**Table S3. Putative common-shared interacted proteins by α-actinin and PaxB.**

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| AccessionNumber | Description |
| AN1306 | Protein with similarity to mammalian gelsolin; predicted role in actin filament severing |
| AN1558 | myoA. Putative myosin I; required for secretion and polarized growth |
| AN2126 | Predicted actin capping protein |
| AN2756 | slaB. Predicted actin binding protein with similarity to Saccharomyces cerevisiae Sla2p; essential for conidial germination |
| 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 |
| AN4706 | myoB. Myosin II; required for normal conidiation, septum formation and for correct chitin deposition |
| AN7540 | Ortholog(s) have role in eukaryotic translation initiation factor 3 complex assembly, gamma-tubulin complex localization |
| AN7707 | Protein with similarity to alpha-actinin; predicted role in actin filament bundling |
| 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 |
| AN0066 | Ortholog(s) have isopropylmalate transmembrane transporter activity, malonate(1-) transmembrane transporter activity, oxaloacetate transmembrane transporter activity, sulfate transmembrane transporter activity |
| AN0089 | rabS. Putative small GTPase involved in endosomal maturation and vacuolar biogenesis |
| AN0123 | Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization |
| 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 |
| AN0490 | Putative CTP synthase with a predicted role in pyrimidine metabolism |
| 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 |
| AN10873 | Ortholog(s) have role in protein import into mitochondrial outer membrane and mitochondrial outer membrane localization |
| AN10946 |  |
| 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 |
| 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 |
| 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 |
| AN3674 | Has domain(s) with predicted phospholipid binding activity |
| 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 |
| 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 |
| AN4234 | pcmA. Uncharacterized ORF; Putative phosphoacetylglucosamine mutase with a predicted role in chitin biosynthesis |
| AN4547 | Ortholog(s) have role in establishment or maintenance of cell polarity and cytosol localization |
| AN4688 | ivdA. Putative acyl-coA dehydrogenase |
| AN5452 | Putative splicing factor 3b, subunit 3; locus contains the conserved upstream open reading frame (uORF) AN5452-uORF |
| 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 |
| AN5918 | catC. Putative catalase with a predicted role in gluconic acid and gluconate metabolism |
| AN6077 | Putative NADH dehydrogenase (ubiquinone) with a predicted role in energy metabolism |
| AN6366 | Ortholog(s) have endoplasmic reticulum, plasma membrane localization |
| AN8038 | Has domain(s) with predicted nucleic acid binding, nucleotide binding activity |
| AN8055 | Ortholog(s) have nucleolus localization |
| AN8810 | Ortholog(s) have endoplasmic reticulum localization |
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