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes; Ask10p	0	1146	7	6.5	13	6	0.000138	7	0.000145	2	3.8	4	2	0.000126	2	0.000119	3	5.9	5	4	0.000251	1	6.48E-05	3	3.1	4	0	1.26E-05	4	0.00027	0.609199
gi|6322722 YKL127W	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p	0	570	8	3.5	44	22	0.000961	22	0.000875	6	3.5	18	8	0.000955	10	0.00112	4	3.5	11	7	0.000868	4	0.000465	5	3.5	15	7	0.001085	8	0.001064	0.610054
gi|6323801 YMR152W	Protein of unknown function; proposed to be involved in responding to DNA damaging agents; Yim1p	0	365	5	18.6	12	6	0.000434	6	0.000395	2	10.7	3	1	0.000213	2	0.000373	1	3.3	3	0	3.15E-05	3	0.000552	3	7.9	6	5	0.001222	1	0.000237	0.612422
gi|6322697 YKL152C	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p	0	247	21	36.4	42	17	0.001725	25	0.002289	10	27.9	15	6	0.001663	9	0.00233	13	29.6	22	9	0.002563	13	0.003391	4	21.5	5	2	0.000757	3	0.000952	0.615502
gi|6324893 YOR317W	Long chain fatty acyl-CoA synthetase with a preference for C12:0-C16:0 fatty acids; involved in the activation of imported fatty acids; not required for growth on nonfermentable carbon sources; essential for stationary phase; Faa1p	0	700	10	11.1	22	13	0.000469	9	0.000301	5	5.6	9	4	0.000397	5	0.000463	5	9.6	11	8	0.000806	3	0.000288	2	4.1	2	1	0.000144	1	0.000124	0.617695
gi|6319679 YBR202W	Component of the hexameric MCM complex, which is important for priming origins of DNA replication in G1 and becomes an active ATP-dependent helicase that promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase; Cdc47p	0	845	9	9.6	18	11	0.000331	7	0.000197	5	9.6	6	3	0.00025	3	0.000235	2	2.8	2	1	9.53E-05	1	8.78E-05	6	5.3	10	7	0.000732	3	0.000278	0.620757
gi|6320784 YEL051W	Subunit D of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; plays a role in the coupling of proton transport and ATP hydrolysis; Vma8p	0	256	4	18.8	15	7	0.000713	8	0.000736	3	14.5	7	2	0.000564	5	0.001267	3	18.8	7	5	0.001394	2	0.000538	1	5.9	1	0	5.62E-05	1	0.000338	0.621099
gi|6319499 YBR025C	hypothetical protein; Ybr025cp	0	394	39	28.4	167	96	0.005962	71	0.004023	26	21.8	75	44	0.007468	31	0.004967	14	21.3	72	43	0.007565	29	0.00471	7	18	20	9	0.002008	11	0.002105	0.621162
gi|6324715 YOR141C	Nuclear actin-related protein involved in chromatin remodeling, component of chromatin-remodeling enzyme complexes; Arp8p	0	881	8	4	21	11	0.000318	10	0.000264	3	4	7	2	0.000164	5	0.000368	3	4	6	5	0.000405	1	8.42E-05	5	2	8	4	0.000408	4	0.000351	0.623214
gi|6324031 YNL298W	Cdc42p activated signal transducing kinase of the PAK (p21-activated kinase) family, involved in septin ring assembly and cytokinesis; directly phosphorylates septins Cdc3p and Cdc10p; other yeast PAK family members are Ste20p and Skm1p; Cla4p	0	842	2	2.3	7	3	0.000101	4	0.000118	2	2.3	2	1	9.23E-05	1	8.7E-05	2	2.3	3	1	9.57E-05	2	0.000164	2	2.3	2	1	0.00012	1	0.000103	0.623538

gi|6325349 YPR091C	hypothetical protein; Ypr091cp	1	770	24	9.6	63	32	0.001028	31	0.000907	18	9.6	33	11	0.000966	22	0.001808	10	6.9	24	17	0.001539	7	0.000592	4	4.7	6	4	0.000467	2	0.000209	0.624353
gi|6319424 YBL047C	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p	0	1381	16	12.5	28	14	0.000256	14	0.000233	8	9.1	13	5	0.000249	8	0.000371	5	5.7	9	6	0.000308	3	0.000146	4	5.1	6	3	0.000198	3	0.00017	0.625964
gi|6323510 YML125C	Essential protein required for maturation of Gas1p and Pho8p; GFP-fusion protein localizes to the endoplasmic reticulum; null mutants have a cell separation defect; Pga3p	2	312	23	28.5	43	21	0.001678	22	0.001599	13	23.4	19	8	0.001744	11	0.002247	9	9	14	7	0.001586	7	0.001461	5	14.7	10	6	0.001706	4	0.000992	0.631096
gi|6321705 YGR266W	Protein of unknown function;predicted to contain a single transmembrane domain; localized to both the mitochondrion and the plasma membrane; Ygr266wp	0	701	6	10	11	5	0.000191	6	0.000206	1	1.7	1	0	1.58E-05	1	0.000105	3	7	5	4	0.00041	1	0.000106	2	5.3	5	1	0.000144	4	0.000441	0.633942
gi|6320266 YDR061W	Mitochondrial protein, member of the ATP-binding cassette (ABC) transporter family; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; Ydr061wp	0	539	12	12.4	54	23	0.001061	31	0.001296	10	9.6	33	15	0.001875	18	0.002116	4	6.1	12	4	0.000534	8	0.000964	4	3.9	9	4	0.000667	5	0.000712	0.635083
gi|6322049 YIL142W	Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo; Cct2p	0	527	6	7	69	38	0.001778	31	0.001325	5	7	32	15	0.001917	17	0.002045	4	4	36	22	0.002905	14	0.00171	1	4	1	1	0.000191	0	2.35E-05	0.639558
gi|6321243 YGL195W	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA; Gcn1p	0	2672	58	9.6	143	73	0.00067	70	0.000585	34	7.7	70	35	0.000877	35	0.000826	17	4.5	35	22	0.000573	13	0.000313	18	3.4	38	16	0.000522	22	0.000616	0.640619
gi|6322723 YKL126W	Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; localized to the bud neck, cytosol and plasma membrane; homolog of mammalian kinase SGK; Ypk1p	0	680	18	14.9	33	15	0.000555	18	0.000603	9	12.2	14	7	0.000702	7	0.000662	9	12.6	12	5	0.000525	7	0.00067	5	5.4	7	3	0.000402	4	0.000455	0.640736
gi|6323279 YLR250W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; Ssp120p	0	234	10	23.5	20	7	0.00078	13	0.001279	8	22.6	16	5	0.001471	11	0.002997	2	15.8	3	2	0.000639	1	0.000317	1	6.4	1	0	6.15E-05	1	0.00037	0.640842
gi|6324575 YOR002W	Glucosyltransferase, involved in transfer of oligosaccharides from dolichyl pyrophosphate to asparagine residues of proteins during N-linked protein glycosylation; mutations in human ortholog are associated with disease; Alg6p	10	544	5	5.5	11	5	0.000246	6	0.000265	3	5.5	3	1	0.000143	2	0.00025	1	2.6	2	2	0.000275	0	1.95E-05	2	2.4	6	2	0.000344	4	0.000569	0.641395
gi|6324992 YPL263C	Cytoplasmic protein of unknown function; Kel3p	0	651	12	5.5	41	18	0.000692	23	0.0008	5	2.9	15	4	0.000426	11	0.001077	5	2.9	10	3	0.000336	7	0.0007	7	5.5	16	11	0.001481	5	0.000589	0.643299
gi|6323956 YMR298W	Ceramide synthase subunit; single-span ER membrane protein associated with Lag1p and Lac1p and required for ceramide synthase activity, null mutant grows extremely slowly and is defective in ceramide synthesis; Lip1p	1	150	31	42.7	106	51	0.008358	55	0.008202	25	42.7	71	40	0.01784	31	0.013047	12	42.7	17	8	0.00376	9	0.003888	5	14	18	3	0.001822	15	0.007509	0.643634
gi|6323087 YLR058C	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p	0	469	47	21.7	217	84	0.004386	133	0.00631	36	19.6	154	63	0.008973	91	0.012206	19	19.2	51	17	0.002528	34	0.004635	8	14.1	12	4	0.000767	8	0.001293	0.644987
gi|6323362 YLR330W	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p localization, also involved in cell fusion during mating; Chs5p	0	671	36	24	75	28	0.001034	47	0.001569	6	10.3	8	3	0.000314	5	0.000484	16	15.6	28	15	0.001561	13	0.001248	16	17.7	39	10	0.001308	29	0.003228	0.646065
gi|6325142 YPL115C	Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton organization; targets the essential Rho-GTPase Cdc42p, which controls establishment and maintenance of cell polarity, including bud-site assembly; Bem3p	0	1128	9	4.7	28	14	0.000313	14	0.000285	7	3.3	15	8	0.000482	7	0.000399	1	1.4	2	0	1.02E-05	2	0.000122	6	3	11	6	0.000472	5	0.00034	0.649037
gi|6325151 YPL106C	ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm; Sse1p	0	693	26	22.4	75	37	0.001317	38	0.001232	1	2.3	2	2	0.000208	0	1.51E-05	9	12.7	13	6	0.000614	7	0.000658	18	14.1	60	29	0.003633	31	0.00334	0.651121
gi|6320267 YDR062W	Component of serine palmitoyltransferase, responsible along with Lcb1p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine; Lcb2p	0	561	8	6.8	31	15	0.000673	16	0.000652	7	6.8	17	8	0.00097	9	0.001026	5	6.8	13	6	0.000759	7	0.000813	1	4.6	1	1	0.000179	0	2.21E-05	0.651786
gi|6324911 YOR335C	Cytoplasmic alanyl-tRNA synthetase, required for protein synthesis; point mutation (cdc64-1 allele) causes cell cycle arrest at G1; lethality of null mutation is functionally complemented by human homolog; Ala1p	0	958	5	4	5	2	6.35E-05	3	8.1E-05	2	2	2	2	0.000151	0	1.09E-05	2	2	2	0	1.2E-05	2	0.000144	1	1.8	1	0	1.5E-05	1	9.04E-05	0.651808
gi|6322411 YJL050W	Dead-box family ATP dependent helicase required for mRNA export from the nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA; Mtr4p	0	1073	31	6.9	77	34	0.000783	43	0.000899	7	2.2	13	8	0.000507	5	0.000302	12	4.3	17	14	0.000912	3	0.000188	17	4.8	47	12	0.000979	35	0.002434	0.652546
gi|6323142 YLR113W	Mitogen-activated protein kinase involved in osmoregulation via three independent osmosensors; mediates the recruitment and activation of RNA Pol II at Hot1p-dependent promoters; localization regulated by Ptp2p and Ptp3p; Hog1p	0	435	5	9.4	17	9	0.000532	8	0.000433	2	3.7	4	2	0.000332	2	0.000313	1	3.7	2	0	2.65E-05	2	0.000317	3	5.7	11	7	0.001422	4	0.000711	0.654489
gi|6320464 YDR258C	Oligomeric mitochondrial matrix chaperone that cooperates with Ssc1p in mitochondrial thermotolerance after heat shock; prevents the aggregation of misfolded matrix proteins; component of the mitochondrial proteolysis system; Hsp78p	0	811	9	9.9	16	7	0.000225	9	0.00026	3	5.3	5	2	0.000178	3	0.000245	4	4.4	6	2	0.000184	4	0.000327	2	3.1	5	3	0.000337	2	0.000198	0.657379
gi|6324280 YNL048W	Alpha-1,2-mannosyltransferase, catalyzes addition of the terminal alpha 1,2-Man to the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Alg11p	1	548	9	8.6	23	12	0.000555	11	0.000465	7	8.4	11	6	0.00075	5	0.000592	2	5.8	3	2	0.000273	1	0.000135	4	2.7	9	4	0.000656	5	0.0007	0.658763
gi|6320689 YDR481C	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides; Pho8p	1	566	26	18.6	60	33	0.001441	27	0.001077	19	15	37	21	0.002491	16	0.001794	9	13.1	19	12	0.001484	7	0.000806	3	2.8	4	0	2.54E-05	4	0.000547	0.659058
gi|6322770 YKL080W	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p	0	392	28	28.6	188	94	0.005869	94	0.005344	16	23.2	67	36	0.006147	31	0.004993	12	11.5	73	38	0.006723	35	0.005707	16	13.3	48	20	0.00444	28	0.005336	0.65931

gi|6323657 YMR015C	C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a target of azole antifungal drugs; Erg5p	0	538	19	9.3	91	37	0.001697	54	0.002246	13	9.3	42	20	0.002497	22	0.002587	4	5.9	9	3	0.000406	6	0.000729	3	1.9	40	14	0.002273	26	0.003612	0.661669
gi|6319597 YBR121C	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bearing tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end formation; Grs1p	0	667	8	9.6	17	7	0.000274	10	0.000349	4	6.7	8	5	0.000516	3	0.000298	5	6.9	7	1	0.000121	6	0.000588	2	5.1	2	1	0.000151	1	0.00013	0.663407
gi|6324737 YOR163W	Diadenosine polyphosphate hydrolase, member of the MutT family of nucleotide hydrolases with high specificity for diadenosine hexa- and pentaphosphates, required for efficient hydrolysis of diphosphorylated inositol polyphosphates; Ddp1p	0	188	2	8	5	2	0.000324	3	0.000413	1	8	1	0	5.91E-05	1	0.00039	1	8	2	0	6.12E-05	2	0.000733	1	8	2	2	0.000995	0	6.58E-05	0.664902
gi|6320009 YDL192W	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p	0	181	14	17.1	36	16	0.002219	20	0.002511	7	17.1	18	10	0.003742	8	0.002833	7	14.9	13	4	0.00159	9	0.003222	4	13.3	5	2	0.001033	3	0.001299	0.667089
gi|6319503 YBR029C	Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diaclglyerol, a critical step in the synthesis of all major yeast phospholipids; Cds1p	6	457	18	5	35	17	0.000932	18	0.000897	9	5	12	7	0.001045	5	0.00071	6	2.6	15	5	0.000781	10	0.001415	6	2.6	8	5	0.000976	3	0.000515	0.668029
gi|6320668 YDR460W	Subunit of TFIIH and nucleotide excision repair factor 3 complexes, involved in transcription initiation, required for nucleotide excision repair; ring finger protein similar to mammalian CAK and TFIIH subunit; Tfb3p	0	321	2	4	7	5	0.000417	2	0.000173	1	4	1	0	3.46E-05	1	0.000228	2	4	5	4	0.000896	1	0.000231	1	4	1	1	0.000314	0	3.86E-05	0.668059
gi|6322065 YIL126W	ATPase component of the ATP-dependent RSC chromatin remodeling complex required for kinetochore function in chromosome segregation; required for expression of early meiotic genes; essential helicase-related protein homologous to Snf2p; Sth1p	0	1359	11	8.5	24	12	0.000224	12	0.000204	5	6.1	10	7	0.000351	3	0.000146	1	1	2	0	8.47E-06	2	0.000101	7	5.1	12	5	0.000328	7	0.000392	0.669938
gi|6323738 YMR091C	Nuclear protein that may have a role in nuclear protein import and maintenance of proper telomere length; Npl6p	0	435	15	9.4	35	19	0.001091	16	0.000841	8	9.2	15	8	0.001251	7	0.001035	1	4.4	3	0	2.65E-05	3	0.000463	10	9.2	17	11	0.002216	6	0.001053	0.673495
gi|6320259 YDR054C	Ubiquitin-conjugating enzyme or E2; together with Skp1p, Rbx1p, Cdc53p, and an F-box protein, forms a ubiquitin-protein ligase called the SCF complex which regulates cell cycle progression by targeting key substrates for degradation; Cdc34p	0	295	12	6.8	25	11	0.000949	14	0.00109	8	6.8	16	9	0.00207	7	0.001526	4	6.8	7	1	0.000273	6	0.00133	2	5.1	2	1	0.000341	1	0.000294	0.674356
gi|6320334 YDR129C	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the organization and maintenance of the actin cytoskeleton; Sac6p	0	642	29	17.1	58	27	0.001043	31	0.001088	17	13.6	32	10	0.001055	22	0.002168	10	8.9	14	11	0.001201	3	0.000314	5	6.4	12	6	0.000829	6	0.000713	0.675235
gi|6319454 YBL017C	Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles between the late-Golgi and prevacuolar endosome-like compartments; Pep1p	1	1579	5	2.2	9	6	0.0001	3	4.91E-05	4	2.2	5	3	0.000134	2	8.62E-05	1	1.3	1	0	7.29E-06	1	4.7E-05	1	0.9	3	3	0.000173	0	7.84E-06	0.677931
gi|6321886 YHR094C	Low-affinity glucose transporter of the major facilitator superfamily, expression is induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose is limiting; Hxt1p	11	570	19	12.5	48	24	0.001046	24	0.000953	4	6.8	7	5	0.000604	2	0.000239	11	8.6	22	11	0.001353	11	0.001246	8	9.6	19	8	0.001237	11	0.001455	0.6781
gi|6324194 YNL135C	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p	0	114	20	41.2	63	32	0.00694	31	0.006126	12	34.2	27	13	0.007695	14	0.007803	12	41.2	35	18	0.011004	17	0.00958	1	14.9	1	1	0.000883	0	0.000109	0.678603
gi|6321881 YHR089C	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA; Gar1p	0	205	27	19.5	80	37	0.004453	43	0.004704	16	19.5	27	14	0.004604	13	0.004033	12	8.8	27	11	0.003761	16	0.005017	12	8.3	26	12	0.005123	14	0.005132	0.681159
gi|6323607 YML034W	Protein with a putative role in sister chromatid segregation, potentially phosphorylated by Cdc28p; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery; Src1p	1	834	8	8.5	16	8	0.000248	8	0.000226	4	8.2	8	6	0.000493	2	0.000163	1	3.7	1	1	9.66E-05	0	1.27E-05	5	4.1	7	1	0.000121	6	0.000549	0.681536
gi|6320077 YDL126C	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p	0	835	56	25.4	150	77	0.002259	73	0.001951	37	20	76	34	0.002726	42	0.003171	29	19.2	62	35	0.002908	27	0.00207	6	5.9	12	8	0.000844	4	0.000371	0.683706
gi|6324485 YOL087C	hypothetical protein; Yol087cp	0	1116	9	5.8	17	7	0.000164	10	0.000209	1	1.7	2	2	0.000129	0	9.38E-06	3	4	6	2	0.000134	4	0.000238	6	4.6	9	3	0.000245	6	0.00041	0.690897
gi|1431851 YFL004W	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in protein localization and non-autophagic vacuolar fusion; Vtc2p	3	828	21	12.7	56	26	0.000779	30	0.000817	12	9.9	28	13	0.001059	15	0.00115	6	6	8	7	0.000598	1	8.96E-05	9	10.7	20	6	0.000643	14	0.001271	0.691766
gi|6320835 YEL002C	Beta subunit of the oligosaccharyl transferase (OST) glycoprotein complex; required for N-linked glycosylation of proteins in the endoplasmic reticulum; Wbp1p	1	430	11	13.3	25	11	0.000651	14	0.000748	8	12.1	13	4	0.000646	9	0.001339	5	9.1	11	6	0.00099	5	0.000764	1	2.8	1	1	0.000234	0	2.88E-05	0.691878
gi|4274225 YJL012C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc4p	3	721	32	20.4	134	71	0.002414	63	0.001952	25	18.9	52	32	0.002972	20	0.001756	5	6.7	7	5	0.000495	2	0.000191	6	3.5	75	34	0.00409	41	0.00424	0.693237
gi|6320236 YDR033W	Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock; Mrh1p	7	320	34	25.9	149	77	0.005896	72	0.005023	6	14.1	20	13	0.002741	7	0.001406	27	20.6	89	45	0.009747	44	0.008781	8	15.6	40	19	0.00517	21	0.004913	0.695959
gi|6320863 YER025W	Gamma subunit of the translation initiation factor eIF2, involved in the identification of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-Met; Gcd11p	0	527	32	25.8	114	50	0.002333	64	0.002713	11	14	17	12	0.001538	5	0.000616	15	19	24	16	0.002118	8	0.000986	17	20.9	73	22	0.003631	51	0.007211	0.698032
gi|6321267 YGL171W	ATP-dependent RNA helicase of the DEAD box family; required for 18S rRNA synthesis; Rok1p	0	564	5	12.1	6	4	0.000194	2	9.83E-05	3	7.8	4	3	0.000374	1	0.00013	1	2.1	1	1	0.000143	0	1.88E-05	1	2.1	1	0	2.55E-05	1	0.000154	0.699147
gi|6323204 YLR175W	Component of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), probable rRNA pseudouridine synthase, binds to snoRNP Nop10p and also interacts with ribosomal biogenesis protein Nop53p; Cbf5p	0	483	19	18.8	40	20	0.001033	20	0.000941	9	13.7	17	9	0.001264	8	0.001062	7	9.9	10	6	0.000882	4	0.000549	8	14.1	13	5	0.000923	8	0.001256	0.702321

gi|6324230 YNL099C	Putative protein tyrosine phosphatase, required for cell cycle arrest in response to oxidative damage of DNA; Oca1p	0	238	5	14.3	10	2	0.000256	8	0.000792	3	14.3	8	1	0.000327	7	0.001891	1	5.9	1	0	4.84E-05	1	0.000312	1	6.7	1	1	0.000423	0	5.2E-05	0.703616
gi|6322838 YKL014C	Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs, associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the biogenesis of the 60S ribosomal subunit; Urb1p	0	1764	13	4.2	21	10	0.000145	11	0.000145	4	1.8	5	3	0.00012	2	7.71E-05	6	3.2	10	3	0.000124	7	0.000258	4	2.6	6	4	0.000204	2	9.12E-05	0.704482
gi|6323453 YLR421C	Subunit of the 19S regulatory particle of the 26S proteasome lid; Rpn13p	0	156	5	21.2	27	15	0.002419	12	0.001776	3	21.2	12	6	0.002634	6	0.002482	2	21.2	13	9	0.004058	4	0.001699	2	15.4	2	0	9.22E-05	2	0.001032	0.70628
gi|6321289 YGL150C	ATPase that forms a large complex, containing actin and several actin-related proteins, that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; shows similarity to the Snf2p family of ATPases; Ino80p	0	1489	8	1.4	16	7	0.000123	9	0.000141	5	1.4	9	5	0.000231	4	0.000176	2	1.4	2	1	5.41E-05	1	4.98E-05	3	1.3	5	1	6.76E-05	4	0.000208	0.709241
gi|6323028 YLL001W	Dynamin-related GTPase required for mitochondrial fission and the maintenance of mitochondrial morphology, assembles on the cytoplasmic face of mitochondrial tubules at sites at which division will occur; also participates in endocytosis; Dnm1p	0	757	12	15.6	21	5	0.000177	16	0.000483	8	11.6	17	4	0.000367	13	0.001092	1	1.6	1	1	0.000106	0	1.4E-05	3	7	3	0	1.9E-05	3	0.000311	0.710496
gi|6323735 YMR088C	Permease of basic amino acids in the vacuolar membrane; Vba1p	12	562	8	5.5	16	6	0.000282	10	0.000414	4	5.3	5	2	0.000257	3	0.000354	2	2.7	2	1	0.000143	1	0.000132	5	4.8	9	3	0.000486	6	0.000815	0.711532
gi|6325238 YPL019C	Vacuolar membrane protein involved in vacuolar polyphosphate accumulation; functions as a regulator of vacuolar H+-ATPase activity and vacuolar transporter chaperones; involved in non-autophagic vacuolar fusion; Vtc3p	3	835	37	22	76	38	0.001122	38	0.001022	18	17.5	35	14	0.00113	21	0.001592	13	15	26	17	0.00142	9	0.000698	10	10.1	15	7	0.000741	8	0.000726	0.715275
gi|6322452 YJL008C	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo; Cct8p	0	568	6	9.7	91	51	0.002207	40	0.001581	5	9.7	69	39	0.004594	30	0.003335	3	6.5	12	6	0.00075	6	0.000691	4	6.5	10	6	0.000937	4	0.000545	0.715842
gi|6319516 YBR042C	hypothetical protein; Ybr042cp	3	397	6	15.6	18	7	0.00046	11	0.000642	4	11.6	8	2	0.000364	6	0.000975	4	11.3	8	3	0.000551	5	0.000828	1	4	2	2	0.000471	0	3.12E-05	0.71617
gi|6319290 YAL029C	One of two type V myosins; required for mother-specific HO expression, for the bud tip localization of ASH1 and IST2 mRNA; facilitates growth and orientation of ER tubules along with She3p; Myo4p	0	1471	5	2.7	14	6	0.000108	8	0.000128	2	1.6	6	2	9.81E-05	4	0.000178	2	2.7	3	3	0.000149	0	7.21E-06	4	1.6	5	1	6.85E-05	4	0.00021	0.71677
gi|6321522 YGR085C	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp	0	174	13	15.5	30	17	0.002448	13	0.00172	7	8	14	6	0.002361	8	0.002947	7	9.2	14	10	0.004035	4	0.001523	2	6.3	2	1	0.000579	1	0.000498	0.718525
gi|6322136 YIL053W	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p	0	271	12	33.9	60	21	0.001931	39	0.003231	10	33.6	19	5	0.00127	14	0.003283	6	11.8	37	12	0.0031	25	0.005908	2	11.4	4	4	0.001327	0	4.57E-05	0.723718
gi|6320438 YDR232W	5-aminolevulinate synthase, catalyzes the first step in the heme biosynthetic pathway; an N-terminal signal sequence is required for localization to the mitochondrial matrix; expression is regulated by Hap2p-Hap3p; Hem1p	0	548	5	3.8	18	10	0.000466	8	0.000344	5	3.8	12	8	0.000993	4	0.000477	1	3.3	3	0	2.1E-05	3	0.000368	2	3.3	3	2	0.000341	1	0.000158	0.723906
gi|6321232 YGL206C	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p	0	1653	25	10.6	53	24	0.000361	29	0.000396	12	8.3	21	10	0.00041	11	0.000424	15	8.5	24	11	0.000466	13	0.000507	5	3.9	8	3	0.000165	5	0.000232	0.724682
gi|6324907 YOR332W	Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma4p	0	233	5	11.6	9	4	0.00047	5	0.000523	2	5.2	4	2	0.00062	2	0.000584	2	6.4	2	1	0.000346	1	0.000319	2	6.4	3	1	0.000432	2	0.000691	0.725612
gi|6324686 YOR112W	hypothetical protein; Yor112wp	0	761	6	3.7	27	12	0.0004	15	0.000452	3	3.7	6	3	0.000277	3	0.000261	2	1.8	7	2	0.000197	5	0.000432	4	3.7	14	7	0.000813	7	0.000699	0.726671
gi|6322999 YLL029W	hypothetical protein; Yll029wp	0	749	11	7.9	48	23	0.000764	25	0.000755	5	4.5	20	12	0.001082	8	0.000685	6	7.9	16	8	0.000753	8	0.000694	3	4.5	12	3	0.000365	9	0.000909	0.727635
gi|6322603 YJR143C	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals; Pmt4p	11	762	20	10.2	46	27	0.000879	19	0.000567	17	10.2	37	24	0.002113	13	0.001085	1	2.2	2	2	0.000196	0	1.39E-05	4	3.5	7	1	0.000132	6	0.000601	0.729408
gi|6323613 YML028W	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion results in mutator phenotype; Tsa1p	1	196	14	10.7	52	28	0.00354	24	0.002771	8	10.7	13	4	0.001416	9	0.002937	11	10.7	21	12	0.004286	9	0.002975	9	10.7	18	12	0.005358	6	0.002337	0.72973
gi|6320308 YDR103W	Scaffold protein that, in response to pheromone, shuttles from the nucleus to the plasma membrane and assembles kinases Ste11p, Ste7p, and Fus3p into a specific signaling complex; active oligomeric form interacts with Ste4p-Ste18p complex; Ste5p	0	917	5	3.9	25	10	0.000279	15	0.000375	1	1.6	1	1	8.48E-05	0	1.14E-05	2	3.8	2	1	8.79E-05	1	8.09E-05	4	1.7	22	8	0.000769	14	0.001147	0.730565
gi|6322988 YLL040C	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention; Vps13p	0	3144	16	4.2	52	33	0.000259	19	0.000137	5	2.4	14	6	0.000131	8	0.000163	2	1	4	2	4.76E-05	2	4.38E-05	10	1.5	34	25	0.000691	9	0.000217	0.730938
gi|6322608 YJR148W	Cytosolic branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during stationary phase and repressed during logarithmic phase; Bat2p	0	376	5	8	17	8	0.00055	9	0.00056	2	8	4	3	0.000561	1	0.000195	3	8	4	2	0.000398	2	0.000367	4	8	9	3	0.000727	6	0.001218	0.731697
gi|6323442 YLR410W	Protein of unknown function probably involved in the function of the cortical actin cytoskeleton; putative ortholog of S. pombe asp1+; Vip1p	0	1146	4	3.3	14	6	0.000138	8	0.000164	2	1.3	5	1	6.78E-05	4	0.000228	2	2	2	1	7.03E-05	1	6.48E-05	2	1.3	7	4	0.000314	3	0.000205	0.733745
gi|6324472 YOL100W	Serine/threonine protein kinase involved in sphingolipid-mediated signaling pathway that controls endocytosis; activates Ypk1p and Ykr2p, components of signaling cascade required for maintenance of cell wall integrity; redundant with Pkh1p; Pkh2p	0	1081	3	3.1	11	4	0.000101	7	0.000154	1	1.7	2	2	0.000134	0	9.68E-06	1	1.7	2	2	0.000138	0	9.81E-06	2	3.1	7	0	1.33E-05	7	0.000492	0.734204

gi|6320813 YEL022W	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in vesicular transport between the Golgi and ER, Golgi organization, and actin cytoskeleton organization; similar to but not functionally redundant with Gea1p; Gea2p	0	1459	10	4.7	15	9	0.000159	6	9.88E-05	7	3.8	10	5	0.000236	5	0.000222	3	2.9	4	4	0.000197	0	7.27E-06	1	0.8	1	0	9.86E-06	1	5.94E-05	0.734299
gi|6321924 YHR132C	Putative metalloprotease with similarity to the zinc carboxypeptidase family, required for normal cell wall assembly; Ecm14p	0	430	5	5.1	21	11	0.000651	10	0.000541	4	5.1	9	5	0.0008	4	0.000608	3	4.7	11	6	0.00099	5	0.000764	1	4.7	1	0	3.35E-05	1	0.000202	0.73735
gi|6324570 YOL004W	DNA binding subunit of Sin3p-Rpd3p histone deacetylase complex, involved in transcriptional repression of meiosis-specific genes during vegetative growth and silencing; involved in telomere maintenance; Sin3p	0	1536	7	5.7	11	4	7.13E-05	7	0.000108	2	1.3	2	1	5.06E-05	1	4.77E-05	1	1.2	1	1	5.24E-05	0	6.9E-06	4	3.2	8	2	0.000122	6	0.000298	0.741777
gi|6324086 YNL243W	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo; Sla2p	0	968	27	8.9	79	41	0.001044	38	0.000882	16	6.6	30	16	0.001113	14	0.000919	6	1.9	14	7	0.000511	7	0.000471	16	6.6	35	18	0.00162	17	0.001317	0.742236
gi|6319666 YBR189W	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp	0	195	13	25.6	31	25	0.003183	6	0.000739	7	25.6	13	11	0.003815	2	0.000698	7	12.3	15	14	0.005017	1	0.000381	2	7.2	3	0	7.38E-05	3	0.001206	0.742334
gi|6325439 YPR181C	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p	0	768	31	11.7	74	33	0.001062	41	0.001198	15	8.2	35	15	0.001316	20	0.001649	10	6.2	15	6	0.000554	9	0.000759	10	2.5	24	12	0.001367	12	0.001177	0.743381
gi|6321899 YHR107C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc12p	0	407	11	12	22	11	0.000688	11	0.000626	6	11.8	9	4	0.000682	5	0.000797	6	11.8	9	5	0.000877	4	0.000651	4	10.1	4	2	0.000459	2	0.000395	0.746698
gi|6323632 YML010W	Protein that forms a complex with Spt4p and mediates both activation and inhibition of transcription elongation; Spt4p-Spt5p complex also plays a role in pre-mRNA processing; Spt5p	0	1063	14	4	80	36	0.000836	44	0.000928	4	4	5	1	7.31E-05	4	0.000246	8	4	27	14	0.00092	13	0.000788	8	3.3	48	21	0.001719	27	0.001898	0.750321
gi|6323635 YML008C	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; Erg6p	0	383	13	21.4	62	28	0.001812	34	0.001997	11	21.1	35	12	0.002116	23	0.003798	6	10.2	11	8	0.001472	3	0.000526	6	12.5	16	8	0.00184	8	0.001584	0.750354
gi|6321315 YGL123W	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p	0	254	21	13.4	67	33	0.003211	34	0.003011	16	13.4	45	23	0.006076	22	0.00548	11	11.8	21	10	0.002764	11	0.002797	1	6.3	1	0	5.66E-05	1	0.000341	0.750815
gi|6319655 YBR177C	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C; Eht1p	0	451	35	26.6	109	40	0.002186	69	0.003416	25	26.6	63	24	0.00357	39	0.005453	17	15.5	40	13	0.002016	27	0.003832	4	7.1	6	3	0.000606	3	0.000521	0.751128
gi|6319618 YBR142W	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits; Mak5p	0	773	12	8.2	29	9	0.000299	20	0.000588	4	2.3	6	3	0.000273	3	0.000257	1	2.8	2	2	0.000194	0	1.37E-05	11	5.3	21	4	0.000465	17	0.001649	0.751801
gi|6323251 YLR222C	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA; Utp13p	0	817	16	5.8	47	27	0.000819	20	0.000556	10	3.5	24	12	0.000992	12	0.000935	2	3.3	3	0	1.41E-05	3	0.000247	9	5.6	20	15	0.001602	5	0.00047	0.752136
gi|6322824 YKL028W	TFIIE large subunit, involved in recruitment of RNA polymerase II to the promoter, activation of TFIIH, and promoter opening; Tfa1p	1	482	6	7.7	17	10	0.00053	7	0.000345	4	7.7	6	3	0.000438	3	0.000413	5	7.7	9	7	0.001027	2	0.000286	1	7.3	2	0	2.98E-05	2	0.000334	0.754331
gi|6323073 YLR044C	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p	0	563	21	21	65	29	0.001276	36	0.001437	15	21	45	21	0.002505	24	0.002695	8	9.9	9	3	0.000388	6	0.000697	7	5.9	11	5	0.000792	6	0.000813	0.757835
gi|6324620 YOR046C	Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in mRNA export from the nucleus; Dbp5p	0	482	19	9.1	45	22	0.001136	23	0.001081	10	6.6	16	7	0.000991	9	0.001194	7	6	13	10	0.001457	3	0.000418	7	8.9	16	5	0.000925	11	0.001721	0.758764
gi|6324258 YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p	0	482	26	20.1	104	48	0.00245	56	0.002599	16	20.1	39	17	0.002373	22	0.002888	13	13.7	35	15	0.002173	20	0.002662	8	9.5	30	16	0.002895	14	0.002183	0.759013
gi|6321013 YER165W	Poly(A) binding protein, part of the 3'-end RNA-processing complex, mediates interactions between the 5' cap structure and the 3' mRNA poly(A) tail, involved in control of poly(A) tail length, interacts with translation factor eIF-4G; Pab1p	0	577	6	9.9	10	7	0.000316	3	0.000134	1	1.6	1	1	0.000135	0	1.81E-05	1	3.6	2	0	1.99E-05	2	0.000239	4	4.7	7	6	0.000922	1	0.00015	0.759806
gi|6324193 YNL136W	Subunit of the NuA4 histone acetyltransferase complex, which acetylates the N-terminal tails of histones H4 and H2A; Eaf7p	0	425	3	5.9	4	2	0.000143	2	0.00013	1	3.3	1	0	2.61E-05	1	0.000172	1	3.8	2	2	0.000352	0	2.49E-05	1	2.1	1	0	3.38E-05	1	0.000204	0.762538
gi|6320226 YDR023W	Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Ses1p	0	462	22	19.7	76	41	0.002187	35	0.001703	13	19	27	18	0.00262	9	0.001246	10	11	31	18	0.002715	13	0.001813	10	15.8	18	5	0.000965	13	0.002117	0.763004
gi|6323218 YLR189C	UDP-glucose:sterol glucosyltransferase, conserved enzyme involved in synthesis of sterol glucoside membrane lipids, involved in autophagy; Atg26p	0	1198	7	2.7	10	6	0.000132	4	8.33E-05	3	1.5	5	2	0.00012	3	0.000166	4	2.7	4	4	0.00024	0	8.85E-06	1	1.5	1	0	1.2E-05	1	7.23E-05	0.769155
gi|6323429 YLR397C	ATPase of the CDC48/PAS1/SEC18 (AAA) family, forms a hexameric complex; may be involved in degradation of aberrant mRNAs; Afg2p	0	780	4	3.5	5	3	0.000109	2	7.11E-05	2	1.8	2	1	9.96E-05	1	9.39E-05	2	1.8	2	2	0.000192	0	1.36E-05	1	1.7	1	0	1.84E-05	1	0.000111	0.770008
gi|6324742 YOR168W	Glutamine tRNA synthetase, monomeric class I tRNA synthetase that catalyzes the specific glutaminylation of tRNA(Glu); N-terminal domain proposed to be involved in enzyme-tRNA interactions; Gln4p	0	809	3	6.1	5	3	0.000105	2	6.85E-05	1	3.2	2	2	0.000178	0	1.29E-05	2	4.9	2	1	9.96E-05	1	9.17E-05	1	1.1	1	0	1.78E-05	1	0.000107	0.770133
gi|6323226 YLR197W	Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation; overexpression causes spindle orientation defects; Sik1p	0	504	34	25.8	73	45	0.002198	28	0.001254	17	12.1	35	22	0.00293	13	0.00164	19	20.4	35	23	0.003174	12	0.001536	2	4.6	3	0	2.85E-05	3	0.000467	0.773386

gi|6323756	YMR109W	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization; Myo5p	0	1219	10	8.3	24	15	0.00031	9	0.000173	6	4.2	12	5	0.000282	7	0.000369	5	4.9	10	10	0.000576	0	8.7E-06	1	1.4	2	0	1.18E-05	2	0.000132	0.773742
gi|6321469	YGR032W	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance; Gsc2p	14	1895	18	6.3	33	21	0.000276	12	0.000146	7	4.8	12	12	0.000428	0	5.52E-06	11	4.2	18	9	0.000334	9	0.000308	3	2.1	3	0	7.59E-06	3	0.000124	0.774944
gi|6319724	YBR247C	Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and 40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the nucleolus; Enp1p	0	483	13	11	37	19	0.000983	18	0.000849	9	11	17	10	0.001402	7	0.000932	1	4.3	1	0	2.38E-05	1	0.000154	6	2.7	19	9	0.001638	10	0.001563	0.777528
gi|6322666	YKL182W	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p	0	2051	22	6.7	53	24	0.000291	29	0.000319	15	4.4	26	8	0.000265	18	0.000556	9	4.2	20	14	0.000477	6	0.000191	6	3	7	2	9.12E-05	5	0.000187	0.778129
gi|6325207	YPL050C	Subunit of Golgi mannosyltransferase complex also containing Anp1p, Mnn10p, Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan backbone; forms a separate complex with Van1p that is also involved in backbone elongation; Mnn9p	1	395	10	10.9	25	13	0.000832	12	0.000702	2	3.8	4	2	0.000365	2	0.000344	6	7.1	13	7	0.001253	6	0.000993	3	3.3	8	4	0.00091	4	0.000783	0.778399
gi|6321341	YGL097W	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; potentially phosphorylated by Cdc28p; Srm1p	0	482	11	19.5	27	16	0.000833	11	0.000529	1	3.7	2	0	2.3E-05	2	0.000282	4	7.5	5	3	0.000454	2	0.000286	8	15.8	20	13	0.002358	7	0.001104	0.779028
gi|6323567	YML073C	N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; Rpl6ap	0	176	12	15.3	41	19	0.002697	22	0.002834	5	8.5	20	10	0.003848	10	0.003627	3	8	6	2	0.00085	4	0.001506	5	14.8	15	7	0.003515	8	0.003446	0.785881
gi|6322536	YJR076C	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM; Cdc11p	0	415	3	6.5	7	2	0.000147	5	0.000294	2	6.5	2	1	0.000187	1	0.000177	1	2.7	1	1	0.000194	0	2.55E-05	1	2.7	4	0	3.47E-05	4	0.000746	0.786665
gi|6321693	YGR254W	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p	0	437	99	27.5	1425	688	0.038355	737	0.037413	50	21.7	376	174	0.026552	202	0.02905	52	24.5	949	446	0.070501	503	0.073251	19	14.6	100	68	0.013464	32	0.005467	0.788525
gi|6323068	YLR039C	Protein involved in retrograde transport to the cis-Golgi network; forms heterodimer with Rgp1p that acts as a GTP exchange factor for Ypt6p; involved in transcription of rRNA and ribosomal protein genes; Ric1p	0	1056	6	2.7	11	6	0.00015	5	0.000115	4	1.5	5	3	0.0002	2	0.000129	1	1.1	1	0	1.09E-05	1	7.03E-05	2	1.1	5	3	0.000259	2	0.000152	0.788799
gi|6324949	YOR373W	Component of the spindle pole body outer plaque, required for exit from mitosis; Nud1p	0	851	4	4.7	5	3	0.0001	2	6.51E-05	1	2	1	1	9.13E-05	0	1.23E-05	1	2.7	1	0	1.35E-05	1	8.72E-05	2	1.8	3	2	0.00022	1	0.000102	0.790341
gi|6323249	YLR220W	Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1 mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial iron accumulation; Ccc1p	3	322	7	6.8	10	6	0.000491	4	0.00031	3	6.8	3	1	0.000241	2	0.000423	4	5.6	6	5	0.001108	1	0.000231	1	5.6	1	0	4.47E-05	1	0.000269	0.795456
gi|6320803	YEL032W	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex that binds chromatin as a part of the pre-replicative complex; Mcm3p	0	971	14	13.8	44	16	0.000414	28	0.000651	3	4.7	5	3	0.000217	2	0.00014	8	11.9	15	6	0.000439	9	0.000601	9	6.6	24	7	0.000637	17	0.001313	0.797316
gi|6321940	YHR146W	Protein that binds to cruciform DNA structures; Crp1p	0	465	18	22.8	68	23	0.00123	45	0.002169	5	8	9	5	0.00074	4	0.000563	8	14.8	14	7	0.001064	7	0.000981	10	11.2	45	11	0.002073	34	0.005457	0.798459
gi|6325441	YPR183W	Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes the formation of Dol-P-Man from Dol-P and GDP-Man; required for glycosyl phosphatidylinositol membrane anchoring, O mannosylation, and protein glycosylation; Dpm1p	1	267	15	18.4	50	20	0.001869	30	0.002532	9	18.4	28	9	0.002287	19	0.004508	4	11.6	9	5	0.001336	4	0.000993	10	18.4	13	6	0.001994	7	0.001993	0.798524
gi|6321362	YGL076C	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap	0	244	38	8.6	138	70	0.007034	68	0.006224	29	8.6	84	37	0.010148	47	0.012139	10	8.2	51	31	0.00882	20	0.005258	3	6.1	3	2	0.000766	1	0.000355	0.798909
gi|6321537	YGR100W	Cytoplasmic GTPase-activating protein for Ypt/Rab transport GTPases Ypt6p, Ypt31p and Sec4p; involved in recycling of internalized proteins and regulation of Golgi secretory function; Mdr1p	0	950	5	5.7	9	3	8.97E-05	6	0.000152	4	3.7	6	2	0.000152	4	0.000275	1	2	1	1	8.48E-05	0	1.12E-05	1	1.8	2	0	1.51E-05	2	0.000169	0.800901
gi|6319522	YBR048W	Protein component of the small (40S) ribosomal subunit; identical to Rps11Ap and has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11bp	0	156	15	24.4	43	21	0.003355	22	0.003197	7	14.7	22	13	0.005623	9	0.00369	5	9.6	11	4	0.001844	7	0.002923	5	21.8	10	4	0.002305	6	0.002936	0.801862
gi|6322524	YJR064W	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo; Cct5p	0	562	4	9.3	8	5	0.000238	3	0.000138	3	6.4	6	4	0.000494	2	0.000242	1	2.8	1	0	2.05E-05	1	0.000132	1	2.7	1	1	0.000179	0	2.2E-05	0.803104
gi|6323354	YLR321C	Subunit of the RSC chromatin remodeling complex required for kinetochore function in chromosome segregation; essential gene required for cell cycle progression; phosphorylated in the G1 phase of the cell cycle; Snf5p paralog; Sfh1p	0	426	3	3.5	7	4	0.000257	3	0.000182	2	3.5	4	2	0.000339	2	0.000319	1	3.5	1	0	2.7E-05	1	0.000174	1	3.1	2	2	0.000439	0	2.91E-05	0.803904
gi|6322790	YKL060C	Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and gluconeogenesis; catalyzes the conversion of fructose 1,6 bisphosphate into two 3-carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone phosphate; Fba1p	0	359	22	17.8	132	61	0.00417	71	0.004415	17	16.2	53	23	0.004299	30	0.005277	12	14.8	37	17	0.003302	20	0.003574	6	8.1	42	21	0.005089	21	0.004379	0.804906
gi|6324905	YOR329C	Protein required for normal cortical actin organization and endocytosis; multicopy suppressor of clathrin deficiency; acts as a targeting subunit for protein phosphatase type 1; Scd5p	0	872	5	8	8	5	0.000154	3	8.9E-05	1	1.8	1	0	1.27E-05	1	8.4E-05	3	6	6	4	0.00033	2	0.000158	1	2.1	1	1	0.000115	0	1.42E-05	0.805856
gi|1431847	YFL042C	Putative protein of unknown function; YFL042C is not an essential gene; Yfl042cp	1	674	4	3.7	7	4	0.000163	3	0.000115	2	3.7	2	0	1.65E-05	2	0.000202	2	3.6	3	2	0.000222	1	0.00011	1	3.6	2	2	0.000277	0	1.84E-05	0.806097
gi|6323404	YLR372W	Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis; Sur4p	6	345	19	11.9	86	39	0.002787	47	0.003052	10	11.9	54	20	0.003894	34	0.006219	7	4.3	17	13	0.002635	4	0.000768	6	4.3	15	6	0.001543	9	0.001973	0.806832

gi|1038378 YCR012W	3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme in glycolysis and gluconeogenesis; Pgk1p	0	416	13	18.5	30	13	0.00079	17	0.000933	5	11.5	9	6	0.000988	3	0.000478	8	12.5	12	2	0.00036	10	0.001555	5	10.3	9	5	0.001072	4	0.000744	0.812844
gi|3736268 YMR214W	One of several homologs of bacterial chaperone DnaJ, located in the ER lumen where it cooperates with Kar2p to mediate maturation of proteins; Scj1p	0	377	6	10.3	12	4	0.000291	8	0.0005	4	10.3	7	1	0.000206	6	0.001027	2	4	3	3	0.00058	0	2.81E-05	1	4	2	0	3.82E-05	2	0.000427	0.817172
gi|1038378 YCR017C	Putative sensor/transporter protein involved in cell wall biogenesis; contains 14-16 transmembrane segments and several putative glycosylation and phosphorylation sites; null mutation is synthetically lethal with pkc1 deletion; Cwh43p	18	953	11	7.9	27	14	0.00037	13	0.000314	4	4.2	8	5	0.000361	3	0.000209	6	4.7	11	7	0.000519	4	0.000278	5	4.6	8	2	0.000196	6	0.000481	0.817329
gi|6321710 YGR271W	Putative RNA helicase related to Ski2p, involved in translation inhibition of non-poly(A) mRNAs; required for repressing propagation of dsRNA viruses; Slh1p	0	1967	6	4.3	16	9	0.000118	7	8.45E-05	4	2.4	8	4	0.000141	4	0.000133	3	2	7	5	0.000181	2	7.01E-05	1	0.9	1	0	7.31E-06	1	4.4E-05	0.820318
gi|6320665 YDR457W	E3 ubiquitin ligase of the hect-domain class; has a role in mRNA export from the nucleus and may regulate transcriptional coactivators; Tom1p	0	3268	3	0.9	11	4	3.35E-05	7	5.09E-05	1	0.5	4	0	3.4E-06	4	8.01E-05	2	0.9	4	1	2.47E-05	3	6.16E-05	1	0.4	3	3	8.36E-05	0	3.79E-06	0.82052
gi|9755337 YLR093C	v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar membrane; Nyv1p	1	253	10	5.9	39	12	0.001203	27	0.00241	6	5.9	13	7	0.001887	6	0.001531	2	5.9	2	2	0.000591	0	4.19E-05	4	5.5	24	3	0.00108	21	0.006213	0.820838
gi|6321299 YGL139W	Putative protein of unknown function; localized to the mitochondrion; Flc3p	10	802	5	3.5	10	6	0.000197	4	0.000124	2	1.5	4	2	0.00018	2	0.00017	1	1.6	2	0	1.44E-05	2	0.000172	2	2	4	4	0.000448	0	1.54E-05	0.821002
gi|6320679 YDR471W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein; Rpl27bp	0	136	17	25.7	78	39	0.007071	39	0.006439	11	25.7	31	14	0.00694	17	0.007926	10	25.7	31	18	0.009224	13	0.006159	5	25	16	7	0.004548	9	0.005006	0.823136
gi|2780871 YNL239W	Aminopeptidase of cysteine protease family, has a DNA binding activity and acts as bleomycin hydrolase in vitro; transcription is regulated by galactose via Gal4p; Lap3p	0	454	6	4.2	24	9	0.000509	15	0.000757	5	4.2	13	5	0.000758	8	0.00113	1	3.7	1	1	0.000177	0	2.34E-05	4	4.2	10	3	0.000602	7	0.001172	0.826926
gi|6324350 YNR023W	73 kDa subunit of the 11-subunit SWI/SNF chromatin remodeling complex involved in transcriptional regulation; homolog of Rsc6p subunit of the RSC chromatin remodeling complex; deletion mutants are temperature-sensitive; Snf12p	0	566	5	5.3	9	5	0.000237	4	0.000176	1	2.7	3	0	1.96E-05	3	0.000351	2	5.3	3	3	0.000386	0	1.87E-05	2	2.7	3	2	0.00033	1	0.000153	0.827306
gi|6324486 YOL086C	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p	0	348	95	25.6	855	398	0.027877	457	0.029144	36	24.7	139	57	0.010944	82	0.014827	43	20.1	206	82	0.016304	124	0.022699	33	13.5	510	259	0.06428	251	0.053603	0.829296
gi|6324177 YNL152W	Protein required for cell viability; Ynl152wp	0	409	7	5.1	15	5	0.000327	10	0.000569	3	5.1	6	4	0.000679	2	0.000333	1	4.9	1	1	0.000197	0	2.59E-05	4	5.1	8	0	3.52E-05	8	0.001483	0.830535
gi|6322466 YJR007W	Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP; Sui2p	0	304	48	22	151	70	0.005646	81	0.005943	14	21.1	34	22	0.004858	12	0.002513	13	17.4	40	20	0.004581	20	0.00422	26	17.4	77	28	0.007997	49	0.012012	0.83224
gi|6320804 YEL031W	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca2+ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by Pichia farinosa KK1; Spf1p	10	1215	78	22.4	210	93	0.001873	117	0.002144	43	17.9	106	48	0.002641	58	0.003006	27	15.1	46	30	0.001714	16	0.000847	30	18.8	58	15	0.001077	43	0.002639	0.834835
gi|6319293 YAL026C	Integral membrane Ca(2+)-ATPase involved in aminophospholipid translocation; required to form a specific class of secretory vesicles that accumulate upon actin cytoskeleton disruption; mutation affects maturation of the 18S rRNA; Drs2p	9	1355	8	5.6	14	10	0.000189	4	7.36E-05	3	4.6	6	5	0.000254	1	5.41E-05	4	3.7	6	5	0.000263	1	5.48E-05	2	2	2	0	1.06E-05	2	0.000119	0.841192
gi|6319804 YCL045C	hypothetical protein; Ycl045cp	1	760	17	15.9	42	26	0.000849	16	0.000481	15	11.7	30	19	0.00168	11	0.000923	5	8.8	9	7	0.000651	2	0.000181	1	1.8	3	0	1.89E-05	3	0.000309	0.843057
gi|6324739 YOR165W	Protein of unknown function, contains two predicted GTP-binding motifs GXXXXGKS and DXXG near the N-terminus, homolog of the Arabidopsis gene RHD3 (Root Hair Defective); Sey1p	2	776	4	5.2	6	2	7.84E-05	4	0.000129	2	3	3	0	1.43E-05	3	0.000256	1	2.2	1	1	0.000104	0	1.37E-05	2	3	2	1	0.00013	1	0.000112	0.843452
gi|6320107 YDL095W	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p	9	817	17	12.6	38	20	0.000611	18	0.000502	7	7.2	16	12	0.000992	4	0.00032	5	3.5	8	3	0.000268	5	0.000402	9	10.4	14	5	0.000546	9	0.000833	0.843807
gi|6321601 YGR162W	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p	0	952	26	24.4	48	29	0.000754	19	0.000454	15	18.2	27	19	0.001341	8	0.000539	11	14.8	18	9	0.000665	9	0.000613	3	2.9	3	1	0.000106	2	0.000169	0.848707
gi|6319699 YBR222C	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p	0	543	17	15.5	43	23	0.001054	20	0.000837	11	15.3	24	13	0.001615	11	0.001291	10	12.9	17	9	0.001166	8	0.000957	2	3.1	2	1	0.000185	1	0.00016	0.848946
gi|6322077 YIL114C	Putative mitochondrial porin (voltage-dependent anion channel), related to Por1p but not required for mitochondrial membrane permeability or mitochondrial osmotic stability; Por2p	0	281	3	3.9	7	4	0.00039	3	0.000276	2	3.9	5	3	0.000751	2	0.000484	1	3.9	1	1	0.000287	0	3.77E-05	1	3.9	1	0	5.12E-05	1	0.000308	0.850349
gi|6324348 YNR021W	hypothetical protein; Ynr021wp	1	404	4	11.9	8	3	0.000211	5	0.000302	2	6.7	4	1	0.000192	3	0.000492	2	8.2	2	2	0.00037	0	2.62E-05	1	5.2	2	0	3.56E-05	2	0.000398	0.85063
gi|6324036 YNL293W	GTPase-activating protein for Sec4p and several other Rab GTPases, regulates exocytosis via its action on Sec4p, also required for proper actin organization; similar to Msb4p; both Msb3p and Msb4p localize to sites of polarized growth; Msb3p	0	633	3	5.4	7	4	0.000173	3	0.000123	2	2.2	3	1	0.000123	2	0.000215	1	2.2	3	3	0.000345	0	1.68E-05	1	3.2	1	0	2.27E-05	1	0.000137	0.851054
gi|1038381 YCR093W	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor; Cdc39p	0	2108	19	4.6	31	15	0.000179	16	0.000174	14	2.6	20	9	0.00029	11	0.000333	4	2	5	2	7.1E-05	3	9.56E-05	3	2	6	4	0.000171	2	7.63E-05	0.851354
gi|6324278 YNL050C	hypothetical protein; Ynl050cp	0	270	4	5.6	8	3	0.000316	5	0.000452	3	5.6	4	2	0.000535	2	0.000504	1	5.6	1	1	0.000298	0	3.93E-05	2	5.6	3	0	5.33E-05	3	0.000871	0.851362
gi|6321673 YGR234W	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses; Yhb1p	0	399	6	8.8	7	4	0.000275	3	0.000194	1	4.3	1	0	2.78E-05	1	0.000184	4	4.5	5	3	0.000548	2	0.000345	1	4.3	1	1	0.000252	0	3.1E-05	0.855017
gi|6324344 YNR017W	Essential protein of the mitochondrial inner membrane, component of the mitochondrial import system; Mas6p	0	222	11	16.2	40	20	0.002248	20	0.002047	9	16.2	25	14	0.004251	11	0.003159	3	9	7	2	0.000674	5	0.001481	5	9	8	4	0.00162	4	0.001394	0.85799

gi|6323374 YLR342W	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p	13	1876	86	11.7	271	122	0.00159	149	0.001767	32	8.7	77	46	0.001639	31	0.001043	38	9	87	38	0.001405	49	0.001667	36	6.9	107	38	0.001756	69	0.002738	0.858321
gi|6321523 YGR086C	Long chain base-responsive inhibitor of protein kinases Pkh1p and Pkh2p, acts along with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p; Pil1p	0	339	19	26.3	92	47	0.003411	45	0.002975	13	21.2	33	20	0.003963	13	0.002439	11	18.3	40	23	0.004719	17	0.003222	6	17.1	19	4	0.001061	15	0.003323	0.858484
gi|3736264 YER178W	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p	0	420	34	18.6	253	150	0.008723	103	0.005463	11	15.7	64	33	0.005261	31	0.00466	13	6.9	167	109	0.017948	58	0.008811	13	11.7	22	8	0.001678	14	0.002505	0.861453
gi|6320490 YDR284C	Diacylglycerol pyrophosphate (DGPP) phosphatase, zinc-regulated vacuolar membrane-associated lipid phosphatase, dephosphorylates DGPP to phosphatidate (PA) and Pi, then PA to diacylglycerol; involved in lipid signaling and cell metabolism; Dpp1p	5	289	2	5.2	11	4	0.000379	7	0.000575	2	5.2	6	2	0.000499	4	0.000905	1	5.2	1	1	0.000279	0	3.67E-05	2	5.2	4	1	0.000348	3	0.000814	0.863646
gi|6320175 YDL029W	Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p	0	391	46	17.1	142	66	0.00414	76	0.004337	21	15.9	69	33	0.005651	36	0.005808	16	13	34	17	0.003032	17	0.002793	21	16.9	39	16	0.003569	23	0.0044	0.864249
gi|6322409 YJL052W	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p	0	332	12	33.7	21	8	0.000623	13	0.000901	6	21.7	11	3	0.000635	8	0.001545	3	9.6	4	3	0.000659	1	0.000224	6	22.6	6	2	0.000563	4	0.000932	0.866842
gi|6320625 YDR418W	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12bp	0	165	40	32.1	126	57	0.008484	69	0.009338	23	23	48	22	0.00895	26	0.009958	27	23	53	22	0.009277	31	0.012017	12	21.8	25	13	0.006888	12	0.005476	0.867225
gi|6319673 YBR196C	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression and completion of the gluconeogenic events of sporulation; Pgi1p	0	554	7	10.8	15	8	0.000374	7	0.0003	3	8.1	4	4	0.000501	0	1.89E-05	7	10.8	9	4	0.000519	5	0.000593	1	2.7	2	0	2.6E-05	2	0.00029	0.874423
gi|6323654 YMR012W	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant; Clu1p	0	1277	20	13.2	43	21	0.00041	22	0.000391	8	7.8	13	10	0.00053	3	0.000156	11	8.4	20	8	0.000442	12	0.000606	7	7.2	10	3	0.000214	7	0.000417	0.877225
gi|6319489 YBR015C	Alpha-1,2-mannosyltransferase, responsible for addition of the first alpha-1,2-linked mannose to form the branches on the mannan backbone of oligosaccharides, localizes to an early Golgi compartment; Mnn2p	1	597	11	16.4	23	13	0.00055	10	0.00039	6	10.9	13	6	0.000688	7	0.000754	6	10.6	9	7	0.000829	2	0.000231	1	2.8	1	0	2.41E-05	1	0.000145	0.878945
gi|6319553 YBR079C	Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p	0	964	39	16.9	121	59	0.001503	62	0.001437	26	15.9	53	28	0.001947	25	0.001639	17	13.8	40	22	0.001588	18	0.001199	14	11.4	28	9	0.000821	19	0.001477	0.878955
gi|6321285 YGL153W	Peroxisomal membrane protein that is a central component of the peroxisomal protein import machinery, interacts with PTS1 (Pex5p) and PTS2 (Pex7p) peroxisomal matrix protein signal recognition factors and membrane receptor Pex13p; Pex14p	0	341	7	10.3	17	9	0.000678	8	0.000553	4	10.3	11	5	0.001009	6	0.001136	4	10.3	5	4	0.000844	1	0.000218	1	5.3	1	0	4.22E-05	1	0.000254	0.879945
gi|6319760 YBR283C	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-translational pathway of protein translocation; not essential; Ssh1p	9	490	26	11	110	56	0.002807	54	0.002466	17	11	71	39	0.005325	32	0.004122	6	11	16	14	0.001996	2	0.000281	6	8.2	23	3	0.000558	20	0.003057	0.880558
gi|3736265 YHR065C	Protein involved in rRNA processing; required for maturation of the 35S primary transcript of pre-rRNA and for cleavage leading to mature 18S rRNA; homologous to eIF-4a, which is a DEAD box RNA-dependent ATPase with helicase activity; Rrp3p	0	501	11	9.6	24	9	0.000462	15	0.000686	5	4.2	8	6	0.00082	2	0.000272	5	7	13	1	0.000161	12	0.001545	2	5.2	3	2	0.000373	1	0.000173	0.881801
gi|6322148 YIL041W	Golgi vesicle protein of unknown function; localizes to both early and late Golgi vesicles; Gvp36p	0	326	10	12.9	22	11	0.000859	11	0.000782	7	12.9	11	6	0.00126	5	0.000995	2	6.4	4	1	0.000247	3	0.000618	3	6.4	7	4	0.001103	3	0.000721	0.882389
gi|6323893 YMR237W	Protein that colocalizes with clathrin-coated vesicles; involved in transport at the trans-Golgi; Bch1p	0	724	9	6.1	25	18	0.000622	7	0.00023	8	6.1	19	14	0.001304	5	0.000448	4	5	5	4	0.000397	1	0.000103	1	2.1	1	0	1.99E-05	1	0.00012	0.882704
gi|6324265 YNL064C	Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family; Ydj1p	0	409	50	28.4	203	98	0.005863	105	0.005718	22	27.4	66	37	0.006054	29	0.004478	20	20	57	26	0.004418	31	0.004848	21	17.1	80	35	0.007421	45	0.008202	0.888484
gi|6323859 YMR203W	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; constitutes the core element of the protein conducting pore; Tom40p	0	387	4	8.5	13	6	0.000409	7	0.00043	2	4.7	4	2	0.000373	2	0.000352	2	3.9	4	2	0.000387	2	0.000356	2	4.7	5	2	0.000483	3	0.000608	0.889124
gi|6321637 YGR198W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; YGR198W is an essential gene; Ygr198wp	0	817	2	2.6	14	9	0.000283	5	0.000149	2	2.6	3	1	9.51E-05	2	0.000167	1	2.6	3	0	1.41E-05	3	0.000247	1	2.6	8	8	0.000863	0	1.52E-05	0.895334
gi|7839160 YDR261C-	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition; Ydr261c-dp	0	1604	64	13.2	184	83	0.001267	101	0.001403	53	13.2	131	55	0.002291	76	0.002982	19	8.1	44	25	0.001083	19	0.00076	6	5.7	9	3	0.00017	6	0.000286	0.897104
gi|6320552 YDR345C	Low affinity glucose transporter of the major facilitator superfamily, expression is induced in low or high glucose conditions; Hxt3p	11	567	30	8.8	81	41	0.001782	40	0.001583	9	5.6	18	11	0.001312	7	0.000794	20	7.1	45	24	0.002943	21	0.002375	12	6	18	6	0.000939	12	0.001594	0.899665
gi|6321430 YGL008C	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-transporting ATPases; Pma1p	10	918	310	51.6	3776	1700	0.045095	2076	0.050146	108	25.3	862	459	0.033323	403	0.027578	201	42.7	2029	855	0.064327	1174	0.081371	122	32.5	885	386	0.036309	499	0.040384	0.899756
gi|6321753 YHL034C	Nucleolar single-strand nucleic acid binding protein; associates with small nuclear RNAs; Sbp1p	0	294	7	19	23	10	0.000869	13	0.001018	3	8.2	7	1	0.000264	6	0.001317	4	14.6	11	5	0.001214	6	0.001334	4	11.9	5	4	0.001223	1	0.000295	0.903238

gi|6319636 YBR160W	Catalytic subunit of the main cell cycle cyclin-dependent kinase (CDK); alternately associates with G1 cyclins (CLNs) and G2/M cyclins (CLBs) which direct the CDK to specific substrates; Cdc28p	0	298	5	12.8	16	9	0.000776	7	0.000558	4	12.8	14	8	0.001826	6	0.001299	1	8.7	1	1	0.00027	0	3.56E-05	1	7.7	1	0	4.83E-05	1	0.000291	0.90364
gi|6319635 YBR159W	Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides.; Ybr159wp	0	347	8	9.8	20	15	0.001087	5	0.000351	7	9.8	14	12	0.002336	2	0.000392	2	5.5	5	3	0.00063	2	0.000397	1	5.5	1	0	4.15E-05	1	0.00025	0.906222
gi|6320952 YER105C	Abundant subunit of the nuclear pore complex (NPC), present on both sides of the NPC, has similarity to Nup170p; Nup157p	0	1391	12	6.1	15	11	0.000201	4	7.17E-05	8	4.9	11	9	0.000439	2	9.78E-05	3	2.3	3	2	0.000108	1	5.34E-05	1	0.9	1	0	1.03E-05	1	6.23E-05	0.908488
gi|6323729 YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p	0	375	106	18.7	904	430	0.027947	474	0.028051	39	15.2	154	66	0.011755	88	0.014764	53	17.9	226	99	0.018261	127	0.021574	42	17.9	524	265	0.061033	259	0.051328	0.910272
gi|6320148 YDL055C	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure; Psa1p	0	361	13	26.3	19	11	0.000776	8	0.000522	3	10.8	4	2	0.0004	2	0.000377	3	12.7	4	1	0.000223	3	0.000558	8	19.1	11	8	0.001953	3	0.000651	0.910373
gi|6324273 YNL055C	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p	0	283	50	39.9	118	53	0.004602	65	0.005131	37	39.6	79	35	0.008279	44	0.0098	13	13.4	28	13	0.003213	15	0.003409	7	13.1	11	5	0.001576	6	0.001618	0.910528
gi|6321540 YGR103W	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit biogenesis; constituent of several different pre-ribosomal particles; Nop7p	0	605	15	19	68	33	0.001348	35	0.001301	10	19	12	4	0.000459	8	0.000848	5	8.8	22	12	0.001389	10	0.001069	8	11.6	34	17	0.002449	17	0.002107	0.910532
gi|6324828 YOR254C	Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-dependent and post-translational SRP-independent protein targeting and import into the ER; Sec63p	3	663	9	6.6	49	23	0.000863	26	0.000886	8	6.6	22	14	0.001424	8	0.000773	4	5.4	8	6	0.000642	2	0.000208	3	2.9	19	3	0.000412	16	0.001811	0.911495
gi|6325128 YPL129W	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, contains a YEATS domain; Taf14p	0	244	31	25	122	64	0.006435	58	0.005315	14	14.8	37	17	0.004687	20	0.00519	12	19.7	28	10	0.002877	18	0.004737	17	24.2	57	37	0.013147	20	0.006138	0.911503
gi|6320298 YDR093W	Non-essential P-type ATPase that is a potential aminophospholipid translocase, localizes to the plasma membrane and late exocytic or early endocytic membranes, likely involved in protein transport; potential Cdc28p substrate; Dnf2p	9	1612	11	5.3	34	15	0.000234	19	0.000268	4	3.5	8	4	0.000172	4	0.000162	8	4.3	21	8	0.00035	13	0.00052	2	1.1	5	3	0.00017	2	9.98E-05	0.911533
gi|6319278 YAL039C	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role in microphthalmia with linear skin defects (MLS); Cyc3p	0	269	8	17.8	23	15	0.001403	8	0.000701	7	17.8	17	12	0.003013	5	0.001206	3	12.3	5	3	0.000813	2	0.000512	1	6.7	1	0	5.35E-05	1	0.000322	0.916425
gi|1431847 YFL041W	Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a role in iron transport; Fet5p	0	622	8	8.5	29	14	0.000568	15	0.000552	7	8.5	19	9	0.000982	10	0.001026	3	3.2	6	3	0.000352	3	0.000324	3	5.3	4	2	0.000301	2	0.000259	0.917177
gi|2780870 YJL019W	Essential integral membrane protein required for spindle pole body duplication and for nuclear fusion, localizes to the spindle pole body half bridge, interacts with DnaJ-like chaperone Jem1p and with centrin homolog Cdc31p; Mps3p	1	682	4	5.1	5	2	8.92E-05	3	0.000114	2	5.1	2	1	0.000114	1	0.000107	1	2.5	2	0	1.69E-05	2	0.000202	1	2.9	1	1	0.000148	0	1.81E-05	0.917821
gi|6324244 YNL085W	Protein that forms a complex with Pbp1p that may mediate posttranscriptional regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; Mkt1p	0	830	7	4.8	13	8	0.000249	5	0.000147	5	4.8	9	6	0.000495	3	0.00024	1	2.2	1	0	1.39E-05	1	8.94E-05	3	3.5	3	2	0.000225	1	0.000104	0.918349
gi|6321184 YGL253W	Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; predominant hexokinase during growth on glucose; functions in the nucleus to repress expression of HXK1 and GLK1 and to induce expression of its own gene; Hxk2p	0	486	6	7.6	34	15	0.000776	19	0.000889	6	7.6	31	13	0.001805	18	0.002347	1	3.9	2	2	0.000308	0	2.18E-05	1	3.9	1	0	2.96E-05	1	0.000178	0.918549
gi|6319523 YBR049C	RNA polymerase I enhancer binding protein; DNA binding protein which binds to genes transcribed by both RNA polymerase I and RNA polymerase II; required for termination of RNA polymerase I transcription; Reb1p	0	810	4	3.8	4	2	7.51E-05	2	6.84E-05	2	2.6	2	1	9.6E-05	1	9.04E-05	1	2.2	1	0	1.42E-05	1	9.16E-05	1	1.2	1	1	0.000124	0	1.53E-05	0.919818
gi|6320054 YDL147W	Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to mammalian p55 subunit and to another S. cerevisiae regulatory subunit, Rpn7p; Rpn5p	0	445	12	7.6	36	16	0.000903	20	0.001021	7	7.6	20	8	0.001223	12	0.001717	4	3.8	10	4	0.000647	6	0.000882	3	3.8	6	4	0.000808	2	0.000362	0.920997
gi|6321792 YHR005C	GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates the pathway via Scp160p; Gpa1p	0	472	6	8.9	11	5	0.000284	6	0.000305	3	5.3	4	3	0.000447	1	0.000155	1	3.2	2	2	0.000317	0	2.25E-05	3	5.7	5	0	3.05E-05	5	0.000813	0.921469
gi|6321643 YGR204W	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p	0	946	15	12.7	33	16	0.000425	17	0.00041	9	11.4	16	8	0.000575	8	0.000542	5	6.6	9	4	0.000304	5	0.000347	4	3.3	8	4	0.00038	4	0.000327	0.922421
gi|6325126 YPL131W	Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and rat L5 ribosomal proteins; binds 5S rRNA and is required for 60S subunit assembly; Rpl5p	0	297	12	27.9	32	15	0.00127	17	0.001306	7	21.2	17	8	0.001832	9	0.001938	5	18.2	8	4	0.000969	4	0.000893	2	4.4	7	3	0.00092	4	0.001042	0.924206
gi|6325097 YPL160W	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p	0	1090	11	10	15	7	0.000168	8	0.000173	3	4.4	4	3	0.000194	1	6.72E-05	3	3.9	3	1	7.39E-05	2	0.000126	5	4.5	8	3	0.000251	5	0.000352	0.925701
gi|6322146 YIL043C	cytochrome b reductase; Cbr1p	1	322	8	6.8	33	17	0.001323	16	0.001136	6	6.2	19	10	0.002103	9	0.001788	2	5.6	4	1	0.00025	3	0.000626	4	5.6	10	6	0.001653	4	0.000961	0.92857
gi|6322468 YJR009C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p	0	332	46	55.4	111	55	0.00407	56	0.003773	23	39.5	49	31	0.006254	18	0.003436	17	24.1	30	11	0.002323	19	0.003673	18	31.9	32	13	0.003423	19	0.004288	0.928626

gi|6320382 YDR177W	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response; Ubc1p	0	215	14	18.1	51	28	0.003227	23	0.002423	11	18.1	23	12	0.00377	11	0.003261	3	18.1	7	2	0.000696	5	0.001529	8	16.7	21	14	0.005687	7	0.002476	0.930404
gi|6320703 YDR495C	Cytoplasmic protein required for the sorting and processing of soluble vacuolar proteins, acidification of the vacuolar lumen, and assembly of the vacuolar H+-ATPase; Vps3p	0	1011	3	3.2	6	3	8.43E-05	3	7.67E-05	2	1.7	4	2	0.000143	2	0.000135	1	1.7	1	1	7.97E-05	0	1.05E-05	1	1.5	1	0	1.42E-05	1	8.57E-05	0.930579
gi|1431848 YFL037W	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules; Tub2p	0	457	12	20.1	47	21	0.001145	26	0.001286	9	13.8	32	15	0.002211	17	0.002359	4	10.3	6	5	0.000781	1	0.000162	3	7.2	9	1	0.00022	8	0.001327	0.931112
gi|6323722 YMR076C	Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes in an interdependent manner, may function as a protein-protein interaction scaffold; Pds5p	0	1277	4	4.6	6	3	6.67E-05	3	6.08E-05	1	1.4	1	0	8.7E-06	1	5.74E-05	2	2.1	4	2	0.000117	2	0.000108	1	1.1	1	1	7.89E-05	0	9.69E-06	0.932904
gi|6324673 YOR099W	Alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr1p	0	393	5	15.3	11	4	0.000279	7	0.000423	2	7.6	3	3	0.000537	0	2.66E-05	1	4.3	1	0	2.93E-05	1	0.000189	3	7.6	7	1	0.000256	6	0.001165	0.933004
gi|6325293 YPR036W	Subunit H of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; serves as an activator or a structural stabilizer of the V-ATPase; Vma13p	0	478	10	10.3	25	8	0.000433	17	0.000812	7	10.3	12	2	0.000302	10	0.001336	2	3.3	5	5	0.000746	0	2.22E-05	5	6.3	8	1	0.000211	7	0.001114	0.934536
gi|6321925 YHR133C	Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p, one of two HMG-CoA isoenzymes that catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIG proteins; Nsg1p	5	291	4	10	31	22	0.001882	9	0.000724	3	10	18	16	0.003701	2	0.000468	3	5.5	12	6	0.001463	6	0.001348	1	5.5	1	0	4.94E-05	1	0.000298	0.936007
gi|6323511 YML124C	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p	0	445	8	12.4	22	11	0.000629	11	0.000573	3	8.1	4	1	0.000175	3	0.000447	3	6.5	5	3	0.000491	2	0.00031	5	9	13	7	0.00139	6	0.001029	0.936421
gi|6320185 YDL019C	Member of an oxysterol-binding protein family with seven members in S. cerevisiae; family members have overlapping, redundant functions in sterol metabolism and collectively perform a function essential for viability; Osh2p	0	1283	4	3	6	3	6.64E-05	3	6.05E-05	1	1.1	1	0	8.65E-06	1	5.71E-05	1	1	1	1	6.28E-05	0	8.26E-06	2	0.9	4	2	0.000146	2	0.000125	0.937468
gi|6322854 YKR002W	Poly(A) polymerase, one of three factors required for mRNA 3'-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for mRNA nuclear export; may also polyadenylate rRNAs; Pap1p	0	568	11	8.3	37	15	0.000664	22	0.000878	4	8.3	9	3	0.000371	6	0.000682	3	8.3	8	6	0.00075	2	0.000243	8	8.3	20	6	0.000937	14	0.001852	0.938199
gi|6319806 YCL043C	Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-surface proteins, unscrambles non-native disulfide bonds; Pdi1p	0	522	22	18	39	26	0.001236	13	0.000573	13	10.2	24	20	0.002574	4	0.000501	10	17.2	14	6	0.000816	8	0.000995	1	2.1	1	0	2.76E-05	1	0.000166	0.938632
gi|2780871 YML032C	Protein that stimulates strand exchange by facilitating Rad51p binding to single-stranded DNA; anneals complementary single-stranded DNA; involved in the repair of double-strand breaks in DNA during vegetative growth and meiosis; Rad52p	0	471	2	3.8	9	5	0.000284	4	0.000212	1	3.8	2	0	2.36E-05	2	0.000289	1	3.8	1	1	0.000171	0	2.25E-05	2	3.8	6	4	0.000764	2	0.000342	0.939089
gi|6319682 YBR205W	Putative alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family; Ktr3p	1	404	12	19.1	39	25	0.001537	14	0.000796	10	18.8	26	17	0.002831	9	0.001425	6	8.9	12	8	0.001396	4	0.000656	1	4.2	1	0	3.56E-05	1	0.000214	0.939579
gi|6319837 YCL009C	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria; Ilv6p	0	309	9	13.3	189	81	0.006421	108	0.007784	7	13.3	71	31	0.00672	40	0.008163	4	9.1	101	39	0.008753	62	0.012799	3	9.1	17	11	0.003119	6	0.001482	0.94169
gi|6320559 YDR352W	hypothetical protein; Ydr352wp	5	317	4	8.8	19	8	0.000653	11	0.000804	2	8.8	5	0	3.5E-05	5	0.001023	2	6.3	5	5	0.001125	0	3.34E-05	2	6.3	9	3	0.000862	6	0.001445	0.942874
gi|6319505 YBR031W	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap	0	362	10	9.7	29	12	0.000841	17	0.001072	8	9.7	16	5	0.000951	11	0.001937	4	3.9	7	3	0.000604	4	0.000732	3	3.6	6	4	0.000993	2	0.000445	0.945885
gi|6321464 YGR027C	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein; Rps25ap	0	108	17	30.6	59	23	0.005297	36	0.007492	10	30.6	37	16	0.009973	21	0.012307	7	30.6	18	4	0.002664	14	0.008345	3	19.4	4	3	0.002531	1	0.000802	0.947315
gi|6320935 YER090W	Anthranilate synthase, catalyzes the initial step of tryptophan biosynthesis, forms multifunctional hetero-oligomeric anthranilate synthase:indole-3-glycerol phosphate synthase enzyme complex with Trp3p; Trp2p	0	507	2	3.4	9	4	0.000216	5	0.00024	2	3.4	6	2	0.000285	4	0.000516	1	3.4	2	2	0.000295	0	2.09E-05	1	3.4	1	0	2.84E-05	1	0.000171	0.94741
gi|6322994 YLL034C	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions; Rix7p	0	837	18	11.2	43	18	0.000538	25	0.000675	5	6	7	5	0.000411	2	0.000163	3	3.9	5	2	0.000179	3	0.000241	12	6.9	31	11	0.001152	20	0.001789	0.948322
gi|6324433 YOL139C	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p	0	213	18	48.8	34	14	0.001657	20	0.002134	8	30.5	14	8	0.002554	6	0.001818	8	31.5	16	3	0.001027	13	0.003933	3	8.9	4	3	0.001283	1	0.000407	0.949428
gi|6320170 YDL035C	Plasma membrane G protein coupled receptor (GPCR) that interacts with the heterotrimeric G protein alpha subunit, Gpa2p, and with Plc1p; sensor that integrates nutritional signals with the modulation of cell fate via PKA and cAMP synthesis; Gpr1p	6	961	5	8.4	14	7	0.00019	7	0.000173	2	3.5	5	0	1.16E-05	5	0.000338	4	8.4	7	5	0.000371	2	0.000143	1	1.9	2	2	0.000195	0	1.29E-05	0.949666
gi|6322363 YJL098W	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p; Sap185p	0	1058	6	9.3	13	5	0.000127	8	0.000178	5	6.4	11	4	0.000262	7	0.000425	1	1.1	1	1	7.61E-05	0	1E-05	1	2.8	1	0	1.36E-05	1	8.19E-05	0.954685
gi|6321968 YHR174W	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p	0	437	168	32.3	1625	757	0.042199	868	0.044059	89	27.2	469	203	0.030973	266	0.038247	76	29.3	1004	469	0.074136	535	0.07791	35	16.9	152	85	0.016822	67	0.011415	0.955061

gi|6321977 YHR183W	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p	0	489	21	23.9	66	30	0.001518	36	0.001655	7	13.9	15	9	0.001249	6	0.000792	10	20.7	24	8	0.001153	16	0.002103	7	5.3	27	13	0.002324	14	0.002152	0.957047
gi|6325025 YPL231W	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p	0	1887	55	14.3	202	88	0.001142	114	0.001345	7	5.4	10	6	0.000218	4	0.000139	8	5.2	13	6	0.000226	7	0.000242	51	13.2	179	76	0.003484	103	0.00406	0.958747
gi|6323961 YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1; Adh2p	0	348	27	9.5	154	78	0.005491	76	0.004873	8	8.9	16	9	0.001755	7	0.001293	14	9.5	30	11	0.002216	19	0.003504	16	8.3	108	58	0.014427	50	0.010706	0.959849
gi|6322368 YJL093C	Outward-rectifier potassium channel of the plasma membrane with two pore domains in tandem, each of which forms a functional channel permeable to potassium; carboxy tail functions to prevent inner gate closures; target of K1 toxin; Tok1p	10	691	6	3.8	12	6	0.000229	6	0.000209	1	2.6	1	1	0.000112	0	1.51E-05	4	3.8	8	5	0.000516	3	0.000292	1	2.6	3	0	2.08E-05	3	0.00034	0.960411
gi|6320844 YER007C-	hypothetical protein; Tma20p	0	181	8	10.5	15	9	0.001278	6	0.000796	3	10.5	5	4	0.001534	1	0.000405	5	10.5	9	5	0.001971	4	0.001465	1	8.3	1	0	7.95E-05	1	0.000479	0.962445
gi|6323016 YLL013C	Protein that regulates degradation of specific mRNAs such as COX17, binds almost exclusively to cytoplasmic mRNAs encoding mitochondrial proteins, member of the PUF protein family that contains Pumilio homology domains; Puf3p	0	879	10	6.1	20	14	0.000402	6	0.000164	5	4.7	6	4	0.000316	2	0.000155	1	1.3	1	0	1.31E-05	1	8.44E-05	6	4.8	13	10	0.000998	3	0.000268	0.969024
gi|3736268 YMR242C	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl20Bp and has similarity to rat L18a ribosomal protein; Rpl20ap	0	178	6	17.4	36	16	0.002257	20	0.002553	3	11.2	17	7	0.002682	10	0.003587	5	13.5	14	6	0.002392	8	0.002919	2	7.3	5	3	0.001536	2	0.000904	0.97816
gi|6321401 YGL037C	Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span; Pnc1p	0	216	18	31	31	14	0.001634	17	0.001796	8	31	13	4	0.001285	9	0.002665	7	18.5	13	7	0.002291	6	0.001816	4	17.1	5	3	0.001265	2	0.000745	0.980749
gi|6324683 YOR109W	Phosphatidylinositol 4,5-bisphosphate 5-phosphatase, synaptojanin-like protein with an N-terminal Sac1 domain, plays a role in a TGN (trans Golgi network)-to-early endosome pathway; hyperosmotic stress causes translocation to actin patches; Inp53p	0	1107	4	3.4	7	3	7.7E-05	4	9.01E-05	3	3.4	4	1	7.02E-05	3	0.00018	1	1.4	1	0	1.04E-05	1	6.7E-05	1	1.4	2	2	0.000169	0	1.12E-05	0.980968
gi|6325329 YPR072W	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation; Not5p	0	560	12	8.9	28	14	0.00063	14	0.000574	8	5.5	12	6	0.000734	6	0.000691	4	5.7	6	2	0.000267	4	0.000473	5	5.9	10	6	0.00095	4	0.000553	0.981654
gi|6319882 YCR034W	Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway; Fen1p	7	347	20	18.7	51	34	0.00242	17	0.001118	15	12.1	30	18	0.003488	12	0.002202	9	13	20	16	0.003217	4	0.000764	1	4.6	1	0	4.15E-05	1	0.00025	0.98396
gi|6324279 YNL049C	Probable component of COPII coated vesicles that binds to Sec23p; similar to and functionally redundant with Sec24p, but expressed at low levels; involved in ER to Golgi transport and in autophagy; Sfb2p	0	876	4	5.4	8	4	0.000125	4	0.000114	2	3.4	3	3	0.000241	0	1.19E-05	3	3.7	3	1	9.2E-05	2	0.000157	1	1.9	2	0	1.64E-05	2	0.000184	0.98905
gi|6322427 YJL033W	Putative nucleolar DEAD box RNA helicase; high-copy number suppression of a U14 snoRNA processing mutant suggests an involvement in 18S rRNA synthesis; Hca4p	0	770	7	5.8	10	5	0.000174	5	0.000158	1	1.8	2	0	1.44E-05	2	0.000177	5	5.8	7	4	0.000374	3	0.000262	1	2.7	1	1	0.000131	0	1.61E-05	0.989743
gi|1038379 YCR030C	Protein with a potential role in actin cytoskeletal organization; overexpression suppresses a pfy1 (profilin) null mutation; Syp1p	0	870	11	6.1	23	11	0.000322	12	0.000319	7	5.9	12	6	0.000472	6	0.000445	3	5.6	4	2	0.000172	2	0.000158	4	1.7	7	3	0.000314	4	0.000356	0.990113
gi|6323798 YMR149W	Delta subunit of the oligosaccharyl transferase glycoprotein complex, which is required for N-linked glycosylation of proteins in the endoplasmic reticulum; Swp1p	2	286	8	15.7	18	11	0.000979	7	0.000581	7	10.5	11	6	0.001436	5	0.001134	2	11.2	6	5	0.001247	1	0.00026	1	4.5	1	0	5.03E-05	1	0.000303	0.99779
gi|6321816 YHR027C	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine-rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p	0	993	19	11.9	40	21	0.000527	19	0.000435	10	5.6	15	8	0.000548	7	0.000453	11	9.9	18	11	0.000777	7	0.000459	4	4.7	7	2	0.000188	5	0.000386	0.997963
gi|6324415 YOL158C	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment; Enb1p	11	606	12	12.9	25	4	0.000181	21	0.000787	2	3.1	2	1	0.000128	1	0.000121	11	11.1	22	2	0.000247	20	0.002117	1	1.8	1	1	0.000166	0	2.04E-05	0.998811
gi|6321631 YGR192C	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p	0	332	59	57.8	218	104	0.007663	114	0.007646	25	38	68	29	0.005853	39	0.007408	23	24.1	79	39	0.008146	40	0.007697	24	31.9	71	36	0.009403	35	0.007867	0.999032
gi|6323077 YLR048W	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Ap; required for maturation of 18S rRNA along with Rps0Ap; deletion of either RPS0 gene reduces growth rate, deletion of both genes is lethal; Rps0bp	0	252	4	9.9	19	10	0.001014	9	0.000836	4	9.9	12	7	0.001895	5	0.001287	2	6	3	1	0.00032	2	0.000547	2	9.9	4	2	0.000742	2	0.000639	0.999826