**Table S6. All over-represented functional categories of target genes for each TF examined in this study.**

Enriched functional annotations for each TF based on the top 200 predicted target genes.

pval = significance of this functional enrichment within target gene set

Bonfp = Bonferroni corrected significance of functional enrichment within target gene set.

| **Aft1** | **n=200** | | |
|---|---|---|---|
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Molecular Function | heavy metal ion porter [GO:0005373] | 7.98E-13 | 1.10E-09 |
| GO Molecular Function | heavy metal ion transporter [GO:0015076] | 1.55E-12 | 2.14E-09 |
| GO Molecular Function | iron transporter [GO:0005381] | 3.99E-11 | 5.50E-08 |
| PFam-A Domains | PF01794 (Ferric_reduct) | 1.04E-09 | 1.23E-06 |
| GO Biological Process | iron-siderochrome transport [GO:0015892] | 9.82E-10 | 1.35E-06 |
| GO Biological Process | siderochrome transport [GO:0015891] | 9.82E-10 | 1.35E-06 |
| GO Molecular Function | ferric-chelate reductase [GO:0000293] | 6.69E-09 | 9.21E-06 |
| GO Biological Process | heavy metal ion transport [GO:0006823] | 1.03E-08 | 1.43E-05 |
| GO Molecular Function | porter [GO:0015291] | 1.08E-08 | 1.48E-05 |
| GO Molecular Function | electrochemical potential-driven transporter [GO:0015290] | 1.08E-08 | 1.48E-05 |
| MIPS Functional Classification | ionic homeostasis | 7.40E-08 | 1.92E-05 |
| GO Biological Process | transition metal transport [GO:0000041] | 1.59E-08 | 2.20E-05 |
| MIPS Functional Classification | homeostasis of cations | 1.19E-07 | 3.07E-05 |
| GO Molecular Function | ion transporter [GO:0015075] | 4.44E-08 | 6.12E-05 |
| GO Biological Process | heavy metal ion homeostasis [GO:0030006] | 5.89E-08 | 8.12E-05 |
| GO Molecular Function | cation transporter [GO:0008324] | 1.03E-07 | 0.00014199 |
| GO Biological Process | metal ion transport [GO:0030001] | 1.44E-07 | 0.00019841 |
| Proteome Localization--Predicted+Obs | en2 | 0.00011581 | 0.00046322 |
| GO Biological Process | copper ion transport [GO:0006825] | 7.72E-07 | 0.0010653 |
| GO Biological Process | metal ion homeostasis [GO:0006875] | 8.42E-07 | 0.00116259 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 9.96E-06 | 0.00189206 |
| GO Biological Process | iron homeostasis [GO:0006879] | 2.41E-06 | 0.00333113 |
| MIPS Functional Classification | REGULATION OF / INTERACTION WITH CELLULAR ENVIRONMENT | 1.53E-05 | 0.00397065 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 1.65E-05 | 0.0042705 |
| GO Biological Process | iron transport [GO:0006826] | 3.58E-06 | 0.00493495 |
| MIPS Functional Classification | ion transporters | 3.17E-05 | 0.00822069 |

| | | | |
|---|---|---|---|
| Published Complexes | Bassler et al. (2001) - Mol Cell 8:517- | 0.00143298 | 0.01003086 |
| MDS Proteomics Complexes | YDR328C (SKP1) | 3.27E-05 | 0.0161103 |
| MIPS Functional Classification | detoxification | 8.69E-05 | 0.02251617 |
| MIPS Functional Classification | cation transporters | 0.00011795 | 0.03054827 |
| GO Molecular Function | carrier [GO:0005386] | 4.48E-05 | 0.06171673 |
| GO Biological Process | ion transport [GO:0006811] | 4.75E-05 | 0.06561845 |
| GO Biological Process | cation transport [GO:0006812] | 7.39E-05 | 0.10203527 |
| GO Biological Process | cation homeostasis [GO:0030003] | 9.41E-05 | 0.12988256 |
| MIPS Functional Classification | drug transporters | 0.00073373 | 0.19003711 |
| GO Biological Process | ion homeostasis [GO:0006873] | 0.00027919 | 0.3852753 |
| MIPS Protein Classes | Zinc-coordinating DNA-binding domains | 0.00207705 | 0.3946395 |
| MIPS Phenotypes | Stress response defects | 0.00245583 | 0.4420494 |
| SMART Domains | TRANS | 0.00152928 | 0.44960832 |
| MIPS Functional Classification | allantoin and allantoate transporters | 0.00233288 | 0.60421592 |
| Cellzome Complexes | YNL061W (NOP2) | 0.00172766 | 0.79299594 |
| MIPS Protein Classes | Histones | 0.00437089 | 0.8304691 |
| GO Biological Process | homeostasis [GO:0019725] | 0.0007653 | >0.999 |
| GO Molecular Function | transporter [GO:0005215] | 0.00161185 | >0.999 |
| GO Biological Process | regulation of transcription from Pol II promoter [GO:0006357] | 0.00183251 | >0.999 |
| Cellzome Complexes | YBR135W (CKS1) | 0.00233288 | >0.999 |
| MDS Proteomics Complexes | YBR217W (APG12) | 0.00251429 | >0.999 |
| PFam-A Domains | PF00125 (histone) | 0.00325479 | >0.999 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 0.0034766 | >0.999 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00434988 | >0.999 |
| Cellzome Complexes | YMR308C (PSE1) | 0.00437089 | >0.999 |
| GO Cellular Component | endosome [GO:0005768] | 0.0046866 | >0.999 |
| | | | |
| **Aro80** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 3.23E-05 | 0.00035521 |
| MIPS Functional Classification | METABOLISM | 2.72E-05 | 0.00705141 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 4.50E-05 | 0.01165259 |
| MIPS Protein Complexes | Nucleosomal protein complex | 6.37E-05 | 0.02007325 |
| MIPS Phenotypes | Silencing mutants | 0.00013224 | 0.02380266 |

|  |  |  |  |
|---|---|---|---|
| MIPS Phenotypes | Transcriptional mutants | 0.00013304 | 0.02394666 |
| MIPS Functional Classification | ENERGY | 0.00013942 | 0.03610874 |
| Proteome Localization--Observed | cell periphery | 0.00403694 | 0.04440634 |
| MIPS Protein Classes | Histones | 0.00027852 | 0.05291785 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00056067 | 0.10652768 |
| GO Cellular Component | nucleosome [GO:0005718] | 0.00040738 | 0.13443639 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 0.00061489 | 0.15925677 |
| MIPS Phenotypes | other transcriptional mutants | 0.00106656 | 0.1919808 |
| PFam-A Domains | PF00125 (histone) | 0.00018176 | 0.21538679 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00089336 | 0.23137895 |
| GO Biological Process | main pathways of carbohydrate metabolism [GO:0006092] | 0.00024113 | 0.3327594 |
| GO Cellular Component | chromatin [GO:0005717] | 0.00115248 | 0.3803184 |
| GO Biological Process | hexose transport [GO:0008645] | 0.00053221 | 0.73444704 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 0.00053221 | 0.73444704 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 0.00316469 | 0.81965471 |
| GO Molecular Function | transporter [GO:0005215] | 0.00070106 | 0.96535687 |
| GO Molecular Function | glucose transporter [GO:0005355] | 0.00172766 | >0.999 |
| GO Biological Process | TCA intermediate metabolism [GO:0006100] | 0.00393128 | >0.999 |
| GO Biological Process | gluconeogenesis [GO:0006094] | 0.00393128 | >0.999 |
| PFam-A Domains | PF00501 (AMP-binding) | 0.00233288 | >0.999 |
| GO Biological Process | organic acid metabolism [GO:0006082] | 0.00085275 | >0.999 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 0.00234057 | >0.999 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 0.00267631 | >0.999 |
| MIPS Functional Classification | transcriptional control | 0.00467695 | >0.999 |
| GO Molecular Function | mannose transporter [GO:0015578] | 0.0010418 | >0.999 |
| GO Molecular Function | carbon-carbon lyase [GO:0016830] | 0.00099658 | >0.999 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 0.0022495 | >0.999 |
| GO Biological Process | amino acid metabolism [GO:0006520] | 0.00493696 | >0.999 |
| GO Molecular Function | hexose transporter [GO:0015149] | 0.00267631 | >0.999 |
| GO Biological Process | carboxylic acid metabolism [GO:0019752] | 0.00085275 | >0.999 |
|  |  |  |  |
| **Asg1** | **n=195** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Protein Classes | Transcription factors | 1.21E-05 | 0.00230088 |

| | | | |
|---|---|---|---|
| MIPS Functional Classification | glyoxylate cycle | 1.30E-05 | 0.00336371 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00031571 | 0.00347283 |
| MIPS Protein Classes | Zinc-coordinating DNA-binding domains | 2.38E-05 | 0.0045246 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 1.24E-05 | 0.01715823 |
| MIPS Functional Classification | drug transporters | 8.13E-05 | 0.02106123 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 9.07E-05 | 0.02349495 |
| PFam-A Domains | PF00083 (sugar_tr) | 3.08E-05 | 0.03645688 |
| GO Biological Process | main pathways of carbohydrate metabolism [GO:0006092] | 3.08E-05 | 0.04245611 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 0.00018236 | 0.04723098 |
| MIPS Subcellular Localization | cytoplasm | 0.00128963 | 0.05416446 |
| MIPS Functional Classification | METABOLISM | 0.00038223 | 0.09899835 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 7.86E-05 | 0.10848304 |
| MIPS Phenotypes | other carbohydrate and lipid biosynthesis defects | 0.00075055 | 0.13509972 |
| GO Biological Process | hexose metabolism [GO:0019318] | 0.00012556 | 0.17327832 |
| MIPS Protein Classes | Cys6 cysteine-zinc cluster | 0.0010344 | 0.196536 |
| MIPS Functional Classification | ENERGY | 0.00079423 | 0.20570479 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00147667 | 0.2805673 |
| MIPS Protein Classes | ABC transporter | 0.00178987 | 0.3400753 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 0.00025593 | 0.35318754 |
| SMART Domains | GAL4 | 0.00129939 | 0.38202066 |
| MIPS Functional Classification | ABC transporters | 0.00151911 | 0.39344949 |
| MIPS Functional Classification | transcriptional control | 0.00153239 | 0.39688901 |
| MIPS Phenotypes | Carbohydrate and lipid biosynthesis defects | 0.00311601 | 0.5608818 |
| MIPS Functional Classification | mRNA synthesis | 0.00356352 | 0.92295168 |
| GO Biological Process | carboxylic acid metabolism [GO:0019752] | 0.00071097 | 0.98114412 |
| GO Biological Process | organic acid metabolism [GO:0006082] | 0.00071097 | 0.98114412 |
| | | | |
| **Bas1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | amino acid metabolism | 1.57E-13 | 4.06E-11 |
| GO Biological Process | amino acid metabolism [GO:0006520] | 5.59E-11 | 7.72E-08 |
| MIPS Functional Classification | amino acid biosynthesis | 6.12E-10 | 1.59E-07 |
| MIPS Functional Classification | purine ribonucleotide metabolism | 7.18E-10 | 1.86E-07 |
| GO Biological Process | amino acid and derivative metabolism [GO:0006519] | 2.06E-10 | 2.84E-07 |

| | | | |
|---|---|---|---|
| GO Biological Process | amine metabolism [GO:0009308] | 2.72E-10 | 3.75E-07 |
| MIPS Functional Classification | METABOLISM | 2.36E-09 | 6.10E-07 |
| GO Biological Process | purine base metabolism [GO:0006144] | 1.05E-09 | 1.45E-06 |
| GO Biological Process | amino acid biosynthesis [GO:0008652] | 1.44E-08 | 1.99E-05 |
| GO Biological Process | amine biosynthesis [GO:0009309] | 3.81E-08 | 5.25E-05 |
| GO Biological Process | nucleobase metabolism [GO:0009112] | 1.17E-07 | 0.00016165 |
| GO Biological Process | aromatic compound metabolism [GO:0006725] | 2.13E-07 | 0.00029447 |
| MDS Proteomics Complexes | YDR388W (RVS167) | 8.92E-07 | 0.00043956 |
| GO Molecular Function | enzyme [GO:0003824] | 4.37E-07 | 0.00060225 |
| GO Molecular Function | ligase [GO:0016874] | 4.60E-07 | 0.00063402 |
| MIPS Functional Classification | nucleotide metabolism | 3.99E-06 | 0.00103358 |
| MIPS Subcellular Localization | mitochondria | 9.10E-05 | 0.0038201 |
| GO Biological Process | heterocycle metabolism [GO:0046483] | 3.24E-06 | 0.00447614 |
| GO Biological Process | one-carbon compound metabolism [GO:0006730] | 3.58E-06 | 0.00493495 |
| GO Biological Process | purine base biosynthesis [GO:0009113] | 1.44E-05 | 0.01982204 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 1.73E-05 | 0.02386268 |
| GO Cellular Component | mitochondrion [GO:0005739] | 7.28E-05 | 0.02401469 |
| GO Biological Process | biosynthesis [GO:0009058] | 1.77E-05 | 0.02439523 |
| GO Biological Process | sulfur amino acid metabolism [GO:0000096] | 2.61E-05 | 0.03597094 |
| Proteome Localization--Observed | cyto | 0.00464306 | 0.05107366 |
| MIPS Functional Classification | mitochondrion | 0.00022648 | 0.05865884 |
| GO Biological Process | serine family amino acid metabolism [GO:0009069] | 7.28E-05 | 0.10051782 |
| MIPS Subcellular Localization | mitochondrial matrix | 0.00353338 | 0.14840196 |
| MIPS Functional Classification | amino acid transport | 0.0006626 | 0.17161236 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 0.00015585 | 0.21460545 |
| MIPS Functional Classification | nitrogen and sulfur metabolism | 0.00121124 | 0.31371116 |
| GO Biological Process | nucleobase biosynthesis [GO:0046112] | 0.00025409 | 0.35064144 |
| MIPS Phenotypes | Methionine auxotrophy (Met) | 0.00233288 | 0.4199184 |
| GO Biological Process | methionine metabolism [GO:0006555] | 0.00033007 | 0.45550074 |
| MIPS Functional Classification | respiration | 0.00184928 | 0.47896352 |
| GO Biological Process | sulfur metabolism [GO:0006790] | 0.00042635 | 0.58835886 |
| GO Cellular Component | cytoplasm [GO:0005737] | 0.00184582 | 0.6091206 |
| GO Molecular Function | ion transporter [GO:0015075] | 0.00337119 | >0.999 |
| GO Molecular Function | other carbon-nitrogen ligase [GO:0016883] | 0.00233288 | >0.999 |

| | | | |
|---|---|---|---|
| GO Molecular Function | amino acid transporter [GO:0015171] | 0.00468663 | >0.999 |
| GO Molecular Function | electron transporter [GO:0005489] | 0.00468663 | >0.999 |
| GO Biological Process | branched chain family amino acid biosynthesis [GO:0009082] | 0.00437089 | >0.999 |
| GO Biological Process | aspartate family amino acid metabolism [GO:0009066] | 0.00173371 | >0.999 |
| GO Biological Process | energy derivation by oxidation of organic compounds [GO:0015980] | 0.00467495 | >0.999 |
| GO Biological Process | ion transport [GO:0006811] | 0.00090342 | >0.999 |
| GO Molecular Function | transporter [GO:0005215] | 0.00353451 | >0.999 |
| GO Biological Process | metabolism [GO:0008152] | 0.00149518 | >0.999 |
| GO Molecular Function | glycine hydroxymethyltransferase [GO:0004372] | 0.00101923 | >0.999 |
| GO Biological Process | branched chain family amino acid metabolism [GO:0009081] | 0.00078341 | >0.999 |
| GO Biological Process | energy pathways [GO:0006091] | 0.00467495 | >0.999 |
| GO Biological Process | serine family amino acid biosynthesis [GO:0009070] | 0.00101923 | >0.999 |
| | | | |
| **Cbf1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Molecular Function | ubiquinol-cytochrome c reductase [GO:0008121] | 0.00233288 | >0.999 |
| GO Cellular Component | cell [GO:0005623] | 1.08E-05 | 0.00356037 |
| GO Cellular Component | respiratory chain complex III (sensu Eukarya) [GO:0005750] | 0.00325479 | >0.999 |
| GO Cellular Component | respiratory chain complex III [GO:0045275] | 0.00325479 | >0.999 |
| MIPS Phenotypes | Methionine auxotrophy (Met) | 0.00233288 | 0.4199184 |
| GO Molecular Function | electron transporter [GO:0005489] | 0.00053221 | 0.73285042 |
| GO Biological Process | sulfur utilization [GO:0006791] | 1.63E-06 | 0.00225164 |
| GO Biological Process | sulfur metabolism [GO:0006790] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | aspartate family amino acid metabolism [GO:0009066] | 3.61E-05 | 0.04982752 |
| GO Biological Process | biosynthesis [GO:0009058] | 0.00143385 | >0.999 |
| MDS Proteomics Complexes | YDR523C (SPS1) | 0.00135467 | 0.66785231 |
| SMART Domains | STYKc | 0.00173371 | 0.50971074 |
| GO Molecular Function | transferase [GO:0016740] | 0.00103 | >0.999 |
| GO Biological Process | energy derivation by oxidation of organic compounds [GO:0015980] | 0.00051343 | 0.70853616 |
| GO Molecular Function | primary active transporter [GO:0015399] | 0.00216403 | >0.999 |
| GO Molecular Function | transporter [GO:0005215] | 0.00011558 | 0.15915779 |
| GO Biological Process | metabolism [GO:0008152] | 3.49E-05 | 0.04821941 |
| GO Molecular Function | kinase [GO:0016301] | 0.00399507 | >0.999 |
| Yeast Two Hybrid - Ito (core) | YER081W (SER3) | 0.0029765 | >0.999 |

| | | | |
|---|---|---|---|
| GO Cellular Component | intracellular [GO:0005622] | 7.66E-05 | 0.02529047 |
| GO Biological Process | amino acid and derivative metabolism [GO:0006519] | 1.26E-09 | 1.74E-06 |
| GO Biological Process | amine biosynthesis [GO:0009309] | 4.28E-05 | 0.05904689 |
| MIPS Functional Classification | amino acid metabolism | 6.00E-12 | 1.55E-09 |
| MIPS Functional Classification | amino acid biosynthesis | 8.53E-11 | 2.21E-08 |
| MIPS Functional Classification | nitrogen and sulfur metabolism | 0.00121124 | 0.31371116 |
| PFam-A Domains | PF03105 (SPX) | 0.00325479 | >0.999 |
| MIPS Functional Classification | METABOLISM | 9.82E-08 | 2.54E-05 |
| GO Cellular Component | cytoplasm [GO:0005737] | 0.00184582 | 0.6091206 |
| GO Molecular Function | carrier [GO:0005386] | 0.00170709 | >0.999 |
| MIPS Functional Classification | regulation of amino acid metabolism | 6.40E-05 | 0.01657787 |
| PFam-A Domains | PF01053 (Cys_Met_Meta_PP) | 0.00159254 | >0.999 |
| SMART Domains | BRLZ | 0.0010418 | 0.3062892 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 0.00046798 | 0.64440158 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 2.06E-06 | 0.00284886 |
| MDS Proteomics Complexes | YNL311C | 0.00101352 | 0.49966536 |
| GO Molecular Function | enzyme [GO:0003824] | 2.00E-07 | 0.00027584 |
| GO Biological Process | amine metabolism [GO:0009308] | 1.63E-09 | 2.25E-06 |
| GO Biological Process | amino acid metabolism [GO:0006520] | 3.68E-10 | 5.08E-07 |
| GO Biological Process | sulfur amino acid metabolism [GO:0000096] | 2.59E-11 | 3.58E-08 |
| GO Biological Process | energy pathways [GO:0006091] | 0.00051343 | 0.70853616 |
| GO Molecular Function | flavin-containing electron transporter [GO:0015933] | 0.0010418 | >0.999 |
| MIPS Protein Classes | Leucine zipper factors | 0.00172766 | 0.3282554 |
| GO Biological Process | electron transport [GO:0006118] | 0.00326287 | >0.999 |
| GO Biological Process | oxidative phosphorylation [GO:0006119] | 0.0010418 | >0.999 |
| GO Biological Process | amino acid biosynthesis [GO:0008652] | 2.20E-05 | 0.03033778 |
| GO Biological Process | sulfate assimilation [GO:0000103] | 1.63E-06 | 0.00225164 |
| GO Biological Process | serine family amino acid biosynthesis [GO:0009070] | 3.27E-05 | 0.04509578 |
| GO Biological Process | sulfur amino acid biosynthesis [GO:0000097] | 3.27E-05 | 0.04509578 |
| GO Biological Process | methionine metabolism [GO:0006555] | 1.65E-06 | 0.00228207 |
| GO Biological Process | regulation of transcription from Pol II promoter [GO:0006357] | 0.00183251 | >0.999 |
| GO Biological Process | serine family amino acid metabolism [GO:0009069] | 3.86E-06 | 0.00532407 |
| | | | |
| **Cep3** | **n=200** | | |

| Source | Annotation | pval | Bonfp |
|---|---|---:|---:|
| MIPS Functional Classification | cell wall | 1.47E-09 | 3.82E-07 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 2.98E-09 | 5.66E-07 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 5.39E-06 | 0.00139691 |
| GO Cellular Component | external protective structure [GO:0030312] | 5.85E-06 | 0.0019311 |
| GO Cellular Component | cell wall [GO:0005618] | 5.85E-06 | 0.0019311 |
| GO Biological Process | aspartate family amino acid catabolism [GO:0009068] | 1.63E-06 | 0.00225164 |
| MIPS Protein Classes | Histones | 1.24E-05 | 0.00236406 |
| PFam-A Domains | PF00125 (histone) | 6.97E-06 | 0.00825587 |
| MIPS Functional Classification | cellular import | 7.15E-05 | 0.0185148 |
| GO Molecular Function | asparaginase [GO:0004067] | 1.44E-05 | 0.01977895 |
| MIPS Protein Complexes | Nucleosomal protein complex | 6.37E-05 | 0.02007325 |
| GO Biological Process | response to starvation [GO:0009267] | 2.08E-05 | 0.02867419 |
| GO Cellular Component | periplasmic space (sensu Fungi) [GO:0030287] | 0.00011184 | 0.03690819 |
| MIPS Functional Classification | plasma membrane | 0.00015139 | 0.03921079 |
| MIPS Phenotypes | Oxidizing agents | 0.00044362 | 0.07985214 |
| GO Cellular Component | extracellular [GO:0005576] | 0.00030825 | 0.1017225 |
| GO Cellular Component | nucleosome [GO:0005718] | 0.00040738 | 0.13443639 |
| GO Biological Process | glutamine family amino acid catabolism [GO:0009065] | 0.00018176 | 0.25083018 |
| GO Biological Process | response to stress [GO:0006950] | 0.00018701 | 0.25807242 |
| MIPS Protein Classes | Cys2His2 zinc-finger | 0.00173371 | 0.3294049 |
| MIPS Functional Classification | stress response | 0.00132605 | 0.34344695 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 0.00025409 | 0.34987918 |
| GO Molecular Function | hexose transporter [GO:0015149] | 0.00025409 | 0.34987918 |
| GO Biological Process | amine catabolism [GO:0009310] | 0.00025409 | 0.35064144 |
| GO Biological Process | amino acid catabolism [GO:0009063] | 0.00025409 | 0.35064144 |
| GO Molecular Function | structural constituent of cell wall [GO:0005199] | 0.00027852 | 0.38351516 |
| GO Molecular Function | monocarboxylic acid transporter [GO:0008028] | 0.00027852 | 0.38351516 |
| PFam-A Domains | PF00107 (adh_zinc) | 0.00042209 | 0.50017665 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00156099 | 0.5151267 |
| MIPS Functional Classification | chromosome | 0.00251429 | 0.65120111 |
| GO Cellular Component | cell wall (sensu Fungi) [GO:0009277] | 0.00212059 | 0.6997947 |
| MDS Proteomics Complexes | YPR165W (RHO1) | 0.00159254 | 0.78512222 |
| GO Molecular Function | organic anion transporter [GO:0008514] | 0.00057382 | 0.79015427 |

| | | | |
|---|---|---|---|
| GO Biological Process | glutamine family amino acid metabolism [GO:0009064] | 0.00062431 | 0.86154918 |
| GO Molecular Function | transporter [GO:0005215] | 0.00070106 | 0.96535687 |
| | | | |
| **Cha4** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Proteome Localization--Predicted+Obs | cyt | 0.00042782 | 0.00171128 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 9.96E-06 | 0.00189206 |
| Proteome Localization--Observed | cyto | 0.00057042 | 0.0062746 |
| MIPS Functional Classification | METABOLISM | 5.52E-05 | 0.01430491 |
| GO Cellular Component | plasma membrane [GO:0005886] | 4.66E-05 | 0.01538236 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 1.88E-05 | 0.02587232 |
| GO Molecular Function | hexose transporter [GO:0015149] | 1.88E-05 | 0.02587232 |
| SMART Domains | Aamy | 0.00011184 | 0.03288184 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00013388 | 0.03467388 |
| MIPS Functional Classification | plasma membrane | 0.00015139 | 0.03921079 |
| PFam-A Domains | PF00083 (sugar_tr) | 3.76E-05 | 0.04454782 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 3.31E-05 | 0.04566185 |
| GO Biological Process | hexose transport [GO:0008645] | 4.77E-05 | 0.06580627 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 4.77E-05 | 0.06580627 |
| GO Molecular Function | fructose transporter [GO:0005353] | 4.98E-05 | 0.06863698 |
| PFam-A Domains | PF00128 (alpha-amylase) | 6.37E-05 | 0.07551365 |
| GO Molecular Function | drug transporter [GO:0015238] | 6.37E-05 | 0.08774877 |
| GO Molecular Function | multidrug transporter [GO:0015239] | 6.37E-05 | 0.08774877 |
| GO Molecular Function | mannose transporter [GO:0015578] | 7.28E-05 | 0.1002993 |
| GO Biological Process | response to chemical substance [GO:0042221] | 0.00011531 | 0.15912228 |
| MIPS Functional Classification | drug transporters | 0.00073373 | 0.19003711 |
| GO Molecular Function | glucose transporter [GO:0005355] | 0.00014246 | 0.19616054 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 0.00020515 | 0.2824943 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 0.0014536 | 0.3764824 |
| MIPS Protein Classes | Zinc-coordinating DNA-binding domains | 0.00207705 | 0.3946395 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 0.00316469 | 0.81965471 |
| GO Molecular Function | ABC-type efflux porter [GO:0015427] | 0.00059642 | 0.82127447 |
| GO Molecular Function | galactose transporter [GO:0005354] | 0.00059642 | 0.82127447 |
| GO Biological Process | response to drug [GO:0042493] | 0.0006626 | 0.91438248 |

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|---|---|---|---|
| PFam-A Domains | PF00005 (ABC_tran) | 0.00271949 | >0.999 |
| GO Cellular Component | cytosolic ribosome (sensu Eukarya) [GO:0005830] | 0.0030707 | >0.999 |
| MIPS Protein Complexes | Cytoplasmic ribosomes | 0.00442721 | >0.999 |
| GO Molecular Function | transporter [GO:0005215] | 0.00353451 | >0.999 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 0.00184928 | >0.999 |
| GO Molecular Function | alpha-glucosidase [GO:0004558] | 0.00101923 | >0.999 |
| GO Molecular Function | carbohydrate kinase [GO:0019200] | 0.0010418 | >0.999 |
| GO Molecular Function | O-acyltransferase [GO:0008374] | 0.00325479 | >0.999 |
| GO Biological Process | amino acid metabolism [GO:0006520] | 0.00493696 | >0.999 |
| | | | |
| **Cup9** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | DNA synthesis and replication | 0.0007653 | 0.19821218 |
| SMART Domains | ZnF_GATA | 0.00325479 | 0.95690826 |
| | | | |
| **Ecm22** | **n=198** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Biological Process | main pathways of carbohydrate metabolism [GO:0006092] | 5.66E-07 | 0.00078072 |
| MIPS Functional Classification | glyoxylate cycle | 1.38E-05 | 0.00357441 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 1.39E-05 | 0.00360344 |
| MIPS Functional Classification | METABOLISM | 1.97E-05 | 0.00510971 |
| MIPS Functional Classification | ENERGY | 3.98E-05 | 0.01032094 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00242093 | 0.02663023 |
| GO Biological Process | energy derivation by oxidation of organic compounds [GO:0015980] | 3.67E-05 | 0.05061826 |
| GO Biological Process | energy pathways [GO:0006091] | 3.67E-05 | 0.05061826 |
| MIPS Subcellular Localization | cytoplasm | 0.00325132 | 0.13655544 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 0.00054262 | 0.14053832 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 0.00020471 | 0.28250256 |
| MIPS Phenotypes | Methionine auxotrophy (Met) | 0.00226655 | 0.407979 |
| GO Cellular Component | cytoplasm [GO:0005737] | 0.00133045 | 0.4390485 |
| Cellzome Complexes | YAR003W (SWD1) | 0.0009933 | 0.45592562 |
| GO Biological Process | TCA intermediate metabolism [GO:0006100] | 0.00040294 | 0.5560503 |
| GO Cellular Component | cytosol [GO:0005829] | 0.00175398 | 0.5788134 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 0.00050819 | 0.70130496 |

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|---|---|---|---|
| GO Biological Process | hexose transport [GO:0008645] | 0.00050819 | 0.70130496 |
| GO Biological Process | glucose transport [GO:0015758] | 0.00057905 | 0.7990821 |
| MIPS Functional Classification | stress response | 0.00345079 | 0.89375461 |
| MIPS Protein Classes | Transcription factors | 0.00482271 | 0.9163149 |
| | | | |
| **Fhl1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 1.90E-08 | 2.62E-05 |
| MIPS Functional Classification | METABOLISM | 1.42E-05 | 0.00367283 |
| GO Biological Process | regulation of cell cycle [GO:0000074] | 4.04E-06 | 0.00557357 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 7.97E-05 | 0.0206472 |
| MIPS Functional Classification | SUBCELLULAR LOCALISATION | 0.00010497 | 0.02718645 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 0.00017043 | 0.04414008 |
| GO Molecular Function | enzyme [GO:0003824] | 4.94E-05 | 0.06796239 |
| MIPS Subcellular Localization | cytoplasm | 0.00277226 | 0.11643492 |
| MIPS Functional Classification | DNA synthesis and replication | 0.00065379 | 0.16933161 |
| MDS Proteomics Complexes | YHR135C (YCK1) | 0.00037713 | 0.18592263 |
| GO Cellular Component | cell [GO:0005623] | 0.00056456 | 0.1863048 |
| MIPS Phenotypes | paromomycin | 0.00220143 | 0.3962574 |
| GO Cellular Component | intracellular [GO:0005622] | 0.00170569 | 0.5628777 |
| MIPS Protein Classes | NPR/HAL5 family | 0.00307287 | 0.5838453 |
| SMART Domains | CYCLIN | 0.00201145 | 0.5913663 |
| PFam-A Domains | PF00682 (HMGL-like) | 0.000562 | 0.66596882 |
| MIPS Functional Classification | other intracellular transport activities | 0.00287754 | 0.74528286 |
| MIPS Protein Classes | Cyclins | 0.00436031 | 0.8284589 |
| MIPS Protein Complexes | Cdc28p complexes | 0.00307287 | 0.96795405 |
| GO Biological Process | pyruvate metabolism [GO:0006090] | 0.00307287 | >0.999 |
| MIPS Functional Classification | deoxyribonucleotide metabolism | 0.00412857 | >0.999 |
| Cellzome Complexes | YER120W (SCS2) | 0.00307287 | >0.999 |
| GO Molecular Function | electron transporter [GO:0005489] | 0.00436031 | >0.999 |
| GO Biological Process | regulation of CDK activity [GO:0000079] | 0.00096582 | >0.999 |
| GO Biological Process | mitotic cell cycle [GO:0000278] | 0.00156851 | >0.999 |
| GO Biological Process | cell cycle [GO:0007049] | 0.00089137 | >0.999 |
| GO Biological Process | metabolism [GO:0008152] | 0.00155404 | >0.999 |

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|---|---|---|---|
| GO Biological Process | G2/M transition of mitotic cell cycle [GO:0000086] | 0.00249012 | >0.999 |
| GO Biological Process | pyruvate dehydrogenase bypass [GO:0006087] | 0.00307287 | >0.999 |
| PFam-A Domains | PF00134 (cyclin) | 0.00125651 | >0.999 |
| | | | |
| **Fkh1** | **n=199** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Cellular Component | cytoskeleton [GO:0005856] | 3.43E-09 | 1.13E-06 |
| GO Cellular Component | spindle [GO:0005819] | 4.06E-09 | 1.34E-06 |
| GO Cellular Component | microtubule cytoskeleton [GO:0015630] | 5.71E-09 | 1.88E-06 |
| GO Cellular Component | spindle pole [GO:0030615] | 2.03E-07 | 6.69E-05 |
| MIPS Subcellular Localization | cytoskeleton | 1.42E-05 | 0.00059457 |
| MIPS Functional Classification | cell differentiation | 8.49E-06 | 0.00219809 |
| MIPS Functional Classification | fungal cell differentiation | 8.49E-06 | 0.00219809 |
| GO Cellular Component | microtubule organizing center [GO:0005815] | 7.40E-06 | 0.00244365 |
| GO Cellular Component | spindle pole body [GO:0005816] | 7.40E-06 | 0.00244365 |
| GO Cellular Component | kinesin [GO:0005871] | 1.41E-05 | 0.00464647 |
| MIPS Functional Classification | CELL FATE | 2.68E-05 | 0.00692859 |
| GO Cellular Component | microtubule associated protein [GO:0005875] | 6.25E-05 | 0.02061929 |
| GO Biological Process | cell cycle [GO:0007049] | 1.72E-05 | 0.02370012 |
| MIPS Subcellular Localization | tubulin cytoskeleton | 0.0006476 | 0.02719924 |
| GO Cellular Component | cell wall (sensu Fungi) [GO:0009277] | 9.02E-05 | 0.02978144 |
| GO Cellular Component | cell wall [GO:0005618] | 0.00014195 | 0.04684185 |
| GO Cellular Component | external protective structure [GO:0030312] | 0.00014195 | 0.04684185 |
| Deletions Consortium (Essentiality, Mo | Morphology - Large | 0.00449122 | 0.04940342 |
| GO Cellular Component | spindle microtubule [GO:0005876] | 0.00017827 | 0.05882745 |
| GO Molecular Function | microtubule binding [GO:0008017] | 4.87E-05 | 0.06700303 |
| GO Molecular Function | microtubule motor [GO:0003777] | 6.25E-05 | 0.08603868 |
| GO Biological Process | mitotic anaphase B [GO:0000092] | 6.25E-05 | 0.08622613 |
| GO Cellular Component | extracellular [GO:0005576] | 0.00029604 | 0.09769419 |
| GO Cellular Component | microtubule [GO:0005874] | 0.00032248 | 0.10641675 |
| MIPS Functional Classification | cell cycle | 0.00042306 | 0.1095715 |
| MIPS Protein Complexes | Microtubules | 0.00043187 | 0.13603874 |
| MIPS Protein Complexes | Cytoskeleton | 0.00045727 | 0.14404068 |
| GO Biological Process | M phase [GO:0000279] | 0.00011708 | 0.1615704 |

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|---|---|---|---|
| GO Cellular Component | bud neck [GO:0005935] | 0.00055612 | 0.18351861 |
| MIPS Functional Classification | cytokinesis (cell division) | 0.00071459 | 0.18507752 |
| GO Molecular Function | motor [GO:0003774] | 0.00013912 | 0.19156824 |
| MIPS Phenotypes | Spindle mutants | 0.00117162 | 0.2108916 |
| MIPS Phenotypes | Cell morphology and organelle mutants | 0.00121123 | 0.2180214 |
| MIPS Protein Complexes | Tubulin-associated motorproteins | 0.00076874 | 0.24215373 |
| SMART Domains | COIL | 0.00112017 | 0.32932998 |
| MIPS Functional Classification | cytoskeleton-dependent transport | 0.00140129 | 0.36293411 |
| MIPS Phenotypes | other cell cycle defects | 0.00230036 | 0.4140648 |
| GO Molecular Function | tubulin binding [GO:0015631] | 0.00032248 | 0.44404808 |
| MIPS Protein Complexes | Kinesin-related motorproteins | 0.0015696 | 0.494424 |
| GO Molecular Function | cytoskeletal protein binding [GO:0008092] | 0.00038963 | 0.53651638 |
| GO Biological Process | cytoskeleton organization and biogenesis [GO:0007010] | 0.0003975 | 0.54854448 |
| GO Cellular Component | bud [GO:0005933] | 0.0017166 | 0.566478 |
| MIPS Functional Classification | CELL CYCLE AND DNA PROCESSING | 0.00237283 | 0.61456297 |
| MIPS Functional Classification | centrosome | 0.00266076 | 0.68913684 |
| GO Cellular Component | actin cytoskeleton [GO:0015629] | 0.00209099 | 0.6900267 |
| MIPS Protein Classes | Protein Kinases | 0.00386273 | 0.7339187 |
| GO Cellular Component | site of polarized growth [GO:0030427] | 0.0022424 | 0.739992 |
| GO Cellular Component | site of polarized growth (sensu Saccharomyces) [GO:0000134] | 0.0022424 | 0.739992 |
| GO Cellular Component | site of polarized growth (sensu Fungi) [GO:0030483] | 0.0022424 | 0.739992 |
| GO Biological Process | cytokinesis [GO:0016288] | 0.00054747 | 0.75551412 |
| GO Biological Process | chromosome segregation [GO:0007059] | 0.00055612 | 0.76744146 |
| MIPS Phenotypes | Tubulin cytoskeleton mutants | 0.00428518 | 0.7713324 |
| MIPS Phenotypes | Bud localization | 0.00458777 | 0.8257986 |
| MIPS Protein Complexes | Spindle pole body (SPB) | 0.00307352 | 0.9681588 |
|  |  |  |  |
| **Fkh2** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Cellular Component | microtubule cytoskeleton [GO:0015630] | 2.67E-06 | 0.00088006 |
| GO Cellular Component | spindle [GO:0005819] | 2.74E-06 | 0.00090546 |
| MIPS Functional Classification | fungal cell differentiation | 9.38E-06 | 0.00242879 |
| MIPS Functional Classification | cell differentiation | 9.38E-06 | 0.00242879 |
| GO Cellular Component | kinesin [GO:0005871] | 1.44E-05 | 0.00474005 |

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|---|---|---:|---:|
| MIPS Functional Classification | CELL FATE | 2.95E-05 | 0.0076449 |
| GO Cellular Component | cytoskeleton [GO:0005856] | 3.00E-05 | 0.00988558 |
| GO Cellular Component | microtubule organizing center [GO:0005815] | 6.17E-05 | 0.02035645 |
| GO Cellular Component | spindle pole body [GO:0005816] | 6.17E-05 | 0.02035645 |
| GO Cellular Component | microtubule associated protein [GO:0005875] | 6.37E-05 | 0.02102912 |
| GO Cellular Component | cell wall (sensu Fungi) [GO:0009277] | 9.41E-05 | 0.03105887 |
| GO Cellular Component | spindle pole [GO:0030615] | 0.00011771 | 0.03884331 |
| MIPS Subcellular Localization | cytoskeleton | 0.00103586 | 0.04350612 |
| Proteome Localization--Predicted+Obs | nuc | 0.011064 | 0.044256 |
| GO Cellular Component | cell wall [GO:0005618] | 0.00014841 | 0.04897464 |
| GO Cellular Component | external protective structure [GO:0030312] | 0.00014841 | 0.04897464 |
| GO Molecular Function | microtubule binding [GO:0008017] | 4.98E-05 | 0.06863698 |
| GO Molecular Function | microtubule motor [GO:0003777] | 6.37E-05 | 0.08774877 |
| GO Biological Process | mitotic anaphase B [GO:0000092] | 6.37E-05 | 0.08793995 |
| GO Cellular Component | extracellular [GO:0005576] | 0.00030825 | 0.1017225 |
| MIPS Protein Complexes | Microtubules | 0.00044362 | 0.13974125 |
| MIPS Phenotypes | Spindle mutants | 0.00119827 | 0.2156886 |
| MIPS Protein Complexes | Tubulin-associated motorproteins | 0.00078341 | 0.24677541 |
| MDS Proteomics Complexes | YER177W (BMH1) | 0.00078341 | 0.3862231 |
| GO Molecular Function | tubulin binding [GO:0015631] | 0.00033007 | 0.45451052 |
| MIPS Protein Complexes | Kinesin-related motorproteins | 0.00159254 | 0.5016501 |
| MIPS Protein Complexes | Cytoskeleton | 0.00212059 | 0.66798585 |
| MIPS Functional Classification | centrosome | 0.00271949 | 0.70434791 |
| MIPS Protein Complexes | Spindle pole body (SPB) | 0.00314095 | 0.98939925 |
|  |  |  |  |
| **Gal4** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 2.89E-10 | 3.99E-07 |
| Proteome Localization--Predicted+Obs | cyt | 1.59E-06 | 6.36E-06 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 7.29E-07 | 0.00018876 |
| Proteome Localization--Observed | cell periphery | 2.95E-05 | 0.00032411 |
| MIPS Functional Classification | METABOLISM | 1.26E-06 | 0.00032687 |
| GO Biological Process | energy pathways [GO:0006091] | 5.67E-07 | 0.00078295 |
| GO Biological Process | energy derivation by oxidation of organic compounds [GO:0015980] | 5.67E-07 | 0.00078295 |

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|---|---|---|---|
| GO Biological Process | main pathways of carbohydrate metabolism [GO:0006092] | 6.26E-07 | 0.00086357 |
| Proteome Localization--Observed | cyto | 0.00017448 | 0.00191931 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 3.52E-06 | 0.00485924 |
| GO Biological Process | galactose metabolism [GO:0006012] | 3.58E-06 | 0.00493495 |
| GO Biological Process | hexose metabolism [GO:0019318] | 3.82E-06 | 0.00527342 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 4.12E-05 | 0.00782321 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 4.81E-05 | 0.01246238 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 9.57E-06 | 0.01320599 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 7.74E-05 | 0.02003637 |
| MIPS Functional Classification | ENERGY | 0.00013942 | 0.03610874 |
| MDS Proteomics Complexes | YBR055C (PRP6) | 8.60E-05 | 0.04238587 |
| PFam-A Domains | PF00083 (sugar_tr) | 3.76E-05 | 0.04454782 |
| GO Biological Process | glutamate biosynthesis [GO:0006537] | 3.29E-05 | 0.04539179 |
| GO Biological Process | TCA intermediate metabolism [GO:0006100] | 3.56E-05 | 0.04915574 |
| GO Biological Process | organic acid metabolism [GO:0006082] | 3.59E-05 | 0.04948542 |
| GO Biological Process | carboxylic acid metabolism [GO:0019752] | 3.59E-05 | 0.04948542 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00016108 | 0.05315772 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 4.88E-05 | 0.06721646 |
| MIPS Subcellular Localization | cytoplasm | 0.00197337 | 0.08288154 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 6.30E-05 | 0.08696208 |
| GO Biological Process | glutamate metabolism [GO:0006536] | 7.28E-05 | 0.10051782 |
| GO Biological Process | tricarboxylic acid cycle [GO:0006099] | 7.28E-05 | 0.10051782 |
| GO Cellular Component | cell [GO:0005623] | 0.00062635 | 0.20669451 |
| GO Cellular Component | intracellular [GO:0005622] | 0.00066949 | 0.22093203 |
| GO Cellular Component | cytoplasm [GO:0005737] | 0.00067571 | 0.22298331 |
| Cellzome Complexes | YDR148C (KGD2) | 0.00101923 | 0.46782657 |
| MDS Proteomics Complexes | YDR394W (RPT3) | 0.00119827 | 0.59074711 |
| GO Biological Process | glutamine family amino acid biosynthesis [GO:0009084] | 0.00053221 | 0.73444704 |
| MIPS Functional Classification | phosphate transport | 0.00325479 | 0.84299061 |
| MIPS Functional Classification | stress response | 0.003762 | 0.974358 |
| | | | |
| **Gat1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | nitrogen and sulfur metabolism | 5.21E-12 | 1.35E-09 |

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|---|---|---|---|
| MIPS Functional Classification | nitrogen and sulfur utilization | 2.76E-11 | 7.16E-09 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 4.18E-06 | 0.00079474 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 8.41E-05 | 0.00092555 |
| MIPS Functional Classification | amino acid degradation (catabolism) | 6.38E-06 | 0.00165253 |
| MIPS Functional Classification | METABOLISM | 6.44E-06 | 0.00166668 |
| GO Molecular Function | hydrolase [GO:0016787] | 2.52E-06 | 0.00347184 |
| GO Molecular Function | solute\:cation symporter [GO:0015294] | 2.56E-06 | 0.00353133 |
| GO Molecular Function | symporter [GO:0015293] | 5.01E-06 | 0.00689201 |
| GO Biological Process | glutamine family amino acid metabolism [GO:0009064] | 5.05E-06 | 0.00696863 |
| MIPS Functional Classification | amino acid metabolism | 3.25E-05 | 0.00842082 |
| GO Molecular Function | asparaginase [GO:0004067] | 1.10E-05 | 0.01513598 |
| MIPS Subcellular Localization | vacuolar lumen | 0.00048933 | 0.02055182 |
| GO Cellular Component | periplasmic space (sensu Fungi) [GO:0030287] | 8.60E-05 | 0.02838799 |
| GO Cellular Component | membrane [GO:0016020] | 0.00019965 | 0.06588483 |
| MIPS Functional Classification | plasma membrane | 0.00025786 | 0.06678574 |
| GO Biological Process | aspartate family amino acid catabolism [GO:0009068] | 4.89E-05 | 0.06752478 |
| MIPS Protein Classes | Cys4 zinc-fingers | 0.00083754 | 0.15913241 |
| PFam-A Domains | PF02133 (Transp_cyt_pur) | 0.00014004 | 0.16594385 |
| GO Biological Process | glutamine family amino acid catabolism [GO:0009065] | 0.00014004 | 0.19325106 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00093696 | 0.24267264 |
| GO Molecular Function | porter [GO:0015291] | 0.00019802 | 0.27267629 |
| GO Molecular Function | electrochemical potential-driven transporter [GO:0015290] | 0.00019802 | 0.27267629 |
| MIPS Functional Classification | mitochondrion | 0.00134672 | 0.34880048 |
| MIPS Functional Classification | nucleotide metabolism | 0.00147343 | 0.38161837 |
| GO Biological Process | response to starvation [GO:0009267] | 0.00031492 | 0.43459236 |
| MIPS Protein Classes | Proteases | 0.00252671 | 0.4800749 |
| MIPS Functional Classification | purine ribonucleotide metabolism | 0.00201348 | 0.52149132 |
| PFam-A Domains | PF00795 (CN_hydrolase) | 0.00048933 | 0.57985487 |
| MIPS Functional Classification | cellular import | 0.00283479 | 0.73421061 |
| SMART Domains | ZnF_GATA | 0.00268719 | 0.79003386 |
| GO Molecular Function | amino acid transporter [GO:0015171] | 0.00368348 | >0.999 |
| GO Biological Process | amino acid catabolism [GO:0009063] | 0.00209311 | >0.999 |
| GO Biological Process | amine catabolism [GO:0009310] | 0.00209311 | >0.999 |
| GO Molecular Function | transporter [GO:0005215] | 0.00338833 | >0.999 |

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| GO Biological Process | amino acid and derivative metabolism [GO:0006519] | 0.00477037 | >0.999 |
| GO Cellular Component | integral membrane protein [GO:0016021] | 0.00485068 | >0.999 |
| GO Biological Process | amino acid transport [GO:0006865] | 0.00435644 | >0.999 |
| GO Biological Process | nitrogen metabolism [GO:0006807] | 0.00202619 | >0.999 |
| GO Biological Process | amino acid metabolism [GO:0006520] | 0.00295681 | >0.999 |
| PFam-A Domains | PF00320 (GATA) | 0.00361428 | >0.999 |
| GO Biological Process | catabolism [GO:0009056] | 0.00232901 | >0.999 |
| GO Biological Process | glutamine family amino acid biosynthesis [GO:0009084] | 0.00368348 | >0.999 |
| | | | |
| **Gat3** | **n=197** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Cellular Component | cell wall (sensu Fungi) [GO:0009277] | 2.27E-06 | 0.00075067 |
| GO Cellular Component | periplasmic space (sensu Fungi) [GO:0030287] | 3.32E-06 | 0.00109515 |
| GO Cellular Component | cell wall [GO:0005618] | 4.95E-06 | 0.00163448 |
| GO Cellular Component | external protective structure [GO:0030312] | 4.95E-06 | 0.00163448 |
| GO Cellular Component | extracellular [GO:0005576] | 1.03E-05 | 0.0034054 |
| GO Molecular Function | asparaginase [GO:0004067] | 1.35E-05 | 0.01862475 |
| GO Cellular Component | integral plasma membrane protein [GO:0005887] | 9.61E-05 | 0.03170076 |
| Proteome Localization--Observed | cell periphery | 0.0037136 | 0.0408496 |
| MIPS Functional Classification | cell wall | 0.00017834 | 0.04619084 |
| GO Biological Process | aspartate family amino acid catabolism [GO:0009068] | 6.01E-05 | 0.08287259 |
| GO Biological Process | glutamine family amino acid catabolism [GO:0009065] | 0.00017142 | 0.23656098 |
| GO Biological Process | response to starvation [GO:0009267] | 0.00038451 | 0.5306169 |
| | | | |
| **Gat4** | **n=198** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Cellular Component | periplasmic space (sensu Fungi) [GO:0030287] | 3.40E-06 | 0.00112291 |
| GO Cellular Component | external protective structure [GO:0030312] | 2.80E-05 | 0.00922416 |
| GO Cellular Component | cell wall [GO:0005618] | 2.80E-05 | 0.00922416 |
| GO Molecular Function | asparaginase [GO:0004067] | 1.38E-05 | 0.0190037 |
| GO Cellular Component | extracellular [GO:0005576] | 5.85E-05 | 0.01930028 |
| GO Cellular Component | cell wall (sensu Fungi) [GO:0009277] | 8.65E-05 | 0.02854896 |
| MIPS Functional Classification | cell wall | 0.00018404 | 0.04766688 |
| GO Biological Process | aspartate family amino acid catabolism [GO:0009068] | 6.13E-05 | 0.08453714 |

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|---|---|---|---|
| GO Biological Process | glutamine family amino acid catabolism [GO:0009065] | 0.00017482 | 0.24125022 |
| SMART Domains | MIR | 0.00098977 | 0.29099356 |
| MIPS Functional Classification | osmosensing | 0.00166466 | 0.43114694 |
| GO Biological Process | response to starvation [GO:0009267] | 0.00039203 | 0.5409945 |
| SMART Domains | CYCLIN | 0.0020879 | 0.6138426 |
| PFam-A Domains | PF02366 (PMT) | 0.00057905 | 0.68616833 |
| GO Molecular Function | dolichyl-phosphate-mannose-protein mannosyltransferase [GO:0004169] | 0.00057905 | 0.79734497 |
| MIPS Protein Classes | Cyclins | 0.00452147 | 0.8590793 |
|  |  |  |  |
| **Gcn4** | **n=195** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | amino acid metabolism | 1.00E-14 | 2.59E-12 |
| MIPS Functional Classification | amino acid biosynthesis | 1.04E-14 | 2.70E-12 |
| GO Biological Process | amino acid metabolism [GO:0006520] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | amino acid biosynthesis [GO:0008652] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | amine biosynthesis [GO:0009309] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | amine metabolism [GO:0009308] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | amino acid and derivative metabolism [GO:0006519] | 1.00E-14 | 1.38E-11 |
| MIPS Functional Classification | METABOLISM | 9.82E-12 | 2.54E-09 |
| GO Biological Process | glutamine family amino acid metabolism [GO:0009064] | 9.00E-12 | 1.24E-08 |
| GO Biological Process | glutamine family amino acid biosynthesis [GO:0009084] | 1.67E-07 | 0.00023113 |
| GO Biological Process | aspartate family amino acid metabolism [GO:0009066] | 3.27E-07 | 0.00045103 |
| GO Biological Process | nitrogen metabolism [GO:0006807] | 3.25E-06 | 0.0044794 |
| GO Biological Process | urea cycle intermediate metabolism [GO:0000051] | 3.33E-06 | 0.00459363 |
| GO Biological Process | biosynthesis [GO:0009058] | 3.75E-06 | 0.00518122 |
| GO Biological Process | glutamine family amino acid catabolism [GO:0009065] | 6.15E-06 | 0.00848907 |
| GO Molecular Function | asparaginase [GO:0004067] | 1.30E-05 | 0.01788351 |
| GO Biological Process | arginine biosynthesis [GO:0006526] | 1.30E-05 | 0.01792247 |
| MIPS Functional Classification | amino acid degradation (catabolism) | 8.13E-05 | 0.02106123 |
| GO Biological Process | amine catabolism [GO:0009310] | 1.63E-05 | 0.02243369 |
| GO Biological Process | amino acid catabolism [GO:0009063] | 1.63E-05 | 0.02243369 |
| GO Biological Process | response to starvation [GO:0009267] | 1.84E-05 | 0.02535226 |
| GO Cellular Component | periplasmic space (sensu Fungi) [GO:0030287] | 0.00010132 | 0.03343659 |
| MIPS Functional Classification | nitrogen and sulfur metabolism | 0.00020374 | 0.05276892 |

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|---|---|---|---|
| PFam-A Domains | PF00153 (mito_carr) | 6.68E-05 | 0.07915101 |
| GO Biological Process | aspartate family amino acid catabolism [GO:0009068] | 5.77E-05 | 0.07961606 |
| GO Molecular Function | lyase [GO:0016829] | 7.07E-05 | 0.09732402 |
| GO Biological Process | aspartate family amino acid biosynthesis [GO:0009067] | 9.15E-05 | 0.12627662 |
| GO Biological Process | lysine metabolism [GO:0006553] | 0.00010132 | 0.13982574 |
| GO Biological Process | lysine biosynthesis [GO:0009085] | 0.00010132 | 0.13982574 |
| MIPS Subcellular Localization | cytoplasm | 0.00348089 | 0.14619738 |
| GO Molecular Function | carbon-carbon lyase [GO:0016830] | 0.0001181 | 0.16262508 |
| MIPS Subcellular Localization | mitochondria | 0.00431001 | 0.18102042 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 0.00018401 | 0.25393656 |
| GO Biological Process | arginine metabolism [GO:0006525] | 0.00025264 | 0.34864734 |
| GO Molecular Function | enzyme [GO:0003824] | 0.00025329 | 0.34878308 |
| MIPS Functional Classification | regulation of nitrogen and sulphur utilization | 0.00178987 | 0.46357633 |
| GO Cellular Component | mitochondrial matrix [GO:0005759] | 0.00178284 | 0.5883372 |
| PFam-A Domains | PF00682 (HMGL-like) | 0.0005536 | 0.656016 |
| GO Molecular Function | transporter [GO:0005215] | 0.00048394 | 0.66638813 |
| GO Molecular Function | aldehyde-lyase [GO:0016832] | 0.0005536 | 0.7623072 |
| GO Molecular Function | aldolase [GO:0016228] | 0.0005536 | 0.7623072 |
| GO Biological Process | leucine metabolism [GO:0006551] | 0.0005536 | 0.763968 |
| MIPS Functional Classification | regulation of amino acid metabolism | 0.00323447 | 0.83772773 |
| MIPS Functional Classification | mitochondrial transport | 0.00323919 | 0.83895021 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00454357 | 0.8632783 |
| GO Biological Process | aromatic compound metabolism [GO:0006725] | 0.0006323 | 0.87256986 |
| GO Cellular Component | mitochondrion [GO:0005739] | 0.00291466 | 0.9618378 |
| GO Biological Process | carboxylic acid metabolism [GO:0019752] | 0.00071097 | 0.98114412 |
| GO Biological Process | organic acid metabolism [GO:0006082] | 0.00071097 | 0.98114412 |
| GO Biological Process | branched chain family amino acid metabolism [GO:0009081] | 0.00071202 | 0.9825807 |
|  |  |  |  |
| **Gln3** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | nitrogen and sulfur utilization | 1.09E-06 | 0.00028241 |
| GO Molecular Function | hydrolase [GO:0016787] | 2.42E-07 | 0.00033295 |
| MIPS Functional Classification | nitrogen and sulfur metabolism | 3.35E-06 | 0.00086777 |
| GO Molecular Function | asparaginase [GO:0004067] | 1.05E-05 | 0.01450119 |

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|---|---|---|---|
| MIPS Subcellular Localization | vacuolar lumen | 0.00047406 | 0.01991052 |
| GO Cellular Component | periplasmic space (sensu Fungi) [GO:0030287] | 8.25E-05 | 0.02721876 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00026339 | 0.0500441 |
| GO Biological Process | aspartate family amino acid catabolism [GO:0009068] | 4.69E-05 | 0.06472683 |
| GO Biological Process | glutamine family amino acid metabolism [GO:0009064] | 4.77E-05 | 0.06586326 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00031395 | 0.08131409 |
| MIPS Functional Classification | cation transporters | 0.00038235 | 0.09902787 |
| MIPS Functional Classification | amino acid degradation (catabolism) | 0.00048511 | 0.12564427 |
| GO Biological Process | glutamine family amino acid catabolism [GO:0009065] | 0.0001343 | 0.18533952 |
| MIPS Subcellular Localization | vacuole | 0.0048562 | 0.2039604 |
| MIPS Functional Classification | amino acid metabolism | 0.00095634 | 0.24769077 |
| GO Biological Process | response to starvation [GO:0009267] | 0.00030219 | 0.4170153 |
| GO Cellular Component | membrane [GO:0016020] | 0.00141809 | 0.4679697 |
| MIPS Functional Classification | ion transporters | 0.001987 | 0.514633 |
| MIPS Functional Classification | lysosomal and vacuolar degradation | 0.00201205 | 0.52112095 |
| MIPS Functional Classification | cellular import | 0.00263605 | 0.68273695 |
| MIPS Functional Classification | homeostasis of protons | 0.00335643 | 0.86931537 |
| GO Molecular Function | enzyme [GO:0003824] | 0.00218231 | >0.999 |
| GO Molecular Function | amino acid transporter [GO:0015171] | 0.00354353 | >0.999 |
| GO Biological Process | amino acid catabolism [GO:0009063] | 0.00201205 | >0.999 |
| MIPS Functional Classification | cell wall | 0.00483249 | >0.999 |
| GO Biological Process | transport [GO:0006810] | 0.00388224 | >0.999 |
| GO Biological Process | catabolism [GO:0009056] | 0.00206664 | >0.999 |
| GO Biological Process | amine catabolism [GO:0009310] | 0.00201205 | >0.999 |
| GO Molecular Function | transporter [GO:0005215] | 0.00130918 | >0.999 |
| GO Biological Process | cation transport [GO:0006812] | 0.00470745 | >0.999 |
| GO Biological Process | amino acid transport [GO:0006865] | 0.00419198 | >0.999 |
| | | | |
| **Gsm1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 1.28E-08 | 3.32E-06 |
| MIPS Functional Classification | METABOLISM | 2.49E-07 | 6.45E-05 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 1.61E-06 | 0.00041673 |
| PFam-A Domains | PF00083 (sugar_tr) | 5.11E-07 | 0.00060537 |

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|---|---|---|---|
| MIPS Functional Classification | ENERGY | 3.07E-06 | 0.00079566 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 2.81E-06 | 0.00387837 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 3.25E-05 | 0.00617472 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 3.45E-05 | 0.00893444 |
| Proteome Localization--Predicted+Obs | cyt | 0.00267231 | 0.01068924 |
| GO Cellular Component | peroxisomal matrix [GO:0005782] | 6.61E-05 | 0.02182307 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 1.67E-05 | 0.02305002 |
| GO Molecular Function | hexose transporter [GO:0015149] | 1.67E-05 | 0.02305002 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00212606 | 0.02338666 |
| GO Biological Process | hexose metabolism [GO:0019318] | 2.14E-05 | 0.02959976 |
| SMART Domains | Aamy | 0.00010337 | 0.0303896 |
| Proteome Localization--Observed | cell periphery | 0.00361035 | 0.03971385 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 2.90E-05 | 0.04007492 |
| GO Molecular Function | alpha-glucosidase [GO:0004558] | 3.02E-05 | 0.04154395 |
| MIPS Subcellular Localization | peroxisome | 0.00136958 | 0.05752236 |
| GO Biological Process | hexose transport [GO:0008645] | 4.26E-05 | 0.05872493 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 4.26E-05 | 0.05872493 |
| GO Molecular Function | fructose transporter [GO:0005353] | 4.52E-05 | 0.06228199 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 4.85E-05 | 0.06688667 |
| PFam-A Domains | PF00128 (alpha-amylase) | 5.89E-05 | 0.06975384 |
| GO Molecular Function | mannose transporter [GO:0015578] | 6.61E-05 | 0.0910617 |
| MIPS Subcellular Localization | peroxisomal matrix | 0.00248619 | 0.10441998 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 0.00049963 | 0.12940391 |
| MIPS Phenotypes | other carbohydrate and lipid biosynthesis defects | 0.00077105 | 0.13878882 |
| MIPS Functional Classification | drug transporters | 0.00065946 | 0.17080118 |
| GO Molecular Function | glucose transporter [GO:0005355] | 0.00012947 | 0.1782857 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 0.00018368 | 0.25293149 |
| GO Biological Process | main pathways of carbohydrate metabolism [GO:0006092] | 0.00020991 | 0.2896758 |
| GO Biological Process | lipid metabolism [GO:0006629] | 0.00022343 | 0.30833754 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.0012863 | 0.424479 |
| GO Cellular Component | peroxisome [GO:0005777] | 0.00136958 | 0.4519614 |
| PFam-A Domains | PF00107 (adh_zinc) | 0.00038445 | 0.45557325 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 0.0003695 | 0.50880012 |
| GO Biological Process | TCA intermediate metabolism [GO:0006100] | 0.00038445 | 0.530541 |

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|---|---|---|---|
| MIPS Phenotypes | Carbohydrate and lipid biosynthesis defects | 0.00319635 | 0.575343 |
| GO Molecular Function | transporter [GO:0005215] | 0.0005219 | 0.71866181 |
| GO Molecular Function | alcohol dehydrogenase [GO:0004022] | 0.000562 | 0.77387262 |
| GO Molecular Function | galactose transporter [GO:0005354] | 0.000562 | 0.77387262 |
| GO Biological Process | sphingoid metabolism [GO:0046519] | 0.000562 | 0.77555862 |
| MIPS Protein Classes | Ubiquitin-system proteins | 0.00437787 | 0.8317953 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 0.0006092 | 0.840696 |
| GO Biological Process | sphingolipid metabolism [GO:0006665] | 0.00365571 | >0.999 |
| GO Biological Process | fatty acid beta-oxidation [GO:0006635] | 0.00150207 | >0.999 |
| MIPS Functional Classification | plasma membrane | 0.00397459 | >0.999 |
| MIPS Functional Classification | detoxification | 0.00442971 | >0.999 |
| GO Biological Process | fatty acid oxidation [GO:0019395] | 0.00220143 | >0.999 |
| GO Biological Process | energy derivation by oxidation of organic compounds [GO:0015980] | 0.00397459 | >0.999 |
| GO Biological Process | ion transport [GO:0006811] | 0.00294426 | >0.999 |
| GO Biological Process | organic acid metabolism [GO:0006082] | 0.00308925 | >0.999 |
| GO Molecular Function | enzyme [GO:0003824] | 0.00251296 | >0.999 |
| GO Biological Process | glucose metabolism [GO:0006006] | 0.00227081 | >0.999 |
| GO Biological Process | energy pathways [GO:0006091] | 0.00397459 | >0.999 |
| GO Molecular Function | anion transporter [GO:0008509] | 0.00303261 | >0.999 |
| MDS Proteomics Complexes | YDL145C (COP1) | 0.00412857 | >0.999 |
| MDS Proteomics Complexes | YDR477W (SNF1) | 0.00220143 | >0.999 |
| GO Biological Process | carboxylic acid metabolism [GO:0019752] | 0.00308925 | >0.999 |
| GO Molecular Function | glucosidase [GO:0015926] | 0.00436031 | >0.999 |
| | | | |
| **Gzf3** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | nitrogen and sulfur metabolism | 5.21E-12 | 1.35E-09 |
| MIPS Functional Classification | nitrogen and sulfur utilization | 4.82E-10 | 1.25E-07 |
| MIPS Functional Classification | amino acid degradation (catabolism) | 5.59E-07 | 0.00014469 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 2.24E-05 | 0.00024644 |
| MIPS Functional Classification | amino acid metabolism | 2.31E-06 | 0.00059757 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 4.18E-06 | 0.00079474 |
| GO Molecular Function | hydrolase [GO:0016787] | 9.21E-07 | 0.00126821 |
| MIPS Functional Classification | METABOLISM | 1.40E-05 | 0.0036217 |

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|---|---|---|---|
| GO Biological Process | glutamine family amino acid metabolism [GO:0009064] | 5.05E-06 | 0.00696863 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 4.70E-05 | 0.01216093 |
| GO Molecular Function | asparaginase [GO:0004067] | 1.10E-05 | 0.01513598 |
| MIPS Subcellular Localization | vacuolar lumen | 0.00048933 | 0.02055182 |
| GO Cellular Component | periplasmic space (sensu Fungi) [GO:0030287] | 8.60E-05 | 0.02838799 |
| GO Cellular Component | membrane [GO:0016020] | 9.12E-05 | 0.03010062 |
| GO Biological Process | amino acid transport [GO:0006865] | 4.31E-05 | 0.05941245 |
| GO Biological Process | aspartate family amino acid catabolism [GO:0009068] | 4.89E-05 | 0.06752478 |
| GO Molecular Function | solute\:cation symporter [GO:0015294] | 8.60E-05 | 0.11845532 |
| MIPS Functional Classification | homeostasis of other cations | 0.00048694 | 0.12611746 |
| MIPS Functional Classification | amino-acid transporters | 0.00073247 | 0.18970973 |
| GO Molecular Function | symporter [GO:0015293] | 0.00014004 | 0.19283095 |
| GO Biological Process | glutamine family amino acid catabolism [GO:0009065] | 0.00014004 | 0.19325106 |
| MIPS Functional Classification | plasma membrane | 0.00086988 | 0.22529918 |
| GO Biological Process | amino acid catabolism [GO:0009063] | 0.00018544 | 0.25590444 |
| GO Biological Process | amine catabolism [GO:0009310] | 0.00018544 | 0.25590444 |
| GO Molecular Function | porter [GO:0015291] | 0.00019802 | 0.27267629 |
| GO Molecular Function | electrochemical potential-driven transporter [GO:0015290] | 0.00019802 | 0.27267629 |
| SMART Domains | TRANS | 0.00127458 | 0.37472652 |
| MIPS Functional Classification | regulation of nitrogen and sulphur utilization | 0.00148621 | 0.38492839 |
| GO Biological Process | response to starvation [GO:0009267] | 0.00031492 | 0.43459236 |
| MIPS Protein Classes | Proteases | 0.00252671 | 0.4800749 |
| GO Molecular Function | amino acid transporter [GO:0015171] | 0.00039044 | 0.53764001 |
| MIPS Functional Classification | lysosomal and vacuolar degradation | 0.00209311 | 0.54211549 |
| MIPS Functional Classification | cellular import | 0.00283479 | 0.73421061 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00243181 | 0.8024973 |
| GO Biological Process | transport [GO:0006810] | 0.00246925 | >0.999 |
| GO Molecular Function | transporter [GO:0005215] | 0.0015077 | >0.999 |
| GO Biological Process | amino acid and derivative metabolism [GO:0006519] | 0.00156144 | >0.999 |
| GO Biological Process | cation transport [GO:0006812] | 0.00499176 | >0.999 |
| GO Biological Process | nitrogen metabolism [GO:0006807] | 0.00202619 | >0.999 |
| PFam-A Domains | PF00324 (aa_permeases) | 0.00368348 | >0.999 |
| GO Biological Process | amine metabolism [GO:0009308] | 0.00175052 | >0.999 |
| PFam-A Domains | PF02133 (Transp_cyt_pur) | 0.00268719 | >0.999 |

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|---|---|---|---|
| GO Biological Process | amino acid metabolism [GO:0006520] | 0.0009062 | >0.999 |
| GO Biological Process | catabolism [GO:0009056] | 0.00232901 | >0.999 |
| GO Biological Process | glutamine family amino acid biosynthesis [GO:0009084] | 0.00368348 | >0.999 |
| MIPS Functional Classification | amino acid transport | 0.00435644 | >0.999 |
|  |  |  |  |
| **Hal9** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | plasma membrane | 2.53E-06 | 0.00065607 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 9.96E-06 | 0.00189206 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00020372 | 0.00224093 |
| GO Cellular Component | plasma membrane [GO:0005886] | 1.26E-05 | 0.00416734 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 1.65E-05 | 0.0042705 |
| MIPS Functional Classification | detoxification | 1.85E-05 | 0.0047936 |
| MIPS Functional Classification | drug transporters | 9.54E-05 | 0.02471787 |
| Proteome Localization--Observed | cyto | 0.00284451 | 0.03128961 |
| Proteome Localization--Observed | cell periphery | 0.00403694 | 0.04440634 |
| PFam-A Domains | PF00083 (sugar_tr) | 3.76E-05 | 0.04454782 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 3.31E-05 | 0.04566185 |
| GO Biological Process | hexose transport [GO:0008645] | 4.77E-05 | 0.06580627 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 4.77E-05 | 0.06580627 |
| MIPS Protein Classes | Zinc-coordinating DNA-binding domains | 0.00056341 | 0.10704752 |
| MIPS Protein Classes | Transcription factors | 0.00065715 | 0.12485755 |
| SMART Domains | ZnF_C2H2 | 0.00094528 | 0.27791232 |
| MIPS Protein Classes | Cys2His2 zinc-finger | 0.00173371 | 0.3294049 |
| GO Molecular Function | hexose transporter [GO:0015149] | 0.00025409 | 0.34987918 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 0.00025409 | 0.34987918 |
| PFam-A Domains | PF00096 (zf-C2H2) | 0.00031682 | 0.37542696 |
| GO Molecular Function | transporter [GO:0005215] | 0.00029115 | 0.40091355 |
| MIPS Protein Complexes | Cytoplasmic ribosomes | 0.0014333 | 0.4514895 |
| PFam-A Domains | PF00107 (adh_zinc) | 0.00042209 | 0.50017665 |
| GO Cellular Component | membrane [GO:0016020] | 0.00152666 | 0.5037978 |
| MIPS Functional Classification | METABOLISM | 0.00228836 | 0.59268524 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 0.00045107 | 0.62247246 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 0.00316469 | 0.81965471 |

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|---|---|---|---|
| GO Molecular Function | galactose transporter [GO:0005354] | 0.00059642 | 0.82127447 |
| | | | |
| **Leu3** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | METABOLISM | 4.13E-10 | 1.07E-07 |
| MIPS Functional Classification | amino acid metabolism | 1.34E-06 | 0.00034707 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 1.54E-06 | 0.00039924 |
| GO Biological Process | amino acid metabolism [GO:0006520] | 1.49E-06 | 0.00205285 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 2.97E-06 | 0.00410545 |
| GO Biological Process | hexose metabolism [GO:0019318] | 3.30E-06 | 0.0045513 |
| GO Biological Process | amino acid biosynthesis [GO:0008652] | 3.39E-06 | 0.00467652 |
| GO Biological Process | amino acid and derivative metabolism [GO:0006519] | 3.56E-06 | 0.00491524 |
| GO Biological Process | amine metabolism [GO:0009308] | 4.28E-06 | 0.00590966 |
| MIPS Protein Classes | Transcription factors | 5.11E-05 | 0.00970379 |
| GO Biological Process | amine biosynthesis [GO:0009309] | 7.12E-06 | 0.00983238 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 8.28E-06 | 0.01142799 |
| GO Biological Process | branched chain family amino acid biosynthesis [GO:0009082] | 1.16E-05 | 0.01594742 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 6.20E-05 | 0.01605339 |
| MIPS Functional Classification | ENERGY | 0.00011311 | 0.02929653 |
| GO Biological Process | main pathways of carbohydrate metabolism [GO:0006092] | 3.34E-05 | 0.04603349 |
| GO Biological Process | branched chain family amino acid metabolism [GO:0009081] | 4.64E-05 | 0.06396493 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 5.44E-05 | 0.07501004 |
| GO Molecular Function | oxo-acid-lyase [GO:0016833] | 6.78E-05 | 0.09330635 |
| MIPS Protein Classes | Zinc-coordinating DNA-binding domains | 0.00049576 | 0.09419383 |
| MIPS Functional Classification | glyoxylate cycle | 0.00057048 | 0.14775432 |
| GO Molecular Function | carbon-carbon lyase [GO:0016830] | 0.00012591 | 0.17337807 |
| MIPS Functional Classification | amino acid biosynthesis | 0.00113314 | 0.29348326 |
| MIPS Protein Classes | Cys2His2 zinc-finger | 0.00160464 | 0.3048816 |
| MIPS Phenotypes | Methionine auxotrophy (Met) | 0.00223384 | 0.4020912 |
| GO Biological Process | glucose metabolism [GO:0006006] | 0.00038898 | 0.53678964 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 0.00039226 | 0.54014202 |
| GO Biological Process | TCA intermediate metabolism [GO:0006100] | 0.00039361 | 0.5431818 |
| SMART Domains | small_GTPase | 0.00223384 | 0.65674896 |
| GO Biological Process | regulation of transcription from Pol II promoter [GO:0006357] | 0.00048525 | 0.669645 |

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|---|---|---|---|
| GO Biological Process | glutamate biosynthesis [GO:0006537] | 0.00054181 | 0.74769504 |
| GO Biological Process | transcription from Pol II promoter [GO:0006366] | 0.00059884 | 0.82640472 |
| GO Molecular Function | transcription regulator [GO:0030528] | 0.00060767 | 0.83675471 |
| GO Biological Process | amino acid transport [GO:0006865] | 0.00061838 | 0.85336716 |
| MIPS Phenotypes | other carbohydrate and lipid biosynthesis defects | 0.00497571 | 0.8956278 |
| PFam-A Domains | PF00096 (zf-C2H2) | 0.00182395 | >0.999 |
| GO Molecular Function | transcription factor [GO:0003700] | 0.00211858 | >0.999 |
| GO Molecular Function | amino acid transporter [GO:0015171] | 0.00444039 | >0.999 |
| GO Molecular Function | lyase [GO:0016829] | 0.00153624 | >0.999 |
| MIPS Functional Classification | detoxification | 0.00458005 | >0.999 |
| GO Molecular Function | specific RNA polymerase II transcription factor [GO:0003704] | 0.00092089 | >0.999 |
| GO Biological Process | gluconeogenesis [GO:0006094] | 0.00372332 | >0.999 |
| GO Biological Process | energy derivation by oxidation of organic compounds [GO:0015980] | 0.00414118 | >0.999 |
| SMART Domains | ZnF_C2H2 | 0.00448824 | >0.999 |
| GO Molecular Function | enzyme [GO:0003824] | 0.00290068 | >0.999 |
| PFam-A Domains | PF00324 (aa_permeases) | 0.00444039 | >0.999 |
| GO Biological Process | energy pathways [GO:0006091] | 0.00414118 | >0.999 |
| PFam-A Domains | PF00107 (adh_zinc) | 0.00372332 | >0.999 |
| GO Biological Process | glutamine family amino acid biosynthesis [GO:0009084] | 0.00444039 | >0.999 |
| GO Biological Process | glutamate metabolism [GO:0006536] | 0.00098444 | >0.999 |
| MDS Proteomics Complexes | YBR055C (PRP6) | 0.002935 | >0.999 |
| MIPS Functional Classification | amino acid degradation (catabolism) | 0.00439463 | >0.999 |
| GO Molecular Function | RNA polymerase II transcription factor [GO:0003702] | 0.00078935 | >0.999 |
| | | | |
| **Lys14** | **n=198** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Biological Process | hexose transport [GO:0008645] | 9.12E-09 | 1.26E-05 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 9.12E-09 | 1.26E-05 |
| GO Biological Process | lysine metabolism [GO:0006553] | 7.16E-08 | 9.88E-05 |
| GO Biological Process | lysine biosynthesis [GO:0009085] | 7.16E-08 | 9.88E-05 |
| GO Molecular Function | mannose transporter [GO:0015578] | 1.47E-07 | 0.00020216 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 2.11E-07 | 0.00029061 |
| GO Molecular Function | glucose transporter [GO:0005355] | 4.20E-07 | 0.00057885 |
| Proteome Localization--Predicted+Obs | cyt | 0.00023142 | 0.00092569 |

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|---|---|---|---|
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 1.03E-06 | 0.001421 |
| GO Molecular Function | hexose transporter [GO:0015149] | 1.03E-06 | 0.001421 |
| MIPS Functional Classification | METABOLISM | 9.36E-06 | 0.00242396 |
| GO Molecular Function | fructose transporter [GO:0005353] | 2.24E-06 | 0.00308708 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 1.38E-05 | 0.00357972 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 1.39E-05 | 0.00360344 |
| GO Biological Process | aspartate family amino acid biosynthesis [GO:0009067] | 5.67E-06 | 0.00782369 |
| MIPS Functional Classification | plasma membrane | 3.67E-05 | 0.00950009 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00089971 | 0.00989681 |
| Proteome Localization--Observed | cyto | 0.00130309 | 0.01433399 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 1.77E-05 | 0.02439467 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 1.90E-05 | 0.02620596 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00014202 | 0.02698285 |
| PFam-A Domains | PF00083 (sugar_tr) | 3.47E-05 | 0.04114533 |
| GO Biological Process | aspartate family amino acid metabolism [GO:0009066] | 3.36E-05 | 0.04635144 |
| GO Molecular Function | carbohydrate kinase [GO:0019200] | 6.94E-05 | 0.09559382 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 0.00053114 | 0.13756422 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00046714 | 0.15415686 |
| MIPS Functional Classification | cellular import | 0.00114992 | 0.29782928 |
| MIPS Functional Classification | regulation of C-compound and carbohydrate utilization | 0.001356 | 0.351204 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 0.00028686 | 0.39586956 |
| Cellzome Complexes | YIL038C (NOT3) | 0.00098977 | 0.45430627 |
| Cellzome Complexes | YDR062W (LCB2) | 0.0010033 | 0.4605147 |
| MIPS Functional Classification | transport mechanism | 0.00199052 | 0.51554468 |
| MIPS Protein Classes | NPR/HAL5 family | 0.00316301 | 0.6009719 |
| SMART Domains | Aamy | 0.00226655 | 0.6663657 |
| Cellzome Complexes | YBL039C (URA7) | 0.00166466 | 0.76407894 |
| GO Biological Process | carbohydrate catabolism [GO:0016052] | 0.00069583 | 0.96024126 |
| | | | |
| **Matalpha2** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Cellular Component | endoplasmic reticulum [GO:0005783] | 0.00070672 | 0.2332176 |
| MIPS Functional Classification | endoplasmic reticulum | 0.00119506 | 0.30952054 |
| MIPS Protein Classes | ion-transport ATPases | 0.00319635 | 0.6073065 |

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|---|---|---|---|
| GO Molecular Function | primary active transporter [GO:0015399] | 0.00046102 | 0.63482592 |
| SMART Domains | COIL | 0.00289502 | 0.85113588 |
| GO Biological Process | ion homeostasis [GO:0006873] | 0.00420041 | >0.999 |
| GO Biological Process | ergosterol biosynthesis [GO:0006696] | 0.00090661 | >0.999 |
| GO Biological Process | ergosterol metabolism [GO:0008204] | 0.00090661 | >0.999 |
| GO Molecular Function | P-P-bond-hydrolysis-driven transporter [GO:0015405] | 0.00117278 | >0.999 |
| GO Biological Process | sterol biosynthesis [GO:0016126] | 0.00183082 | >0.999 |
| GO Biological Process | steroid biosynthesis [GO:0006694] | 0.00486952 | >0.999 |
| GO Molecular Function | hydrogen-transporting two-sector ATPase [GO:0003936] | 0.00214203 | >0.999 |
| GO Biological Process | lipid biosynthesis [GO:0008610] | 0.00338723 | >0.999 |
| GO Molecular Function | hydrogen-/sodium-translocating ATPase [GO:0015442] | 0.00214203 | >0.999 |
| GO Biological Process | sterol metabolism [GO:0016125] | 0.00287754 | >0.999 |
|  |  |  |  |
| **Mbp1** | **n=199** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | DNA synthesis and replication | 1.00E-14 | 2.59E-12 |
| MIPS Functional Classification | DNA processing | 1.00E-14 | 2.59E-12 |
| GO Biological Process | DNA replication and chromosome cycle [GO:0000067] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | DNA dependent DNA replication [GO:0006261] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | DNA metabolism [GO:0006259] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | DNA replication [GO:0006260] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | S phase of mitotic cell cycle [GO:0000084] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | cell cycle [GO:0007049] | 8.35E-14 | 1.15E-10 |
| MIPS Functional Classification | CELL CYCLE AND DNA PROCESSING | 6.96E-13 | 1.80E-10 |
| MIPS Protein Complexes | Replication complexes | 7.72E-13 | 2.43E-10 |
| MIPS Phenotypes | Nucleic acid metabolism defects | 5.13E-12 | 9.23E-10 |
| GO Biological Process | mitotic cell cycle [GO:0000278] | 1.41E-12 | 1.95E-09 |
| MIPS Protein Complexes | Replication fork complexes | 3.96E-11 | 1.25E-08 |
| MIPS Phenotypes | DNA repair mutants | 1.96E-10 | 3.52E-08 |
| MIPS Phenotypes | Cell cycle defects | 3.73E-10 | 6.71E-08 |
| GO Biological Process | DNA repair [GO:0006281] | 5.53E-11 | 7.63E-08 |
| Proteome Localization--Predicted+Obs | nuc | 5.17E-08 | 2.07E-07 |
| GO Biological Process | DNA strand elongation [GO:0006271] | 3.37E-10 | 4.65E-07 |
| GO Cellular Component | replication fork [GO:0005657] | 3.62E-09 | 1.19E-06 |

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|---|---|---|---|
| MIPS Protein Classes | Histones | 8.69E-09 | 1.65E-06 |
| MIPS Subcellular Localization | nucleus | 1.14E-07 | 4.79E-06 |
| MIPS Phenotypes | other DNA repair mutants | 2.92E-08 | 5.25E-06 |
| GO Cellular Component | nucleosome [GO:0005718] | 2.03E-08 | 6.70E-06 |
| MIPS Protein Complexes | Nucleosomal protein complex | 2.53E-08 | 7.96E-06 |
| MIPS Functional Classification | DNA recombination and DNA repair | 5.72E-08 | 1.48E-05 |
| GO Biological Process | double-strand break repair [GO:0006302] | 1.44E-08 | 1.98E-05 |
| Synthetic Genetic Array Analysis | YMR190C (SGS1) | 6.41E-06 | 5.12E-05 |
| GO Cellular Component | chromatin [GO:0005717] | 1.81E-07 | 5.97E-05 |
| MIPS Functional Classification | chromosome | 8.04E-07 | 0.00020834 |
| PFam-A Domains | PF00125 (histone) | 1.80E-07 | 0.00021292 |
| GO Biological Process | double-strand break repair via synthesis-dependent strand annealing [GO:0045003] | 1.80E-07 | 0.00024795 |
| GO Cellular Component | chromosome [GO:0005694] | 7.85E-07 | 0.00025908 |
| MIPS Protein Classes | associated subunits | 1.59E-06 | 0.00030238 |
| MIPS Phenotypes | other cell cycle defects | 2.01E-06 | 0.00036155 |
| GO Biological Process | lagging strand elongation [GO:0006273] | 2.63E-07 | 0.00036289 |
| GO Biological Process | double-strand break repair via homologous recombination [GO:0000724] | 2.63E-07 | 0.00036289 |
| GO Biological Process | recombinational repair [GO:0000725] | 2.63E-07 | 0.00036289 |
| MIPS Phenotypes | UV light sensitivity | 3.97E-06 | 0.00071547 |
| GO Biological Process | DNA recombination [GO:0006310] | 5.93E-07 | 0.00081768 |
| GO Biological Process | mitotic recombination [GO:0006312] | 6.11E-07 | 0.00084266 |
| GO Biological Process | double-strand break repair via single-strand annealing [GO:0045002] | 7.49E-07 | 0.00103421 |
| GO Biological Process | chromosome organization and biogenesis (sensu Eukarya) [GO:0007001] | 7.74E-07 | 0.00106821 |
| MIPS Phenotypes | Alkylating agents sensitivity | 6.30E-06 | 0.00113347 |
| GO Cellular Component | cell [GO:0005623] | 7.41E-06 | 0.00244501 |
| MIPS Functional Classification | SUBCELLULAR LOCALISATION | 1.07E-05 | 0.0027712 |
| MIPS Functional Classification | deoxyribonucleotide metabolism | 1.21E-05 | 0.00314457 |
| MIPS Protein Classes | DNA-directed DNA polymerases | 2.03E-05 | 0.00385286 |
| GO Biological Process | nuclear organization and biogenesis [GO:0006997] | 3.82E-06 | 0.00527611 |
| Deletions Consortium (Essentiality, Mo | Morphology - Large | 0.00048809 | 0.00536898 |
| GO Molecular Function | DNA binding [GO:0003677] | 4.01E-06 | 0.00551824 |
| MIPS Phenotypes | DNA replication mutants | 3.20E-05 | 0.0057663 |
| MIPS Protein Classes | DNA-dependent ATPases | 3.21E-05 | 0.00609999 |
| GO Biological Process | chromatin assembly/disassembly [GO:0006333] | 4.66E-06 | 0.0064329 |

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|---|---|---|---|
| GO Biological Process | post-replication repair [GO:0006301] | 6.80E-06 | 0.00938045 |
| GO Biological Process | establishment and/or maintenance of chromatin architecture [GO:0006325] | 8.52E-06 | 0.0117633 |
| GO Biological Process | DNA packaging [GO:0006323] | 8.52E-06 | 0.0117633 |
| MIPS Phenotypes | other cell morphology mutants | 6.57E-05 | 0.01182884 |
| GO Cellular Component | intracellular [GO:0005622] | 5.61E-05 | 0.0185067 |
| Deletions Consortium (Essentiality, Mo | Morphology - Elongate | 0.00209825 | 0.02308075 |
| GO Cellular Component | bud [GO:0005933] | 7.09E-05 | 0.02338938 |
| MIPS Functional Classification | DNA repair | 9.44E-05 | 0.02445892 |
| GO Cellular Component | bud neck [GO:0005935] | 9.94E-05 | 0.03281672 |
| GO Cellular Component | site of polarized growth (sensu Fungi) [GO:0030483] | 0.00010151 | 0.03349665 |
| GO Cellular Component | site of polarized growth (sensu Saccharomyces) [GO:0000134] | 0.00010151 | 0.03349665 |
| GO Cellular Component | site of polarized growth [GO:0030427] | 0.00010151 | 0.03349665 |
| MIPS Functional Classification | transcriptional control | 0.00013054 | 0.03380986 |
| GO Cellular Component | cell cortex [GO:0005938] | 0.00010481 | 0.03458598 |
| GO Biological Process | non-recombinational repair [GO:0000726] | 2.54E-05 | 0.03504952 |
| GO Biological Process | mismatch repair [GO:0006298] | 2.54E-05 | 0.03504952 |
| GO Biological Process | maintenance of fidelity during DNA dependent DNA replication [GO:0045005] | 2.54E-05 | 0.03504952 |
| Synthetic Genetic Array Analysis | YNL271C (BNI1) | 0.00520575 | 0.041646 |
| MIPS Subcellular Localization | cytoskeleton | 0.00099406 | 0.04175031 |
| GO Biological Process | nucleotide-excision repair [GO:0006289] | 3.20E-05 | 0.0442083 |
| MIPS Functional Classification | cell cycle | 0.00018156 | 0.047023 |
| MIPS Phenotypes | Recombination mutants | 0.00030313 | 0.0545625 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 4.19E-05 | 0.05775355 |
| GO Molecular Function | DNA-directed DNA polymerase [GO:0003887] | 4.64E-05 | 0.06383565 |
| GO Biological Process | DNA replication initiation [GO:0006270] | 4.64E-05 | 0.06397473 |
| GO Biological Process | metabolism [GO:0008152] | 4.73E-05 | 0.06530822 |
| MDS Proteomics Complexes | YPL153C (RAD53) | 0.00013912 | 0.06858616 |
| Cellzome Complexes | YBL035C (POL12) | 0.00017827 | 0.08182364 |
| GO Cellular Component | nucleus [GO:0005634] | 0.00029792 | 0.09831195 |
| PFam-A Domains | PF00176 (SNF2_N) | 0.00013912 | 0.1648572 |
| GO Cellular Component | alpha DNA polymerase\:primase complex [GO:0005658] | 0.00058769 | 0.19393836 |
| GO Molecular Function | kinase [GO:0016301] | 0.00015562 | 0.21428599 |
| MIPS Functional Classification | fungal cell differentiation | 0.00094944 | 0.24590367 |
| MIPS Functional Classification | cell differentiation | 0.00094944 | 0.24590367 |

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|---|---|---|---|
| GO Biological Process | double-strand break repair via break-induced replication [GO:0000727] | 0.00017827 | 0.2460057 |
| MIPS Protein Classes | CaMK group | 0.00132964 | 0.2526316 |
| Cellzome Complexes | YJL115W (ASF1) | 0.00058769 | 0.26975063 |
| GO Molecular Function | transferase [GO:0016740] | 0.00019833 | 0.27309766 |
| MDS Proteomics Complexes | YOL054W (PSH1) | 0.000563 | 0.27756097 |
| MIPS Phenotypes | Mating and sporulation defects | 0.0015587 | 0.280566 |
| GO Molecular Function | protein kinase [GO:0004672] | 0.00024239 | 0.33377241 |
| GO Biological Process | DNA unwinding [GO:0006268] | 0.00027319 | 0.37700634 |
| MIPS Functional Classification | meiosis | 0.00161426 | 0.41809334 |
| MIPS Functional Classification | mitotic cell cycle and cell cycle control | 0.00166612 | 0.43152508 |
| MIPS Phenotypes | Cell morphology and organelle mutants | 0.00246108 | 0.4429944 |
| MIPS Phenotypes | Sporulation efficiency | 0.00281053 | 0.5058954 |
| GO Cellular Component | pre-replicative complex [GO:0005656] | 0.0015696 | 0.517968 |
| MIPS Functional Classification | CELL FATE | 0.00201161 | 0.52100699 |
| GO Cellular Component | nucleoplasm [GO:0005654] | 0.00163963 | 0.5410779 |
| MIPS Functional Classification | mRNA synthesis | 0.0021825 | 0.5652675 |
| SMART Domains | CYCLIN | 0.00212688 | 0.62530272 |
| SMART Domains | BROMO | 0.00229957 | 0.67607358 |
| GO Biological Process | cell cycle checkpoint [GO:0000075] | 0.00051406 | 0.70940694 |
| GO Biological Process | telomerase-independent telomere maintenance [GO:0000722] | 0.00058769 | 0.81101496 |
| MIPS Protein Complexes | Replication complex | 0.00262786 | 0.8277759 |
| MIPS Protein Classes | Cyclins | 0.00460355 | 0.8746745 |
| Cellzome Complexes | YBL002W (HTB2) | 0.00212688 | 0.97623792 |
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| **Mcm1** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Cellular Component | cell wall [GO:0005618] | 5.19E-12 | 1.71E-09 |
| GO Cellular Component | external protective structure [GO:0030312] | 5.19E-12 | 1.71E-09 |
| GO Cellular Component | extracellular [GO:0005576] | 8.20E-11 | 2.71E-08 |
| Proteome Localization--Predicted+Obs | en2 | 4.26E-06 | 1.70E-05 |
| MIPS Subcellular Localization | extracellular | 1.10E-06 | 4.64E-05 |
| MIPS Functional Classification | cell wall | 2.48E-07 | 6.43E-05 |
| GO Cellular Component | cell wall (sensu Fungi) [GO:0009277] | 3.86E-07 | 0.00012731 |
| MIPS Functional Classification | extracellular / secretion proteins | 1.65E-06 | 0.0004283 |

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|---|---|---|---|
| MIPS Functional Classification | stress response | 2.49E-06 | 0.00064376 |
| MIPS Functional Classification | CELL FATE | 2.95E-05 | 0.0076449 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00170882 | 0.01879702 |
| MIPS Functional Classification | cell differentiation | 0.00017805 | 0.04611547 |
| MIPS Functional Classification | fungal cell differentiation | 0.00017805 | 0.04611547 |
| MIPS Functional Classification | plasma membrane | 0.00051343 | 0.13297889 |
| MIPS Phenotypes | Galactose fermentation (Gal) | 0.00078341 | 0.14101452 |
| MIPS Functional Classification | other cell division and DNA synthesis activities | 0.00059642 | 0.15447356 |
| MIPS Phenotypes | other mating and sporulation defects | 0.001505 | 0.2709 |
| GO Molecular Function | structural constituent of cell wall [GO:0005199] | 0.00027852 | 0.38351516 |
| MIPS Functional Classification | cellular sensing and response | 0.00212059 | 0.54923281 |
| MIPS Functional Classification | chemoperception and response | 0.00212059 | 0.54923281 |
| GO Biological Process | development [GO:0007275] | 0.00060501 | 0.83491104 |
| GO Biological Process | pheromone response (sensu Fungi) [GO:0030434] | 0.00062431 | 0.86154918 |
| GO Biological Process | pheromone response (sensu Saccharomyces) [GO:0007328] | 0.00062431 | 0.86154918 |
| GO Biological Process | pheromone response [GO:0019236] | 0.00064531 | 0.89052504 |
| GO Biological Process | cell communication [GO:0007154] | 0.00065219 | 0.90002496 |
| GO Biological Process | signal transduction [GO:0007165] | 0.00134565 | >0.999 |
| GO Biological Process | intracellular signaling cascade [GO:0007242] | 0.00132967 | >0.999 |
| GO Biological Process | mating (sensu Fungi) [GO:0030461] | 0.00155725 | >0.999 |
| GO Biological Process | perception of abiotic stimulus [GO:0009582] | 0.00094528 | >0.999 |
| GO Biological Process | perception of external stimulus [GO:0009581] | 0.00094528 | >0.999 |
| GO Biological Process | sensory perception [GO:0007600] | 0.00094528 | >0.999 |
| GO Biological Process | small GTPase mediated signal transduction [GO:0007264] | 0.001505 | >0.999 |
| GO Biological Process | cell adhesion [GO:0007155] | 0.00437089 | >0.999 |
| GO Molecular Function | transcription regulator [GO:0030528] | 0.00183314 | >0.999 |
| PFam-A Domains | PF00399 (yeast_PIR) | 0.00233288 | >0.999 |
| GO Biological Process | cell-cell fusion [GO:0006947] | 0.00167601 | >0.999 |
| GO Biological Process | chemosensory perception [GO:0007606] | 0.00094528 | >0.999 |
| GO Biological Process | reproduction [GO:0000003] | 0.00155725 | >0.999 |
| GO Biological Process | regulation of meiosis [GO:0040020] | 0.00267631 | >0.999 |
| GO Biological Process | perception of chemical substance [GO:0009593] | 0.00094528 | >0.999 |
| GO Biological Process | cell cycle [GO:0007049] | 0.00253439 | >0.999 |
| GO Biological Process | RAS protein signal transduction [GO:0007265] | 0.0010418 | >0.999 |

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|---|---|---|---|
| GO Biological Process | mating (sensu Saccharomyces) [GO:0007322] | 0.00144542 | >0.999 |
| GO Molecular Function | signal transducer [GO:0004871] | 0.00207705 | >0.999 |
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| **Met32** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Biological Process | sulfur amino acid metabolism [GO:0000096] | 2.44E-11 | 3.37E-08 |
| GO Biological Process | sulfur metabolism [GO:0006790] | 3.34E-11 | 4.61E-08 |
| MIPS Functional Classification | amino acid metabolism | 2.04E-08 | 5.28E-06 |
| GO Biological Process | methionine metabolism [GO:0006555] | 8.16E-08 | 0.00011256 |
| MIPS Functional Classification | METABOLISM | 4.54E-07 | 0.00011749 |
| MIPS Functional Classification | amino acid biosynthesis | 7.85E-07 | 0.00020334 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 4.91E-06 | 0.00127208 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 9.34E-06 | 0.00177478 |
| MIPS Functional Classification | amino acid transport | 6.11E-05 | 0.01581843 |
| MIPS Phenotypes | Methionine auxotrophy (Met) | 0.00010968 | 0.01974204 |
| MIPS Functional Classification | amino-acid transporters | 0.00010161 | 0.02631595 |
| MIPS Functional Classification | pentose-phosphate pathway | 0.00010968 | 0.0284066 |
| GO Biological Process | sulfur amino acid biosynthesis [GO:0000097] | 3.20E-05 | 0.0442112 |
| GO Biological Process | aspartate family amino acid metabolism [GO:0009066] | 3.48E-05 | 0.04806305 |
| GO Molecular Function | amino acid transporter [GO:0015171] | 4.64E-05 | 0.06383566 |
| MIPS Functional Classification | homeostasis of anions | 0.000563 | 0.14581804 |
| SMART Domains | WW | 0.00058769 | 0.17278145 |
| GO Biological Process | amino acid metabolism [GO:0006520] | 0.00012864 | 0.17752044 |
| MIPS Functional Classification | nitrogen and sulfur metabolism | 0.00117265 | 0.30371635 |
| GO Biological Process | amino acid and derivative metabolism [GO:0006519] | 0.00024954 | 0.3443583 |
| GO Biological Process | amine metabolism [GO:0009308] | 0.00028686 | 0.39586818 |
| MIPS Functional Classification | lysosomal and vacuolar degradation | 0.00262786 | 0.68061574 |
| GO Molecular Function | L-amino acid transporter [GO:0015179] | 0.00058769 | 0.80925188 |
| GO Biological Process | amino acid transport [GO:0006865] | 0.0006476 | 0.89368938 |
| MDS Proteomics Complexes | YHR030C (SLT2) | 0.00195782 | 0.96520526 |
| MIPS Functional Classification | drug transporters | 0.00458777 | >0.999 |
| GO Biological Process | hexose metabolism [GO:0019318] | 0.00359177 | >0.999 |
| GO Molecular Function | transporter [GO:0005215] | 0.00332302 | >0.999 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 0.00178636 | >0.999 |

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|---|---|---|---|
| GO Biological Process | inorganic anion transport [GO:0015698] | 0.00102243 | >0.999 |
| GO Biological Process | hexose catabolism [GO:0019320] | 0.00460355 | >0.999 |
| PFam-A Domains | PF01053 (Cys_Met_Meta_PP) | 0.0015696 | >0.999 |
| PFam-A Domains | PF00324 (aa_permeases) | 0.00460355 | >0.999 |
| GO Biological Process | glucose metabolism [GO:0006006] | 0.00245165 | >0.999 |
| GO Biological Process | glucose catabolism [GO:0006007] | 0.00460355 | >0.999 |
| PFam-A Domains | PF00155 (aminotran_1_2) | 0.00229957 | >0.999 |
| | | | |
| **Mga1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Protein Complexes | Cytoplasmic translation elongation | 3.58E-06 | 0.00112646 |
| Cellzome Complexes | YAL029C (MYO4) | 2.08E-05 | 0.00953729 |
| MIPS Protein Classes | other ATPases | 0.00016555 | 0.03145355 |
| MIPS Subcellular Localization | cytoplasm | 0.00098914 | 0.04154375 |
| GO Molecular Function | translation elongation factor [GO:0003746] | 3.29E-05 | 0.04529311 |
| MIPS Protein Complexes | eEF1 | 0.00059642 | 0.18787325 |
| GO Molecular Function | heat shock protein [GO:0003773] | 0.00019217 | 0.26461396 |
| GO Molecular Function | translation regulator [GO:0045182] | 0.00021041 | 0.28973044 |
| MIPS Functional Classification | SUBCELLULAR LOCALISATION | 0.00123621 | 0.32017839 |
| SMART Domains | HATPase | 0.00159254 | 0.46820676 |
| GO Biological Process | translational elongation [GO:0006414] | 0.00042209 | 0.5824842 |
| Cellzome Complexes | YBR126C (TPS1) | 0.00135467 | 0.62179353 |
| GO Molecular Function | signal transducer [GO:0004871] | 0.00056341 | 0.77581282 |
| MIPS Phenotypes | Bud localization | 0.0046866 | 0.843588 |
| MDS Proteomics Complexes | YMR001C (CDC5) | 0.00233288 | >0.999 |
| MDS Proteomics Complexes | YDR398W (UTP5) | 0.00233288 | >0.999 |
| PFam-A Domains | PF02518 (HATPase_c) | 0.00159254 | >0.999 |
| GO Molecular Function | receptor signaling protein [GO:0005057] | 0.00133589 | >0.999 |
| MDS Proteomics Complexes | YDL145C (COP1) | 0.00437089 | >0.999 |
| GO Biological Process | protein folding [GO:0006457] | 0.00196986 | >0.999 |
| | | | |
| **Mig1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 1.00E-14 | 2.59E-12 |

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|---|---|---|---|
| MIPS Functional Classification | METABOLISM | 5.38E-14 | 1.39E-11 |
| GO Biological Process | hexose transport [GO:0008645] | 3.92E-13 | 5.41E-10 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 3.92E-13 | 5.41E-10 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 4.60E-12 | 1.19E-09 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 4.99E-12 | 1.29E-09 |
| GO Molecular Function | mannose transporter [GO:0015578] | 2.29E-12 | 3.16E-09 |
| GO Molecular Function | glucose transporter [GO:0005355] | 1.40E-11 | 1.93E-08 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 1.56E-11 | 2.15E-08 |
| PFam-A Domains | PF00083 (sugar_tr) | 4.62E-11 | 5.47E-08 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 4.20E-11 | 5.79E-08 |
| GO Molecular Function | fructose transporter [GO:0005353] | 5.01E-11 | 6.90E-08 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 6.31E-11 | 8.68E-08 |
| GO Molecular Function | hexose transporter [GO:0015149] | 6.31E-11 | 8.68E-08 |
| MIPS Functional Classification | plasma membrane | 2.37E-08 | 6.13E-06 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 8.96E-09 | 1.24E-05 |
| MIPS Functional Classification | cellular import | 8.06E-08 | 2.09E-05 |
| MIPS Functional Classification | ENERGY | 8.59E-08 | 2.22E-05 |
| SMART Domains | Aamy | 7.61E-08 | 2.24E-05 |
| GO Biological Process | energy reserve metabolism [GO:0006112] | 2.30E-07 | 0.00031675 |
| Proteome Localization--Predicted+Obs | cyt | 0.00014341 | 0.00057365 |
| GO Biological Process | glycogen metabolism [GO:0005977] | 6.35E-07 | 0.00087561 |
| Proteome Localization--Observed | cyto | 9.33E-05 | 0.00102626 |
| PFam-A Domains | PF00128 (alpha-amylase) | 1.63E-06 | 0.00193347 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 4.12E-05 | 0.00782321 |
| MIPS Phenotypes | Galactose fermentation (Gal) | 4.98E-05 | 0.00897215 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00103917 | 0.01143087 |
| GO Biological Process | glucan metabolism [GO:0006073] | 1.05E-05 | 0.01447137 |
| GO Biological Process | disaccharide metabolism [GO:0005984] | 1.24E-05 | 0.01717051 |
| GO Molecular Function | transporter [GO:0005215] | 1.60E-05 | 0.02200157 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 1.96E-05 | 0.02699321 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00013388 | 0.03467388 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00016108 | 0.05315772 |
| GO Biological Process | polysaccharide metabolism [GO:0005976] | 0.00010081 | 0.13912056 |
| MIPS Protein Classes | Ubiquitin-system proteins | 0.00094528 | 0.1796032 |

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|---|---|---|---|
| MIPS Protein Classes | Cys2His2 zinc-finger | 0.00173371 | 0.3294049 |
| GO Cellular Component | unlocalized [GO:0005941] | 0.00234057 | 0.7723881 |
| MIPS Phenotypes | Accumulation of storage carbohydrates | 0.00437089 | 0.7867602 |
| MIPS Functional Classification | phosphate transport | 0.00325479 | 0.84299061 |
| MIPS Functional Classification | CELLULAR TRANSPORT AND TRANSPORT MECHANISMS | 0.00380586 | 0.98571774 |
| PFam-A Domains | PF00096 (zf-C2H2) | 0.00196986 | >0.999 |
| MDS Proteomics Complexes | YPL031C (PHO85) | 0.00233288 | >0.999 |
| GO Biological Process | carbohydrate catabolism [GO:0016052] | 0.0046866 | >0.999 |
| GO Biological Process | mitotic checkpoint [GO:0007093] | 0.00172766 | >0.999 |
| GO Molecular Function | transferase [GO:0016740] | 0.00418089 | >0.999 |
| GO Biological Process | energy derivation by oxidation of organic compounds [GO:0015980] | 0.00161284 | >0.999 |
| GO Biological Process | hexose metabolism [GO:0019318] | 0.00080198 | >0.999 |
| GO Biological Process | ion transport [GO:0006811] | 0.00337119 | >0.999 |
| MIPS Functional Classification | regulation of C-compound and carbohydrate utilization | 0.00479665 | >0.999 |
| SMART Domains | ZnF_C2H2 | 0.00483174 | >0.999 |
| GO Molecular Function | alpha-glucosidase [GO:0004558] | 0.00101923 | >0.999 |
| GO Molecular Function | inorganic anion transporter [GO:0015103] | 0.00159254 | >0.999 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 0.00147054 | >0.999 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 0.00173164 | >0.999 |
| GO Molecular Function | enzyme [GO:0003824] | 0.00439284 | >0.999 |
| GO Biological Process | glucose metabolism [GO:0006006] | 0.00251429 | >0.999 |
| MDS Proteomics Complexes | YKL166C (TPK3) | 0.00437089 | >0.999 |
| GO Biological Process | energy pathways [GO:0006091] | 0.00161284 | >0.999 |
| GO Molecular Function | anion transporter [GO:0008509] | 0.00326287 | >0.999 |
| GO Molecular Function | glucosidase [GO:0015926] | 0.00468663 | >0.999 |
| GO Biological Process | mitotic spindle checkpoint [GO:0007094] | 0.00172766 | >0.999 |
| | | | |
| **Mig2** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 1.00E-14 | 2.59E-12 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 1.00E-14 | 2.59E-12 |
| MIPS Functional Classification | METABOLISM | 1.05E-14 | 2.73E-12 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 1.05E-14 | 2.73E-12 |
| GO Molecular Function | glucose transporter [GO:0005355] | 1.00E-14 | 1.38E-11 |

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|---|---|---|---|
| GO Molecular Function | fructose transporter [GO:0005353] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 1.00E-14 | 1.38E-11 |
| GO Molecular Function | mannose transporter [GO:0015578] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | hexose transport [GO:0008645] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 1.00E-14 | 1.38E-11 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 1.00E-14 | 1.38E-11 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 3.50E-14 | 4.82E-11 |
| GO Molecular Function | hexose transporter [GO:0015149] | 3.50E-14 | 4.82E-11 |
| PFam-A Domains | PF00083 (sugar_tr) | 2.14E-13 | 2.53E-10 |
| SMART Domains | Aamy | 8.21E-12 | 2.41E-09 |
| PFam-A Domains | PF00128 (alpha-amylase) | 2.37E-10 | 2.81E-07 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 1.65E-09 | 2.28E-06 |
| MIPS Functional Classification | ENERGY | 8.59E-08 | 2.22E-05 |
| MIPS Functional Classification | cellular import | 4.98E-07 | 0.00012894 |
| GO Biological Process | energy reserve metabolism [GO:0006112] | 2.30E-07 | 0.00031675 |
| MIPS Phenotypes | Galactose fermentation (Gal) | 2.38E-06 | 0.00042799 |
| GO Biological Process | disaccharide metabolism [GO:0005984] | 3.96E-07 | 0.00054715 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 5.79E-07 | 0.00079933 |
| GO Molecular Function | alpha-glucosidase [GO:0004558] | 6.28E-07 | 0.00086495 |
| Proteome Localization--Predicted+Obs | cyt | 0.00025031 | 0.00100124 |
| MIPS Functional Classification | plasma membrane | 1.06E-05 | 0.00274594 |
| GO Biological Process | glycogen metabolism [GO:0005977] | 8.95E-06 | 0.01235063 |
| GO Cellular Component | plasma membrane [GO:0005886] | 4.66E-05 | 0.01538236 |
| GO Molecular Function | transporter [GO:0005215] | 1.60E-05 | 0.02200157 |
| MIPS Functional Classification | regulation of C-compound and carbohydrate utilization | 0.00010456 | 0.02708182 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.000158 | 0.03002019 |
| Proteome Localization--Observed | cyto | 0.00284451 | 0.03128961 |
| GO Biological Process | hexose metabolism [GO:0019318] | 2.56E-05 | 0.0352757 |
| GO Molecular Function | glucosidase [GO:0015926] | 4.77E-05 | 0.06566321 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 5.76E-05 | 0.0794339 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00035466 | 0.09185668 |
| MIPS Phenotypes | Carbon utilization | 0.00060998 | 0.10979694 |
| GO Biological Process | glucan metabolism [GO:0006073] | 9.54E-05 | 0.1317014 |
| GO Molecular Function | enzyme [GO:0003824] | 0.00019377 | 0.26681854 |

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|---|---|---|---|
| GO Biological Process | energy derivation by oxidation of organic compounds [GO:0015980] | 0.00051343 | 0.70853616 |
| GO Biological Process | energy pathways [GO:0006091] | 0.00051343 | 0.70853616 |
| GO Biological Process | disaccharide catabolism [GO:0046352] | 0.00059642 | 0.82306374 |
| GO Biological Process | glucose transport [GO:0015758] | 0.00059642 | 0.82306374 |
| MIPS Protein Classes | Histones | 0.00437089 | 0.8304691 |
| GO Biological Process | polysaccharide metabolism [GO:0005976] | 0.00064531 | 0.89052504 |
| PFam-A Domains | PF00125 (histone) | 0.00325479 | >0.999 |
| GO Biological Process | carbohydrate catabolism [GO:0016052] | 0.0046866 | >0.999 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 0.0034766 | >0.999 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 0.00173164 | >0.999 |
| GO Biological Process | galactose metabolism [GO:0006012] | 0.00233288 | >0.999 |
| GO Biological Process | glucose metabolism [GO:0006006] | 0.00251429 | >0.999 |
| GO Biological Process | trehalose metabolism [GO:0005991] | 0.00101923 | >0.999 |
| MDS Proteomics Complexes | YAL015C (NTG1) | 0.00325479 | >0.999 |
| MDS Proteomics Complexes | YKL166C (TPK3) | 0.00437089 | >0.999 |
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| **Mig3** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 1.00E-14 | 2.59E-12 |
| MIPS Functional Classification | METABOLISM | 1.05E-14 | 2.73E-12 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 6.74E-14 | 9.30E-11 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 9.45E-13 | 2.45E-10 |
| GO Biological Process | hexose transport [GO:0008645] | 3.92E-13 | 5.41E-10 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 3.92E-13 | 5.41E-10 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 5.94E-13 | 8.19E-10 |
| GO Molecular Function | fructose transporter [GO:0005353] | 7.85E-13 | 1.08E-09 |
| GO Molecular Function | mannose transporter [GO:0015578] | 2.29E-12 | 3.16E-09 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 7.05E-11 | 1.83E-08 |
| GO Molecular Function | glucose transporter [GO:0005355] | 1.40E-11 | 1.93E-08 |
| PFam-A Domains | PF00083 (sugar_tr) | 4.62E-11 | 5.47E-08 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 6.31E-11 | 8.68E-08 |
| GO Molecular Function | hexose transporter [GO:0015149] | 6.31E-11 | 8.68E-08 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 8.96E-09 | 1.24E-05 |
| SMART Domains | Aamy | 7.61E-08 | 2.24E-05 |

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|---|---|---|---|
| GO Biological Process | energy reserve metabolism [GO:0006112] | 2.30E-07 | 0.00031675 |
| PFam-A Domains | PF00128 (alpha-amylase) | 1.63E-06 | 0.00193347 |
| Proteome Localization--Predicted+Obs | cyt | 0.00071618 | 0.00286472 |
| MIPS Functional Classification | ENERGY | 1.46E-05 | 0.00377272 |
| Proteome Localization--Observed | cyto | 0.00057042 | 0.0062746 |
| MIPS Phenotypes | Galactose fermentation (Gal) | 4.98E-05 | 0.00897215 |
| MIPS Functional Classification | plasma membrane | 4.15E-05 | 0.01074617 |
| GO Biological Process | glycogen metabolism [GO:0005977] | 8.95E-06 | 0.01235063 |
| GO Cellular Component | plasma membrane [GO:0005886] | 4.66E-05 | 0.01538236 |
| GO Biological Process | disaccharide metabolism [GO:0005984] | 1.24E-05 | 0.01717051 |
| MIPS Functional Classification | cellular import | 7.15E-05 | 0.0185148 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 1.96E-05 | 0.02699321 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.000158 | 0.03002019 |
| GO Molecular Function | alpha-glucosidase [GO:0004558] | 3.27E-05 | 0.04499774 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00432221 | 0.04754431 |
| GO Molecular Function | transporter [GO:0005215] | 4.39E-05 | 0.06046187 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00035466 | 0.09185668 |
| MIPS Functional Classification | regulation of C-compound and carbohydrate utilization | 0.00041012 | 0.10622186 |
| GO Biological Process | glucan metabolism [GO:0006073] | 9.54E-05 | 0.1317014 |
| GO Biological Process | energy derivation by oxidation of organic compounds [GO:0015980] | 0.00015139 | 0.20892234 |
| GO Biological Process | energy pathways [GO:0006091] | 0.00015139 | 0.20892234 |
| GO Molecular Function | enzyme [GO:0003824] | 0.00019377 | 0.26681854 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 0.00046798 | 0.64440158 |
| Yeast Two Hybrid - Ito (core) | YNL189W (SRP1) | 0.00157355 | 0.70652395 |
| GO Molecular Function | glucosidase [GO:0015926] | 0.00053221 | 0.73285042 |
| MIPS Phenotypes | Carbon utilization | 0.00431598 | 0.7768764 |
| MIPS Protein Classes | Histones | 0.00437089 | 0.8304691 |
| GO Biological Process | polysaccharide metabolism [GO:0005976] | 0.00064531 | 0.89052504 |
| PFam-A Domains | PF00125 (histone) | 0.00325479 | >0.999 |
| GO Molecular Function | transferase [GO:0016740] | 0.00418089 | >0.999 |
| GO Biological Process | hexose metabolism [GO:0019318] | 0.00080198 | >0.999 |
| MDS Proteomics Complexes | YPL022W (RAD1) | 0.00216637 | >0.999 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 0.00147054 | >0.999 |
| GO Biological Process | glucose metabolism [GO:0006006] | 0.00251429 | >0.999 |

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|---|---|---|---|
| GO Biological Process | trehalose metabolism [GO:0005991] | 0.00101923 | >0.999 |
| MDS Proteomics Complexes | YAL015C (NTG1) | 0.00325479 | >0.999 |
| MDS Proteomics Complexes | YKL166C (TPK3) | 0.00437089 | >0.999 |
| MDS Proteomics Complexes | YGL137W (SEC27) | 0.0028255 | >0.999 |
|  |  |  |  |
| **Ndt80** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Biological Process | spore wall assembly (sensu Fungi) [GO:0030476] | 1.59E-08 | 2.20E-05 |
| GO Biological Process | spore wall assembly [GO:0042244] | 1.59E-08 | 2.20E-05 |
| GO Biological Process | sporulation [GO:0030435] | 2.29E-08 | 3.16E-05 |
| GO Biological Process | spore wall assembly (sensu Saccharomyces) [GO:0007152] | 2.04E-07 | 0.00028119 |
| GO Biological Process | sporulation (sensu Fungi) [GO:0030437] | 2.75E-07 | 0.00037932 |
| Proteome Localization--Predicted+Obs | nuc | 0.00032927 | 0.00131709 |
| MIPS Functional Classification | sporulation and germination | 1.35E-05 | 0.00350702 |
| GO Biological Process | hexose transport [GO:0008645] | 3.45E-06 | 0.00475443 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 3.45E-06 | 0.00475443 |
| GO Biological Process | sporulation (sensu Saccharomyces) [GO:0007151] | 5.25E-06 | 0.00724805 |
| GO Cellular Component | ascus [GO:0005627] | 4.98E-05 | 0.01644895 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 3.31E-05 | 0.04566185 |
| GO Molecular Function | fructose transporter [GO:0005353] | 4.98E-05 | 0.06863698 |
| GO Molecular Function | mannose transporter [GO:0015578] | 7.28E-05 | 0.1002993 |
| MIPS Functional Classification | cell cycle | 0.00045963 | 0.11904417 |
| GO Molecular Function | glucose transporter [GO:0005355] | 0.00014246 | 0.19616054 |
| MIPS Functional Classification | CELL FATE | 0.00099435 | 0.25753665 |
| MIPS Functional Classification | cell differentiation | 0.00101949 | 0.26404791 |
| MIPS Functional Classification | fungal cell differentiation | 0.00101949 | 0.26404791 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 0.00025409 | 0.34987918 |
| GO Molecular Function | hexose transporter [GO:0015149] | 0.00025409 | 0.34987918 |
| MIPS Functional Classification | meiosis | 0.00167601 | 0.43408659 |
| Yeast Two Hybrid - Ito (core) | YDL239C (ADY3) | 0.00099326 | 0.44597419 |
| GO Molecular Function | protein serine/threonine kinase [GO:0004674] | 0.00037401 | 0.51500902 |
| GO Cellular Component | spore wall (sensu Fungi) [GO:0005619] | 0.00159254 | 0.5255382 |
| SMART Domains | SANT | 0.00216637 | 0.63691278 |
| MIPS Functional Classification | CELL CYCLE AND DNA PROCESSING | 0.00257896 | 0.66795064 |

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|---|---|---|---|
| SMART Domains | Aamy | 0.00233288 | 0.68586672 |
| GO Cellular Component | prospore membrane [GO:0005628] | 0.00233288 | 0.7698504 |
| GO Biological Process | regulation of transcription from Pol II promoter [GO:0006357] | 0.00056067 | 0.77372736 |
| SMART Domains | HMG | 0.0029765 | 0.875091 |
| GO Biological Process | transcription from Pol II promoter [GO:0006366] | 0.00071186 | 0.98236128 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00434988 | >0.999 |
| GO Biological Process | mitotic cell cycle [GO:0000278] | 0.00471142 | >0.999 |
| GO Molecular Function | enzyme regulator [GO:0030234] | 0.00271478 | >0.999 |
| GO Biological Process | nuclear division [GO:0000280] | 0.00290622 | >0.999 |
| GO Biological Process | regulation of transcription [GO:0045449] | 0.00455154 | >0.999 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 0.00173164 | >0.999 |
| PFam-A Domains | PF00128 (alpha-amylase) | 0.00159254 | >0.999 |
| GO Biological Process | DNA replication and chromosome cycle [GO:0000067] | 0.00477914 | >0.999 |
| GO Biological Process | M phase of mitotic cell cycle [GO:0000087] | 0.0045195 | >0.999 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 0.0016999 | >0.999 |
| GO Molecular Function | protein kinase [GO:0004672] | 0.00296353 | >0.999 |
| GO Biological Process | negative regulation of transcription from Pol II promoter [GO:0000122] | 0.00314095 | >0.999 |
| GO Molecular Function | glucosidase [GO:0015926] | 0.00468663 | >0.999 |
| GO Biological Process | mitosis [GO:0007067] | 0.00400314 | >0.999 |
| | | | |
| **Nhp6A** | **n=184** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Subcellular Localization | nucleus | 0.00098155 | 0.04122489 |
| MIPS Subcellular Localization | nuclear envelope | 0.00185445 | 0.0778869 |
| MIPS Subcellular Localization | ER membrane | 0.00233002 | 0.09786084 |
| GO Biological Process | mitotic prophase [GO:0000088] | 8.08E-05 | 0.11143541 |
| GO Biological Process | mitotic chromosome condensation [GO:0007076] | 8.08E-05 | 0.11143541 |
| GO Cellular Component | mitotic chromosome [GO:0005708] | 0.00041774 | 0.13785255 |
| GO Cellular Component | commitment complex [GO:0000243] | 0.00057149 | 0.18859104 |
| MIPS Functional Classification | endoplasmic reticulum | 0.00212553 | 0.55051227 |
| GO Biological Process | chromosome condensation [GO:0030261] | 0.00045199 | 0.62375172 |
| GO Cellular Component | chromosome [GO:0005694] | 0.00233002 | 0.7689066 |
| Cellzome Complexes | YBR119W (MUD1) | 0.00183549 | 0.84248991 |
| MIPS Functional Classification | meiosis | 0.00331988 | 0.85984892 |

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|---|---|---|---|
| **Nhp6B** | **n=187** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Cellular Component | chromosome [GO:0005694] | 4.38E-05 | 0.01445311 |
| Proteome Localization--Predicted+Obs | nuc | 0.00924913 | 0.03699652 |
| MIPS Functional Classification | meiosis | 0.00024688 | 0.06394063 |
| MIPS Subcellular Localization | nucleus | 0.00252531 | 0.10606302 |
| GO Biological Process | mitotic prophase [GO:0000088] | 8.60E-05 | 0.1187134 |
| GO Biological Process | mitotic chromosome condensation [GO:0007076] | 8.60E-05 | 0.1187134 |
| GO Cellular Component | mitotic chromosome [GO:0005708] | 0.00044433 | 0.14662857 |
| MIPS Subcellular Localization | chromosome structure | 0.00435644 | 0.18297048 |
| GO Cellular Component | commitment complex [GO:0000243] | 0.00060764 | 0.20051988 |
| MIPS Functional Classification | chromosome | 0.00178858 | 0.46324222 |
| MIPS Protein Classes | Protein Kinases | 0.00246342 | 0.4680498 |
| Cellzome Complexes | YFL017W-A (SMX2) | 0.00134672 | 0.61814448 |
| GO Biological Process | chromosome condensation [GO:0030261] | 0.00048694 | 0.6719772 |
| GO Molecular Function | binding [GO:0005488] | 0.00059735 | 0.82254682 |
| Cellzome Complexes | YBR119W (MUD1) | 0.00192304 | 0.88267536 |
| | | | |
| **Nrg1** | **n=199** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 5.38E-07 | 5.92E-06 |
| PFam-A Domains | PF00660 (SRP1_TIP1) | 1.44E-08 | 1.70E-05 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 2.34E-05 | 0.00605508 |
| MIPS Protein Classes | Cys2His2 zinc-finger | 3.48E-05 | 0.00661738 |
| Proteome Localization--Predicted+Obs | en2 | 0.00597167 | 0.02388668 |
| MIPS Protein Classes | Zinc-coordinating DNA-binding domains | 0.00013223 | 0.02512351 |
| SMART Domains | ZnF_C2H2 | 0.00015313 | 0.04502051 |
| PFam-A Domains | PF00096 (zf-C2H2) | 4.19E-05 | 0.04961038 |
| SMART Domains | ZnF_GATA | 0.00017827 | 0.05240991 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 0.00025611 | 0.06633171 |
| GO Molecular Function | glucosyltransferase [GO:0046527] | 4.87E-05 | 0.06700303 |
| MIPS Protein Classes | Transcription factors | 0.00062351 | 0.11846614 |
| MIPS Functional Classification | METABOLISM | 0.00064434 | 0.16688458 |

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|---|---|---|---|
| GO Biological Process | response to stress [GO:0006950] | 0.00017598 | 0.24285378 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 0.00021639 | 0.29862234 |
| PFam-A Domains | PF00320 (GATA) | 0.00027319 | 0.32373371 |
| MIPS Functional Classification | stress response | 0.00126358 | 0.32726722 |
| Cellzome Complexes | YBR126C (TPS1) | 0.00132964 | 0.61030476 |
| | | | |
| **Oaf1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | METABOLISM | 4.00E-08 | 1.04E-05 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 2.36E-07 | 6.12E-05 |
| GO Cellular Component | peroxisome [GO:0005777] | 3.22E-07 | 0.00010619 |
| GO Molecular Function | fructose transporter [GO:0005353] | 8.62E-08 | 0.00011873 |
| GO Molecular Function | mannose transporter [GO:0015578] | 1.57E-07 | 0.00021663 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 2.65E-07 | 0.00036483 |
| GO Molecular Function | glucose transporter [GO:0005355] | 4.50E-07 | 0.00061994 |
| MIPS Subcellular Localization | peroxisomal matrix | 1.88E-05 | 0.00078913 |
| MIPS Subcellular Localization | peroxisome | 2.99E-05 | 0.00125454 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 1.10E-06 | 0.00152099 |
| GO Molecular Function | hexose transporter [GO:0015149] | 1.10E-06 | 0.00152099 |
| GO Biological Process | lipid metabolism [GO:0006629] | 1.33E-06 | 0.00184099 |
| GO Biological Process | fatty acid beta-oxidation [GO:0006635] | 1.63E-06 | 0.00225164 |
| MIPS Phenotypes | Carbohydrate and lipid biosynthesis defects | 1.36E-05 | 0.00245626 |
| MIPS Functional Classification | ENERGY | 1.46E-05 | 0.00377272 |
| GO Biological Process | hexose transport [GO:0008645] | 3.45E-06 | 0.00475443 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 3.45E-06 | 0.00475443 |
| GO Biological Process | fatty acid oxidation [GO:0019395] | 3.58E-06 | 0.00493495 |
| GO Molecular Function | enzyme [GO:0003824] | 4.02E-06 | 0.00553639 |
| Proteome Localization--Predicted+Obs | cyt | 0.00188715 | 0.0075486 |
| GO Biological Process | organic acid metabolism [GO:0006082] | 6.28E-06 | 0.00866265 |
| GO Biological Process | carboxylic acid metabolism [GO:0019752] | 6.28E-06 | 0.00866265 |
| GO Biological Process | fatty acid metabolism [GO:0006631] | 8.31E-06 | 0.01147467 |
| MIPS Functional Classification | cellular import | 7.15E-05 | 0.0185148 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 7.74E-05 | 0.02003637 |
| MIPS Phenotypes | other carbohydrate and lipid biosynthesis defects | 0.00011531 | 0.02075508 |

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|---|---|---|---|
| GO Cellular Component | peroxisomal matrix [GO:0005782] | 7.28E-05 | 0.02403687 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 2.03E-05 | 0.02797858 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.000158 | 0.03002019 |
| SMART Domains | Aamy | 0.00011184 | 0.03288184 |
| PFam-A Domains | PF00083 (sugar_tr) | 3.76E-05 | 0.04454782 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 3.31E-05 | 0.04566185 |
| PFam-A Domains | PF00128 (alpha-amylase) | 6.37E-05 | 0.07551365 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00035466 | 0.09185668 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 0.00056421 | 0.14613117 |
| MIPS Functional Classification | drug transporters | 0.00073373 | 0.19003711 |
| GO Cellular Component | membrane [GO:0016020] | 0.00078169 | 0.2579577 |
| MIPS Functional Classification | oxidation of fatty acids | 0.00101923 | 0.26398057 |
| MIPS Functional Classification | detoxification | 0.00144542 | 0.37436378 |
| GO Biological Process | sterol metabolism [GO:0016125] | 0.00044362 | 0.61219974 |
| PFam-A Domains | PF00173 (heme_1) | 0.00059642 | 0.70676126 |
| GO Molecular Function | galactose transporter [GO:0005354] | 0.00059642 | 0.82127447 |
| GO Biological Process | ergosterol metabolism [GO:0008204] | 0.00099326 | >0.999 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00434988 | >0.999 |
| GO Biological Process | steroid metabolism [GO:0008202] | 0.00151969 | >0.999 |
| GO Biological Process | sterol biosynthesis [GO:0016126] | 0.00200157 | >0.999 |
| GO Biological Process | TCA intermediate metabolism [GO:0006100] | 0.00393128 | >0.999 |
| GO Biological Process | transport [GO:0006810] | 0.0022345 | >0.999 |
| GO Molecular Function | alpha-glucosidase [GO:0004558] | 0.00101923 | >0.999 |
| GO Biological Process | ergosterol biosynthesis [GO:0006696] | 0.00099326 | >0.999 |
| PFam-A Domains | PF00107 (adh_zinc) | 0.00393128 | >0.999 |
| GO Molecular Function | glucosidase [GO:0015926] | 0.00468663 | >0.999 |
| | | | |
| **Pbf1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Biological Process | ribosome biogenesis [GO:0007046] | 2.04E-11 | 2.81E-08 |
| GO Cellular Component | nucleolus [GO:0005730] | 3.66E-10 | 1.21E-07 |
| GO Biological Process | ribosome biogenesis and assembly [GO:0042254] | 1.09E-10 | 1.50E-07 |
| GO Biological Process | rRNA processing [GO:0006364] | 6.00E-09 | 8.28E-06 |
| GO Biological Process | transcription from Pol I promoter [GO:0006360] | 1.14E-08 | 1.58E-05 |

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|---|---|---|---|
| Deletions Consortium (Essentiality, Mo | essential | 7.70E-06 | 8.47E-05 |
| Published Complexes | Andersen et al. (2002) - Curr Bio 12:1- | 3.73E-05 | 0.00026077 |
| Cellzome Complexes | YCR057C (PWP2) | 1.12E-06 | 0.00051273 |
| Cellzome Complexes | YPL043W (NOP4) | 4.88E-06 | 0.0022391 |
| Cellzome Complexes | YDR060W (MAK21) | 6.60E-06 | 0.00303028 |
| GO Biological Process | RNA processing [GO:0006396] | 2.91E-06 | 0.0040218 |
| Cellzome Complexes | YNL110C (NOP15) | 8.80E-06 | 0.00404062 |
| MDS Proteomics Complexes | YER082C (UTP7) | 1.44E-05 | 0.0071171 |
| Proteome Localization--Predicted+Obs | nuc | 0.00226644 | 0.00906576 |
| Cellzome Complexes | YGR090W (UTP22) | 2.01E-05 | 0.00922764 |
| Cellzome Complexes | YGL099W (LSG1) | 3.68E-05 | 0.01688018 |
| MIPS Subcellular Localization | nucleus | 0.00047881 | 0.02010989 |
| Published Complexes | Harnicharnpai et al. (2001) - Mol Cell 8:505- | 0.00338241 | 0.02367687 |
| GO Biological Process | RNA metabolism [GO:0016070] | 2.12E-05 | 0.02930099 |
| GO Cellular Component | nucleus [GO:0005634] | 9.88E-05 | 0.0325907 |
| SMART Domains | COIL | 0.00011297 | 0.03321347 |
| MDS Proteomics Complexes | YJL069C (UTP18) | 8.09E-05 | 0.0398693 |
| GO Biological Process | cytoplasm organization and biogenesis [GO:0007028] | 4.37E-05 | 0.06034547 |
| GO Cellular Component | small nucleolar ribonucleoprotein complex [GO:0005732] | 0.00019594 | 0.06465987 |
| MDS Proteomics Complexes | YMR049C (ERB1) | 0.00015204 | 0.07495424 |
| MDS Proteomics Complexes | YLR074C (BUD20) | 0.00020482 | 0.10097429 |
| GO Biological Process | transcription [GO:0006350] | 0.00010841 | 0.14960856 |
| GO Molecular Function | snoRNA binding [GO:0030515] | 0.00019594 | 0.269808 |
| Cellzome Complexes | YHR066W (SSF1) | 0.00066132 | 0.30354496 |
| MDS Proteomics Complexes | YIL035C (CKA1) | 0.00063496 | 0.31303676 |
| GO Biological Process | processing of 20S pre-rRNA [GO:0030490] | 0.00023878 | 0.32952054 |
| MDS Proteomics Complexes | YOR005C (DNL4) | 0.0008765 | 0.43211253 |
| MIPS Functional Classification | rRNA transcription | 0.00169547 | 0.43912673 |
| Cellzome Complexes | YBR247C (ENP1) | 0.00097403 | 0.44708161 |
| MDS Proteomics Complexes | YDL213C (FYV14) | 0.00091558 | 0.45137848 |
| Cellzome Complexes | YKR081C (RPF2) | 0.00114103 | 0.52373277 |
| MIPS Functional Classification | purine ribonucleotide metabolism | 0.00224141 | 0.58052519 |
| GO Biological Process | ribosomal large subunit biogenesis [GO:0042273] | 0.00048166 | 0.66468666 |
| Cellzome Complexes | YNL061W (NOP2) | 0.00145687 | 0.66870333 |

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|---|---|---|---|
| MDS Proteomics Complexes | YPR017C (DSS4) | 0.0013937 | 0.6870941 |
| MIPS Functional Classification | lipid and fatty-acid transport | 0.00333028 | 0.86254252 |
| GO Molecular Function | RNA binding [GO:0003723] | 0.00065087 | 0.89624248 |
| GO Molecular Function | helicase [GO:0004386] | 0.00440583 | >0.999 |
| MDS Proteomics Complexes | YDL047W (SIT4) | 0.00469845 | >0.999 |
| GO Molecular Function | ATP dependent RNA helicase [GO:0004004] | 0.00080643 | >0.999 |
| MDS Proteomics Complexes | YHR052W (CIC1) | 0.00204383 | >0.999 |
| GO Molecular Function | RNA dependent adenosinetriphosphatase [GO:0008186] | 0.00080643 | >0.999 |
| GO Molecular Function | RNA helicase [GO:0003724] | 0.00104458 | >0.999 |
| GO Molecular Function | ATP dependent helicase [GO:0008026] | 0.0038503 | >0.999 |
|  |  |  |  |
| **Pbf2** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Cellular Component | nucleolus [GO:0005730] | 4.04E-10 | 1.33E-07 |
| GO Biological Process | ribosome biogenesis [GO:0007046] | 1.66E-10 | 2.29E-07 |
| GO Biological Process | ribosome biogenesis and assembly [GO:0042254] | 7.31E-10 | 1.01E-06 |
| Deletions Consortium (Essentiality, Mo | essential | 9.19E-06 | 0.00010111 |
| Published Complexes | Andersen et al. (2002) - Curr Bio 12:1- | 3.97E-05 | 0.00027804 |
| Cellzome Complexes | YPL043W (NOP4) | 5.05E-06 | 0.00231819 |
| GO Biological Process | rRNA processing [GO:0006364] | 1.74E-06 | 0.00240798 |
| GO Biological Process | transcription from Pol I promoter [GO:0006360] | 2.02E-06 | 0.00278934 |
| Cellzome Complexes | YDR060W (MAK21) | 6.83E-06 | 0.00313688 |
| Cellzome Complexes | YNL110C (NOP15) | 9.11E-06 | 0.00418217 |
| Cellzome Complexes | YCR057C (PWP2) | 1.21E-05 | 0.0055422 |
| Published Complexes | Harnicharnpai et al. (2001) - Mol Cell 8:505- | 0.00345941 | 0.02421587 |
| MIPS Functional Classification | rRNA transcription | 0.00011247 | 0.02913025 |
| MIPS Subcellular Localization | nucleolus | 0.00074231 | 0.0311771 |
| GO Biological Process | RNA processing [GO:0006396] | 3.36E-05 | 0.04633654 |
| Cellzome Complexes | YBR247C (ENP1) | 0.0001055 | 0.04842588 |
| MIPS Subcellular Localization | nucleus | 0.0011664 | 0.0489888 |
| GO Biological Process | cytoplasm organization and biogenesis [GO:0007028] | 4.93E-05 | 0.06803566 |
| GO Cellular Component | nucleus [GO:0005634] | 0.00022503 | 0.0742599 |
| MDS Proteomics Complexes | YMR049C (ERB1) | 0.00015515 | 0.07648895 |
| SMART Domains | COIL | 0.00026554 | 0.07806847 |

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|---|---|---|---|
| MDS Proteomics Complexes | YER082C (UTP7) | 0.00020989 | 0.10347774 |
| MDS Proteomics Complexes | YLR074C (BUD20) | 0.00020989 | 0.10347774 |
| Cellzome Complexes | YGR090W (UTP22) | 0.00027296 | 0.12528635 |
| MIPS Functional Classification | other rRNA-transcription activities | 0.00052889 | 0.13698329 |
| Cellzome Complexes | YGL099W (LSG1) | 0.00044105 | 0.20244287 |
| Cellzome Complexes | YML126C (ERG13) | 0.00052889 | 0.24276189 |
| GO Biological Process | RNA metabolism [GO:0016070] | 0.00018864 | 0.26031906 |
| Cellzome Complexes | YHR066W (SSF1) | 0.00067726 | 0.31086418 |
| MDS Proteomics Complexes | YIL035C (CKA1) | 0.0006551 | 0.32296184 |
| MDS Proteomics Complexes | YJL069C (UTP18) | 0.00082577 | 0.40710264 |
| MDS Proteomics Complexes | YOR005C (DNL4) | 0.00089387 | 0.44067791 |
| MDS Proteomics Complexes | YDL213C (FYV14) | 0.00094421 | 0.46549701 |
| Cellzome Complexes | YKR081C (RPF2) | 0.0011635 | 0.5340465 |
| GO Cellular Component | small nucleolar ribonucleoprotein complex [GO:0005732] | 0.00167109 | 0.5514597 |
| MIPS Functional Classification | purine ribonucleotide metabolism | 0.00230133 | 0.59604447 |
| GO Biological Process | ribosomal large subunit biogenesis [GO:0042273] | 0.00049133 | 0.67803678 |
| Cellzome Complexes | YNL061W (NOP2) | 0.00148537 | 0.68178483 |
| MDS Proteomics Complexes | YPR017C (DSS4) | 0.00141496 | 0.69757528 |
| GO Cellular Component | cell [GO:0005623] | 0.00223772 | 0.7384476 |
| MIPS Functional Classification | lipid and fatty-acid transport | 0.0033937 | 0.8789683 |
| MDS Proteomics Complexes | YDL047W (SIT4) | 0.00478672 | >0.999 |
| GO Biological Process | cell organization and biogenesis [GO:0016043] | 0.00354704 | >0.999 |
| GO Biological Process | processing of 20S pre-rRNA [GO:0030490] | 0.00195617 | >0.999 |
| MDS Proteomics Complexes | YHR052W (CIC1) | 0.00207476 | >0.999 |
| GO Biological Process | transcription [GO:0006350] | 0.00139268 | >0.999 |
| GO Molecular Function | snoRNA binding [GO:0030515] | 0.00167109 | >0.999 |
| GO Molecular Function | RNA binding [GO:0003723] | 0.00452206 | >0.999 |
| GO Biological Process | heavy metal ion transport [GO:0006823] | 0.00167109 | >0.999 |
| GO Biological Process | transition metal transport [GO:0000041] | 0.00478672 | >0.999 |
| | | | |
| **Pdr1** | **n=199** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | TRANSPORT FACILITATION | 1.51E-05 | 0.00391129 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00014982 | 0.02846637 |

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|---|---|---|---|
| GO Cellular Component | hydrogen-translocating V-type ATPase complex [GO:0016471] | 0.00010079 | 0.03325938 |
| MIPS Functional Classification | transport mechanism | 0.00045727 | 0.11843345 |
| GO Molecular Function | transporter [GO:0005215] | 0.00010627 | 0.14632691 |
| GO Biological Process | vacuolar acidification [GO:0007035] | 0.00024821 | 0.3425229 |
| Cellzome Complexes | YNL313C | 0.00100443 | 0.46103337 |
| MIPS Functional Classification | transport ATPases | 0.00245165 | 0.63497735 |
| MIPS Protein Classes | ion-transport ATPases | 0.00344674 | 0.6548806 |
| SMART Domains | CBS | 0.00229957 | 0.67607358 |
| Cellzome Complexes | YGR020C (VMA7) | 0.0015696 | 0.7204464 |
| GO Biological Process | transport [GO:0006810] | 0.0005381 | 0.74257662 |
| MIPS Functional Classification | cation transporters | 0.0029873 | 0.7737107 |
| MIPS Functional Classification | ion transporters | 0.00313155 | 0.81107145 |
| | | | |
| **Phd1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00014982 | 0.02846637 |
| GO Biological Process | thiamin biosynthesis [GO:0009228] | 4.87E-05 | 0.06714901 |
| GO Biological Process | thiamin metabolism [GO:0006772] | 7.11E-05 | 0.09813801 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00049284 | 0.16263687 |
| MIPS Functional Classification | plasma membrane | 0.00154138 | 0.39921742 |
| MDS Proteomics Complexes | YDL017W (CDC7) | 0.00169595 | 0.83610335 |
| MIPS Protein Complexes | Mitochondrial ribosomes | 0.00425946 | >0.999 |
| PFam-A Domains | PF02776 (TPP_enzymes_N) | 0.00100443 | >0.999 |
| PFam-A Domains | PF00205 (TPP_enzymes) | 0.00100443 | >0.999 |
| GO Biological Process | vitamin biosynthesis [GO:0009110] | 0.00307352 | >0.999 |
| GO Biological Process | water-soluble vitamin biosynthesis [GO:0042364] | 0.00307352 | >0.999 |
| PFam-A Domains | PF03105 (SPX) | 0.0032087 | >0.999 |
| PFam-A Domains | PF02775 (TPP_enzymes_C) | 0.00100443 | >0.999 |
| | | | |
| **Pho2** | **n=186** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Cellzome Complexes | YFL017W-A (SMX2) | 0.000101 | 0.04635808 |
| MIPS Functional Classification | transport mechanism | 0.00027732 | 0.07182666 |
| MIPS Subcellular Localization | chromosome structure | 0.00427367 | 0.17949414 |

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|---|---|---|---|
| GO Cellular Component | commitment complex [GO:0000243] | 0.00059541 | 0.1964853 |
| GO Molecular Function | binding [GO:0005488] | 0.00027608 | 0.38015665 |
| Cellzome Complexes | YBR119W (MUD1) | 0.00189357 | 0.86914863 |
| MDS Proteomics Complexes | YDR386W (MUS81) | 0.0019789 | 0.9755977 |
|  |  |  |  |
| **Pho4** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | amino acid metabolism | 4.78E-09 | 1.24E-06 |
| PFam-A Domains | PF03105 (SPX) | 3.36E-09 | 3.98E-06 |
| MIPS Functional Classification | METABOLISM | 1.59E-08 | 4.13E-06 |
| MIPS Functional Classification | amino acid biosynthesis | 2.60E-08 | 6.73E-06 |
| GO Biological Process | amino acid metabolism [GO:0006520] | 1.34E-08 | 1.85E-05 |
| GO Biological Process | amino acid and derivative metabolism [GO:0006519] | 3.95E-08 | 5.45E-05 |
| GO Biological Process | amine metabolism [GO:0009308] | 4.97E-08 | 6.86E-05 |
| MIPS Functional Classification | phosphate metabolism | 5.69E-07 | 0.00014745 |
| GO Biological Process | sulfur metabolism [GO:0006790] | 8.42E-07 | 0.00116259 |
| MIPS Functional Classification | regulation of amino acid metabolism | 6.54E-06 | 0.00169275 |
| GO Biological Process | amino acid biosynthesis [GO:0008652] | 4.01E-06 | 0.00553268 |
| GO Biological Process | amine biosynthesis [GO:0009309] | 8.41E-06 | 0.01160108 |
| Proteome Localization--Observed | cyto | 0.0017033 | 0.0187363 |
| MIPS Phenotypes | Methionine auxotrophy (Met) | 0.00011184 | 0.02013174 |
| MIPS Functional Classification | glycolysis and gluconeogenesis | 9.54E-05 | 0.02471787 |
| MIPS Protein Classes | Basic domains | 0.00013224 | 0.02512503 |
| MIPS Protein Classes | Leucine zipper factors | 0.00014246 | 0.02706645 |
| GO Biological Process | sulfur amino acid metabolism [GO:0000096] | 2.61E-05 | 0.03597094 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 5.76E-05 | 0.0794339 |
| GO Biological Process | inorganic anion transport [GO:0015698] | 7.28E-05 | 0.10051782 |
| MIPS Phenotypes | Divalent cations and heavy metals resistance | 0.00057382 | 0.10328814 |
| GO Cellular Component | cell [GO:0005623] | 0.00037317 | 0.12314511 |
| GO Biological Process | glycolysis [GO:0006096] | 0.00010322 | 0.14243808 |
| MIPS Functional Classification | homeostasis of anions | 0.00057382 | 0.14862016 |
| GO Biological Process | phosphate transport [GO:0006817] | 0.00011184 | 0.15434334 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 0.00011603 | 0.16011588 |
| GO Biological Process | hexose metabolism [GO:0019318] | 0.00015233 | 0.2102154 |

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|---|---|---|---|
| MIPS Phenotypes | Divalent cations and heavy metals | 0.00122023 | 0.2196414 |
| MIPS Functional Classification | homeostasis of phosphate | 0.00101923 | 0.26398057 |
| GO Molecular Function | enzyme [GO:0003824] | 0.00019377 | 0.26681854 |
| MIPS Functional Classification | ENERGY | 0.00106776 | 0.27654984 |
| SMART Domains | BRLZ | 0.0010418 | 0.3062892 |
| MIPS Functional Classification | nitrogen and sulfur metabolism | 0.00121124 | 0.31371116 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 0.00022865 | 0.31553424 |
| GO Biological Process | aromatic amino acid family metabolism [GO:0009072] | 0.00025409 | 0.35064144 |
| GO Cellular Component | intracellular [GO:0005622] | 0.00109494 | 0.3613302 |
| GO Biological Process | methionine metabolism [GO:0006555] | 0.00033007 | 0.45550074 |
| MIPS Phenotypes | Inositol auxotrophy (Ino) | 0.00325479 | 0.5858622 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 0.00045107 | 0.62247246 |
| GO Molecular Function | electron transporter [GO:0005489] | 0.00053221 | 0.73285042 |
| GO Biological Process | glucose catabolism [GO:0006007] | 0.00053221 | 0.73444704 |
| GO Biological Process | hexose catabolism [GO:0019320] | 0.00053221 | 0.73444704 |
| SMART Domains | ANK | 0.00267631 | 0.78683514 |
| GO Cellular Component | cell wall [GO:0005618] | 0.0025201 | 0.831633 |
| GO Cellular Component | external protective structure [GO:0030312] | 0.0025201 | 0.831633 |
| MIPS Functional Classification | phosphate transport | 0.00325479 | 0.84299061 |
| GO Biological Process | monosaccharide catabolism [GO:0046365] | 0.0006626 | 0.91438248 |
| | | | |
| **Put3** | **n=198** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | glyoxylate cycle | 1.38E-05 | 0.00357441 |
| Proteome Localization--Predicted+Obs | cyt | 0.00178211 | 0.00712844 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00089971 | 0.00989681 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.0001148 | 0.02973398 |
| Proteome Localization--Observed | cyto | 0.00365118 | 0.04016298 |
| GO Biological Process | main pathways of carbohydrate metabolism [GO:0006092] | 3.47E-05 | 0.04791608 |
| MIPS Functional Classification | drug transporters | 0.00069583 | 0.18021919 |
| PFam-A Domains | PF00083 (sugar_tr) | 0.00022507 | 0.26671269 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 0.00020471 | 0.28250256 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00168253 | 0.3196807 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 0.00142072 | 0.36796648 |

| | | | |
|---|---|---|---|
| MIPS Phenotypes | Methionine auxotrophy (Met) | 0.00226655 | 0.407979 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 0.00041642 | 0.57465684 |
| MIPS Phenotypes | Carbohydrate and lipid biosynthesis defects | 0.0033617 | 0.605106 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 0.00272429 | 0.70559111 |
| GO Cellular Component | cytoplasm [GO:0005737] | 0.00216715 | 0.7151595 |
| GO Cellular Component | cell wall [GO:0005618] | 0.00235362 | 0.7766946 |
| GO Cellular Component | external protective structure [GO:0030312] | 0.00235362 | 0.7766946 |
| MIPS Functional Classification | phosphate transport | 0.00316301 | 0.81921959 |
| GO Biological Process | response to drug [GO:0042493] | 0.00063286 | 0.87335232 |
| MIPS Functional Classification | stress response | 0.00345079 | 0.89375461 |
| | | | |
| **Rap1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Subcellular Localization | cytoplasm | 1.00E-14 | 4.20E-13 |
| MIPS Functional Classification | ribosome biogenesis | 1.00E-14 | 2.59E-12 |
| MIPS Functional Classification | PROTEIN SYNTHESIS | 1.00E-14 | 2.59E-12 |
| MIPS Protein Complexes | Cytoplasmic ribosomes | 1.00E-14 | 3.15E-12 |
| MIPS Protein Complexes | cytoplasmic ribosomal large subunit | 1.00E-14 | 3.15E-12 |
| MIPS Protein Complexes | Translation complexes | 1.00E-14 | 3.15E-12 |
| GO Cellular Component | cytosolic ribosome (sensu Eukarya) [GO:0005830] | 1.00E-14 | 3.30E-12 |
| GO Cellular Component | cytosol [GO:0005829] | 1.00E-14 | 3.30E-12 |
| GO Cellular Component | ribosome [GO:0005840] | 1.00E-14 | 3.30E-12 |
| GO Cellular Component | ribonucleoprotein complex [GO:0030529] | 1.00E-14 | 3.30E-12 |
| GO Cellular Component | cytosolic large ribosomal subunit (sensu Eukarya) [GO:0005842] | 1.00E-14 | 3.30E-12 |
| GO Cellular Component | large ribosomal subunit [GO:0015934] | 1.00E-14 | 3.30E-12 |
| GO Biological Process | biosynthesis [GO:0009058] | 1.00E-14 | 1.38E-11 |
| GO Molecular Function | structural molecule [GO:0005198] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | protein biosynthesis [GO:0006412] | 1.00E-14 | 1.38E-11 |
| GO Molecular Function | structural constituent of ribosome [GO:0003735] | 1.00E-14 | 1.38E-11 |
| GO Biological Process | macromolecule biosynthesis [GO:0009059] | 1.00E-14 | 1.38E-11 |
| MIPS Protein Complexes | cytoplasmic ribosomal small subunit | 5.06E-14 | 1.59E-11 |
| GO Cellular Component | cytosolic small ribosomal subunit (sensu Eukarya) [GO:0005843] | 2.09E-13 | 6.91E-11 |
| GO Cellular Component | eukaryotic 48S initiation complex [GO:0016283] | 2.09E-13 | 6.91E-11 |
| GO Cellular Component | eukaryotic 43S pre-initiation complex [GO:0016282] | 1.30E-12 | 4.28E-10 |

|  |  |  |  |
|---|---|---|---|
| GO Cellular Component | cytoplasm [GO:0005737] | 5.12E-11 | 1.69E-08 |
| GO Biological Process | protein metabolism [GO:0019538] | 1.87E-11 | 2.58E-08 |
| GO Cellular Component | small ribosomal subunit [GO:0015935] | 1.86E-10 | 6.15E-08 |
| MIPS Functional Classification | SUBCELLULAR LOCALISATION | 2.02E-08 | 5.23E-06 |
| Published Complexes | Andersen et al. (2002) - Curr Bio 12:1- | 1.74E-05 | 0.00012161 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 1.96E-07 | 0.00026992 |
| Yeast Fitness Data | Slow Growers | 0.00047742 | 0.00047742 |
| Proteome Localization--Observed | cyto | 4.88E-05 | 0.00053659 |
| Proteome Localization--Predicted+Obs | cyt | 0.00014341 | 0.00057365 |
| GO Biological Process | regulation of translational fidelity [GO:0006450] | 6.28E-07 | 0.00086683 |
| GO Cellular Component | intracellular [GO:0005622] | 3.22E-06 | 0.00106288 |
| Cellzome Complexes | YBR031W (RPL4A) | 2.65E-06 | 0.0012157 |
| GO Biological Process | metabolism [GO:0008152] | 1.31E-06 | 0.00180935 |
| GO Cellular Component | cell [GO:0005623] | 1.08E-05 | 0.00356037 |
| MIPS Protein Complexes | Cytoplasmic translation elongation | 0.00011184 | 0.03523055 |
| MIPS Protein Complexes | eEF1 | 0.00059642 | 0.18787325 |
| MIPS Phenotypes | paromomycin | 0.00233288 | 0.4199184 |
| PFam-A Domains | PF00467 (KOW) | 0.00040738 | 0.48274886 |
| GO Biological Process | translational elongation [GO:0006414] | 0.00042209 | 0.5824842 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 0.00045107 | 0.62247246 |
| GO Molecular Function | translation elongation factor [GO:0003746] | 0.00057382 | 0.79015427 |
| GO Biological Process | carbohydrate catabolism [GO:0016052] | 0.0046866 | >0.999 |
| GO Biological Process | hexose metabolism [GO:0019318] | 0.00080198 | >0.999 |
| GO Biological Process | alcohol catabolism [GO:0046164] | 0.00119827 | >0.999 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 0.00147054 | >0.999 |
| GO Biological Process | ribosomal subunit assembly [GO:0042257] | 0.00073539 | >0.999 |
| GO Biological Process | hexose catabolism [GO:0019320] | 0.00468663 | >0.999 |
| GO Biological Process | glucose metabolism [GO:0006006] | 0.00251429 | >0.999 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 0.0022495 | >0.999 |
| GO Biological Process | glucose catabolism [GO:0006007] | 0.00468663 | >0.999 |
| GO Biological Process | regulation of translation [GO:0006445] | 0.00099326 | >0.999 |
| MIPS Functional Classification | glycolysis and gluconeogenesis | 0.0046866 | >0.999 |
| GO Biological Process | ribosome assembly [GO:0042255] | 0.00094528 | >0.999 |
| GO Molecular Function | chaperone [GO:0003754] | 0.00479726 | >0.999 |

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|---|---|---|---|
| MIPS Functional Classification | C-compound and carbohydrate utilization | 0.00388782 | >0.999 |
|  |  |  |  |
| **Rdr1** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 9.28E-08 | 1.76E-05 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 5.23E-08 | 7.20E-05 |
| GO Molecular Function | hexose transporter [GO:0015149] | 5.23E-08 | 7.20E-05 |
| GO Molecular Function | fructose transporter [GO:0005353] | 8.62E-08 | 0.00011873 |
| GO Molecular Function | mannose transporter [GO:0015578] | 1.57E-07 | 0.00021663 |
| GO Biological Process | hexose transport [GO:0008645] | 2.04E-07 | 0.00028119 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 2.04E-07 | 0.00028119 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 2.30E-07 | 0.00031675 |
| GO Molecular Function | glucose transporter [GO:0005355] | 4.50E-07 | 0.00061994 |
| PFam-A Domains | PF00083 (sugar_tr) | 6.26E-07 | 0.00074154 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 5.39E-06 | 0.00139691 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 1.68E-06 | 0.00231169 |
| MIPS Functional Classification | plasma membrane | 1.06E-05 | 0.00274594 |
| Proteome Localization--Predicted+Obs | cyt | 0.00071618 | 0.00286472 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00035892 | 0.00394808 |
| GO Cellular Component | plasma membrane [GO:0005886] | 1.26E-05 | 0.00416734 |
| GO Molecular Function | galactose transporter [GO:0005354] | 1.44E-05 | 0.01977895 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 8.60E-05 | 0.02226763 |
| MIPS Functional Classification | detoxification | 8.69E-05 | 0.02251617 |
| MIPS Functional Classification | drug transporters | 9.54E-05 | 0.02471787 |
| MIPS Functional Classification | cellular import | 0.00031291 | 0.08104473 |
| GO Molecular Function | drug transporter [GO:0015238] | 6.37E-05 | 0.08774877 |
| GO Molecular Function | multidrug transporter [GO:0015239] | 6.37E-05 | 0.08774877 |
| MIPS Functional Classification | METABOLISM | 0.00039781 | 0.10303227 |
| GO Biological Process | response to chemical substance [GO:0042221] | 0.00011531 | 0.15912228 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 0.00064984 | 0.16830804 |
| GO Molecular Function | transporter [GO:0005215] | 0.00029115 | 0.40091355 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 0.00045107 | 0.62247246 |
| SMART Domains | Aamy | 0.00233288 | 0.68586672 |
| GO Molecular Function | ABC-type efflux porter [GO:0015427] | 0.00059642 | 0.82127447 |

|  |  |  |  |
|---|---|---|---|
| GO Biological Process | response to drug [GO:0042493] | 0.0006626 | 0.91438248 |
| GO Molecular Function | oxo-acid-lyase [GO:0016833] | 0.0010418 | >0.999 |
| GO Biological Process | hexose metabolism [GO:0019318] | 0.00080198 | >0.999 |
| GO Molecular Function | alpha-glucosidase [GO:0004558] | 0.00101923 | >0.999 |
| GO Molecular Function | inorganic anion transporter [GO:0015103] | 0.00159254 | >0.999 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 0.00147054 | >0.999 |
| PFam-A Domains | PF00128 (alpha-amylase) | 0.00159254 | >0.999 |
| GO Molecular Function | anion transporter [GO:0008509] | 0.00326287 | >0.999 |
|  |  |  |  |
| **Rds1** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00061778 | 0.00679554 |
| Proteome Localization--Observed | cyto | 0.00284451 | 0.03128961 |
| MIPS Functional Classification | plasma membrane | 0.00015139 | 0.03921079 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00056067 | 0.10652768 |
| MIPS Functional Classification | lipid and fatty-acid transport | 0.00042209 | 0.10932131 |
| GO Cellular Component | nuclear chromosome [GO:0000228] | 0.00040738 | 0.13443639 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00089336 | 0.23137895 |
| GO Molecular Function | transporter [GO:0005215] | 0.00029115 | 0.40091355 |
| GO Cellular Component | cell [GO:0005623] | 0.00166059 | 0.5479947 |
| GO Cellular Component | integral membrane protein [GO:0016021] | 0.00200172 | 0.6605676 |
| MIPS Functional Classification | ion transporters | 0.00322967 | 0.83648453 |
| MIPS Functional Classification | phosphate transport | 0.00325479 | 0.84299061 |
| MDS Proteomics Complexes | YOR181W (LAS17) | 0.00172766 | 0.85173638 |
| SMART Domains | HMG | 0.0029765 | 0.875091 |
|  |  |  |  |
| **Rds2** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 4.71E-07 | 8.96E-05 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 5.39E-06 | 0.00139691 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00170882 | 0.01879702 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 1.88E-05 | 0.02587232 |
| GO Molecular Function | hexose transporter [GO:0015149] | 1.88E-05 | 0.02587232 |
| PFam-A Domains | PF00083 (sugar_tr) | 3.76E-05 | 0.04454782 |

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|---|---|---|---|
| GO Biological Process | carbohydrate transport [GO:0008643] | 3.31E-05 | 0.04566185 |
| GO Biological Process | hexose transport [GO:0008645] | 4.77E-05 | 0.06580627 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 4.77E-05 | 0.06580627 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 0.00027825 | 0.07206701 |
| GO Molecular Function | mannose transporter [GO:0015578] | 7.28E-05 | 0.1002993 |
| GO Cellular Component | membrane [GO:0016020] | 0.00038759 | 0.12790569 |
| SMART Domains | TRANS | 0.00051001 | 0.14994323 |
| GO Biological Process | transport [GO:0006810] | 0.0001399 | 0.19305924 |
| GO Molecular Function | glucose transporter [GO:0005355] | 0.00014246 | 0.19616054 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 0.00020515 | 0.2824943 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00156099 | 0.5151267 |
| MIPS Functional Classification | METABOLISM | 0.00228836 | 0.59268524 |
| MIPS Functional Classification | allantoin and allantoate transporters | 0.00233288 | 0.60421592 |
| MIPS Phenotypes | Carbohydrate and lipid biosynthesis defects | 0.00353338 | 0.6360084 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 0.00316469 | 0.81965471 |
| GO Molecular Function | galactose transporter [GO:0005354] | 0.00059642 | 0.82127447 |
| MDS Proteomics Complexes | YOR181W (LAS17) | 0.00172766 | 0.85173638 |
| GO Molecular Function | fructose transporter [GO:0005353] | 0.00078341 | >0.999 |
| MIPS Functional Classification | plasma membrane | 0.00467495 | >0.999 |
| GO Molecular Function | anion transporter [GO:0008509] | 0.00326287 | >0.999 |
| GO Molecular Function | transporter [GO:0005215] | 0.00353451 | >0.999 |
| GO Biological Process | carboxylic acid metabolism [GO:0019752] | 0.0034975 | >0.999 |
| GO Biological Process | organic acid metabolism [GO:0006082] | 0.0034975 | >0.999 |
| GO Molecular Function | monocarboxylic acid transporter [GO:0008028] | 0.00437089 | >0.999 |
| MIPS Functional Classification | cellular import | 0.00443397 | >0.999 |
|  |  |  |  |
| **Rgt1** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 1.31E-10 | 3.38E-08 |
| GO Biological Process | hexose transport [GO:0008645] | 4.06E-10 | 5.60E-07 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 4.06E-10 | 5.60E-07 |
| GO Molecular Function | mannose transporter [GO:0015578] | 4.97E-09 | 6.85E-06 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 1.51E-08 | 2.08E-05 |
| GO Molecular Function | glucose transporter [GO:0005355] | 1.78E-08 | 2.45E-05 |

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|---|---|---|---|
| MIPS Functional Classification | METABOLISM | 9.82E-08 | 2.54E-05 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 5.23E-08 | 7.20E-05 |
| GO Molecular Function | hexose transporter [GO:0015149] | 5.23E-08 | 7.20E-05 |
| GO Molecular Function | fructose transporter [GO:0005353] | 8.62E-08 | 0.00011873 |
| Proteome Localization--Predicted+Obs | cyt | 0.00014341 | 0.00057365 |
| PFam-A Domains | PF00083 (sugar_tr) | 6.26E-07 | 0.00074154 |
| GO Molecular Function | alpha-glucosidase [GO:0004558] | 6.28E-07 | 0.00086495 |
| SMART Domains | Aamy | 3.58E-06 | 0.00105136 |
| PFam-A Domains | PF00128 (alpha-amylase) | 1.63E-06 | 0.00193347 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 1.68E-06 | 0.00231169 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 2.53E-05 | 0.00655205 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00061778 | 0.00679554 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 4.12E-05 | 0.00782321 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 8.60E-05 | 0.02226763 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00013388 | 0.03467388 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00016108 | 0.05315772 |
| MIPS Functional Classification | cellular import | 0.00031291 | 0.08104473 |
| MIPS Subcellular Localization | cytoplasm | 0.00197337 | 0.08288154 |
| MIPS Protein Classes | Transcription factors | 0.00065715 | 0.12485755 |
| MIPS Functional Classification | plasma membrane | 0.00051343 | 0.13297889 |
| MIPS Functional Classification | glyoxylate cycle | 0.00059642 | 0.15447356 |
| MIPS Protein Classes | Helix-turn-helix | 0.00099326 | 0.18871959 |
| MIPS Functional Classification | ENERGY | 0.00106776 | 0.27654984 |
| SMART Domains | ZnF_C2H2 | 0.00094528 | 0.27791232 |
| MIPS Protein Classes | Cys2His2 zinc-finger | 0.00173371 | 0.3294049 |
| PFam-A Domains | PF00096 (zf-C2H2) | 0.00031682 | 0.37542696 |
| MIPS Functional Classification | regulation of C-compound and carbohydrate utilization | 0.00147075 | 0.38092425 |
| MIPS Protein Classes | Zinc-coordinating DNA-binding domains | 0.00207705 | 0.3946395 |
| GO Molecular Function | glucosidase [GO:0015926] | 0.00053221 | 0.73285042 |
| GO Molecular Function | galactose transporter [GO:0005354] | 0.00059642 | 0.82127447 |
| GO Biological Process | sphingolipid metabolism [GO:0006665] | 0.00393128 | >0.999 |
| GO Molecular Function | structural constituent of cell wall [GO:0005199] | 0.00437089 | >0.999 |
| GO Molecular Function | oxo-acid-lyase [GO:0016833] | 0.0010418 | >0.999 |
| GO Biological Process | response to osmotic stress [GO:0006970] | 0.0028255 | >0.999 |

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|---|---|---|---|
| GO Molecular Function | transporter [GO:0005215] | 0.00353451 | >0.999 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 0.00184928 | >0.999 |
| GO Biological Process | organic acid metabolism [GO:0006082] | 0.00085275 | >0.999 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 0.0034766 | >0.999 |
| GO Molecular Function | carbon-carbon lyase [GO:0016830] | 0.00099658 | >0.999 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 0.0022495 | >0.999 |
| GO Biological Process | lipid metabolism [GO:0006629] | 0.00263813 | >0.999 |
| GO Biological Process | carboxylic acid metabolism [GO:0019752] | 0.00085275 | >0.999 |
| Cellzome Complexes | YDR172W (SUP35) | 0.00233288 | >0.999 |
| | | | |
| **Rph1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 4.10E-06 | 4.51E-05 |
| GO Biological Process | response to stress [GO:0006950] | 5.73E-05 | 0.07902487 |
| MIPS Protein Classes | Transcription factors | 0.00192745 | 0.3662155 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 0.0014536 | 0.3764824 |
| MIPS Functional Classification | other transcription activities | 0.00207275 | 0.53684225 |
| PFam-A Domains | PF00498 (FHA) | 0.00057382 | 0.67998026 |
| MIPS Functional Classification | stress response | 0.003762 | 0.974358 |
| PFam-A Domains | PF02786 (CPSase_L_D2) | 0.00101923 | >0.999 |
| GO Biological Process | carbohydrate catabolism [GO:0016052] | 0.0046866 | >0.999 |
| PFam-A Domains | PF00289 (CPSase_L_chain) | 0.00101923 | >0.999 |
| GO Molecular Function | transcriptional repressor [GO:0016564] | 0.00437089 | >0.999 |
| GO Biological Process | sporulation [GO:0030435] | 0.00378224 | >0.999 |
| | | | |
| **Rpn4** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Proteome Localization--Observed | cyto | 0.00284451 | 0.03128961 |
| Cellzome Complexes | YDR062W (LCB2) | 7.28E-05 | 0.0334331 |
| MIPS Subcellular Localization | vacuolar membrane | 0.0013264 | 0.0557088 |
| MIPS Subcellular Localization | vacuole | 0.001505 | 0.06321 |
| MIPS Functional Classification | purine ribonucleotide metabolism | 0.00049144 | 0.12728244 |
| GO Biological Process | purine nucleotide metabolism [GO:0006163] | 0.00010322 | 0.14243808 |
| SMART Domains | KISc | 0.00059642 | 0.17534836 |

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|---|---|---|---|
| GO Biological Process | sporulation [GO:0030435] | 0.00020538 | 0.28342026 |
| MIPS Protein Classes | Cys2His2 zinc-finger | 0.00173371 | 0.3294049 |
| PFam-A Domains | PF00096 (zf-C2H2) | 0.00031682 | 0.37542696 |
| GO Biological Process | ion homeostasis [GO:0006873] | 0.00027919 | 0.3852753 |
| MIPS Functional Classification | vacuolar transport | 0.00167874 | 0.43479366 |
| MIPS Protein Classes | Kinesines | 0.00233288 | 0.4432472 |
| GO Cellular Component | hydrogen-translocating V-type ATPase complex [GO:0016471] | 0.00135467 | 0.4470411 |
| Cellzome Complexes | YBR207W (FTH1) | 0.00101923 | 0.46782657 |
| GO Biological Process | vacuolar transport [GO:0007034] | 0.00044362 | 0.61219974 |
| MIPS Functional Classification | transport ATPases | 0.00251429 | 0.65120111 |
| GO Biological Process | cation homeostasis [GO:0030003] | 0.00047438 | 0.65464992 |
| MIPS Protein Classes | ion-transport ATPases | 0.00353338 | 0.6713422 |
| PFam-A Domains | PF00225 (kinesin) | 0.00059642 | 0.70676126 |
| Cellzome Complexes | YGR020C (VMA7) | 0.00159254 | 0.73097586 |
| GO Biological Process | ribonucleotide metabolism [GO:0009259] | 0.00057382 | 0.79187574 |
| GO Biological Process | purine ribonucleotide metabolism [GO:0009150] | 0.00057382 | 0.79187574 |
| MIPS Functional Classification | cation transporters | 0.00307229 | 0.79572311 |
| GO Biological Process | copper homeostasis [GO:0006878] | 0.00059642 | 0.82306374 |
| GO Cellular Component | 26S proteasome [GO:0005837] | 0.00251429 | 0.8297157 |
| MIPS Functional Classification | ion transporters | 0.00322967 | 0.83648453 |
| GO Cellular Component | vacuolar membrane [GO:0005774] | 0.00353338 | >0.999 |
| GO Biological Process | nicotinamide adenine dinucleotide metabolism [GO:0019674] | 0.00437089 | >0.999 |
| GO Biological Process | homeostasis [GO:0019725] | 0.0007653 | >0.999 |
| GO Biological Process | nucleotide metabolism [GO:0009117] | 0.00099326 | >0.999 |
| GO Biological Process | hydrogen ion homeostasis [GO:0030641] | 0.00099326 | >0.999 |
| GO Biological Process | sporulation (sensu Saccharomyces) [GO:0007151] | 0.00440471 | >0.999 |
| GO Biological Process | purine nucleoside monophosphate metabolism [GO:0009126] | 0.00325479 | >0.999 |
| GO Biological Process | regulation of pH [GO:0006885] | 0.00099326 | >0.999 |
| GO Molecular Function | transferase [GO:0016740] | 0.00418089 | >0.999 |
| GO Biological Process | ribonucleotide biosynthesis [GO:0009260] | 0.00437089 | >0.999 |
| GO Molecular Function | kinase [GO:0016301] | 0.00399507 | >0.999 |
| GO Biological Process | ribonucleoside monophosphate metabolism [GO:0009161] | 0.00325479 | >0.999 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00484406 | >0.999 |
| GO Molecular Function | hydrogen-/sodium-translocating ATPase [GO:0015442] | 0.00234057 | >0.999 |

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|---|---|---|---|
| SMART Domains | ZnF_C2H2 | 0.00483174 | >0.999 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 0.00105549 | >0.999 |
| MIPS Functional Classification | homeostasis of protons | 0.0046866 | >0.999 |
| GO Biological Process | monovalent inorganic cation homeostasis [GO:0030004] | 0.00271949 | >0.999 |
| GO Biological Process | vacuolar acidification [GO:0007035] | 0.00267631 | >0.999 |
| MDS Proteomics Complexes | YPR110C (RPC40) | 0.00436537 | >0.999 |
| GO Biological Process | purine nucleotide biosynthesis [GO:0006164] | 0.00078341 | >0.999 |
| GO Biological Process | purine ribonucleoside monophosphate metabolism [GO:0009167] | 0.00325479 | >0.999 |
| GO Biological Process | nucleoside monophosphate metabolism [GO:0009123] | 0.00437089 | >0.999 |
| GO Molecular Function | hydrogen-transporting two-sector ATPase [GO:0003936] | 0.00234057 | >0.999 |
| GO Biological Process | nucleotide biosynthesis [GO:0009165] | 0.00326287 | >0.999 |
| GO Biological Process | purine ribonucleotide biosynthesis [GO:0009152] | 0.00437089 | >0.999 |
| | | | |
| **Rsc3** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Protein Classes | Histones | 8.69E-09 | 1.65E-06 |
| PFam-A Domains | PF00125 (histone) | 3.25E-09 | 3.85E-06 |
| MIPS Protein Complexes | Nucleosomal protein complex | 2.53E-08 | 7.96E-06 |
| GO Cellular Component | nucleosome [GO:0005718] | 7.49E-07 | 0.00024731 |
| MIPS Functional Classification | DNA synthesis and replication | 7.06E-06 | 0.0018296 |
| MIPS Phenotypes | other carbohydrate and lipid biosynthesis defects | 1.26E-05 | 0.00227588 |
| MIPS Functional Classification | deoxyribonucleotide metabolism | 1.21E-05 | 0.00314457 |
| GO Cellular Component | chromatin [GO:0005717] | 1.93E-05 | 0.00638454 |
| Proteome Localization--Predicted+Obs | en2 | 0.00175664 | 0.00702656 |
| PFam-A Domains | PF00674 (DUP) | 6.41E-06 | 0.00759021 |
| MIPS Phenotypes | Carbohydrate and lipid biosynthesis defects | 9.73E-05 | 0.01751861 |
| GO Cellular Component | chromosome [GO:0005694] | 8.34E-05 | 0.02753731 |
| GO Biological Process | DNA replication [GO:0006260] | 2.63E-05 | 0.03626516 |
| GO Biological Process | S phase of mitotic cell cycle [GO:0000084] | 3.28E-05 | 0.0452876 |
| GO Biological Process | chromatin assembly/disassembly [GO:0006333] | 6.11E-05 | 0.0842835 |
| MIPS Functional Classification | lipid and fatty-acid transport | 0.00041243 | 0.10681885 |
| MIPS Functional Classification | chromosome | 0.00041358 | 0.107118 |
| MIPS Protein Classes | Helix-turn-helix | 0.00097104 | 0.18449798 |
| MIPS Functional Classification | transcriptional control | 0.00083913 | 0.21733441 |

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|---|---|---|---|
| GO Cellular Component | cell [GO:0005623] | 0.00078586 | 0.25933314 |
| MDS Proteomics Complexes | YOL054W (PSH1) | 0.000563 | 0.27756097 |
| MIPS Phenotypes | Killer toxin hypersensitivity | 0.0015696 | 0.282528 |
| MIPS Protein Classes | associated subunits | 0.0015696 | 0.298224 |
| MIPS Functional Classification | METABOLISM | 0.00116218 | 0.30100462 |
| MIPS Protein Classes | Transcription factors | 0.00183853 | 0.3493207 |
| MIPS Phenotypes | other cell morphology mutants | 0.00201431 | 0.3625758 |
| GO Cellular Component | extracellular [GO:0005576] | 0.00128371 | 0.4236243 |
| MIPS Protein Classes | Homeodomain | 0.00229957 | 0.4369183 |
| SMART Domains | CYCLIN | 0.00212688 | 0.62530272 |
| SMART Domains | HOX | 0.00229957 | 0.67607358 |
| GO Cellular Component | cell wall (sensu Fungi) [GO:0009277] | 0.00205474 | 0.6780642 |
| PFam-A Domains | PF00682 (HMGL-like) | 0.00058769 | 0.69641502 |
| MIPS Protein Complexes | Replication fork complexes | 0.00228972 | 0.7212618 |
| GO Cellular Component | cell wall [GO:0005618] | 0.00243573 | 0.8037909 |
| GO Cellular Component | external protective structure [GO:0030312] | 0.00243573 | 0.8037909 |
| GO Biological Process | DNA metabolism [GO:0006259] | 0.0006324 | 0.87270786 |
| MIPS Protein Classes | Cyclins | 0.00460355 | 0.8746745 |
| MDS Proteomics Complexes | YER133W (GLC7) | 0.00430951 | >0.999 |
| GO Biological Process | double-strand break repair via synthesis-dependent strand annealing [GO:0045003] | 0.0032087 | >0.999 |
| GO Molecular Function | DNA binding [GO:0003677] | 0.00260697 | >0.999 |
| MIPS Protein Complexes | Replication complexes | 0.00425946 | >0.999 |
| MIPS Functional Classification | mRNA synthesis | 0.00459568 | >0.999 |
| PFam-A Domains | PF00134 (cyclin) | 0.00132964 | >0.999 |
| GO Biological Process | DNA replication and chromosome cycle [GO:0000067] | 0.00457128 | >0.999 |
| GO Biological Process | lipid metabolism [GO:0006629] | 0.00084774 | >0.999 |
| | | | |
| **Rsc30** | **n=199** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| PFam-A Domains | PF00674 (DUP) | 4.27E-07 | 0.00050571 |
| Proteome Localization--Observed | cyto | 0.00250785 | 0.02758635 |
| MIPS Subcellular Localization | cytoplasm | 0.00181589 | 0.07626738 |
| MIPS Functional Classification | lipid and fatty-acid transport | 0.00041243 | 0.10681885 |
| GO Cellular Component | nuclear chromosome [GO:0000228] | 0.00039965 | 0.13188483 |

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|---|---|---|---|
| MIPS Functional Classification | METABOLISM | 0.00064434 | 0.16688458 |
| PFam-A Domains | PF02133 (Transp_cyt_pur) | 0.00017827 | 0.21124403 |
| MIPS Phenotypes | Killer toxin hypersensitivity | 0.0015696 | 0.282528 |
| PFam-A Domains | PF00660 (SRP1_TIP1) | 0.00029836 | 0.35355897 |
| MIPS Protein Classes | Histones | 0.00430951 | 0.8188069 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 0.00070884 | 0.97819368 |
|  |  |  |  |
| **Rtg3** | **n=199** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Proteome Localization--Predicted+Obs | en2 | 0.00097084 | 0.00388335 |
| GO Biological Process | amine metabolism [GO:0009308] | 4.91E-06 | 0.00678155 |
| GO Biological Process | glutamine family amino acid catabolism [GO:0009065] | 6.80E-06 | 0.00938045 |
| GO Biological Process | amino acid metabolism [GO:0006520] | 7.77E-06 | 0.01072502 |
| GO Molecular Function | asparaginase [GO:0004067] | 1.41E-05 | 0.01938844 |
| GO Biological Process | amino acid and derivative metabolism [GO:0006519] | 1.73E-05 | 0.02387621 |
| GO Cellular Component | periplasmic space (sensu Fungi) [GO:0030287] | 0.00010968 | 0.03619374 |
| GO Biological Process | aspartate family amino acid metabolism [GO:0009066] | 3.48E-05 | 0.04806305 |
| MIPS Functional Classification | amino acid metabolism | 0.00023739 | 0.06148505 |
| GO Biological Process | aspartate family amino acid catabolism [GO:0009068] | 6.25E-05 | 0.08622613 |
| MIPS Functional Classification | transport ATPases | 0.00041358 | 0.107118 |
| MIPS Protein Classes | ion-transport ATPases | 0.00062625 | 0.11898769 |
| MIPS Functional Classification | purine ribonucleotide metabolism | 0.00047679 | 0.12348913 |
| MIPS Functional Classification | homeostasis of protons | 0.00071459 | 0.18507752 |
| GO Molecular Function | enzyme [GO:0003824] | 0.00016167 | 0.22262097 |
| MIPS Functional Classification | cell wall | 0.00112286 | 0.29082074 |
| MIPS Protein Classes | AGC group | 0.00169595 | 0.3222305 |
| GO Biological Process | amino acid catabolism [GO:0009063] | 0.00024821 | 0.3425229 |
| GO Biological Process | amine catabolism [GO:0009310] | 0.00024821 | 0.3425229 |
| GO Molecular Function | hydrogen-transporting two-sector ATPase [GO:0003936] | 0.00029836 | 0.41084447 |
| GO Molecular Function | hydrogen-/sodium-translocating ATPase [GO:0015442] | 0.00029836 | 0.41084447 |
| Cellzome Complexes | YNL313C | 0.00100443 | 0.46103337 |
| GO Biological Process | response to starvation [GO:0009267] | 0.00039965 | 0.55151838 |
| GO Cellular Component | cell [GO:0005623] | 0.00205075 | 0.6767475 |
| Cellzome Complexes | YGR020C (VMA7) | 0.0015696 | 0.7204464 |

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|---|---|---|---|
| GO Cellular Component | intracellular [GO:0005622] | 0.00219324 | 0.7237692 |
| GO Biological Process | glutamine family amino acid metabolism [GO:0009064] | 0.00060794 | 0.8389503 |
| MIPS Functional Classification | METABOLISM | 0.0035034 | 0.9073806 |
| MIPS Functional Classification | regulation of amino acid metabolism | 0.00353056 | 0.91441504 |
| GO Cellular Component | nuclear membrane [GO:0005635] | 0.00288721 | 0.9527793 |

| **Sfl1** | **n=200** | | |
|---|---|---|---|
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Proteome Localization--Predicted+Obs | cyt | 0.00188715 | 0.0075486 |
| Proteome Localization--Observed | cyto | 0.00284451 | 0.03128961 |
| MIPS Protein Complexes | Cytoplasmic translation elongation | 0.00011184 | 0.03523055 |
| GO Molecular Function | translation elongation factor [GO:0003746] | 3.29E-05 | 0.04529311 |
| MIPS Protein Classes | Transcription factors | 0.00065715 | 0.12485755 |
| Cellzome Complexes | YAL029C (MYO4) | 0.00040738 | 0.1869888 |
| MIPS Functional Classification | perception of nutrients and nutritional adaptation | 0.00099326 | 0.2572546 |
| MIPS Functional Classification | plasma membrane | 0.00161284 | 0.41772556 |
| GO Biological Process | translational elongation [GO:0006414] | 0.00042209 | 0.5824842 |
| MIPS Functional Classification | METABOLISM | 0.00228836 | 0.59268524 |
| MIPS Protein Classes | Cyclins | 0.00468663 | 0.8904597 |
| GO Biological Process | hydrogen ion homeostasis [GO:0030641] | 0.00099326 | >0.999 |
| GO Biological Process | monovalent inorganic cation homeostasis [GO:0030004] | 0.00271949 | >0.999 |
| GO Molecular Function | transcriptional repressor [GO:0016564] | 0.00437089 | >0.999 |
| GO Biological Process | regulation of pH [GO:0006885] | 0.00099326 | >0.999 |
| MIPS Functional Classification | translation | 0.00403694 | >0.999 |
| GO Molecular Function | transferase [GO:0016740] | 0.00418089 | >0.999 |
| GO Molecular Function | kinase [GO:0016301] | 0.00148127 | >0.999 |
| GO Molecular Function | hydrogen-transporting two-sector ATPase [GO:0003936] | 0.00234057 | >0.999 |
| Yeast Two Hybrid - Ito (core) | YER081W (SER3) | 0.0029212 | >0.999 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00484406 | >0.999 |
| GO Molecular Function | hydrogen-/sodium-translocating ATPase [GO:0015442] | 0.00234057 | >0.999 |
| MDS Proteomics Complexes | YJL173C (RFA3) | 0.00325479 | >0.999 |
| GO Molecular Function | carbohydrate kinase [GO:0019200] | 0.0010418 | >0.999 |
| | | | |
| **Sfp1** | **n=200** | | |

| **Source** | **Annotation** | **pval** | **Bonfp** |
|---|---|---|---|
| Published Complexes | Harnicharnpai et al. (2001) - Mol Cell 8:505- | 0.00060794 | 0.00425555 |
| MIPS Subcellular Localization | cytoplasm | 0.00351619 | 0.14767998 |
| SMART Domains | ZnF_C2H2 | 0.00091774 | 0.26981674 |
| MIPS Protein Classes | Cys2His2 zinc-finger | 0.00168984 | 0.3210696 |
| MIPS Phenotypes | other cell wall mutants | 0.00205474 | 0.3698532 |
| MDS Proteomics Complexes | YNL175C (NOP13) | 0.00076874 | 0.37898981 |
| MDS Proteomics Complexes | YBL036C | 0.00100443 | 0.49518399 |
| MDS Proteomics Complexes | YNL230C (ELA1) | 0.00140129 | 0.69083597 |
| MIPS Protein Complexes | Cytoplasmic translation elongation | 0.00229957 | 0.72436455 |
| GO Biological Process | aromatic compound metabolism [GO:0006725] | 0.00071377 | 0.98499846 |
| GO Biological Process | membrane lipid biosynthesis [GO:0046467] | 0.00425946 | >0.999 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 0.00329331 | >0.999 |
| GO Cellular Component | cell [GO:0005623] | 0.00321478 | >0.999 |
| PFam-A Domains | PF00096 (zf-C2H2) | 0.00192027 | >0.999 |
| MIPS Functional Classification | homeostasis of protons | 0.00458777 | >0.999 |
| MDS Proteomics Complexes | YPL259C (APM1) | 0.00262786 | >0.999 |
| GO Biological Process | protein-nucleus import [GO:0006606] | 0.00275548 | >0.999 |
| GO Biological Process | nucleobase metabolism [GO:0009112] | 0.00166253 | >0.999 |
| GO Biological Process | biosynthesis [GO:0009058] | 0.00446223 | >0.999 |
| Cellzome Complexes | YKL081W (TEF4) | 0.00430951 | >0.999 |
| MIPS Functional Classification | translation | 0.00392687 | >0.999 |
| MDS Proteomics Complexes | YIL035C (CKA1) | 0.00425946 | >0.999 |
| GO Biological Process | nucleobase biosynthesis [GO:0046112] | 0.00262786 | >0.999 |
| | | | |
| **Sip4** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 7.85E-06 | 0.00203401 |
| MIPS Functional Classification | glyoxylate cycle | 1.44E-05 | 0.00372022 |
| MIPS Functional Classification | ENERGY | 1.46E-05 | 0.00377272 |
| MIPS Subcellular Localization | cytoplasm | 0.00010113 | 0.00424746 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 4.33E-06 | 0.00597053 |
| GO Biological Process | main pathways of carbohydrate metabolism [GO:0006092] | 5.15E-06 | 0.00710926 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 1.96E-05 | 0.02699321 |

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|---|---|---|---|
| Proteome Localization--Predicted+Obs | cyt | 0.0103009 | 0.0412036 |
| GO Biological Process | energy derivation by oxidation of organic compounds [GO:0015980] | 4.15E-05 | 0.05725758 |
| GO Biological Process | energy pathways [GO:0006091] | 4.15E-05 | 0.05725758 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 0.00027825 | 0.07206701 |
| MDS Proteomics Complexes | YLR340W (RPP0) | 0.00018176 | 0.08960817 |
| MIPS Functional Classification | METABOLISM | 0.00039781 | 0.10303227 |
| MIPS Subcellular Localization | mitochondria | 0.00278128 | 0.11681376 |
| GO Cellular Component | cytoplasm [GO:0005737] | 0.00039662 | 0.13088427 |
| GO Cellular Component | cytosol [GO:0005829] | 0.00082212 | 0.27129927 |
| MDS Proteomics Complexes | YDR499W (LCD1) | 0.00059642 | 0.29403654 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00183251 | 0.3481769 |
| MIPS Functional Classification | detoxification | 0.00144542 | 0.37436378 |
| GO Cellular Component | ribosome [GO:0005840] | 0.00139752 | 0.4611816 |
| MIPS Protein Complexes | Translation complexes | 0.00160867 | 0.50673105 |
| GO Molecular Function | amino acid-polyamine transporter [GO:0005279] | 0.00059642 | 0.82127447 |
| GO Molecular Function | polyamine transporter [GO:0015203] | 0.00059642 | 0.82127447 |
| MIPS Protein Classes | Histones | 0.00437089 | 0.8304691 |
| MIPS Functional Classification | ribosome biogenesis | 0.0034766 | 0.9004394 |
|  |  |  |  |
| **Skn7** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Cellular Component | extracellular [GO:0005576] | 0.00132967 | 0.4387911 |
| GO Cellular Component | oligosaccharyl transferase complex [GO:0008250] | 0.00159254 | 0.5255382 |
| GO Cellular Component | cell wall (sensu Fungi) [GO:0009277] | 0.00212059 | 0.6997947 |
| MIPS Protein Complexes | Oligosaccharyltransferase | 0.00233288 | 0.7348572 |
| GO Biological Process | glutathione metabolism [GO:0006749] | 0.00059642 | 0.82306374 |
| GO Cellular Component | cell wall [GO:0005618] | 0.0025201 | 0.831633 |
| GO Cellular Component | external protective structure [GO:0030312] | 0.0025201 | 0.831633 |
|  |  |  |  |
| **Smp1** | **n=198** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MDS Proteomics Complexes | YDL175C (AIR2) | 0.00098977 | 0.48795858 |
|  |  |  |  |
| **Spt15** | **n=200** |  |  |

| Source | Annotation | pval | Bonfp |
|---|---|---|---|
| GO Cellular Component | chromosome [GO:0005694] | 7.14E-05 | 0.0235556 |
| MIPS Subcellular Localization | chromosome structure | 0.00060415 | 0.02537438 |
| GO Cellular Component | mitotic chromosome [GO:0005708] | 0.00053143 | 0.17537091 |
| MDS Proteomics Complexes | YCR002C (CDC10) | 0.000562 | 0.27706551 |
| MIPS Functional Classification | chromosome | 0.00227081 | 0.58813979 |
| PFam-A Domains | PF00970 (FAD_binding_6) | 0.000562 | 0.66596882 |
| Cellzome Complexes | YFL017W-A (SMX2) | 0.00160329 | 0.73591011 |
| GO Biological Process | mitotic chromosome condensation [GO:0007076] | 0.00220143 | >0.999 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 0.00286598 | >0.999 |
| PFam-A Domains | PF00175 (NAD_binding) | 0.00150207 | >0.999 |
| GO Biological Process | amine metabolism [GO:0009308] | 0.00259873 | >0.999 |
| GO Biological Process | amino acid metabolism [GO:0006520] | 0.00136469 | >0.999 |
| GO Biological Process | biosynthesis [GO:0009058] | 0.00097008 | >0.999 |
| GO Biological Process | amino acid and derivative metabolism [GO:0006519] | 0.00232405 | >0.999 |
| GO Biological Process | amino acid biosynthesis [GO:0008652] | 0.00174138 | >0.999 |
| GO Biological Process | amine biosynthesis [GO:0009309] | 0.00274067 | >0.999 |
| GO Biological Process | mitotic prophase [GO:0000088] | 0.00220143 | >0.999 |
| | | | |
| **Srd1** | **n=197** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Proteome Localization--Predicted+Obs | en2 | 0.00277149 | 0.01108596 |
| GO Molecular Function | asparaginase [GO:0004067] | 1.35E-05 | 0.01862475 |
| GO Cellular Component | periplasmic space (sensu Fungi) [GO:0030287] | 0.00010544 | 0.0347952 |
| GO Cellular Component | cell wall [GO:0005618] | 0.00012974 | 0.04281288 |
| GO Cellular Component | external protective structure [GO:0030312] | 0.00012974 | 0.04281288 |
| GO Biological Process | aspartate family amino acid catabolism [GO:0009068] | 6.01E-05 | 0.08287259 |
| GO Cellular Component | cell wall (sensu Fungi) [GO:0009277] | 0.00042458 | 0.14010975 |
| GO Biological Process | glutamine family amino acid catabolism [GO:0009065] | 0.00017142 | 0.23656098 |
| MIPS Functional Classification | CLASSIFICATION NOT YET CLEAR-CUT | 0.00091464 | 0.23689228 |
| MIPS Functional Classification | cell wall | 0.00106538 | 0.27593342 |
| GO Cellular Component | extracellular [GO:0005576] | 0.00119564 | 0.3945612 |
| GO Biological Process | response to starvation [GO:0009267] | 0.00038451 | 0.5306169 |
| MIPS Functional Classification | regulation of amino acid metabolism | 0.00338017 | 0.87546403 |

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|---|---|---|---|
| **Stb3** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Cellular Component | nucleolus [GO:0005730] | 3.15E-08 | 1.04E-05 |
| GO Biological Process | ribosome biogenesis and assembly [GO:0042254] | 4.59E-08 | 6.33E-05 |
| MIPS Functional Classification | PROTEIN SYNTHESIS | 8.81E-07 | 0.00022829 |
| GO Biological Process | ribosome biogenesis [GO:0007046] | 4.53E-07 | 0.00062579 |
| MIPS Subcellular Localization | cytoplasm | 1.87E-05 | 0.00078465 |
| GO Cellular Component | ribonucleoprotein complex [GO:0030529] | 2.90E-06 | 0.00095806 |
| GO Biological Process | transcription from Pol I promoter [GO:0006360] | 7.11E-07 | 0.00098163 |
| GO Cellular Component | polysome [GO:0005844] | 3.58E-06 | 0.0011801 |
| Published Complexes | Andersen et al. (2002) - Curr Bio 12:1- | 0.00022865 | 0.00160054 |
| GO Biological Process | biosynthesis [GO:0009058] | 1.32E-06 | 0.0018197 |
| GO Cellular Component | ribosome [GO:0005840] | 6.47E-06 | 0.00213565 |
| MDS Proteomics Complexes | YOL115W (TRF4) | 6.97E-06 | 0.00343472 |
| GO Biological Process | rRNA processing [GO:0006364] | 2.84E-06 | 0.00391676 |
| Published Complexes | Harnicharnpai et al. (2001) - Mol Cell 8:505- | 0.00062431 | 0.00437018 |
| Cellzome Complexes | YJL033W (HCA4) | 1.32E-05 | 0.00606082 |
| MIPS Subcellular Localization | nucleolus | 0.00015855 | 0.0066591 |
| GO Biological Process | RNA metabolism [GO:0016070] | 5.08E-06 | 0.00701665 |
| GO Biological Process | RNA processing [GO:0006396] | 6.58E-06 | 0.00908244 |
| Cellzome Complexes | YLR175W (CBF5) | 2.08E-05 | 0.00953729 |
| Published Complexes | Kressler et al. (1999) - Mol Cell Bio 19(12)7897- (C/D Box) | 0.00233288 | 0.01633016 |
| GO Biological Process | protein biosynthesis [GO:0006412] | 1.70E-05 | 0.02348691 |
| Deletions Consortium (Essentiality, Mo | Morphology - Football | 0.00255218 | 0.02807398 |
| MDS Proteomics Complexes | YOR080W (DIA2) | 6.40E-05 | 0.03155555 |
| GO Biological Process | macromolecule biosynthesis [GO:0009059] | 2.35E-05 | 0.03248727 |
| GO Biological Process | metabolism [GO:0008152] | 3.49E-05 | 0.04821941 |
| Cellzome Complexes | YBR079C (RPG1) | 0.00011184 | 0.05133594 |
| Cellzome Complexes | YPR086W (SUA7) | 0.00011184 | 0.05133594 |
| MIPS Protein Complexes | Cytoplasmic translation initiation | 0.00016555 | 0.05214668 |
| Cellzome Complexes | YBR247C (ENP1) | 0.00013224 | 0.06069678 |
| MIPS Protein Complexes | Translation complexes | 0.00021276 | 0.06701814 |
| MDS Proteomics Complexes | YNL230C (ELA1) | 0.00016555 | 0.08161369 |

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|---|---|---|---|
| MDS Proteomics Complexes | YDL213C (FYV14) | 0.00021041 | 0.10373065 |
| MDS Proteomics Complexes | YMR059W (SEN15) | 0.00027543 | 0.13578847 |
| MIPS Functional Classification | rRNA transcription | 0.00065997 | 0.17093145 |
| GO Cellular Component | eukaryotic translation initiation factor 3 complex [GO:0005852] | 0.00059642 | 0.19681959 |
| GO Cellular Component | cell [GO:0005623] | 0.00062635 | 0.20669451 |
| MIPS Functional Classification | rRNA processing | 0.00080198 | 0.20771334 |
| GO Cellular Component | intracellular [GO:0005622] | 0.00066949 | 0.22093203 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 0.00020863 | 0.28790802 |
| MIPS Functional Classification | SUBCELLULAR LOCALISATION | 0.00123621 | 0.32017839 |
| MIPS Protein Complexes | eIF3 | 0.00101923 | 0.32105745 |
| MIPS Functional Classification | amino acid biosynthesis | 0.00128165 | 0.33194735 |
| GO Molecular Function | translation initiation factor [GO:0003743] | 0.00025187 | 0.34682637 |
| Cellzome Complexes | YPR016C (TIF6) | 0.00078341 | 0.35958703 |
| MDS Proteomics Complexes | YNL175C (NOP13) | 0.00078341 | 0.3862231 |
| MDS Proteomics Complexes | YIL035C (CKA1) | 0.00083514 | 0.41172303 |
| Cellzome Complexes | YCR057C (PWP2) | 0.00099658 | 0.45743114 |
| Cellzome Complexes | YGR162W (TIF4631) | 0.0010418 | 0.4781862 |
| MDS Proteomics Complexes | YLR427W | 0.00099326 | 0.48967767 |
| MDS Proteomics Complexes | YOL087C | 0.0010418 | 0.5136074 |
| GO Biological Process | 35S primary transcript processing [GO:0006365] | 0.00042635 | 0.58835886 |
| Cellzome Complexes | YDL208W (NHP2) | 0.00135467 | 0.62179353 |
| Cellzome Complexes | YPR041W (TIF5) | 0.00135467 | 0.62179353 |
| GO Cellular Component | small nucleolar ribonucleoprotein complex [GO:0005732] | 0.00200157 | 0.6605181 |
| SMART Domains | COIL | 0.00230265 | 0.6769791 |
| Cellzome Complexes | YOR361C (PRT1) | 0.00159254 | 0.73097586 |
| Cellzome Complexes | YNL061W (NOP2) | 0.00172766 | 0.79299594 |
| MIPS Functional Classification | cell death | 0.00325479 | 0.84299061 |
| Cellzome Complexes | YNL016W (PUB1) | 0.00216637 | 0.99436383 |
| GO Molecular Function | lyase [GO:0016829] | 0.00170628 | >0.999 |
| GO Cellular Component | cytosolic ribosome (sensu Eukarya) [GO:0005830] | 0.0030707 | >0.999 |
| GO Biological Process | rRNA metabolism [GO:0016072] | 0.00172766 | >0.999 |
| GO Biological Process | processing of 20S pre-rRNA [GO:0030490] | 0.00234057 | >0.999 |
| GO Biological Process | ribosomal subunit assembly [GO:0042257] | 0.00073539 | >0.999 |
| PFam-A Domains | PF00076 (rrm) | 0.00483174 | >0.999 |

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|---|---|---|---|
| GO Molecular Function | enzyme [GO:0003824] | 0.00168829 | >0.999 |
| Cellzome Complexes | YAL035W (FUN12) | 0.00233288 | >0.999 |
| MDS Proteomics Complexes | YER161C (SPT2) | 0.00393128 | >0.999 |
| GO Cellular Component | cytosolic large ribosomal subunit (sensu Eukarya) [GO:0005842] | 0.00474504 | >0.999 |
| GO Biological Process | ribosomal large subunit assembly and maintenance [GO:0000027] | 0.0046866 | >0.999 |
| GO Molecular Function | ligase [GO:0016874] | 0.00311086 | >0.999 |
| GO Biological Process | RNA modification [GO:0009451] | 0.0013264 | >0.999 |
| MDS Proteomics Complexes | YER082C (UTP7) | 0.00267631 | >0.999 |
| GO Biological Process | aspartate family amino acid metabolism [GO:0009066] | 0.00173371 | >0.999 |
| GO Biological Process | rRNA modification [GO:0000154] | 0.00135467 | >0.999 |
| MIPS Protein Complexes | Cytoplasmic ribosomes | 0.00442721 | >0.999 |
| MIPS Functional Classification | translation | 0.00403694 | >0.999 |
| GO Molecular Function | snoRNA binding [GO:0030515] | 0.00200157 | >0.999 |
| PFam-A Domains | PF00587 (tRNA-synt_2b) | 0.00233288 | >0.999 |
| GO Biological Process | ribosome assembly [GO:0042255] | 0.00094528 | >0.999 |
| GO Biological Process | translational initiation [GO:0006413] | 0.00099658 | >0.999 |
| | | | |
| **Stp2** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | amino acid metabolism | 1.66E-10 | 4.29E-08 |
| MIPS Functional Classification | amino acid transport | 6.65E-10 | 1.72E-07 |
| PFam-A Domains | PF00324 (aa_permeases) | 3.86E-10 | 4.58E-07 |
| MIPS Functional Classification | amino-acid transporters | 1.80E-09 | 4.65E-07 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 2.72E-09 | 5.16E-07 |
| GO Molecular Function | amino acid transporter [GO:0015171] | 3.86E-10 | 5.32E-07 |
| MIPS Functional Classification | METABOLISM | 3.22E-08 | 8.34E-06 |
| GO Cellular Component | plasma membrane [GO:0005886] | 3.37E-08 | 1.11E-05 |
| GO Biological Process | amino acid transport [GO:0006865] | 1.52E-08 | 2.10E-05 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 1.29E-07 | 3.35E-05 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 7.59E-05 | 0.00083481 |
| Proteome Localization--Observed | cell periphery | 0.000166 | 0.00182602 |
| GO Molecular Function | amine/polyamine transporter [GO:0005275] | 1.59E-06 | 0.00219147 |
| GO Molecular Function | transporter [GO:0005215] | 1.68E-06 | 0.00230897 |
| MIPS Functional Classification | plasma membrane | 9.92E-06 | 0.0025683 |

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|---|---|---|---|
| PFam-A Domains | PF00674 (DUP) | 6.41E-06 | 0.00759021 |
| Proteome Localization--Predicted+Obs | cyt | 0.00360971 | 0.01443884 |
| GO Molecular Function | polyamine transporter [GO:0015203] | 1.41E-05 | 0.01938844 |
| GO Molecular Function | amino acid-polyamine transporter [GO:0005279] | 1.41E-05 | 0.01938844 |
| Proteome Localization--Observed | cyto | 0.00250785 | 0.02758635 |
| MIPS Functional Classification | amino acid biosynthesis | 0.00033517 | 0.08681007 |
| MIPS Phenotypes | Nitrogen utilization | 0.0015696 | 0.282528 |
| SMART Domains | HMG | 0.00100443 | 0.29530242 |
| GO Cellular Component | integral plasma membrane protein [GO:0005887] | 0.00097104 | 0.32044386 |
| SMART Domains | TRANS | 0.00133526 | 0.39256644 |
| GO Cellular Component | membrane [GO:0016020] | 0.00139256 | 0.4595448 |
| MDS Proteomics Complexes | YOL126C (MDH2) | 0.00100443 | 0.49518399 |
| MIPS Functional Classification | ion transporters | 0.00313155 | 0.81107145 |
| GO Molecular Function | vitamin/cofactor transporter [GO:0015223] | 0.00100443 | >0.999 |
| GO Molecular Function | porter [GO:0015291] | 0.00163096 | >0.999 |
| PFam-A Domains | PF00501 (AMP-binding) | 0.00229957 | >0.999 |
| MDS Proteomics Complexes | YDR142C (PEX7) | 0.00294706 | >0.999 |
| MIPS Functional Classification | cellular import | 0.0042903 | >0.999 |
| MIPS Functional Classification | transcriptional control | 0.00441946 | >0.999 |
| PFam-A Domains | PF00505 (HMG_box) | 0.00100443 | >0.999 |
| GO Biological Process | nitrogen metabolism [GO:0006807] | 0.00266076 | >0.999 |
| GO Molecular Function | transcriptional repressor [GO:0016564] | 0.00430951 | >0.999 |
| GO Molecular Function | channel/pore class transporter [GO:0015267] | 0.00430951 | >0.999 |
| MIPS Functional Classification | lipid and fatty-acid transport | 0.0038611 | >0.999 |
| GO Molecular Function | alpha-type channel [GO:0015268] | 0.0032087 | >0.999 |
| GO Molecular Function | electrochemical potential-driven transporter [GO:0015290] | 0.00163096 | >0.999 |
| | | | |
| **Stp4** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 2.72E-09 | 5.16E-07 |
| Proteome Localization--Predicted+Obs | cyt | 5.70E-05 | 0.00022819 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 7.59E-05 | 0.00083481 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 4.91E-06 | 0.00127208 |
| Proteome Localization--Observed | cyto | 0.00086686 | 0.00953547 |

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|---|---|---|---|
| GO Cellular Component | plasma membrane [GO:0005886] | 4.37E-05 | 0.01442909 |
| MIPS Functional Classification | amino-acid transporters | 0.00010161 | 0.02631595 |
| MIPS Functional Classification | plasma membrane | 0.00014315 | 0.03707585 |
| Proteome Localization--Observed | cell periphery | 0.00392687 | 0.04319557 |
| PFam-A Domains | PF00324 (aa_permeases) | 4.64E-05 | 0.05493482 |
| GO Molecular Function | amino acid transporter [GO:0015171] | 4.64E-05 | 0.06383566 |
| MIPS Functional Classification | homeostasis of anions | 0.000563 | 0.14581804 |
| MIPS Functional Classification | amino acid transport | 0.0006476 | 0.16772866 |
| GO Molecular Function | transporter [GO:0005215] | 0.0002692 | 0.37069391 |
| GO Molecular Function | anion transporter [GO:0008509] | 0.00032248 | 0.44404808 |
| GO Cellular Component | cell [GO:0005623] | 0.00205075 | 0.6767475 |
| MIPS Functional Classification | phosphate transport | 0.0032087 | 0.8310533 |
| GO Biological Process | amino acid transport [GO:0006865] | 0.0006476 | 0.89368938 |
| GO Biological Process | phosphate transport [GO:0006817] | 0.00229957 | >0.999 |
| GO Molecular Function | channel/pore class transporter [GO:0015267] | 0.00430951 | >0.999 |
| GO Biological Process | anion transport [GO:0006820] | 0.00079715 | >0.999 |
| GO Molecular Function | amine/polyamine transporter [GO:0005275] | 0.0015696 | >0.999 |
| GO Molecular Function | alpha-type channel [GO:0015268] | 0.0032087 | >0.999 |
| GO Biological Process | inorganic anion transport [GO:0015698] | 0.00102243 | >0.999 |
| MDS Proteomics Complexes | YDR142C (PEX7) | 0.00294706 | >0.999 |
| MIPS Functional Classification | cellular import | 0.0042903 | >0.999 |
| GO Molecular Function | inorganic anion transporter [GO:0015103] | 0.0015696 | >0.999 |
| | | | |
| **Sum1** | **n=199** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Proteome Localization--Observed | mixed (cyto / nuc) | 0.00028258 | 0.00310841 |
| Proteome Localization--Predicted+Obs | nuc | 0.00086602 | 0.00346408 |
| Published Complexes | Andersen et al. (2002) - Curr Bio 12:1- | 0.00215171 | 0.01506197 |
| MIPS Subcellular Localization | nucleus | 0.00037949 | 0.01593862 |
| GO Cellular Component | nucleus [GO:0005634] | 7.80E-05 | 0.02572485 |
| MIPS Functional Classification | transport mechanism | 0.00205474 | 0.53217766 |
| | | | |
| **Sut2** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |

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|---|---|---|---|
| Proteome Localization--Observed | cyto | 0.00284451 | 0.03128961 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00432221 | 0.04754431 |
| GO Biological Process | organic anion transport [GO:0015711] | 0.00018176 | 0.25083018 |
| GO Cellular Component | peroxisomal matrix [GO:0005782] | 0.0010418 | 0.343794 |
| GO Molecular Function | hexose transporter [GO:0015149] | 0.00025409 | 0.34987918 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 0.00025409 | 0.34987918 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 0.00030657 | 0.42306108 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 0.00053221 | 0.73444704 |
| GO Biological Process | hexose transport [GO:0008645] | 0.00053221 | 0.73444704 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 0.00316469 | 0.81965471 |
| MDS Proteomics Complexes | YOR181W (LAS17) | 0.00172766 | 0.85173638 |
|  |  |  |  |
| **Tbf1** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Phenotypes | Flocculence | 0.00078341 | 0.14101452 |
| Yeast Two Hybrid - Ito (core) | YDL239C (ADY3) | 0.00099326 | 0.44597419 |
| MIPS Protein Classes | Protein Kinases | 0.00400314 | 0.7605966 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 0.00062906 | 0.86810694 |
|  |  |  |  |
| **Tbs1** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | TRANSPORT FACILITATION | 4.54E-07 | 0.00011757 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00013926 | 0.00153189 |
| MIPS Protein Complexes | Cytoplasmic ribosomes | 0.0001101 | 0.03468182 |
| MIPS Functional Classification | phosphate transport | 0.00017827 | 0.04617064 |
| MIPS Functional Classification | METABOLISM | 0.00018366 | 0.04756872 |
| GO Molecular Function | transporter [GO:0005215] | 4.01E-05 | 0.05526975 |
| GO Cellular Component | cytosolic ribosome (sensu Eukarya) [GO:0005830] | 0.00028686 | 0.09466413 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.0005345 | 0.10155481 |
| MIPS Functional Classification | ribosome biogenesis | 0.00044144 | 0.114334 |
| MIPS Functional Classification | plasma membrane | 0.00048809 | 0.12641505 |
| MIPS Functional Classification | glyoxylate cycle | 0.00058769 | 0.15221223 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00049284 | 0.16263687 |
| GO Cellular Component | ribosome [GO:0005840] | 0.00050058 | 0.16518975 |

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|---|---|---|---|
| MIPS Functional Classification | drug transporters | 0.00071459 | 0.18507752 |
| MIPS Functional Classification | ion transporters | 0.00074916 | 0.19403322 |
| MIPS Protein Complexes | cytoplasmic ribosomal large subunit | 0.00098738 | 0.31102565 |
| GO Molecular Function | structural constituent of ribosome [GO:0003735] | 0.00026675 | 0.36731888 |
| GO Cellular Component | cytosolic large ribosomal subunit (sensu Eukarya) [GO:0005842] | 0.00117788 | 0.3887004 |
| GO Cellular Component | membrane [GO:0016020] | 0.00139256 | 0.4595448 |
| MIPS Protein Complexes | Translation complexes | 0.00152318 | 0.4798017 |
| GO Cellular Component | large ribosomal subunit [GO:0015934] | 0.00161591 | 0.5332503 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 0.00308668 | 0.79945012 |
| GO Molecular Function | ABC-type efflux porter [GO:0015427] | 0.00058769 | 0.80925188 |
| GO Molecular Function | galactose transporter [GO:0005354] | 0.00058769 | 0.80925188 |
| GO Biological Process | response to drug [GO:0042493] | 0.0006476 | 0.89368938 |
| PFam-A Domains | PF00096 (zf-C2H2) | 0.00192027 | >0.999 |
| PFam-A Domains | PF00083 (sugar_tr) | 0.00130695 | >0.999 |
| GO Biological Process | phosphate transport [GO:0006817] | 0.00229957 | >0.999 |
| MIPS Functional Classification | detoxification | 0.00489268 | >0.999 |
| GO Biological Process | TCA intermediate metabolism [GO:0006100] | 0.0038611 | >0.999 |
| GO Molecular Function | structural molecule [GO:0005198] | 0.00186394 | >0.999 |
| GO Biological Process | ion transport [GO:0006811] | 0.00326014 | >0.999 |
| GO Molecular Function | drug transporter [GO:0015238] | 0.0015696 | >0.999 |
| SMART Domains | ZnF_C2H2 | 0.00471515 | >0.999 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 0.00228972 | >0.999 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 0.00262786 | >0.999 |
| GO Biological Process | hexose transport [GO:0008645] | 0.00460355 | >0.999 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 0.00460355 | >0.999 |
| PFam-A Domains | PF00107 (adh_zinc) | 0.0038611 | >0.999 |
| GO Molecular Function | multidrug transporter [GO:0015239] | 0.0015696 | >0.999 |
| GO Molecular Function | hexose transporter [GO:0015149] | 0.00262786 | >0.999 |
|  |  |  |  |
| **Tea1** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | METABOLISM | 1.03E-12 | 2.66E-10 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 4.25E-10 | 1.10E-07 |
| SMART Domains | Aamy | 7.38E-08 | 2.17E-05 |

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|---|---|---|---|
| PFam-A Domains | PF00128 (alpha-amylase) | 2.53E-08 | 2.99E-05 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 5.92E-07 | 0.00015327 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 5.45E-07 | 0.00075182 |
| GO Molecular Function | alpha-glucosidase [GO:0004558] | 6.13E-07 | 0.00084355 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 4.03E-06 | 0.00555867 |
| MIPS Functional Classification | ENERGY | 4.30E-05 | 0.01112783 |
| Proteome Localization--Observed | mixed (cyto / ER) | 0.00107923 | 0.01187153 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 1.97E-05 | 0.02708022 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00014982 | 0.02846637 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00012401 | 0.03211963 |
| MIPS Protein Classes | Cys6 cysteine-zinc cluster | 0.00020327 | 0.03862206 |
| PFam-A Domains | PF00083 (sugar_tr) | 3.61E-05 | 0.04281784 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 3.20E-05 | 0.0442083 |
| GO Biological Process | hexose transport [GO:0008645] | 4.64E-05 | 0.06397473 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 4.64E-05 | 0.06397473 |
| GO Molecular Function | enzyme [GO:0003824] | 4.75E-05 | 0.06545996 |
| SMART Domains | GAL4 | 0.00026617 | 0.07825427 |
| GO Biological Process | carbohydrate catabolism [GO:0016052] | 9.25E-05 | 0.12759839 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 0.00054747 | 0.14179577 |
| GO Molecular Function | transporter [GO:0005215] | 0.00010627 | 0.14632691 |
| MIPS Functional Classification | glycolysis and gluconeogenesis | 0.00071459 | 0.18507752 |
| GO Biological Process | hexose metabolism [GO:0019318] | 0.00014663 | 0.20234388 |
| PFam-A Domains | PF00172 (Zn_clus) | 0.00023299 | 0.27609078 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 0.00024821 | 0.34177829 |
| GO Molecular Function | hexose transporter [GO:0015149] | 0.00024821 | 0.34177829 |
| MIPS Protein Classes | Zinc-coordinating DNA-binding domains | 0.00200137 | 0.3802603 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 0.00029784 | 0.41101506 |
| GO Biological Process | glucose metabolism [GO:0006006] | 0.00041358 | 0.57074454 |
| GO Biological Process | energy derivation by oxidation of organic compounds [GO:0015980] | 0.00048809 | 0.67356282 |
| GO Biological Process | energy pathways [GO:0006091] | 0.00048809 | 0.67356282 |
| GO Molecular Function | glucosidase [GO:0015926] | 0.0005201 | 0.71617082 |
| GO Molecular Function | galactose transporter [GO:0005354] | 0.00058769 | 0.80925188 |
| Yeast Two Hybrid - Ito (core) | YNL189W (SRP1) | 0.00491135 | >0.999 |
| GO Molecular Function | glucose transporter [GO:0005355] | 0.00169595 | >0.999 |

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|---|---|---|---|
| GO Molecular Function | fructose transporter [GO:0005353] | 0.00076874 | >0.999 |
| MIPS Functional Classification | plasma membrane | 0.00449122 | >0.999 |
| GO Biological Process | gluconeogenesis [GO:0006094] | 0.0038611 | >0.999 |
| GO Biological Process | carbohydrate biosynthesis [GO:0016051] | 0.00130695 | >0.999 |
| GO Biological Process | alcohol catabolism [GO:0046164] | 0.00117162 | >0.999 |
| MIPS Functional Classification | cellular import | 0.0042903 | >0.999 |
| GO Biological Process | main pathways of carbohydrate metabolism [GO:0006092] | 0.00130695 | >0.999 |
| GO Biological Process | hexose catabolism [GO:0019320] | 0.00460355 | >0.999 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 0.00206668 | >0.999 |
| GO Biological Process | disaccharide metabolism [GO:0005984] | 0.00430951 | >0.999 |
| GO Biological Process | alcohol biosynthesis [GO:0046165] | 0.00097104 | >0.999 |
| GO Molecular Function | mannose transporter [GO:0015578] | 0.00102243 | >0.999 |
| GO Biological Process | glucose catabolism [GO:0006007] | 0.00460355 | >0.999 |
| GO Biological Process | lipid metabolism [GO:0006629] | 0.00252454 | >0.999 |
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| **Tec1** | **n=197** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| PFam-A Domains | PF00660 (SRP1_TIP1) | 1.00E-14 | 1.19E-11 |
| MIPS Functional Classification | stress response | 0.00011038 | 0.0285892 |
| MDS Proteomics Complexes | YGR040W (KSS1) | 0.00012591 | 0.06207363 |
| MIPS Subcellular Localization | extracellular | 0.00253281 | 0.10637802 |
| GO Biological Process | bud growth [GO:0007117] | 0.00023198 | 0.32013378 |
| GO Cellular Component | bud [GO:0005933] | 0.00160974 | 0.5312142 |
| MIPS Functional Classification | extracellular / secretion proteins | 0.00308909 | 0.80007431 |
| GO Biological Process | pseudohyphal growth [GO:0007124] | 0.00058948 | 0.81348792 |
| | | | |
| **Tye7** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Biological Process | sulfur metabolism [GO:0006790] | 2.18E-12 | 3.01E-09 |
| MIPS Functional Classification | amino acid metabolism | 1.86E-10 | 4.82E-08 |
| GO Biological Process | amino acid metabolism [GO:0006520] | 2.29E-09 | 3.15E-06 |
| GO Biological Process | aspartate family amino acid metabolism [GO:0009066] | 2.81E-09 | 3.88E-06 |
| GO Biological Process | amino acid and derivative metabolism [GO:0006519] | 7.26E-09 | 1.00E-05 |
| GO Biological Process | amine metabolism [GO:0009308] | 9.28E-09 | 1.28E-05 |

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|---|---|---|---|
| GO Biological Process | sulfur amino acid metabolism [GO:0000096] | 1.03E-08 | 1.43E-05 |
| MIPS Functional Classification | amino acid biosynthesis | 1.53E-07 | 3.97E-05 |
| MIPS Functional Classification | METABOLISM | 2.82E-06 | 0.00073025 |
| GO Biological Process | amino acid catabolism [GO:0009063] | 1.10E-06 | 0.00152431 |
| GO Biological Process | amine catabolism [GO:0009310] | 1.10E-06 | 0.00152431 |
| GO Biological Process | sulfur utilization [GO:0006791] | 1.63E-06 | 0.00225164 |
| GO Biological Process | aspartate family amino acid catabolism [GO:0009068] | 1.63E-06 | 0.00225164 |
| GO Biological Process | sulfate assimilation [GO:0000103] | 1.63E-06 | 0.00225164 |
| GO Biological Process | methionine metabolism [GO:0006555] | 1.65E-06 | 0.00228206 |
| GO Biological Process | serine family amino acid metabolism [GO:0009069] | 3.86E-06 | 0.00532407 |
| GO Biological Process | glutamine family amino acid catabolism [GO:0009065] | 6.97E-06 | 0.00961443 |
| GO Molecular Function | asparaginase [GO:0004067] | 1.44E-05 | 0.01977895 |
| GO Molecular Function | enzyme [GO:0003824] | 1.59E-05 | 0.02190036 |
| MIPS Functional Classification | amino acid degradation (catabolism) | 9.54E-05 | 0.02471787 |
| Proteome Localization--Observed | cyto | 0.00284451 | 0.03128961 |
| MDS Proteomics Complexes | YGL237C (HAP2) | 6.40E-05 | 0.03155555 |
| GO Cellular Component | periplasmic space (sensu Fungi) [GO:0030287] | 0.00011184 | 0.03690819 |
| GO Biological Process | sulfur amino acid biosynthesis [GO:0000097] | 3.27E-05 | 0.04509578 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 3.34E-05 | 0.04611104 |
| GO Molecular Function | electron transporter [GO:0005489] | 4.77E-05 | 0.06566321 |
| GO Biological Process | glutamine family amino acid metabolism [GO:0009064] | 7.84E-05 | 0.10825548 |
| GO Biological Process | regulation of transcription from Pol II promoter [GO:0006357] | 0.000158 | 0.21804138 |
| GO Biological Process | metabolism [GO:0008152] | 0.0001967 | 0.27144738 |
| GO Cellular Component | cell [GO:0005623] | 0.00103017 | 0.3399561 |
| GO Biological Process | response to starvation [GO:0009267] | 0.00040738 | 0.56218854 |
| MDS Proteomics Complexes | YMR059W (SEN15) | 0.001505 | 0.741965 |
| Yeast Two Hybrid - Ito (core) | YNL189W (SRP1) | 0.00200157 | 0.89870493 |
| GO Molecular Function | transporter [GO:0005215] | 0.00070106 | 0.96535687 |
| | | | |
| **Ume6** | **n=199** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Protein Classes | Zinc-coordinating DNA-binding domains | 0.00013223 | 0.02512351 |
| MIPS Functional Classification | METABOLISM | 0.00034835 | 0.09022136 |
| PFam-A Domains | PF00674 (DUP) | 7.93E-05 | 0.09396849 |

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|---|---|---|---|
| MIPS Subcellular Localization | peroxisomal matrix | 0.00262786 | 0.11037012 |
| GO Cellular Component | peroxisomal matrix [GO:0005782] | 0.00102243 | 0.3374019 |
| SMART Domains | S_TKc | 0.00244328 | 0.71832432 |
| Yeast Two Hybrid - Ito (core) | YNL189W (SRP1) | 0.00163096 | 0.73230104 |
| MIPS Functional Classification | sporulation and germination | 0.00319966 | 0.82871194 |
| SMART Domains | ZnF_GATA | 0.0032087 | 0.9433578 |
|  |  |  |  |
| **Usv1** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | ENERGY | 1.00E-14 | 2.59E-12 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 1.70E-13 | 4.40E-11 |
| GO Biological Process | energy reserve metabolism [GO:0006112] | 6.74E-14 | 9.30E-11 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 4.55E-13 | 1.18E-10 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 1.61E-13 | 2.22E-10 |
| GO Biological Process | glycogen metabolism [GO:0005977] | 8.02E-11 | 1.11E-07 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 7.85E-08 | 8.63E-07 |
| Proteome Localization--Observed | cyto | 1.23E-07 | 1.35E-06 |
| GO Biological Process | energy derivation by oxidation of organic compounds [GO:0015980] | 4.42E-09 | 6.11E-06 |
| GO Biological Process | energy pathways [GO:0006091] | 4.42E-09 | 6.11E-06 |
| GO Biological Process | glucan metabolism [GO:0006073] | 5.67E-09 | 7.83E-06 |
| MIPS Functional Classification | stress response | 1.29E-07 | 3.34E-05 |
| GO Cellular Component | unlocalized [GO:0005941] | 2.30E-07 | 7.57E-05 |
| GO Biological Process | response to stress [GO:0006950] | 6.32E-08 | 8.73E-05 |
| Proteome Localization--Predicted+Obs | cyt | 2.37E-05 | 9.49E-05 |
| GO Biological Process | polysaccharide metabolism [GO:0005976] | 1.69E-07 | 0.00023344 |
| MIPS Subcellular Localization | cytoplasm | 1.87E-05 | 0.00078465 |
| GO Biological Process | trehalose metabolism [GO:0005991] | 6.28E-07 | 0.00086683 |
| GO Molecular Function | glucosyltransferase [GO:0046527] | 2.38E-06 | 0.00327415 |
| MIPS Functional Classification | METABOLISM | 5.52E-05 | 0.01430491 |
| GO Biological Process | disaccharide metabolism [GO:0005984] | 1.24E-05 | 0.01717051 |
| GO Molecular Function | heat shock protein [GO:0003773] | 1.32E-05 | 0.01818246 |
| SMART Domains | Aamy | 0.00011184 | 0.03288184 |
| Cellzome Complexes | YBR126C (TPS1) | 0.00010322 | 0.04737614 |
| PFam-A Domains | PF00128 (alpha-amylase) | 6.37E-05 | 0.07551365 |

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|---|---|---|---|
| GO Biological Process | hexose metabolism [GO:0019318] | 0.00015233 | 0.2102154 |
| GO Biological Process | main pathways of carbohydrate metabolism [GO:0006092] | 0.00024113 | 0.3327594 |
| MDS Proteomics Complexes | YER177W (BMH1) | 0.00078341 | 0.3862231 |
| GO Biological Process | monosaccharide metabolism [GO:0005996] | 0.00030916 | 0.42663942 |
| MIPS Functional Classification | intracellular signalling | 0.00167874 | 0.43479366 |
| Cellzome Complexes | YDR099W (BMH2) | 0.00101923 | 0.46782657 |
| GO Biological Process | sporulation (sensu Fungi) [GO:0030437] | 0.0003845 | 0.53061414 |
| GO Biological Process | glucose metabolism [GO:0006006] | 0.00042635 | 0.58835886 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 0.00045107 | 0.62247246 |
| MIPS Functional Classification | CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM | 0.00253479 | 0.65651061 |
| GO Biological Process | glutamine family amino acid biosynthesis [GO:0009084] | 0.00053221 | 0.73444704 |
| MIPS Phenotypes | Accumulation of storage carbohydrates | 0.00437089 | 0.7867602 |
| GO Biological Process | glutamate biosynthesis [GO:0006537] | 0.00057382 | 0.79187574 |
| MIPS Functional Classification | sporulation and germination | 0.00331737 | 0.85919883 |
| | | | |
| **Xbp1** | **n=193** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| PFam-A Domains | PF00674 (DUP) | 1.81E-08 | 2.15E-05 |
| Proteome Localization--Predicted+Obs | en2 | 5.05E-05 | 0.00020205 |
| Cellzome Complexes | YDR170C (SEC7) | 4.20E-05 | 0.01927479 |
| MDS Proteomics Complexes | YLR442C (SIR3) | 0.00050114 | 0.24706399 |
| MIPS Functional Classification | cell wall | 0.00095727 | 0.24793267 |
| GO Cellular Component | bud [GO:0005933] | 0.00141191 | 0.4659303 |
| GO Cellular Component | cell cortex [GO:0005938] | 0.00156459 | 0.5163147 |
| MIPS Functional Classification | allantoin and allantoate transporters | 0.00210598 | 0.54544882 |
| GO Cellular Component | external protective structure [GO:0030312] | 0.00197559 | 0.6519447 |
| GO Cellular Component | cell wall [GO:0005618] | 0.00197559 | 0.6519447 |
| Cellzome Complexes | YBL087C (RPL23A) | 0.00210598 | 0.96664482 |
| | | | |
| **Yap1** | **n=197** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 1.26E-05 | 0.00325364 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 6.20E-05 | 0.01605339 |
| SMART Domains | Aamy | 0.00010544 | 0.03099936 |

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|---|---|---|---|
| PFam-A Domains | PF00128 (alpha-amylase) | 6.01E-05 | 0.07116233 |
| Cellzome Complexes | YNL016W (PUB1) | 0.00017899 | 0.08215457 |
| MDS Proteomics Complexes | YHR135C (YCK1) | 0.00038898 | 0.19176615 |
| GO Biological Process | redox homeostasis [GO:0045454] | 0.00017142 | 0.23656098 |
| GO Biological Process | regulation of redox homeostasis [GO:0030503] | 0.00017142 | 0.23656098 |
| | | | |
| **Yap6** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MDS Proteomics Complexes | YNL323W (LEM3) | 0.00101923 | 0.50248039 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00213654 | 0.55336386 |
| | | | |
| **Ybr239c** | **n=198** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Proteome Localization--Observed | cell periphery | 0.00083511 | 0.00918624 |
| Proteome Localization--Predicted+Obs | cyt | 0.00281951 | 0.01127804 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00030756 | 0.07965778 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00050937 | 0.09678011 |
| MIPS Functional Classification | plasma membrane | 0.00046382 | 0.1201299 |
| PFam-A Domains | PF00083 (sugar_tr) | 0.00022507 | 0.26671269 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 0.00125871 | 0.32600589 |
| MIPS Functional Classification | cell wall | 0.00125924 | 0.32614316 |
| GO Molecular Function | hexose transporter [GO:0015149] | 0.00024243 | 0.33382336 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 0.00024243 | 0.33382336 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 0.00029033 | 0.40065816 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 0.00041642 | 0.57465684 |
| GO Biological Process | hexose transport [GO:0008645] | 0.00050819 | 0.70130496 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 0.00050819 | 0.70130496 |
| GO Cellular Component | external protective structure [GO:0030312] | 0.00235362 | 0.7766946 |
| GO Cellular Component | cell wall [GO:0005618] | 0.00235362 | 0.7766946 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 0.00301012 | 0.77962108 |
| GO Molecular Function | galactose transporter [GO:0005354] | 0.00057905 | 0.79734497 |
| | | | |
| **Ydr520c** | **n=199** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |

|  |  |  |  |
|---|---|---|---|
| GO Molecular Function | hexose transporter [GO:0015149] | 1.52E-12 | 2.10E-09 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 1.52E-12 | 2.10E-09 |
| GO Molecular Function | mannose transporter [GO:0015578] | 2.18E-12 | 3.00E-09 |
| GO Molecular Function | glucose transporter [GO:0005355] | 1.33E-11 | 1.84E-08 |
| GO Molecular Function | fructose transporter [GO:0005353] | 4.79E-11 | 6.59E-08 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 1.57E-09 | 4.08E-07 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 3.37E-10 | 4.64E-07 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 3.86E-10 | 5.33E-07 |
| GO Biological Process | hexose transport [GO:0008645] | 3.86E-10 | 5.33E-07 |
| PFam-A Domains | PF00083 (sugar_tr) | 5.43E-10 | 6.43E-07 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 8.10E-10 | 1.12E-06 |
| MIPS Functional Classification | METABOLISM | 4.91E-09 | 1.27E-06 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 8.56E-08 | 1.63E-05 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 1.27E-07 | 3.28E-05 |
| MIPS Functional Classification | plasma membrane | 2.36E-06 | 0.00061025 |
| MIPS Functional Classification | cellular import | 1.41E-05 | 0.00365211 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 7.19E-05 | 0.01862052 |
| GO Molecular Function | galactose transporter [GO:0005354] | 1.41E-05 | 0.01938844 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00012401 | 0.03211963 |
| SMART Domains | Aamy | 0.00010968 | 0.03224533 |
| Proteome Localization--Predicted+Obs | cyt | 0.00830198 | 0.03320792 |
| PFam-A Domains | PF00128 (alpha-amylase) | 6.25E-05 | 0.074042 |
| MIPS Functional Classification | ENERGY | 0.0010074 | 0.2609166 |
| GO Biological Process | nucleotide biosynthesis [GO:0009165] | 0.00032248 | 0.4450155 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.0014881 | 0.491073 |
| SMART Domains | CBS | 0.00229957 | 0.67607358 |
|  |  |  |  |
| **Yer130c** | **n=200** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| PFam-A Domains | PF00660 (SRP1_TIP1) | 1.51E-08 | 1.79E-05 |
| GO Cellular Component | unlocalized [GO:0005941] | 2.30E-07 | 7.57E-05 |
| MIPS Functional Classification | stress response | 9.96E-06 | 0.00258025 |
| Proteome Localization--Predicted+Obs | cyt | 0.00117447 | 0.00469788 |
| Proteome Localization--Observed | cell periphery | 0.00089192 | 0.00981109 |

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|---|---|---|---|
| MIPS Functional Classification | C-compound and carbohydrate utilization | 7.74E-05 | 0.02003637 |
| Proteome Localization--Observed | cyto | 0.00284451 | 0.03128961 |
| MIPS Subcellular Localization | cytoplasm | 0.00098914 | 0.04154375 |
| GO Biological Process | energy reserve metabolism [GO:0006112] | 3.31E-05 | 0.04566185 |
| GO Molecular Function | protein serine/threonine phosphatase [GO:0004722] | 4.16E-05 | 0.05727604 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 0.00027825 | 0.07206701 |
| MIPS Functional Classification | ENERGY | 0.00039709 | 0.10284709 |
| SMART Domains | PP2Ac | 0.00040738 | 0.1197706 |
| GO Biological Process | glycogen metabolism [GO:0005977] | 0.00010447 | 0.14416998 |
| GO Cellular Component | protein serine/threonine phosphatase complex [GO:0008287] | 0.00057382 | 0.18936159 |
| GO Molecular Function | heat shock protein [GO:0003773] | 0.00019217 | 0.26461396 |
| Cellzome Complexes | YOR014W (RTS1) | 0.00059642 | 0.27375816 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 0.00022865 | 0.31553424 |
| Cellzome Complexes | YDR099W (BMH2) | 0.00101923 | 0.46782657 |
| GO Molecular Function | enzyme [GO:0003824] | 0.00034356 | 0.47308074 |
| MIPS Functional Classification | METABOLISM | 0.00228836 | 0.59268524 |
| MIPS Functional Classification | pentose-phosphate pathway | 0.00233288 | 0.60421592 |
| Cellzome Complexes | YBR126C (TPS1) | 0.00135467 | 0.62179353 |
| GO Biological Process | response to stress [GO:0006950] | 0.0005725 | 0.79005414 |
| MIPS Protein Classes | PPP family | 0.00437089 | 0.8304691 |
| GO Molecular Function | protein phosphatase [GO:0004721] | 0.00064531 | 0.88858912 |
| GO Molecular Function | intramolecular transferase [GO:0016866] | 0.00233288 | >0.999 |
| GO Biological Process | hexose metabolism [GO:0019318] | 0.00369296 | >0.999 |
| GO Biological Process | protein folding [GO:0006457] | 0.00196986 | >0.999 |
| GO Biological Process | glucan metabolism [GO:0006073] | 0.00073373 | >0.999 |
| GO Biological Process | disaccharide metabolism [GO:0005984] | 0.00437089 | >0.999 |
| GO Molecular Function | phosphoric monoester hydrolase [GO:0016791] | 0.00378224 | >0.999 |
| GO Biological Process | glucose metabolism [GO:0006006] | 0.00251429 | >0.999 |
| GO Biological Process | trehalose metabolism [GO:0005991] | 0.00101923 | >0.999 |
| GO Biological Process | polysaccharide metabolism [GO:0005976] | 0.00353338 | >0.999 |
| PFam-A Domains | PF00149 (Metallophos) | 0.00393128 | >0.999 |
| | | | |
| **Ygr067c** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |

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|---|---|---|---|
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 1.00E-14 | 2.59E-12 |
| MIPS Functional Classification | METABOLISM | 1.45E-12 | 3.75E-10 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 9.73E-10 | 2.52E-07 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 2.55E-09 | 6.61E-07 |
| GO Molecular Function | mannose transporter [GO:0015578] | 4.97E-09 | 6.85E-06 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 6.96E-09 | 9.59E-06 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 1.51E-08 | 2.08E-05 |
| GO Molecular Function | glucose transporter [GO:0005355] | 1.78E-08 | 2.45E-05 |
| MIPS Functional Classification | plasma membrane | 1.19E-07 | 3.09E-05 |
| GO Molecular Function | hexose transporter [GO:0015149] | 5.23E-08 | 7.20E-05 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 5.23E-08 | 7.20E-05 |
| PFam-A Domains | PF00083 (sugar_tr) | 6.79E-08 | 8.04E-05 |
| GO Molecular Function | fructose transporter [GO:0005353] | 8.62E-08 | 0.00011873 |
| GO Cellular Component | plasma membrane [GO:0005886] | 7.68E-07 | 0.00025348 |
| GO Biological Process | hexose transport [GO:0008645] | 2.04E-07 | 0.00028118 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 2.04E-07 | 0.00028118 |
| Proteome Localization--Predicted+Obs | cyt | 0.00071618 | 0.00286472 |
| MIPS Functional Classification | cellular import | 1.49E-05 | 0.0038549 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 3.52E-06 | 0.00485924 |
| Proteome Localization--Observed | cyto | 0.00099696 | 0.01096651 |
| GO Molecular Function | transporter [GO:0005215] | 1.60E-05 | 0.02200157 |
| GO Biological Process | glycerol metabolism [GO:0006071] | 3.27E-05 | 0.04509578 |
| GO Biological Process | polyol metabolism [GO:0019751] | 3.27E-05 | 0.04509578 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 6.53E-05 | 0.09005535 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00035466 | 0.09185668 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00056067 | 0.10652768 |
| GO Biological Process | triacylglycerol metabolism [GO:0006641] | 0.00011184 | 0.15434334 |
| GO Biological Process | neutral lipid metabolism [GO:0006638] | 0.00011184 | 0.15434334 |
| GO Biological Process | acylglycerol metabolism [GO:0006639] | 0.00011184 | 0.15434334 |
| GO Biological Process | glycerolipid metabolism [GO:0046486] | 0.00011184 | 0.15434334 |
| GO Biological Process | disaccharide metabolism [GO:0005984] | 0.00027852 | 0.3843507 |
| MIPS Functional Classification | CELLULAR TRANSPORT AND TRANSPORT MECHANISMS | 0.00188804 | 0.48900236 |
| GO Cellular Component | mitochondrial intermembrane space [GO:0005758] | 0.00172766 | 0.5701278 |
| MIPS Functional Classification | phosphate transport | 0.00325479 | 0.84299061 |

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|---|---|---|---|
| GO Cellular Component | membrane [GO:0016020] | 0.00288616 | 0.9524328 |
| | | | |
| **Ykl222c** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | detoxification | 6.48E-07 | 0.00016781 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 2.16E-06 | 0.00056061 |
| SMART Domains | Aamy | 3.58E-06 | 0.00105136 |
| MIPS Protein Classes | Zinc-coordinating DNA-binding domains | 6.41E-06 | 0.00121883 |
| MIPS Functional Classification | METABOLISM | 6.15E-06 | 0.00159295 |
| PFam-A Domains | PF00128 (alpha-amylase) | 1.63E-06 | 0.00193347 |
| MIPS Functional Classification | drug transporters | 1.05E-05 | 0.002716 |
| MIPS Protein Classes | Cys6 cysteine-zinc cluster | 3.21E-05 | 0.006096 |
| PFam-A Domains | PF00083 (sugar_tr) | 5.15E-06 | 0.00610469 |
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 0.00061778 | 0.00679554 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 4.12E-05 | 0.00782321 |
| MIPS Functional Classification | ENERGY | 4.63E-05 | 0.01199072 |
| SMART Domains | GAL4 | 4.39E-05 | 0.01290131 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 7.74E-05 | 0.02003637 |
| PFam-A Domains | PF00172 (Zn_clus) | 3.76E-05 | 0.04454782 |
| GO Molecular Function | alpha-glucosidase [GO:0004558] | 3.27E-05 | 0.04499774 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 4.77E-05 | 0.06580627 |
| GO Biological Process | hexose transport [GO:0008645] | 4.77E-05 | 0.06580627 |
| MIPS Protein Classes | Transcription factors | 0.00065715 | 0.12485755 |
| MIPS Functional Classification | glyoxylate cycle | 0.00059642 | 0.15447356 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00089336 | 0.23137895 |
| SMART Domains | ZnF_C2H2 | 0.00094528 | 0.27791232 |
| MIPS Functional Classification | plasma membrane | 0.00161284 | 0.41772556 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 0.00030657 | 0.42306108 |
| GO Biological Process | TCA intermediate metabolism [GO:0006100] | 0.00042209 | 0.5824842 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 0.00045107 | 0.62247246 |
| GO Molecular Function | ABC-type efflux porter [GO:0015427] | 0.00059642 | 0.82127447 |
| GO Biological Process | response to drug [GO:0042493] | 0.0006626 | 0.91438248 |
| | | | |
| **Yll054c** | **n=200** | | |

| **Source** | **Annotation** | **pval** | **Bonfp** |
|---|---|---|---|
| Deletions Consortium (Essentiality, Mo | Morphology - WT | 1.96E-06 | 2.16E-05 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 1.69E-06 | 0.0004367 |
| MIPS Functional Classification | plasma membrane | 1.06E-05 | 0.00274594 |
| Proteome Localization--Observed | cyto | 0.00031906 | 0.00350968 |
| MIPS Functional Classification | transport mechanism | 9.41E-05 | 0.02437651 |
| Proteome Localization--Predicted+Obs | cyt | 0.00694139 | 0.02776556 |
| MIPS Functional Classification | METABOLISM | 0.00010933 | 0.02831725 |
| Proteome Localization--Observed | cell periphery | 0.00403694 | 0.04440634 |
| MIPS Protein Classes | ABC transporter | 0.00025187 | 0.04785549 |
| GO Biological Process | organic acid metabolism [GO:0006082] | 3.59E-05 | 0.04948542 |
| GO Biological Process | carboxylic acid metabolism [GO:0019752] | 3.59E-05 | 0.04948542 |
| MIPS Functional Classification | ABC transporters | 0.00020515 | 0.05313437 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00016108 | 0.05315772 |
| MDS Proteomics Complexes | YMR059W (SEN15) | 0.00027543 | 0.13578847 |
| GO Molecular Function | ATP-binding cassette (ABC) transporter [GO:0004009] | 0.00010447 | 0.14385657 |
| MIPS Subcellular Localization | mitochondrial matrix | 0.00353338 | 0.14840196 |
| MIPS Functional Classification | glyoxylate cycle | 0.00059642 | 0.15447356 |
| MIPS Functional Classification | drug transporters | 0.00073373 | 0.19003711 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 0.00015585 | 0.21460545 |
| GO Biological Process | main pathways of carbohydrate metabolism [GO:0006092] | 0.00024113 | 0.3327594 |
| GO Cellular Component | peroxisomal matrix [GO:0005782] | 0.0010418 | 0.343794 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00183251 | 0.3481769 |
| PFam-A Domains | PF00005 (ABC_tran) | 0.00037016 | 0.43863842 |
| GO Biological Process | TCA intermediate metabolism [GO:0006100] | 0.00042209 | 0.5824842 |
| GO Cellular Component | cytoplasm [GO:0005737] | 0.00184582 | 0.6091206 |
| GO Molecular Function | ABC-type efflux porter [GO:0015427] | 0.00059642 | 0.82127447 |
| | | | |
| **Yml081w** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 4.55E-13 | 1.18E-10 |
| MIPS Functional Classification | METABOLISM | 8.76E-10 | 2.27E-07 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 4.46E-08 | 1.16E-05 |
| Proteome Localization--Predicted+Obs | cyt | 4.42E-05 | 0.00017668 |

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|---|---|---|---|
| GO Molecular Function | mannose transporter [GO:0015578] | 1.57E-07 | 0.00021663 |
| GO Biological Process | hexose transport [GO:0008645] | 2.04E-07 | 0.00028119 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 2.04E-07 | 0.00028119 |
| GO Molecular Function | glucose transporter [GO:0005355] | 4.50E-07 | 0.00061994 |
| MIPS Functional Classification | cellular import | 2.84E-06 | 0.0007351 |
| Proteome Localization--Observed | cyto | 9.33E-05 | 0.00102626 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 1.10E-06 | 0.00152099 |
| GO Molecular Function | hexose transporter [GO:0015149] | 1.10E-06 | 0.00152099 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 1.68E-06 | 0.00231169 |
| MIPS Functional Classification | plasma membrane | 1.06E-05 | 0.00274594 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 1.13E-05 | 0.00293771 |
| GO Molecular Function | fructose transporter [GO:0005353] | 2.38E-06 | 0.00327415 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 2.99E-06 | 0.00412908 |
| GO Biological Process | alcohol metabolism [GO:0006066] | 3.52E-06 | 0.00485924 |
| PFam-A Domains | PF00083 (sugar_tr) | 3.76E-05 | 0.04454782 |
| MDS Proteomics Complexes | YPL022W (RAD1) | 0.00019217 | 0.09473833 |
| MIPS Phenotypes | Galactose fermentation (Gal) | 0.00078341 | 0.14101452 |
| GO Molecular Function | transporter [GO:0005215] | 0.00011558 | 0.15915779 |
| MDS Proteomics Complexes | YGL137W (SEC27) | 0.00049144 | 0.24227893 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 0.00022865 | 0.31553424 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00156099 | 0.5151267 |
| GO Molecular Function | oxidoreductase [GO:0016491] | 0.00046798 | 0.64440158 |
| MIPS Functional Classification | ENERGY | 0.00270516 | 0.70063644 |
| MIPS Functional Classification | CELLULAR TRANSPORT AND TRANSPORT MECHANISMS | 0.00380586 | 0.98571774 |
| GO Biological Process | glycerol metabolism [GO:0006071] | 0.00101923 | >0.999 |
| GO Biological Process | triacylglycerol metabolism [GO:0006641] | 0.00233288 | >0.999 |
| GO Biological Process | polyol metabolism [GO:0019751] | 0.00101923 | >0.999 |
| MDS Proteomics Complexes | YPL031C (PHO85) | 0.00233288 | >0.999 |
| MDS Proteomics Complexes | YPL204W (HRR25) | 0.00253479 | >0.999 |
| GO Biological Process | hexose metabolism [GO:0019318] | 0.00369296 | >0.999 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00484406 | >0.999 |
| GO Biological Process | acylglycerol metabolism [GO:0006639] | 0.00233288 | >0.999 |
| GO Biological Process | glucose metabolism [GO:0006006] | 0.00251429 | >0.999 |
| MDS Proteomics Complexes | YKL166C (TPK3) | 0.00437089 | >0.999 |

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|---|---|---|---|
| MIPS Functional Classification | lipid and fatty-acid transport | 0.00393128 | >0.999 |
| GO Biological Process | neutral lipid metabolism [GO:0006638] | 0.00233288 | >0.999 |
| GO Biological Process | glycerolipid metabolism [GO:0046486] | 0.00233288 | >0.999 |
| MDS Proteomics Complexes | YLR340W (RPP0) | 0.00325479 | >0.999 |
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| **Ynr063w** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 3.32E-11 | 8.60E-09 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 2.01E-09 | 2.77E-06 |
| GO Molecular Function | hexose transporter [GO:0015149] | 2.01E-09 | 2.77E-06 |
| GO Molecular Function | mannose transporter [GO:0015578] | 4.97E-09 | 6.85E-06 |
| PFam-A Domains | PF00083 (sugar_tr) | 6.61E-09 | 7.83E-06 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 4.46E-08 | 1.16E-05 |
| GO Biological Process | hexose transport [GO:0008645] | 9.97E-09 | 1.38E-05 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 9.97E-09 | 1.38E-05 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 9.28E-08 | 1.76E-05 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 1.51E-08 | 2.08E-05 |
| GO Molecular Function | glucose transporter [GO:0005355] | 1.78E-08 | 2.45E-05 |
| GO Molecular Function | fructose transporter [GO:0005353] | 8.62E-08 | 0.00011873 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 1.17E-07 | 0.00016129 |
| Proteome Localization--Predicted+Obs | cyt | 4.42E-05 | 0.00017668 |
| MIPS Functional Classification | METABOLISM | 2.82E-06 | 0.00073025 |
| SMART Domains | Aamy | 3.58E-06 | 0.00105136 |
| PFam-A Domains | PF00128 (alpha-amylase) | 1.63E-06 | 0.00193347 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 1.13E-05 | 0.00293771 |
| GO Molecular Function | galactose transporter [GO:0005354] | 1.44E-05 | 0.01977895 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00013388 | 0.03467388 |
| GO Molecular Function | alpha-glucosidase [GO:0004558] | 3.27E-05 | 0.04499774 |
| MIPS Functional Classification | cellular import | 0.00031291 | 0.08104473 |
| MIPS Functional Classification | ENERGY | 0.00039709 | 0.10284709 |
| MIPS Functional Classification | plasma membrane | 0.00051343 | 0.13297889 |
| MIPS Functional Classification | drug transporters | 0.00073373 | 0.19003711 |
| MIPS Protein Classes | Zinc-coordinating DNA-binding domains | 0.00207705 | 0.3946395 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00156099 | 0.5151267 |

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| **Yox1** | **n=191** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | transport mechanism | 0.00033786 | 0.08750548 |
| MIPS Phenotypes | G2/M arrest | 0.00090651 | 0.1631709 |
| GO Biological Process | cell growth and/or maintenance [GO:0008151] | 0.00013007 | 0.17950074 |
| MIPS Protein Classes | other transcription factors | 0.00145687 | 0.2768053 |
| GO Biological Process | mitosis [GO:0007067] | 0.00021145 | 0.291801 |
| GO Biological Process | M phase of mitotic cell cycle [GO:0000087] | 0.00024821 | 0.34253394 |
| MIPS Protein Classes | ion-transport ATPases | 0.00280972 | 0.5338468 |
| Cellzome Complexes | YFL017W-A (SMX2) | 0.00145687 | 0.66870333 |
| MIPS Functional Classification | REGULATION OF / INTERACTION WITH CELLULAR ENVIRONMENT | 0.0027524 | 0.7128716 |
| GO Biological Process | M phase [GO:0000279] | 0.00052693 | 0.72716064 |
| MIPS Protein Classes | ATPases | 0.00388289 | 0.7377491 |
| GO Biological Process | nuclear division [GO:0000280] | 0.00065648 | 0.90594792 |
| Cellzome Complexes | YBR119W (MUD1) | 0.00204383 | 0.93811797 |
|  |  |  |  |
| **Ypr013c** | **n=198** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Cellular Component | bud [GO:0005933] | 6.79E-05 | 0.02241492 |
| MIPS Subcellular Localization | golgi membrane | 0.00195716 | 0.08220072 |
| GO Cellular Component | site of polarized growth (sensu Fungi) [GO:0030483] | 0.00048821 | 0.16111062 |
| GO Cellular Component | site of polarized growth [GO:0030427] | 0.00048821 | 0.16111062 |
| GO Cellular Component | site of polarized growth (sensu Saccharomyces) [GO:0000134] | 0.00048821 | 0.16111062 |
| GO Biological Process | metal ion transport [GO:0030001] | 0.00012997 | 0.17935998 |
| MDS Proteomics Complexes | YDR200C (VPS64) | 0.00057905 | 0.28546919 |
| GO Cellular Component | spore wall (sensu Fungi) [GO:0005619] | 0.00154688 | 0.5104704 |
| MIPS Phenotypes | Heat-sensitivity (ts) | 0.00449441 | 0.8089938 |
| GO Cellular Component | bud neck [GO:0005935] | 0.00264 | 0.8712 |
| MIPS Functional Classification | homeostasis of cations | 0.00350185 | 0.90697915 |
|  |  |  |  |
| **Ypr015c** | **n=199** |  |  |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 4.09E-05 | 0.01060214 |

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|---|---|---|---|
| MDS Proteomics Complexes | YPL031C (PHO85) | 0.00010968 | 0.05407125 |
| MIPS Functional Classification | METABOLISM | 0.00064434 | 0.16688458 |
| MIPS Protein Classes | Cys2His2 zinc-finger | 0.00168984 | 0.3210696 |
| MIPS Functional Classification | C-compound and carbohydrate utilization | 0.00150455 | 0.38967845 |
| Cellzome Complexes | YDR062W (LCB2) | 0.00102243 | 0.46929537 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.0014881 | 0.491073 |
| MDS Proteomics Complexes | YBL036C | 0.00100443 | 0.49518399 |
| GO Molecular Function | transporter [GO:0005215] | 0.00065187 | 0.89762361 |
| GO Biological Process | carbohydrate metabolism [GO:0005975] | 0.00070884 | 0.97819368 |
| | | | |
| **Ypr196w** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Molecular Function | mannose transporter [GO:0015578] | 4.97E-09 | 6.85E-06 |
| GO Biological Process | hexose transport [GO:0008645] | 9.97E-09 | 1.38E-05 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 9.97E-09 | 1.38E-05 |
| GO Molecular Function | glucose transporter [GO:0005355] | 1.78E-08 | 2.45E-05 |
| MIPS Functional Classification | METABOLISM | 2.36E-07 | 6.10E-05 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 5.23E-08 | 7.20E-05 |
| GO Molecular Function | hexose transporter [GO:0015149] | 5.23E-08 | 7.20E-05 |
| GO Molecular Function | fructose transporter [GO:0005353] | 8.62E-08 | 0.00011873 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 7.29E-07 | 0.00018877 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 2.30E-07 | 0.00031675 |
| SMART Domains | Aamy | 3.58E-06 | 0.00105136 |
| Proteome Localization--Predicted+Obs | cyt | 0.00042782 | 0.00171128 |
| PFam-A Domains | PF00128 (alpha-amylase) | 1.63E-06 | 0.00193347 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 1.68E-06 | 0.00231169 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 1.13E-05 | 0.00293771 |
| Proteome Localization--Observed | cyto | 0.00031906 | 0.00350968 |
| PFam-A Domains | PF00083 (sugar_tr) | 5.15E-06 | 0.00610469 |
| MIPS Functional Classification | plasma membrane | 4.15E-05 | 0.01074617 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00013388 | 0.03467388 |
| MIPS Subcellular Localization | cytoplasm | 0.00098914 | 0.04154375 |
| GO Molecular Function | alpha-glucosidase [GO:0004558] | 3.27E-05 | 0.04499774 |
| SMART Domains | ZnF_C2H2 | 0.00015855 | 0.0466137 |

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|---|---|---|---|
| PFam-A Domains | PF00096 (zf-C2H2) | 4.34E-05 | 0.05142426 |
| MIPS Protein Classes | Cys2His2 zinc-finger | 0.00027125 | 0.05153674 |
| MIPS Functional Classification | nucleotide metabolism | 0.00024497 | 0.06344619 |
| MIPS Functional Classification | cellular import | 0.00031291 | 0.08104473 |
| MIPS Functional Classification | purine ribonucleotide metabolism | 0.00049144 | 0.12728244 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 0.00183251 | 0.3481769 |
| MIPS Functional Classification | regulation of C-compound and carbohydrate utilization | 0.00147075 | 0.38092425 |
| Cellzome Complexes | YDR099W (BMH2) | 0.00101923 | 0.46782657 |
| Cellzome Complexes | YDR062W (LCB2) | 0.0010418 | 0.4781862 |
| GO Cellular Component | plasma membrane [GO:0005886] | 0.00156099 | 0.5151267 |
| SMART Domains | CBS | 0.00233288 | 0.68586672 |
| GO Molecular Function | glucosidase [GO:0015926] | 0.00053221 | 0.73285042 |
| MIPS Protein Complexes | Cytoplasmic translation elongation | 0.00233288 | 0.7348572 |
| GO Molecular Function | galactose transporter [GO:0005354] | 0.00059642 | 0.82127447 |
| GO Cellular Component | membrane [GO:0016020] | 0.00288616 | 0.9524328 |
| MIPS Functional Classification | CELLULAR TRANSPORT AND TRANSPORT MECHANISMS | 0.00380586 | 0.98571774 |
| GO Biological Process | sphingolipid metabolism [GO:0006665] | 0.00393128 | >0.999 |
| GO Molecular Function | other carbon-nitrogen ligase [GO:0016883] | 0.00233288 | >0.999 |
| PFam-A Domains | PF00571 (CBS) | 0.00325479 | >0.999 |
| GO Biological Process | transport [GO:0006810] | 0.00117216 | >0.999 |
| GO Biological Process | ribonucleotide biosynthesis [GO:0009260] | 0.00437089 | >0.999 |
| MIPS Functional Classification | homeostasis of protons | 0.0046866 | >0.999 |
| GO Biological Process | translational elongation [GO:0006414] | 0.00393128 | >0.999 |
| GO Biological Process | purine nucleotide metabolism [GO:0006163] | 0.00135467 | >0.999 |
| GO Biological Process | purine nucleotide biosynthesis [GO:0006164] | 0.00078341 | >0.999 |
| GO Biological Process | RAS protein signal transduction [GO:0007265] | 0.0010418 | >0.999 |
| GO Biological Process | nucleotide biosynthesis [GO:0009165] | 0.00326287 | >0.999 |
| GO Biological Process | purine ribonucleotide biosynthesis [GO:0009152] | 0.00437089 | >0.999 |
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| **Yrm1** | **n=199** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| Proteome Localization--Predicted+Obs | nuc | 0.00245152 | 0.00980608 |
| MIPS Subcellular Localization | nucleus | 0.00445438 | 0.18708396 |
| GO Biological Process | negative regulation of transcription [GO:0016481] | 0.00018989 | 0.26204682 |

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| Cellzome Complexes | YNL313C | 0.00100443 | 0.46103337 |
| MIPS Phenotypes | Slow-growth (slg) | 0.00325195 | 0.585351 |
| GO Biological Process | negative regulation of transcription from Pol II promoter [GO:0000122] | 0.00043187 | 0.59597922 |
| MIPS Functional Classification | phosphate metabolism | 0.00353056 | 0.91441504 |
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| **Yrr1** | **n=200** | | |
| **Source** | **Annotation** | **pval** | **Bonfp** |
| GO Molecular Function | fructose transporter [GO:0005353] | 2.38E-06 | 0.00327415 |
| GO Molecular Function | mannose transporter [GO:0015578] | 3.86E-06 | 0.00531249 |
| PFam-A Domains | PF00083 (sugar_tr) | 5.15E-06 | 0.00610469 |
| MIPS Functional Classification | METABOLISM | 2.72E-05 | 0.0070514 |
| MIPS Protein Classes | Major facilitator superfamily proteins (MFS) | 4.12E-05 | 0.00782321 |
| Proteome Localization--Predicted+Obs | cyt | 0.0029717 | 0.0118868 |
| GO Molecular Function | glucose transporter [GO:0005355] | 9.04E-06 | 0.01245068 |
| MIPS Functional Classification | drug transporters | 9.54E-05 | 0.02471787 |
| GO Molecular Function | monosaccharide transporter [GO:0015145] | 1.88E-05 | 0.02587232 |
| GO Molecular Function | hexose transporter [GO:0015149] | 1.88E-05 | 0.02587232 |
| MIPS Protein Classes | Cys6 cysteine-zinc cluster | 0.00021041 | 0.03997733 |
| MIPS Subcellular Localization | peroxisome | 0.00151969 | 0.06382698 |
| GO Biological Process | hexose transport [GO:0008645] | 4.77E-05 | 0.06580627 |
| GO Biological Process | monosaccharide transport [GO:0015749] | 4.77E-05 | 0.06580627 |
| SMART Domains | GAL4 | 0.00027543 | 0.0809773 |
| MIPS Functional Classification | detoxification | 0.00037229 | 0.09642363 |
| MIPS Functional Classification | plasma membrane | 0.00051343 | 0.13297889 |
| MIPS Functional Classification | C-compound and carbohydrate transporters | 0.00056421 | 0.14613117 |
| MIPS Functional Classification | TRANSPORT FACILITATION | 0.00089336 | 0.23137895 |
| GO Molecular Function | carbohydrate transporter [GO:0015144] | 0.00020515 | 0.2824943 |
| PFam-A Domains | PF00172 (Zn_clus) | 0.00024113 | 0.28573905 |
| MIPS Functional Classification | C-compound and carbohydrate metabolism | 0.0014536 | 0.3764824 |
| MIPS Protein Classes | Zinc-coordinating DNA-binding domains | 0.00207705 | 0.3946395 |
| GO Biological Process | carbohydrate transport [GO:0008643] | 0.00030657 | 0.42306108 |
| GO Cellular Component | peroxisome [GO:0005777] | 0.00151969 | 0.5014977 |
| GO Biological Process | response to drug [GO:0042493] | 0.0006626 | 0.91438248 |

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