

Supplemental_Data

Genes repressed by overexpression of DhGzf3 in synthetic medium (ND, no data or signal too low))

| ypd_ID | Gene Name | DhGZF3 vs wt synthetic med (log2) | DhGZF3 vs wt YPD med (log2) | Description |
|---------|-----------|---|-----------------------------------|---|
| YGR125W | | -3.42 | -0.29 | Hypothetical ORF |
| YIR034C | LYS1 | -3.13 | 0.53 | saccharopine dehydrogenase |
| YJL153C | INO1 | -2.92 | ND | L-myo-inositol-1-phosphate synthase |
| YDL182W | LYS20 | -2.82 | 0.15 | YDL131W (LYS21) homolog homocitrate synthase |
| YAR064W | | -2.68 | ND | Hypothetical ORF |
| YJL170C | ASG7 | -2.63 | -1.98 | an a-specific gene that is induced to a higher expression level by alpha factor |
| YIL160C | POT1 | -2.56 | 0.45 | 3-oxoacyl CoA thiolase |
| YNR050C | LYS9 | -2.52 | 0.30 | Seventh step in lysine biosynthesis pathway |
| YBR291C | CTP1 | -2.47 | -0.03 | citrate transporter |
| YJL200C | | -2.46 | 0.24 | Hypothetical ORF |
| YJL195C | | -2.42 | ND | Protein required for cell viability |
| YIL094C | LYS12 | -2.41 | 0.38 | homo-isocitrate dehydrogenase |
| YOR341W | RPA190 | -2.37 | -2.62 | RNA polymerase I subunit |
| YBR072W | HSP26 | -2.34 | 0.88 | heat shock protein 26 |
| YDR234W | LYS4 | -2.31 | 0.28 | homoaconitase |
| YIR032C | DAL3 | -2.27 | ND | ureidoglycolate hydrolase |
| YKL070W | | -2.26 | ND | Hypothetical ORF |
| YGR031W | | -2.18 | -2.30 | Hypothetical ORF |
| YCR098C | GIT1 | -2.13 | -0.85 | permease involved in the uptake of glycerophosphoinositol (GroPIns) |
| YEL021W | URA3 | -2.06 | -3.05 | orotidine-5'-phosphate decarboxylase |
| YHR082C | KSP1 | -2.04 | -2.52 | Serine/threonine kinase similar to casein kinase II and other serine/threonine protein kinases |
| YLR458W | | -2.04 | ND | Protein required for cell viability |
| YBR018C | GAL7 | -2.02 | ND | galactose-1-phosphate uridyl transferase |
| YDR461W | MFA1 | -2.00 | ND | a-factor mating pheromone precursor |
| YNL142W | MEP2 | -1.93 | -0.04 | ammonia transport protein |
| YJR150C | DAN1 | -1.91 | -1.44 | cell wall mannoprotein induced during anaerobic growth |
| YKR039W | GAP1 | -1.88 | -0.34 | general amino acid permease |
| YLR081W | GAL2 | -1.87 | ND | galactose permease |
| YOR387C | | -1.80 | ND | Hypothetical ORF |
| YBR115C | LYS2 | -1.79 | 0.32 | alpha aminoadipate reductase |
| YHL043W | ECM34 | -1.78 | -2.30 | Non-essential protein of unknown function |
| YEL072W | RMD6 | -1.76 | ND | Protein required for sporulation |
| YGL028C | SCW11 | -1.73 | -1.57 | glucanase |
| YOR203W | | -1.72 | -0.95 | Protein required for cell viability |
| YCR105W | ADH7 | -1.72 | ND | medium chain alcohol dehydrogenase |
| YDR535C | | -1.71 | ND | Hypothetical ORF |
| YML100W | TSL1 | -1.71 | ND | similar to TPS3 gene product trehalose-6-phosphate synthase/phosphatase complex 123 kDa regulatory subunit |
| YDR070C | FMP16 | -1.70 | -1.64 | The authentic, non-tagged protein was localized to the mitochondria |
| YDR355C | | -1.69 | -1.03 | Protein required for cell viability |
| YLR142W | PUT1 | -1.68 | ND | proline oxidase |
| YPL082C | MOT1 | -1.68 | -2.04 | helicase (putative) |
| YDR220C | | -1.65 | -1.38 | Hypothetical ORF |
| YGR059W | SPR3 | -1.63 | -1.92 | a sporulation-specific homologue of the yeast CDC3/10/11/12 family of bud neck microfilament genes; regulated by ABFI |
| YLR004C | | -1.63 | -1.36 | Hypothetical ORF |
| YMR111C | | -1.63 | -0.33 | Hypothetical ORF |
| YOL166C | | -1.63 | ND | Hypothetical ORF |
| YML099C | ARG81 | -1.62 | -1.62 | zinc finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type |
| YBR184W | | -1.60 | ND | Hypothetical ORF |
| YOR348C | PUT4 | -1.60 | ND | proline specific permease |
| YER085C | | -1.59 | -1.72 | Hypothetical ORF |
| YDR090C | | -1.57 | -1.58 | Hypothetical ORF |
| YLR227C | ADY4 | -1.57 | -0.37 | Component of the meiotic outer plaque, a membrane- organizing center that assembles on the cytoplasmic face of the spindle pole body during meiosis II and triggers the formation of the prospore membrane |
| YKR105C | | -1.56 | ND | Hypothetical ORF |

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|---------|-------|-------|-------|--|
| YGL258W | | -1.54 | 0.24 | Increased in velum formation in flor strain |
| YJL110C | GZF3 | -1.52 | -0.36 | GATA zinc finger protein 3 homologous to Dal80 in structure and function |
| YBR128C | ATG14 | -1.51 | -1.52 | Required for autophagy |
| YGR121C | MEP1 | -1.50 | -0.55 | ammonia permease |
| YHL042W | | -1.50 | -1.76 | Hypothetical ORF |
| YDR016C | DAD1 | -1.48 | -0.97 | Duo1 And Dam1 interacting; localized to intranuclear spindles and spindle pole bodies |
| YJL038C | | -1.47 | ND | Hypothetical ORF |
| YOR391C | HSP33 | -1.47 | -0.99 | Possible chaperone and cysteine protease with similarity to E. coli Hsp31 and S. cerevisiae Hsp32p, Hsp33p, and Sno4p; member of the DJ-1/ThiJ/Pfpl superfamily, which includes human DJ-1 involved in Parkinson's disease |
| YEL070W | DSF1 | -1.46 | ND | Hypothetical ORF |
| YBL089W | AVT5 | -1.46 | ND | transporter |
| YMR306W | FKS3 | -1.46 | -1.85 | Protein of unknown function, has similarity to 1,3-beta-D-glucan synthase catalytic subunits Fks1p and Gsc2p |
| YJL113W | | -1.46 | -1.50 | TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition |
| YCL048W | | -1.46 | -1.62 | Hypothetical ORF |
| YBL112C | | -1.45 | -1.18 | Hypothetical ORF |
| YMR053C | STB2 | -1.44 | -2.33 | binds Sin3p in two-hybrid assay and is part of large protein complex with Sin3p and Stb1p |
| YML047C | PRM6 | -1.44 | -1.12 | Pheromone-regulated protein, predicted to have 2 transmembrane segments; regulated by Ste12p during mating |
| YOR300W | | -1.44 | -1.26 | Hypothetical ORF |
| YPL280W | HSP32 | -1.43 | -1.71 | Possible chaperone and cysteine protease with similarity to E. coli Hsp31 and S. cerevisiae Hsp31p, Hsp33p, and Sno4p; member of the DJ-1/ThiJ/Pfpl superfamily, which includes human DJ-1 involved in Parkinson's disease |
| YDL196W | | -1.42 | -2.41 | Protein required for cell viability |
| YDL169C | UGX2 | -1.42 | ND | Product of gene unknown |
| YDR480W | DIG2 | -1.42 | -1.37 | MAP kinase-associated protein |
| YER096W | SHC1 | -1.41 | -1.23 | Sporulation-specific activator of Chs3p (chitin synthase III), required for the synthesis of the chitosan layer of ascospores; has similarity to Skt5p, which activates Chs3p during vegetative growth; transcriptionally induced at alkaline pH |
| YFL066C | | -1.41 | -1.32 | Hypothetical ORF |
| YDR139C | RUB1 | -1.40 | -0.57 | ubiquitin-like protein |
| YAL018C | | -1.39 | -1.29 | Hypothetical ORF |
| YLR054C | OSW2 | -1.39 | ND | Outer Spore Wall |
| YKR097W | PCK1 | -1.39 | ND | phosphoenolpyruvate carboxylkinase |
| YCR095C | | -1.39 | ND | Hypothetical ORF |
| YMR113W | FOL3 | -1.39 | -0.11 | dihydrofolate synthetase |
| YEL041W | | -1.38 | -1.21 | Hypothetical ORF |
| YBR285W | | -1.37 | ND | Hypothetical ORF |
| YGL128C | CWC23 | -1.36 | -0.98 | Complexed with Cef1p |
| YDL090C | RAM1 | -1.35 | 0.21 | farnesyltransferase beta subunit |
| YER103W | SSA4 | -1.34 | 0.16 | HSP70 family |
| YFL021W | GAT1 | -1.33 | -0.59 | transcriptional activator with GATA-1-type Zn finger DNA-binding motif |
| YBR116C | | -1.33 | ND | Hypothetical ORF |
| YBR050C | REG2 | -1.33 | -1.91 | Glc7p regulatory subunit |
| YMR017W | SPO20 | -1.33 | ND | SNAP 25 homolog |
| YIL164C | NIT1 | -1.33 | -0.15 | nitrilase |
| YGR154C | | -1.32 | -1.21 | Hypothetical ORF |
| YGR004W | PEX31 | -1.32 | -0.80 | Peroxisomal integral membrane protein, involved in negative regulation of peroxisome size; partially functionally redundant with Pex30p and Pex32p; probably acts at a step downstream of steps mediated by Pex28p and Pex29p |
| YIL167W | SDL1 | -1.32 | -0.55 | Hypothetical ORF |
| YGL138C | | -1.31 | -2.06 | Hypothetical ORF |
| YIR041W | | -1.30 | ND | Hypothetical ORF |
| YIL104C | SHQ1 | -1.30 | -0.61 | Essential nuclear protein, required for accumulation of box H/ACA snoRNAs and for rRNA processing; interacts with Naf1p |
| YEL063C | CAN1 | -1.30 | -0.10 | arginine permease |

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|---------|-------|-------|-------|---|
| YEL004W | YEA4 | -1.29 | -1.30 | Shows sequence similarity to GOG5, a gene involved in vanadate resistance |
| YBR201W | DER1 | -1.28 | ND | Endoplasmic reticulum membrane protein, required for the protein degradation process associated with the ER, involved in the retrograde transport of misfolded or unassembled proteins |
| YCL061C | MRC1 | -1.28 | -1.01 | Mediator of the Replication Checkpoint; required for full activation of Rad53p in response to replication stress. |
| YML130C | ERO1 | -1.28 | 0.25 | Glycoprotein required for oxidative protein folding in the endoplasmic reticulum |
| YIR030C | DCG1 | -1.28 | -0.27 | Protein of unknown function, expression is sensitive to nitrogen catabolite repression and regulated by Dal80p; contains transmembrane domain |
| YDR290W | | -1.28 | ND | Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 42% of ORF overlaps the verified gene RTT103; deletion causes hydroxvuracil sensitivity |
| YJL075C | | -1.27 | ND | Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 85% of ORF overlaps the verified gene NET1 |
| YFR055W | | -1.27 | -0.02 | Hypothetical ORF |
| YBR218C | PYC2 | -1.27 | -1.02 | pyruvate carboxylase |
| YER038C | KRE29 | -1.27 | -0.80 | Killer toxin RESistant |
| YJL219W | HXT9 | -1.27 | ND | hexose permease |
| YGR239C | PEX21 | -1.27 | -0.14 | peroxin |
| YPR116W | | -1.27 | -0.83 | Hypothetical ORF |
| YIL121W | QDR2 | -1.27 | -0.26 | plasma membrane transporter |
| YFL007W | BLM3 | -1.26 | -0.88 | involved in protecting the cell against bleomycin damage |
| YGR142W | BTN2 | -1.25 | 0.00 | Gene/protein whose expression is elevated in a btn1 minus/Btn1p lacking yeast strain. |
| YLR171W | | -1.24 | -0.39 | Hypothetical ORF |
| YDL131W | LYS21 | -1.23 | -0.14 | YDL182W (LYS20) homolog/homocitrate synthase |
| YKL115C | | -1.21 | -0.76 | Hypothetical ORF |
| YGL033W | HOP2 | -1.21 | -1.80 | meiosis-specific gene required for the pairing of similar chromosomes |
| YDR340W | | -1.20 | -0.89 | Hypothetical ORF |
| YFL040W | | -1.20 | -0.77 | Hypothetical ORF |
| YNL332W | THI12 | -1.19 | ND | thiamine regulated gene, homologous to nmt1a in Schizosaccharomyces pombe; putatively involved in pyrimidine biosynthesis |
| YML107C | | -1.19 | -0.12 | Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery |
| YIL166C | | -1.19 | 0.33 | Hypothetical ORF, member of the Dal5p subfamily of the major facilitator family |
| YBL031W | SHE1 | -1.18 | -0.66 | Cytoskeletal protein of unknown function; overexpression causes growth arrest |
| YKL191W | DPH2 | -1.18 | -0.09 | Protein of unknown function, involved in diphtheria toxicity and diphthamide biosynthesis, not essential for viability |
| YOL031C | SIL1 | -1.17 | 0.18 | Nucleotide exchange factor |
| YEL064C | AVT2 | -1.16 | -0.85 | transporter |
| YDR034C | LYS14 | -1.16 | 0.20 | Transcriptional activator of lysine pathway genes with 2-aminoadipate semialdehyde as co-inducer; saccharopine reductase synthesis |
| YHL035C | VMR1 | -1.16 | -1.08 | ABC transporter |
| YFL062W | COS4 | -1.14 | ND | Protein of unknown function, member of a family of conserved, often subtelomerically-encoded proteins |
| YDR540C | | -1.14 | -0.79 | Hypothetical ORF |
| YAL064W | | -1.13 | -0.89 | Hypothetical ORF |
| YGL156W | AMS1 | -1.13 | ND | alpha mannosidase |
| YGR212W | SLI1 | -1.13 | ND | Hypothetical ORF |
| YBL074C | AAR2 | -1.12 | -1.10 | Component of the U5 snRNP, required for splicing of U3 precursors; originally described as a splicing factor specifically required for splicing pre-mRNA of the MATa1 cistron |
| YLR136C | TIS11 | -1.11 | ND | Zinc finger containing homolog of mammalian TIS11, glucose repressible gene |
| YNL183C | NPR1 | -1.11 | -0.37 | protein kinase homolog |
| YIL001W | | -1.10 | -0.45 | Hypothetical ORF |
| YBR147W | | -1.10 | -0.14 | Hypothetical ORF |
| YJL043W | | -1.10 | -0.80 | Hypothetical ORF |

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|---------|-------|-------|-------|---|
| YIL150C | MCM10 | -1.09 | -0.17 | Protein required for S-phase (DNA synthesis) initiation or completion |
| YGL018C | JAC1 | -1.09 | ND | E. coli Hsc20 co-chaperone protein homolog J-protein co-chaperone family 20 kDa |
| YEL076C | | -1.09 | -1.26 | Hypothetical ORF |
| YAL028W | FRT2 | -1.09 | -1.33 | Exhibits physical and genetic interactions with FRT1 and genetic interactions with TCP1; contains a C-terminal transmembrane domain and shows localization to the plasma membrane, the ER, and cytoplasmic vesicular or granule-like structures |
| YDR428C | | -1.08 | -1.08 | Hypothetical ORF |
| YJL144W | | -1.08 | -0.83 | Hypothetical ORF |
| YPL166W | | -1.07 | -0.51 | Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern |
| YMR040W | YET2 | -1.06 | ND | homolog of mammalian BAP31 |
| YDR123C | INO2 | -1.06 | -0.58 | helix-loop-helix protein |
| YOR191W | RIS1 | -1.06 | ND | SWI2/SNF2 DNA-dependent ATPase family member (putative) |
| YLR423C | ATG17 | -1.05 | -0.15 | required for activation of App1 protein kinase |
| YGR101W | PCP1 | -1.05 | -0.59 | rhomboid protease |
| YLR211C | | -1.04 | -0.89 | Hypothetical ORF |
| YMR170C | ALD2 | -1.03 | -0.34 | aldehyde dehydrogenase |
| YGL045W | RIM8 | -1.03 | -0.65 | Regulator of IME2 (RIM) Involved in proteolytic processing of Rim1p |
| YDR114C | | -1.02 | -0.74 | Hypothetical ORF |
| YJR097W | JJJ3 | -1.02 | -0.29 | Protein that may function as a cochaperone, as suggested by the presence of a DnaJ-like domain |
| YCL069W | | -1.02 | -0.65 | Hypothetical ORF |
| YLL063C | AYT1 | -1.01 | ND | Acetyltransferase; catalyzes trichothecene 3-O-acetylation, suggesting a possible role in trichothecene biosynthesis |
| YER037W | PHM8 | -1.01 | -0.42 | Protein of unknown function, expression is induced by low phosphate levels and by inactivation of Pho85p |
| YGL175C | SAE2 | -1.00 | -0.65 | Involved in meiotic recombination and chromosome metabolism |
| YJR140C | HIR3 | -1.00 | -0.87 | Transcriptional corepressor involved in the cell cycle-regulated transcription of histone genes HTA1, HTB1, HHT1, and HHT2; involved in position-dependent gene silencing and nucleosome reassembly |

Genes induced by overexpression of DhGzf3 in synthetic medium

| ypd_ID | Gene Name | DhGZF3 vs wt synthetic med (log2) | DhGZF3 vs wt YPD med (log2) | Description |
|---------|-----------|-----------------------------------|-----------------------------|--|
| YKL216W | URA1 | 1.97 | 0.04 | dihydroorotate dehydrogenase |
| YMR011W | HXT2 | 1.80 | ND | high affinity hexose transporter-2 |
| YEL039C | CYC7 | 1.69 | ND | iso-2-cytochrome c |
| YJR048W | CYC1 | 1.69 | 0.83 | iso-1-cytochrome c |
| YOL126C | MDH2 | 1.53 | 0.25 | malate dehydrogenase |
| YOR028C | CIN5 | 1.45 | ND | bZIP (basic-leucine zipper) protein can activate transcription from a promoter containing a Yap recognition site |
| YER076C | | 1.42 | 0.10 | Hypothetical ORF |
| YOL036W | | 1.41 | ND | Protein of unknown function; potential Cdc28p substrate |
| YJL130C | URA2 | 1.41 | 0.08 | aspartate transcarbamylase carbamoyl phosphate synthetase glutamine amidotransferase |
| YAR073W | IMD1 | 1.39 | 0.83 | IMP dehydrogenase homolog |
| YBL075C | SSA3 | 1.36 | 0.22 | heat shock protein of HSP70 family |
| YER067W | | 1.33 | 0.26 | Hypothetical ORF |
| YAR010C | | 1.33 | -0.02 | TyA Gag protein; the main structural constituent of virus-like particles (VLPs) |
| YHL036W | MUP3 | 1.31 | -0.74 | very low affinity methionine permease |
| YJR026W | | 1.31 | 0.04 | TyA Gag protein; the main structural constituent of virus-like particles (VLPs) |
| YML040W | | 1.29 | -0.12 | TyA Gag protein; the main structural constituent of virus-like particles (VLPs) |
| YFR015C | GSY1 | 1.28 | ND | glycogen synthase (UDP-glucose-starch glucosyltransferase) |
| YMR051C | | 1.28 | -0.11 | TyA Gag protein; the main structural constituent of virus-like particles (VLPs) |

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|---------|--------|------|-------|--|
| YML045W | | 1.27 | -0.12 | TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition |
| YJR028W | | 1.24 | 0.02 | Ty ORF |
| YLR432W | IMD3 | 1.21 | 0.55 | IMP dehydrogenase homolog |
| YJL084C | | 1.20 | 0.22 | Cytoplasmic protein of unknown function that interacts with Pcl7p, phosphorylated in vitro; potential Cdc28p substrate |
| YGR052W | FMP48 | 1.19 | ND | The authentic, non-tagged protein was localized to the mitochondria |
| YOL143C | RIB4 | 1.18 | 0.36 | 6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase) |
| YOL041C | NOP12 | 1.17 | -0.05 | Nucleolar protein, required for pre-25S rRNA processing; contains an RNA recognition motif (RRM) and has similarity to Nop13p, Nsr1p, and putative orthologs in <i>Drosophila</i> and <i>S. pombe</i> |
| YMR046C | | 1.15 | -0.11 | TyA Gag protein; the main structural constituent of virus-like particles (VLPs) |
| YIL066C | RNR3 | 1.12 | 0.39 | ribonucleotide reductase, large (R1) subunit |
| YHR216W | IMD2 | 1.09 | 0.58 | IMP dehydrogenase homolog |
| YKR075C | | 1.08 | 0.06 | Protein of unknown function; similar to YOR062Cp and Reg1p; expression regulated by glucose and Rqt1p |
| YMR288W | HSH155 | 1.06 | 0.15 | U2-snRNP associated splicing factor that forms extensive associations with the branch site-3' splice site-3' exon region upon prespliceosome formation; ortholog of the mammalian U2 snRNP-associated splicing factor SAP155 |
| YKL109W | HAP4 | 1.04 | 0.38 | transcriptional activator protein of CYC1 (component of HAP2/HAP3 heteromer) |
| YGR243W | FMP43 | 0.99 | 0.30 | The authentic, non-tagged protein was localized to mitochondria |
| YDL079C | MRK1 | 0.99 | 0.18 | MDS1 related protein kinase |
| YEL011W | GLC3 | 0.99 | ND | 1,4-glucan-6-(1,4-glucano)-transferase |
| YDR074W | TPS2 | 0.98 | 0.07 | trehalose-6-phosphate phosphatase |
| YBR069C | TAT1 | 0.98 | 0.44 | amino acid transport protein for valine, leucine, isoleucine, and tyrosine |
| YMR068W | AVO2 | 0.97 | -0.06 | Component of a complex containing the Tor2p kinase and other proteins, which may have a role in regulation of cell growth |
| YJR115W | | 0.96 | -1.02 | Hypothetical ORF |
| YLR106C | MDN1 | 0.95 | ND | midasin |
| YDR343C | HXT6 | 0.94 | 0.60 | hexose transporter |
| YMR153W | NUP53 | 0.93 | -0.08 | karyopherin docking complex component of the nuclear pore complex nuclear pore complex subunit |
| YBR068C | BAP2 | 0.93 | ND | amino acid permease for leucine, valine, and isoleucine (putative) |
| YHR136C | SPL2 | 0.92 | -0.05 | Protein with similarity to cyclin-dependent kinase inhibitors, overproduction suppresses a <i>plc1</i> null mutation; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern |
| YLL061W | MMP1 | 0.92 | 0.09 | high affinity S-methylmethionine permease |
| YBL004W | UTP20 | 0.91 | ND | U3 snoRNP protein |
| YGR269W | | 0.91 | 0.29 | Hypothetical ORF |
| YML056C | IMD4 | 0.90 | 0.20 | IMP dehydrogenase homolog |
| YPL042C | SSN3 | 0.90 | 0.50 | cyclin (SSN8)-dependent serine/threonine protein kinase |
| YOR273C | TPO4 | 0.89 | ND | Polyamine transport protein |
| YJL108C | PRM10 | 0.89 | 0.36 | Pheromone-regulated protein, predicted to have 5 transmembrane segments |
| YDL153C | SAS10 | 0.89 | ND | U3 snoRNP protein |
| YPR010C | RPA135 | 0.89 | -0.03 | RNA polymerase I subunit |
| YER110C | KAP123 | 0.88 | -0.13 | karyopherin beta 4 |
| YOL113W | SKM1 | 0.88 | 0.15 | Serine/threonine protein kinase with similarity to Ste20p and Cla4p |
| YBR092C | PHO3 | 0.85 | -0.30 | acid phosphatase |