

| Supplemental Table S1. Gene Expression Responses to 6NDA in <i>S.cerevisiae</i> | | | |
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| ORF | Gene symbol | Description | Fold Change |
| YOR134W | BAG7 | Rho GTPase activating protein (RhoGAP), stimulates the intrinsic GTPase activity of Rho1p, which plays a role in actin cytoskeleton organization and | 156.5 |
| YGR213C | RTA1 | Protein involved in 7-aminocholesterol resistance; has seven potential membrane-spanning regions | 84.1 |
| YGR043C | | Putative protein of unknown function; transcription is repressed by MOT1/YPL082C and induced by alpha-factor and during diauxic shift; green | 73.0 |
| YLR054C | OSW2 | Protein of unknown function proposed to be involved in the assembly of the spore wall | 44.4 |
| YFL014W | HSP12 | Plasma membrane localized protein that protects membranes from desiccation; induced by heat shock, oxidative stress, osmostress, stationary | 42.1 |
| YAR050W | FLO1 | Lectin-like protein involved in flocculation, cell wall protein that binds to mannose chains on the surface of other cells, confers floc-forming ability that is | 32.9 |
| YDR034W-B | | Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery | 31.7 |
| YJL116C | NCA3 | 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 | 23.2 |
| YOL101C | IZH4 | Membrane protein involved in zinc metabolism, member of the four-protein IZH family, expression induced by fatty acids and altered zinc levels; deletion | 22.7 |
| YIL101C | XBP1 | Transcriptional repressor that binds to promoter sequences of the cyclin genes, CYS3, and SMF2; expression is induced by stress or starvation during mitosis, | 22.5 |
| YHR139C | SPS100 | Protein required for spore wall maturation; expressed during sporulation; may be a component of the spore wall | 22.5 |
| YHR087W | | Protein involved in RNA metabolism, one of two yeast homologs (with Sdo1p/Ylr022cp) of the human protein SBDS responsible for autosomal | 21.5 |
| YGR236C | SPG1 | Protein required for survival at high temperature during stationary phase; not required for growth on nonfermentable carbon sources; the authentic, non- | 21.2 |
| YNL160W | YGP1 | Cell wall-related secretory glycoprotein; induced by nutrient deprivation-associated growth arrest and upon entry into stationary phase; may be involved | 18.9 |
| YGL156W | AMS1 | Vacuolar alpha mannosidase, involved in free oligosaccharide (fOS) degradation; delivered to the vacuole in a novel pathway separate from the | 18.8 |
| YJL144W | | Cytoplasmic hydrophilin of unknown function, proposed to be involved in the dessication response; expression induced by osmotic stress, starvation | 18.6 |
| YLR121C | YPS3 | Aspartic protease, attached to the plasma membrane via a glycosylphosphatidylinositol (GPI) anchor | 18.2 |
| YHR209W | | Putative S-adenosylmethionine-dependent methyltransferase | 18.0 |
| YNL093W | YPT53 | GTPase, similar to Ypt51p and Ypt52p and to mammalian rab5; required for vacuolar protein sorting and endocytosis | 17.9 |
| YGL121C | GPG1 | Proposed gamma subunit of the heterotrimeric G protein that interacts with the receptor Grp1p; involved in regulation of pseudohyphal growth; requires Gpb1p | 17.8 |
| YMR315W-A | | Putative protein of unknown function | 17.6 |
| YHR096C | HXT5 | Hexose transporter with moderate affinity for glucose, may function in accumulation of reserve carbohydrates during stress, expression induced by a | 17.0 |
| YKL163W | PIR3 | O-glycosylated covalently-bound cell wall protein required for cell wall stability; expression is cell cycle regulated, peaking in M/G1 and also subject to | 16.1 |
| YER037W | PHM8 | Protein of unknown function, expression is induced by low phosphate levels and by inactivation of Pho85p | 13.8 |
| YOL052C-A | DDR2 | Multistress response protein, expression is activated by a variety of xenobiotic agents and environmental or physiological stresses | 13.8 |
| YGR256W | GND2 | 6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth | 13.6 |

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| YAL061W | | putative polyol dehydrogenase | 13.2 |
| YJL107C | | Putative protein of unknown function; expression is induced by activation of the HOG1 mitogen-activated signaling pathway and this induction is Hog1p/Pbs2p | 12.8 |
| YOL047C | | Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern | 12.6 |
| YNL194C | | Integral membrane protein localized to eisosomes, large immobile protein structures at the cell cortex associated with endocytosis; sporulation and | 12.4 |
| YOR049C | RSB1 | Suppressor of sphingoid long chain base (LCB) sensitivity of an LCB-lyase mutation; putative integral membrane transporter or flippase that may transport | 12.0 |
| YER185W | | Hypothetical protein | 11.5 |
| YLR327C | TMA10 | Protein of unknown function that associates with ribosomes | 11.4 |
| YPL088W | | Putative aryl alcohol dehydrogenase; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug | 10.8 |
| YJR078W | BNA2 | Tryptophan 2,3-dioxygenase, required for biosynthesis of nicotinic acid from tryptophan via kynurenine pathway | 10.7 |
| YJL108C | PRM10 | Pheromone-regulated protein, predicted to have 5 transmembrane segments | 10.5 |
| YNR064C | | Epoxide hydrolase, member of the alpha/beta hydrolase fold family; may have a role in detoxification of epoxides | 10.1 |
| YLR194C | | Structural constituent of the cell wall attached to the plasma membrane by a GPI-anchor; expression is upregulated in response to cell wall stress | 10.1 |
| YAL063C | FLO9 | Lectin-like protein with similarity to Flo1p, thought to be expressed and involved in flocculation | 9.7 |
| YDR380W | ARO10 | Phenylpyruvate decarboxylase, catalyzes decarboxylation of phenylpyruvate to phenylacetaldehyde, which is the first specific step in the Ehrlich pathway | 9.7 |
| YGR032W | GSC2 | Catalytic subunit of 1,3-beta-glucan synthase, involved in formation of the inner layer of the spore wall; activity positively regulated by Rho1p and negatively by | 9.5 |
| YLR099C | ICT1 | Protein of unknown function, null mutation leads to an increase in sensitivity to Calcofluor white; expression of the gene is induced in the presence of | 9.4 |
| YHR138C | | Putative protein of unknown function; has similarity to Pbi2p; double null mutant lacking Pbi2p and Yhr138p exhibits highly fragmented vacuoles | 9.4 |
| YLR149C | | Putative protein of unknown function; YLR149C is not an essential gene | 9.3 |
| YCR007C | | Putative integral membrane protein, member of DUP240 gene family; YCR007C is not an essential gene | 9.1 |
| YMR169C | ALD3 | Cytoplasmic aldehyde dehydrogenase, involved in beta-alanine synthesis; uses NAD+ as the preferred coenzyme; very similar to Ald2p; expression is induced | 9.1 |
| YKR091W | SRL3 | Cytoplasmic protein that, when overexpressed, suppresses the lethality of a rad53 null mutation; potential Cdc28p substrate | 9.1 |
| YNL237W | YTP1 | Probable type-III integral membrane protein of unknown function, has regions of similarity to mitochondrial electron transport proteins | 8.9 |
| YLR136C | TIS11 | mRNA-binding protein expressed during iron starvation; binds to a sequence element in the 3'-untranslated regions of specific mRNAs to mediate their | 8.8 |
| YHR160C | PEX18 | Part of a two-member peroxin family (Pex18p and Pex21p) specifically required for peroxisomal targeting of the Pex7p peroxisomal signal recognition factor | 8.8 |
| YKL161C | | Protein kinase implicated in the Sit2p mitogen-activated (MAP) kinase signaling pathway; associates with Rlm1p | 8.7 |
| YBR085C-A | | Hypothetical protein | 8.7 |
| YBL049W | MOH1 | Protein of unknown function, has homology to kinase Snf7p; not required for growth on nonfermentable carbon sources; essential for viability in stationary | 8.2 |
| YMR316W | DIA1 | Protein of unknown function, involved in invasive and pseudohyphal growth; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a | 8.1 |

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| YMR107W | SPG4 | Protein required for survival at high temperature during stationary phase; not required for growth on nonfermentable carbon sources | 8.1 |
| YDL244W | THI13 | Protein involved in synthesis of the thiamine precursor hydroxymethylpyrimidine (HMP); member of a subtelomeric gene family | 7.9 |
| YBR054W | YRO2 | Putative plasma membrane protein of unknown function, transcriptionally regulated by Haa1p; green fluorescent protein (GFP)-fusion protein localizes to | 7.7 |
| YOL151W | GRE2 | NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase); stress induced (osmotic, ionic, oxidative, heat shock and heavy metals); | 7.7 |
| YOR237W | HES1 | Protein implicated in the regulation of ergosterol biosynthesis; one of a seven member gene family with a common essential function and non-essential | 7.6 |
| YGR146C | | Putative protein of unknown function; induced by iron homeostasis transcription factor Aft2p; multicopy suppressor of a temperature sensitive <i>hsf1</i> mutant | 7.6 |
| YIR039C | YPS6 | Putative GPI-anchored aspartic protease | 7.5 |
| YKR076W | ECM4 | Putative omega class glutathione transferase; not essential; similar to Ygr154cp; green fluorescent protein (GFP)-fusion protein localizes to the | 7.5 |
| YMR174C | PAI3 | Cytoplasmic proteinase A inhibitor, dependent on Pbs2p and Hog1p protein kinases for osmotic induction; intrinsically unstructured, N-terminal half | 7.4 |
| YLR346C | | Putative protein of unknown function found in mitochondria; expression is regulated by transcription factors involved in pleiotropic drug resistance, Pdr1p | 7.4 |
| YOR273C | TPO4 | Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily | 7.3 |
| YMR008C | PLB1 | Phospholipase B (lysophospholipase) involved in lipid metabolism, required for deacylation of phosphatidylcholine and phosphatidylethanolamine but not | 7.3 |
| YMR084W | | Hypothetical protein | 7.3 |
| YDR453C | TSA2 | Stress inducible cytoplasmic thioredoxin peroxidase; cooperates with Tsa1p in the removal of reactive oxygen, nitrogen and sulfur species using thioredoxin | 7.3 |
| YGR088W | CTT1 | Cytosolic catalase T, has a role in protection from oxidative damage by hydrogen peroxide | 7.2 |
| YMR034C | | Putative protein of unknown function with similarity to transporters; identified in a transposon mutagenesis screen as a gene involved in azole resistance; | 7.2 |
| YEL057C | | Protein of unknown function involved in telomere maintenance; target of UME6 regulation | 6.9 |
| YGR131W | | Hypothetical protein | 6.7 |
| YBR117C | TKL2 | Transketolase, similar to Tkl1p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3- | 6.6 |
| YLR031W | | Hypothetical protein | 6.6 |
| YBR214W | SDS24 | One of two <i>S. cerevisiae</i> homologs (Sds23p and Sds24p) of the <i>Schizosaccharomyces pombe</i> Sds23 protein, which genetic studies have | 6.6 |
| YMR085W | | Hypothetical protein | 6.6 |
| YPL240C | HSP82 | Cytoplasmic chaperone (Hsp90 family) required for pheromone signaling and negative regulation of Hsf1p; docks with the mitochondrial import receptor | 6.6 |
| YLR461W | PAU4 | Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by | 6.4 |
| YMR322C | SNO4 | Possible chaperone and cysteine protease with similarity to <i>E. coli</i> Hsp31 and <i>S. cerevisiae</i> Hsp31p, Hsp32p, and Hsp33p; member of the DJ-1/ThiJ/Pfpl | 6.4 |
| YLL039C | UBI4 | Ubiquitin, becomes conjugated to proteins, marking them for selective degradation via the ubiquitin-26S proteasome system; essential for the cellular | 6.3 |
| YKR049C | FMP46 | Mitochondrial protein of unknown function; putative redox protein containing a thioredoxin fold | 6.3 |
| YOL084W | PHM7 | Protein of unknown function, expression is regulated by phosphate levels; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery | 6.1 |

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| YDR055W | PST1 | Cell wall protein that contains a putative GPI-attachment site; secreted by regenerating protoplasts; up-regulated by activation of the cell integrity | 6.0 |
| YER150W | SPI1 | GPI-anchored, serine/threonine rich cell wall protein of unknown function; basal expression requires Msn2p/Msn4p; expression is induced under conditions of | 6.0 |
| YNR075W | COS10 | Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins | 6.0 |
| YOR173W | DCS2 | Non-essential protein containing a HIT (histidine triad) motif; regulated by Msn2p, Msn4p, and the Ras-cAMP-cAPK signaling pathway, transcript | 6.0 |
| YOR338W | | Hypothetical protein | 6.0 |
| YBR072W | HSP26 | 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 | 6.0 |
| YDR223W | CRF1 | Transcriptional corepressor involved in the regulation of ribosomal protein gene transcription via the TOR signaling pathway and protein kinase A, | 5.9 |
| YOL016C | CMK2 | Calmodulin-dependent protein kinase; may play a role in stress response, many CA ⁺⁺ /calmodulin dependent phosphorylation substrates demonstrated | 5.9 |
| YML100W | TSL1 | Large subunit of trehalose 6-phosphate synthase (Tps1p)/phosphatase (Tps2p) complex, which converts uridine-5'-diphosphoglucose and glucose 6-phosphate | 5.9 |
| YBR033W | | Non-essential protein of unknown function | 5.8 |
| YGL179C | TOS3 | Protein kinase, related to and functionally redundant with Elm1p and Sak1p for the phosphorylation and activation of Snf1p; functionally orthologous to LKB1, | 5.8 |
| YBR295W | PCA1 | P-type metal-transporting ATPase with a role in copper and iron homeostasis; R970G-substitution in the C-terminal region confers cadmium resistance | 5.8 |
| YAL068C | | Hypothetical protein | 5.6 |
| YKL096W | CWP1 | Cell wall mannoprotein, linked to a beta-1,3- and beta-1,6-glucan heteropolymer through a phosphodiester bond; involved in cell wall | 5.6 |
| YOR289W | | Hypothetical protein | 5.5 |
| YEL060C | PRB1 | Vacuolar proteinase B (yscB), a serine protease of the subtilisin family; involved in protein degradation in the vacuole and required for full protein | 5.5 |
| YER184C | | Hypothetical protein | 5.4 |
| YJL161W | | The authentic, non-tagged protein was localized to the mitochondria | 5.3 |
| YKL159C | RCN1 | Protein involved in calcineurin regulation during calcium signaling; has similarity to H. sapiens DSCR1 which is found in the Down Syndrome | 5.2 |
| YPR001W | CIT3 | Citrate synthase, catalyzes the condensation of acetyl coenzyme A and oxaloacetate to form citrate, mitochondrial isozyme involved in the TCA cycle | 5.2 |
| YBR056W | | Hypothetical protein | 5.2 |
| YGR059W | SPR3 | Sporulation-specific homolog of the yeast CDC3/10/11/12 family of bud neck microfilament genes; septin protein involved in sporulation; regulated by ABFI | 5.1 |
| YNR060W | FRE4 | Ferric reductase, reduces a specific subset of siderophore-bound iron prior to uptake by transporters; expression induced by low iron levels | 5.1 |
| YBL078C | ATG8 | Protein required for autophagy; modified by the serial action of Atg4p, Atg7p, and Atg3p, and conjugated at the C terminus with phosphatidylethanolamine, | 5.1 |
| YLR205C | HMX1 | ER localized, heme-binding peroxidase involved in the degradation of heme; does not exhibit heme oxygenase activity despite similarity to heme | 5.1 |
| YMR053C | STB2 | Protein that interacts with Sin3p in a two-hybrid assay and is part of a large protein complex with Sin3p and Stb1p | 5.1 |
| YKL151C | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm | 5.0 |
| YHR097C | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus | 5.0 |

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| YKL107W | | Putative protein of unknown function | 5.0 |
| YOR385W | | Hypothetical protein | 5.0 |
| YMR040W | YET2 | Endoplasmic reticulum transmembrane protein, homolog of human BAP31 protein | 4.9 |
| YGR144W | THI4 | Protein required for thiamine biosynthesis and for mitochondrial genome stability | 4.8 |
| YLL064C | PAU6 | Hypothetical protein /// Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, | 4.8 |
| YKR061W | KTR2 | Mannosyltransferase involved in N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family | 4.8 |
| YOR152C | | Hypothetical protein | 4.8 |
| YDR085C | AFR1 | Alpha-factor pheromone receptor regulator, negatively regulates pheromone receptor signaling; required for normal mating projection (shmoo) formation; | 4.7 |
| YNR002C | ATO2 | Putative transmembrane protein, involved in the export of ammonia, a starvation signal that promotes cell death in the center of aging colonies; | 4.7 |
| YOR220W | | protein that interacts genetically with the Pat1 mRNA-decapping factor | 4.7 |
| YJL153C | INO1 | Inositol 1-phosphate synthase, involved in synthesis of inositol phosphates and inositol-containing phospholipids; transcription is coregulated with other | 4.6 |
| YGL183C | MND1 | Protein required for recombination and meiotic nuclear division; forms a complex with Hop2p, which is involved in chromosome pairing and repair of | 4.6 |
| YNR019W | ARE2 | Acyl-CoA:sterol acyltransferase, isozyme of Are1p; endoplasmic reticulum enzyme that contributes the major sterol esterification activity in the presence | 4.6 |
| YER106W | MAM1 | Monopolin, kinetochore associated protein involved in chromosome attachment to meiotic spindle | 4.6 |
| YER062C | HOR2 | One of two redundant DL-glycerol-3-phosphatases (RHR2/GPP1 encodes the other) involved in glycerol biosynthesis; induced in response to hyperosmotic | 4.6 |
| YNL092W | | Putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family; YNL092W is not an essential gene | 4.6 |
| YOR377W | ATF1 | Alcohol acetyltransferase with potential roles in lipid and sterol metabolism; responsible for the major part of volatile acetate ester production during | 4.5 |
| YHR124W | NDT80 | Meiosis-specific transcription factor required for exit from pachytene and for full meiotic recombination; activates middle sporulation genes; competes with | 4.5 |
| YDL246C | SOR2 | Protein of unknown function, computational analysis of large-scale protein-protein interaction data suggests a possible role in fructose or mannose | 4.5 |
| YMR250W | GAD1 | Glutamate decarboxylase, converts glutamate into gamma-aminobutyric acid (GABA) during glutamate catabolism; involved in response to oxidative stress | 4.5 |
| YDR171W | HSP42 | Small cytosolic stress-induced chaperone that forms barrel-shaped oligomers and suppresses the aggregation of non-native proteins; oligomer dissociation is | 4.5 |
| YCR104W | PAU3 | Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by | 4.4 |
| YGL039W | | Oxidoreductase, catalyzes NADPH-dependent reduction of the bicyclic diketone bicyclo[2.2.2]octane-2,6-dione (BCO _{2,6D}) to the chiral ketoalcohol | 4.4 |
| YNL202W | SPS19 | Peroxisomal 2,4-dienoyl-CoA reductase, auxiliary enzyme of fatty acid beta-oxidation; homodimeric enzyme required for growth and sporulation on | 4.4 |
| YFR022W | ROG3 | Protein that binds to Rsp5p, which is a hect-type ubiquitin ligase, via its 2 PY motifs; has similarity to Rod1p; mutation suppresses the temperature | 4.4 |
| YLR030W | | Hypothetical protein | 4.4 |
| YMR102C | | Protein of unknown function; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug | 4.3 |
| YOR185C | GSP2 | GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; interacts with Kap121p, | 4.3 |

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| YLR307W | CDA1 | Chitin deacetylase, together with Cda2p involved in the biosynthesis ascospore wall component, chitosan; required for proper rigidity of the ascospore wall | 4.3 |
| YKR003W | OSH6 | Member of an oxysterol-binding protein family with overlapping, redundant functions in sterol metabolism and which collectively perform a function | 4.3 |
| YGL258W-A | | Putative protein of unknown function | 4.3 |
| YGR174W-A | | Putative protein of unknown function | 4.2 |
| YDR379C-A | | Hypothetical protein identified by homology. See FEBS Letters [2000] 487:31-36. | 4.2 |
| YDL114W | | Putative protein of unknown function with similarity to acyl-carrier-protein reductases; YDL114W is not an essential gene | 4.2 |
| YOR036W | PEP12 | Target membrane receptor (t-SNARE) for vesicular intermediates traveling between the Golgi apparatus and the vacuole; controls entry of biosynthetic, | 4.2 |
| YBR203W | COS111 | Protein required for wild-type resistance to the antifungal drug ciclopirox olamine; not related to the COS family of subtelomerically-encoded proteins | 4.2 |
| YNL192W | CHS1 | Chitin synthase I, requires activation from zymogenic form in order to catalyze the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for repairing | 4.2 |
| YHL021C | | The authentic, non-tagged protein was localized to the mitochondria | 4.1 |
| YMR196W | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YMR196W is not an essential gene | 4.1 |
| YPL223C | GRE1 | Hydrophilin of unknown function; stress induced (osmotic, ionic, oxidative, heat shock and heavy metals); regulated by the HOG pathway | 4.1 |
| YLR178C | TFS1 | Carboxypeptidase Y inhibitor, function requires acetylation by the NatB N-terminal acetyltransferase; phosphatidylethanolamine-binding protein involved | 4.1 |
| YOL083W | | Hypothetical protein | 4.0 |
| YHR030C | SLT2 | Serine/threonine MAP kinase involved in regulating the maintenance of cell wall integrity and progression through the cell cycle; regulated by the PKC1- | 4.0 |
| YLR120C | YPS1 | Aspartic protease, attached to the plasma membrane via a glycosylphosphatidylinositol (GPI) anchor | 4.0 |
| YIL099W | SGA1 | Intracellular sporulation-specific glucoamylase involved in glycogen degradation; induced during starvation of a/a diploids late in sporulation, but | 4.0 |
| YDL110C | TMA17 | Protein of unknown function that associates with ribosomes | 4.0 |
| YLR267W | | Protein of unknown function, overproduction suppresses a pam1 slv3 double null mutation | 3.9 |
| YDL234C | GYP7 | GTPase-activating protein for yeast Rab family members including: Ypt7p (most effective), Ypt1p, Ypt31p, and Ypt32p (in vitro); involved in vesicle | 3.9 |
| YDR258C | HSP78 | Oligomeric mitochondrial matrix chaperone that cooperates with Ssc1p in mitochondrial thermotolerance after heat shock; prevents the aggregation of | 3.9 |
| YLL026W | HSP104 | Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold and reactivate previously denatured, aggregated proteins; responsive to | 3.9 |
| YIL176C | PAU1 | Hypothetical protein /// Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, | 3.9 |
| YKR046C | PET10 | Protein of unknown function that co-purifies with lipid particles; expression pattern suggests a role in respiratory growth; computational analysis of large- | 3.9 |
| YLR080W | EMP46 | Integral membrane component of endoplasmic reticulum-derived COPII-coated vesicles, which function in ER to Golgi transport | 3.9 |
| YMR323W | ERR3 | Protein of unknown function, has similarity to enolases /// Protein of unknown function, has similarity to enolases /// Protein of unknown function, has | 3.9 |
| YGL157W | | Oxidoreductase, catalyzes NADPH-dependent reduction of the bicyclic diketone bicyclo[2.2.2]octane-2,6-dione (BCO _{2,6} D) to the chiral ketoalcohol | 3.8 |
| YDL222C | FMP45 | Integral membrane protein localized to mitochondria (untagged protein) and eisosomes, immobile patches at the cortex associated with endocytosis; | 3.8 |

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| YNR059W | MNT4 | Putative alpha-1,3-mannosyltransferase, not required for protein O-glycosylation | 3.8 |
| YGR142W | BTN2 | Cytosolic coiled-coil protein that modulates arginine uptake, interacts with Rhb1p, possible role in mediating pH homeostasis between the vacuole and | 3.8 |
| YGR268C | HUA1 | Cytoplasmic protein containing a zinc finger domain with sequence similarity to that of Type I J-proteins; computational analysis of large-scale protein-protein | 3.8 |
| YGR243W | | The authentic, non-tagged protein was localized to mitochondria | 3.8 |
| YGL053W | PRM8 | Pheromone-regulated protein with 2 predicted transmembrane segments and an FF sequence, a motif involved in COPII binding; forms a complex with | 3.8 |
| YGR110W | | Putative protein of unknown function; transcription is increased in response to genotoxic stress | 3.8 |
| YGR052W | | The authentic, non-tagged protein was localized to the mitochondria | 3.8 |
| YMR181C | | Protein of unknown function; mRNA transcribed as part of a bicistronic transcript with a predicted transcriptional repressor RGM1/YMR182C; mRNA is | 3.8 |
| YPL170W | DAP1 | Heme-binding protein involved in regulation of cytochrome P450 protein Erg11p; damage response protein, related to mammalian membrane | 3.8 |
| YDL223C | HBT1 | Substrate of the Hub1p ubiquitin-like protein that localizes to the shmoo tip (mating projection); mutants are defective for mating projection formation, | 3.8 |
| YML128C | MSC1 | Protein of unknown function, green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; msc1 mutants are defective in directing | 3.8 |
| YJR096W | | Putative xylose and arabinose reductase | 3.8 |
| YJL048C | UBX6 | UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p, transcription is repressed when cells are grown in media containing | 3.7 |
| YIR033W | MGA2 | ER membrane protein involved, with its homolog Spt23p, in regulation of OLE1 transcription; inactive ER form dimerizes and one subunit is then activated by | 3.7 |
| YAL005C | SSA1 | ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; | 3.7 |
| YER179W | DMC1 | Meiosis-specific protein required for repair of double-strand breaks and pairing between homologous chromosomes; homolog of Rad51p and the bacterial | 3.7 |
| YDR074W | TPS2 | Phosphatase subunit of the trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; expression is | 3.7 |
| YIL160C | POT1 | 3-ketoacyl-CoA thiolase with broad chain length specificity, cleaves 3-ketoacyl-CoA into acyl-CoA and acetyl-CoA during beta-oxidation of fatty acids | 3.6 |
| YDR001C | NTH1 | Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses; may be phosphorylated by | 3.6 |
| YGR149W | | Putative protein of unknown function; predicted to be an integral membrane protein | 3.6 |
| YMR020W | FMS1 | Polyamine oxidase, converts spermine to spermidine, which is required for the essential hypusination modification of translation factor eIF-5A; also involved in | 3.6 |
| YCL048W | SPS22 | Protein of unknown function, redundant with Sps2p for the organization of the beta-glucan layer of the spore wall | 3.6 |
| YGR189C | CRH1 | Putative glycosidase of the cell wall, may have a role in cell wall architecture | 3.5 |
| YMR175W | SIP18 | Protein of unknown function whose expression is induced by osmotic stress | 3.5 |
| YDR058C | TGL2 | Protein with lipolytic activity towards triacylglycerols and diacylglycerols when expressed in E. coli; role in yeast lipid degradation is unclear | 3.5 |
| YOR208W | PTP2 | Phosphotyrosine-specific protein phosphatase involved in the inactivation of mitogen-activated protein kinase (MAPK) during osmolarity sensing; | 3.5 |
| YJR019C | TES1 | Peroxisomal acyl-CoA thioesterase likely to be involved in fatty acid oxidation rather than fatty acid synthesis; conserved protein also found in human | 3.5 |
| YDR391C | | Hypothetical protein | 3.5 |

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| YDR402C | DIT2 | N-formyltyrosine oxidase, sporulation-specific microsomal enzyme required for spore wall maturation, involved in the production of a soluble LL-dityrosine- | 3.5 |
| YFL041W-A | | Putative protein of unknown function; identified by fungal homology and RT-PCR | 3.5 |
| YPL149W | ATG5 | Conserved autophagy-related protein that undergoes conjugation with Atg12p and then associates with Atg16p to form a cytosolic complex essential for | 3.5 |
| YBL064C | PRX1 | Mitochondrial peroxiredoxin (1-Cys Prx) with thioredoxin peroxidase activity, has a role in reduction of hydroperoxides; induced during respiratory growth | 3.4 |
| YFL030W | AGX1 | Alanine : glyoxylate aminotransferase, catalyzes the synthesis of glycine from glyoxylate, which is one of three pathways for glycine biosynthesis in yeast; | 3.4 |
| YGR161C | RTS3 | Putative component of the protein phosphatase type 2A complex | 3.4 |
| YDR070C | | The authentic, non-tagged protein was localized to the mitochondria | 3.4 |
| YGL166W | CUP2 | Copper-binding transcription factor; activates transcription of the metallothionein genes CUP1-1 and CUP1-2 in response to elevated copper | 3.4 |
| YNL115C | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to mitochondria; YNL115C is not an essential gene | 3.4 |
| YBL093C | ROX3 | RNA polymerase II holoenzyme component | 3.4 |
| YIL055C | | Hypothetical protein | 3.4 |
| YCR018C | SRD1 | Protein involved in the processing of pre-rRNA to mature rRNA; contains a C2/C2 zinc finger motif; srd1 mutation suppresses defects caused by the rrp1- | 3.4 |
| YBR053C | | Hypothetical protein | 3.3 |
| YBR169C | SSE2 | Member of the heat shock protein 70 (HSP70) family; may be involved in protein folding; localized to the cytoplasm; highly homologous to the heat | 3.3 |
| YAL008W | FUN14 | Mitochondrial protein of unknown function | 3.3 |
| YML118W | NGL3 | Putative endonuclease, has a domain similar to a magnesium-dependent endonuclease motif in mRNA deadenylase Ccr4p; similar to Ngl1p and Ngl2p | 3.3 |
| YKL086W | SRX1 | Sulfiredoxin, contributes to oxidative stress resistance by reducing cysteine-sulfenic acid groups in the peroxiredoxins Tsa1p and Ahp1p that are formed | 3.3 |
| YDL124W | | NADPH-dependent alpha-keto amide reductase; reduces aromatic alpha-keto amides, aliphatic alpha-keto esters, and aromatic alpha-keto esters | 3.3 |
| YGL248W | PDE1 | Low-affinity cyclic AMP phosphodiesterase, controls glucose and intracellular acidification-induced cAMP signaling, target of the cAMP-protein kinase A | 3.3 |
| YDR358W | GGA1 | Golgi-localized protein with homology to gamma-adaptin, interacts with and regulates Arf1p and Arf2p in a GTP-dependent manner in order to facilitate | 3.3 |
| YLR414C | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the bud and cytoplasm; Hog1p is required for transcriptional | 3.2 |
| YOL002C | IZH2 | Membrane protein involved in zinc metabolism, member of the four-protein IZH family, direct target of the Zap1p transcription factor, expression induced by | 3.2 |
| YLR107W | REX3 | RNA exonuclease; required for maturation of the RNA component of RNase MRP; functions redundantly with Rnh70p and Rex2p in processing of U5 | 3.2 |
| YBR005W | RCR1 | Protein of the endoplasmic reticulum membrane involved in chitin deposition in the cell wall; overproduction confers resistance to Congo Red | 3.2 |
| YGR008C | STF2 | Protein involved in regulation of the mitochondrial F1F0-ATP synthase; Stf1p and Stf2p act as stabilizing factors that enhance inhibitory action of the Inh1p | 3.2 |
| YIL072W | HOP1 | Meiosis-specific DNA binding protein that displays Red1p dependent localization to the unsynapsed axial-lateral elements of the synaptonemal | 3.2 |
| YCL038C | ATG22 | Protein required for the breakdown of autophagic vesicles in the vacuole during autophagy, putative integral membrane protein that localizes to vacuolar | 3.2 |
| YGL104C | VPS73 | Mitochondrial protein of unknown function involved in vacuolar protein sorting | 3.2 |

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| YDL204W | RTN2 | Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily | 3.2 |
| YGR249W | MGA1 | Protein similar to heat shock transcription factor; multicopy suppressor of pseudohyphal growth defects of ammonium permease mutants | 3.2 |
| YOL155C | HPF1 | Haze-protective mannoprotein that reduces the particle size of aggregated proteins in white wines | 3.2 |
| YGR126W | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus | 3.2 |
| YBR280C | SAF1 | F-Box protein involved in proteasome-dependent degradation of Aah1p during entry of cells into quiescence; interacts with Skp1 | 3.2 |
| YGR138C | TPO2 | Polyamine transport protein specific for spermine; localizes to the plasma membrane; transcription of TPO2 is regulated by Haa1p; member of the major | 3.2 |
| YOL131W | | Hypothetical protein | 3.1 |
| YJL066C | MPM1 | Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches | 3.1 |
| YOR120W | GCY1 | Putative NADP(+) coupled glycerol dehydrogenase, proposed to be involved in an alternative pathway for glycerol catabolism | 3.1 |
| YPL221W | FLC1 | Putative FAD transporter; required for uptake of FAD into endoplasmic reticulum; involved in cell wall maintenance | 3.1 |
| YKL221W | MCH2 | Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma membrane; | 3.1 |
| YGL126W | SCS3 | Protein required for inositol prototrophy, appears to be involved in the synthesis of inositol phospholipids from inositol but not in the control of inositol synthesis | 3.1 |
| YJL082W | IML2 | Protein of unknown function, green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus | 3.1 |
| YGR066C | | Putative protein of unknown function | 3.1 |
| YGL006W | PMC1 | Vacuolar Ca ²⁺ ATPase involved in depleting cytosol of Ca ²⁺ ions; prevents growth inhibition by activation of calcineurin in the presence of elevated | 3.1 |
| YIL169C | | Putative protein of unknown function; serine/threonine rich and highly similar to YOL155C, a putative glucan alpha-1,4-glucosidase; transcript is induced in | 3.1 |
| YDL113C | ATG20 | Protein required for transport of aminopeptidase I (Lap4p) through the cytoplasm-to-vacuole targeting pathway; binds phosphatidylinositol-3- | 3.1 |
| YBR046C | ZTA1 | Zeta-crystallin homolog, found in the cytoplasm and nucleus; has similarity to E. coli quinone oxidoreductase and to human zeta-crystallin, which has | 3.1 |
| YJR116W | | Hypothetical protein | 3.1 |
| YCR061W | | Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern | 3.1 |
| YGL015C | | Hypothetical protein | 3.0 |
| YLL019C | KNS1 | Nonessential putative protein kinase of unknown cellular role; member of the LAMMER family of protein kinases, which are serine/threonine kinases also | 3.0 |
| YLR251W | SYM1 | Protein required for ethanol metabolism; induced by heat shock and localized to the inner mitochondrial membrane; homologous to mammalian peroxisomal | 3.0 |
| YAL037C-A | | Identified by SAGE | 3.0 |
| YJL163C | | Hypothetical protein | 3.0 |
| YGR237C | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm | 3.0 |
| YDL169C | UGX2 | Protein of unknown function, transcript accumulates in response to any combination of stress conditions | 3.0 |
| YJL057C | IKS1 | Putative serine/threonine kinase; expression is induced during mild heat stress; deletion mutants are hypersensitive to copper sulphate and resistant to | 3.0 |

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| YKR098C | UBP11 | Ubiquitin-specific protease that cleaves ubiquitin from ubiquitinated proteins | 3.0 |
| YKL183C-A | | Putative protein of unknown function; identified by fungal homology and RT-PCR | 3.0 |
| YNL036W | NCE103 | Carbonic anhydrase; poorly transcribed under aerobic conditions and at an undetectable level under anaerobic conditions; involved in non-classical protein | 3.0 |
| YIL136W | OM45 | Protein of unknown function, major constituent of the mitochondrial outer membrane; located on the outer (cytosolic) face of the outer membrane | 2.9 |
| YBR076W | ECM8 | Non-essential protein of unknown function | 2.9 |
| YBR149W | ARA1 | Large subunit of NADP ⁺ dependent arabinose dehydrogenase, involved in carbohydrate metabolism; small subunit is unidentified | 2.9 |
| YHR140W | | Putative integral membrane protein of unknown function | 2.9 |
| YGR087C | PDC6 | Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde, regulation is glucose- | 2.9 |
| YKR053C | YSR3 | Dihydro sphingosine 1-phosphate phosphatase, membrane protein involved in sphingolipid metabolism; has similarity to Lcb3p | 2.9 |
| YJR142W | | Putative protein of unknown function | 2.9 |
| YCR068W | ATG15 | Lipase, required for intravacuolar lysis of autophagic bodies; located in the endoplasmic reticulum membrane and targeted to intravacuolar vesicles during | 2.9 |
| YDL020C | RPN4 | Transcription factor that stimulates expression of proteasome genes; Rpn4p levels are in turn regulated by the 26S proteasome in a negative feedback | 2.9 |
| YDL130W-A | STF1 | Protein involved in regulation of the mitochondrial F1F0-ATP synthase; Stf1p and Stf2p act as stabilizing factors that enhance inhibitory action of the Inh1p | 2.9 |
| YBR284W | | Putative protein of unknown function; YBR284W is not an essential gene; null mutant exhibits decreased resistance to rapamycin and wortmannin | 2.9 |
| YPL230W | | Up in StarVation | 2.9 |
| YCL049C | | Protein of unknown function; localizes to membrane fraction; YCL049C is not an essential gene; | 2.9 |
| YOR019W | | Hypothetical protein | 2.9 |
| YMR173W | DDR48 | DNA damage-responsive protein, expression is increased in response to heat-shock stress or treatments that produce DNA lesions; contains multiple repeats | 2.9 |
| YDR072C | IPT1 | Inositolphosphotransferase 1, involved in synthesis of mannose-(inositol-P) ₂ -ceramide (M(IP) ₂ C), which is the most abundant sphingolipid in cells, mutation | 2.9 |
| YKL026C | GPX1 | Phospholipid hydroperoxide glutathione peroxidase induced by glucose starvation that protects cells from phospholipid hydroperoxides and | 2.9 |
| YMR104C | YPK2 | Protein kinase with similarity to serine/threonine protein kinase Ypk1p; functionally redundant with YPK1 at the genetic level; participates in a signaling | 2.9 |
| YMR096W | SNZ1 | Protein involved in vitamin B6 biosynthesis; member of a stationary phase-induced gene family; coregulated with SNO1; interacts with Sno1p and with | 2.9 |
| YDR018C | | Hypothetical protein | 2.9 |
| YPL070W | MUK1 | Protein of unknown function, localized to the cytoplasm; computational analysis of large-scale protein-protein interaction data suggests a possible role in | 2.8 |
| YER035W | EDC2 | RNA-binding protein, activates mRNA decapping directly by binding to the mRNA substrate and enhancing the activity of the decapping proteins Dcp1p | 2.8 |
| YJR149W | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm | 2.8 |
| YIL154C | IMP2 | Transcriptional activator involved in maintenance of ion homeostasis and protection against DNA damage caused by bleomycin and other oxidants, | 2.8 |
| YNL208W | | Hypothetical protein | 2.8 |

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| YGR136W | LSB1 | Protein containing an N-terminal SH3 domain; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch | 2.8 |
| YNL094W | APP1 | Protein of unknown function, interacts with Rvs161p and Rvs167p; computational analysis of protein-protein interactions in large-scale studies | 2.8 |
| YLR162W-A | | Putative protein of unknown function identified by fungal homology comparisons and RT-PCR | 2.8 |
| YPL186C | UIP4 | Protein of unknown function that interacts with Ulp1p, a Ubl (ubiquitin-like protein)-specific protease for Smt3p protein conjugates | 2.8 |
| YNL012W | SPO1 | Meiosis-specific protein with similarity to phospholipase B, required for meiotic spindle pole body duplication and separation; required for spore formation | 2.8 |
| YJL164C | TPK1 | Subunit of cytoplasmic cAMP-dependent protein kinase, which contains redundant catalytic subunits Tpk1p, Tpk2p, and Tpk3p and regulatory subunit | 2.8 |
| YJL020C | BBC1 | 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 | 2.8 |
| YJL149W | | Putative SCF ubiquitin ligase F-box protein of unknown function; interacts physically with both Cdc53p and Skp1 and genetically with CDC34; similar to | 2.8 |
| YMR140W | SIP5 | Protein of unknown function; interacts with both the Reg1p/Glc7p phosphatase and the Snf1p kinase | 2.8 |
| YER144C | UBP5 | Putative ubiquitin-specific protease that does not associate with the proteasome | 2.7 |
| YDR255C | RMD5 | Cytosolic protein required for sporulation; also required for the ubiquitination of the gluconeogenic enzyme fructose-1,6-bisphosphatase, which is degraded | 2.7 |
| YDL024C | DIA3 | Protein of unknown function, involved in invasive and pseudohyphal growth | 2.7 |
| YPR078C | | Hypothetical protein | 2.7 |
| YOL048C | | Hypothetical protein | 2.7 |
| YDR222W | | Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern | 2.7 |
| YAL062W | GDH3 | NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs | 2.7 |
| YOL107W | | Hypothetical protein | 2.7 |
| YMR170C | ALD2 | Cytoplasmic aldehyde dehydrogenase, involved in ethanol oxidation and beta-alanine biosynthesis; uses NAD+ as the preferred coenzyme; expression is | 2.7 |
| YBR108W | | Protein interacting with Rsv167p | 2.7 |
| YAR027W | UIP3 | Putative integral membrane protein of unknown function; interacts with Ulp1p at the nuclear periphery; member of DUP240 gene family | 2.7 |
| YGR010C | ADY2 | Acetate transporter required for normal sporulation | 2.7 |
| YER103W | SSA4 | Heat shock protein that is highly induced upon stress; plays a role in SRP-dependent cotranslational protein-membrane targeting and translocation; | 2.7 |
| YLR099W-A | | Putative protein of unknown function | 2.7 |
| YDR435C | PPM1 | Carboxyl methyl transferase, methylates the C terminus of the protein phosphatase 2A catalytic subunit (Pph21p or Pph22p), which is important for | 2.7 |
| YKR013W | PRY2 | Protein of unknown function, has similarity to Pry1p and Pry3p and to the plant PR-1 class of pathogen related proteins | 2.7 |
| YAL053W | FLC2 | Putative FAD transporter; required for uptake of FAD into endoplasmic reticulum; involved in cell wall maintenance | 2.7 |
| YFL059W | SNZ3 | 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- | 2.7 |
| YDL057W | | Putative protein of unknown function; YDL057W is not an essential gene | 2.7 |

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| YOR394W | | Hypothetical protein /// Hypothetical protein | 2.7 |
| YNL015W | PBI2 | Cytosolic inhibitor of vacuolar proteinase B, required for efficient vacuole inheritance; with thioredoxin forms protein complex LMA1, which assists in | 2.7 |
| YJL103C | | Putative zinc cluster protein of unknown function; computationally predicted involvement in oxidative phosphorylation, based on patterns of expression and | 2.7 |
| YKR011C | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus | 2.7 |
| YMR303C | ADH2 | Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate | 2.7 |
| YDL085W | NDE2 | Mitochondrial external NADH dehydrogenase, catalyzes the oxidation of cytosolic NADH; Nde1p and Nde2p are involved in providing the cytosolic | 2.7 |
| YNL024C | | Putative protein of unknown function with seven beta-strand methyltransferase motif; green fluorescent protein (GFP)-fusion protein localizes to the | 2.7 |
| YLR270W | DCS1 | Non-essential hydrolase involved in mRNA decapping, may function in a feedback mechanism to regulate deadenylation, contains pyrophosphatase | 2.7 |
| YDL027C | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondrion; YDL027C is not an essential gene | 2.6 |
| YIL117C | PRM5 | Pheromone-regulated protein, predicted to have 1 transmembrane segment; induced during cell integrity signaling | 2.6 |
| YPL123C | RNY1 | RNAse; member of the T(2) family of endoribonucleases | 2.6 |
| YPL166W | ATG29 | Protein specifically required for autophagy; may function in autophagosome formation at the pre-autophagosomal structure in collaboration with other | 2.6 |
| YDR317W | HIM1 | Protein of unknown function involved in DNA repair | 2.6 |
| YIL108W | | Putative metalloprotease | 2.6 |
| YPL222W | | The authentic, non-tagged protein was localized to the mitochondria. | 2.6 |
| YJR008W | | Putative protein of unknown function; expression repressed by inosine and choline in an Opi1p-dependent manner; expression induced by mild heat-stress | 2.6 |
| YGR019W | UGA1 | Gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase) involved in the 4-aminobutyrate and glutamate degradation | 2.6 |
| YER019W | ISC1 | Inositol phosphosphingolipid phospholipase C, hydrolyzes inositolphosphosphingolipids, activated by phosphatidylserine, cardiolipin, and | 2.6 |
| YDR275W | BSC2 | Protein of unknown function, ORF exhibits genomic organization compatible with a translational readthrough-dependent mode of expression | 2.6 |
| YPR198W | SGE1 | Membrane-associated multidrug transporter, acts as an extrusion permease, member of the drug-resistance protein family within the major facilitator | 2.6 |
| YHR075C | PPE1 | Protein with carboxyl methyl esterase activity that may have a role in demethylation of the phosphoprotein phosphatase catalytic subunit; also | 2.6 |
| YKL126W | YPK1 | Serine/threonine protein kinase required for receptor-mediated endocytosis; involved in sphingolipid-mediated and cell integrity signaling pathways; | 2.6 |
| YOR035C | SHE4 | Protein containing a UCS (UNC-45/CRO1/SHE4) domain, binds to myosin motor domains to regulate myosin function; involved in endocytosis, | 2.6 |
| YML054C | CYB2 | Cytochrome b2 (L-lactate cytochrome-c oxidoreductase), component of the mitochondrial intermembrane space, required for lactate utilization; expression | 2.6 |
| YBR045C | GIP1 | Meiosis-specific regulatory subunit of the Glc7p protein phosphatase, regulates spore wall formation and septin organization, required for expression of some | 2.6 |
| YKL091C | | Putative homolog of Sec14p, which is a phosphatidylinositol/phosphatidylcholine transfer protein involved in lipid | 2.6 |
| YPL067C | | Hypothetical protein | 2.6 |
| YKL142W | MRP8 | Putative mitochondrial ribosomal protein, has similarity to E. coli ribosomal protein S2 | 2.6 |

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| YNL014W | HEF3 | Translational elongation factor EF-3; paralog of YEF3 and member of the ABC superfamily; stimulates EF-1 alpha-dependent binding of aminoacyl-tRNA by | 2.6 |
| YJR079W | | Putative protein of unknown function; mutation results in impaired mitochondrial respiration | 2.5 |
| YGL259W | YPS5 | Protein with similarity to GPI-anchored aspartic proteases such as Yap1p and Yap3p | 2.5 |
| YNR010W | CSE2 | Component of the Med9/10 module, which is a subcomplex within the RNA polymerase II Mediator complex; required for regulation of RNA polymerase II | 2.5 |
| YJL045W | | Minor succinate dehydrogenase isozyme; homologous to Sdh1p, the major isozyme responsible for the oxidation of succinate and transfer of electrons to | 2.5 |
| YLR214W | FRE1 | Ferric reductase and cupric reductase, reduces siderophore-bound iron and oxidized copper prior to uptake by transporters; expression induced by low | 2.5 |
| YPL171C | OYE3 | Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN), homologous to Oye2p with slight differences in ligand binding and | 2.5 |
| YDR030C | RAD28 | Protein involved in transcription-coupled repair nucleotide excision repair of UV-induced DNA lesions; homolog of human CSA protein | 2.5 |
| YFL040W | | Putative protein of unknown function; YFL040W is not an essential gene | 2.5 |
| YGL051W | MST27 | Putative integral membrane protein, involved in vesicle formation; forms complex with Mst28p; member of DUP240 gene family; binds COPI and COPII | 2.5 |
| YDL239C | ADY3 | Protein required for spore wall formation, thought to mediate assembly of a Don1p-containing structure at the leading edge of the prospore membrane via | 2.5 |
| YPR154W | PIN3 | Protein that induces appearance of [PIN+] prion when overproduced | 2.5 |
| YLR417W | VPS36 | Component of the ESCRT-II complex; contains the GLUE (GRAM Like Ubiquitin binding in EAP45) domain which is involved in interactions with | 2.5 |
| YPR081C | GRS2 | Protein with sequence similarity to Grs1p, which is a glycyl-tRNA synthetase; cannot substitute for Grs1p; possible pseudogene that is expressed at very low | 2.5 |
| YPR030W | CSR2 | Nuclear protein with a potential regulatory role in utilization of galactose and nonfermentable carbon sources; overproduction suppresses the lethality at | 2.5 |
| YGL038C | OCH1 | Mannosyltransferase of the cis-Golgi apparatus, initiates the polymannose outer chain elongation of N-linked oligosaccharides of glycoproteins | 2.5 |
| YCR083W | TRX3 | Mitochondrial thioredoxin, highly conserved oxidoreductase required to maintain the redox homeostasis of the cell, forms the mitochondrial thioredoxin | 2.5 |
| YKL103C | LAP4 | Vacuolar aminopeptidase, often used as a marker protein in studies of autophagy and cytosol to vacuole targeting (CVT) pathway | 2.5 |
| YMR087W | | Putative ADP-ribose-1"-monophosphatase that converts ADP-ribose-1"-monophosphate to ADP-ribose; may have a role in tRNA splicing; contains an | 2.5 |
| YDL238C | GUD1 | Guanine deaminase, a catabolic enzyme of the guanine salvage pathway producing xanthine and ammonia from guanine; activity is low in exponentially- | 2.4 |
| YMR090W | | Putative protein of unknown function with similarity to DTDP-glucose 4,6-dehydratases; green fluorescent protein (GFP)-fusion protein localizes to the | 2.4 |
| YLR271W | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus; YLR271W is not an | 2.4 |
| YDR285W | ZIP1 | Transverse filament protein of the synaptonemal complex; required for normal levels of meiotic recombination and pairing between homologous chromosome | 2.4 |
| YLR241W | | Hypothetical protein | 2.4 |
| YLR213C | CRR1 | Putative glycoside hydrolase of the spore wall envelope; required for normal spore wall assembly, possibly for cross-linking between the glucan and | 2.4 |
| YDR077W | SED1 | Major stress-induced structural GPI-cell wall glycoprotein in stationary-phase cells, associates with translating ribosomes, possible role in mitochondrial | 2.4 |
| YJL094C | KHA1 | Putative K ⁺ /H ⁺ antiporter | 2.4 |
| YLR307C-A | | Putative protein of unknown function | 2.4 |

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| YLR094C | GIS3 | Protein of unknown function | 2.4 |
| YDR218C | SPR28 | Sporulation-specific homolog of the yeast CDC3/10/11/12 family of bud neck microfilament genes; meiotic septin expressed at high levels during meiotic | 2.4 |
| YER169W | RPH1 | Transcriptional repressor of PHR1, which is a photolyase induced by DNA damage; binds to AG(4) (C(4)T) sequence upstream of PHR1; Rph1p | 2.4 |
| YML130C | ERO1 | Glycoprotein required for oxidative protein folding in the endoplasmic reticulum | 2.4 |
| YGL242C | | Putative protein of unknown function; deletion mutant is viable | 2.4 |
| YAL028W | FRT2 | Tail-anchored endoplasmic reticulum membrane protein, interacts with homolog Frt1p but is not a substrate of calcineurin (unlike Frt1p), promotes | 2.4 |
| YGL037C | PNC1 | Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; | 2.4 |
| YNL157W | | Hypothetical protein | 2.4 |
| YIR038C | GTT1 | ER associated glutathione S-transferase capable of homodimerization; expression induced during the diauxic shift and throughout stationary phase; | 2.4 |
| YKR097W | PCK1 | Phosphoenolpyruvate carboxykinase, key enzyme in gluconeogenesis, catalyzes early reaction in carbohydrate biosynthesis, glucose represses | 2.4 |
| YKL129C | MYO3 | 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 | 2.4 |
| YMR009W | ADI1 | Acireductone dioxygenase involved in the methionine salvage pathway; ortholog of human MTCBP-1; transcribed with YMR010W and regulated post- | 2.4 |
| YGL249W | ZIP2 | Meiosis-specific protein involved in normal synaptonemal complex formation and pairing between homologous chromosomes during meiosis | 2.4 |
| YLR345W | | Similar to 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase enzymes responsible for the metabolism of fructoso-2,6-bisphosphate; mRNA | 2.4 |
| YCL033C | | Putative protein-methionine-R-oxide reductase; involved in response to oxidative stress; similar to mouse Sepx1p and fly SelRp; YCL033C is not an | 2.4 |
| YML042W | CAT2 | Carnitine acetyl-CoA transferase present in both mitochondria and peroxisomes, transfers activated acetyl groups to carnitine to form | 2.4 |
| YDR122W | KIN1 | Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; closely related to Kin2p | 2.4 |
| YFL020C | PAU5 | Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by | 2.4 |
| YFL012W | | Putative protein of unknown function; transcribed during sporulation; null mutant exhibits increased resistance to rapamycin | 2.3 |
| YMR258C | | Protein of unknown function with similarity to F-box proteins; physically interacts with Skp1p; green fluorescent protein (GFP)-fusion protein localizes | 2.3 |
| YNL165W | | Hypothetical protein | 2.3 |
| YDR486C | VPS60 | Cytoplasmic and vacuolar membrane protein involved in late endosome to vacuole transport; required for normal filament maturation during pseudohyphal | 2.3 |
| YDR436W | PPZ2 | Serine/threonine protein phosphatase Z, isoform of Ppz1p; involved in regulation of potassium transport, which affects osmotic stability, cell cycle | 2.3 |
| YMR114C | | Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus and cytoplasm; YMR114C is not an essential gene | 2.3 |
| YOL082W | ATG19 | Protein involved in the cytoplasm-to-vacuole targeting pathway and in autophagy, recognizes cargo proteins and delivers them to the | 2.3 |
| YNL305C | | Hypothetical protein | 2.3 |
| YGL045W | RIM8 | Protein of unknown function, involved in the proteolytic activation of Rim101p in response to alkaline pH; has similarity to A. nidulans PalF | 2.3 |
| YDL243C | AAD4 | Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase, involved in the oxidative stress response | 2.3 |

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|---------|-------|---|-----|
| YEL020C | | Hypothetical protein with low sequence identity to Pdc1p | 2.3 |
| YDL010W | | Putative thiol-disulfide oxidoreductase; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; YDL010W is not an essential gene | 2.3 |
| YOR275C | RIM20 | Protein involved in proteolytic activation of Rim101p in response to alkaline pH; member of the PalA/AIP1/Alix family; interacts with the ESCRT-III subunits | 2.3 |
| YIL017C | VID28 | Protein involved in proteasome-dependent catabolite degradation of fructose-1,6-bisphosphatase (FBPase); localized to the nucleus and the cytoplasm | 2.3 |
| YLR216C | CPR6 | Peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; binds to Hsp82p | 2.3 |
| YHR104W | GRE3 | Aldose reductase involved in methylglyoxal, d-xylose and arabinose metabolism; stress induced (osmotic, ionic, oxidative, heat shock, starvation) | 2.3 |
| YBR269C | | The authentic, non-tagged protein was localized to the mitochondria | 2.3 |
| YIL010W | DOT5 | Nuclear thiol peroxidase which functions as an alkyl-hydroperoxide reductase during post-diauxic growth | 2.3 |
| YJL165C | HAL5 | Putative protein kinase; overexpression increases sodium and lithium tolerance, whereas gene disruption increases cation and low pH sensitivity and | 2.3 |
| YMR165C | PAH1 | Mg ²⁺ -dependent phosphatidate (PA) phosphatase, catalyzes the dephosphorylation of PA to yield diacylglycerol and Pi, responsible for de novo | 2.3 |
| YDR059C | UBC5 | Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins, central component of the cellular stress response; | 2.3 |
| YDR403W | DIT1 | Sporulation-specific enzyme required for spore wall maturation, involved in the production of a soluble LL-dityrosine-containing precursor of the spore wall; | 2.3 |
| YNL020C | ARK1 | Serine/threonine protein kinase involved in regulation of the cortical actin cytoskeleton; involved in control of endocytosis | 2.3 |
| YOR389W | | Hypothetical protein | 2.3 |
| YHR004C | NEM1 | Protein of the nuclear envelope required for the spherical shape of the nucleus; required for normal sporulation | 2.3 |
| YIL073C | SPO22 | Meiosis-specific protein with similarity to phospholipase A2, involved in completion of nuclear divisions during meiosis; induced early in meiosis | 2.3 |
| YPR134W | MSS18 | Nuclear encoded protein needed for efficient splicing of mitochondrial COX1 a15beta intron; mss18 mutations block cleavage of 5' exon - intron junction; | 2.3 |
| YPL154C | PEP4 | Vacuolar aspartyl protease (proteinase A), required for the posttranslational precursor maturation of vacuolar proteinases; synthesized as a zymogen, self- | 2.3 |
| YER130C | | Hypothetical protein | 2.3 |
| YPL110C | GDE1 | Major cellular glycerophosphocholine (GroPCho) phosphodiesterase; hydrolyzes GroPCho to choline and glycerolphosphate after its uptake by Git1p | 2.3 |
| YOL032W | OPI10 | Protein with a possible role in phospholipid biosynthesis, based on inositol-excreting phenotype of the null mutant and its suppression by exogenous | 2.3 |
| YOR177C | MPC54 | Component of the meiotic outer plaque, a membrane-organizing center which is assembled on the cytoplasmic face of the spindle pole body during meiosis II | 2.3 |
| YLR350W | ORM2 | Evolutionarily conserved protein with similarity to Orm1p, required for resistance to agents that induce the unfolded protein response; human | 2.3 |
| YGL227W | VID30 | Protein involved in proteasome-dependent catabolite degradation of fructose-1,6-bisphosphatase (FBPase); shifts the balance of nitrogen metabolism | 2.3 |
| YJL036W | SNX4 | Sorting nexin, involved in the retrieval of late-Golgi SNAREs from the post-Golgi endosome to the trans-Golgi network and in cytoplasm to vacuole | 2.3 |
| YOR162C | YRR1 | Zn ²⁺ -Cys ⁶ zinc-finger transcription factor that activates genes involved in multidrug resistance; paralog of Yrm1p, acting on an overlapping set of target | 2.3 |
| YOR062C | | Protein of unknown function; similar to YKR075Cp and Reg1p; expression regulated by glucose and Rgt1p | 2.3 |
| YGR057C | LST7 | Protein possibly involved in a post-Golgi secretory pathway; required for the transport of nitrogen-regulated amino acid permease Gap1p from the Golgi to | 2.3 |

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| YFL044C | OTU1 | Deubiquitylation enzyme that binds to the chaperone-ATPase Cdc48p; may contribute to regulation of protein degradation by deubiquitylating substrates | 2.3 |
| YMR105W-A | | Putative protein of unknown function | 2.3 |
| YML057W | CMP2 | Calcineurin A; one isoform (the other is CNA1) of the catalytic subunit of calcineurin, a Ca ⁺⁺ /calmodulin-regulated protein phosphatase which regulates | 2.3 |
| YAL034C | FUN19 | Non-essential protein of unknown function | 2.3 |
| YOR274W | MOD5 | Delta 2-isopentenyl pyrophosphate:tRNA isopentenyl transferase, required for biosynthesis of the modified base isopentenyladenosine in mitochondrial and | 2.3 |
| YPL167C | REV3 | Catalytic subunit of DNA polymerase zeta, which is involved in DNA repair and translesion synthesis; required for mutagenesis induced by DNA damage | 2.3 |
| YKL150W | MCR1 | Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis | 2.2 |
| YER143W | DDI1 | DNA damage-inducible v-SNARE binding protein, contains a ubiquitin-associated (UBA) domain, may act as a negative regulator of constitutive | 2.2 |
| YML131W | | Putative protein of unknown function with similarity to oxidoreductases; mRNA expression is increased in a HOG1 and SKO1-dependent manner after osmotic | 2.2 |
| YEL012W | UBC8 | Ubiquitin-conjugating enzyme that negatively regulates gluconeogenesis by mediating the glucose-induced ubiquitination of fructose-1,6-bisphosphatase | 2.2 |
| YNL134C | | Putative protein of unknown function with similarity to dehydrogenases from other model organisms; green fluorescent protein (GFP)-fusion protein | 2.2 |
| YGR036C | CAX4 | Dolichyl pyrophosphate (Dol-P-P) phosphatase with a lumenally oriented active site in the ER, cleaves the anhydride linkage in Dol-P-P, required for Dol-P-P- | 2.2 |
| YMR095C | SNO1 | Protein of unconfirmed function, involved in pyridoxine metabolism; expression is induced during stationary phase; forms a putative glutamine | 2.2 |
| YBR006W | UGA2 | Succinate semialdehyde dehydrogenase involved in the utilization of gamma-aminobutyrate (GABA) as a nitrogen source; part of the 4-aminobutyrate and | 2.2 |
| YHR105W | YPT35 | Endosomal protein of unknown function that contains a phox (PX) homology domain and binds to both phosphatidylinositol-3-phosphate (PtdIns(3)P) and | 2.2 |
| YJR151C | DAN4 | Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p, and Tir4p; expressed under anaerobic conditions, completely repressed during aerobic | 2.2 |
| YPL249C | GYP5 | GTPase-activating protein (GAP) for yeast Rab family members, involved in ER to Golgi trafficking; exhibits GAP activity toward Ypt1p that is stimulated by | 2.2 |
| YLR337C | VRP1 | Proline-rich actin-associated protein involved in cytoskeletal organization and cytokinesis; related to mammalian Wiskott-Aldrich syndrome protein (WASP)- | 2.2 |
| YML070W | DAK1 | Dihydroxyacetone kinase, required for detoxification of dihydroxyacetone (DHA); involved in stress adaptation | 2.2 |
| YAL010C | MDM10 | Subunit of the mitochondrial sorting and assembly machinery (SAM complex); has a role in assembly of the TOM complex, which mediates protein import | 2.2 |
| YHR016C | YSC84 | Protein involved in the organization of the actin cytoskeleton; contains SH3 domain similar to Rvs167p | 2.2 |
| YMR304W | UBP15 | Ubiquitin-specific protease that may play a role in ubiquitin precursor processing | 2.2 |
| YOR018W | ROD1 | Membrane protein; overexpression confers resistance to the GST substrate o-dinitrobenzene as well as to zinc and calcium; contains 2 PY motifs, which are | 2.2 |
| YLR225C | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YLR225C is not an essential gene | 2.2 |
| YPL087W | YDC1 | Alkaline dihydroceramidase, involved in sphingolipid metabolism; preferentially hydrolyzes dihydroceramide to a free fatty acid and dihydrosphingosine; has a | 2.2 |
| YLR047C | FRE8 | Protein with sequence similarity to iron/copper reductases, involved in iron homeostasis; deletion mutant has iron deficiency/accumulation growth defects; | 2.2 |
| YOL132W | GAS4 | Putative 1,3-beta-glucanosyltransferase, has similarity to Gas1p; localizes to the cell wall | 2.2 |
| YOR175C | | Member of the MBOAT family of putative membrane-bound O-acyltransferases | 2.2 |

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| YOL104C | NDJ1 | Meiosis-specific telomere protein, required for bouquet formation, effective homolog pairing, ordered cross-over distribution (interference), sister chromatid | 2.2 |
| YPR127W | | Hypothetical protein | 2.2 |
| YFL057C | AAD16 | alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role | 2.2 |
| YDL072C | YET3 | Endoplasmic reticulum transmembrane protein, homolog of human BAP31 protein | 2.2 |
| YER015W | FAA2 | Long chain fatty acyl-CoA synthetase; accepts a wider range of acyl chain lengths than Faa1p, preferring C9:0-C13:0; involved in the activation of | 2.2 |
| YBR170C | NPL4 | Endoplasmic reticulum and nuclear membrane protein, forms a complex with Cdc48p and Ufd1p that recognizes ubiquitinated proteins in the endoplasmic | 2.2 |
| YGL056C | SDS23 | One of two <i>S. cerevisiae</i> homologs (Sds23p and Sds24p) of the <i>Schizosaccharomyces pombe</i> Sds23 protein, which genetic studies have | 2.2 |
| YGR223C | HSV2 | Phosphatidylinositol 3,5-bisphosphate-binding protein, predicted to fold as a seven-bladed beta-propeller; displays punctate cytoplasmic localization | 2.1 |
| YOR020W-A | | Identified by homology to <i>Ashbya gossypii</i> | 2.1 |
| YER142C | MAG1 | 3-methyl-adenine DNA glycosylase involved in protecting DNA against alkylating agents; initiates base excision repair by removing damaged bases to | 2.1 |
| YCL035C | GRX1 | Hydroperoxide and superoxide-radical responsive heat-stable glutathione-dependent disulfide oxidoreductase with active site cysteine pair; protects cells | 2.1 |
| YJR106W | ECM27 | Non-essential protein of unknown function | 2.1 |
| YPR026W | ATH1 | Acid trehalase required for utilization of extracellular trehalose | 2.1 |
| YOL087C | | Hypothetical protein | 2.1 |
| YDR490C | PKH1 | Serine/threonine protein kinase involved in sphingolipid-mediated signaling pathway that controls endocytosis; activates Ypk1p and Ykr2p, components of | 2.1 |
| YGL144C | ROG1 | Protein with putative serine active lipase domain | 2.1 |
| YOL071W | EMI5 | Non-essential protein of unknown function required for transcriptional induction of the early meiotic-specific transcription factor IME1, also required for | 2.1 |
| YOL013C | HRD1 | Ubiquitin-protein ligase required for endoplasmic reticulum-associated degradation (ERAD) of misfolded proteins; genetically linked to the unfolded | 2.1 |
| YKL133C | | Hypothetical protein | 2.1 |
| YPL163C | SVS1 | Cell wall and vacuolar protein, required for wild-type resistance to vanadate | 2.1 |
| YDR530C | APA2 | Diadenosine 5',5''-P1,P4-tetraphosphate phosphorylase II (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; | 2.1 |
| YLR438W | CAR2 | L-ornithine transaminase (OTase), catalyzes the second step of arginine degradation, expression is dually-regulated by allophanate induction and a | 2.1 |
| YHL002W | HSE1 | Subunit of the endosomal Vps27p-Hse1p complex required for sorting of ubiquitinated membrane proteins into intraluminal vesicles prior to vacuolar | 2.1 |
| YKL037W | | Putative protein of unknown function | 2.1 |
| YOR347C | PYK2 | Pyruvate kinase that appears to be modulated by phosphorylation; PYK2 transcription is repressed by glucose, and Pyk2p may be active under low | 2.1 |
| YMR238W | DFG5 | Putative mannosidase, essential glycosylphosphatidylinositol (GPI)-anchored membrane protein required for cell wall biogenesis in bud formation, involved in | 2.1 |
| YER163C | | Hypothetical protein | 2.1 |
| YOL018C | TLG2 | Syntaxin-like t-SNARE that forms a complex with Tlg1p and Vti1p and mediates fusion of endosome-derived vesicles with the late Golgi; binds | 2.1 |

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| YPL119C-A | | Identified by expression profiling and mass spectrometry | 2.1 |
| YNL195C | | Hypothetical protein | 2.1 |
| YDR123C | INO2 | Component of the heteromeric Ino2p/Ino4p basic helix-loop-helix transcription activator that binds inositol/choline-responsive elements (ICREs), required for | 2.1 |
| YJL171C | | GPI-anchored cell wall protein of unknown function; induced in response to cell wall damaging agents and by mutations in genes involved in cell wall | 2.1 |
| YKL007W | CAP1 | Alpha subunit of the capping protein (CP) heterodimer (Cap1p and Cap2p) which binds to the barbed ends of actin filaments preventing further | 2.1 |
| YBR223C | TDP1 | Tyrosyl-DNA Phosphodiesterase I, hydrolyzes 3'-phosphotyrosyl bonds to generate 3'-phosphate DNA and tyrosine, involved in the repair of DNA lesions | 2.1 |
| YLR257W | | Hypothetical protein | 2.1 |
| YIL107C | PFK26 | 6-phosphofructo-2-kinase, inhibited by phosphoenolpyruvate and sn-glycerol 3-phosphate, has negligible fructose-2,6-bisphosphatase activity, transcriptional | 2.1 |
| YIL065C | FIS1 | Mitochondrial outer membrane protein involved in membrane fission, required for localization of Dnm1p and Mdv1p during mitochondrial division | 2.1 |
| YOL055C | THI20 | Hydroxymethylpyrimidine phosphate kinase, involved in the last steps in thiamine biosynthesis; member of a gene family with THI21 and THI22; | 2.1 |
| YJL016W | | Putative protein of unknown function; GFP-fusion protein localizes to the cytoplasm; conserved in closely related Saccharomyces species | 2.1 |
| YLR362W | STE11 | Signal transducing MEK kinase involved in pheromone response and pseudohyphal/invasive growth pathways where it phosphorylates Ste7p, and | 2.1 |
| YFR012W-A | | Putative protein of unknown function; identified by homology | 2.1 |
| YPL017C | | Putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family; null mutant displays increased levels of spontaneous Rad52 foci | 2.1 |
| YHR015W | MIP6 | Putative RNA-binding protein, interacts with Mex67p, which is a component of the nuclear pore involved in nuclear mRNA export | 2.1 |
| YDL206W | | Hypothetical protein | 2.1 |
| YCR036W | RBK1 | Putative ribokinase | 2.1 |
| YPL119C | DBP1 | Putative ATP-dependent RNA helicase of the DEAD-box protein family; mutants show reduced stability of the 40S ribosomal subunit scanning through | 2.1 |
| YKL064W | MNR2 | Putative magnesium transporter; has similarity to Alr1p and Alr2p, which mediate influx of Mg ²⁺ and other divalent cations | 2.1 |
| YOL015W | | Hypothetical protein; null mutant displays increased levels of spontaneous Rad52 foci | 2.1 |
| YDR107C | | multispanning membrane protein | 2.1 |
| YOR153W | PDR5 | Short-lived membrane ABC (ATP-binding cassette) transporter, actively exports various drugs, expression regulated by Pdr1p; also involved in steroid | 2.1 |
| YFL056C | AAD6 | Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase, involved in the oxidative stress response | 2.0 |
| YMR110C | HFD1 | Putative fatty aldehyde dehydrogenase, located in the mitochondrial outer membrane and also in lipid particles; has similarity to human fatty aldehyde | 2.0 |
| YPL057C | SUR1 | Probable catalytic subunit of a mannosylinositol phosphorylceramide (MIPC) synthase, forms a complex with probable regulatory subunit Csg2p; function in | 2.0 |
| YGR295C | COS6 | Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins | 2.0 |
| YML007C-A | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to mitochondria | 2.0 |
| YPR172W | | Protein of unknown function, transcriptionally activated by Yrm1p along with genes involved in multidrug resistance | 2.0 |

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| YNL003C | PET8 | S-adenosylmethionine transporter of the mitochondrial inner membrane, member of the mitochondrial carrier family; required for biotin biosynthesis and | 2.0 |
| YKL051W | SFK1 | Plasma membrane protein that may act together with or upstream of Stt4p to generate normal levels of the essential phospholipid PI4P, at least partially | 2.0 |
| YFL062W | COS4 | Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins | 2.0 |
| YDR406W | PDR15 | ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, | 2.0 |
| YLR361C-A | | Putative protein of unknown function | 2.0 |
| YGR287C | | Putative protein of unknown function; similarity to alpha-D-glucosidase (maltase); localizes to the mitochondrion | 2.0 |
| YOR052C | | Hypothetical protein | 2.0 |
| YJL185C | | Putative protein of unknown function; mRNA is weakly cell cycle regulated, peaking in G2 phase; YJL185C is a non-essential gene | 2.0 |
| YML002W | | Hypothetical protein | 2.0 |
| YLR093C | NYV1 | v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the | 2.0 |
| YGR141W | VPS62 | Vacuolar protein sorting (VPS) protein required for cytoplasm to vacuole targeting of proteins | 2.0 |
| YDR216W | ADR1 | Carbon source-responsive zinc-finger transcription factor, required for transcription of the glucose-repressed gene ADH2, of peroxisomal protein | 2.0 |
| YPL203W | TPK2 | Subunit of cytoplasmic cAMP-dependent protein kinase, which contains redundant catalytic subunits Tpk1p, Tpk2p, and Tpk3p and regulatory subunit | 2.0 |
| YGL180W | ATG1 | Protein serine/threonine kinase, required for autophagy and for the cytoplasm-to-vacuole targeting (Cvt) pathway | 2.0 |
| YLR024C | UBR2 | Cytoplasmic ubiquitin-protein ligase (E3) | 2.0 |
| YMR271C | URA10 | One of two orotate phosphoribosyltransferase isozymes (see also URA5) that catalyze the fifth enzymatic step in the de novo biosynthesis of pyrimidines, | 2.0 |
| YKL188C | PXA2 | Subunit of a heterodimeric peroxisomal ATP-binding cassette transporter complex (Pxa1p-Pxa2p), required for import of long-chain fatty acids into | 2.0 |
| YMR119W | ASI1 | Putative integral membrane E3 ubiquitin ligase; genetic interactions suggest a role in negative regulation of amino acid uptake | 2.0 |
| YGR028W | MSP1 | Mitochondrial protein involved in sorting of proteins in the mitochondria; putative membrane-spanning ATPase | 2.0 |
| YPL179W | PPQ1 | Putative protein serine/threonine phosphatase; null mutation enhances efficiency of translational suppressors | 2.0 |
| YOR005C | DNL4 | DNA ligase required for nonhomologous end-joining (NHEJ), forms stable heterodimer with required cofactor Lif1p, catalyzes DNA ligation as part of a | 2.0 |
| YBL039W-A | | Putative protein of unknown function | 2.0 |
| YOR176W | HEM15 | Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of ferrous iron into protoporphyrin IX, the eighth and final step in the | 2.0 |
| YBR126C | TPS1 | Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a | 2.0 |
| YGR127W | | Hypothetical protein | 2.0 |
| YKR009C | FOX2 | Multifunctional enzyme of the peroxisomal fatty acid beta-oxidation pathway; has 3-hydroxyacyl-CoA dehydrogenase and enoyl-CoA hydratase activities | 2.0 |
| YDL214C | PRR2 | Protein kinase with a possible role in MAP kinase signaling in the pheromone response pathway | 2.0 |
| YBL005W-A | | Retrotransposon TYA Gag gene co-transcribed with TYB Pol; translated as TYA or TYA-TYB polyprotein; Gag is a nucleocapsid protein that is the | 2.0 |

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| YCR091W | KIN82 | Putative serine/threonine protein kinase, most similar to cyclic nucleotide-dependent protein kinase subfamily and the protein kinase C subfamily | 2.0 |
| YBR230C | OM14 | Integral mitochondrial outer membrane protein; abundance is decreased in cells grown in glucose relative to other carbon sources; appears to contain 3 | 2.0 |
| YFR003C | YPI1 | Inhibitor of the type I protein phosphatase Glc7p, which is involved in regulation of a variety of metabolic processes; overproduction causes decreased cellular | 2.0 |
| YOL011W | PLB3 | Phospholipase B (lysophospholipase) involved in phospholipid metabolism; hydrolyzes phosphatidylinositol and phosphatidylserine and displays | 2.0 |
| YPL277C | | Hypothetical protein /// Hypothetical protein | 2.0 |
| YCR014C | POL4 | DNA polymerase IV, undergoes pair-wise interactions with Dnl4p-Lif1p and Rad27p to mediate repair of DNA double-strand breaks by non-homologous | 2.0 |
| YDR003W | RCR2 | Probable integral membrane protein with similarity to Rcr1p; C-terminal region can functionally replace the corresponding region of Rcr1p in conferring Congo | 2.0 |
| YHR161C | YAP1801 | Protein involved in clathrin cage assembly; binds Pan1p and clathrin; homologous to Yap1802p, member of the AP180 protein family | 2.0 |
| YKL144C | RPC25 | RNA polymerase III subunit C25 | -2.0 |
| YCR084C | TUP1 | General repressor of transcription, forms complex with Cyc8p, involved in the establishment of repressive chromatin structure through interactions with | -2.0 |
| YCR075C | ERS1 | Protein with similarity to human cystinosin, which is a H(+)-driven transporter involved in L-cystine export from lysosomes and implicated in the disease | -2.0 |
| YOL119C | MCH4 | Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma membrane; | -2.0 |
| YPR137W | RRP9 | Protein involved in pre-rRNA processing, associated with U3 snRNP; component of small ribosomal subunit (SSU) processosome; ortholog of the | -2.0 |
| YHR149C | SKG6 | Protein of unknown function; found in the bud tip and bud neck, potential Cdc28p substrate; Skg6p interacts with Zds1p and Zds2p | -2.0 |
| YNL268W | LYP1 | Lysine permease; one of three amino acid permeases (Alp1p, Can1p, Lyp1p) responsible for uptake of cationic amino acids | -2.0 |
| YDL036C | PUS9 | Mitochondrial tRNA pseudouridine synthase involved in pseudouridylation of mitochondrial tRNAs at position 32 | -2.0 |
| YHR197W | RIX1 | Essential protein involved in the processing of the ITS2 region of the rRNA locus; required for the maturation and nuclear export of the 60S ribosomal | -2.0 |
| YDR044W | HEM13 | Coproporphyrinogen III oxidase, an oxygen requiring enzyme that catalyzes the sixth step in the heme biosynthetic pathway; localizes to the mitochondrial | -2.0 |
| YKR081C | RPF2 | Essential protein involved in the processing of pre-rRNA and the assembly of the 60S ribosomal subunit; interacts with ribosomal protein L11; localizes | -2.0 |
| YAL067C | SEO1 | Putative permease, member of the allantoin transporter subfamily of the major facilitator superfamily; mutation confers resistance to ethionine sulfoxide | -2.0 |
| YPL267W | | Protein of unknown function, potential Cdc28p substrate | -2.0 |
| YGR041W | BUD9 | Protein involved in bud-site selection; diploid mutants display a unipolar budding pattern instead of the wild-type bipolar pattern, and bud at the distal | -2.0 |
| YIL118W | RHO3 | Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins involved in the establishment of cell polarity; GTPase activity positively | -2.0 |
| YAR008W | SEN34 | Subunit of the tRNA splicing endonuclease, which is composed of Sen2p, Sen15p, Sen34p, and Sen54p; Sen34p contains the active site for tRNA 3' | -2.0 |
| YBL004W | UTP20 | Component of the small-subunit (SSU) processosome, which is involved in the biogenesis of the 18S rRNA | -2.0 |
| YOL092W | | Hypothetical protein | -2.0 |
| YNL299W | TRF5 | Poly (A) polymerase involved in nuclear RNA quality control based on: homology with Trf4p, genetic interactions with TRF4 mutants, physical | -2.0 |
| YDR120C | TRM1 | tRNA methyltransferase, localizes to both the nucleus and mitochondrion to produce the modified base N2,N2-dimethylguanosine in tRNAs in both | -2.0 |

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| YIL127C | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleolus | -2.0 |
| YPL211W | NIP7 | Nucleolar protein required for 60S ribosome subunit biogenesis, constituent of 66S pre-ribosomal particles; physically interacts with Nop8p and the exosome | -2.0 |
| YCR057C | PWP2 | Conserved 90S pre-ribosomal component essential for proper endonucleolytic cleavage of the 35 S rRNA precursor at A0, A1, and A2 sites; contains eight | -2.0 |
| YDR091C | RLI1 | Essential iron-sulfur protein required for ribosome biogenesis and translation initiation; facilitates binding of a multifactor complex (MFC) of translation | -2.0 |
| YOL149W | DCP1 | Subunit of the Dcp1p-Dcp2p decapping enzyme complex, which removes the 5' cap structure from mRNAs prior to their degradation; enhances the activity of | -2.0 |
| YBL052C | SAS3 | Histone acetyltransferase catalytic subunit of NuA3 complex that acetylates histone H3, involved in transcriptional silencing; homolog of the mammalian | -2.0 |
| YOR337W | TEA1 | Ty1 enhancer activator required for full levels of Ty enhancer-mediated transcription; C6 zinc cluster DNA-binding protein | -2.0 |
| YJL200C | ACO2 | Putative mitochondrial aconitase isozyme; similarity to Aco1p, an aconitase required for the TCA cycle; expression induced during growth on glucose, by | -2.0 |
| YIL020C | HIS6 | Phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase, catalyzes the fourth step in histidine biosynthesis; mutations cause | -2.0 |
| YPL269W | KAR9 | Karyogamy protein required for correct positioning of the mitotic spindle and for orienting cytoplasmic microtubules, localizes at the shmoo tip in mating cells | -2.0 |
| YER148W | SPT15 | TATA-binding protein, general transcription factor that interacts with other factors to form the preinitiation complex at promoters, essential for viability | -2.0 |
| YPL058C | PDR12 | Plasma membrane weak-acid-inducible ATP-binding cassette (ABC) transporter, required for weak organic acid resistance, strongly induced by | -2.0 |
| YFL034C-A | RPL22B | Protein component of the large (60S) ribosomal subunit, has similarity to Rpl22Ap and to rat L22 ribosomal protein | -2.0 |
| YGL012W | ERG4 | C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants are viable, but lack ergosterol | -2.0 |
| YLR348C | DIC1 | Mitochondrial dicarboxylate carrier, integral membrane protein, catalyzes a dicarboxylate-phosphate exchange across the inner mitochondrial membrane, | -2.0 |
| YMR290C | HAS1 | ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S | -2.0 |
| YDR113C | PDS1 | Securin that inhibits anaphase by binding separin Esp1p, also blocks cyclin destruction and mitotic exit, essential for cell cycle arrest in mitosis in the | -2.0 |
| YOR011W | AUS1 | Transporter of the ATP-binding cassette family, involved in uptake of sterols and anaerobic growth | -2.0 |
| YJR109C | CPA2 | Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor | -2.0 |
| YNL216W | RAP1 | DNA-binding protein involved in either activation or repression of transcription, depending on binding site context; also binds telomere sequences and plays a | -2.0 |
| YDR449C | UTP6 | Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA | -2.0 |
| YHR196W | UTP9 | Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA | -2.0 |
| YCL063W | VAC17 | Protein involved in vacuole inheritance; acts as a vacuole-specific receptor for myosin Myo2p | -2.0 |
| YLR008C | PAM18 | Constituent of the mitochondrial import motor associated with the presequence translocase, along with Ssc1p, Tim44p, Mge1p, and Pam16p; stimulates the | -2.1 |
| YLR186W | EMG1 | Protein required for the maturation of the 18S rRNA and for 40S ribosome production; associated with spindle/microtubules; nuclear localization depends | -2.1 |
| YML116W | ATR1 | Multidrug efflux pump of the major facilitator superfamily, required for resistance to aminotriazole and 4-nitroquinoline-N-oxide | -2.1 |
| YFL026W | STE2 | Receptor for alpha-factor pheromone; seven transmembrane-domain GPCR that interacts with both pheromone and a heterotrimeric G protein to initiate the | -2.1 |
| YNL191W | | Hypothetical protein | -2.1 |

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| YKL191W | DPH2 | Protein required, along with Dph1p, Kti11p, Jjj3p, and Dph5p, for synthesis of diphthamide, which is a modified histidine residue of translation elongation | -2.1 |
| YML087C | | Hypothetical protein | -2.1 |
| YBL009W | | haspin | -2.1 |
| YLR413W | | Putative protein of unknown function; YLR413W is not an essential gene | -2.1 |
| YNL180C | RHO5 | Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, likely involved in protein kinase C (Pkc1p)-dependent signal transduction | -2.1 |
| YDL060W | TSR1 | Protein required for processing of 20S pre-rRNA in the cytoplasm, associates with pre-40S ribosomal particles | -2.1 |
| YGR065C | VHT1 | High-affinity plasma membrane H ⁺ -biotin (vitamin H) symporter; mutation results in fatty acid auxotrophy; 12 transmembrane domain containing major | -2.1 |
| YER156C | | Hypothetical protein | -2.1 |
| YMR003W | | Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria; YMR003W is not an essential gene | -2.1 |
| YAL025C | MAK16 | Essential nuclear protein, constituent of 66S pre-ribosomal particles; required for normal concentration of free 60S ribosomal subunits; required for | -2.1 |
| YLR019W | PSR2 | Functionally redundant Psr1p homolog, a plasma membrane phosphatase involved in the general stress response; required with Psr1p and Whi2p for full | -2.1 |
| YBR145W | ADH5 | Alcohol dehydrogenase isoenzyme V; involved in ethanol production | -2.1 |
| YLR304C | ACO1 | Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of | -2.1 |
| YJR112W | NNF1 | Essential component of the MIND kinetochore complex (Mtw1p Including Nnf1p, Nsl1p-Dsn1p) which joins kinetochore subunits contacting DNA to those | -2.1 |
| YMR209C | | Hypothetical protein | -2.1 |
| YCL036W | GFD2 | Protein of unknown function, identified as a high-copy suppressor of a dbp5 mutation | -2.1 |
| YKR058W | GLG1 | Self-glucosylating initiator of glycogen synthesis, also glucosylates n-dodecyl-beta-D-maltoside; similar to mammalian glycogenin | -2.1 |
| YJR124C | | Hypothetical protein | -2.1 |
| YHR049W | FSH1 | Serine hydrolase that localizes to both the nucleus and cytoplasm; sequence is similar to Fsh2p and Fsh3p | -2.1 |
| YOL115W | PAP2 | Catalytic subunit of TRAMP (Trf4/Pap2p-Mtr4p-Air1p/2p), a nuclear poly (A) polymerase complex involved in RNA quality control; catalyzes polyadenylation | -2.1 |
| YNL151C | RPC31 | RNA polymerase III subunit C31; contains HMG-like C-terminal domain | -2.1 |
| YPR009W | SUT2 | Putative transcription factor; multicopy suppressor of mutations that cause low activity of the cAMP/protein kinase A pathway; highly similar to Sut1p | -2.1 |
| YDL205C | HEM3 | Phorphobilinogen deaminase, catalyzes the conversion of 4-porphobilinogen to hydroxymethylbilane, the third step in the heme biosynthetic pathway; localizes | -2.1 |
| YDL170W | UGA3 | Transcriptional activator necessary for gamma-aminobutyrate (GABA)-dependent induction of GABA genes (such as UGA1, UGA2, UGA4); zinc- | -2.1 |
| YMR006C | PLB2 | Phospholipase B (lysophospholipase) involved in phospholipid metabolism; displays transacylase activity in vitro; overproduction confers resistance to | -2.1 |
| YNL301C | RPL18B | Protein component of the large (60S) ribosomal subunit, identical to Rpl18Ap and has similarity to rat L18 ribosomal protein | -2.2 |
| YOR264W | DSE3 | Daughter cell-specific protein, may help establish daughter fate | -2.2 |
| YBR028C | | Hypothetical protein | -2.2 |

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| YOL093W | TRM10 | tRNA methyltransferase, methylates the N-1 position of guanosine in tRNAs | -2.2 |
| YLR437C | | Hypothetical protein | -2.2 |
| YIL074C | SER33 | 3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p | -2.2 |
| YGR125W | | Putative protein of unknown function; deletion mutant has decreased rapamycin resistance but normal wormannin resistance; green fluorescent | -2.2 |
| YLR056W | ERG3 | 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 | -2.2 |
| YER069W | ARG5,6 | Protein that is processed in the mitochondrion to yield acetylglutamate kinase and N-acetyl-gamma-glutamyl-phosphate reductase, which catalyze the 2nd | -2.2 |
| YJL077C | ICS3 | Protein of unknown function | -2.2 |
| YIL162W | SUC2 | Invertase, sucrose hydrolyzing enzyme; a secreted, glycosylated form is regulated by glucose repression, and an intracellular, nonglycosylated enzyme | -2.2 |
| YBR233W-A | DAD3 | Essential subunit of the Dam1 complex (aka DASH complex), couples kinetochores to the force produced by MT depolymerization thereby aiding in | -2.2 |
| YPR157W | | Hypothetical protein | -2.2 |
| YGL201C | MCM6 | Protein involved in DNA replication; component of the Mcm2-7 hexameric complex that binds chromatin as a part of the pre-replicative complex | -2.2 |
| YBR213W | MET8 | Bifunctional dehydrogenase and ferredoxin, involved in the biosynthesis of siroheme; also involved in the expression of PAPS reductase and sulfite | -2.2 |
| YOR302W | | CPA1 uORF , Arginine attenuator peptide, regulates translation of the CPA1 mRNA | -2.2 |
| YCL055W | KAR4 | Transcription factor required for induction of KAR3 and CIK1 during mating, also required during meiosis; exists in two forms, a slower-migrating form more | -2.2 |
| YOR390W | | Hypothetical protein /// Hypothetical protein | -2.3 |
| YDR078C | SHU2 | Protein of unassigned function involved in mutation suppression, important for error-free repair of spontaneous and induced DNA lesions to protect the | -2.3 |
| YFR055W | | Putative cystathionine beta-lyase; involved in copper ion homeostasis and sulfur metabolism; null mutant displays increased levels of spontaneous Rad52 | -2.3 |
| YGR177C | ATF2 | Alcohol acetyltransferase, may play a role in steroid detoxification; forms volatile esters during fermentation, which is important in brewing | -2.3 |
| YOR073W | SGO1 | Component of the spindle checkpoint, involved in sensing lack of tension on mitotic chromosomes; protects centromeric Rec8p at meiosis I; required for | -2.3 |
| YJL134W | LCB3 | Long-chain base-1-phosphate phosphatase, regulates ceramide and long-chain base phosphates levels, involved in incorporation of exogenous long | -2.3 |
| YJL051W | | Bud tip localized protein of unknown function; mRNA is targeted to the bud by a She2p dependent transport system; mRNA is cell cycle regulated via Fkh2p, | -2.3 |
| YMR266W | | Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant | -2.3 |
| YIL132C | CSM2 | Protein required for accurate chromosome segregation during meiosis | -2.3 |
| YOR004W | UTP23 | Essential nucleolar protein that is a component of the SSU (small subunit) processome involved in 40S ribosomal subunit biogenesis; has homology to | -2.3 |
| YOR375C | GDH1 | NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs | -2.3 |
| YGL117W | | Hypothetical protein | -2.3 |
| YMR030W-A | | Putative protein of unknown function | -2.3 |
| YOR342C | | Hypothetical protein | -2.3 |

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| YDR461W | MFA1 | Mating pheromone a-factor, made by a cells; interacts with alpha cells to induce cell cycle arrest and other responses leading to mating; biogenesis | -2.3 |
| YMR189W | GCV2 | P subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels | -2.3 |
| YER070W | RNR1 | Ribonucleotide-diphosphate reductase (RNR), large subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA | -2.3 |
| YGL032C | AGA2 | Adhesion subunit of a-agglutinin of a-cells, C-terminal sequence acts as a ligand for alpha-agglutinin (Sag1p) during agglutination, modified with O-linked | -2.3 |
| YMR015C | ERG5 | 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 | -2.3 |
| YPL241C | CIN2 | Tubulin folding factor C (putative) involved in beta-tubulin (Tub2p) folding; isolated as mutant with increased chromosome loss and sensitivity to benomyl | -2.4 |
| YBL016W | FUS3 | Mitogen-activated protein kinase involved in mating pheromone response; activated by phosphorylation by Ste7p; provides specificity during the mating | -2.4 |
| YLR073C | | Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to endosomes; YLR073C is not an essential gene | -2.4 |
| YLL012W | YEH1 | Steryl ester hydrolase, one of three gene products (Yeh1p, Yeh2p, Tgl1p) responsible for steryl ester hydrolase activity and involved in sterol | -2.4 |
| YEL032W | MCM3 | Protein involved in DNA replication; component of the Mcm2-7 hexameric complex that binds chromatin as a part of the pre-replicative complex | -2.4 |
| YDR207C | UME6 | Key transcriptional regulator of early meiotic genes, binds URS1 upstream regulatory sequence, couples metabolic responses to nutritional cues with | -2.4 |
| YGL101W | | Hypothetical protein | -2.4 |
| YDR528W | HLR1 | Protein involved in regulation of cell wall composition and integrity and response to osmotic stress; overproduction suppresses a lysis sensitive PKC | -2.4 |
| YKL106W | AAT1 | Mitochondrial aspartate aminotransferase, catalyzes the conversion of oxaloacetate to aspartate in aspartate and asparagine biosynthesis | -2.4 |
| YIL121W | QDR2 | Multidrug transporter required for resistance to quinidine, barban, cisplatin, and bleomycin; member of the major facilitator superfamily of transporters | -2.4 |
| YER052C | HOM3 | Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine | -2.4 |
| YKR092C | SRP40 | Nucleolar, serine-rich protein with a role in preribosome assembly or transport; may function as a chaperone of small nucleolar ribonucleoprotein particles | -2.4 |
| YDR089W | | Hypothetical protein | -2.4 |
| YKL120W | OAC1 | Mitochondrial inner membrane transporter, transports oxaloacetate, sulfate, and thiosulfate; member of the mitochondrial carrier family | -2.4 |
| YLL055W | | Putative protein of unknown function with similarity to transporters; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; | -2.4 |
| YOL064C | MET22 | Bisphosphate-3'-nucleotidase, involved in salt tolerance and methionine biogenesis; dephosphorylates 3'-phosphoadenosine-5'-phosphate and 3'- | -2.4 |
| YGR221C | TOS2 | Protein involved in localization of Cdc24p to the site of bud growth; may act as a membrane anchor; localizes to the bud neck and bud tip; potentially | -2.5 |
| YOL012C | HTZ1 | Histone variant H2AZ, exchanged for histone H2A in nucleosomes by the SWR1 complex; involved in transcriptional regulation through prevention of the | -2.5 |
| YDL167C | NRP1 | Protein of unknown function, rich in asparagine residues | -2.5 |
| YJR070C | LIA1 | Deoxyhypusine hydroxylase, a HEAT-repeat containing metalloenzyme that catalyses hypusine formation; binds to and is required for the modification of | -2.5 |
| YOR317W | FAA1 | Long chain fatty acyl-CoA synthetase with a preference for C12:0-C16:0 fatty acids; involved in the activation of imported fatty acids; localized to both lipid | -2.5 |
| YGL125W | MET13 | Isozyme of methylenetetrahydrofolate reductase, catalyzes the reduction of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate in the methionine | -2.5 |
| YPL279C | | Hypothetical protein | -2.5 |

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| YNL112W | DBP2 | Essential ATP-dependent RNA helicase of the DEAD-box protein family, involved in nonsense-mediated mRNA decay and rRNA processing | -2.5 |
| YPL158C | | Hypothetical protein | -2.5 |
| YGR245C | SDA1 | Highly conserved nuclear protein required for actin cytoskeleton organization and passage through Start, plays a critical role in G1 events, binds Nap1p, also | -2.5 |
| YNL111C | CYB5 | Cytochrome b5, involved in the sterol and lipid biosynthesis pathways; required for sterol C5-6 and fatty acid desaturation | -2.5 |
| YOL140W | ARG8 | Acetylmethionine aminotransferase, catalyzes the fourth step in the biosynthesis of the arginine precursor ornithine | -2.6 |
| YHR128W | FUR1 | Uracil phosphoribosyltransferase, synthesizes UMP from uracil; involved in the pyrimidine salvage pathway | -2.6 |
| YNL141W | AAH1 | Adenine deaminase (adenine aminohydrolase), involved in purine salvage and nitrogen catabolism | -2.6 |
| YPL250C | ICY2 | Protein of unknown function; potential Cdc28p substrate | -2.6 |
| YGR109W-B | | Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), | -2.6 |
| YPL252C | YAH1 | Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur proteins; involved in heme A biosynthesis; homologous to human | -2.6 |
| YIL131C | FKH1 | Transcription factor of the forkhead family that regulates the cell cycle and pseudohyphal growth; also involved in chromatin silencing at HML and HMR | -2.6 |
| YML091C | RPM2 | Protein component of mitochondrial RNase P, along with the mitochondrially-encoded RNA subunit RPM1; RNase P removes 5' extensions from tRNA | -2.6 |
| YEL038W | UTR4 | Protein of unknown function, found in both the cytoplasm and nucleus | -2.6 |
| YJL122W | ALB1 | Shuttling pre-60S factor; involved in the biogenesis of ribosomal large subunit; interacts directly with Arx1p; responsible for Tif6p recycling defects in absence | -2.7 |
| YIL037C | PRM2 | Pheromone-regulated protein, predicted to have 4 transmembrane segments and a coiled coil domain; regulated by Ste12p | -2.7 |
| YML018C | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the membrane of the vacuole; YML018C is not an essential | -2.7 |
| YBL028C | | Hypothetical protein | -2.7 |
| YIL082W-A | | Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), | -2.7 |
| YER124C | DSE1 | Daughter cell-specific protein, may participate in pathways regulating cell wall metabolism; deletion affects cell separation after division and sensitivity to | -2.7 |
| YJR147W | HMS2 | Protein with similarity to heat shock transcription factors; overexpression suppresses the pseudohyphal filamentation defect of a diploid mep1 mep2 | -2.7 |
| YGR280C | PXR1 | Essential protein involved in rRNA and snoRNA maturation; competes with TLC1 RNA for binding to Est2p, suggesting a role in regulation of telomerase; | -2.7 |
| YEL040W | UTR2 | Putative glycosidase, glycosylphosphatidylinositol (GPI)-anchored protein localized to the bud neck; has a role in cell wall maintenance | -2.7 |
| YNL078W | NIS1 | Protein localized in the bud neck at G2/M phase; physically interacts with septins; possibly involved in a mitotic signaling network | -2.7 |
| YGL162W | SUT1 | Transcription factor of the Zn[II]2Cys6 family involved in sterol uptake; involved in induction of hypoxic gene expression | -2.7 |
| YDL171C | GLT1 | NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamine and alpha-ketoglutarate; with Gln1p, forms the secondary pathway | -2.8 |
| YKL001C | MET14 | Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine metabolism | -2.8 |
| YDR384C | ATO3 | Plasma membrane protein, regulation pattern suggests a possible role in export of ammonia from the cell; member of the TC 9.B.33 YaaH family of | -2.8 |
| YBR291C | CTP1 | Mitochondrial inner membrane citrate transporter, member of the mitochondrial carrier family | -2.8 |

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| YNR028W | CPR8 | Peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; similarity to | -2.8 |
| YBR157C | ICS2 | Protein of unknown function; null mutation does not confer any obvious defects in growth, spore germination, viability, or carbohydrate utilization | -2.8 |
| YMR032W | HOF1 | Bud neck-localized, SH3 domain-containing protein required for cytokinesis; regulates actomyosin ring dynamics and septin localization; interacts with the | -2.8 |
| YDR075W | PPH3 | Catalytic subunit of an evolutionarily conserved protein phosphatase complex containing Psy2p and the regulatory subunit Psy4p; required for cisplatin | -2.8 |
| YHR153C | SPO16 | Protein of unknown function, required for spore formation | -2.8 |
| YMR243C | ZRC1 | Vacuolar membrane zinc transporter, transports zinc from the cytosol into the vacuole for storage; also has a role in resistance to zinc shock resulting from a | -2.8 |
| YGR108W | CLB1 | 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 | -2.8 |
| YCL027W | FUS1 | Membrane protein localized to the shmoo tip, required for cell fusion; expression regulated by mating pheromone; proposed to coordinate signaling, | -2.8 |
| YEL063C | CAN1 | Plasma membrane arginine permease, requires phosphatidyl ethanolamine (PE) for localization, exclusively associated with lipid rafts; mutation confers | -2.8 |
| YMR058W | FET3 | Ferro-O ₂ -oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral | -2.9 |
| YPR145W | ASN1 | Asparagine synthetase, isozyme of Asn2p; catalyzes the synthesis of L-asparagine from L-aspartate in the asparagine biosynthetic pathway | -2.9 |
| YHL026C | | Putative protein of unknown function; YHL026C is not an essential gene; in 2005 the start site was moved 141 nt upstream (see Locus History) | -2.9 |
| YKL201C | MNN4 | Putative positive regulator of mannosylphosphate transferase (Mnn6p), involved in mannosylphosphorylation of N-linked oligosaccharides; expression | -3.0 |
| YOR095C | RK11 | Ribose-5-phosphate ketol-isomerase, catalyzes the interconversion of ribose 5-phosphate and ribulose 5-phosphate in the pentose phosphate pathway; | -3.0 |
| YPL144W | | Hypothetical protein | -3.0 |
| YEL072W | RMD6 | Protein required for sporulation | -3.0 |
| YDR281C | PHM6 | Protein of unknown function, expression is regulated by phosphate levels | -3.0 |
| YBR085W | AAC3 | Mitochondrial inner membrane ADP/ATP translocator, exchanges cytosolic ADP for mitochondrially synthesized ATP; expressed under anaerobic | -3.0 |
| YBR184W | | Putative protein of unknown function; YBR184W is not an essential gene | -3.0 |
| YBR202W | CDC47 | Component of the hexameric MCM complex, which is important for priming origins of DNA replication in G1 and becomes an active ATP-dependent | -3.0 |
| YLR452C | SST2 | GTPase-activating protein for Gpa1p, regulates desensitization to alpha factor pheromone; also required to prevent receptor-independent signaling of the | -3.1 |
| YJL047C-A | | Putative protein of unknown function | -3.1 |
| YDL198C | GGC1 | Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the | -3.1 |
| YBL044W | | Hypothetical protein | -3.1 |
| YOL154W | ZPS1 | Putative GPI-anchored protein; transcription is induced under low-zinc conditions, as mediated by the Zap1p transcription factor, and at alkaline pH | -3.1 |
| YIL164C | NIT1 | Nitrilase, member of the widely found nitrilase branch (EC:3.5.5.1) of the nitrilase superfamily | -3.2 |
| YKL043W | PHD1 | Transcriptional activator that enhances pseudohyphal growth; regulates expression of FLO11, an adhesin required for pseudohyphal filament formation; | -3.2 |
| YIL158W | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole | -3.2 |

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| YJR152W | DAL5 | Allantoin permease; ureidosuccinate permease; expression is constitutive but sensitive to nitrogen catabolite repression | -3.2 |
| YGR121C | MEP1 | Ammonium permease; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport only ammonium (NH ₄ ⁺); expression is under | -3.2 |
| YNL327W | EGT2 | Glycosylphosphatidylinositol (GPI)-anchored cell wall endoglucanase required for proper cell separation after cytokinesis, expression is activated by Swi5p | -3.3 |
| YCL024W | KCC4 | Protein kinase of the bud neck involved in the septin checkpoint, associates with septin proteins, negatively regulates Swe1p by phosphorylation, shows | -3.3 |
| YFL021W | GAT1 | Transcriptional activator of genes involved in nitrogen catabolite repression, member of the GATA family of DNA binding proteins; activity and localization | -3.3 |
| YBR265W | TSC10 | 3-ketosphinganine reductase, catalyzes the second step in phytosphingosine synthesis, essential for growth in the absence of exogenous | -3.3 |
| YOR101W | RAS1 | GTPase involved in G-protein signaling in the adenylate cyclase activating pathway, plays a role in cell proliferation; localized to the plasma membrane; | -3.4 |
| YBR218C | PYC2 | Pyruvate carboxylase isoform, cytoplasmic enzyme that converts pyruvate to oxaloacetate; highly similar to isoform Pyc1p but differentially regulated; | -3.4 |
| YIR017C | MET28 | Transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in the regulation of sulfur metabolism | -3.4 |
| YML052W | SUR7 | Putative integral membrane protein; component of eisosomes; associated with endocytosis, along with Pil1p and Lsp1p; sporulation and plasma membrane | -3.5 |
| YJL078C | PRY3 | Protein of unknown function, has similarity to Pry1p and Pry2p and to the plant PR-1 class of pathogen related proteins | -3.6 |
| YGR234W | YHB1 | Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses | -3.6 |
| YHR092C | HXT4 | High-affinity glucose transporter of the major facilitator superfamily, expression is induced by low levels of glucose and repressed by high levels of glucose | -3.6 |
| YFR030W | MET10 | Subunit alpha of assimilatory sulfite reductase, which is responsible for the conversion of sulfite into sulfide | -3.6 |
| YJR010W | MET3 | ATP sulfurylase, catalyzes the primary step of intracellular sulfate activation, essential for assimilatory reduction of sulfate to sulfide, involved in methionine | -3.6 |
| YJL088W | ARG3 | Ornithine carbamoyltransferase (carbamoylphosphate:L-ornithine carbamoyltransferase), catalyzes the sixth step in the biosynthesis of the | -3.6 |
| YDL059C | RAD59 | Protein involved in the repair of double-strand breaks in DNA during vegetative growth via recombination and single-strand annealing; anneals complementary | -3.6 |
| YGR109W-A | | Retrotransposon TYA Gag gene co-transcribed with TYB Pol; translated as TYA or TYA-TYB polyprotein; Gag is a nucleocapsid protein that is the | -3.6 |
| YJL079C | PRY1 | Protein of unknown function, has similarity to Pry2p and Pry3p and to the plant PR-1 class of pathogen related proteins | -3.7 |
| YNR067C | DSE4 | Daughter cell-specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate from mother | -3.7 |
| YER056C | FCY2 | Purine-cytosine permease, mediates purine (adenine, guanine, and hypoxanthine) and cytosine accumulation | -3.7 |
| YBR092C | PHO3 | Constitutively expressed acid phosphatase similar to Pho5p; brought to the cell surface by transport vesicles; hydrolyzes thiamin phosphates in the periplasmic | -3.7 |
| YBR147W | | Putative protein of unknown function; YBR147W is not an essential gene; resistant to fluconazole | -3.7 |
| YBR158W | AMN1 | Protein required for daughter cell separation, multiple mitotic checkpoints, and chromosome stability; contains 12 degenerate leucine-rich repeat motifs; | -3.7 |
| YIL165C | | Hypothetical protein | -3.7 |
| YPL092W | SSU1 | Plasma membrane sulfite pump involved in sulfite metabolism and required for efficient sulfite efflux; major facilitator superfamily protein | -3.7 |
| YMR215W | GAS3 | Putative 1,3-beta-glucanosyltransferase, has similarity to Gas1p; localizes to the cell wall | -3.8 |
| YNR009W | NRM1 | Transcriptional co-repressor of MBF (MCB binding factor)-regulated gene expression; Nrm1p associates stably with promoters via MBF to repress | -3.8 |

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| YKL109W | HAP4 | Subunit of the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex, a transcriptional activator and global regulator of respiratory | -3.8 |
| YLR364W | | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YLR364W is not an essential gene | -3.8 |
| YGL028C | SCW11 | Cell wall protein with similarity to glucanases; may play a role in conjugation during mating based on its regulation by Ste12p | -3.8 |
| YER145C | FTR1 | High affinity iron permease involved in the transport of iron across the plasma membrane; forms complex with Fet3p; expression is regulated by iron | -3.9 |
| YGL035C | MIG1 | Transcription factor involved in glucose repression; C2H2 zinc finger protein similar to mammalian Egr and Wilms tumor proteins | -3.9 |
| YPL265W | DIP5 | Dicarboxylic amino acid permease, mediates high-affinity and high-capacity transport of L-glutamate and L-aspartate; also a transporter for Gln, Asn, Ser, | -3.9 |
| YLR049C | | Hypothetical protein | -3.9 |
| YPR167C | MET16 | 3'-phosphoadenylylsulfate reductase, reduces 3'-phosphoadenylyl sulfate to adenosine-3',5'-bisphosphate and free sulfite using reduced thioredoxin as | -3.9 |
| YIL011W | TIR3 | Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins; expressed under anaerobic conditions and required for anaerobic | -4.1 |
| YGR109C | CLB6 | B-type cyclin involved in DNA replication during S phase; activates Cdc28p to promote initiation of DNA synthesis; functions in formation of mitotic spindles | -4.2 |
| YHL036W | MUP3 | Low affinity methionine permease, similar to Mup1p | -4.3 |
| YOR108W | LEU9 | Alpha-isopropylmalate synthase II (2-isopropylmalate synthase), catalyzes the first step in the leucine biosynthesis pathway; the minor isozyme, responsible | -4.3 |
| YCR089W | FIG2 | Cell wall adhesin, expressed specifically during mating; may be involved in maintenance of cell wall integrity during mating | -4.3 |
| YJR137C | ECM17 | Sulfite reductase beta subunit, involved in amino acid biosynthesis, transcription repressed by methionine | -4.3 |
| YIR031C | DAL7 | Malate synthase, role in allantoin degradation unknown; expression sensitive to nitrogen catabolite repression and induced by allophanate, an intermediate in | -4.4 |
| YNL065W | AQR1 | Plasma membrane transporter of the major facilitator superfamily that confers resistance to short-chain monocarboxylic acids and quinidine | -4.4 |
| YKL029C | MAE1 | Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor | -4.4 |
| YKL068W-A | | Putative protein of unknown function; identified by homology to <i>Ashbya gossypii</i> | -4.5 |
| YPR138C | MEP3 | Ammonium permease of high capacity and low affinity; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport only ammonium | -4.7 |
| YDR253C | MET32 | Zinc-finger DNA-binding protein, involved in regulating expression of the methionine biosynthetic genes, similar to Met31p | -4.9 |
| YKR069W | MET1 | S-adenosyl-L-methionine uroporphyrinogen III transmethylase, involved in sulfate assimilation, methionine metabolism, and siroheme biosynthesis | -5.0 |
| YJR004C | SAG1 | Alpha-agglutinin of alpha-cells, binds to Aga1p during agglutination, N-terminal half is homologous to the immunoglobulin superfamily and contains binding | -5.0 |
| YJL212C | OPT1 | Plasma membrane transporter that transports tetra- and pentapeptides and glutathione; member of the OPT family | -5.0 |
| YHR214C-E | | Hypothetical protein /// Identified by gene-trapping, microarray-based expression analysis, and genome-wide homology searching | -5.0 |
| YLR130C | ZRT2 | Low-affinity zinc transporter of the plasma membrane; transcription is induced under low-zinc conditions by the Zap1p transcription factor | -5.1 |
| YHR143W | DSE2 | Daughter cell-specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate from mother; | -5.1 |
| YIR032C | DAL3 | Ureidoglycolate hydrolase, converts ureidoglycolate to glyoxylate and urea in the third step of allantoin degradation; expression sensitive to nitrogen | -5.3 |
| YNL277W | MET2 | L-homoserine-O-acetyltransferase, catalyzes the conversion of homoserine to O-acetyl homoserine which is the first step of the methionine biosynthetic | -5.3 |

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| YJL157C | FAR1 | Cyclin-dependent kinase inhibitor that mediates cell cycle arrest in response to pheromone; also forms a complex with Cdc24p, Ste4p, and Ste18p that may | -5.3 |
| YHR136C | SPL2 | Protein with similarity to cyclin-dependent kinase inhibitors, overproduction suppresses a plc1 null mutation; green fluorescent protein (GFP)-fusion protein | -5.4 |
| YLR092W | SUL2 | High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous | -5.5 |
| YHL016C | DUR3 | Plasma membrane urea transporter, expression is highly sensitive to nitrogen catabolite repression and induced by allophanate, the last intermediate of the | -5.6 |
| YDR508C | GNP1 | High-affinity glutamine permease, also transports Leu, Ser, Thr, Cys, Met and Asn; expression is fully dependent on Grr1p and modulated by the Ssy1p-Ptr3p | -5.6 |
| YKR034W | DAL80 | Negative regulator of genes in multiple nitrogen degradation pathways; expression is regulated by nitrogen levels and by Gln3p; member of the GATA- | -5.7 |
| YDL227C | HO | Site-specific endonuclease required for gene conversion at the MAT locus (homothallic switching) through the generation of a ds DNA break; expression | -6.0 |
| YGR055W | MUP1 | High affinity methionine permease, integral membrane protein with 13 putative membrane-spanning regions; also involved in cysteine uptake | -6.0 |
| YBR208C | DUR1,2 | Urea amidolyase, contains both urea carboxylase and allophanate hydrolase activities, degrades urea to CO ₂ and NH ₃ ; expression sensitive to nitrogen | -6.0 |
| YNL279W | PRM1 | Pheromone-regulated multispinning membrane protein involved in membrane fusion during mating; predicted to have 5 transmembrane segments and a | -6.2 |
| YIL119C | RPI1 | Putative transcriptional regulator; overexpression suppresses the heat shock sensitivity of wild-type RAS2 overexpression and also suppresses the cell lysis | -6.2 |
| YJL218W | | Putative protein of unknown function, similar to bacterial galactoside O-acetyltransferases; induced by oleate in an OAF1/PIP2-dependent manner; | -6.2 |
| YNL066W | SUN4 | Cell wall protein related to glucanases, possibly involved in cell wall septation; member of the SUN family | -6.3 |
| YAR071W | PHO11 | One of three repressible acid phosphatases, a glycoprotein that is transported to the cell surface by the secretory pathway; induced by phosphate starvation | -6.5 |
| YNR044W | AGA1 | Anchorage subunit of a-agglutinin of a-cells, highly O-glycosylated protein with N-terminal secretion signal and C-terminal signal for addition of GPI anchor to | -6.6 |
| YGL089C | MF(ALPHA)2 | 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; | -7.1 |
| YBR040W | FIG1 | Integral membrane protein required for efficient mating; may participate in or regulate the low affinity Ca ²⁺ influx system, which affects intracellular signaling | -7.3 |
| YKR039W | GAP1 | General amino acid permease; localization to the plasma membrane is regulated by nitrogen source | -7.3 |
| YBL042C | FUI1 | High affinity uridine permease, localized to the plasma membrane; not involved in uracil transport | -7.5 |
| YPL274W | SAM3 | High-affinity S-adenosylmethionine permease, required for utilization of S-adenosylmethionine as a sulfur source; has similarity to S-methylmethionine | -7.8 |
| YLL062C | MHT1 | S-methylmethionine-homocysteine methyltransferase, functions along with Sam4p in the conversion of S-adenosylmethionine (AdoMet) to methionine to | -8.1 |
| YOR313C | SPS4 | Protein whose expression is induced during sporulation; not required for sporulation; heterologous expression in E. coli induces the SOS response that | -8.1 |
| YNL142W | MEP2 | Ammonium permease involved in regulation of pseudohyphal growth; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport only | -8.2 |
| YOR315W | SFG1 | Nuclear protein, putative transcription factor required for growth of superficial pseudohyphae (which do not invade the agar substrate) but not for invasive | -9.4 |
| YMR230W-A | | Putative protein of unknown function | -9.5 |
| YCL025C | AGP1 | Low-affinity amino acid permease with broad substrate range, involved in uptake of asparagine, glutamine, and other amino acids; expression is | -10.1 |
| YLL061W | MMP1 | High-affinity S-methylmethionine permease, required for utilization of S-methylmethionine as a sulfur source; has similarity to S-adenosylmethionine | -10.3 |
| YML047C | PRM6 | Pheromone-regulated protein, predicted to have 2 transmembrane segments; regulated by Ste12p during mating | -12.0 |

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| YBL029W | | Hypothetical protein | -13.5 |
| YPR194C | OPT2 | Oligopeptide transporter; member of the OPT family, with potential orthologs in <i>S. pombe</i> and <i>C. albicans</i> | -13.7 |
| YGL255W | ZRT1 | High-affinity zinc transporter of the plasma membrane, responsible for the majority of zinc uptake; transcription is induced under low-zinc conditions by | -20.0 |
| YHL028W | WSC4 | ER membrane protein involved in the translocation of soluble secretory proteins and insertion of membrane proteins into the ER membrane; may also | -24.4 |
| YBR294W | SUL1 | High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous | -37.0 |