

Systemic name	Gene name	Description	Fold change VPA+/VPA-	
			Inositol+	Inositol-
YCR034W	<i>FEN1</i>	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-	2.46	2.86
YLR372W	<i>SUR4</i>	Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers; involved in	2.77	2.47
YNR056C	<i>BIO5</i>	Putative transmembrane protein involved in the biotin biosynthesis pathway; responsible for uptake of 7-keto 8-aminopelargonic acid; BIO5 is in a cluster	-	-8.92
YCL025C	<i>AGP1</i>	Low-affinity amino acid permease with broad substrate range, involved in uptake of asparagine, glutamine, and other amino acids; expression is	-	-3.77
YKR039W	<i>GAP1</i>	General amino acid permease; localization to the plasma membrane is regulated by nitrogen source	-	-2.85
YBR068C	<i>BAP2</i>	High-affinity leucine permease, functions as a branched-chain amino acid permease involved in the	-	-6.22
YPL265W	<i>DIP5</i>	Dicarboxylic amino acid permease, mediates high-affinity and high-capacity transport of L-glutamate	-2.22	-2.36
YDL210W	<i>UGA4</i>	Permease that serves as a gamma-aminobutyrate (GABA) transport protein involved in the utilization of GABA as a nitrogen source; catalyzes the transport of	-	-2.26
YEL063C	<i>CAN1</i>	Plasma membrane arginine permease, requires phosphatidyl ethanolamine (PE) for localization,	-	-2.31
YPL274W	<i>SAM3</i>	High-affinity S-adenosylmethionine permease, required for utilization of S-adenosylmethionine as a	-	-13.79
YDR518W	<i>EUG1</i>	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of	-	2.39
YJL073W	<i>JEM1</i>	DnaJ-like chaperone required for nuclear membrane fusion during mating, localizes to the ER membrane;	-	5.81
YKL073W	<i>LHS1</i>	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; nucleotide exchange factor for the ER	-	3.50
YCL043C	<i>PDI1</i>	Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in	-	2.83
YPL187W	<i>MF(ALPHA)1</i>	Mating pheromone alpha-factor, made by alpha cells; interacts with mating type a cells to induce cell cycle arrest and other responses leading to mating; also	11.29	-
YOR153W	<i>PDR5</i>	Plasma membrane ATP-binding cassette (ABC) transporter, multidrug transporter actively regulated by Pdr1p; also involved in steroid transport, cation	10.09	12.10

YLR307W	<i>CDA1</i>	Chitin deacetylase, together with Cda2p involved in the biosynthesis ascospore wall component,	8.54	8.31
YJL116C	<i>NCA3</i>	Protein that functions with Nca2p to regulate mitochondrial expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase; member of the	7.43	–
YKL121W	<i>DGR2</i>	Protein of unknown function; null mutant is resistant to 2-deoxy-D-glucose and displays abnormally	5.55	2.68
YKL178C	<i>STE3</i>	Receptor for a factor pheromone, couples to MAP kinase cascade to mediate pheromone response; transcribed in alpha cells and required for mating by	5.53	–
YBR040W	<i>FIG1</i>	Integral membrane protein required for efficient mating; may participate in or regulate the low affinity Ca <sup>2+</sup> influx system, which affects intracellular	5.37	–
YOL101C	<i>IZH4</i>	Membrane protein involved in zinc ion homeostasis, member of the four-protein IZH family, expression induced by fatty acids and altered zinc levels;	5.35	5.88
YEL057C	<i>YEL057C</i>	Protein of unknown function involved in telomere	5.30	–
YNL289W	<i>PCL1</i>	Cyclin, interacts with cyclin-dependent kinase Pho85p; member of the Pcl1,2-like subfamily, involved in the regulation of polarized growth and	5.25	–
YJR078W	<i>BNA2</i>	Putative tryptophan 2,3-dioxygenase or indoleamine 2,3-dioxygenase, required for de novo biosynthesis of NAD from tryptophan via kynurenine; interacts	5.13	–
YGR225W	<i>AMA1</i>	Activator of meiotic anaphase promoting complex (APC/C); Cdc20p family member; required for	5.03	2.59
YOR315W	<i>SFG1</i>	Nuclear protein, putative transcription factor required for growth of superficial pseudohyphae (which do not invade the agar substrate) but not for	4.94	–
YDR317W	<i>HIM1</i>	Protein of unknown function involved in DNA repair	4.78	–
YML027W	<i>YOX1</i>	Homeodomain-containing transcriptional repressor, binds to Mcm1p and to early cell cycle boxes (ECBs) in the promoters of cell cycle-regulated genes	4.59	–
YGL055W	<i>OLE1</i>	Delta(9) fatty acid desaturase, required for monounsaturated fatty acid synthesis and for normal	4.59	–
YER060W	<i>FCY21</i>	Putative purine-cytosine permease, very similar to	4.56	–
YPR119W	<i>CLB2</i>	B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the transition from G2 to M phase; accumulates during G2 and M, then	4.54	–
YOL014W	<i>YOL014W</i>	Putative protein of unknown function	4.43	11.01
YHL028W	<i>WSC4</i>	ER membrane protein involved in the translocation of soluble secretory proteins and insertion of membrane proteins into the ER membrane; may also	4.22	–

YLR183C	<i>TOS4</i>	Forkhead Associated domain containing protein and putative transcription factor found associated with chromatin; target of SBF transcription factor;	4.22	5.96
YBR021W	<i>FUR4</i>	Uracil permease, localized to the plasma membrane; expression is tightly regulated by uracil levels and	4.20	-
YDL101C	<i>DUN1</i>	Cell-cycle checkpoint serine-threonine kinase required for DNA damage-induced transcription of certain target genes, phosphorylation of Rad55p and	4.19	-
YCL048W	<i>SPS22</i>	Protein of unknown function, redundant with Sps2p for the organization of the beta-glucan layer of the	4.12	2.53
YMR215W	<i>GAS3</i>	Putative 1,3-beta-glucanosyltransferase, has	4.07	
YKL216W	<i>URA1</i>	Dihydroorotate dehydrogenase, catalyzes the fourth enzymatic step in the de novo biosynthesis of	3.93	4.66
YKR090W	<i>PXL1</i>	LIM domain-containing protein that localizes to sites of polarized growth, required for selection and/or maintenance of polarized growth sites, may	3.88	
YPL081W	<i>RPS9A</i>	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity	3.88	3.15
YJL158C	<i>CIS3</i>	Mannose-containing glycoprotein constituent of the cell wall; member of the PIR (proteins with internal	3.85	3.06
YMR199W	<i>CLN1</i>	G1 cyclin involved in regulation of the cell cycle; activates Cdc28p kinase to promote the G1 to S phase transition; late G1 specific expression depends	3.80	-
YPL256C	<i>CLN2</i>	G1 cyclin involved in regulation of the cell cycle; activates Cdc28p kinase to promote the G1 to S phase transition; late G1 specific expression depends	3.80	-
YHL024W	<i>RIM4</i>	Putative RNA-binding protein required for the expression of early and middle sporulation genes	3.75	-
YMR076C	<i>PDS5</i>	Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes, may	3.75	-
YHR184W	<i>SSP1</i>	Protein involved in the control of meiotic nuclear division and coordination of meiosis with spore	3.66	-
YLR012C	<i>YLR012C</i>	Putative protein of unknown function; YLR012C is not	3.64	-
YHR172W	<i>SPC97</i>	Component of the microtubule-nucleating Tub4p (gamma-tubulin) complex; interacts with Spc110p at	3.56	-
YJL037W	<i>IRC18</i>	Putative protein of unknown function; expression induced in respiratory-deficient cells and in carbon-limited chemostat cultures; similar to adjacent ORF,	3.55	-
YLR103C	<i>CDC45</i>	DNA replication initiation factor; recruited to MCM pre-RC complexes at replication origins; promotes release of MCM from Mcm10p, recruits elongation	3.50	-

YHR154W	<i>RTT107</i>	Protein implicated in Mms22-dependent DNA repair during S phase, DNA damage induces phosphorylation by Mec1p at one or more SQ/TQ	3.49	-
YHR153C	<i>SPO16</i>	Meiosis-specific protein involved in synaptonemal complex assembly; implicated in regulation of	3.49	5.79
YDR451C	<i>YHP1</i>	One of two homeobox transcriptional repressors (see also Yox1p), that bind to Mcm1p and to early cell cycle box (ECB) elements of cell cycle regulated	3.37	-
YJL194W	<i>CDC6</i>	Essential ATP-binding protein required for DNA replication, component of the pre-replicative complex (pre-RC) which requires ORC to associate	3.36	-
YBR088C	<i>POL30</i>	Proliferating cell nuclear antigen (PCNA), functions as the sliding clamp for DNA polymerase delta; may function as a docking site for other proteins required	3.36	5.26
YJR053W	<i>BFA1</i>	Component of the GTPase-activating Bfa1p-Bub2p complex involved in multiple cell cycle checkpoint	3.34	2.67
YJR092W	<i>BUD4</i>	Protein involved in bud-site selection and required for axial budding pattern; localizes with septins to bud neck in mitosis and may constitute an axial	3.33	-
YDR146C	<i>SWI5</i>	Transcription factor that activates transcription of genes expressed at the M/G1 phase boundary and in G1 phase; localization to the nucleus occurs during	3.33	-
YDR042C	<i>YDR042C</i>	Putative protein of unknown function; expression is	3.33	-
YPL231W	<i>FAS2</i>	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains the acyl-carrier protein domain and	3.31	2.66
YMR101C	<i>SRT1</i>	Cis-prenyltransferase involved in synthesis of long-chain dolichols (19-22 isoprene units; as opposed to Rer2p which synthesizes shorter-chain dolichols);	3.30	-
YNR030W	<i>ALG12</i>	Alpha-1,6-mannosyltransferase localized to the ER; responsible for the addition of the alpha-1,6	3.30	-
YMR305C	<i>SCW10</i>	Cell wall protein with similarity to glucanases; may play a role in conjugation during mating based on	3.30	-
YOL151W	<i>GRE2</i>	3-methylbutanal reductase and NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase); stress induced (osmotic, ionic,	3.26	-
YNL301C	<i>RPL18B</i>	Protein component of the large (60S) ribosomal subunit, identical to Rpl18Ap and has similarity to rat	3.19	2.86
YNR073C	<i>YNR073C</i>	Putative mannitol dehydrogenase	3.17	-
YMR144W	<i>YMR144W</i>	Putative protein of unknown function; localized to the nucleus; YMR144W is not an essential gene	3.11	-

YDL003W	<i>MCD1</i>	Essential subunit of the cohesin complex required for sister chromatid cohesion in mitosis and meiosis; apoptosis induces cleavage and translocation of a C-	3.10	3.70
YCL026C-B	<i>HBN1</i>	Putative protein of unknown function; similar to bacterial nitroreductases; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and	3.05	2.68
YMR032W	<i>HOF1</i>	Bud neck-localized, SH3 domain-containing protein required for cytokinesis; regulates actomyosin ring dynamics and septin localization; interacts with the	3.03	-
YER187W	<i>YER187W</i>	Putative protein of unknown function; induced in	2.98	-
YJL092W	<i>SRS2</i>	DNA helicase and DNA-dependent ATPase involved in DNA repair, needed for proper timing of commitment to meiotic recombination and transition from Meiosis	2.93	-
YBR078W	<i>ECM33</i>	GPI-anchored protein of unknown function, has a possible role in apical bud growth; GPI-anchoring on the plasma membrane crucial to function;	2.91	-
YLR054C	<i>OSW2</i>	Protein of unknown function proposed to be involved	2.89	2.17
YMR303C	<i>ADH2</i>	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde;	2.89	-
YDL114W	<i>YDL114W</i>	Putative protein of unknown function with similarity to acyl-carrier-protein reductases; YDL114W is not an	2.82	-
YGR286C	<i>BIO2</i>	Biotin synthase, catalyzes the conversion of dethiobiotin to biotin, which is the last step of the	2.79	-
YOL132W	<i>GAS4</i>	1,3-beta-glucanosyltransferase, involved with Gas2p in spore wall assembly; has similarity to Gas1p;	2.77	-
YAL061W	<i>BDH2</i>	Putative medium-chain alcohol dehydrogenase with similarity to BDH1; transcription induced by	2.76	-
YDR528W	<i>HLR1</i>	Protein involved in regulation of cell wall composition and integrity and response to osmotic stress; overproduction suppresses a lysis sensitive PKC	2.75	-
YIL123W	<i>SIM1</i>	Protein of the SUN family (Sim1p, Uth1p, Nca3p, Sun4p) that may participate in DNA replication, promoter contains SCB regulation box at -300 bp	2.74	-
YJL080C	<i>SCP160</i>	Essential RNA-binding G protein effector of mating response pathway, mainly associated with nuclear envelope and ER, interacts in mRNA-dependent	2.72	-
YBL031W	<i>SHE1</i>	Mitotic spindle protein that interacts with components of the Dam1 (DASH) complex, its effector Sli15p, and microtubule-associated protein	2.71	2.20
YBR092C	<i>PHO3</i>	Constitutively expressed acid phosphatase similar to Pho5p; brought to the cell surface by transport vesicles; hydrolyzes thiamin phosphates in the	2.71	-
YJL102W	<i>MEF2</i>	Mitochondrial elongation factor involved in	2.70	3.61

YAR007C	<i>RFA1</i>	Subunit of heterotrimeric Replication Protein A (RPA), which is a highly conserved single-stranded DNA	2.68	2.97
YLR131C	<i>ACE2</i>	Transcription factor that activates expression of early G1-specific genes, localizes to daughter cell nuclei after cytokinesis and delays G1 progression in	2.66	2.33
YER095W	<i>RAD51</i>	Strand exchange protein, forms a helical filament with DNA that searches for homology; involved in the recombinational repair of double-strand breaks in	2.66	-
YOR049C	<i>RSB1</i>	Suppressor of sphingoid long chain base (LCB) sensitivity of an LCB-lyase mutation; putative integral membrane transporter or flippase that may transport	2.65	-
YDR503C	<i>LPP1</i>	Lipid phosphate phosphatase, catalyzes Mg(2+)-independent dephosphorylation of phosphatidic acid (PA), lysophosphatidic acid, and diacylglycerol	2.62	-
YBR184W	<i>YBR184W</i>	Putative protein of unknown function; YBR184W is	2.62	-
YPL248C	<i>GAL4</i>	DNA-binding transcription factor required for the activation of the GAL genes in response to galactose;	2.58	-
YER043C	<i>SAH1</i>	S-adenosyl-L-homocysteine hydrolase, catabolizes S-adenosyl-L-homocysteine which is formed after donation of the activated methyl group of S-adenosyl-	2.57	2.62
YDR497C	<i>ITR1</i>	Myo-inositol transporter with strong similarity to the minor myo-inositol transporter Itr2p, member of the sugar transporter superfamily; expression is	2.57	-
YER032W	<i>FIR1</i>	Protein involved in 3' mRNA processing, interacts	2.56	2.28
YPL127C	<i>HHO1</i>	Histone H1, a linker histone required for nucleosome packaging at restricted sites; suppresses DNA repair involving homologous recombination; not required	2.55	-
YER085C	<i>YER085C</i>	Putative protein of unknown function	2.54	-
YCR088W	<i>ABP1</i>	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3	2.54	-
YNR019W	<i>ARE2</i>	Acyl-CoA:sterol acyltransferase, isozyme of Are1p; endoplasmic reticulum enzyme that contributes the	2.52	2.74
YLR045C	<i>STU2</i>	Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates microtubule dynamics during spindle orientation and metaphase	2.51	-
YBR069C	<i>TAT1</i>	Amino acid transport protein for valine, leucine, isoleucine, and tyrosine, low-affinity tryptophan and	2.51	-
YEL070W	<i>DSF1</i>	Deletion suppressor of mpt5 mutation	2.50	-
YDR501W	<i>PLM2</i>	Forkhead Associated domain containing protein and putative transcription factor found associated with chromatin; target of SBF transcription factor; induced	2.50	-

YNL333W	<i>SNZ2</i>	Member of a stationary phase-induced gene family; transcription of SNZ2 is induced prior to diauxic shift, and also in the absence of thiamin in a Thi2p-	2.50	2.15
YIR033W	<i>MGA2</i>	ER membrane protein involved in regulation of OLE1 transcription, acts with homolog Spt23p; inactive ER form dimerizes and one subunit is then activated by	2.48	2.54
YMR116C	<i>ASC1</i>	G-protein beta subunit and guanine nucleotide dissociation inhibitor for Gpa2p; ortholog of RACK1 that inhibits translation; core component of the small	2.48	2.55
YER070W	<i>RNR1</i>	Major isoform of the large subunit of ribonucleotide-diphosphate reductase; the RNR complex catalyzes rate-limiting step in dNTP synthesis, regulated by	2.47	7.99
YAR018C	<i>KIN3</i>	Nonessential protein kinase with unknown cellular	2.46	-
YDR507C	<i>GIN4</i>	Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities;	2.46	-
YBR071W	<i>YBR071W</i>	Putative protein of unknown function; (GFP)-fusion and epitope-tagged proteins localize to the	2.46	-
YEL040W	<i>UTR2</i>	Chitin transglycosylase that functions in the transfer of chitin to beta(1-6) and beta(1-3) glucans in the cell wall; similar to and functionally redundant with Crh1;	2.46	-
YFL037W	<i>TUB2</i>	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes	2.46	2.34
YML085C	<i>TUB1</i>	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form	2.45	2.30
YBL063W	<i>KIP1</i>	Kinesin-related motor protein required for mitotic spindle assembly, chromosome segregation, and 2 micron plasmid partitioning; functionally redundant	2.44	-
YPL163C	<i>SVS1</i>	Cell wall and vacuolar protein, required for wild-type	2.43	-
YOR025W	<i>HST3</i>	Member of the Sir2 family of NAD(+)-dependent protein deacetylases; involved along with Hst4p in telomeric silencing, cell cycle progression, radiation	2.43	-
YNL135C	<i>FPR1</i>	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and	2.43	2.31
YJR118C	<i>ILM1</i>	Protein of unknown function; may be involved in mitochondrial DNA maintenance; required for slowed	2.41	2.05
YML028W	<i>TSA1</i>	Thioredoxin peroxidase, acts as both a ribosome-associated and free cytoplasmic antioxidant; self-associates to form a high-molecular weight	2.41	3.43
YJL045W	<i>YJL045W</i>	Minor succinate dehydrogenase isozyme; homologous to Sdh1p, the major isozyme responsible for the oxidation of succinate and transfer of	2.40	-

YKL107W	<i>YKL107W</i>	Putative protein of unknown function; proposed to	2.38	2.30
YLR413W	<i>YLR413W</i>	Putative protein of unknown function; YLR413W is	2.38	4.85
YDR113C	<i>PDS1</i>	Securin, inhibits anaphase by binding separin Esp1p; blocks cyclin destruction and mitotic exit, essential for meiotic progression and mitotic cell cycle arrest;	2.36	-
YNL067W	<i>RPL9B</i>	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl9Ap and has similarity	2.35	-
YPL255W	<i>BBP1</i>	Protein required for the spindle pole body (SPB) duplication, localized at the central plaque periphery; forms a complex with a nuclear envelope protein	2.35	2.17
YGL242C	<i>YGL242C</i>	Putative protein of unknown function; deletion	2.35	4.01
YJR047C	<i>ANB1</i>	Translation elongation factor eIF-5A, previously thought to function in translation initiation; similar to and functionally redundant with Hyp2p; undergoes	2.33	-
YAL024C	<i>LTE1</i>	Protein similar to GDP/GTP exchange factors but without detectable GEF activity; required for asymmetric localization of Bfa1p at daughter-directed	2.32	-
YBR160W	<i>CDC28</i>	Catalytic subunit of the main cell cycle cyclin-dependent kinase (CDK); alternately associates with	2.31	2.15
YMR179W	<i>SPT21</i>	Protein with a role in transcriptional silencing; required for normal transcription at several loci including HTA2-HTB2 and HHF2-HHT2, but not	2.30	-
YKL165C	<i>MCD4</i>	Protein involved in glycosylphosphatidylinositol (GPI) anchor synthesis; multimembrane-spanning protein that localizes to the endoplasmic reticulum; highly	2.30	6.19
YLL002W	<i>RTT109</i>	Histone acetyltransferase critical for cell survival in the presence of DNA damage during S phase; acetylates H3-K56 and H3-K9; involved in non-	2.30	-
YJL091C	<i>GWT1</i>	Protein involved in the inositol acylation of glucosaminyl phosphatidylinositol (GlcN-PI) to form glucosaminyl(acyl)phosphatidylinositol (GlcN(acyl)PI),	2.30	3.32
YML058W	<i>SML1</i>	Ribonucleotide reductase inhibitor involved in regulating dNTP production; regulated by Mec1p and	2.29	2.11
YKR042W	<i>UTH1</i>	Mitochondrial outer membrane and cell wall localized SUN family member involved in cell wall biogenesis and required for mitochondrial autophagy;	2.29	-
YBL035C	<i>POL12</i>	B subunit of DNA polymerase alpha-primase complex, required for initiation of DNA replication during mitotic and premeiotic DNA synthesis; also functions	2.29	-
YMR001C	<i>CDC5</i>	Polo-like kinase with multiple functions in mitosis and cytokinesis through substrate phosphorylation, also functions in adaptation to DNA damage during	2.27	-



YLR273C	<i>PIG1</i>	Putative targeting subunit for the type-1 protein phosphatase Glc7p that tethers it to the Gsy2p	2.27	-
YHR061C	<i>GIC1</i>	Protein of unknown function involved in initiation of budding and cellular polarization, interacts with	2.26	-
YGR260W	<i>TNA1</i>	High affinity nicotinic acid plasma membrane permease, responsible for uptake of low levels of nicotinic acid; expression of the gene increases in the	2.26	-
YGR014W	<i>MSB2</i>	Mucin family member involved in the Cdc42p- and MAP kinase-dependent filamentous growth signaling pathway; also functions as an osmosensor in parallel	2.24	-
YJL219W	<i>HXT9</i>	Putative hexose transporter that is nearly identical to Hxt11p, has similarity to major facilitator superfamily (MFS) transporters, expression of HXT9 is regulated	2.24	-
YOR071C	<i>NRT1</i>	High-affinity nicotinamide riboside transporter; also transports thiamine with low affinity; shares sequence similarity with Thi7p and Thi72p; proposed	2.21	-
YAR008W	<i>SEN34</i>	Subunit of the tRNA splicing endonuclease, which is composed of Sen2p, Sen15p, Sen34p, and Sen54p; Sen34p contains the active site for tRNA 3' splice site	2.21	2.59
YGR254W	<i>ENO1</i>	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the	2.20	2.67
YDR368W	<i>YPR1</i>	NADPH-dependent aldo-keto reductase, reduces multiple substrates including 2-methylbutyraldehyde and D,L-glyceraldehyde, expression is induced by	2.20	2.25
YGL038C	<i>OCH1</i>	Mannosyltransferase of the cis-Golgi apparatus, initiates the polymannose outer chain elongation of N-	2.19	-
YOL120C	<i>RPL18A</i>	Protein component of the large (60S) ribosomal subunit, identical to Rpl18Bp and has similarity to rat L18 ribosomal protein; intron of RPL18A pre-mRNA	2.19	-
YNL012W	<i>SPO1</i>	Meiosis-specific prospore protein; required for meiotic spindle pole body duplication and separation; required to produce bending force necessary for	2.19	-
YLR231C	<i>BNA5</i>	Kynureninase, required for the de novo biosynthesis of NAD from tryptophan via kynurenine; expression	2.19	2.41
YGR049W	<i>SCM4</i>	Potential regulatory effector of CDC4 function, suppresses a temperature-sensitive allele of CDC4, tripartite protein structure in which a charged region	2.19	-
YPR175W	<i>DPB2</i>	Second largest subunit of DNA polymerase II (DNA polymerase epsilon), required for normal yeast chromosomal replication; expression peaks at the	2.18	-

YHR043C	<i>DOG2</i>	2-deoxyglucose-6-phosphate phosphatase, member of a family of low molecular weight phosphatases, similar to Dog1p, induced by oxidative and osmotic	2.18	3.70
YGR037C	<i>ACB1</i>	Acyl-CoA-binding protein, transports newly synthesized acyl-CoA esters from fatty acid synthetase (Fas1p-Fas2p) to acyl-CoA-consuming	2.16	2.74
YER154W	<i>OXA1</i>	Mitochondrial inner membrane insertase, mediates the insertion of both mitochondrial- and nuclear-encoded proteins from the matrix into the inner	2.16	-
YJL115W	<i>ASF1</i>	Nucleosome assembly factor, involved in chromatin assembly and disassembly, anti-silencing protein that causes derepression of silent loci when	2.15	-
YDL164C	<i>CDC9</i>	DNA ligase found in the nucleus and mitochondria, an essential enzyme that joins Okazaki fragments during DNA replication; also acts in nucleotide excision	2.15	-
YPL158C	<i>AIM44</i>	Protein of unknown function; GFP-fusion protein localizes to the bud neck; transcription is regulated by	2.14	-
YGL226C-A	<i>OST5</i>	Zeta subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-	2.14	2.22
YBR243C	<i>ALG7</i>	UDP-N-acetyl-glucosamine-1-P transferase, transfers Glc-Nac-P from UDP-GlcNac to Dol-P in the ER in the first step of the dolichol pathway of protein	2.14	-
YMR198W	<i>CIK1</i>	Kinesin-associated protein required for both karyogamy and mitotic spindle organization, interacts stably and specifically with Kar3p and may function to	2.14	-
YDR309C	<i>GIC2</i>	Redundant rho-like GTPase Cdc42p effector; homolog of Gic1p; involved in initiation of budding and cellular polarization; interacts with Cdc42p via the Cdc42/Rac-	2.14	-
YLR187W	<i>SKG3</i>	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; potential	2.14	-
YKR010C	<i>TOF2</i>	Protein required for rDNA silencing and mitotic rDNA condensation; stimulates Cdc14p phosphatase activity and biphasic release to promote rDNA repeat	2.13	-
YDR009W	<i>GAL3</i>	Transcriptional regulator involved in activation of the GAL genes in response to galactose; forms a complex with Gal80p to relieve Gal80p inhibition of Gal4p;	2.12	-
YPL227C	<i>ALG5</i>	UDP-glucose:dolichyl-phosphate glucosyltransferase, involved in asparagine-linked glycosylation in the	2.11	-
YGR156W	<i>PTI1</i>	Essential protein that is a component of CPF (cleavage and polyadenylation factor); involved in 3' end formation of snoRNA and mRNA; interacts	2.11	-

YML078W	<i>CPR3</i>	Mitochondrial peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues;	2.11	-
YNL246W	<i>VPS75</i>	NAP family histone chaperone; binds to histones and Rtt109p, stimulating histone acetyltransferase activity; possesses nucleosome assembly activity in	2.10	-
YLR084C	<i>RAX2</i>	N-glycosylated protein involved in the maintenance of bud site selection during bipolar budding;	2.10	-
YLR209C	<i>PNP1</i>	Purine nucleoside phosphorylase, specifically metabolizes inosine and guanosine nucleosides;	2.09	-
YOL143C	<i>RIB4</i>	Lumazine synthase (6,7-dimethyl-8-ribityllumazine synthase, also known as DMRL synthase); catalyzes	2.07	3.24
YJL181W	<i>YJL181W</i>	Putative protein of unknown function; expression is cell-cycle regulated as shown by microarray analysis	2.07	-
YLR134W	<i>PDC5</i>	Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde, regulation is glucose- and	2.07	3.16
YGR292W	<i>MAL12</i>	Maltase (alpha-D-glucosidase), inducible protein involved in maltose catabolism; encoded in the MAL1 complex locus; hydrolyzes the disaccharides maltose,	2.07	-
YAL062W	<i>GDH3</i>	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization	2.06	2.11
YFL045C	<i>SEC53</i>	Phosphomannomutase, involved in synthesis of GDP-mannose and dolichol-phosphate-mannose; required	2.06	-
YDR261C	<i>EXG2</i>	Exo-1,3-beta-glucanase, involved in cell wall beta-glucan assembly; may be anchored to the plasma	2.04	-
YKL113C	<i>RAD27</i>	5' to 3' exonuclease, 5' flap endonuclease, required for Okazaki fragment processing and maturation as well as for long-patch base-excision repair; member	2.04	-
YLR293C	<i>GSP1</i>	Ran GTPase, GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport;	2.04	2.36
YNL072W	<i>RNH201</i>	Ribonuclease H2 catalytic subunit, removes RNA primers during Okazaki fragment synthesis and errant ribonucleotides misincorporated during DNA	2.03	2.49
YHR149C	<i>SKG6</i>	Integral membrane protein that localizes primarily to growing sites such as the bud tip or the cell	2.03	-
YPL208W	<i>RKM1</i>	SET-domain lysine-N-methyltransferase, catalyzes the formation of dimethyllysine residues on the large	2.03	-
YGL251C	<i>HFM1</i>	Meiosis specific DNA helicase involved in the conversion of double-stranded breaks to later recombination intermediates and in crossover	2.03	-

YDL145C	<i>COP1</i>	Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles in the early	2.02	2.15
YGR221C	<i>TOS2</i>	Protein involved in localization of Cdc24p to the site of bud growth; may act as a membrane anchor;	2.02	2.09
YML009C	<i>MRPL39</i>	Mitochondrial ribosomal protein of the large subunit	2.01	-
YJR048W	<i>CYC1</i>	Cytochrome c, isoform 1; electron carrier of the mitochondrial intermembrane space that transfers electrons from ubiquinone-cytochrome c	2.00	3.06
YLR272C	<i>YCS4</i>	Subunit of the condensin complex; required for establishment and maintenance of chromosome condensation, chromosome segregation, chromatin	2.00	-
YDR361C	<i>BCP1</i>	Essential protein involved in nuclear export of Mss4p, which is a lipid kinase that generates phosphatidylinositol 4,5-biphosphate and plays a role	-2.01	-
YML099C	<i>ARG81</i>	Zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type, involved in the	-2.01	-
YGR030C	<i>POP6</i>	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors	-2.01	-
YLL056C	<i>YLL056C</i>	Putative protein of unknown function, transcription is activated by paralogous transcription factors Yrm1p and Yrr1p and genes involved in pleiotropic drug	-2.02	-
YPR086W	<i>SUA7</i>	Transcription factor TFIIIB, a general transcription factor required for transcription initiation and start	-2.02	-2.18
YDL169C	<i>UGX2</i>	Protein of unknown function, transcript accumulates in response to any combination of stress conditions	-2.02	-
YBR293W	<i>VBA2</i>	Permease of basic amino acids in the vacuolar	-2.03	-2.58
YDR465C	<i>RMT2</i>	Arginine N5 methyltransferase; methylates ribosomal	-2.04	-
YNL314W	<i>DAL82</i>	Positive regulator of allophanate inducible genes; binds a dodecanucleotide sequence upstream of all genes that are induced by allophanate; contains an	-2.04	-
YDL025C	<i>YDL025C</i>	Putative protein kinase, potentially phosphorylated by Cdc28p; interacts with ribosome biogenesis	-2.04	-
YPR157W	<i>YPR157W</i>	Putative protein of unknown function; induced by treatment with 8-methoxypsoralen and UVA	-2.05	-
YPL199C	<i>YPL199C</i>	Putative protein of unknown function, predicted to	-2.06	-2.56
YDR244W	<i>PEX5</i>	Peroxisomal membrane signal receptor for the C-terminal tripeptide signal sequence (PTS1) of peroxisomal matrix proteins, required for	-2.07	-
YNL004W	<i>HRB1</i>	Poly(A+) RNA-binding protein, involved in the export of mRNAs from the nucleus to the cytoplasm; similar	-2.07	-2.15
YBR297W	<i>MAL33</i>	MAL-activator protein, part of complex locus MAL3; nonfunctional in genomic reference strain S288C	-2.07	-

YHR066W	<i>SSF1</i>	Constituent of 66S pre-ribosomal particles, required for ribosomal large subunit maturation; functionally	-2.07	-4.63
YMR265C	<i>YMR265C</i>	Putative protein of unknown function	-2.08	-2.35
YDL121C	<i>YDL121C</i>	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to	-2.08	-2.47
YPR112C	<i>MRD1</i>	Essential conserved protein that is part of the 90S preribosome; required for production of 18S rRNA	-2.08	-
YNL119W	<i>NCS2</i>	Protein required for thiolation of the uridine at the wobble position of Lys(UUU) and Glu(UUC) tRNAs; has a role in urmylation and in invasive and	-2.11	-
YOR213C	<i>SAS5</i>	Subunit of the SAS complex (Sas2p, Sas4p, Sas5p), which acetylates free histones and nucleosomes and	-2.11	-
YER015W	<i>FAA2</i>	Medium chain fatty acyl-CoA synthetase, activates imported fatty acids; accepts a wide range of fatty acid chain lengths with a preference for medium	-2.11	-2.09
YOR179C	<i>SYC1</i>	Subunit of the APT subcomplex of cleavage and polyadenylation factor, may have a role in 3' end	-2.11	-
YLR161W	<i>YLR161W</i>	Putative protein of unknown function; YLR156W, YLR159W, and YLR161W are three identical open	-2.11	-
YPR048W	<i>TAH18</i>	Conserved NADPH-dependent diflavin reductase, component of an early step in the cytosolic Fe-S protein assembly (CIA) machinery; transfers electrons	-2.11	-
YDR312W	<i>SSF2</i>	Protein required for ribosomal large subunit maturation, functionally redundant with Ssf1p;	-2.11	-
YHR166C	<i>CDC23</i>	Subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase	-2.13	-2.12
YOL136C	<i>PFK27</i>	6-phosphofructo-2-kinase, catalyzes synthesis of fructose-2,6-bisphosphate; inhibited by phosphoenolpyruvate and sn-glycerol 3-phosphate,	-2.14	-
YOR101W	<i>RAS1</i>	GTPase involved in G-protein signaling in the adenylate cyclase activating pathway, plays a role in cell proliferation; localized to the plasma membrane;	-2.14	-
YDL223C	<i>HBT1</i>	Substrate of the Hub1p ubiquitin-like protein that localizes to the shmoo tip (mating projection); mutants are defective for mating projection	-2.14	-
YNL113W	<i>RPC19</i>	RNA polymerase subunit AC19, common to RNA	-2.14	-
YKL099C	<i>UTP11</i>	Subunit of U3-containing Small Subunit (SSU) processome complex involved in production of 18S	-2.15	-
YGL153W	<i>PEX14</i>	Peroxisomal membrane peroxin that is a central component of the peroxisomal protein import machinery; interacts with both PTS1 (Pex5p) and	-2.15	-

YJL212C	<i>OPT1</i>	Proton-coupled oligopeptide transporter of the plasma membrane; also transports glutathione and	-2.16	-3.25
YLR407W	<i>YLR407W</i>	Putative protein of unknown function; null mutant displays elongated buds and a large fraction of	-2.18	-
YLR159W	<i>YLR159W</i>	Putative protein of unknown function; YLR156W, YLR159W, and YLR161W are three identical open	-2.18	-
YKR058W	<i>GLG1</i>	Self-glucosylating initiator of glycogen synthesis, also glucosylates n-dodecyl-beta-D-maltoside; similar to	-2.18	-
YJL112W	<i>MDV1</i>	Peripheral protein of the cytosolic face of the mitochondrial outer membrane, required for mitochondrial fission; interacts with Fis1p and with	-2.19	-
YCR100C	<i>YCR100C</i>	Putative protein of unknown function	-2.19	-2.34
YLL051C	<i>FRE6</i>	Putative ferric reductase with similarity to Fre2p;	-2.19	-
YGR202C	<i>PCT1</i>	Cholinephosphate cytidyltransferase, also known as CTP:phosphocholine cytidyltransferase, rate-determining enzyme of the CDP-choline pathway for	-2.20	-
YDR030C	<i>RAD28</i>	Protein involved in DNA repair, related to the human CSA protein that is involved in transcription-coupled	-2.20	-
YGR081C	<i>SLX9</i>	Protein required for pre-rRNA processing; associated with the 90S pre-ribosome and 43S small ribosomal subunit precursor; interacts with U3 snoRNA;	-2.20	-2.57
YIL113W	<i>SDP1</i>	Stress-inducible dual-specificity MAP kinase phosphatase, negatively regulates Slt2p MAP kinase by direct dephosphorylation, diffuse localization	-2.20	-
YPL202C	<i>AFT2</i>	Iron-regulated transcriptional activator; activates genes involved in intracellular iron use and required	-2.21	-
YER037W	<i>PHM8</i>	Protein of unknown function, expression is induced by low phosphate levels and by inactivation of	-2.22	-
YBL033C	<i>RIB1</i>	GTP cyclohydrolase II; catalyzes the first step of the	-2.22	-2.34
YGR129W	<i>SYF2</i>	Member of the NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of the spliceosome containing U2, U5, and U6	-2.22	-
YOR056C	<i>NOB1</i>	Essential nuclear protein involved in proteasome maturation and synthesis of 40S ribosomal subunits;	-2.23	-
YOR262W	<i>YOR262W</i>	Protein of unknown function required for establishment of sister chromatid cohesion; contains an ATP/GTP binding site motif; similar to YLR243W	-2.23	-
YPL212C	<i>PUS1</i>	tRNA:pseudouridine synthase, introduces pseudouridines at positions 26-28, 34-36, 65, and 67	-2.24	-
YMR185W	<i>YMR185W</i>	Putative protein of unknown function; conflicting evidence on whether null mutant is viable with	-2.25	-
YER184C	<i>YER184C</i>	Putative zinc cluster protein; deletion confers sensitivity to Calcufluor white, and prevents growth	-2.25	-3.03

YIR031C	<i>DAL7</i>	Malate synthase, role in allantoin degradation unknown; expression sensitive to nitrogen catabolite	-2.26	-
YJL072C	<i>PSF2</i>	Subunit of the GINS complex (Sld5p, Psf1p, Psf2p, Psf3p), which is localized to DNA replication origins	-2.26	-3.81
YKL106W	<i>AAT1</i>	Mitochondrial aspartate aminotransferase, catalyzes the conversion of oxaloacetate to aspartate in	-2.26	-
YBR141C	<i>YBR141C</i>	Putative S-adenosylmethionine-dependent methyltransferase; green fluorescent protein (GFP)-	-2.26	-
YNL221C	<i>POP1</i>	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors	-2.29	-2.07
YOR004W	<i>UTP23</i>	Essential nucleolar protein that is a component of the SSU (small subunit) processome involved in 40S ribosomal subunit biogenesis; has homology to PINc	-2.30	-2.09
YHR150W	<i>PEX28</i>	Peroxisomal integral membrane peroxin, involved in the regulation of peroxisomal size, number and distribution; genetic interactions suggest that Pex28p	-2.30	-
YKR024C	<i>DBP7</i>	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; essential	-2.31	-
YLR284C	<i>ECI1</i>	Peroxisomal delta3,delta2-enoyl-CoA isomerase, hexameric protein that converts 3-hexenoyl-CoA to trans-2-hexenoyl-CoA, essential for the beta-	-2.32	-
YDR421W	<i>ARO80</i>	Zinc finger transcriptional activator of the Zn2Cys6 family; activates transcription of aromatic amino acid	-2.32	-
YER137C	<i>YER137C</i>	Putative protein of unknown function	-2.35	-
YOR338W	<i>YOR338W</i>	Putative protein of unknown function; YOR338W transcription is regulated by Azf1p and its transcript is a specific target of the G protein effector Scp160p;	-2.35	-
YCR107W	<i>AAD3</i>	Putative aryl-alcohol dehydrogenase with similarity to <i>P. chrysosporium</i> aryl-alcohol dehydrogenase;	-2.35	-
YMR201C	<i>RAD14</i>	Protein that recognizes and binds damaged DNA during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 1 (NEF1); contains	-2.37	-
YBL054W	<i>TOD6</i>	PAC motif binding protein involved in rRNA and ribosome biogenesis; subunit of the RPD3L histone deacetylase complex; Myb-like HTH transcription	-2.37	-
YBR257W	<i>POP4</i>	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors	-2.38	-2.59
YBR105C	<i>VID24</i>	Peripheral membrane protein located at Vid (vacuole import and degradation) vesicles; regulates fructose-1,6-bisphosphatase (FBPase) targeting to the vacuole;	-2.39	-3.67
YKL072W	<i>STB6</i>	Protein that binds Sin3p in a two-hybrid assay	-2.39	-2.55

YGR121C	<i>MEP1</i>	Ammonium permease; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport only ammonium (NH <sub>4</sub> <sup>+</sup> ); expression is under the	-2.39	-2.92
YNL014W	<i>HEF3</i>	Translational elongation factor EF-3; paralog of YEF3 and member of the ABC superfamily; stimulates EF-1 alpha-dependent binding of aminoacyl-tRNA by the	-2.40	-
YPL230W	<i>USV1</i>	Putative transcription factor containing a C2H2 zinc finger; mutation affects transcriptional regulation of genes involved in growth on non-fermentable carbon	-2.40	-
YLR312C	<i>YLR312C</i>	Putative protein of unknown function	-2.40	-2.10
YLR023C	<i>IZH3</i>	Membrane protein involved in zinc ion homeostasis, member of the four-protein IZH family, expression induced by zinc deficiency; deletion reduces	-2.42	-
YMR009W	<i>ADI1</i>	Acireductone dioxygenase involved in the methionine salvage pathway; ortholog of human MTCBP-1; transcribed with YMR010W and regulated	-2.42	-
YMR145C	<i>NDE1</i>	Mitochondrial external NADH dehydrogenase, a type II NAD(P)H:quinone oxidoreductase that catalyzes the oxidation of cytosolic NADH; Nde1p and Nde2p	-2.43	-
YHR046C	<i>INM1</i>	Inositol monophosphatase, involved in biosynthesis of inositol and in phosphoinositide second messenger signaling; INM1 expression increases in the presence	-2.44	-2.11
YEL029C	<i>BUD16</i>	Putative pyridoxal kinase, a key enzyme involved in pyridoxal 5'-phosphate synthesis, the active form of vitamin B6; required for genome integrity; involved in	-2.44	-
YFL030W	<i>AGX1</i>	Alanine:glyoxylate aminotransferase (AGT), catalyzes the synthesis of glycine from glyoxylate, which is one of three pathways for glycine biosynthesis in yeast;	-2.49	-2.27
YKL023W	<i>YKL023W</i>	Putative protein of unknown function, predicted by computational methods to be involved in mRNA	-2.50	-3.03
YOR192C	<i>THI72</i>	Transporter of thiamine or related compound; shares	-2.52	-3.27
YLR387C	<i>REH1</i>	Cytoplasmic 60S subunit biogenesis factor, associates with pre-60S particles; similar to Rei1p and shares partially redundant function in cytoplasmic 60S	-2.52	-
YLL061W	<i>MMP1</i>	High-affinity S-methylmethionine permease, required for utilization of S-methylmethionine as a sulfur	-2.53	-
YBL069W	<i>AST1</i>	Peripheral membrane protein that interacts with the plasma membrane ATPase Pma1p and has a role in its targeting to the plasma membrane, possibly by	-2.54	-
YPL017C	<i>IRC15</i>	Microtubule associated protein; regulates microtubule dynamics; required for accurate meiotic chromosome segregation; null mutant displays large	-2.56	-2.27



YNL234W	<i>YNL234W</i>	Protein of unknown function with similarity to globins; has a functional heme-binding domain; mutant has aneuploidy tolerance; transcription	-2.57	-
YOL165C	<i>AAD15</i>	Putative aryl-alcohol dehydrogenase with similarity to <i>P. chrysosporium</i> aryl-alcohol dehydrogenase;	-2.60	-2.72
YGR159C	<i>NSR1</i>	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and	-2.61	-
YDR120C	<i>TRM1</i>	tRNA methyltransferase; two forms of the protein are made by alternative translation starts; localizes to both the nucleus and mitochondrion to produce the	-2.65	-
YKL143W	<i>LTV1</i>	Component of the GSE complex, which is required for proper sorting of amino acid permease Gap1p; required for ribosomal small subunit export from	-2.68	-
YLR460C	<i>YLR460C</i>	Member of the quinone oxidoreductase family, up-regulated in response to the fungicide mancozeb;	-2.71	-
YPR111W	<i>DBF20</i>	Ser/Thr kinase involved in late nuclear division, one of the mitotic exit network (MEN) proteins; necessary	-2.73	-3.36
YHR088W	<i>RPF1</i>	Nucleolar protein involved in the assembly and export of the large ribosomal subunit; constituent of 66S pre-ribosomal particles; contains a sigma(70)-like	-2.76	-2.13
YLL053C	<i>YLL053C</i>	Putative protein; in the Sigma 1278B strain background YLL053C is contiguous with AQY2 which	-2.79	-2.85
YDR342C	<i>HXT7</i>	High-affinity glucose transporter of the major facilitator superfamily, nearly identical to Hxt6p, expressed at high basal levels relative to other HXTs,	-2.80	-
YFL061W	<i>DDI2</i>	Protein of unknown function; expression is induced over 100-fold by DNA damage; induction decreased	-2.87	-5.18
YLR297W	<i>YLR297W</i>	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; YLR297W is not an essential gene;	-2.88	-
YLL052C	<i>AQY2</i>	Water channel that mediates the transport of water across cell membranes, only expressed in proliferating cells, controlled by osmotic signals, may	-2.89	-3.13
YOR363C	<i>PIP2</i>	Autoregulatory oleate-specific transcriptional activator of peroxisome proliferation, contains Zn(2)-Cys(6) cluster domain, forms heterodimer with	-2.90	-
YMR189W	<i>GCV2</i>	P subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels	-2.90	-5.24
YKR099W	<i>BAS1</i>	Myb-related transcription factor involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways; also	-2.91	-4.06
YIL019W	<i>FAF1</i>	Protein required for pre-rRNA processing and 40S	-2.94	-

YHR033W	<i>YHR033W</i>	Putative protein of unknown function; epitope-	-2.95	-
YGR239C	<i>PEX21</i>	Peroxin required for targeting of peroxisomal matrix proteins containing PTS2; interacts with Pex7p;	-3.02	-4.21
YDR343C	<i>HXT6</i>	High-affinity glucose transporter of the major facilitator superfamily, nearly identical to Hxt7p, expressed at high basal levels relative to other HXTs,	-3.02	-
YLR152C	<i>YLR152C</i>	Putative protein of unknown function; YLR152C is not	-3.03	-4.74
YIL003W	<i>CFD1</i>	Highly conserved, iron-sulfur cluster binding protein localized in the cytoplasm; forms a complex with	-3.03	-3.22
YDR533C	<i>HSP31</i>	Possible chaperone and cysteine protease with similarity to E. coli Hsp31; member of the DJ-1/ThiJ/Pfpl superfamily, which includes human DJ-1	-3.03	-2.24
YER176W	<i>ECM32</i>	DNA dependent ATPase/DNA helicase belonging to the Dna2p- and Nam7p-like family of helicases that is involved in modulating translation termination;	-3.05	-
YDL170W	<i>UGA3</i>	Transcriptional activator necessary for gamma-aminobutyrate (GABA)-dependent induction of GABA genes (such as UGA1, UGA2, UGA4); zinc-finger	-3.18	-5.69
YOL158C	<i>ENB1</i>	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated	-3.21	-3.60
YDR019C	<i>GCV1</i>	T subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels	-3.24	-4.41
YNL162W-A	<i>YNL162W-A</i>	Putative protein of unknown function; identified by	-3.25	-
YNL279W	<i>PRM1</i>	Pheromone-regulated multispinning membrane protein involved in membrane fusion during mating; predicted to have 5 transmembrane segments and a	-3.29	-
YKL155C	<i>RSM22</i>	Mitochondrial ribosomal protein of the small subunit; also predicted to be an S-adenosylmethionine-	-3.63	-
YER145C	<i>FTR1</i>	High affinity iron permease involved in the transport of iron across the plasma membrane; forms complex	-3.64	-5.70
YNL142W	<i>MEP2</i>	Ammonium permease involved in regulation of pseudohyphal growth; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport	-3.66	-
YMR107W	<i>SPG4</i>	Protein required for survival at high temperature during stationary phase; not required for growth on	-4.07	-
YOR306C	<i>MCH5</i>	Plasma membrane riboflavin transporter; facilitates the uptake of vitamin B2; required for FAD-dependent processes; sequence similarity to	-4.11	-
YML123C	<i>PHO84</i>	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to	-4.19	-

YNL112W	<i>DBP2</i>	Essential ATP-dependent RNA helicase of the DEAD-box protein family, involved in nonsense-mediated	-4.19	-
YNR069C	<i>BSC5</i>	Protein of unknown function, ORF exhibits genomic organization compatible with a translational	-4.47	-
YJL213W	<i>YJL213W</i>	Protein of unknown function that may interact with ribosomes; periodically expressed during the yeast metabolic cycle; phosphorylated in vitro by the	-4.50	-13.17
YPL092W	<i>SSU1</i>	Plasma membrane sulfite pump involved in sulfite metabolism and required for efficient sulfite efflux;	-4.79	-6.75
YGR230W	<i>BNS1</i>	Protein with some similarity to Spo12p; overexpression bypasses need for Spo12p, but not	-4.87	-3.61
YIR032C	<i>DAL3</i>	Ureidoglycolate hydrolase, converts ureidoglycolate to glyoxylate and urea in the third step of allantoin	-5.20	-4.19
YPR192W	<i>AQY1</i>	Spore-specific water channel that mediates the transport of water across cell membranes, developmentally controlled; may play a role in spore	-5.28	-
YHR048W	<i>YHK8</i>	Presumed antiporter of the DHA1 family of multidrug resistance transporters; contains 12 predicted transmembrane spans; expression of gene is up-	-5.55	-6.38
YLL055W	<i>YCT1</i>	High-affinity cysteine-specific transporter with similarity to the Dal5p family of transporters; green fluorescent protein (GFP)-fusion protein localizes to	-5.99	-
YIL165C	<i>YIL165C</i>	Putative protein of unknown function; mutant exhibits mitophagy defects; in closely related species and other <i>S. cerevisiae</i> strain backgrounds YIL165C	-6.03	-7.59
YIL164C	<i>NIT1</i>	Nitrilase, member of the nitrilase branch of the nitrilase superfamily; in closely related species and other <i>S. cerevisiae</i> strain backgrounds YIL164C and	-6.31	-7.94
YOR186W	<i>YOR186W</i>	Putative protein of unknown function; proper regulation of expression during heat stress is	-6.37	-6.03
YMR058W	<i>FET3</i>	Ferro-O <sub>2</sub> -oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to	-6.64	-11.97
YFR055W	<i>IRC7</i>	Putative cystathionine beta-lyase; involved in copper ion homeostasis and sulfur metabolism; null mutant displays increased levels of spontaneous Rad52p foci;	-6.82	-11.69
YDR242W	<i>AMD2</i>	Putative amidase	-7.12	-8.88
YBL043W	<i>ECM13</i>	Non-essential protein of unknown function; induced by treatment with 8-methoxypsoralen and UVA	-7.22	-9.22
YHL016C	<i>DUR3</i>	Plasma membrane transporter for both urea and polyamines, expression is highly sensitive to nitrogen catabolite repression and induced by allophanate, the	-7.66	-8.79

YPL095C	<i>EEB1</i>	Acyl-coenzymeA:ethanol O-acyltransferase responsible for the major part of medium-chain fatty acid ethyl ester biosynthesis during fermentation;	-8.32	-3.60
YCL064C	<i>CHA1</i>	Catabolic L-serine (L-threonine) deaminase, catalyzes the degradation of both L-serine and L-threonine; required to use serine or threonine as the sole	-9.36	-12.61
YHR096C	<i>HXT5</i>	Hexose transporter with moderate affinity for glucose, induced in the presence of non-fermentable carbon sources, induced by a decrease in growth	-9.51	-8.23
YHR137W	<i>ARO9</i>	Aromatic aminotransferase II, catalyzes the first step of tryptophan, phenylalanine, and tyrosine	-16.37	-10.86
YKR034W	<i>DAL80</i>	Negative regulator of genes in multiple nitrogen degradation pathways; expression is regulated by nitrogen levels and by Gln3p; member of the GATA-	-22.06	-
YJL153C	<i>INO1</i>	Inositol-3-phosphate synthase, involved in synthesis of inositol phosphates and inositol-containing phospholipids; transcription is coregulated with other	-	32.84
YER003C	<i>PMI40</i>	Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and mannose-6-P;	-	8.04
YGR109C	<i>CLB6</i>	B-type cyclin involved in DNA replication during S phase; activates Cdc28p to promote initiation of DNA synthesis; functions in formation of mitotic spindles	-	6.29
YKL165C	<i>MCD4</i>	Protein involved in glycosylphosphatidylinositol (GPI) anchor synthesis; multimembrane-spanning protein that localizes to the endoplasmic reticulum; highly	-	6.19
YGR256W	<i>GND2</i>	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating	-	6.06
YOR387C	<i>YOR387C</i>	Putative protein of unknown function; regulated by the metal-responsive Aft1p transcription factor;	-	5.85
YBR088C	<i>POL30</i>	Proliferating cell nuclear antigen (PCNA), functions as the sliding clamp for DNA polymerase delta; may function as a docking site for other proteins required	-	5.26
YML058W-A	<i>HUG1</i>	Protein involved in the Mec1p-mediated checkpoint pathway that responds to DNA damage or replication	-	5.03
YGR213C	<i>RTA1</i>	Protein involved in 7-aminocholesterol resistance; has seven potential membrane-spanning regions; expression is induced under both low-heme and low-	-	4.73
YNR016C	<i>ACC1</i>	Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form	-	4.40
YLR099C	<i>ICT1</i>	Lysophosphatidic acid acyltransferase, responsible for enhanced phospholipid synthesis during organic solvent stress; null displays increased sensitivity to	-	4.32

YGL253W	<i>HXK2</i>	Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; predominant hexokinase during growth on glucose;	-	4.18
YGR234W	<i>YHB1</i>	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in	-	3.97
YAL023C	<i>PMT2</i>	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein Ser/Thr residues; involved in ER quality	-	3.84
YML070W	<i>DAK1</i>	Dihydroxyacetone kinase, required for detoxification of dihydroxyacetone (DHA); involved in stress	-	3.75
YOR388C	<i>FDH1</i>	NAD(+)-dependent formate dehydrogenase, may	-	3.45
YML028W	<i>TSA1</i>	Thioredoxin peroxidase, acts as both a ribosome-associated and free cytoplasmic antioxidant; self-associates to form a high-molecular weight	-	3.43
YKL182W	<i>FAS1</i>	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl	-	3.41
YJL167W	<i>ERG20</i>	Farnesyl pyrophosphate synthetase, has both dimethylallyltranstransferase and geranyltranstransferase activities; catalyzes the	-	3.41
YOL143C	<i>RIB4</i>	Lumazine synthase (6,7-dimethyl-8-ribityllumazine synthase, also known as DMRL synthase); catalyzes	-	3.24
YHR174W	<i>ENO2</i>	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the	-	3.20
YLR134W	<i>PDC5</i>	Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde, regulation is glucose- and	-	3.16
YOR321W	<i>PMT3</i>	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts in a complex	-	3.15
YHR183W	<i>GND1</i>	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required	-	3.13
YLR354C	<i>TAL1</i>	Transaldolase, enzyme in the non-oxidative pentose phosphate pathway; converts sedoheptulose 7-phosphate and glyceraldehyde 3-phosphate to	-	3.10
YOR198C	<i>BFR1</i>	Component of mRNP complexes associated with polyribosomes; implicated in secretion and nuclear	-	3.03
YOR393W	<i>ERR1</i>	Protein of unknown function, has similarity to	-	3.02
YFL011W	<i>HXT10</i>	Putative hexose transporter, expressed at low levels	-	3.00
YPL281C	<i>ERR2</i>	Protein of unknown function, has similarity to	-	3.00
YMR323W	<i>ERR3</i>	Protein of unknown function, has similarity to	-	2.98

YOR288C	<i>MPD1</i>	Member of the protein disulfide isomerase (PDI) family; interacts with and inhibits the chaperone activity of Cne1p; MPD1 overexpression in a pdi1 null	-	2.96
YLR259C	<i>HSP60</i>	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and	-	2.81
YMR214W	<i>SCJ1</i>	One of several homologs of bacterial chaperone DnaJ, located in the ER lumen where it cooperates	-	2.76
YPL240C	<i>HSP82</i>	Hsp90 chaperone required for pheromone signaling and negative regulation of Hsf1p; docks with Tom70p for mitochondrial preprotein delivery; promotes	-	2.76
YOR176W	<i>HEM15</i>	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of ferrous iron into	-	2.75
YNR019W	<i>ARE2</i>	Acyl-CoA:sterol acyltransferase, isozyme of Are1p; endoplasmic reticulum enzyme that contributes the	-	2.74
YGR037C	<i>ACB1</i>	Acyl-CoA-binding protein, transports newly synthesized acyl-CoA esters from fatty acid synthetase (Fas1p-Fas2p) to acyl-CoA-consuming	-	2.74
YJR030C	<i>YJR030C</i>	Putative protein of unknown function; expression repressed in carbon limited vs carbon replete	-	2.72
YLR304C	<i>ACO1</i>	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance;	-	2.72
YOL031C	<i>SIL1</i>	Nucleotide exchange factor for the endoplasmic reticulum (ER) luminal Hsp70 chaperone Kar2p, required for protein translocation into the ER;	-	2.69
YKL121W	<i>DGR2</i>	Protein of unknown function; null mutant is resistant to 2-deoxy-D-glucose and displays abnormally	-	2.68
YBR011C	<i>IPP1</i>	Cytoplasmic inorganic pyrophosphatase (PPase), homodimer that catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and	-	2.67
YBR029C	<i>CDS1</i>	Phosphatidate cytidyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate +	-	2.62
YPL058C	<i>PDR12</i>	Plasma membrane ATP-binding cassette (ABC) transporter, weak-acid-inducible multidrug transporter required for weak organic acid resistance;	-	2.60
YNL102W	<i>POL1</i>	Catalytic subunit of the DNA polymerase I alpha-primase complex, required for the initiation of DNA	-	2.60
YLR234W	<i>TOP3</i>	DNA Topoisomerase III, conserved protein that functions in a complex with Sgs1p and Rmi1p to relax single-stranded negatively-supercoiled DNA	-	2.56

YHR104W	<i>GRE3</i>	Aldose reductase involved in methylglyoxal, d-xylose, arabinose, and galactose metabolism; stress induced (osmotic, ionic, oxidative, heat shock, starvation and	-	2.53
YGL256W	<i>ADH4</i>	Alcohol dehydrogenase isoenzyme type IV, dimeric enzyme demonstrated to be zinc-dependent despite sequence similarity to iron-activated alcohol	-	2.51
YOR073W	<i>SGO1</i>	Component of the spindle checkpoint, involved in sensing lack of tension on mitotic chromosomes; protects centromeric Rec8p at meiosis I; required for	-	2.51
YDR148C	<i>KGD2</i>	Dihydrolipoyl transsuccinylase, component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes the oxidative	-	2.49
YKL103C	<i>LAP4</i>	Vacuolar aminopeptidase yscI; zinc metalloproteinase that belongs to the peptidase family M18; often used as a marker protein in studies of autophagy and	-	2.48
YOR247W	<i>SRL1</i>	Mannoprotein that exhibits a tight association with the cell wall, required for cell wall stability in the absence of GPI-anchored mannoproteins; has a high	-	2.47
YOR385W	<i>YOR385W</i>	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to	-	2.43
YOR254C	<i>SEC63</i>	Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-	-	2.42
YDR050C	<i>TPI1</i>	Triose phosphate isomerase, abundant glycolytic enzyme; mRNA half-life is regulated by iron availability; transcription is controlled by activators	-	2.41
YCL050C	<i>APA1</i>	Diadenosine 5',5''-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase), involved in	-	2.40
YDL103C	<i>QRI1</i>	UDP-N-acetylglucosamine pyrophosphorylase, catalyzes the formation of UDP-N-acetylglucosamine (UDP-GlcNAc), which is important in cell wall	-	2.38
YDL022W	<i>GPD1</i>	NAD-dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression	-	2.38
YBL032W	<i>HEK2</i>	RNA binding protein involved in the asymmetric localization of ASH1 mRNA; represses translation of ASH1 mRNA, an effect reversed by Yck1p-dependent	-	2.38
YER103W	<i>SSA4</i>	Heat shock protein that is highly induced upon stress; plays a role in SRP-dependent cotranslational protein-membrane targeting and translocation; member of	-	2.38
YBR072W	<i>HSP26</i>	Small heat shock protein (sHSP) with chaperone activity; forms hollow, sphere-shaped oligomers that suppress unfolded proteins aggregation; oligomer	-	2.37

YJR143C	<i>PMT4</i>	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; appears to form	-	2.37
YGR285C	<i>ZUO1</i>	Ribosome-associated chaperone, functions in ribosome biogenesis and, in partnership with Ssz1p and Ssb1/2, as a chaperone for nascent polypeptide	-	2.36
YGL137W	<i>SEC27</i>	Essential beta <sup>1</sup> -coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective	-	2.34
YBL002W	<i>HTB2</i>	Histone H2B, core histone protein required for chromatin assembly and chromosome function; nearly identical to HTB1; Rad6p-Bre1p-Lge1p	-	2.34
YLR131C	<i>ACE2</i>	Transcription factor that activates expression of early G1-specific genes, localizes to daughter cell nuclei after cytokinesis and delays G1 progression in	-	2.33
YGR240C	<i>PFK1</i>	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by	-	2.33
YKL152C	<i>GPM1</i>	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-	-	2.29
YLR132C	<i>YLR132C</i>	Essential protein of unknown function; fluorescent protein (GFP or YFP)-tagged protein localizes to	-	2.28
YNL082W	<i>PMS1</i>	ATP-binding protein required for mismatch repair in mitosis and meiosis; functions as a heterodimer with Mlh1p, binds double- and single-stranded DNA via its	-	2.28
YIL041W	<i>GVP36</i>	BAR domain-containing protein that localizes to both early and late Golgi vesicles; required for adaptation to varying nutrient concentrations, fluid-phase	-	2.27
YHR064C	<i>SSZ1</i>	Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome-associated complex that binds the ribosome via the Zuo1p subunit; also	-	2.26
YDR508C	<i>GNP1</i>	High-affinity glutamine permease, also transports Leu, Ser, Thr, Cys, Met and Asn; expression is fully dependent on Grr1p and modulated by the Ssy1p-	-	2.26
YFL059W	<i>SNZ3</i>	Member of a stationary phase-induced gene family; transcription of SNZ2 is induced prior to diauxic shift, and also in the absence of thiamin in a Thi2p-	-	2.25
YHL018W	<i>YHL018W</i>	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to	-	2.24
YOR083W	<i>WHI5</i>	Repressor of G1 transcription that binds to SCB binding factor (SBF) at SCB target promoters in early G1; phosphorylation of Whi5p by the CDK,	-	2.20



YLR133W	<i>CKI1</i>	Choline kinase, catalyzing the first step in phosphatidylcholine synthesis via the CDP-choline (Kennedy pathway); exhibits some ethanolamine	-	2.19
YNL071W	<i>LAT1</i>	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes	-	2.19
YDL004W	<i>ATP16</i>	Delta subunit of the central stalk of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily	-	2.18
YPR183W	<i>DPM1</i>	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	-	2.17
YFL053W	<i>DAK2</i>	Dihydroxyacetone kinase, required for detoxification of dihydroxyacetone (DHA); involved in stress	-	2.16
YOR388C	<i>FDH1</i>	NAD(+)-dependent formate dehydrogenase, may	-	2.16
YDL192W	<i>ARF1</i>	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated vesicle	-	2.14
YGL175C	<i>SAE2</i>	Endonuclease that processes hairpin DNA structures with the MRX complex; involved in meiotic and mitotic double-strand break repair; phosphorylated in	-	2.14
YBR053C	<i>YBR053C</i>	Putative protein of unknown function; induced by cell	-	2.13
YDL140C	<i>RPO21</i>	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association	-	2.12
YDL219W	<i>DTD1</i>	D-Tyr-tRNA(Tyr) deacylase, functions in protein translation, may affect nonsense suppression via	-	2.12
YDR226W	<i>ADK1</i>	Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the mitochondria;	-	2.11
YHR068W	<i>DYS1</i>	Deoxyhypusine synthase, catalyzes formation of deoxyhypusine, the first step in hypusine biosynthesis; triggers posttranslational hypusination	-	2.10
YMR205C	<i>PFK2</i>	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by	-	2.09
YDR432W	<i>NPL3</i>	RNA-binding protein that promotes elongation, regulates termination, and carries poly(A) mRNA from nucleus to cytoplasm; required for pre-mRNA	-	2.08
YNL233W	<i>BNI4</i>	Targeting subunit for Glc7p protein phosphatase, localized to the bud neck, required for localization of chitin synthase III to the bud neck via interaction with	-	2.07
YMR027W	<i>YMR027W</i>	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to	-	2.06
YDR111C	<i>ALT2</i>	Putative alanine transaminase (glutamic pyruvic	-	2.06

YFL038C	<i>YPT1</i>	Rab family GTPase, involved in the ER-to-Golgi step of the secretory pathway; complex formation with the Rab escort protein Mrs6p is required for prenylation	-	2.05
YNR035C	<i>ARC35</i>	Subunit of the ARP2/3 complex, which is required for the motility and integrity of cortical actin patches;	-	2.04
YGL105W	<i>ARC1</i>	Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring	-	2.04
YNL010W	<i>YNL010W</i>	Putative protein of unknown function with similarity to phosphoserine phosphatases; green fluorescent protein (GFP)-fusion protein localizes to the	-	2.04
YPL032C	<i>SVL3</i>	Protein of unknown function, mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to	-	2.02
YDR510W	<i>SMT3</i>	Ubiquitin-like protein of the SUMO family, conjugated to lysine residues of target proteins; regulates chromatid cohesion, chromosome segregation, APC-	-	2.01
YDL185W	<i>TFP1</i>	Subunit A of the eight-subunit V1 peripheral membrane domain of the vacuolar H <sup>+</sup> -ATPase; protein precursor undergoes self-catalyzed splicing to	-	2.01
YHL031C	<i>GOS1</i>	v-SNARE protein involved in Golgi transport, homolog	-	2.01
YML054C	<i>CYB2</i>	Cytochrome b2 (L-lactate cytochrome-c oxidoreductase), component of the mitochondrial intermembrane space, required for lactate utilization;	-	2.00
YGR279C	<i>SCW4</i>	Cell wall protein with similarity to glucanases; scw4 scw10 double mutants exhibit defects in mating	-	2.00
YOL164W	<i>BDS1</i>	Bacterially-derived sulfatase required for use of alkyl-	-	-2.00
YGR074W	<i>SMD1</i>	Core Sm protein Sm D1; part of heteroheptameric complex (with Smb1p, Smd2p, Smd3p, Sme1p, Smx3p, and Smx2p) that is part of the spliceosomal	-	-2.00
YMR126C	<i>DLT1</i>	Protein of unknown function, mutant sensitive to 6-azauracil (6AU) and mycophenolic acid (MPA)	-	-2.00
YLR266C	<i>PDR8</i>	Transcription factor; targets include ATP-binding cassette (ABC) transporters, major facilitator superfamily transporters, and other genes involved in	-	-2.01
YKR009C	<i>FOX2</i>	Multifunctional enzyme of the peroxisomal fatty acid beta-oxidation pathway; has 3-hydroxyacyl-CoA	-	-2.01
YIL046W	<i>MET30</i>	F-box protein containing five copies of the WD40 motif, controls cell cycle function, sulfur metabolism, and methionine biosynthesis as part of the ubiquitin	-	-2.03
YGR166W	<i>KRE11</i>	Subunit of TRAPP II, a multimeric guanine nucleotide-exchange factor for Ypt1p; involved in intra-Golgi traffic and the retrograde pathway from the	-	-2.04

YBR212W	<i>NGR1</i>	RNA binding protein that negatively regulates growth rate; interacts with the 3' UTR of the mitochondrial porin (POR1) mRNA and enhances its degradation;	-	-2.05
YDL231C	<i>BRE4</i>	Zinc finger protein containing five transmembrane domains; null mutant exhibits strongly fragmented vacuoles and sensitivity to brefeldin A, a drug which is	-	-2.05
YFR046C	<i>CNN1</i>	Kinetochores protein of unknown function; associated with the essential kinetochores proteins Nnf1p and	-	-2.06
YMR132C	<i>JLP2</i>	Protein of unknown function, contains sequence that closely resembles a J domain (typified by the E. coli	-	-2.06
YNL221C	<i>POP1</i>	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors	-	-2.07
YDL215C	<i>GDH2</i>	NAD(+)-dependent glutamate dehydrogenase, degrades glutamate to ammonia and alpha-ketoglutarate; expression sensitive to nitrogen	-	-2.08
YER015W	<i>FAA2</i>	Medium chain fatty acyl-CoA synthetase, activates imported fatty acids; accepts a wide range of fatty acid chain lengths with a preference for medium	-	-2.09
YOR004W	<i>UTP23</i>	Essential nucleolar protein that is a component of the SSU (small subunit) processome involved in 40S ribosomal subunit biogenesis; has homology to PINc	-	-2.09
YFR025C	<i>HIS2</i>	Histidinolphosphatase, catalyzes the eighth step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts;	-	-2.10
YLL048C	<i>YBT1</i>	Transporter of the ATP-binding cassette (ABC) family involved in bile acid transport; similar to mammalian	-	-2.10
YER092W	<i>IES5</i>	Protein that associates with the INO80 chromatin remodeling complex under low-salt conditions	-	-2.11
YNR074C	<i>AIF1</i>	Mitochondrial cell death effector that translocates to the nucleus in response to apoptotic stimuli, homolog	-	-2.11
YJR050W	<i>ISY1</i>	Member of NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of spliceosome containing U2, U5, and U6 snRNAs,	-	-2.11
YIR013C	<i>GAT4</i>	Protein containing GATA family zinc finger motifs	-	-2.12
YLR193C	<i>UPS1</i>	Mitochondrial intermembrane space protein that regulates mitochondrial cardiolipin levels, null has defects in Mgm1p processing, integrity of	-	-2.12
YGR280C	<i>PXR1</i>	Essential protein involved in rRNA and snoRNA maturation; competes with TLC1 RNA for binding to Est2p, suggesting a role in negative regulation of	-	-2.15
YPR200C	<i>ARR2</i>	Arsenate reductase required for arsenate resistance; converts arsenate to arsenite which can then be	-	-2.16
YDR249C	<i>YDR249C</i>	Putative protein of unknown function	-	-2.16

YOL044W	<i>PEX15</i>	Phosphorylated tail-anchored type II integral peroxisomal membrane protein required for peroxisome biogenesis, cells lacking Pex15p	-	-2.19
YBL049W	<i>MOH1</i>	Protein of unknown function, has homology to kinase Snf7p; not required for growth on nonfermentable	-	-2.20
YOR184W	<i>SER1</i>	3-phosphoserine aminotransferase, catalyzes the formation of phosphoserine from 3-phosphohydroxypyruvate, required for serine and	-	-2.20
YOL047C	<i>YOL047C</i>	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the	-	-2.21
YER040W	<i>GLN3</i>	Transcriptional activator of genes regulated by nitrogen catabolite repression (NCR), localization and	-	-2.21
YPR168W	<i>NUT2</i>	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; required for	-	-2.21
YLR130C	<i>ZRT2</i>	Low-affinity zinc transporter of the plasma membrane; transcription is induced under low-zinc	-	-2.21
YKL220C	<i>FRE2</i>	Ferric reductase and cupric reductase, reduces siderophore-bound iron and oxidized copper prior to uptake by transporters; expression induced by low	-	-2.22
YLR004C	<i>THI73</i>	Putative plasma membrane permease proposed to be involved in carboxylic acid uptake and repressed by thiamine; substrate of Dbf2p/Mob1p kinase;	-	-2.22
YOL084W	<i>PHM7</i>	Protein of unknown function, expression is regulated by phosphate levels; green fluorescent protein (GFP)-	-	-2.23
YNL046W	<i>YNL046W</i>	Putative protein of unknown function; expression depends on Swi5p; GFP-fusion protein localizes to the endoplasmic reticulum; deletion confers sensitivity to	-	-2.25
YDR257C	<i>RKM4</i>	Ribosomal lysine methyltransferase specific for monomethylation of Rpl42ap and Rpl42bp (lysine	-	-2.29
YNL116W	<i>DMA2</i>	Protein involved in ubiquitination; plays a role in regulating spindle position and orientation; functionally redundant with Dma1p; orthologous to	-	-2.30
YEL065W	<i>SIT1</i>	Ferrioxamine B transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; transcription is induced	-	-2.35
YBR043C	<i>QDR3</i>	Multidrug transporter of the major facilitator superfamily, required for resistance to quinidine,	-	-2.37
YNL129W	<i>NRK1</i>	Nicotinamide riboside kinase, catalyzes the phosphorylation of nicotinamide riboside and	-	-2.37
YBL029W	<i>YBL029W</i>	Non-essential protein of unknown function	-	-2.38
YPR128C	<i>ANT1</i>	Peroxisomal adenine nucleotide transporter; involved in beta-oxidation of medium-chain fatty acid;	-	-2.41

YBR166C	<i>TYR1</i>	Prephenate dehydrogenase involved in tyrosine biosynthesis, expression is dependent on	-	-2.41
YLL027W	<i>ISA1</i>	Mitochondrial matrix protein involved in biogenesis of the iron-sulfur (Fe/S) cluster of Fe/S proteins, isa1 deletion causes loss of mitochondrial DNA and	-	-2.43
YGL146C	<i>RRT6</i>	Putative protein of unknown function; non-essential gene identified in a screen for mutants with increased levels of rDNA transcription; contains two putative	-	-2.45
YIL117C	<i>PRM5</i>	Pheromone-regulated protein, predicted to have 1 transmembrane segment; induced during cell	-	-2.46
YBL103C	<i>RTG3</i>	Basic helix-loop-helix-leucine zipper (bHLH/Zip) transcription factor that forms a complex with	-	-2.46
YDR090C	<i>YDR090C</i>	Putative protein of unknown function	-	-2.46
YMR187C	<i>YMR187C</i>	Putative protein of unknown function; YMR187C is	-	-2.46
YGR029W	<i>ERV1</i>	Flavin-linked sulfhydryl oxidase of the mitochondrial intermembrane space (IMS), oxidizes Mia40p as part of a disulfide relay system that promotes IMS	-	-2.47
YDL121C	<i>YDL121C</i>	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to	-	-2.47
YCR089W	<i>FIG2</i>	Cell wall adhesin, expressed specifically during mating; may be involved in maintenance of cell wall	-	-2.48
YER039C	<i>HVG1</i>	Protein of unknown function, has homology to Vrg4p	-	-2.52
YNL125C	<i>ESBP6</i>	Protein with similarity to monocarboxylate permeases, appears not to be involved in transport of	-	-2.53
YAL044C	<i>GCV3</i>	H subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; also required for all protein	-	-2.53
YBL095W	<i>YBL095W</i>	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified	-	-2.54
YHR160C	<i>PEX18</i>	Peroxin required for targeting of peroxisomal matrix proteins containing PTS2; interacts with Pex7p;	-	-2.54
YBR115C	<i>LYS2</i>	Alpha amino adipate reductase, catalyzes the reduction of alpha-amino adipate to alpha-amino adipate 6-semialdehyde, which is the fifth step	-	-2.55
YGL205W	<i>POX1</i>	Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta-oxidation pathway; localized to the	-	-2.56
YGL114W	<i>YGL114W</i>	Putative protein of unknown function; predicted member of the oligopeptide transporter (OPT) family	-	-2.62
YFL021W	<i>GAT1</i>	Transcriptional activator of genes involved in nitrogen catabolite repression; contains a GATA-1-type zinc finger DNA-binding motif; activity and localization	-	-2.64
YCR023C	<i>YCR023C</i>	Vacuolar membrane protein of unknown function; member of the multidrug resistance family; YCR023C	-	-2.64

YML097C	<i>VPS9</i>	A guanine nucleotide exchange factor involved in vesicle-mediated vacuolar protein transport; specifically stimulates the intrinsic guanine nucleotide	-	-2.66
YOR221C	<i>MCT1</i>	Predicted malonyl-CoA:ACP transferase, putative component of a type-II mitochondrial fatty acid	-	-2.68
YKL033W-A	<i>YKL033W-A</i>	Putative protein of unknown function; similar to	-	-2.75
YLL057C	<i>JLP1</i>	Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase, involved in sulfonate catabolism for use as a sulfur source; contains sequence that resembles	-	-2.76
YMR019W	<i>STB4</i>	Protein that binds Sin3p in a two-hybrid assay; contains a Zn(II)2Cys6 zinc finger domain characteristic of DNA-binding proteins;	-	-2.78
YBR248C	<i>HIS7</i>	Imidazole glycerol phosphate synthase (glutamine amidotransferase:cyclase), catalyzes the fifth and sixth steps of histidine biosynthesis and also produces	-	-2.82
YNR065C	<i>YNR065C</i>	Protein of unknown function; protein-protein interactions suggest a possible role in actin patch	-	-2.84
YOR339C	<i>UBC11</i>	Ubiquitin-conjugating enzyme most similar in sequence to <i>Xenopus</i> ubiquitin-conjugating enzyme E2-C, but not a true functional homolog of this E2;	-	-2.86
YOR008C-A	<i>YOR008C-A</i>	Putative protein of unknown function, includes a potential transmembrane domain; deletion results in	-	-2.87
YDR384C	<i>ATO3</i>	Plasma membrane protein, regulation pattern suggests a possible role in export of ammonia from the cell; phosphorylated in mitochondria; member of	-	-2.89
YBR249C	<i>ARO4</i>	3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase, catalyzes the first step in aromatic amino acid biosynthesis and is feedback-inhibited by	-	-2.91
YGR121C	<i>MEP1</i>	Ammonium permease; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport only ammonium (NH <sub>4</sub> <sup>+</sup> ); expression is under the	-	-2.92
YPL052W	<i>OAZ1</i>	Regulator of ornithine decarboxylase (Spe1p), antizyme that binds to Spe1p to regulate ubiquitin-independent degradation; ribosomal frameshifting	-	-2.95
YBL071W-A	<i>KT111</i>	Zn-ribbon protein that co-purifies with Dph1 and Dph2 in a complex required for synthesis of diphthamide on translation factor eEF2 and with	-	-2.96
YER055C	<i>HIS1</i>	ATP phosphoribosyltransferase, a hexameric enzyme, catalyzes the first step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity	-	-2.97
YIR034C	<i>LYS1</i>	Saccharopine dehydrogenase (NAD <sup>+</sup> , L-lysine-forming), catalyzes the conversion of saccharopine to L-lysine, which is the final step in the lysine	-	-2.98

YER184C	<i>YER184C</i>	Putative zinc cluster protein; deletion confers sensitivity to Calcufluor white, and prevents growth	-	-3.03
YDR487C	<i>RIB3</i>	3,4-dihydroxy-2-butanone-4-phosphate synthase (DHBP synthase), required for riboflavin biosynthesis from ribulose-5-phosphate, also has an unrelated	-	-3.03
YDR076W	<i>RAD55</i>	Protein that stimulates strand exchange by stabilizing the binding of Rad51p to single-stranded DNA; involved in the recombinational repair of double-	-	-3.05
YNL311C	<i>YNL311C</i>	F-box protein of unknown function predicted to be part of an SCF ubiquitin protease complex; involved in regulating protein levels of sulfur metabolism	-	-3.11
YPL135W	<i>ISU1</i>	Conserved protein of the mitochondrial matrix, performs a scaffolding function during assembly of iron-sulfur clusters, interacts physically and	-	-3.13
YGR197C	<i>SNG1</i>	Protein involved in resistance to nitrosoguanidine (MNNG) and 6-azauracil (6-AU); expression is	-	-3.13
YLR090W	<i>XDJ1</i>	Putative chaperone, homolog of E. coli DnaJ, closely related to Ydj1p; the authentic, non-tagged protein is	-	-3.14
YGL154C	<i>LYS5</i>	Phosphopantetheinyl transferase involved in lysine biosynthesis; converts inactive apo-form of Lys2p (alpha-aminoadipate reductase) into catalytically	-	-3.23
YLR348C	<i>DIC1</i>	Mitochondrial dicarboxylate carrier, integral membrane protein, catalyzes a dicarboxylate-phosphate exchange across the inner mitochondrial	-	-3.25
YOR192C	<i>THI72</i>	Transporter of thiamine or related compound; shares	-	-3.27
YJR010W	<i>MET3</i>	ATP sulfurylase, catalyzes the primary step of intracellular sulfate activation, essential for	-	-3.33
YGR154C	<i>GTO1</i>	Omega-class glutathione transferase; induced under oxidative stress; putative peroxisomal localization	-	-3.34
YHR208W	<i>BAT1</i>	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly	-	-3.37
YER039C-A	<i>YER039C-A</i>	Putative protein of unknown function; YER039C-A is	-	-3.37
YGL186C	<i>TPN1</i>	Plasma membrane pyridoxine (vitamin B6) transporter; member of the purine-cytosine permease subfamily within the major facilitator	-	-3.38
YHR122W	<i>YHR122W</i>	Protein of unknown function required for establishment of sister chromatid cohesion; synthetically lethal with RFC5, an RF-C subunit that	-	-3.41
YKL211C	<i>TRP3</i>	Bifunctional enzyme exhibiting both indole-3-glycerol-phosphate synthase and anthranilate synthase activities, forms multifunctional hetero-oligomeric	-	-3.43
YPR078C	<i>YPR078C</i>	Putative protein of unknown function; possible role in DNA metabolism and/or in genome stability;	-	-3.45

YDL054C	<i>MCH1</i>	Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma	-	-3.51
YLR042C	<i>YLR042C</i>	Protein of unknown function; localizes to the	-	-3.58
YOR161C	<i>PNS1</i>	Protein of unknown function; has similarity to Torpedo californica tCTL1p, which is postulated to be	-	-3.59
YJR155W	<i>AAD10</i>	Putative aryl-alcohol dehydrogenase with similarity to <i>P. chrysosporium</i> aryl-alcohol dehydrogenase;	-	-3.59
YPL188W	<i>POS5</i>	Mitochondrial NADH kinase, phosphorylates NADH; also phosphorylates NAD(+) with lower specificity;	-	-3.60
YGL059W	<i>PKP2</i>	Mitochondrial protein kinase that negatively regulates activity of the pyruvate dehydrogenase complex by phosphorylating the ser-133 residue of	-	-3.63
YBR105C	<i>VID24</i>	Peripheral membrane protein located at Vid (vacuole import and degradation) vesicles; regulates fructose-1,6-bisphosphatase (FBPase) targeting to the vacuole;	-	-3.67
YKR071C	<i>DRE2</i>	Conserved component of an early step in the cytosolic Fe-S protein assembly (CIA) machinery; contains an Fe-S cluster that receives electrons from	-	-3.70
YBR104W	<i>YMC2</i>	Mitochondrial protein, putative inner membrane transporter with a role in oleate metabolism and glutamate biosynthesis; member of the	-	-3.74
YJL072C	<i>PSF2</i>	Subunit of the GINS complex (Sld5p, Psf1p, Psf2p, Psf3p), which is localized to DNA replication origins	-	-3.81
YDR158W	<i>HOM2</i>	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression	-	-3.82
YPL273W	<i>SAM4</i>	S-adenosylmethionine-homocysteine methyltransferase, functions along with Mht1p in the conversion of S-adenosylmethionine (AdoMet) to	-	-3.83
YPL033C	<i>SRL4</i>	Protein of unknown function; involved in regulation of dNTP production; null mutant suppresses the	-	-3.84
YCL030C	<i>HIS4</i>	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase	-	-3.85
YNL036W	<i>NCE103</i>	Carbonic anhydrase; poorly transcribed under aerobic conditions and at an undetectable level under	-	-3.86
YBR045C	<i>GIP1</i>	Meiosis-specific regulatory subunit of the Glc7p protein phosphatase, regulates spore wall formation and septin organization, required for expression of	-	-3.88
YER056C	<i>FCY2</i>	Purine-cytosine permease, mediates purine (adenine, guanine, and hypoxanthine) and cytosine	-	-4.04
YMR321C	<i>YMR321C</i>	Putative protein of unknown function; proposed to	-	-4.07



YHR018C	<i>ARG4</i>	Argininosuccinate lyase, catalyzes the final step in the	-	-4.10
YPR058W	<i>YMC1</i>	Mitochondrial protein, putative inner membrane transporter with a role in oleate metabolism and glutamate biosynthesis; member of the	-	-4.10
YOL141W	<i>PPM2</i>	AdoMet-dependent tRNA methyltransferase also involved in methoxycarbonylation; required for the synthesis of wybutosine ( $\gamma$ W), a modified guanosine	-	-4.15
YKL218C	<i>SRY1</i>	3-hydroxyaspartate dehydratase, deaminates L-threo-3-hydroxyaspartate to form oxaloacetate and ammonia; required in the presence of	-	-4.31
YOL091W	<i>SPO21</i>	Component of the meiotic outer plaque of the spindle pole body, involved in modifying the meiotic	-	-4.32
YDR253C	<i>MET32</i>	Zinc-finger DNA-binding protein, involved in transcriptional regulation of the methionine	-	-4.35
YPL252C	<i>YAH1</i>	Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur proteins; involved in	-	-4.39
YIL056W	<i>VHR1</i>	Transcriptional activator, required for the vitamin H-responsive element (VHRE) mediated induction of VHT1 (Vitamin H transporter) and BIO5 (biotin	-	-4.41
YOR303W	<i>CPA1</i>	Small subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor; translationally regulated by an	-	-4.45
YDR354W	<i>TRP4</i>	Anthranilate phosphoribosyl transferase of the tryptophan biosynthetic pathway, catalyzes the phosphoribosylation of anthranilate, subject to the	-	-4.58
YOR130C	<i>ORT1</i>	Ornithine transporter of the mitochondrial inner membrane, exports ornithine from mitochondria as part of arginine biosynthesis; human ortholog is	-	-4.59
YER060W-A	<i>FCY22</i>	Putative purine-cytosine permease, very similar to	-	-4.59
YNR057C	<i>BIO4</i>	Dethiobiotin synthetase, catalyzes the third step in the biotin biosynthesis pathway; BIO4 is in a cluster of 3 genes (BIO3, BIO4, and BIO5) that mediate biotin	-	-4.68
YGL224C	<i>SDT1</i>	Pyrimidine nucleotidase; overexpression suppresses the 6-AU sensitivity of transcription elongation factor	-	-4.89
YNL095C	<i>YNL095C</i>	Putative protein of unknown function predicted to contain a transmembrane domain; YNL095C is not an	-	-4.94
YMR062C	<i>ARG7</i>	Mitochondrial ornithine acetyltransferase, catalyzes the fifth step in arginine biosynthesis; also possesses acetylglutamate synthase activity, regenerates	-	-4.99
YJL198W	<i>PHO90</i>	Low-affinity phosphate transporter; deletion of <i>pho84</i> , <i>pho87</i> , <i>pho89</i> , <i>pho90</i> , and <i>pho91</i> causes synthetic lethality; transcription independent of Pi	-	-5.08
YOR302W	<i>YOR302W</i>	CPA1 uORF, Arginine attenuator peptide, regulates	-	-5.18

YOL058W	<i>ARG1</i>	Arginosuccinate synthetase, catalyzes the formation of L-argininosuccinate from citrulline and L-aspartate	-	-5.19
YBR256C	<i>RIB5</i>	Riboflavin synthase; catalyzes the last step of the	-	-5.28
YDL198C	<i>GGC1</i>	Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in	-	-5.29
YOR032C	<i>HMS1</i>	Basic helix-loop-helix (bHLH) protein with similarity to myc-family transcription factors; overexpression confers hyperfilamentous growth and suppresses the	-	-5.29
YIR017C	<i>MET28</i>	Basic leucine zipper (bZIP) transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in	-	-5.33
YLR089C	<i>ALT1</i>	Alanine transaminase (glutamic pyruvic transaminase); involved in alanine biosynthetic and catabolic processes; the authentic, non-tagged	-	-5.33
YJR111C	<i>YJR111C</i>	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to	-	-5.38
YJR154W	<i>YJR154W</i>	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to	-	-5.49
YJR137C	<i>MET5</i>	Sulfite reductase beta subunit, involved in amino acid biosynthesis, transcription repressed by methionine	-	-5.66
YNL104C	<i>LEU4</i>	Alpha-isopropylmalate synthase (2-isopropylmalate synthase); the main isozyme responsible for the first	-	-5.87
YER174C	<i>GRX4</i>	Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase; monothiol glutaredoxin subfamily member along with Grx3p and	-	-5.88
YPR167C	<i>MET16</i>	3'-phosphoadenylylsulfate reductase, reduces 3'-phosphoadenylyl sulfate to adenosine-3',5'-bisphosphate and free sulfite using reduced	-	-5.95
YJR109C	<i>CPA2</i>	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an	-	-6.23
YER024W	<i>YAT2</i>	Carnitine acetyltransferase; has similarity to Yat1p, which is a carnitine acetyltransferase associated with	-	-6.25
YNR068C	<i>YNR068C</i>	Putative protein of unknown function	-	-6.35
YKR069W	<i>MET1</i>	S-adenosyl-L-methionine uroporphyrinogen III transmethylase, involved in the biosynthesis of siroheme, a prosthetic group used by sulfite	-	-6.40
YER069W	<i>ARG5,6</i>	Protein that is processed in the mitochondrion to yield acetylglutamate kinase and N-acetyl-gamma-glutamyl-phosphate reductase, which catalyze the	-	-6.44
YKL029C	<i>MAE1</i>	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for	-	-6.47
YML116W	<i>ATR1</i>	Multidrug efflux pump of the major facilitator superfamily, required for resistance to aminotriazole	-	-6.51

YGR065C	<i>VHT1</i>	High-affinity plasma membrane H <sup>+</sup> -biotin (vitamin H) symporter; mutation results in fatty acid auxotrophy; 12 transmembrane domain containing major	-	-6.60
YJR130C	<i>STR2</i>	Cystathionine gamma-synthase, converts cysteine	-	-6.63
YLR092W	<i>SUL2</i>	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of	-	-6.83
YMR108W	<i>ILV2</i>	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the	-	-6.90
YOL140W	<i>ARG8</i>	Acetylornithine aminotransferase, catalyzes the fourth step in the biosynthesis of the arginine	-	-7.11
YPL264C	<i>YPL264C</i>	Putative membrane protein of unknown function; physically interacts with Hsp82p; YPL264C is not an	-	-7.16
YOL119C	<i>MCH4</i>	Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma	-	-7.39
YPR027C	<i>YPR027C</i>	Putative protein of unknown function	-	-7.46
YGR224W	<i>AZR1</i>	Plasma membrane transporter of the major facilitator superfamily, involved in resistance to azole drugs	-	-7.62
YFR030W	<i>MET10</i>	Subunit alpha of assimilatory sulfite reductase, which	-	-7.71
YHR071W	<i>PCL5</i>	Cyclin, interacts with and phosphorylated by Pho85p cyclin-dependent kinase (Cdk), induced by Gcn4p at level of transcription, specifically required for Gcn4p	-	-7.71
YNR058W	<i>BIO3</i>	7,8-diamino-pelargonic acid aminotransferase (DAPA), catalyzes the second step in the biotin biosynthesis pathway; BIO3 is in a cluster of 3 genes	-	-8.23
YBR296C	<i>PHO89</i>	Na <sup>+</sup> /Pi cotransporter, active in early growth phase; similar to phosphate transporters of Neurospora	-	-9.20
YHR029C	<i>YHI9</i>	Protein of unknown function; null mutant is defective in unfolded protein response; possibly involved in a membrane regulation metabolic pathway; member of	-	-9.30
YER175C	<i>TMT1</i>	Trans-aconitate methyltransferase, cytosolic enzyme that catalyzes the methyl esterification of 3-isopropylmalate, an intermediate of the leucine	-	-9.72
YGL117W	<i>YGL117W</i>	Putative protein of unknown function	-	-9.72
YGL184C	<i>STR3</i>	Cystathionine beta-lyase, converts cystathionine into	-	-9.83
YBR148W	<i>YSW1</i>	Protein required for normal prospore membrane formation; interacts with Gip1p, which is the meiosis-specific regulatory subunit of the Glc7p protein	-	-10.31
YBR047W	<i>FMP23</i>	Putative protein of unknown function; proposed to be involved in iron or copper homeostasis; the authentic, non-tagged protein is detected in highly	-	-12.46

YJL088W	<i>ARG3</i>	Ornithine carbamoyltransferase (carbamoylphosphate:L-ornithine	-	-14.12
YMR096W	<i>SNZ1</i>	Protein involved in vitamin B6 biosynthesis; member of a stationary phase-induced gene family; coregulated with SNO1; interacts with Sno1p and	-	-17.82
YPL250C	<i>ICY2</i>	Protein of unknown function; mobilized into polysomes upon a shift from a fermentable to	-	-18.06
YDR380W	<i>ARO10</i>	Phenylpyruvate decarboxylase, catalyzes decarboxylation of phenylpyruvate to	-	-25.87
YMR095C	<i>SNO1</i>	Protein of unconfirmed function, involved in pyridoxine metabolism; expression is induced during stationary phase; forms a putative glutamine	-	-33.55
YBR294W	<i>SUL1</i>	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of	-	-39.15