**Table S1. Putative interacted proteins identified in the strain of expressing GFP-α-actinin and GFP**

**(GFP-α-actinin pulled-down protein list ; red highlights are common shared with GFP only).**

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| Accession  Number | Description |
| AN10396 | Ortholog(s) have farnesyl-diphosphate farnesyltransferase activity, squalene synthase activity and role in ergosterol biosynthetic process, establishment or maintenance of cell polarity |
| AN4770 | sA. Adenosine 3-phosphate 5-phosphosulfate (PAPS) reductase involved in sulfate assimilation |
| AN3674 | Has domain(s) with predicted phospholipid binding activity |
| AN7707 | Protein with similarity to alpha-actinin; predicted role in actin filament bundling |
| AN6630 | Putative nascent polypeptide-associated complex subunit alpha; induced by rapamycin-induced autophagy |
| AN4380 | Putative ribonucleotide reductase large chain with a predicted role in nucleotide salvage pathways; transcript upregulated in response to camptothecin |
| AN10518 | Protein of unknown function; protein induced by farnesol |
| AN10087 | Uncharacterized ORF; PASA transcript |
| AN4762 | Ortholog(s) have mitochondrion localization |
| AN11102 | Ortholog(s) have ubiquitin-specific protease activity, role in protein deubiquitination and nucleoplasm localization |
| AN6346 | Putative dihydroxy-acid dehydratase with a predicted role in valine, leucine, and isoleucine metabolism; intracellular, menadione stress-induced protein |
| AN0641 | tcpA. TCTP (translationally controlled tumor protein); high expression during germination, germ tube elongation, early vegetative growth, decreased in stationary phase; protein levels increase in osmoadaptation; mutant makes no cleistothecia |
| AN0858 | hsp104. Putative chaperone |
| AN3739 | snxA. SR/RRM family mRNA binding protein involved in control of G2/M transition |
| AN6341 | Protein with similarity to Saccharomyces cerevisiae Crn1p; predicted role in actin patch assembly |
| AN4939 | Ortholog(s) have enzyme activator activity, heme binding activity, role in ergosterol biosynthetic process, regulation of ergosterol biosynthetic process and endoplasmic reticulum, endosome localization |
| AN2056 | Ortholog(s) have endoplasmic reticulum localization |
| AN1429 | codA. Putative choline oxidase; intracellular, menadione stress-induced protein |
| AN5883 | metF. Putative methylenetetrahydrofolate reductase (NADPH) with predicted role in one-carbon metabolism; mutation causes methionine auxotrophy and decreased mycelial pigment production; expression induced by homocysteine and decreased by farnesol |
| AN4168 |  |
| AN1211 | Has domain(s) with predicted hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, proton-transporting ATPase activity, rotational mechanism activity |
| AN6900 | tpiA. Putative triose-phosphate isomerase with a predicted role in gluconeogenesis and glycolysis; protein induced by farnesol |
| AN10609 | Ortholog(s) have role in mitochondrial respiratory chain complex III assembly and integral component of mitochondrial inner membrane localization |
| AN2213 | Ortholog(s) have proteasome-activating ATPase activity |
| AN10337 | Has domain(s) with predicted enzyme regulator activity, role in regulation of protein catabolic process and proteasome complex localization |
| AN3461 | Ortholog(s) have mitochondrion localization |
| AN2756 | slaB. Predicted actin binding protein with similarity to Saccharomyces cerevisiae Sla2p; essential for conidial germination |
| AN4940 | Ortholog(s) have role in reciprocal meiotic recombination and endoplasmic reticulum, mitochondrion, nuclear envelope, plasma membrane localization |
| AN5662 | Ortholog(s) have cytosol localization |
| AN1528 | Ortholog(s) have role in regulation of transcription from RNA polymerase II promoter, transcription from RNA polymerase II promoter and cytosol, nucleus localization |
| AN1558 | myoA. Putative myosin I; required for secretion and polarized growth |
| AN2903 | pepE. Aspartic protease; protein expressed at decreased levels in a hapX mutant versus wild-type |
| AN8571 | Putative cytidine deaminase with a predicted role in pyrimidine metabolism |
| AN1677 | Short-chain dehydrogenase; transcriptionally induced by growth on xylose |
| AN9408 | fasB. Fatty acid synthase, beta subunit; multifunctional enzyme with a predicted role in cytosolic fatty acid formation |
| AN10778 | Ortholog(s) have mitochondrion localization |
| AN8023 | vpsA. Protein required for vacuole biogenesis |
| AN6338 | Putative aromatic-amino-acid transaminase with a predicted role in aromatic amino acid biosynthesis |
| AN6227 | Ortholog(s) have hercynylcysteine sulfoxide lyase activity (ergothioneine-forming), hercynylselenocysteine lyase activity (selenoneine-forming) activity and role in ergothioneine biosynthetic process, selenoneine biosynthetic process |
| AN1549 |  |
| AN10946 |  |
| AN10844 | fbpZ. Putative fructose-2,6-bisphosphate 2-phosphatase |
| AN3634 | Putative anthranilate phosphoribosyltransferase with a predicted role in aromatic amino acid biosynthesis |
| AN7602 | rabC. Putative GTPase with a role in retrograde traffic from endosomes to the Golgi; partially localizes to the late Golgi and to the Spitzenkorper; mutants display an increase in abundance of early endosomes |
| AN6931 | Has domain(s) with predicted oxidoreductase activity and role in metabolic process |
| AN4977 | Ortholog(s) have mitochondrion localization |
| AN8191 | Has domain(s) with predicted translation initiation factor activity, role in translational initiation and cytoplasm localization |
| AN8022 | Protein of unknown function |
| AN5601 | Putative saccharopine dehydrogenase (NADP+, L-glutamate-forming) with a predicted role in lysine metabolism |
| AN2523 | chsB. Class III chitin synthase with a role in chitin biosynthesis; required for normal growth and conidiation; constitutively expressed during vegetative growth, sexual and asexual development |
| AN6874 | Putative mannosyltransferase; transcript levels increase during the unfolded-protein response (UPR); ortholog Alg2p has glycolipid 6-alpha-mannosyltransferase activity |
| AN8274 | Ortholog(s) have DNA binding, tricarboxylate secondary active transmembrane transporter activity and role in alpha-ketoglutarate transport, mitochondrial citrate transport, mitochondrial genome maintenance |
| AN2953 |  |
| AN10020 | Ortholog(s) have role in proteasome-mediated ubiquitin-dependent protein catabolic process and cytosol, nuclear periphery localization |
| AN1539 | csnD. Subunit 4 of the COP9 signalosome; required for light-dependent asexual and sexual development and cleistothecia production; regulates secondary metabolite production, mutant hyphae are aberrant with abnormal red pigmentation |
| AN0347 | rabE. Putative GTPase with a predicted role in intra-Golgi transport; transcript levels increase during the unfolded-protein response (UPR) |
| AN12475 | Ortholog(s) have eukaryotic initiation factor 4G binding, mRNA binding, single-stranded telomeric DNA binding activity and role in negative regulation of translation in response to stress |
| AN1358 | Ortholog(s) have protein serine/threonine phosphatase activity |
| AN10873 | Ortholog(s) have role in protein import into mitochondrial outer membrane and mitochondrial outer membrane localization |
| AN2126 | Predicted actin capping protein |
| AN4688 | ivdA. Putative acyl-coA dehydrogenase |
| AN8055 | Ortholog(s) have nucleolus localization |
| AN5969 |  |
| AN3843 | Ortholog(s) have role in cristae formation, protein import into mitochondrial intermembrane space and MICOS complex, mitochondrial crista, mitochondrial crista junction, plasma membrane localization |
| AN5442 | cpyA. Putative carboxypeptidase Y |
| AN2896 | Has domain(s) with predicted catalytic activity and role in metabolic process |
| AN3789 | Ortholog(s) have cytosol, nucleus localization |
| AN4401 | Putative asparagine synthase with a predicted role in asparagine metabolism |
| AN6126 | accA. Putative acetyl-CoA carboxylase with a predicted role in cytosolic fatty acid formation |
| AN3098 | nsfA. Putative secretory component; ortholog of Sec18p |
| AN8874 | Ortholog(s) have GTPase activity, protein homodimerization activity |
| AN1700 | Putative 26S proteasome regulatory subunit; transcript upregulated in response to camptothecin |
| AN6906 | Ortholog(s) have Prp19 complex, cytosol, nuclear envelope, spliceosomal complex localization |
| AN8639 | Putative alpha,alpha-trehalose-phosphate synthase (UDP-forming) with a predicted role in trehalose biosynthesis |
| AN0034 | Putative glycerone kinase with a predicted role in glycerol metabolism; transcript upregulated by growth in glycerol |
| AN4236 | Probable 26S proteasome subunit and member of the CDC48/PAS1/SEC18 family of ATPases; transcript upregulated in response to camptothecin |
| AN1306 | Protein with similarity to mammalian gelsolin; predicted role in actin filament severing |
| AN0595 | Putative NADPH-cytochrome P450 reductase with a predicted role in energy metabolism |
| AN4085 | Ortholog(s) have role in asymmetric protein localization to old mitotic spindle pole body, establishment or maintenance of cytoskeleton polarity, negative regulation of septation initiation signaling |
| AN1047 | Putative heat shock protein |
| AN1503 | Protein expressed at increased levels during osmoadaptation; contains dihydrodipicolinate synthase family DHDPS-like conserved domain |
| AN10540 | Ortholog(s) have dipeptidyl-peptidase activity and cytoplasm, nucleus localization |
| AN3720 | Ortholog(s) have cytosol, endoplasmic reticulum exit site localization |
| AN8702 | Ortholog(s) have ubiquitin conjugating enzyme activity, ubiquitin-protein transferase activity and role in UV-damage excision repair, free ubiquitin chain polymerization, postreplication repair, protein K63-linked ubiquitination |
| AN2743 | Ortholog(s) have role in regulation of translation in response to nitrogen starvation |
| AN6804 | Predicted transporter of the major facilitator superfamily (MFS); expression upregulated after exposure to farnesol |
| AN1063 | Putative NADH dehydrogenase (ubiquinone) with a predicted role in energy metabolism |
| AN7472 | Ortholog(s) have dolichyl-diphosphooligosaccharide-protein glycotransferase activity, role in protein N-linked glycosylation via asparagine and oligosaccharyltransferase complex, plasma membrane localization |
| AN3168 | Ortholog(s) have proton-transporting ATPase activity, rotational mechanism activity, role in asexual sporulation, cellular response to drug, vacuolar transport and fungal-type vacuole membrane, nucleus localization |
| AN6366 | Ortholog(s) have endoplasmic reticulum, plasma membrane localization |
| AN0182 | rasA. Small monomeric GTPase of the Ras superfamily involved in regulation of development; involved in conidiophore formation and conidial germination |
| AN4288 | Protein expressed at decreased levels in a hapX mutant versus wild-type; AN4288 and AN9411 in version 4 of the A. nidulans annotation were identical, AN9411 has been merged with AN4288 such that AN4288 remains and AN9411 was deleted |
| AN6489 | Ortholog(s) have mitochondrial ribosome localization |
| AN2069 | Ortholog(s) have electron carrier activity, role in ergosterol biosynthetic process and endoplasmic reticulum membrane, mitochondrion localization |
| AN3709 |  |
| AN5602 | Ortholog(s) have ATPase activator activity, chaperone binding activity, role in cellular response to heat, positive regulation of ATPase activity, protein folding and cytosol localization |
| AN5666 | mpkA. Putative mitogen-activated protein kinase (MAP kinase) involved in conidial germination and polarized growth; mutants arrest as branched germlings, phenotype is remediated by sucrose and NaCl; reduced growth on AVICEL medium |
| AN3468 | H2A.X. Histone H2A |
| AN2909 | Ortholog(s) have cytosol, nucleus localization |
| AN8169 | apnA. Uncharacterized ORF; Putative asparaginase with a predicted role in asparagine metabolism |
| AN7540 | Ortholog(s) have role in eukaryotic translation initiation factor 3 complex assembly, gamma-tubulin complex localization |
| AN4859 | pmaA. Plasma membrane ATPase with a predicted role in energy metabolism |
| AN4234 | pcmA. Putative phosphoacetylglucosamine mutase with a predicted role in chitin biosynthesis |
| AN1635 | Ortholog(s) have U1 snRNP localization |
| AN5146 | Has domain(s) with predicted catalytic activity, heme binding, oxidoreductase activity |
| AN10837 | Ortholog(s) have amidophosphoribosyltransferase activity, role in 'de novo' IMP biosynthetic process, adenine metabolic process and cytoplasm localization |
| AN10170 | Ortholog(s) have ATPase activity and cytosol, nucleus localization |
| AN2762 | Putative acyl-coA dehydrogenase |
| AN4086 | Ortholog(s) have phenylalanine-tRNA ligase activity, role in cellular response to drug, phenylalanyl-tRNA aminoacylation and cytosol, nucleus, phenylalanine-tRNA ligase complex localization |
| AN0673 | Protein with a predicted role in actin assembly; similar to Saccharomyces cerevisiae Arp2p |
| AN8170 | napB. Nap/SET family member; exits nuclei at the onset of mitosis; cytosolic role in vacuolar protein sorting; interacts directly with KapA |
| AN1971 | Ortholog(s) have ATP-dependent 3'-5' DNA helicase activity, ATP-dependent 5'-3' DNA helicase activity, sequence-specific DNA binding activity |
| AN1177 | Ortholog(s) have cytosol, plasma membrane localization |
| AN6077 | Putative NADH dehydrogenase (ubiquinone) with a predicted role in energy metabolism |
| AN0086 | Ortholog(s) have cytosol, nucleus localization |
| AN0123 | Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization |
| AN3807 | Ortholog(s) have lipid binding activity |
| AN1689 | Putative oxidoreductase; putative salicylaldehyde dehydrogenase with a predicted role in naphthalene degradation; upregulated under hypoxic growth conditions |
| AN4908 | Putative eukaryotic translation initiation factor subunit; PalA-dependent expression independent of pH |
| AN2516 | ampA. S. cerevisiae RVS167 ortholog; component of the endocytic internalization machinery; localized to peripheral patches, to the cytosol and to hyphal tips; colocalizes with AbpA-GFP |
| AN10519 | Ortholog(s) have cytosol, nucleus localization |
| AN2458 | candA-C. C-terminal subunit of Cand1; which is split into two subunits (candA-N and candA-C) that bind to each other and to unneddylated cullin-RING complexes; role in sexual development, secondary metabolism and light control of asexual development |
| AN0381 | Ortholog(s) have unfolded protein binding activity, role in protein folding and chaperonin-containing T-complex, nucleus localization |
| AN5743 | Putative potassium-transporting ATPase with a predicted role in energy metabolism |
| AN7625 | Putative myo-inositol-1-phosphate synthase with a predicted role in phospholipid metabolism; intracellular, menadione stress-induced protein; palA-dependent expression independent of pH |
| AN3594 | sogA. Putative vacuolar protein-sorting protein with homology to Saccharomyces cerevisiae Vps5p; identified as a suppressor of xprG |
| AN2882 | Putative homoserine dehydrogenase with a predicted role in glycine, serine, and threonine metabolism; protein expressed at increased levels during osmoadaptation |
| AN0290 | Ortholog(s) have actin filament binding activity and role in barbed-end actin filament capping, filamentous growth, mitotic actomyosin contractile ring contraction |
| AN4038 | Putative translation initiation factor eIF5B |
| AN4547 | Ortholog(s) have role in establishment or maintenance of cell polarity and cytosol localization |
| AN2286 | alcC. Alcohol dehydrogenase III with a predicted role in two-carbon compound metabolism; required for long-term survival under anaerobic conditions; regulated at both the transcriptional and translational levels |
| AN8038 | Has domain(s) with predicted nucleic acid binding, nucleotide binding activity |
| AN6252 | Ortholog(s) have DNA binding, RNA polymerase II activity, RNA-directed RNA polymerase activity, role in response to drug, termination of RNA polymerase II transcription and DNA-directed RNA polymerase II, core complex, cytosol localization |
| AN0926 | kapC. Non-essential nuclear transport receptor importin-beta2 subunit; karyopherin superfamily; expression reduced after exposure to farnesol |
| AN10743 | Ortholog(s) have role in endocytosis, establishment or maintenance of actin cytoskeleton polarity, vacuole organization and integral component of Golgi membrane localization |
| AN1167 | Has domain(s) with predicted cytoplasm, nucleus localization |
| AN0327 | Ortholog(s) have ATP-dependent 3'-5' DNA helicase activity, ATP-dependent 5'-3' DNA helicase activity and role in box C/D snoRNP assembly, histone exchange, rRNA processing, regulation of transcription from RNA polymerase II promoter |
| AN0432 | Ortholog(s) have cytochrome-b5 reductase activity, acting on NAD(P)H activity and role in cellular response to oxidative stress, ergosterol biosynthetic process |
| AN4317 | sec13. Putative nuclear pore complex protein with homology to Saccharomyces cerevisiae Sec13p |
| AN5719 | Ortholog(s) have protein kinase activator activity, structural constituent of ribosome activity, role in cytoplasmic translation, positive regulation of protein kinase activity and cytosolic large ribosomal subunit localization |
| AN3349 | CYP659A1. Putative cytochrome P450 |
| AN8795 | Ortholog(s) have role in endosomal transport, vacuole fusion, non-autophagic, vesicle-mediated transport and AP-1 adaptor complex, cell division site, cell tip, cytosol, endosome, mitotic spindle pole body, nucleus localization |
| AN0943 | atp20. Putative mitochondrial F1F0-ATP synthase subunit g; ortholog of Atp20p; expression reduced after exposure to farnesol |
| AN8810 | Ortholog(s) have endoplasmic reticulum localization |
| AN1094 | ndiF. Putative mitochondrial NADH dehydrogenase (ubiquinone) with a predicted role in energy metabolism |
| AN4182 | nimX. Cyclin-dependent protein kinase involved in cell cycle control; required for cell cycle progression through G1 and G2; regulated by NimE cyclin and NimT phosphatase; homolog of S. pombe cdc2; transcript camptothecin upregulated |
| AN7206 | spgA. Ortholog(s) have GTPase activity, role in cellular protein localization, exit from mitosis, mitotic M phase, positive regulation of barrier septum assembly, septation initiation signaling and mitotic spindle pole body localization |
| AN3581 | trxR. Thioredoxin reductase with a predicted role in pyrimidine metabolism; putative flavoprotein; intracellular, menadione stress-induced protein; transcripts of two different sizes have been detected |
| AN2224 | sogB. Putative vacuolar protein-sorting protein with homology to Saccharomyces cerevisiae Vps17p; identified as a suppressor of xprG |
| AN2294 | elp3. Putative GNAT-type acetyltransferase |
| AN6066 | Has domain(s) with predicted catalytic activity and role in metabolic process |
| AN3628 | Putative peptide alpha-N-acetyltransferase with a predicted role in protein, peptide, and amino acid metabolism |
| AN6257 | Ortholog(s) have role in ER to Golgi vesicle-mediated transport, intracellular protein transport, nuclear envelope organization and cytosol localization |
| AN1401 | kapK. Essential exportin 1 involved in nuclear export |
| AN0490 | Putative CTP synthase with a predicted role in pyrimidine metabolism |
| AN9419 | Ortholog(s) have alanine-tRNA ligase activity, role in alanyl-tRNA aminoacylation and cytosol, mitochondrion localization |
| AN10229 | Ortholog(s) have role in ascospore formation, mitochondrial respiratory chain complex I assembly, programmed cell death and mitochondrion, plasma membrane localization |
| AN8866 | Putative phosphoglycerate dehydrogenase with a predicted role in glycine, serine, and threonine metabolism |
| AN1017 | hogA. Putative mitogen-activated protein kinase (MAPK) involved in osmotic stress response; highly up-regulated under osmotic stress conditions; required for sexual development and sporulation; mutant sensitive to NaCl |
| AN3830 | ileA. L-threonine dehydratase with a predicted role in glycine, serine, and threonine metabolism |
| AN5634 | acuD. Isocitrate lyase, required for utilization of acetate and fatty acids as carbon sources; transcriptional induction in response to acetate is mediated by FacB; transcriptional induction in response to long-chain fatty acids mediated by FarA |
| AN2968 | ippA. Putative inorganic diphosphatase with a predicted role in energy metabolism; intracellular; protein abundance decreased by menadione stress; protein expressed at increased levels during osmoadaptation |
| AN10527 | Ortholog(s) have trimethyllysine dioxygenase activity, role in carnitine biosynthetic process, mitochondrion organization and mitochondrion localization |
| AN4051 | Has domain(s) with predicted heme binding, iron ion binding, oxygen binding activity and role in oxygen transport |
| AN10350 | Ortholog(s) have cytosol, nucleus localization |
| AN0665 | aneA. Coatomer subunit epsilon involved in vesicle transport; mutants are defective in cleistothecium formation |
| AN12335 | acdA. Protein with an acyl-CoA dehydrogenase domain |
| AN6508 | gsk3. Protein kinase; transcript upregulated in response to camptothecin; mutants have brown pigment, a conidiaton defect and a strong growth defect but defects remediated by sucrose; required for nuclear import of CrzA under alkaline pH stress |
| AN2530 | hsp30. Heat shock protein 30; expression and protein levels upregulated after exposure to farnesol |
| AN10172 | Ortholog(s) have dicarboxylic acid transmembrane transporter activity, role in mitochondrial transport and mitochondrial inner membrane localization |
| AN3456 | Putative cystathionine gamma-synthase with a predicted role in methionine metabolism |
| AN10734 | Ortholog(s) have role in regulation of translational elongation and cytosolic ribosome, mitochondrion localization |
| AN8815 | Putative isoflavone reductase family protein; intracellular, menadione stress-induced protein |
| AN3695 | Putative anthranilate synthase with a predicted role in aromatic amino acid biosynthesis |
| AN5028 | ppoC. Fatty acid oxygenase that plays a role in oxylipin biosynthesis; responsible for the formation of the psi-factor component psiB-beta; expression reduced after exposure to farnesol |
| AN5747 | Ortholog(s) have protein domain specific binding activity |
| AN4015 | Ortholog(s) have ribosome binding, translation elongation factor activity, translation initiation factor activity |
| AN1683 | Putative oligosaccharyltransferase delta subunit; ortholog of Swp1p |
| AN4820 | Putative succinate-semialdehyde dehydrogenase [NAD(P)+] with a predicted role in 4-aminobutyrate (GABA) shunt |
| AN4583 | cyp7. Putative peptidyl-prolyl cis-trans isomerase D (PPIase); cyclophilin family member; protein abundance decreased by menadione stress; transcript levels increase during the unfolded-protein response (UPR) and in response to camptothecin |
| AN10466 | Ortholog(s) have role in inner mitochondrial membrane organization and integral component of mitochondrial inner membrane localization |
| AN2343 | Putative nitroreductase; intracellular, menadione stress-induced protein |
| AN5918 | catC. Putative catalase with a predicted role in gluconic acid and gluconate metabolism |
| AN1485 | cka1. Protein kinase; mutants are lethal forming only microcolonies |
| AN6368 | Putative arginyl-tRNA synthetase with a predicted role in tRNA charging for translation |
| AN8224 | Ortholog(s) have cytosol, nucleus localization |
| AN10351 | Ortholog(s) have metalloaminopeptidase activity, role in cellular response to drug, chaperone-mediated protein folding, proteolysis and cytosol, fungal-type vacuole lumen, ribosome localization |
| AN3499 | Has domain(s) with predicted ATP binding, phosphotransferase activity, alcohol group as acceptor activity and role in amino sugar metabolic process, peptidoglycan turnover |
| AN0261 | sec23. COPII coat component; considered a prototypic marker of transitional ER (endoplasmic reticulum); localizes to a cytosolic haze and to numerous small foci that predominate near the hyphal tips |
| AN6004 | Protein with an RNA recognition motif; protein expressed at increased levels in a hapX mutant versus wild-type; expression upregulated after exposure to farnesol |
| AN5121 | Protein similar to proteasome regulatory subunit 8; menadione stress-induced protein |
| AN3169 | prs3. Putative ribose-phosphate pyrophosphokinase with a predicted role in histidine metabolism; interacts with prs1 and prs2 |
| AN5529 | cotA. Essential NDR ser/thr protein kinase; role in cell polarity; RAM-signaling pathway component; MobB/CotA kinase complex thought to regulate cell polarity growth by maintaining cellular calcium homeostasis; mutant forms brown microcolonies |
| AN3070 | Ortholog(s) have chaperonin-containing T-complex, nucleus localization |
| AN0066 | Ortholog(s) have isopropylmalate transmembrane transporter activity, malonate(1-) transmembrane transporter activity, oxaloacetate transmembrane transporter activity, sulfate transmembrane transporter activity |
| AN0912 | Putative Beta-isopropylmalate dehydrogenase with a predicted role in valine, leucine, and isoleucine metabolism |
| AN7687 | Ortholog(s) have preprotein binding activity, role in conidium formation, hyphal growth, protein targeting to mitochondrion and mitochondrial outer membrane translocase complex localization |
| AN0907 | Ortholog(s) have structural constituent of ribosome activity and cytosolic small ribosomal subunit, nucleus localization |
| AN3842 | rabB. Putative GTPase required for early endosome trafficking; recruits prototypical Rab5 effectors Vps19, Vps45 and Vps34 and plays the major role in endocytic degradation; involved in vacuolar biogenesis; synthetically lethal with srgG/rabA |
| AN12408 | Ortholog(s) have role in cellular response to biotic stimulus, filamentous growth of a population of unicellular organisms in response to biotic stimulus, hyphal growth, vacuole inheritance |
| AN8843 | Putative homoserine kinase with a predicted role in glycine, serine, and threonine metabolism |
| AN7105 | Putative translation initiation factor 3, subunit c (eIF-3c); ortholog of Nip1p; expression reduced after exposure to farnesol |
| AN3102 | phkA. Putative histidine-containing phosphotransfer protein |
| AN2317 | Predicted actin depolymerizing protein with similarity to Saccharomyces cerevisiae Cof1p |
| AN10156 | Has domain(s) with predicted kinase activity, transferase activity, transferring phosphorus-containing groups activity and role in glycerophospholipid biosynthetic process |
| AN1989 | Putative dihydrosphingosine-1-phosphate lyase with a predicted role in sphingoglycolipid metabolism |
| AN0089 | rabS. Putative small GTPase involved in endosomal maturation and vacuolar biogenesis |
| AN10783 | Has domain(s) with predicted coenzyme binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, phosphogluconate dehydrogenase (decarboxylating) activity |
| AN4706 | myoB. Myosin II; required for normal conidiation, septum formation and for correct chitin deposition |
| AN0224 | Ortholog(s) have Golgi apparatus, cytosol, nucleus localization |
| AN5823 | sidA. L-ornithine N5-monooxygenase; involved in siderophore biosynthesis; null mutant inviable unless medium is supplemented with siderophores |
| AN7707 | Protein with similarity to alpha-actinin; predicted role in actin filament bundling |
| AN6341 | Protein with similarity to Saccharomyces cerevisiae Crn1p; predicted role in actin patch assembly |
| AN2756 | slaB. Predicted actin binding protein with similarity to Saccharomyces cerevisiae Sla2p; essential for conidial germination |
| AN1558 | myoA. Putative myosin I; required for secretion and polarized growth |
| AN2126 | Predicted actin capping protein |
| AN1306 | Protein with similarity to mammalian gelsolin; predicted role in actin filament severing |
| AN4085 | Ortholog(s) have role in asymmetric protein localization to old mitotic spindle pole body, establishment or maintenance of cytoskeleton polarity, negative regulation of septation initiation signaling |
| AN0673 | Protein with a predicted role in actin assembly; similar to Saccharomyces cerevisiae Arp2p |
| AN0290 | Ortholog(s) have actin filament binding activity and role in barbed-end actin filament capping, filamentous growth, mitotic actomyosin contractile ring contraction |
| AN8795 | Ortholog(s) have role in endosomal transport, vacuole fusion, non-autophagic, vesicle-mediated transport and AP-1 adaptor complex, cell division site, cell tip, cytosol, endosome, mitotic spindle pole body, nucleus localization |
| AN4182 | nimX. Cyclin-dependent protein kinase involved in cell cycle control; required for cell cycle progression through G1 and G2; regulated by NimE cyclin and NimT phosphatase; homolog of S. pombe cdc2; transcript camptothecin upregulated |
| AN7206 | spgA. Ortholog(s) have GTPase activity, role in cellular protein localization, exit from mitosis, mitotic M phase, positive regulation of barrier septum assembly, septation initiation signaling and mitotic spindle pole body localization |
| AN3169 | prs3. Putative ribose-phosphate pyrophosphokinase with a predicted role in histidine metabolism; interacts with prs1 and prs2 |
| AN2317 | Predicted actin depolymerizing protein with similarity to Saccharomyces cerevisiae Cof1p |
| AN4706 | myoB. Myosin II; required for normal conidiation, septum formation and for correct chitin deposition |
| AN0081 | sfaD. Beta subunit of a heterotrimeric G protein composed of FadA, SfaD, GpgA and involved in regulation of proliferation and conidiophore development; mutant produces increased amounts of extracellular proteinase during carbon starvation |
| AN5566 | Putative GMP synthase (glutamine-hydrolyzing) with a predicted role in purine metabolism |
| AN2508 | Ortholog(s) have cysteine desulfurase activity and role in cellular iron ion homeostasis, iron-sulfur cluster assembly, mitochondrial tRNA thio-modification, tRNA wobble uridine modification |
| AN1923 | Putative alanine transaminase with a predicted role in alanine and aspartate metabolism; intracellular, menadione stress-induced protein |
| AN7354 | Ortholog(s) have structural constituent of ribosome activity, role in translation and cytosolic large ribosomal subunit, nucleus localization |
| AN5525 | acoA. Putative aconitate hydratase with a predicted role in the TCA cycle; intracellular; protein abundance decreased by menadione stress; protein expressed at increased levels in a hapX mutant versus wild-type |
| AN8176 | Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization |
| AN2412 | cmkA. Calcium/calmodulin-dependent protein kinase A; essential for growth and nuclear division; expression downregulated by farnesol; transcript upregulated by camptothecin; mutants have a moderate growth defect and increased pigment production |
| AN5520 | Ortholog(s) have role in maturation of LSU-rRNA and cytosolic large ribosomal subunit localization |
| AN5790 | Putative isocitrate dehydrogenase (NAD+) with a predicted role in the TCA cycle |
| AN3172 | Ortholog of RPS0A and RPS0B; expression reduced after exposure to farnesol |
| AN8853 | snpA. Putative eukaryotic polypeptide releasing factor; suppressor of nonsense mutations |
| AN4443 | metH. Putative methionine synthase with a predicted role in methionine metabolism; protein expressed at increased levels in a hapX mutant versus wild-type |
| AN7146 | Putative S-adenosyl-methionine delta-24-sterol-C-methyltransferase with a predicted role in sterol metabolism |
| AN2149 | cct1. Putative chaperonin complex component, TCP-1 alpha subunit; ortholog of Tcp1p; expression reduced after exposure to farnesol |
| AN4388 | Putative ubiquinol-cytochrome-c reductase subunit with a predicted role in energy metabolism |
| AN1246 | pgkA. Putative phosphoglycerate kinase with a predicted role in gluconeogenesis and glycolysis; intracellular, menadione stress-induced protein; promoter activity is greater on gluconeogenic than on glycolytic carbon sources |
| AN1095 | Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit, nucleolus localization |
| AN10417 | Ortholog(s) have chromatin binding, mRNA binding, translation regulator activity, nucleic acid binding activity |
| AN4222 | Ortholog(s) have cytosolic large ribosomal subunit, nucleus, small-subunit processome localization |
| AN4667 | aspA. Septin, involved in development; prevents formation of inappropriate germ tubes and branches; required for formation of normal conidiophores; protein induced by farnesol |
| AN3466 | kgdB. Putative dihydrolipoamide S-succinyl transferase with a predicted role in the TCA cycle |
| AN4430 | Small subunit of acetolactate synthase involved in branched-chain amino acid biosynthesis under hypoxic conditions |
| AN2867 | pgmB. Putative phosphoglucomutase with a predicted role in carbohydrate metabolism; intracellular; protein abundance decreased by menadione stress; transcript levels increase during asexual development |
| AN4494 | Ortholog(s) have cytosolic large ribosomal subunit, hyphal cell wall, mitochondrion, nucleus localization |
| AN1990 | Putative homocitrate synthase with a predicted role in pyruvate metabolism |
| AN8021 | vmaA. Putative vacuolar ATPase (V-ATPase), subunit A; required for normal growth and conidiation; mutation confers resistance to concanamycin; mutant fails to grow at alkaline pH; protein induced by farnesol |
| AN2904 | Putative 26S proteasome regulatory subunit; ortholog of Rpt3p |
| AN5907 | Putative ribose-5-phosphate isomerase; intracellular, menadione stress-induced protein |
| AN0354 | aroG. Putative 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase with a predicted role in aromatic amino acid family biosynthesis; protein expressed at increased levels in a hapX mutant versus wild-type; feedback-inhibited by phenylalanine |
| AN4163 | cpcB. Protein with seven WD repeats, involved in cross-pathway control of the response to amino acid starvation; required for sexual development; palA-dependent expression independent of pH; protein induced by farnesol |
| AN5482 | Ran. Putative Ran GTPase, GTP binding protein; protein abundance decreased by menadione stress; palA-dependent expression independent of pH |
| AN4060 | rps16. Putative ribosomal protein S16 |
| AN3744 | Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization |
| AN5670 | Ortholog(s) have role in mitochondrial respiratory chain complex I assembly and mitochondrial membrane localization |
| AN7721 | Putative translocon, alpha subunit; ortholog of Sec61p |
| AN0443 | Putative zinc containing alcohol dehydrogenase; protein expressed at decreased levels in a hapX mutant versus wild-type |
| AN9407 | fasA. Fatty acid synthase, alpha subunit; multifunctional enzyme with a predicted role in cytosolic fatty acid biosynthesis |
| AN1904 | Ortholog(s) have chaperonin-containing T-complex localization |
| AN1007 | niiA. Putative nitrite reductase with a predicted role in nitrogen metabolism; transcript stabilized by intracellular nitrate |
| AN2080 | Ortholog(s) have translation release factor activity, role in cytoplasmic translational termination and cytosolic ribosome, translation release factor complex localization |
| AN6202 | rpl3. Putative ribosomal protein L3 |
| AN6689 | Ortholog(s) have structural constituent of nuclear pore activity |
| AN8698 | Ortholog(s) have structural molecule activity and role in Arp2/3 complex-mediated actin nucleation, actin cortical patch assembly, cellular response to drug, spore germination |
| AN6037 | swoM. Putative glucose-6-phosphate isomerase with a predicted role in gluconeogenesis and glycolysis; mutant defective in hyphal polarity and conidiation |
| AN6010 | sgdE. Hsp70-family protein; required for conidial germination; protein expressed at increased levels during osmoadaptation |
| AN2731 | Ortholog(s) have ATPase activator activity, unfolded protein binding activity |
| AN10164 | Ortholog(s) have mRNA binding, poly(U) RNA binding activity and role in nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, regulation of mRNA stability, stress granule assembly |
| AN4376 | gdhA. Putative NADP-linked glutamate dehydrogenase; predicted role in glutamate/glutamine metabolism; involved in nitrogen catabolite repression; induced by low nitrate; intracellular, menadione stress-induced protein; protein induced by farnesol |
| AN8870 | Expression increased in salt-adapted strains |
| AN1084 | Putative elongation factor EF-Tu; intracellular, menadione stress-induced protein |
| AN3134 | Ortholog(s) have role in cellular response to drug and chaperonin-containing T-complex, nucleus localization |
| AN3413 | Protein with homology to ribosomal protein S2 and S5; ortholog of Rps2p; expression reduced after exposure to farnesol |
| AN4594 | Ortholog(s) have mRNA binding activity, role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytosolic small ribosomal subunit, hyphal cell wall, yeast-form cell wall localization |
| AN8863 | Nap/SET family protein; putative nucleosome assembly protein; transcript upregulated in response to camptothecin; protein induced by farnesol |
| AN8216 | swoH. Putative nucleoside diphosphate kinase with a predicted role in phospholipid metabolism; required for normal hyphal growth and conidiation; mutants display increased hyphal cell lysis; transcript upregulated in response to camptothecin |
| AN6525 | aciA. Putative formate dehydrogenase with a predicted role in oxalic acid metabolism; intracellular; protein abundance decreased by menadione stress; inducible by acetate; expression reduced after exposure to farnesol |
| AN7725 | pyroA. Protein required for biosynthesis of pyridoxine; highly conserved throughout fungi, plants and bacteria |
| AN9403 | pdhC. Putative pyruvate dehydrogenase (lipoamide) with a predicted role in pyruvate metabolism |
| AN4192 | Ortholog(s) have cytosol localization |
| AN0411 | Putative GTPase with a predicted role in ER to Golgi transport |
| AN2436 | aclB. Putative ATP citrate synthase with a predicted role in TCA intermediate metabolism; transcript downregulated upon shift from glucose to ethanol and after exposure to farnesol |
| AN2295 | Putative succinate-CoA ligase (GDP-forming) with a predicted role in the TCA cycle |
| AN2316 | Putative cytochrome c oxidase subunit with a predicted role in energy metabolism |
| AN4888 | pdcA. Putative pyruvate decarboxylase with a predicted role in pyruvate metabolism or penicillin biosynthesis; intracellular; protein abundance decreased by menadione stress |
| AN7107 | Ortholog(s) have cell surface, nucleolus localization |
| AN6083 | Ortholog(s) have role in ribosomal large subunit assembly, translational termination and cell surface, cytosolic large ribosomal subunit localization |
| AN11008 | Ortholog(s) have drug binding, squalene monooxygenase activity |
| AN2917 | Ortholog(s) have role in positive regulation of RNA polymerase II transcriptional preinitiation complex assembly, positive regulation of protein catabolic process and proteasome regulatory particle assembly. |
| AN2275 | Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleus, preribosome, large subunit precursor localization |
| AN8722 | sub2. Putative ATP-dependent RNA helicase; PalA-dependent expression independent of pH |
| AN12478 | IMP dehydrogenase/GMP reductase; expression reduced after exposure to farnesol |
| AN0840 | Putative alpha-isopropylmalate synthase with a predicted role in valine, leucine, and isoleucine metabolism |
| AN4250 | Ortholog(s) have organic acid transmembrane transporter activity, role in mitochondrial transport and fungal-type vacuole, mitochondrion localization |
| AN5716 | Putative inosine-5'-monophosphate dehydrogenase with a predicted role in purine metabolism |
| AN2140 | Ortholog(s) have plasma membrane localization |
| AN5954 | Protein with reduced expression after exposure to farnesol |
| AN1182 | benA. Beta-tubulin, highly conserved component of microtubules; <I>A. nidulans</I> has two beta-tubulin genes, benA and tubC; temperature sensitive mutants are blocked in mitosis and in nuclear division |
| AN0570 | Ortholog(s) have RNA binding, structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus, yeast-form cell wall localization |
| AN1964 | Ortholog of RPS6B and RPS6A; palA-dependent expression independent of pH |
| AN8275 | citA. Mitochondrial citrate synthase with a predicted role in the TCA cycle |
| AN4947 | Ortholog(s) have endoplasmic reticulum, plasma membrane localization |
| AN6700 | Ortholog(s) have cytosol localization |
| AN4997 | Ortholog(s) have phosphatidylcholine transporter activity, phosphatidylinositol transporter activity |
| AN5589 | Putative glycerol kinase with a predicted role in glycerol metabolism; required for growth on glycerol; transcript upregulated by growth in glycerol |
| AN9465 | Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleus localization |
| AN2435 | aclA. Putative ATP citrate synthase with a predicted role in TCA intermediate metabolism; transcript downregulated upon shift from glucose to ethanol and after exposure to farnesol; protein induced by farnesol |
| AN6563 | Putative translation elongation factor EF-1 gamma; ortholog of Cam1p; expression reduced after exposure to farnesol |
| AN2997 | Ortholog(s) have sequence-specific DNA binding activity and role in cellular response to drug, cellular response to osmotic stress, cytoplasmic translational initiation |
| AN7570 | tubB. Alpha-tubulin, forms a heterodimer with beta-tubulin that promotes microtubule assembly; non-essential subunit required for meiosis and formation of ascospores |
| AN3814 | cypA. Putative peptidyl-prolyl cis-trans isomerase (PPIase); cyclophilin |
| AN3716 |  |
| AN6636 | Ortholog(s) have role in reciprocal meiotic recombination and cytosol, endoplasmic reticulum, nucleus localization |
| AN5441 | Ortholog(s) have role in endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), rRNA export from nucleus |
| AN1534 | Putative F1F0-ATPase complex subunit with a predicted role in energy metabolism |
| AN4202 | rpl16a. Predicted ribosomal protein of the large (60S) ribosomal subunit; differentially expressed during sexual development |
| AN4802 | 60S ribosomal protein L21; ortholog of Rpl21Ap; expression reduced after exposure to farnesol |
| AN5778 | Ortholog(s) have role in Arp2/3 complex-mediated actin nucleation, cellular response to biotic stimulus and cellular response to starvation. |
| AN3748 | Putative ATP phosphoribosyltransferase with a predicted role in histidine metabolism |
| AN2150 | Prolyl-tRNA synthetase; protein induced by farnesol |
| AN4775 | Ortholog(s) have role in cullin deneddylation, positive regulation of mitotic metaphase/anaphase transition, proteasome-mediated ubiquitin-dependent protein catabolic process |
| AN4803 | Ortholog(s) have rRNA binding, structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), positive regulation of translational fidelity |
| AN5895 | gdiA. Putative Rab GDP-dissociation inhibitor; ortholog of Gdi1p |
| AN5960 | Ortholog(s) have mRNA binding activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), ribosomal small subunit assembly |
| AN4259 | Ortholog(s) have role in cytoplasmic translational initiation and cytosol, eukaryotic 43S preinitiation complex, eukaryotic translation initiation factor 3 complex, nucleus localization |
| AN7299 | Ortholog(s) have DNA binding activity and cytosol, nucleus localization |
| AN3223 | pfkA. Putative 6-phosphofructokinase with a predicted role in gluconeogenesis and glycolysis; upregulated under hypoxic growth conditions |
| AN4462 | pycA. Putative pyruvate carboxylase or glutathione synthase |
| AN0075 | tigA. Putative protein disulfide isomerase |
| AN5912 | arlA. Predicted ADP ribosylation factor GTPase |
| AN1396 | Putative FAD dependent glycerol 3-phosphate dehydrogenase with a predicted role in glycerol metabolism; transcript upregulated by growth in glycerol and after exposure to farnesol; protein induced by farnesol |
| AN4916 | Ortholog(s) have role in ribosome biogenesis and cell surface, cytosol, nucleolus, small-subunit processome localization |
| AN1345 | Ortholog(s) have structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), regulation of translational fidelity |
| AN1993 | Putative aspartate transaminase with a predicted role in alanine, aspartate, and aromatic amino acid metabolism |
| AN2260 | Predicted NADH-ubiquinone oxidoreductase subunit |
| AN4777 | Ortholog(s) have structural constituent of ribosome activity |
| AN2208 | Putative galactose 1-dehydrogenase with a predicted role in galactonic acid and galactonate metabolism; NAD binding Rossmann fold oxidoreductase; intracellular, menadione stress-induced protein |
| AN1965 | prs2. Putative ribose-phosphate pyrophosphokinase with a predicted role in histidine metabolism; interacts with prs1 and prs3 |
| AN6838 | tubC. Beta-tubulin, highly conserved component of microtubules; A. nidulans has two beta-tubulin genes, tubC and benA; expression of tubC increases during conidiation |
| AN8009 | nmt1. Ortholog of nmt1 and THI13; repressed by starvation-induced autophagy; this locus is reported to contain an upstream open reading frame (uORF) |
| AN2306 | Putative ubiquinol-cytochrome-c reductase subunit with a predicted role in energy metabolism; intracellular, menadione stress-induced protein |
| AN1380 | Ortholog(s) have cytosol localization |
| AN1270 | Putative translation initiation factor 3, subunit h (eIF-3h); expression reduced after exposure to farnesol |
| AN3954 | Putative phosphogluconate dehydrogenase (decarboxylating) with a predicted role in the pentose-phosphate shunt |
| AN10223 | Putative 1-Cys peroxiredoxin; intracellular; protein abundance decreased by menadione stress; expression reduced after exposure to farnesol |
| AN4501 | artA. Putative 14-3-3 protein; induced by carbon starvation-induced autophagy |
| AN4794 | Putative ribosomal protein; expression increased in salt-adapted strains |
| AN5800 | Ortholog(s) have cytosol localization |
| AN2980 | Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization |
| AN1150 | Putative transaminase with a predicted role in arginine metabolism |
| AN4695 | hexA. Putative Woronin body protein; HapX-regulated gene; protein induced by farnesol |
| AN6515 | Ortholog(s) have role in posttranslational protein targeting to membrane, protein insertion into ER membrane and TRC complex, nucleus localization |
| AN4492 | Ortholog(s) have ubiquitin-specific protease activity and role in mitochondrial fission, peroxisome fission, proteasome storage granule assembly, proteasome-mediated ubiquitin-dependent protein catabolic process, protein deubiquitination |
| AN0922 | Ortholog(s) have role in ER to Golgi vesicle-mediated transport, Golgi inheritance, Golgi localization, retrograde vesicle-mediated transport, Golgi to ER and COPI vesicle coat localization |
| AN5744 | Putative 14-3-3-like protein; transcript upregulated in response to camptothecin |
| AN7350 | Has domain(s) with predicted nucleic acid binding, nucleotide binding activity |
| AN1954 | Ortholog(s) have mitochondrial ribosome localization |
| AN9094 | ungA. Putative UDP-N-acetylglucosamine pyrophosphorylase with a predicted role in chitin biosynthesis; menadione stress-induced protein; repressed by and starvation- and rapamycin-induced autophagy |
| AN4475 | Ortholog(s) have role in ribosomal large subunit assembly and cytosolic large ribosomal subunit localization |
| AN5746 | acuN. Putative phosphopyruvate hydratase with a predicted role in gluconeogenesis and glycolysis; intracellular; protein abundance decreased by menadione stress; protein induced by farnesol |
| AN9097 | Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytosol, mitochondrion, nucleolus localization |
| AN5740 | rhoA. Protein with similarity to Saccharomyces cerevisiae Rho family GTPase Rho1p; involved in polar growth, hyphal branching, and cell wall synthesis |
| AN6631 | Putative F1F0-ATPase complex subunit with a predicted role in energy metabolism; protein expressed at increased levels in a hapX mutant versus wild-type |
| AN2526 | Putative ketol-acid reductoisomerase with a predicted role in Coenzyme A and pantothenate biosynthesis or amino acid metabolism |
| AN5701 | aroF. Putative 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase with a predicted role in aromatic amino acid biosynthesis; feedback-inhibited by tyrosine |
| AN0316 | tubA. Alpha-tubulin, forms a heterodimer with beta-tubulin that promotes microtubule assembly |
| AN8979 | alcA. Alcohol dehydrogenase with a role in two-carbon compound metabolism; expression is negatively regulated by glucose; transcript upregulated by exposure to ethanol; protein levels decrease in response to farnesol |
| AN0252 | Putative F1F0-ATPase complex gamma subunit with a predicted role in energy metabolism; expression reduced after exposure to farnesol |
| AN10296 | Ortholog(s) have fumarate reductase (NADH) activity, role in cellular response to anoxia and cytosol, mitochondrion, plasma membrane, ribosome localization |
| AN1394 | aspD. Putative septin |
| AN9148 | galF. Putative UTP-glucose-1-phosphate uridylyltransferase with a predicted role in galactose and galactitol metabolism; protein expressed at decreased levels in a hapX mutant versus wild-type |
| AN11411 | Ortholog(s) have structural constituent of ribosome activity and cytosolic small ribosomal subunit, nucleus, yeast-form cell wall localization |
| AN8016 | fal1. Putative ATP-dependent RNA helicase; expression reduced after exposure to farnesol |
| AN7143 | Ortholog(s) have cytosol localization |
| AN4956 | Large subunit of acetolactate synthase involved in branched-chain amino acid biosynthesis under hypoxic conditions |
| AN4522 | Ortholog(s) have cytosolic large ribosomal subunit localization |
| AN1003 | Putative isocitrate dehydrogenase (NAD+) with a predicted role in the TCA cycle; intracellular, menadione stress-induced protein |
| AN6232 | vmaB. Putative F1F0-ATPase complex subunit with a predicted role in energy metabolism |
| AN0686 | Ortholog(s) have role in inner mitochondrial membrane organization, mitochondrion inheritance, mitochondrion morphogenesis, negative regulation of proteolysis, protein folding, replicative cell aging |
| AN7699 | Ortholog(s) have mitochondrial ribosome localization |
| AN8283 | cyp51B. Putative sterol 14-demethylase with a predicted role in sterol metabolism; putative cytochrome P450 |
| AN2210 | Probable ABC-transporter; transcript upregulated in response to camptothecin |
| AN5591 | Putative aminotransferase; protein expressed at decreased levels in a hapX mutant versus wild-type |
| AN8704 | 60S ribosomal protein L24a; PalA-dependent expression independent of pH |
| AN4080 | Ortholog(s) have GTP binding activity, role in cytoplasmic translation, filamentous growth and cytosol, nucleus, polysomal ribosome, polysome localization |
| AN1013 | Putative 60S ribosomal protein L5; ortholog of Rpl5p which is an RNA binding protein with a role in ribosomal large subunit assembly |
| AN7659 | Ortholog(s) have RNA helicase activity, RNA-dependent ATPase activity, inositol hexakisphosphate binding activity and role in mRNA export from nucleus, translational termination |
| AN1281 | Ortholog(s) have chaperone binding, protein binding, bridging activity, role in protein import into mitochondrial matrix and plasma membrane, presequence translocase-associated import motor localization |
| AN7254 | Protein with a conserved CDC48, cell division protein N-terminal domain and two ATPase domains of the AAA-superfamily; protein expressed at increased levels during osmoadaptation; protein induced by farnesol |
| AN4546 | Ortholog(s) have mRNA 3'-UTR AU-rich region binding activity, role in 3'-UTR-mediated mRNA stabilization, negative regulation of MAPK cascade and cytosol localization |
| AN2998 | Putative multifunctional enzyme with a predicted role in one-carbon metabolism; palA-dependent expression independent of pH |
| AN9297 | Has domain(s) with predicted FAD binding, oleate hydratase activity and role in fatty acid metabolic process |
| AN2907 | Ortholog(s) have role in cellular protein localization, eukaryotic translation initiation factor 3 complex assembly, positive regulation of proteasomal ubiquitin-dependent protein catabolic process |
| AN4452 | Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization |
| AN2977 | Putative transporter with a predicted role in small molecule transport; putative mitochondrial phosphate carrier protein; expression upregulated after exposure to farnesol |
| AN2916 | Putative succinate dehydrogenase with a predicted role in the TCA cycle |
| AN5586 | Putative mannose-1-phosphate guanylyltransferase with a predicted role in mannose/mannitol, fructose, and sorbose/sorbitol metabolism |
| AN6209 | Putative 5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole lyase with a predicted role in purine metabolism; adenylosuccinate lyase; expression reduced after exposure to farnesol |
| AN1263 | Putative adenosylhomocysteinase with a predicted role in methionine metabolism; expression reduced after exposure to farnesol |
| AN12246 | Ortholog(s) have cytosolic large ribosomal subunit localization |
| AN10901 | Ortholog(s) have glycine dehydrogenase (decarboxylating) activity, role in glycine decarboxylation via glycine cleavage system, one-carbon metabolic process and mitochondrion localization |
| AN5222 | Ortholog(s) have structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), ribosomal small subunit assembly |
| AN5132 | Ortholog(s) have guanine nucleotide transmembrane transporter activity and role in cellular iron ion homeostasis, guanine nucleotide transport, mitochondrial genome maintenance, transmembrane transport |
| AN5979 | Ortholog(s) have role in ribosomal small subunit assembly and cytosol localization |
| AN1122 | Ortholog(s) have cytosolic large ribosomal subunit, preribosome, large subunit precursor localization |
| AN12473 | hscA. Putative heat shock protein |
| AN6207 | pkpC. Putative protein kinase; reduced growth on AVICEL medium |
| AN1913 | Putative lysyl-tRNA synthetase with a predicted role in lysine metabolism |
| AN0776 | Ortholog(s) have structural constituent of ribosome activity, role in cellular response to drug, cytoplasmic translation and cell surface, cytosolic large ribosomal subunit localization |
| AN8269 | hsp90. 90 kilodalton heat shock protein; physically associates with importin-alpha, KapA; palA-dependent expression independent of pH |
| AN6629 | Putative ribosomal protein L14; ortholog of Rpl14Ap; expression reduced after exposure to farnesol |
| AN9090 | rrmA. RNA binding protein involved in regulation of arginine catabolism; controls stability of mRNAs in response to nitrogen sources and oxidative stress |
| AN3019 | Ortholog(s) have role in proteasome-mediated ubiquitin-dependent protein catabolic process and CENP-A containing chromatin, nucleus, proteasome regulatory particle, lid subcomplex, proteasome storage granule localization |
| AN2875 | fbaA. Putative fructose-bisphosphate aldolase with a predicted role in gluconeogenesis and glycolysis; intracellular, menadione stress-induced protein; palA-dependent expression independent of pH |
| AN6505 | rcoA. WD40 repeat protein; required for sexual development and for sterigmatocystin production; experimentally studied orthologs present in Neurospora crassa, Candida albicans, Schizosaccharomyces pombe and Penicillium marneffei |
| AN8041 | gpdA. Glyceraldehyde-3-phosphate dehydrogenase with a predicted role in gluconeogenesis and glycolysis; the gpdA promoter is a commonly used regulatory sequence for driving constitutive heterologous gene expression |
| AN5713 | cct7. Putative chaperonin complex component, TCP-1 eta subunit; ortholog of Cct7p; expression reduced after exposure to farnesol |
| AN6708 | pdhA. Putative dihydrolipoamide S-acetyltransferase with a predicted role in pyruvate metabolism |
| AN6267 | Ortholog(s) have role in negative regulation of G0 to G1 transition |
| AN10257 | Ortholog(s) have mRNA binding activity, role in telomere maintenance and cytoplasm, nucleus localization |
| AN0262 | Ortholog(s) have role in ribosomal large subunit assembly and cytosolic large ribosomal subunit, nucleolus, preribosome, large subunit precursor localization |
| AN10526 | rmtA. Arginine methyltransferase |
| AN6639 | mcdB. Putative 2-methylcitrate dehydratase with a predicted role in lysine metabolism |
| AN10557 | Putative ATP-dependent RNA helicase; protein levels decrease in response to farnesol |
| AN5975 | Putative mannitol-1-phosphate 5-dehydrogenase with a predicted role in mannose/mannitol, fructose, and sorbose/sorbitol metabolism; expression upregulated after exposure to farnesol |
| AN6048 | Putative aspartate transaminase with a predicted role in amino acid metabolism; palA-dependent expression independent of pH; induced by carbon starvation-induced autophagy |
| AN5129 | hsp70. 70 kilodalton heat shock protein; protein abundance decreased by menadione stress; physically associates with importin-alpha, KapA; palA-dependent expression independent of pH; protein induced by farnesol |
| AN6168 | maeA. Putative malate dehydrogenase with a predicted role in oxidation of malate to pyruvate |
| AN5122 | Putative kinase with a predicted role in nucleotide salvage pathways |
| AN6499 | mdhC. Putative malate dehydrogenase with a predicted role in the methylglyoxal bypass or the TCA cycle; intracellular; protein abundance decreased by menadione stress |
| AN1523 | Putative F1F0-ATPase complex subunit with a predicted role in energy metabolism |
| AN12465 | Ortholog(s) have role in cellular response to biotic stimulus, filamentous growth of a population of unicellular organisms in response to biotic stimulus and mitochondrion localization |
| AN7430 | hisHF. Putative glutamine amidotransferase with a predicted role in histidine metabolism |
| AN1256 | Ortholog(s) have cytosol localization |
| AN4470 | Ortholog(s) have GTP binding, tRNA binding, translation initiation factor activity, translation initiation factor binding activity |
| AN3626 | Putative phosphoribosylamino-imidazole-carboxylase with a predicted role in purine metabolism |
| AN5626 | facA. Acetyl-CoA synthase, required for utilization of acetate as a carbon source; transcriptional induction by acetate is mediated by FacB; carbon catabolite repression is mediated by CreA |
| AN5134 | gltA. Glutamate synthase, NAD(+)-dependent (GOGAT) with a predicted role in glutamate and glutamine metabolism; required for ammonium uptake in the absence of NADP-glutamate dehydrogenase GdhA; transcript upregulated by nitrate limitation |
| AN4064 | Putative ADP/ATP carrier protein with a predicted role in energy metabolism; palA-dependent expression independent of pH |
| AN0651 | fadA. Alpha subunit of a heterotrimeric G protein composed of FadA, SfaD, GpgA and involved in regulation of proliferation and conidiophore development; mutant produces increased amounts of extracellular proteinase during carbon starvation |
| AN2734 | Ortholog(s) have large ribosomal subunit rRNA binding, structural constituent of ribosome activity and role in cytoplasmic translation, ribosomal large subunit assembly |
| AN8707 | Putative fumarate dehydratase with a predicted role in the TCA cycle |
| AN6330 | Putative elongation factor 2; intracellular; protein abundance decreased by menadione stress |
| AN2918 | cct4. Putative chaperonin complex component, TCP-1 delta subunit; ortholog of Cct4p; expression reduced after exposure to farnesol |
| AN0445 | Ortholog(s) have RNA binding, structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization |
| AN1162 | Ortholog(s) have guanyl-nucleotide exchange factor activity, translation elongation factor activity |
| AN8605 | cyp1. Putative peptidyl-prolyl cis-trans isomerase (PPIase); cyclophilin |
| AN5629 | Putative NADH dehydrogenase (ubiquinone) with a predicted role in energy metabolism |
| AN7169 | fhbA. NirA-dependent flavohemoprotein; required for nitrate and nitrite reductase enzyme activity, regulates sexual development; menadione stress-induced protein; induced by nitrate; palA-dependent, pH-independent expression |
| AN6014 | faaA. Putative long-chain-fatty-acid-CoA ligase with a predicted role in fatty acid metabolism |
| AN0046 | Putative histidyl-tRNA synthetase with a predicted role in tRNA aminoacylation; intracellular, menadione stress-induced protein; expression reduced after exposure to farnesol |
| AN5206 | lysB. Putative homoisocitrate dehydrogenase with a predicted role in lysine metabolism |
| AN7003 | Ortholog(s) have cell surface, cytosolic large ribosomal subunit localization |
| AN6679 | Ortholog(s) have small ribosomal subunit rRNA binding, structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) |
| AN2142 | kapA. Karyopherin (importin) alpha, involved in protein import into nucleus |
| AN2414 | Putative NADH dehydrogenase (ubiquinone) with a predicted role in energy metabolism |
| AN1883 | Putative argininosuccinate synthase with a predicted role in arginine metabolism; intracellular; protein abundance decreased by menadione stress |
| AN6082 | Ortholog(s) have pre-mRNA 5'-splice site binding, structural constituent of ribosome activity, role in negative regulation of mRNA splicing, via spliceosome, rRNA processing and cytosolic large ribosomal subunit localization |
| AN6653 | acuE. Malate synthase, required for utilization of acetate as carbon source; transcription induction by acetate mediated by FacB; carbon catabolite repression mediated by CreA; transcription induction by long-chain fatty acids mediated by FarA |
| AN6231 | trpB. Tryptophan synthase involved in tryptophan biosynthesis; transcription is regulated by the cross-pathway control of amino acid biosynthesis; repressed by starvation-induced autophagy; protein induced by farnesol |
| AN8346 | Ortholog(s) have FAD binding, sulfide:quinone oxidoreductase activity |
| AN3059 | pgmA. Putative phosphoglycerate mutase with a predicted role in gluconeogenesis and glycolysis; expression upregulated after exposure to farnesol |
| AN2062 | bipA. Putative ER-resident chaperone of the HSP70 family; unfolded-protein response (UPR) target gene; transcript levels increase during the UPR |
| AN10709 | gfaA. Putative glutamine-fructose-6-phosphate transaminase |
| AN4563 | ckiA. Casein kinase I; required for delivery of amino acid transporters to the plasma membrane; mutants arrest as short germings |
| AN3928 | thiF. Putative thiazole synthase, enzyme of the thiamine biosynthesis pathway |
| AN10416 | Putative 60s ribosomal protein similar to subunits L15 and L27; ortholog of RPL28; expression reduced after exposure to farnesol; palA-dependent expression independent of pH |
| AN0870 | Putative transporter with a predicted role in small molecule transport |
| AN4683 | Putative oligosaccharyltransferase beta subunit; ortholog of Wbp1p |
| AN10681 | Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation, regulation of translational fidelity and cytosolic large ribosomal subunit localization |
| AN11565 | Ortholog(s) have proton-transporting ATP synthase activity, rotational mechanism activity and role in ATP synthesis coupled proton transport |
| AN1166 | Ortholog(s) have RNA binding, structural constituent of ribosome activity |
| AN6643 | bioB. Putative biotin synthase with a predicted role in Coenzyme A and pantothenate biosynthesis |
| AN0843 | Ortholog(s) have structural constituent of ribosome activity, role in rRNA export from nucleus and 90S preribosome, cytosolic small ribosomal subunit, membrane, nucleolus localization |
| AN5162 | pdhB. Putative pyruvate dehydrogenase (lipoamide) with a predicted role in pyruvate metabolism |
| AN10182 | Putative translation initiation factor 3, subunit f (eIF-3f); expression reduced after exposure to farnesol |
| AN8182 | aspC. Septin, involved in development; prevents formation of inappropriate germ tubes and branches; required for formation of normal conidiophores |
| AN2279 | Ortholog(s) have role in cellular protein localization, endoplasmic reticulum inheritance, endoplasmic reticulum tubular network organization, nuclear pore complex assembly, vesicle-mediated transport |
| AN4218 | Ortholog(s) have GDP binding, GTP binding, calmodulin binding, translation elongation factor activity and role in cytoplasmic translational elongation, interaction with host, tRNA export from nucleus |
| AN2914 | Putative argininosuccinate lyase with a predicted role in arginine metabolism |
| AN4872 | ubi1. Fusion protein consisting of N-terminal ubiquitin and C-terminal extension protein (CEP) of the small ribosomal subunit; transcript upregulated in response to camptothecin |
| AN5356 | acuH. Putative carnitine transporter; transcriptional induction in response to acetate is mediated by FacB; transcriptional induction in response to long-chain fatty acids is mediated by FarA |
| AN10195 | Ortholog(s) have valine-tRNA ligase activity |
| AN4464 | purH. Putative bifunctional enzyme with a predicted role in purine metabolism; protein expressed at increased levels in a hapX mutant versus wild-type |
| AN10745 | Ortholog(s) have mitochondrion localization |
| AN3459 | Ortholog(s) have metallodipeptidase activity, omega peptidase activity, role in glutathione catabolic process and cytosol, mitochondrion, nucleus, ribosome localization |
| AN7000 | Putative succinate-CoA ligase (ADP-forming) with a predicted role in the TCA cycle |
| AN0433 | Ortholog(s) have cell surface, cytosolic large ribosomal subunit, nucleolus localization |
| AN1922 | Ortholog(s) have structural molecule activity, role in positive regulation of mitotic metaphase/anaphase transition and cytosol, nucleus, proteasome regulatory particle, lid subcomplex localization |
| AN0057 | Ortholog(s) have cytosol localization |
| AN1543 | Putative succinate dehydrogenase |
| AN8770 | Putative bifunctional enzyme with a predicted role in arginine metabolism; putative acetylglutamate kinase |
| AN9468 | Ortholog(s) have role in DNA recombination, maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and 90S preribosome, cytosol localization |
| AN1222 | sasA. Putative S-adenosylmethionine synthetase; predicted role in methionine metabolism; expression reduced after exposure to farnesol; strongly expressed during vegetative growth, downregulated during development in asexual or sexual cultures |
| AN4793 | Putative aspartate semialdehyde dehydrogenase with a predicted role in glycine, serine, and threonine metabolism |
| AN2185 | nucA. Putative homolog of mammalian EndoG and S. cerevisiae Nuc1p; plays no role in cell death, unlike its mammalian ortholog |
| AN10512 | mthA. Putative mitochondrial ketoacyl-CoA thiolase with a role in fatty acid beta-oxidation |
| AN5580 |  |
| AN3112 | ugmA. UDP-galactopyranose mutase, a flavoenzyme that converts UDP-galactopyranose to UDP-galactofuranose, a central enzyme in in galactofuranose biosynthesis; involved in cell wall biogenesis |
| AN5210 | pkiA. Putative pyruvate kinase with a predicted role in gluconeogenesis and glycolysis; intracellular, menadione stress-induced protein |
| AN8277 | cysD. Putative bifunctional enzyme with a predicted role in methionine metabolism; O-acetlylhomoserine (homocysteine synthase) |
| AN5715 | Putative 40s ribosomal protein S26; ortholog of Rps26Bp which has role in rRNA export from nucleus; expression reduced after exposure to farnesol |
| AN6688 | aspB. Putative septin B; localizes to septa during early septum formation and to branch points during vegetative growth; localizes to the vesicle/metula, the metula/phialide and the phialide/conidium interfaces during conidiophore development |
| AN4159 | glnA. Putative glutamate-ammonia ligase with a predicted role in glutamate and glutamine metabolism; intracellular; transcript upregulated by nitrate limitation; protein abundance decreased by menadione stress and induced by farnesol |
| AN11125 | Ortholog(s) have glycine-tRNA ligase activity, role in DNA-templated transcription, termination, mitochondrial glycyl-tRNA aminoacylation and cytosol, mitochondrion localization |
| AN2873 | lysA. Putative saccharopine dehydrogenase (NAD+, L-lysine-forming) with a predicted role in lysine metabolism |
| AN2120 | kapJ. Putative karyopherin (importin) beta 3; expression reduced after exposure to farnesol |
| AN3497 | CYP623B2. Putative cytochrome P450 |
| AN10474 | Has domain(s) with predicted tRNA binding activity |
| AN1851 | Ortholog(s) have unfolded protein binding activity |
| AN0747 | Putative ubiquinol-cytochrome-c reductase subunit with a predicted role in energy metabolism; hapX-repressed protein; protein induced by farnesol |
| AN0565 | pyrABCN. Multifunctional enzyme with carbamoyl-phosphate synthase (CPSase) and aspartate carbamoyltransferase (ATCase) activities that catalyze the first two steps in pyrimidine biosynthesis |
| AN10130 | Ortholog(s) have structural constituent of ribosome activity and cytosolic small ribosomal subunit localization |
| AN5799 | Putative gamma-glutamyl phosphate reductase with a predicted role in proline metabolism |
| AN8859 | Putative aspartate kinase with a predicted role in glycine, serine, and threonine metabolism |
| AN8273 | Putative ubiquinol-cytochrome-c reductase subunit with a predicted role in energy metabolism; hapX-repressed; protein levels decrease in response to farnesol |
| AN10475 | Ortholog(s) have cytosol localization |
| AN2964 | pdhX. Putative pyruvate dehydrogenase complex component |
| AN1409 | Putative acetyl-CoA C-acetyltransferase with a predicted role in fatty acid metabolism; intracellular; protein abundance decreased by menadione stress |
| AN5523 | tpsA. Putative alpha,alpha-trehalose-phosphate synthase (UDP-forming) with a role in trehalose biosynthesis; transcriptionally induced during spore germination and exponential growth; required for viability of conidia during prolonged storage |
| AN2932 | Putative eukaryotic initiation factor 4A; expression reduced after exposure to farnesol |
| AN2999 | idpA. Putative isocitrate dehydrogenase (NADP+) with a predicted role in the TCA cycle; regulated by carbon source; alternative transcription start sites specify mitochondrial or cytoplasmic and peroxisomal protein localization |
| AN10440 | Ortholog(s) have membrane, mitochondrion localization |
| AN4727 | ugeA. UDP-glucose 4-epimerase, involved in galactose metabolism; converts UDP-galactose to UDP-glucose; intracellular; protein abundance decreased by menadione stress |
| AN8867 | Ortholog(s) have cytosol localization |
| AN0688 | Putative transketolase with a predicted role in the pentose-phosphate shunt or xylulose metabolism |
| AN4616 | ssz1. Putative 70 kilodalton heat shock protein; protein induced by farnesol |
| AN4000 | fabM. Protein with similarity to poly(A)-binding proteins; overexpression results in increased brlA expression and asexual development; expression reduced after exposure to farnesol |
| AN2332 | Putative succinate dehydrogenase with a predicted role in the TCA cycle |
| AN0554 | aldA. Aldehyde dehydrogenase; possible roles in beta-alanine, acetate, acetaldehyde and ethanol metabolism, methylglyoxal bypass, penicillin biosynthesis; menadione stress-decreased; carbon starvation autophagy-induced; hypoxia upregulated |
| AN6988 | Ortholog(s) have protein domain specific binding activity |
| AN7375 | Has domain(s) with predicted role in lipid biosynthetic process |
| AN6500 | Ortholog(s) have cytosol localization |
| AN0306 | Ortholog(s) have role in Arp2/3 complex-mediated actin nucleation and Arp2/3 protein complex, actin cortical patch, cell division site, cell tip, cytosol, nucleus localization |
| AN5741 | Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit, mitochondrial membrane localization |
| AN5604 | acuG. Putative fructose-bisphosphatase with a predicted role in gluconeogenesis and glycolysis; intracellular; protein abundance decreased by menadione stress; expression upregulated after exposure to farnesol |
| AN6542 | actA. Gamma-actin |
| AN5931 | Putative ATP-dependent RNA helicase; ortholog of Dbp2p; expression reduced after exposure to farnesol |
| AN2272 | Putative kinase with a predicted role in ribose metabolism or nucleotide salvage pathways |
| AN3719 | mpkB. MAP kinase, component of a signaling module SteD-SteC-MkkB-MpkB that controls coordination of development and secondary metabolism; phosphorylates VeA in vitro; mutant has moderate growth defect and arrested sexual development |
| AN4087 | Putative 40S ribosomal protein subunit; ortholog of Rps3p; expression reduced after exposure to farnesol |
| AN0240 | pppA. Putative transaldolase with a predicted role in the pentose-phosphate shunt; intracellular, menadione stress-induced protein; protein induced by farnesol |
| AN5571 | kgdA. Putative oxoglutarate dehydrogenase (lipoamide) with a predicted role in the TCA cycle |
| AN4323 | Putative branched chain amino acid aminotransferase with a predicted role in valine, leucine, and isoleucine metabolism |
| AN4402 | Ortholog(s) have voltage-gated anion channel activity and role in DNA transport, apoptotic process, cell redox homeostasis, ion transport, mitochondrion organization |
| AN7479 | Putative asparaginyl-tRNA synthetase with a predicted role in tRNA charging for translation |
| AN0140 | Protein with a predicted role in actin assembly; similar to Saccharomyces cerevisiae Arp3p |
| AN6089 | Putative 60 kilodalton heat shock protein |
| AN0465 | Ortholog of RPS8A and RPS8B; palA-dependent expression independent of pH |
| AN1059 | facC. Carnitine acetyltransferase, required for utilization of acetate as carbon source; transcriptional induction by acetate is mediated by FacB; carbon catabolite repression is mediated by CreA; predicted role in the carnitine shuttle |
| AN2315 | Putative F1F0-ATPase complex subunit with a predicted role in energy metabolism; expression increased in salt-adapted strains |
| AN4769 | sC. ATP sulfurylase involved in sulfate assimilation; mutants are resistant to selenate |
| AN4281 | rabO. Putative GTPase with a predicted role in transport between cis and medial Golgi compartments |
| AN3416 | ssoA. Similar to syntaxin proteins; SsoA-GFP localizes to the plasma membrane and to the hyphal tip |
| AN3823 | Ortholog(s) have structural constituent of ribosome activity |
| AN2992 | Ortholog(s) have mRNA binding, translation initiation factor activity, translation initiation factor binding activity and role in formation of translation preinitiation complex |
| AN10740 | Ortholog(s) have cell surface, cytosolic large ribosomal subunit, preribosome, large subunit precursor localization |
| AN10220 | ccp1. Putatice cytochrome c peroxidase; intracellular; protein abundance decreased by menadione stress |
| AN3058 | Putative glycine hydroxymethyltransferase with a predicted role in glycine, serine, and threonine metabolism |
| AN8856 | Ortholog(s) have RNA binding activity, role in ribosomal large subunit assembly and cytosolic large ribosomal subunit localization |
| AN3839 | swoF. Putative glycylpeptide N-tetradecanoyltransferase involved in control of polar growth; predicted role in protein, peptide, and amino acid metabolism |
| AN1911 | Putative mannose-1-phosphate guanyltransferase |
| AN2243 | Cpa. Putative carbamoyl-phosphate synthase or aspartate carbamoyltransferase with a predicted role in arginine or pyrimidine metabolism |
| AN0705 | Ortholog(s) have isoleucine-tRNA ligase activity, role in isoleucyl-tRNA aminoacylation and cytosol localization |
| AN4042 | CYP61A1. Putative C-22 sterol desaturase with a predicted role in sterol metabolism; putative cytochrome P450 |
| AN6650 | mcsA. Methylcitrate synthase with a predicted role in the methylcitrate pathway or the TCA cycle; transcript upregulated by exposure to ethanol |
| AN10298 | 3-phosphoserine aminotransferase; intracellular; protein abundance decreased by menadione stress |
| AN2981 | gsdA. Putative glucose 6-phosphate 1-dehydrogenase with a predicted role in the pentose-phosphate shunt; intracellular, menadione stress-induced protein; transcript downregulated by growth in ethanol |
| AN1198 | Putative aminomethyltransferase with a predicted role in glycine, serine, and threonine metabolism |
| AN0357 | Putative ubiquinol-cytochrome-c reductase subunit with a predicted role in energy metabolism |