**S2 Table. Biofilm vesicle compared to biofilm matrix proteome profile**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Protein Characteristics** | | | | **Quantitative Value**  **(Normalized Total Spectra)1** | |  |
| **Protein Name** | **Gene Name** | **ORF Number** | **UniProt ID** | **Biofilm EVs** | **Extracellular matrix** | **Biofilm/Planktonic**  **Ratio** |
| Beta-hexosaminidase | HEX1 | CAALFM\_C503610WA | A0A1D8PNR7 | 50.95 | 0.00 | EV unique |
| Gca2p | GCA2 | CAALFM\_C110550CA | A0A1D8PEW1 | 49.09 | 0.00 | EV unique |
| Putative glucan endo-1\3-beta-D-glucosidase | SCW11 | CAALFM\_C504110WA | A0A1D8PNW1 | 35.85 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C209800CA | Q59YF6 | 18.96 | 0.00 | EV unique |
| Predicted GPI-anchored protein 45 | PGA45 | CAALFM\_C105960WA | Q5AA33 | 17.04 | 0.00 | EV unique |
| Predicted GPI-anchored protein 17 | PGA17 | CAALFM\_C203350WA | A0A1D8PGU3 | 16.18 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C210150WA | A0A1D8PIN7 | 15.37 | 0.00 | EV unique |
| Glycolipid 2-alpha-mannosyltransferase 2 | MNT2 | CAALFM\_C301830CA | P46592 | 13.49 | 0.00 | EV unique |
| Beta-mannosyltransferase 6 | BMT6 | CAALFM\_C603160CA | A0A1D8PQ28 | 12.23 | 0.00 | EV unique |
| Alpha-1,2-mannosyltransferase | MNN24 | CAALFM\_C201300CA | Q5AD72 | 11.50 | 0.00 | EV unique |
| Repressed by EFG1 protein 1 | RBE1 | CAALFM\_C114120CA | Q59ZX3 | 9.25 | 0.00 | EV unique |
| Alpha-1,2-mannosyltransferase | MNN26 | CAALFM\_C703600WA | Q59R28 | 9.16 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_CR07460CA | A0A1D8PTI1 | 7.65 | 0.00 | EV unique |
| Chitinase 1 | CHT1 | CAALFM\_CR00180CA | Q5AAH2 | 7.17 | 0.00 | EV unique |
| ADP-ribosylation factor | ARF1 | CAALFM\_CR08700CA | P22274 | 7.04 | 0.00 | EV unique |
| Candidapepsin-2 | SAP2 | CAALFM\_CR07800WA | P0DJ06 | 5.94 | 0.00 | EV unique |
| Glucan 1,4-alpha-glucosidase | SGA1 | CAALFM\_C301320CA | Q5AJ73 | 5.69 | 0.00 | EV unique |
| Candidapepsin-8 | SAP8 | CAALFM\_C302510CA | Q5AEM6 | 5.48 | 0.00 | EV unique |
| Candidapepsin-10 | SAP10 | CAALFM\_C404470WA | Q5A651 | 4.93 | 0.00 | EV unique |
| Phosphatidylglycerol/phosphatidylinositol transfer protein (PG/PI-TP) | NPC2 | CAALFM\_CR01280CA | Q5A8A2 | 4.17 | 0.00 | EV unique |
| Beta-mannosyltransferase 1 | BMT1 | CAALFM\_C307180CA | Q5ADQ9 | 4.01 | 0.00 | EV unique |
| Emp46p | EMP46 | CAALFM\_C105960WA | A0A1D8PTF1 | 3.79 | 0.00 | EV unique |
| Mid1p | MID1 | CAALFM\_C503990WA | A0A1D8PNU4 | 3.47 | 0.00 | EV unique |
| Axl2p | AXL2 | CAALFM\_C404170CA | A0A1D8PM01 | 3.26 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C403480CA | A0A1D8PLU2 | 2.99 | 0.00 | EV unique |
| Acid phosphatase | PHO113 | CAALFM\_CR02180WA | Q59UY6 | 2.94 | 0.00 | EV unique |
| Secreted protein | PRY1 | CAALFM\_C107580CA | Q59PV6 | 2.82 | 0.00 | EV unique |
| Pho114p | PHO114 | CAALFM\_C402070WA | Q5AMR2 | 2.81 | 0.00 | EV unique |
| Beta-mannosyltransferase 8 | BMT8 | CAALFM\_C203600WA | Q5AHD6 | 2.31 | 0.00 | EV unique |
| Alkaline phosphatase | PHO8 | CAALFM\_C110430WA | A0A1D8PEV2 | 2.25 | 0.00 | EV unique |
| Cell wall protein | IFF11 | CAALFM\_C300600WA | Q5A7R7 | 2.20 | 0.00 | EV unique |
| Alpha-1,2-mannosyltransferase | MNN2 | CAALFM\_C110720CA | Q59WF4 | 2.17 | 0.00 | EV unique |
| Cell wall protein | RHD3 | CAALFM\_C404050CA | Q5A5U4 | 2.13 | 0.00 | EV unique |
| Putative alpha-1,3-mannosyltransferase | MNN12 | CAALFM\_C110300WA | Q5APQ8 | 2.12 | 0.00 | EV unique |
| Ldg3p | LDG3 | CAALFM\_C702270WA | A0A1D8PR06 | 2.10 | 0.00 | EV unique |
| Sap99p | SAP99 | CAALFM\_C203670WA | A0A1D8PGZ9 | 2.05 | 0.00 | EV unique |
| mRNA splicing protein |  | CAALFM\_C203880CA | A0A1D8PH20 | 2.04 | 0.00 | EV unique |
| Phosphoserine phosphatase | SER2 | CAALFM\_C202690WA | Q5A0H3 | 1.98 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C503930CA | A0A1D8PNT7 | 1.95 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C210120WA | A0A1D8PIN9 | 1.79 | 0.00 | EV unique |
| Glutathione-disulfide reductase |  | CAALFM\_C501560CA | Q59NQ2 | 1.79 | 0.00 | EV unique |
| Dag7p | DAG7 | CAALFM\_C401010CA | Q5AMF9 | 1.69 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C110170WA | Q5AP78 | 1.54 | 0.00 | EV unique |
| Lip1p | LIP1 | CAALFM\_C109580CA | A0A1D8PER6 | 1.53 | 0.00 | EV unique |
| Probable pathogenesis-related protein |  | CAALFM\_C107040CA | Q5AB49 | 1.44 | 0.00 | EV unique |
| Peptide hydrolase |  | CAALFM\_C105670WA | Q5AA00 | 1.39 | 0.00 | EV unique |
| Translation initiation factor eIF1 | SUI1 | CAALFM\_C504090CA | Q59LQ6 | 1.34 | 0.00 | EV unique |
| Peptidyl-prolyl cis-trans isomerase (PPIase) |  | CAALFM\_C305550CA | A0A1D8PKA6 | 1.06 | 0.00 | EV unique |
| Transcription factor TFIIIC subunit |  | CAALFM\_CR07180WA | A0A1D8PQW6 | 1.05 | 0.00 | EV unique |
| Guanosine-diphosphatase (GDPase) | GDA1 | CAALFM\_C306120CA | Q8TGH6 | 1.04 | 0.00 | EV unique |
| Candidapepsin-7 | SAP7 | CAALFM\_C104870WA | Q59VH7 | 0.99 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C208770CA | Q59Y55 | 0.98 | 0.00 | EV unique |
| Kre5p | KRE5 | CAALFM\_C302960CA | A0A1D8PJN6 | 0.89 | 0.00 | EV unique |
| Ribonuclease T2-like 1-B (RNase T2-like B) | RNY1-B | CAALFM\_C504260WA | Q5AKB1 | 0.82 | 0.00 | EV unique |
| ADP-ribosylation factor GTPase-activating protein | GLO3 | CAALFM\_C300240CA | Q5A7M1 | 0.79 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C104150CA | Q59VP4 | 0.72 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C202000WA | A0A1D8PGG5 | 0.69 | 0.00 | EV unique |
| Anthranilate phosphoribosyltransferase | TRP4 | CAALFM\_C407090CA | A0A1D8PMR2 | 0.64 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C403500CA | A0A1D8PLV4 | 0.59 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C103240WA | A0A1D8PD02 | 0.50 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C204850CA | A0A1D8PH89 | 0.50 | 0.00 | EV unique |
| Co-chaperone | SGT1 | CAALFM\_C209270CA | A0A1D8PIG5 | 0.50 | 0.00 | EV unique |
| Vacuolar protein sorting-associated protein 27 | VPS27 | CAALFM\_C100750CA | Q5ABD9 | 0.48 | 0.00 | EV unique |
| Candidapepsin-3 | SAP3 | CAALFM\_C305230WA | P0CY29 | 0.41 | 0.00 | EV unique |
| Pho112p | PHO112 | CAALFM\_CR02400WA | A0A1D8PS71 | 0.38 | 0.00 | EV unique |
| ATP synthase subunit beta | ATP2 | CAALFM\_C400270WA | A0A1D8PKZ9 | 0.38 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C304650WA | Q5ANH8 | 0.37 | 0.00 | EV unique |
| Tubulin-binding prefolding complex subunit |  | CAALFM\_C111110CA | A0A1D8PF30 | 0.34 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_CR06530WA | A0A1D8PT84 | 0.34 | 0.00 | EV unique |
| Ribonuclease H |  | CAALFM\_C603260WA | A0A1D8PQ43 | 0.33 | 0.00 | EV unique |
| Fmp45p | FMP45 | CAALFM\_C702240WA | A0A1D8PR25 | 0.33 | 0.00 | EV unique |
| F-actin-capping protein subunit alpha | CAP01 | CAALFM\_CR01180WA | A0A1D8PRV7 | 0.33 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C203020CA | Q5A0L2 | 0.29 | 0.00 | EV unique |
| Carboxypeptidase | PRC2 | CAALFM\_C501450WA | A0A1D8PN69 | 0.25 | 0.00 | EV unique |
| mRNA-binding protein | PUF3 | CAALFM\_C405370WA | A0A1D8PMA5 | 0.25 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C702260WA | Q5AH51 | 0.25 | 0.00 | EV unique |
| AMP-activated serine/threonine-protein kinase regulatory subunit | SNF4 | CAALFM\_C603920WA | A0A1D8PQA6 | 0.25 | 0.00 | EV unique |
| Class E vacuolar protein-sorting machinery protein HSE1 | HSE1 | CAALFM\_CR01210CA | Q5A895 | 0.23 | 0.00 | EV unique |
| Cystathionine gamma-lyase | CYS3 | CAALFM\_CR08340WA | Q5A362 | 0.23 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C406130WA | A0A1D8PMG9 | 0.20 | 0.00 | EV unique |
| Putative mannosyltransferase | KTR4 | CAALFM\_C104000CA | Q59QH4 | 0.18 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C209070CA | A0A1D8PIC6 | 0.18 | 0.00 | EV unique |
| Phosphoribomutase |  | CAALFM\_C307490WA | Q5ADV2 | 0.18 | 0.00 | EV unique |
| Bifunctional choline kinase/ethanolamine kinase |  | CAALFM\_C305300CA | A0A1D8PK80 | 0.17 | 0.00 | EV unique |
| Peptidylprolyl isomerase |  | CAALFM\_C113260WA | A0A1D8PFM9 | 0.17 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C400710WA | A0A1D8PL57 | 0.17 | 0.00 | EV unique |
| Glycylpeptide N-tetradecanoyltransferase | NMT1 | CAALFM\_C401440WA | P30418 | 0.17 | 0.00 | EV unique |
| Aldehyde dehydrogenase (NAD(P)(+)) | ALD5 | CAALFM\_C202970CA | A0A1D8PGT5 | 0.17 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C204330CA | Q59TB0 | 0.17 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C100700WA | Q5ABD5 | 0.16 | 0.00 | EV unique |
| Rho family GTPase | CRL1 | CAALFM\_C101420CA | Q5A904 | 0.16 | 0.00 | EV unique |
| 4-nitrophenylphosphatase (PNPPase) | PHO15 | CAALFM\_C107230WA | Q59WC5 | 0.16 | 0.00 | EV unique |
| Pho100p | PHO100 | CAALFM\_C107430WA | Q59WE5 | 0.16 | 0.00 | EV unique |
| Putative GTPase | RHB1 | CAALFM\_C305180WA | Q5ANA9 | 0.16 | 0.00 | EV unique |
| mRNA splicing protein |  | CAALFM\_C503110CA | A0A1D8PNM3 | 0.16 | 0.00 | EV unique |
| Bifunctional AP-4-A phosphorylase/ADP sulfurylase | APA2 | CAALFM\_C603410CA | A0A1D8PQ57 | 0.16 | 0.00 | EV unique |
| DNA-directed RNA polymerases I, II, and III subunit RPABC3 | RPB8 | CAALFM\_CR04780WA | Q59MZ8 | 0.16 | 0.00 | EV unique |
| Vac7p | VAC7 | CAALFM\_C404370CA | Q59PA6 | 0.15 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C108770WA | A0A1D8PEE6 | 0.10 | 0.00 | EV unique |
| Spa2p | SPA2 | CAALFM\_C112620WA | A0A1D8PFH4 | 0.10 | 0.00 | EV unique |
| Nuclear pore protein |  | CAALFM\_C201220WA | A0A1D8PGB0 | 0.10 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C207810WA | Q5A2K5 | 0.10 | 0.00 | EV unique |
| Translation initiation factor eIF4G | TIF4631 | CAALFM\_C208760CA | A0A1D8PI73 | 0.10 | 0.00 | EV unique |
| Imp2'p |  | CAALFM\_C406730CA | Q5A0W0 | 0.10 | 0.00 | EV unique |
| Translation initiation factor eIF-2B subunit epsilon | GCD6 | CAALFM\_C108600CA | P87163 | 0.10 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_CR00230WA | A0A1D8PRM4 | 0.10 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_CR09580CA | A0A1D8PU09 | 0.10 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C104600CA | A0A1D8PDC7 | 0.10 | 0.00 | EV unique |
| Hgt7p | HGT7 | CAALFM\_C201000WA | A0A1D8PG81 | 0.10 | 0.00 | EV unique |
| Acyl-coenzyme A oxidase | PXP2 | CAALFM\_C301930WA | Q5AJD6 | 0.10 | 0.00 | EV unique |
| Myosin 1 | MYO1 | CAALFM\_C501650CA | A0A1D8PN92 | 0.10 | 0.00 | EV unique |
| DNA-directed RNA polymerase subunit beta | RPA135 | CAALFM\_C700570WA | A0A1D8PQM4 | 0.10 | 0.00 | EV unique |
| Trm2p | TRM2 | CAALFM\_C101380CA | A0A1D8PCG3 | 0.08 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C206770WA | A0A1D8PHR2 | 0.08 | 0.00 | EV unique |
| Prb1p | PRB1 | CAALFM\_C206880CA | Q59Z57 | 0.08 | 0.00 | EV unique |
| Putative flavin adenine dinucleotide transporter | FLC1 | CAALFM\_C300980WA | A0A1D8PJ45 | 0.08 | 0.00 | EV unique |
| Skn1p | SKN1 | CAALFM\_C305810CA | A0A1D8PKE1 | 0.08 | 0.00 | EV unique |
| Midasin | MDN1 | CAALFM\_C400970CA | A0A1D8PL61 | 0.08 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C505340WA | A0A1D8PP79 | 0.08 | 0.00 | EV unique |
| Long-chain fatty acid transporter | FAT1 | CAALFM\_C600740WA | Q59NN4 | 0.08 | 0.00 | EV unique |
| Long chronological lifespan protein 2 | LCL2 | CAALFM\_CR05800CA | Q59PT4 | 0.08 | 0.00 | EV unique |
| Nucleosome assembly protein 1 | NAP1 | CAALFM\_CR00320CA | Q5AAI8 | 0.08 | 0.00 | EV unique |
| Fre7p | FRE7 | CAALFM\_CR07290WA | A0A1D8PTG2 | 0.08 | 0.00 | EV unique |
| Glycerophosphodiester transporter GIT2 | GIT2 | CAALFM\_C500890CA | A0A1D8PN12 | 0.08 | 0.00 | EV unique |
| Uncharacterized protein |  | CAALFM\_C105890WA | A0A1D8PDR3 | 88.98 | 0.32 | 275.73 |
| Lysophospholipase | PLB4.5 | CAALFM\_C201380WA | A0A1D8PGF0 | 50.69 | 0.22 | 235.68 |
| Candidapepsin-4 | SAP4 | CAALFM\_C603500CA | Q5A8N2 | 34.28 | 0.32 | 106.23 |
| Endo-1,3(4)-beta-glucanase 1 | ENG1 | CAALFM\_C103680WA | Q5AIR7 | 46.76 | 0.44 | 106.11 |
| Putative aspartic endopeptidase | YPS7 | CAALFM\_C702300WA | Q5AH56 | 31.33 | 0.33 | 95.02 |
| Scw4p | SCW4 | CAALFM\_C102520WA | Q5AIB2 | 10.22 | 0.11 | 95.00 |
| Op4p | OP4 | CAALFM\_C113080WA | A0A1D8PFJ9 | 104.80 | 1.11 | 94.82 |
| Cell wall protein | RBT1 | CAALFM\_C403520CA | Q59TP1 | 79.39 | 1.32 | 60.05 |
| Msb2p | MSB2 | CAALFM\_C201780WA | A0A1D8PGF8 | 44.11 | 0.75 | 58.59 |
| Candidapepsin-6 | SAP6 | CAALFM\_C602710CA | Q5AC08 | 164.74 | 3.02 | 54.51 |
| Candidapepsin-5 | SAP5 | CAALFM\_C603030WA | P43094 | 1361.70 | 31.45 | 43.29 |
| Kexin | KEX2 | CAALFM\_C108990CA | A0A1D8PEG3 | 13.87 | 0.33 | 42.31 |
| Hsp70 family chaperone | LHS1 | CAALFM\_C202760WA | A0A1D8PGU0 | 4.45 | 0.11 | 41.36 |
| Lipase 4 | LIP4 | CAALFM\_C604490WA | Q9P8W1 | 26.53 | 0.66 | 40.46 |
| Cell wall acid trehalase | ATC1 | CAALFM\_C106940CA | Q5AAU5 | 15.92 | 0.44 | 36.14 |
| Glucoamylase 1 | GAM1 | CAALFM\_C110290WA | O74254 | 37.13 | 1.05 | 35.46 |
| Rax2p | RAX2 | CAALFM\_C112510WA | A0A1D8PFE5 | 22.03 | 0.65 | 33.85 |
| Agglutinin-like protein 3 | ALS3 | CAALFM\_CR07070CA | Q59L12 | 354.54 | 10.92 | 32.47 |
| ER oxidoreductin | ERO1 | CAALFM\_C110040WA | A0A1D8PER8 | 8.85 | 0.28 | 31.35 |
| Uncharacterized protein |  | CAALFM\_CR06030CA | A0A1D8PT50 | 16.21 | 0.52 | 30.96 |
| Uncharacterized protein |  | CAALFM\_C405580CA | Q5A470 | 173.17 | 5.62 | 30.84 |
| Dynein light chain |  | CAALFM\_C201440CA | A0A1D8PGE0 | 3.07 | 0.11 | 28.53 |
| Glucan 1,3-beta-glucosidase | BGL2 | CAALFM\_C402250CA | Q5AMT2 | 178.63 | 6.33 | 28.21 |
| Agglutinin-like protein 4 | ALS4 | CAALFM\_C604130CA | A0A1D8PQB9 | 9.01 | 0.33 | 27.19 |
| Agglutinin-like protein 1 | ALS1 | CAALFM\_C603700WA | Q5A8T4 | 26.57 | 1.05 | 25.38 |
| Chitinase 3 | CHT3 | CAALFM\_CR10110WA | P40954 | 27.70 | 1.10 | 25.10 |
| Hyphally regulated cell wall protein 1 | HYR1 | CAALFM\_C113450WA | A0A1D8PFM8 | 296.70 | 12.76 | 23.26 |
| Protein OS-9 homolog | YOS9 | CAALFM\_CR10020CA | Q5ACR4 | 13.34 | 0.62 | 21.69 |
| Het1p | HET1 | CAALFM\_C600100CA | A0A1D8PPA5 | 22.92 | 1.11 | 20.70 |
| Secreted beta-glucosidase | SIM1 | CAALFM\_C113940WA | Q5AKU5 | 35.33 | 1.72 | 20.60 |
| Covalently-linked cell wall protein 14 | SSR1 | CAALFM\_C700860WA | Q5AFN8 | 10.68 | 0.55 | 19.35 |
| Repressed by TUP1 protein 5 | RBT5 | CAALFM\_C400130WA | Q59UT4 | 32.14 | 1.72 | 18.64 |
| Secreted protein | RBT4 | CAALFM\_C107030CA | A0A1D8PDY8 | 89.46 | 4.85 | 18.45 |
| Chitinase 2 | CHT2 | CAALFM\_C504130CA | P40953 | 91.98 | 5.20 | 17.68 |
| Cell surface superoxide dismutase [Cu-Zn] 4 | SOD4 | CAALFM\_C200660CA | Q5AD05 | 1.86 | 0.11 | 16.73 |
| Inosine triphosphate pyrophosphatase | HAM1 | CAALFM\_C503860WA | Q59N80 | 1.59 | 0.11 | 14.80 |
| High osmolarity signaling protein | SHO1 | CAALFM\_C109140CA | Q5AQ36 | 1.48 | 0.11 | 13.74 |
| Peptide hydrolase | APE3 | CAALFM\_C208800CA | A0A1D8PI95 | 2.69 | 0.22 | 12.50 |
| Surface antigen protein 2 | CSA2 | CAALFM\_C406920CA | Q5A0X8 | 15.69 | 1.36 | 11.55 |
| Asm3p | ASM3 | CAALFM\_C100680WA | Q5ABD3 | 41.64 | 3.78 | 11.03 |
| Adh1p | ADH1 | CAALFM\_C505050WA | A0A1D8PP43 | 24.86 | 2.35 | 10.57 |
| Uncharacterized protein |  | CAALFM\_C109670CA | Q5APD5 | 2.17 | 0.22 | 10.07 |
| Uncharacterized protein |  | CAALFM\_C307470WA | A0A1D8PKU6 | 11.26 | 1.19 | 9.47 |
| Glucan 1,3-beta-glucosidase | XOG1 | CAALFM\_C102990CA | P29717 | 38.73 | 4.25 | 9.11 |
| 3-hydroxyanthranilate 3,4-dioxygenase | BNA1 | CAALFM\_CR05440WA | Q59K86 | 1.99 | 0.22 | 9.05 |
| Cell surface GPI-anchored protein | ECM33 | CAALFM\_C502460CA | Q5AGC4 | 0.96 | 0.11 | 8.88 |
| S-(hydroxymethyl)glutathione dehydrogenase | FDH3 | CAALFM\_CR10250CA | A0A1D8PU61 | 4.96 | 0.56 | 8.79 |
| Uncharacterized protein |  | CAALFM\_C703370CA | A0A1D8PRB4 | 1.83 | 0.22 | 8.50 |
| Tos1p | TOS1 | CAALFM\_C301550CA | A0A1D8PJA8 | 111.69 | 14.24 | 7.84 |
| Cell wall mannoprotein | PIR1 | CAALFM\_C208870CA | Q59SF7 | 9.07 | 1.21 | 7.50 |
| Oxysterol-binding protein |  | CAALFM\_C205720CA | A0A1D8PHG1 | 3.96 | 0.57 | 6.94 |
| Aha1p | AHA1 | CAALFM\_CR10270CA | A0A1D8PU72 | 2.71 | 0.39 | 6.86 |
| Uncharacterized protein |  | CAALFM\_C401660WA | A0A1D8PLF7 | 0.73 | 0.11 | 6.59 |
| Fet31p | FET31 | CAALFM\_C600480CA | A0A1D8PPE2 | 6.29 | 0.98 | 6.39 |
| Glycolipid 2-alpha-mannosyltransferase 1 | MNT1 | CAALFM\_C301810CA | Q00310 | 20.71 | 3.32 | 6.24 |
| Pbr1p | PBR1 | CAALFM\_C106370CA | Q5AAN7 | 10.35 | 1.67 | 6.20 |
| Acyl-protein thioesterase 1 |  | CAALFM\_C502400WA | A0A1D8PNF2 | 5.44 | 0.89 | 6.13 |
| Uncharacterized protein |  | CAALFM\_CR09240CA | A0A1D8PTY0 | 9.25 | 1.55 | 5.97 |
| Isopentenyl-diphosphate delta-isomerase | IDI1 | CAALFM\_C402280WA | A0A1D8PLI2 | 10.80 | 1.84 | 5.87 |
| Pheromone-processing carboxypeptidase | KEX1 | CAALFM\_C700940WA | Q5AFP8 | 3.75 | 0.68 | 5.52 |
| pH-regulated antigen | PRA1 | CAALFM\_C406980WA | P87020 | 408.40 | 75.18 | 5.43 |
| Uncharacterized protein |  | CAALFM\_C701710WA | A0A1D8PQW4 | 2.12 | 0.40 | 5.33 |
| Fructose 1,6-bisphosphate 1-phosphatase | FBP1 | CAALFM\_C307830WA | A0A1D8PKW2 | 5.29 | 0.99 | 5.32 |
| Importin-alpha export receptor |  | CAALFM\_C107690CA | A0A1D8PE78 | 3.40 | 0.66 | 5.14 |
| E2 ubiquitin-conjugating protein | UBC4 | CAALFM\_CR09970WA | A0A1D8PU40 | 5.83 | 1.17 | 4.99 |
| Flavodoxin-like fold family protein | PST3 | CAALFM\_CR05390WA | A0A1D8PT02 | 5.36 | 1.09 | 4.90 |
| L-methionine (R)-S-oxide reductase |  | CAALFM\_C602800WA | A0A1D8PPZ9 | 2.05 | 0.44 | 4.70 |
| Nucleoporin |  | CAALFM\_C104200CA | A0A1D8PD79 | 3.71 | 0.79 | 4.69 |
| Phosphatidylinositol 4-phosphate-binding protein | GGA2 | CAALFM\_C103130CA | A0A1D8PCX6 | 1.51 | 0.32 | 4.68 |
| Uncharacterized protein (Fragment) |  | CAALFM\_C100270WA | A0A1D8PC75 | 0.50 | 0.11 | 4.50 |
| Mannan endo-1,6-alpha-mannosidase | DCW1 | CAALFM\_C201360CA | Q5AD78 | 9.66 | 2.16 | 4.48 |
| Cell surface Cu-only superoxide dismutase 5 | SOD5 | CAALFM\_C200680CA | Q5AD07 | 52.36 | 11.94 | 4.39 |
| Cell surface mannoprotein | MP65 | CAALFM\_C210030CA | Q59XX2 | 189.21 | 43.23 | 4.38 |
| Uncharacterized protein |  | CAALFM\_C101300WA | Q5A915 | 1.39 | 0.35 | 3.99 |
| Sortilin | PEP1 | CAALFM\_C112490WA | A0A1D8PFH5 | 11.70 | 2.94 | 3.98 |
| Secreted beta-glucosidase | SUN41 | CAALFM\_C600820WA | Q59NP5 | 176.15 | 44.91 | 3.92 |
| GPI-anchored protein 52 | PGA52 | CAALFM\_C200100CA | Q59L72 | 5.73 | 1.51 | 3.79 |
| SEC14 cytosolic factor (Phosphatidylinositol/phosphatidylcholine transfer protein) (PI/PC TP) | SEC14 | CAALFM\_C500480CA | P46250 | 2.39 | 0.65 | 3.70 |
| Uncharacterized protein |  | CAALFM\_C105630CA | A0A1D8PDL7 | 15.77 | 4.35 | 3.63 |
| Coatomer subunit gamma | SEC21 | CAALFM\_C104830WA | A0A1D8PDE3 | 5.63 | 1.57 | 3.58 |
| Extracellular glycosidase | CRH11 | CAALFM\_C402900CA | Q5AFA2 | 37.77 | 10.68 | 3.54 |
| Lysophospholipase | PLB3 | CAALFM\_CR09690CA | A0A1D8PU17 | 7.78 | 2.21 | 3.52 |
| Coatomer subunit zeta |  | CAALFM\_CR03600CA | Q5A006 | 2.30 | 0.66 | 3.47 |
| 1,3-beta-glucanosyltransferase | PGA4 | CAALFM\_C505390CA | Q5AJY5 | 31.81 | 9.17 | 3.47 |
| Uncharacterized protein |  | CAALFM\_C101910WA | A0A1D8PCL4 | 1.59 | 0.46 | 3.46 |
| Trehalose 6-phosphate synthase/phosphatase complex subunit | TPS3 | CAALFM\_C210690WA | A0A1D8PIS4 | 0.60 | 0.17 | 3.42 |
| RNA-binding protein |  | CAALFM\_C304590WA | A0A1D8PK11 | 1.35 | 0.39 | 3.42 |
| Exportin | CRM1 | CAALFM\_CR00520CA | A0A1D8PRR9 | 9.01 | 2.65 | 3.40 |
| Peptidyl-prolyl cis-trans isomerase (PPIase) | CYP5 | CAALFM\_C306360CA | A0A1D8PKL0 | 10.66 | 3.17 | 3.36 |
| pH-responsive protein 1 | PHR1 | CAALFM\_C404530CA | P43076 | 180.03 | 55.69 | 3.23 |
| Trifunctional fatty acid synthase subunit | FAS2 | CAALFM\_C304830CA | A0A1D8PK65 | 21.03 | 6.54 | 3.21 |
| Uncharacterized protein |  | CAALFM\_C600980CA | A0A1D8PPI4 | 1.02 | 0.33 | 3.13 |
| Arf family GTPase | ARL1 | CAALFM\_C401890CA | Q5AMP3 | 1.18 | 0.39 | 3.03 |
| Protein ROT1 | ROT1 | CAALFM\_C100770CA | Q5ABP8 | 2.31 | 0.77 | 3.00 |
| Coatomer subunit beta' | SEC27 | CAALFM\_C602260CA | A0A1D8PPV5 | 3.67 | 1.23 | 2.98 |
| H(+)-transporting V1 sector ATPase subunit H | VMA13 | CAALFM\_CR05080WA | A0A1D8PSX0 | 6.66 | 2.24 | 2.97 |
| Ecm33p | ECM33 | CAALFM\_C103190CA | A0A1D8PCY4 | 98.54 | 33.20 | 2.97 |
| Spermidine synthase | SPE3 | CAALFM\_C206960WA | Q59Z50 | 3.40 | 1.16 | 2.92 |
| Glutamate-5-semialdehyde dehydrogenase | PRO2 | CAALFM\_C307220CA | Q5ADR2 | 2.09 | 0.74 | 2.83 |
| pH-responsive protein 2 | PHR2 | CAALFM\_C100220WA | O13318 | 4.92 | 1.78 | 2.77 |
| Glucan 1,3-beta-glucosidase 2 | EXG2 | CAALFM\_C102630CA | Q5AIA1 | 16.26 | 5.88 | 2.76 |
| Extracellular glycosidase | UTR2 | CAALFM\_C301730CA | Q5AJC0 | 27.01 | 9.84 | 2.75 |
| Cfl2p | CFL2 | CAALFM\_C405780CA | A0A1D8PME3 | 3.00 | 1.10 | 2.74 |
| Proteasome core particle subunit beta 3 | PUP3 | CAALFM\_C703390CA | A0A1D8PRB6 | 2.71 | 1.00 | 2.72 |
| Ferroxidase | FET34 | CAALFM\_C600440CA | A0A1D8PPC9 | 12.48 | 4.69 | 2.66 |
| Metalloendopeptidase | STE23 | CAALFM\_C602860WA | A0A1D8PQ06 | 4.25 | 1.60 | 2.66 |
| Proteasome endopeptidase complex | PRE6 | CAALFM\_CR04550WA | A0A1D8PSS4 | 3.16 | 1.20 | 2.63 |
| 3-hydroxy-3-methylglutaryl coenzyme A synthase (HMG-CoA synthase) | ERG13 | CAALFM\_CR09160CA | A0A1D8PTW6 | 3.52 | 1.36 | 2.59 |
| Arf family GTPase | ARF2 | CAALFM\_C304950WA | Q5AND9 | 17.05 | 6.68 | 2.55 |
| Putative methyltransferase | HRT2 | CAALFM\_C401690CA | A0A1D8PLC6 | 5.05 | 1.99 | 2.54 |
| Glutathione peroxidase |  | CAALFM\_C600850WA | Q59WW7 | 7.44 | 2.96 | 2.51 |
| Lysophospholipase | PLB5 | CAALFM\_C108230CA | A0A1D8PEB1 | 6.83 | 2.73 | 2.50 |
| Candidapepsin-9 | SAP9 | CAALFM\_C303870CA | Q59SU1 | 13.07 | 5.33 | 2.45 |
| Asparagine synthase (Glutamine-hydrolyzing) 2 | ASN1 | CAALFM\_C209060CA | A0A1D8PIB2 | 2.37 | 0.99 | 2.38 |
| Proteasome core particle subunit beta 6 |  | CAALFM\_C402470CA | A0A1D8PLK1 | 3.38 | 1.44 | 2.35 |
| Alcohol dehydrogenase 2 | ADH2 | CAALFM\_C108330CA | O94038 | 13.27 | 5.72 | 2.32 |
| Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) | DUT1 | CAALFM\_C101330CA | P0CY19 | 0.81 | 0.35 | 2.31 |
| Protein YOP1 |  | CAALFM\_C208160CA | A0A1D8PI76 | 2.06 | 0.90 | 2.28 |
| Transmembrane 9 superfamily member | EMP70 | CAALFM\_C402550CA | Q5AF62 | 0.50 | 0.22 | 2.26 |
| Importin subunit alpha |  | CAALFM\_C500150CA | A0A1D8PMU8 | 0.96 | 0.44 | 2.17 |
| Translation elongation factor EF1B gamma | CAM1 | CAALFM\_C306010WA | A0A1D8PKC3 | 10.65 | 4.98 | 2.14 |
| Uncharacterized protein |  | CAALFM\_C201690WA | Q5ALU6 | 0.98 | 0.46 | 2.13 |
| Extent of cell elongation protein 1 | ECE1 | CAALFM\_C403470CA | Q07730 | 36.47 | 17.31 | 2.11 |
| Rab geranylgeranyltransferase | BET2 | CAALFM\_CR09890CA | A0A1D8PU24 | 0.60 | 0.29 | 2.09 |
| Guanine nucleotide-binding protein subunit beta-like protein (Cytoplasmic antigenic protein 1) | ASC1 | CAALFM\_C701250WA | P83774 | 22.00 | 10.78 | 2.04 |
| ATP-dependent RNA helicase eIF4A | TIF1 | CAALFM\_C101350CA | P87206 | 31.37 | 15.40 | 2.04 |
| Hch1p | HCH1 | CAALFM\_C601860CA | A0A1D8PPR5 | 2.00 | 0.99 | 2.03 |
| Epsin |  | CAALFM\_C201390WA | A0A1D8PGB7 | 0.35 | 0.17 | 2.01 |
| Eukaryotic translation initiation factor 4E (eIF-4E) (eIF4E) | TIF45 | CAALFM\_CR10490WA | Q9P975 | 1.71 | 0.85 | 2.01 |
| Hsp70 family ATPase | KAR2 | CAALFM\_C201120WA | A0A1D8PG96 | 20.06 | 10.01 | 2.00 |
| Profilin | PFY1 | CAALFM\_C108030WA | Q5A786 | 17.01 | 8.66 | 1.96 |
| PRA1 family protein |  | CAALFM\_C106480CA | A0A1D8PDT9 | 1.29 | 0.66 | 1.96 |
| Cell wall protein | PGA31 | CAALFM\_C404080CA | A0A1D8PM04 | 2.30 | 1.18 | 1.96 |
| Orotate phosphoribosyltransferase | URA5 | CAALFM\_CR01650WA | A0A1D8PS11 | 3.97 | 2.10 | 1.89 |
| DNA mismatch repair protein HSM3 | HSM3 | CAALFM\_C703450CA | Q59PP0 | 2.10 | 1.12 | 1.88 |
| RNA export factor | GLE2 | CAALFM\_C604360CA | A0A1D8PQE5 | 0.31 | 0.17 | 1.78 |
| Ribosomal 60S subunit protein L14B | RPL14 | CAALFM\_C113050WA | A0A1D8PFL9 | 3.47 | 1.97 | 1.76 |
| Fum12p | FUM12 | CAALFM\_C307640CA | A0A1D8PKV4 | 4.37 | 2.53 | 1.73 |
| Cofilin | COF1 | CAALFM\_C500370WA | A0A1D8PMW6 | 8.83 | 5.20 | 1.70 |
| 1,3-beta-glucan synthase | GSC1 | CAALFM\_C102420CA | A0A1D8PCT0 | 4.68 | 2.76 | 1.69 |
| Rab GDP dissociation inhibitor | GDI1 | CAALFM\_C114440CA | A0A1D8PFX8 | 5.16 | 3.11 | 1.66 |
| Rho family GTPase | RAC1 | CAALFM\_C106730WA | A0A1D8PDV5 | 1.64 | 0.99 | 1.65 |
| Ribosomal 60S subunit protein L12A | RPL12 | CAALFM\_C302110WA | Q5AJF7 | 6.04 | 3.69 | 1.63 |
| Phosphoglucomutase | PGM2 | CAALFM\_CR02820WA | A0A1D8PSA9 | 20.92 | 12.94 | 1.62 |
| Homocitrate synthase | LYS21 | CAALFM\_C104730CA | Q59VG1 | 5.37 | 3.33 | 1.61 |
| Uncharacterized protein |  | CAALFM\_C202410WA | A0A1D8PGL1 | 1.56 | 0.97 | 1.61 |
| C-8 sterol isomerase | ERG2 | CAALFM\_C100800CA | A0A1D8PCB9 | 0.17 | 0.11 | 1.59 |
| Endoplasmic reticulum vesicle protein 25 | ERV25 | CAALFM\_C306250WA | Q5A302 | 3.26 | 2.05 | 1.59 |
| Phosphoenolpyruvate carboxykinase | PCK1 | CAALFM\_CR00200WA | A0A1D8PRM7 | 12.53 | 7.93 | 1.58 |
| Chorismate synthase | ARO2 | CAALFM\_CR07710WA | A0A1D8PTK1 | 1.33 | 0.85 | 1.57 |
| Cwh41p | CWH41 | CAALFM\_C406100WA | A0A1D8PMH9 | 0.17 | 0.11 | 1.57 |
| Survival factor 1 | SVF1 | CAALFM\_C100400WA | Q5ABA2 | 4.02 | 2.57 | 1.56 |
| 60S ribosomal protein L10a | RPL10A | CAALFM\_C602240CA | Q9UVJ4 | 16.45 | 10.56 | 1.56 |
| Putative phosphoric monoester hydrolase |  | CAALFM\_C207140WA | A0A1D8PHU6 | 2.06 | 1.33 | 1.55 |
| Acetyl-CoA C-acetyltransferase | ERG10 | CAALFM\_C204310WA | A0A1D8PH52 | 7.12 | 4.65 | 1.53 |
| Uncharacterized protein |  | CAALFM\_C209980WA | A0A1D8PIK6 | 0.27 | 0.17 | 1.53 |
| S-adenosylmethionine synthase | SAM2 | CAALFM\_C111450CA | A0A1D8PF68 | 6.45 | 4.23 | 1.52 |
| Proteasome subunit beta |  | CAALFM\_C502230WA | A0A1D8PNC8 | 1.51 | 1.00 | 1.52 |
| 1,4-alpha-glucan branching enzyme | GLC3 | CAALFM\_C603340CA | A0A1D8PQ59 | 5.95 | 3.96 | 1.50 |
| Kinase | IPK2 | CAALFM\_C209730CA | Q59YE9 | 0.16 | 0.11 | 1.46 |
| Uncharacterized protein |  | CAALFM\_C700340CA | A0A1D8PQJ7 | 1.27 | 0.88 | 1.44 |
| Uncharacterized protein |  | CAALFM\_C602100WA | A0A1D8PPT3 | 27.96 | 19.49 | 1.43 |
| Elf1p | ELF1 | CAALFM\_CR09370WA | A0A1D8PTY4 | 0.25 | 0.17 | 1.42 |
| Ribosomal 40S subunit protein S23B | RPS23A | CAALFM\_C106580WA | A0A1D8PDU3 | 0.56 | 0.39 | 1.42 |
| mRNA export factor MEX67 | MEX67 | CAALFM\_CR04050CA | P84149 | 0.16 | 0.11 | 1.41 |
| Elongation factor 2 | EFT2 | CAALFM\_C203100WA | Q5A0M4 | 50.63 | 36.06 | 1.40 |
| Glucose-6-phosphate 1-epimerase |  | CAALFM\_C501230CA | Q5A1Q0 | 9.26 | 6.62 | 1.40 |
| 60S acidic ribosomal protein P0 | RPP0 | CAALFM\_C700990WA | A0A1D8PQS0 | 3.05 | 2.20 | 1.38 |
| Cam1-1p | CAM1-1 | CAALFM\_C503280WA | A0A1D8PNN8 | 5.70 | 4.20 | 1.36 |
| Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial | LSC1 | CAALFM\_C101690CA | Q5A8X6 | 3.36 | 2.50 | 1.34 |
| Hypoxanthine phosphoribosyltransferase | HPT1 | CAALFM\_C202740CA | A0A1D8PGN7 | 0.59 | 0.44 | 1.32 |
| Induced during hyphae development protein 1 (GPI-anchored protein 36) | IHD1 | CAALFM\_C603850CA | Q5A8I8 | 7.72 | 5.87 | 1.32 |
| Phosphoribosylaminoimidazolesuccinocarboxamide synthase | ADE1 | CAALFM\_CR00510CA | A0A1D8PRQ1 | 1.49 | 1.14 | 1.30 |
| Ardp | ARD | CAALFM\_C600150WA | A0A1D8PPB1 | 0.55 | 0.43 | 1.29 |
| Doa1p | DOA1 | CAALFM\_C109660WA | A0A1D8PEM3 | 1.45 | 1.14 | 1.27 |
| Cell division control protein 10 | CDC10 | CAALFM\_CR04570CA | P39827 | 2.62 | 2.09 | 1.25 |
| Tetrafunctional fatty acid synthase subunit | FAS1 | CAALFM\_C500190CA | Q5A4W7 | 27.76 | 22.28 | 1.25 |
| Metalloaminopeptidase | LAP41 | CAALFM\_C302170CA | A0A1D8PJE0 | 9.81 | 7.93 | 1.24 |
| Coi1p | COI1 | CAALFM\_C107900WA | Q5A799 | 14.34 | 11.65 | 1.23 |
| Adenosylhomocysteinase (AdoHcyase) | SAH1 | CAALFM\_C504270CA | P83783 | 32.77 | 26.78 | 1.22 |
| L-iditol 2-dehydrogenase | XYL2 | CAALFM\_CR10840CA | A0A1D8PUB4 | 8.03 | 6.67 | 1.21 |
| Proteasome endopeptidase complex | PRE8 | CAALFM\_CR09380WA | A0A1D8PTY6 | 2.39 | 1.99 | 1.20 |
| 17-beta-hydroxysteroid dehydrogenase-like protein |  | CAALFM\_C114060WA | A0A1D8PFV8 | 8.75 | 7.53 | 1.16 |
| Rab family GTPase | YPT1 | CAALFM\_C103500WA | Q5AI00 | 4.26 | 3.68 | 1.16 |
| Thioredoxin peroxidase | AHP1 | CAALFM\_C402410CA | Q5AF44 | 14.31 | 12.49 | 1.15 |
| Uncharacterized protein |  | CAALFM\_C200770WA | Q5AD20 | 0.25 | 0.22 | 1.15 |
| Triosephosphate isomerase (TIM) | TPI1 | CAALFM\_C307440WA | Q9P940 | 33.08 | 29.15 | 1.13 |
| Saccharopine dehydrogenase [NAD(+), L-lysine-forming] | LYS1 | CAALFM\_C405320WA | A0A1D8PMA1 | 2.35 | 2.07 | 1.13 |
| Fimbrin | SAC6 | CAALFM\_C602730WA | A0A1D8PPY8 | 2.24 | 2.00 | 1.12 |
| Hsp90 cochaperone | SBA1 | CAALFM\_C603750CA | A0A1D8PQ94 | 2.06 | 1.85 | 1.11 |
| Uncharacterized protein |  | CAALFM\_CR03020CA | Q5A1X9 | 1.64 | 1.50 | 1.10 |
| Actin-related protein 2/3 complex subunit 4 | ARC19 | CAALFM\_CR01040CA | A0A1D8PRU4 | 0.50 | 0.46 | 1.09 |
| Protein transport protein SEC13 | SEC13 | CAALFM\_C303170WA | Q5AEF2 | 1.68 | 1.55 | 1.08 |
| Cell-surface associated glycoprotein DFI1 (Defective in filamentous invasion protein 1) | DFI1 | CAALFM\_C700360WA | Q5AFI4 | 1.29 | 1.19 | 1.08 |
| Adenylosuccinate lyase (ASL) | ADE13 | CAALFM\_CR06150CA | A0A1D8PT56 | 6.37 | 5.93 | 1.07 |
| E1 ubiquitin-activating protein | UBA1 | CAALFM\_C306500WA | A0A1D8PKJ3 | 7.25 | 6.84 | 1.06 |
| Protein disulfide isomerase | PDI1 | CAALFM\_C703250CA | A0A1D8PR99 | 7.60 | 7.23 | 1.05 |
| 40S ribosomal protein S0 | RPS0 | CAALFM\_C305370CA | O42817 | 5.24 | 5.14 | 1.02 |
| Rdi1p | RDI1 | CAALFM\_C305000WA | Q5AND4 | 9.30 | 9.28 | 1.00 |
| Cell division control protein 42 homolog | CDC42 | CAALFM\_C108450CA | P0CY33 | 2.32 | 2.33 | 1.00 |
| Ran GTPase-binding protein | YRB1 | CAALFM\_CR00580WA | A0A1D8PRQ3 | 0.71 | 0.71 | 0.99 |
| Proteasome regulatory particle base subunit | RPN1 | CAALFM\_C113300CA | A0A1D8PFL7 | 2.73 | 2.77 | 0.99 |
| Mir1p | MIR1 | CAALFM\_C110160WA | Q5AP79 | 15.20 | 15.45 | 0.98 |
| Hsp70 nucleotide exchange factor | FES1 | CAALFM\_C600760WA | Q59NN8 | 2.35 | 2.40 | 0.98 |
| GTP-binding protein | RHO1 | CAALFM\_CR02860WA | O42825 | 10.08 | 10.35 | 0.97 |
| Copper transport protein CTR1 | CTR1 | CAALFM\_C600790CA | Q59NP1 | 5.88 | 6.07 | 0.97 |
| Palmitoyltransferase | YKT6 | CAALFM\_C102860CA | Q5AI79 | 3.74 | 3.87 | 0.97 |
| 60S ribosomal protein L6 | RPL6 | CAALFM\_C103110WA | A0A1D8PCX8 | 2.59 | 2.70 | 0.96 |
| Methylthioribose-1-phosphate isomerase (M1Pi) (MTR-1-P isomerase) | MRI1 | CAALFM\_C201160WA | A0A1D8PGB1 | 0.31 | 0.33 | 0.94 |
| 6-phosphogluconate dehydrogenase, decarboxylating | GND1 | CAALFM\_C113860CA | A0A1D8PFS4 | 56.95 | 61.23 | 0.93 |
| Isoleucine--tRNA ligase | ILS1 | CAALFM\_C604520WA | Q59RI1 | 6.97 | 7.52 | 0.93 |
| Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial | LSC2 | CAALFM\_CR06760CA | A0A1D8PTB5 | 0.69 | 0.75 | 0.92 |
| Putative amidotransferase |  | CAALFM\_C205590CA | Q59T45 | 0.98 | 1.07 | 0.92 |
| Glutamate decarboxylase | GAD1 | CAALFM\_C111660WA | A0A1D8PF79 | 16.95 | 18.65 | 0.91 |
| Phosphomannomutase (PMM) | PMM1 | CAALFM\_C102480WA | P31353 | 11.51 | 12.67 | 0.91 |
| Homoserine dehydrogenase (HDH) | HOM6 | CAALFM\_C102620CA | Q5AIA2 | 2.56 | 2.82 | 0.91 |
| Arginase | CAR1 | CAALFM\_C504490CA | A0A1D8PP00 | 2.74 | 3.05 | 0.90 |
| Heat shock protein 90 homolog | HSP90 | CAALFM\_C702030WA | P46598 | 38.73 | 43.09 | 0.90 |
| AMP deaminase |  | CAALFM\_C203360WA | Q5AHA6 | 0.16 | 0.17 | 0.90 |
| Monothiol glutaredoxin | GRX3 | CAALFM\_C402710CA | Q5AF81 | 0.16 | 0.17 | 0.90 |
| Emp24p | EMP24 | CAALFM\_CR07590WA | Q59V63 | 1.96 | 2.19 | 0.89 |
| Aspartyl aminopeptidase |  | CAALFM\_C110820CA | Q59WG6 | 2.04 | 2.31 | 0.88 |
| Pfk26p | PFK26 | CAALFM\_C108950WA | A0A1D8PEF9 | 0.10 | 0.11 | 0.88 |
| 40S ribosomal protein S27 | RPS27 | CAALFM\_CR07630CA | A0A1D8PTI7 | 0.10 | 0.11 | 0.88 |
| E3 ubiquitin-protein ligase | RSP5 | CAALFM\_C208500WA | Q59Y21 | 1.77 | 2.01 | 0.88 |
| Proteasome endopeptidase complex | PRE5 | CAALFM\_C704020CA | A0A1D8PRH6 | 1.54 | 1.75 | 0.88 |
| Nucleoside diphosphate kinase | YNK1 | CAALFM\_C502890WA | Q5AG68 | 11.43 | 13.08 | 0.87 |
| Malate synthase | MLS1 | CAALFM\_C109690WA | Q5APD2 | 14.64 | 16.78 | 0.87 |
| Hsp12p (Lipid-binding protein) | HSP12 | CAALFM\_C502080CA CAALFM\_C502110WA | A0A1D8PNC7 | 0.34 | 0.39 | 0.87 |
| Corticosteroid-binding protein | CBP1 | CAALFM\_CR09270CA | P31225 | 7.44 | 8.87 | 0.84 |
| 6-phosphogluconolactonase | SOL3 | CAALFM\_CR06700CA | Q59PZ6 | 1.77 | 2.11 | 0.84 |
| Reticulon-like protein |  | CAALFM\_C404800WA | A0A1D8PM53 | 3.54 | 4.25 | 0.83 |
| Proteasome endopeptidase complex | SCL1 | CAALFM\_C300770CA | A0A1D8PJ20 | 1.20 | 1.44 | 0.83 |
| Ribosomal 40S subunit protein S18B | RPS18 | CAALFM\_C700960WA | A0A1D8PQQ5 | 2.89 | 3.52 | 0.82 |
| Uncharacterized protein |  | CAALFM\_C202720WA | A0A1D8PGN9 | 0.63 | 0.78 | 0.82 |
| Proteasome core particle subunit beta 2 | PUP1 | CAALFM\_CR10300WA | A0A1D8PU67 | 0.27 | 0.33 | 0.82 |
| Exportin-T (Exportin(tRNA)) (Karyopherin-beta) (tRNA exportin) | LOS1 | CAALFM\_C704200CA | Q5A0E2 | 0.17 | 0.22 | 0.81 |
| Kre9p | KRE9 | CAALFM\_C304180WA | Q5ANN9 | 2.69 | 3.32 | 0.81 |
| Asparagine--tRNA ligase | DED81 | CAALFM\_C703670WA | Q59R18 | 3.92 | 4.84 | 0.81 |
| Proteasome endopeptidase complex (EC 3.4.25.1) | PRE9 | CAALFM\_C303520CA | Q5AEB8 | 2.32 | 2.87 | 0.81 |
| Flavodoxin-like fold family protein | YCP4 | CAALFM\_CR05380CA | A0A1D8PT03 | 0.94 | 1.17 | 0.81 |
| Peptidyl-prolyl cis-trans isomerase (PPIase) | CYP1 | CAALFM\_C702380CA | P22011 | 16.26 | 20.21 | 0.80 |
| Uncharacterized protein |  | CAALFM\_C201340WA | A0A1D8PGD2 | 0.17 | 0.22 | 0.80 |
| 6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase) | RIB4 | CAALFM\_C105560WA | A0A1D8PDK6 | 0.17 | 0.22 | 0.80 |
| Ifr2p | IFR2 | CAALFM\_CR03280WA | A0A1D8PSE7 | 3.70 | 4.66 | 0.79 |
| Tubulin alpha chain | TUB1 | CAALFM\_CR09120CA | A0A1D8PTV4 | 6.14 | 7.78 | 0.79 |
| S-adenosylmethionine-homocysteine S-methyltransferase | SAM4 | CAALFM\_C108410CA | A0A1D8PEB0 | 0.34 | 0.44 | 0.78 |
| Ent3p | ENT3 | CAALFM\_C202340CA | A0A1D8PGL6 | 0.34 | 0.44 | 0.77 |
| Protein phosphatase 2A structural subunit | TPD3 | CAALFM\_C306910CA | Q5ADN1 | 4.03 | 5.21 | 0.77 |
| Pyruvate decarboxylase | PDC11 | CAALFM\_C406570CA | P83779 | 35.27 | 45.63 | 0.77 |
| Saccharopine dehydrogenase (NADP+, L-glutamate-forming) | LYS9 | CAALFM\_C306590WA | A0A1D8PKJ4 | 2.08 | 2.70 | 0.77 |
| S-adenosylmethionine permease | GAP4 | CAALFM\_C107120WA | Q59WB3 | 1.17 | 1.52 | 0.77 |
| Rho family GTPase | RHO3 | CAALFM\_C205030CA | A0A1D8PH96 | 1.90 | 2.51 | 0.76 |
| Glycerol-3-phosphate dehydrogenase [NAD(+)] | GPD2 | CAALFM\_C602010CA | Q59W33 | 0.25 | 0.33 | 0.76 |
| Karyopherin beta |  | CAALFM\_C102240WA | Q59VX7 | 4.16 | 5.50 | 0.76 |
| Proteasome endopeptidase complex | PRE10 | CAALFM\_C701470CA | A0A1D8PQW1 | 0.74 | 0.99 | 0.75 |
| Fructose-bisphosphate aldolase | FBA1 | CAALFM\_C401750CA | Q9URB4 | 39.11 | 52.02 | 0.75 |
| Mtr10p | MTR10 | CAALFM\_C503760CA | A0A1D8PNS3 | 0.96 | 1.30 | 0.74 |
| Ribosomal 60S subunit protein L18A | RPL18 | CAALFM\_C305100CA | A0A1D8PK43 | 1.44 | 1.96 | 0.73 |
| Rab family GTPase | YPT31 | CAALFM\_CR07520CA | A0A1D8PTI2 | 0.78 | 1.08 | 0.72 |
| Actin | ACT1 | CAALFM\_C113700WA | A0A1D8PFR4 | 13.69 | 18.93 | 0.72 |
| Proteasome core particle subunit beta 1 | PRE3 | CAALFM\_C305560WA | A0A1D8PK85 | 1.18 | 1.63 | 0.72 |
| Ribosomal 60S subunit protein L22B |  | CAALFM\_C404390WA | A0A1D8PM41 | 1.26 | 1.75 | 0.72 |
| Uncharacterized protein |  | CAALFM\_C104360CA | A0A1D8PD97 | 0.08 | 0.11 | 0.71 |
| Rad23p | RAD23 | CAALFM\_C201850WA | A0A1D8PGE3 | 0.08 | 0.11 | 0.71 |
| Uncharacterized protein |  | CAALFM\_C202540WA | A0A1D8PGR5 | 0.08 | 0.11 | 0.71 |
| Ribosomal 40S subunit protein S16A | RPS16A | CAALFM\_C103030WA | A0A1D8PCW6 | 1.44 | 2.02 | 0.71 |
| Ras family GTPase | RSR1 | CAALFM\_CR02140WA | A0A1D8PS50 | 1.56 | 2.21 | 0.70 |
| Pyridoxine 4-dehydrogenase |  | CAALFM\_CR09100CA | A0A1D8PTW9 | 1.06 | 1.52 | 0.70 |
| Serine/threonine-protein phosphatase | SIT4 | CAALFM\_C104380WA | Q59KY8 | 0.08 | 0.11 | 0.69 |
| Transaldolase | TAL1 | CAALFM\_CR03720WA | Q5A017 | 36.12 | 52.97 | 0.68 |
| Proteasome core particle subunit beta 5 | PRE2 | CAALFM\_C206820CA | Q59Z65 | 1.53 | 2.31 | 0.66 |
| Ribosomal 40S subunit protein S9B | RPS9B | CAALFM\_C203820CA | A0A1D8PGY8 | 1.48 | 2.25 | 0.66 |
| 3,4-dihydroxy-2-butanone 4-phosphate synthase | RIB3 | CAALFM\_C112360CA | Q5A3V6 | 3.87 | 5.99 | 0.65 |
| Pyruvate kinase | CDC19 | CAALFM\_C205460WA | P46614 | 13.15 | 20.64 | 0.64 |
| Uncharacterized protein |  | CAALFM\_C300640WA | Q5A7S3 | 2.63 | 4.18 | 0.63 |
| Hexokinase-2 | HXK2 | CAALFM\_CR04510WA | P83776 | 22.87 | 36.51 | 0.63 |
| 40S ribosomal protein S12 | RPS12 | CAALFM\_C307150CA | Q5ADQ6 | 2.83 | 4.53 | 0.63 |
| ATP-dependent RNA helicase | SUB2 | CAALFM\_C400220CA | A0A1D8PKZ3 | 1.09 | 1.75 | 0.62 |
| Nascent polypeptide-associated complex subunit alpha | EGD2 | CAALFM\_C304140CA | Q5ANP2 | 0.98 | 1.58 | 0.62 |
| Tyrosine protein phosphatase | LTP1 | CAALFM\_C108260CA | A0A1D8PE91 | 0.87 | 1.41 | 0.62 |
| Exomer complex subunit | BUD7 | CAALFM\_C503820CA | Q59N76 | 0.96 | 1.58 | 0.61 |
| Respiratory growth induced protein 1 | RGI1 | CAALFM\_C208290CA | Q59KG2 | 0.81 | 1.33 | 0.61 |
| Pst1p | PST1 | CAALFM\_C206870CA | A0A1D8PHR5 | 5.81 | 9.71 | 0.60 |
| Tubulin beta chain | TUB2 | CAALFM\_C100710CA | A0A1D8PC97 | 3.53 | 5.96 | 0.59 |
| High-affinity iron permease | FTR1 | CAALFM\_C114130WA | A0A1D8PFV0 | 1.81 | 3.06 | 0.59 |
| Sfc1p | SFC1 | CAALFM\_C504440CA | A0A1D8PNY6 | 1.59 | 2.72 | 0.58 |
| Septin | CDC3 | CAALFM\_C104210CA | A0A1D8PD83 | 1.48 | 2.54 | 0.58 |
| Uncharacterized protein |  | CAALFM\_CR03520CA | A0A1D8PSI3 | 1.54 | 2.65 | 0.58 |
| Hsp90 co-chaperone | CDC37 | CAALFM\_C602610CA | Q8X1E6 | 0.50 | 0.86 | 0.58 |
| 14-3-3 protein homolog | BMH1 | CAALFM\_C103220CA | O42766 | 20.35 | 36.02 | 0.57 |
| Proliferating cell nuclear antigen | POL30 | CAALFM\_C401770WA | Q5AMN0 | 2.18 | 3.88 | 0.56 |
| GTP-binding nuclear protein | GSP1 | CAALFM\_C206310CA | Q59P43 | 3.68 | 6.62 | 0.56 |
| Arf3p | ARF3 | CAALFM\_C301470WA | A0A1D8PJ64 | 0.80 | 1.44 | 0.55 |
| Ornithine-oxo-acid transaminase | CAR2 | CAALFM\_C400160CA | A0A1D8PL14 | 14.43 | 26.04 | 0.55 |
| Ifd6p | IFD6 | CAALFM\_C104140WA | A0A1D8PD78 | 4.50 | 8.16 | 0.55 |
| Uncharacterized protein |  | CAALFM\_C110890CA | A0A1D8PEZ3 | 0.10 | 0.17 | 0.55 |
| Psa2p | PSA2 | CAALFM\_C113160WA | Q5AL34 | 2.69 | 4.95 | 0.54 |
| FK506-binding protein 1 | RBP1; RBP2 | CAALFM\_C702570CA | P28870 | 2.52 | 4.64 | 0.54 |
| Argininosuccinate synthase | ARG1 | CAALFM\_CR00620CA | A0A1D8PRR5 | 2.61 | 4.84 | 0.54 |
| 40S ribosomal protein S7 | RPS7A | CAALFM\_C301490WA | Q5AJ93 | 0.80 | 1.52 | 0.53 |
| Ubiquitin-related modifier 1 | URM1 | CAALFM\_C111160CA | Q59JW3 | 0.17 | 0.33 | 0.52 |
| Protein transport protein SEC31 | PGA63 | CAALFM\_C106930WA | Q5AAU3 | 2.18 | 4.24 | 0.51 |
| Ras-like protein 1 | RAS1 | CAALFM\_C210210CA | Q59XU5 | 6.50 | 12.83 | 0.51 |
| Adenine phosphoribosyltransferase (APRT) | APT1 | CAALFM\_C201430WA | Q5ALX8 | 0.55 | 1.10 | 0.50 |
| NADH-cytochrome b5 reductase 2 | MCR1 | CAALFM\_C602040WA | Q59M70 | 3.27 | 6.60 | 0.50 |
| 40S ribosomal protein S22-B | RPS22B | CAALFM\_C103620CA | P0CU35 | 2.75 | 5.61 | 0.49 |
| Peptidyl-prolyl cis-trans isomerase D | CPR6 | CAALFM\_CR10670WA | Q5ACI8 | 2.97 | 6.05 | 0.49 |
| Glutamate dehydrogenase | GDH3 | CAALFM\_C406120WA | A0A1D8PMH8 | 3.20 | 6.53 | 0.49 |
| Mitochondrial outer membrane protein porin (Cytoplasmic antigenic protein 4) | POR1 | CAALFM\_C104100CA | P83781 | 18.12 | 37.05 | 0.49 |
| Putative NADPH-dependent methylglyoxal reductase | GRP2 | CAALFM\_C502860CA | P83775 | 9.29 | 18.99 | 0.49 |
| Uncharacterized protein |  | CAALFM\_C401460CA | A0A1D8PLE6 | 0.63 | 1.31 | 0.49 |
| High-affinity glucose transporter 1 | HGT1 | CAALFM\_C101980WA | A0A1D8PCL1 | 3.29 | 6.77 | 0.49 |
| Metalloendopeptidase | PRD1 | CAALFM\_C105300CA | Q5A2A7 | 3.75 | 7.76 | 0.48 |
| Oye32p | OYE32 | CAALFM\_C406780CA | A0A1D8PMP0 | 0.16 | 0.33 | 0.48 |
| Eukaryotic translation initiation factor 5A | ANB1 | CAALFM\_C601610WA | O94083 | 1.89 | 3.98 | 0.48 |
| Bifunctional (2E,6E)-farnesyl diphosphate synthase/dimethylallyltranstransferase | ERG20 | CAALFM\_C204580WA | A0A1D8PH78 | 3.88 | 8.17 | 0.48 |
| Phosphoglycerate kinase | PGK1 | CAALFM\_C600750CA | P46273 | 39.13 | 83.87 | 0.47 |
| ADP/ATP carrier protein | PET9 | CAALFM\_C500590WA | Q5A516 | 24.37 | 52.85 | 0.46 |
| NAD-specific glutamate dehydrogenase | GDH2 | CAALFM\_C207900WA | A0A1D8PI00 | 3.36 | 7.29 | 0.46 |
| Autophagy-related protein 27 | ATG27 | CAALFM\_C210470CA | Q5A5S7 | 0.23 | 0.51 | 0.46 |
| Leu42p | LEU42 | CAALFM\_C209750WA | A0A1D8PIF8 | 2.22 | 4.92 | 0.45 |
| Isocitrate dehydrogenase [NAD] subunit, mitochondrial | IDH2 | CAALFM\_C203080WA | A0A1D8PGS5 | 2.84 | 6.30 | 0.45 |
| Proteinase B |  | CAALFM\_C703860WA | A0A1D8PRH0 | 1.78 | 3.98 | 0.45 |
| Glucose-6-phosphate 1-dehydrogenase | ZWF1 | CAALFM\_C108980CA | A0A1D8PEG2 | 9.70 | 21.84 | 0.44 |
| Mannan endo-1,6-alpha-mannosidase | DFG5 | CAALFM\_C200520WA | Q5ACZ2 | 1.70 | 3.84 | 0.44 |
| Ubiquitin-ribosomal 40S subunit protein S31 fusion protein | UBI3 | CAALFM\_C407180WA | Q5A109 | 12.18 | 27.47 | 0.44 |
| Ribosomal 60S subunit protein L34B |  | CAALFM\_C106890CA | A0A1D8PDZ1 | 0.10 | 0.22 | 0.44 |
| Mannose-1-phosphate guanyltransferase | MPG1 | CAALFM\_C307950CA | O93827 | 2.04 | 4.64 | 0.44 |
| cAMP-dependent protein kinase regulatory subunit (PKA regulatory subunit) (PKA-R) | BCY1 | CAALFM\_C201110CA | Q9HEW1 | 0.58 | 1.31 | 0.44 |
| Ribosomal 40S subunit protein S3 | RPS3 | CAALFM\_CR04810WA | A0A1D8PSV5 | 2.03 | 4.64 | 0.44 |
| Glucose-6-phosphate isomerase (GPI) | PGI1 | CAALFM\_CR06340CA | P83780 | 24.51 | 56.25 | 0.44 |
| Acyl-coenzyme A oxidase | POX1-3 | CAALFM\_C301960CA | Q5AJD9 | 5.36 | 12.37 | 0.43 |
| Coproporphyrinogen oxidase | HEM13 | CAALFM\_C304060CA | Q59MR4 | 3.59 | 8.33 | 0.43 |
| Mannose-6-phosphate isomerase | PMI1 | CAALFM\_C209640WA | P34948 | 2.70 | 6.43 | 0.42 |
| Phosphotransferase | GLK1 | CAALFM\_CR07150WA | Q59TZ8 | 6.19 | 14.73 | 0.42 |
| Enolase 1 | ENO1 | CAALFM\_C108500CA | P30575 | 53.48 | 128.85 | 0.42 |
| ATP synthase subunit d, mitochondrial | ATP7 | CAALFM\_C107600WA | Q59PV8 | 2.06 | 4.97 | 0.42 |
| Csh1p | CSH1 | CAALFM\_C104020CA | Q59QH2 | 17.67 | 42.80 | 0.41 |
| Protein | SUR7 | CAALFM\_C601720CA | Q5A4M8 | 4.94 | 12.00 | 0.41 |
| Ras-related protein | SEC4 | CAALFM\_CR01750CA | P0CY31 | 1.60 | 3.93 | 0.41 |
| Phosphoacetylglucosamine mutase | AGM1 | CAALFM\_C113760WA | Q5AKW4 | 1.65 | 4.06 | 0.41 |
| Adenylyl cyclase-associated protein | SRV2 | CAALFM\_CR04190WA | Q5A6P9 | 2.08 | 5.17 | 0.40 |
| Elongation factor 1-alpha 2 | TEF2 | CAALFM\_C108380WA | Q59QD6 | 23.54 | 58.71 | 0.40 |
| ATP-dependent 6-phosphofructokinase | PFK2 | CAALFM\_C701800CA | Q5AGZ8 | 2.13 | 5.34 | 0.40 |
| Ubiquinol--cytochrome-c reductase subunit |  | CAALFM\_C505230CA | A0A1D8PP59 | 1.50 | 3.76 | 0.40 |
| Phospho-2-dehydro-3-deoxyheptonate aldolase | ARO3 | CAALFM\_C202030WA | A0A1D8PGI8 | 0.16 | 0.39 | 0.40 |
| Plasma membrane ATPase | PMA1 | CAALFM\_C300720WA | A0A1D8PJ01 | 17.94 | 45.27 | 0.40 |
| Clathrin heavy chain (Fragment) | CHC1 | CAALFM\_C602120WA | A0A1D8PPS9 | 2.78 | 7.02 | 0.40 |
| Peroxisomal catalase | CAT1 | CAALFM\_C106810WA | O13289 | 3.24 | 8.22 | 0.39 |
| UTP--glucose-1-phosphate uridylyltransferase | UGP1 | CAALFM\_CR04660CA | Q59KI0 | 5.39 | 13.77 | 0.39 |
| Bifunctional aminoimidazole ribotide synthase/glycinamide ribotide synthase | ADE5,7 | CAALFM\_C107890CA | A0A1D8PE67 | 0.63 | 1.63 | 0.39 |
| Bifunctional UDP-glucose 4-epimerase/aldose 1-epimerase | GAL10 | CAALFM\_C102150WA | A0A1D8PCN0 | 0.25 | 0.65 | 0.39 |
| Aromatic-amino-acid:2-oxoglutarate transaminase | ARO9 | CAALFM\_C405560CA | A0A1D8PMC5 | 0.70 | 1.85 | 0.38 |
| Low-affinity Zn(2+) transporter | ZRT2 | CAALFM\_C202590WA | A0A1D8PGN5 | 3.93 | 10.39 | 0.38 |
| 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase | MET6 | CAALFM\_CR01620CA | P82610 | 21.54 | 57.17 | 0.38 |
| E2 ubiquitin-conjugating protein |  | CAALFM\_C604280WA | A0A1D8PQD4 | 0.50 | 1.33 | 0.38 |
| Glutathione peroxidase | GPX2 | CAALFM\_C600840WA | Q59WW8 | 0.78 | 2.08 | 0.37 |
| Proteasome endopeptidase complex | PUP2 | CAALFM\_CR06750CA | Q59PZ1 | 1.50 | 4.03 | 0.37 |
| Dip5p | DIP5 | CAALFM\_C102530CA | A0A1D8PCR4 | 0.40 | 1.09 | 0.37 |
| Pyruvate carboxylase | PYC2 | CAALFM\_C403940CA | A0A1D8PLY4 | 1.85 | 5.01 | 0.37 |
| Uncharacterized protein |  | CAALFM\_CR06500CA | A0A1D8PTA6 | 1.56 | 4.24 | 0.37 |
| Putative ammonium permease | FRP3 | CAALFM\_C206680WA | A0A1D8PHP8 | 1.60 | 4.43 | 0.36 |
| Proteasome regulatory particle lid subunit |  | CAALFM\_C201320WA | A0A1D8PGA6 | 0.19 | 0.54 | 0.36 |
| Protein transport protein SEC23 | SEC23 | CAALFM\_C405690WA | Q5A455 | 1.71 | 4.77 | 0.36 |
| Acetyltransferase component of pyruvate dehydrogenase complex | LAT1 | CAALFM\_C701640WA | Q5AGX8 | 2.52 | 7.07 | 0.36 |
| Age3p | AGE3 | CAALFM\_C102260CA | A0A1D8PCP6 | 0.08 | 0.22 | 0.36 |
| D-arabinose 1-dehydrogenase (NAD(P)(+)) |  | CAALFM\_C400380WA | A0A1D8PL15 | 0.23 | 0.66 | 0.36 |
| Uncharacterized protein |  | CAALFM\_C402340WA | Q5AF37 | 1.82 | 5.10 | 0.36 |
| F1F0 ATP synthase subunit 4 | ATP4 | CAALFM\_C205500WA | Q59ZE0 | 2.72 | 7.68 | 0.35 |
| F1F0 ATP synthase subunit e |  | CAALFM\_C400330CA | A0A1D8PL02 | 0.19 | 0.55 | 0.35 |
| Lmo1p | LMO1 | CAALFM\_C703080WA | A0A1D8PR98 | 0.08 | 0.22 | 0.35 |
| 40S ribosomal protein S21 | RPS21B | CAALFM\_C101370CA | A0A1D8PCG7 | 0.17 | 0.50 | 0.35 |
| Uncharacterized protein |  | CAALFM\_C113190WA | A0A1D8PFM0 | 0.26 | 0.75 | 0.35 |
| Bifunctional cysteine synthase/O-acetylhomoserine aminocarboxypropyltransferase | MET15 | CAALFM\_C400200CA | Q59US5 | 2.55 | 7.41 | 0.34 |
| Alpha-1,4 glucan phosphorylase | GPH1 | CAALFM\_C700930WA | A0A1D8PQQ3 | 6.09 | 17.72 | 0.34 |
| Proteinase A | APR1 | CAALFM\_C207400CA | Q59U59 | 5.43 | 15.83 | 0.34 |
| Translation initiation factor eIF2 subunit gamma | GCD11 | CAALFM\_C502170CA | Q5AGF6 | 1.28 | 3.72 | 0.34 |
| Ribosomal 60S subunit protein L11B | RPL11 | CAALFM\_C206810CA | A0A1D8PHW1 | 0.63 | 1.86 | 0.34 |
| Ali1p | ALI1 | CAALFM\_C301410CA | A0A1D8PJ73 | 0.16 | 0.46 | 0.34 |
| Isocitrate dehydrogenase [NADP] | IDP2 | CAALFM\_CR02360WA | A0A1D8PS79 | 6.78 | 20.11 | 0.34 |
| Acetyl-coenzyme A synthetase 2 | ACS2 | CAALFM\_C104290CA | Q8NJN3 | 3.68 | 10.99 | 0.33 |
| Translationally-controlled tumor protein homolog (TCTP) | TMA19 | CAALFM\_CR00860CA | Q5A860 | 1.84 | 5.49 | 0.33 |
| Uncharacterized protein |  | CAALFM\_C209970CA | Q59YH1 | 1.45 | 4.34 | 0.33 |
| Uncharacterized protein |  | CAALFM\_C502380WA | A0A1D8PNE5 | 0.63 | 1.89 | 0.33 |
| Phosphoglycerate mutase | GPM1 | CAALFM\_C203270WA | P82612 | 8.91 | 26.70 | 0.33 |
| Ribosomal 60S subunit protein L7A |  | CAALFM\_C105720WA | A0A1D8PDL6 | 0.94 | 2.82 | 0.33 |
| Protein transport protein SEC24 | SEC24 | CAALFM\_C108740CA | Q5AQ76 | 1.98 | 6.09 | 0.32 |
| Uncharacterized protein |  | CAALFM\_C103510CA | A0A1D8PD11 | 3.74 | 11.67 | 0.32 |
| Ribonucleotide-diphosphate reductase subunit | RNR21 | CAALFM\_C203010CA | Q5A0L0 | 0.56 | 1.75 | 0.32 |
| Elongation factor 3 | CEF3 | CAALFM\_C501580CA | P25997 | 9.35 | 29.58 | 0.32 |
| Ribosomal 60S subunit protein L9B | RPL9B | CAALFM\_C302470CA | Q5AEN2 | 2.32 | 7.36 | 0.31 |
| Uncharacterized protein |  | CAALFM\_C104010CA | A0A1D8PD74 | 5.97 | 19.19 | 0.31 |
| 60S ribosomal protein L36 | RPL39 | CAALFM\_C203960WA | A0A1D8PH21 | 0.16 | 0.51 | 0.31 |
| Isocitrate lyase | ICL1 | CAALFM\_C104500WA | Q59RB8 | 4.45 | 14.46 | 0.31 |
| Alpha-mannosidase | AMS1 | CAALFM\_C402360WA | Q5AF38 | 16.55 | 54.18 | 0.31 |
| Phosphatidylinositol transfer protein | SFH5 | CAALFM\_C110270CA | Q5AP66 | 1.18 | 3.86 | 0.30 |
| Yim1p | YIM1 | CAALFM\_C203750WA | Q5AHE9 | 1.35 | 4.46 | 0.30 |
| Transketolase | TKL1 | CAALFM\_C108320WA | Q5A750 | 11.28 | 37.43 | 0.30 |
| Alpha,alpha-trehalose-phosphate synthase [UDP-forming] | TPS1 | CAALFM\_CR05720WA | Q92410 | 1.68 | 5.66 | 0.30 |
| Methionine--tRNA ligase | MES1 | CAALFM\_C504700CA | A0A1D8PP21 | 0.60 | 2.01 | 0.30 |
| Superoxide dismutase | SOD3 | CAALFM\_C700110WA | A0A1D8PQH5 | 4.60 | 15.58 | 0.29 |
| T-complex protein 1 subunit delta |  | CAALFM\_C402780WA | A0A1D8PLN3 | 0.10 | 0.32 | 0.29 |
| Transcriptional repressor TUP1 | TUP1 | CAALFM\_C100060WA | P0CY34 | 2.92 | 9.90 | 0.29 |
| Nmd5p | NMD5 | CAALFM\_C400540CA | Q59SI4 | 0.10 | 0.33 | 0.29 |
| Lys22p | LYS22 | CAALFM\_C204460WA | Q59TC4 | 1.17 | 4.01 | 0.29 |
| Cys-Gly metallodipeptidase | DUG1 | CAALFM\_C504300CA | Q5AKA5 | 2.90 | 10.07 | 0.29 |
| Putative Rab GTPase-binding protein | SRO77 | CAALFM\_C600410CA | Q59RK1 | 0.10 | 0.33 | 0.29 |
| Uncharacterized protein |  | CAALFM\_CR09140CA | A0A1D8PTW2 | 0.17 | 0.62 | 0.28 |
| Phosphoglycerate dehydrogenase | SER33 | CAALFM\_C112030WA | Q5A3K7 | 0.70 | 2.54 | 0.28 |
| Inorganic pyrophosphatase | IPP1 | CAALFM\_C208810CA | P83777 | 7.39 | 26.69 | 0.28 |
| Cdr11p | CDR11 | CAALFM\_C304070CA | A0A1D8PK15 | 0.73 | 2.65 | 0.27 |
| Branched-chain-amino-acid aminotransferase | BAT22 | CAALFM\_C305590CA | A0A1D8PKB9 | 1.44 | 5.23 | 0.27 |
| Pyrroline-5-carboxylate reductase | PRO3 | CAALFM\_C400240CA | A0A1D8PKZ7 | 0.08 | 0.28 | 0.27 |
| Hgt2p | HGT2 | CAALFM\_C102110CA | Q59VZ0 | 0.42 | 1.55 | 0.27 |
| Ribosomal 60S subunit protein L5 | RPL5 | CAALFM\_C701790CA | Q5AGZ7 | 1.29 | 4.73 | 0.27 |
| Uncharacterized protein |  | CAALFM\_C503490CA | A0A1D8PNP4 | 0.17 | 0.65 | 0.27 |
| Thioredoxin peroxidase | PRX1 | CAALFM\_C702810WA | Q5A5A0 | 1.43 | 5.44 | 0.26 |
| Uncharacterized protein |  | CAALFM\_CR00090CA | A0A1D8PRL3 | 0.31 | 1.20 | 0.26 |
| Peroxiredoxin TSA1-A | TSA1 | CAALFM\_C306180CA | Q9Y7F0 | 11.76 | 45.97 | 0.26 |
| Superoxide dismutase | SOD2 | CAALFM\_C101520CA | Q5A8Z4 | 1.87 | 7.32 | 0.26 |
| Non-classical export protein 102 | NCE102 | CAALFM\_C304910CA | Q5ANE3 | 1.70 | 6.74 | 0.25 |
| ATP synthase subunit alpha | ATP1 | CAALFM\_C104610WA | A0A1D8PDC4 | 2.16 | 8.77 | 0.25 |
| Bleomycin hydrolase | LAP3 | CAALFM\_CR04480CA | Q5A6L5 | 5.79 | 23.64 | 0.24 |
| Cytochrome c oxidase subunit 1 | COX1 | CaalfMp08 | P0C8K9 | 0.33 | 1.35 | 0.24 |
| Uncharacterized protein |  | CAALFM\_C205550WA | A0A1D8PHE5 | 0.16 | 0.65 | 0.24 |
| Ketol-acid reductoisomerase, mitochondrial | ILV5 | CAALFM\_C600870CA | A0A1D8PPG7 | 1.44 | 6.04 | 0.24 |
| Osm1p | OSM1 | CAALFM\_C205700WA | Q59T35 | 1.22 | 5.29 | 0.23 |
| Gcr3p | GCR3 | CAALFM\_C108420WA | A0A1D8PEB4 | 0.08 | 0.33 | 0.23 |
| Putative cystathionine beta-lyase |  | CAALFM\_CR09010CA | A0A1D8PTV7 | 1.47 | 6.37 | 0.23 |
| Sgt2p | SGT2 | CAALFM\_C202830CA | Q5A0I8 | 0.33 | 1.44 | 0.23 |
| Mrf1p | MRF1 | CAALFM\_C111700CA | Q59TU5 | 2.55 | 11.28 | 0.23 |
| Proteasome core particle subunit beta 4 | PRE1 | CAALFM\_C505310WA | Q5AJZ5 | 0.25 | 1.10 | 0.22 |
| Omega-class glutathione transferase | ECM4 | CAALFM\_CR02130WA | A0A1D8PS56 | 1.63 | 7.32 | 0.22 |
| Uncharacterized protein |  | CAALFM\_C603320WA | A0A1D8PQ54 | 0.31 | 1.40 | 0.22 |
| Riboflavin synthase | RIB5 | CAALFM\_C505300WA | A0A1D8PP67 | 0.58 | 2.61 | 0.22 |
| Cta3p | CTA3 | CAALFM\_C111540CA | A0A1D8PF53 | 0.10 | 0.44 | 0.22 |
| Bifunctional 2-aminoadipate transaminase/aromatic-amino-acid:2-oxoglutarate transaminase | ARO8 | CAALFM\_C200340CA | A0A1D8PG20 | 0.63 | 2.92 | 0.22 |
| Sphingolipid C9-methyltransferase | MTS1 | CAALFM\_C109680WA | Q5APD4 | 1.87 | 8.73 | 0.21 |
| H(+)-transporting V1 sector ATPase subunit E | VMA4 | CAALFM\_CR01970CA | A0A1D8PS38 | 0.34 | 1.60 | 0.21 |
| ATP-dependent RNA helicase | DHH1 | CAALFM\_C107070CA | Q5AAW3 | 0.17 | 0.84 | 0.21 |
| Proteasome regulatory particle lid subunit |  | CAALFM\_C104230WA | A0A1D8PDB0 | 0.16 | 0.75 | 0.21 |
| Arginine--tRNA ligase |  | CAALFM\_C101530CA | A0A1D8PCI5 | 0.31 | 1.51 | 0.21 |
| Carboxypeptidase | CPY1 | CAALFM\_C703360WA | A0A1D8PRC2 | 1.02 | 4.98 | 0.20 |
| Cytochrome b-c1 complex subunit 2, mitochondrial | QCR2 | CAALFM\_C503350WA | P83782 | 1.54 | 7.60 | 0.20 |
| Pyridoxine biosynthesis protein | SNZ1 | CAALFM\_C102590CA | Q5AIA6 | 2.67 | 13.13 | 0.20 |
| Glyoxalase 3 | GLX3 | CAALFM\_C302610CA | Q5AF03 | 33.69 | 167.15 | 0.20 |
| Heat shock protein SSA1 | SSA1 | CAALFM\_C113480WA | P41797 | 16.75 | 83.45 | 0.20 |
| Proteasome regulatory particle lid subunit | RPN5 | CAALFM\_C505380WA | A0A1D8PP77 | 0.16 | 0.79 | 0.20 |
| Uncharacterized protein |  | CAALFM\_C602330WA | A0A1D8PPV6 | 1.11 | 5.63 | 0.20 |
| Cytochrome c | CYC1 | CAALFM\_C210110WA | P53698 | 1.04 | 5.29 | 0.20 |
| Diphosphomevalonate decarboxylase | MVD | CAALFM\_C100070WA | A0A1D8PC43 | 0.16 | 0.81 | 0.19 |
| Zrt1p | ZRT1 | CAALFM\_C406970CA | A0A1D8PMR6 | 1.59 | 8.20 | 0.19 |
| 40S ribosomal protein S4 | RPS4A | CAALFM\_C210620WA | Q5A5Q8 | 1.61 | 8.38 | 0.19 |
| Sbp1p | SBP1 | CAALFM\_C304090WA | Q5ANP6 | 0.18 | 0.95 | 0.19 |
| Adenylosuccinate synthetase | ADE12 | CAALFM\_C109640WA | P0CH96 | 0.96 | 5.06 | 0.19 |
| Acetyl-CoA carboxylase | ACC1 | CAALFM\_CR00640WA | A0A1D8PRR7 | 0.78 | 4.14 | 0.19 |
| Ribosomal 40S subunit protein S19A | RPS19A | CAALFM\_C305200WA | A0A1D8PK61 | 0.34 | 1.79 | 0.19 |
| Hsp70 family ATPase | SSB1 | CAALFM\_CR08090WA | Q5A397 | 3.54 | 19.27 | 0.18 |
| Formate dehydrogenase | FDH1 | CAALFM\_CR05170CA | Q59QN6 | 6.92 | 38.53 | 0.18 |
| Citrate synthase | CIT1 | CAALFM\_CR03500WA | A0A1D8PSH3 | 15.00 | 83.67 | 0.18 |
| Peptide-methionine-S-sulfoxide reductase | MXR1 | CAALFM\_C200960CA | Q5AD39 | 0.16 | 0.88 | 0.18 |
| Hexose transporter | HGT6 | CAALFM\_C201020WA | Q5AD47 | 1.25 | 7.09 | 0.18 |
| Acetyl-coenzyme A synthetase | ACS1 | CAALFM\_C210350CA | Q59XW4 | 5.06 | 29.27 | 0.17 |
| SCF ubiquitin ligase subunit | SKP1 | CAALFM\_C107410CA | Q59WE2 | 0.62 | 3.69 | 0.17 |
| F1F0 ATP synthase subunit i | ATP18 | CAALFM\_C200610CA | A0A1D8PG50 | 0.10 | 0.57 | 0.17 |
| AAA family ATPase | SEC18 | CAALFM\_C113580WA | A0A1D8PFN6 | 0.18 | 1.10 | 0.16 |
| Glyceraldehyde-3-phosphate dehydrogenase | TDH3 | CAALFM\_C306870WA | Q5ADM7 | 20.32 | 124.05 | 0.16 |
| Leukotriene A-4 hydrolase homolog (LTA-4 hydrolase) | LKH1 | CAALFM\_C110490WA | Q59NB8 | 0.75 | 4.57 | 0.16 |
| Csp37p | CSP37 | CAALFM\_CR01470WA | Q5A9D4 | 0.80 | 5.03 | 0.16 |
| Ribosomal 40S subunit protein S10A | RPS10 | CAALFM\_C208040CA | A0A1D8PI15 | 0.16 | 0.99 | 0.16 |
| Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit | WBP1 | CAALFM\_C111170WA | A0A1D8PF22 | 0.17 | 1.11 | 0.16 |
| Sla2p | SLA2 | CAALFM\_C703810WA | A0A1D8PRF5 | 0.33 | 2.10 | 0.16 |
| Dap2p | DAP2 | CAALFM\_C502970WA | A0A1D8PNK0 | 0.17 | 1.11 | 0.16 |
| Serine/threonine-protein phosphatase | PPH21 | CAALFM\_C301600WA | A0A1D8PJ80 | 0.15 | 0.99 | 0.15 |
| Histone H4 | HHF1 | CAALFM\_C104240CA | Q59VN4 | 1.37 | 9.08 | 0.15 |
| Uncharacterized protein |  | CAALFM\_C703830CA | A0A1D8PRF3 | 0.10 | 0.65 | 0.15 |
| Proline--tRNA ligase |  | CAALFM\_C703660CA | Q59R20 | 0.41 | 2.76 | 0.15 |
| Pleiotropic ABC efflux transporter of multiple drugs | CDR1 | CAALFM\_C305220WA | Q5ANA3 | 6.15 | 41.54 | 0.15 |
| Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial | SDH12 | CAALFM\_C406610CA | Q5A1E8 | 0.57 | 3.92 | 0.14 |
| Lactoylglutathione lyase | GLO1 | CAALFM\_C100500CA | Q5ABB2 | 0.16 | 1.10 | 0.14 |
| Proteasome regulatory particle lid subunit | RPN7 | CAALFM\_CR08910CA | A0A1D8PTV0 | 0.08 | 0.56 | 0.14 |
| Uncharacterized protein |  | CAALFM\_C101490WA | Q5A8Z9 | 0.56 | 4.20 | 0.13 |
| Chaperone ATPase | HSP104 | CAALFM\_CR08250CA | A0A1D8PTP9 | 1.36 | 10.28 | 0.13 |
| Ribosomal 60S subunit protein L21A | RPL21A | CAALFM\_C203810CA | A0A1D8PGY0 | 0.16 | 1.19 | 0.13 |
| Chaperonin-containing T-complex subunit | CCT7 | CAALFM\_C501690CA | Q59YH4 | 0.17 | 1.32 | 0.13 |
| Coatomer subunit delta | RET2 | CAALFM\_C502300CA | A0A1D8PND9 | 0.08 | 0.60 | 0.13 |
| Eukaryotic translation initiation factor 2A |  | CAALFM\_C102430CA | A0A1D8PCQ3 | 0.16 | 1.30 | 0.12 |
| Ribosomal 40S subunit protein S14B | RPS14B | CAALFM\_C106450CA | A0A1D8PDT3 | 0.18 | 1.53 | 0.12 |
| Erv29p | ERV29 | CAALFM\_C402120WA | Q5AMR7 | 0.17 | 1.48 | 0.12 |
| Carboxypeptidase | PRC3 | CAALFM\_C105770CA | A0A1D8PDM9 | 0.08 | 0.66 | 0.12 |
| Histone H2A.Z | HTZ1 | CAALFM\_C303280CA | Q5AEE1 | 0.18 | 1.57 | 0.12 |
| Isocitrate dehydrogenase [NAD] subunit, mitochondrial | IDH1 | CAALFM\_C109630WA | A0A1D8PEM5 | 1.51 | 13.19 | 0.11 |
| UDP-N-acetylglucosamine diphosphorylase | UAP1 | CAALFM\_C502530WA | A0A1D8PNG6 | 0.17 | 1.54 | 0.11 |
| Cytochrome c oxidase subunit Va | COX5 | CAALFM\_C109030CA | Q5APK5 | 0.63 | 5.88 | 0.11 |
| Histidine biosynthesis trifunctional protein | HIS4 | CAALFM\_C400140CA | A0A1D8PKY7 | 0.08 | 0.71 | 0.11 |
| Trifunctional aldehyde reductase/xylose reductase/glucose 1-dehydrogenase (NADP(+)) | GRE3 | CAALFM\_C502930CA | A0A1D8PNK3 | 2.19 | 20.65 | 0.11 |
| ATP-binding cassette glutathione S-conjugate transporter | YCF1 | CAALFM\_C702330WA | A0A1D8PR42 | 0.16 | 1.49 | 0.11 |
| Cip1p | CIP1 | CAALFM\_C601070CA | A0A1D8PPI6 | 2.46 | 23.46 | 0.10 |
| Adenylate kinase | ADK1 | CAALFM\_C601910WA | Q5A4Q1 | 0.64 | 6.16 | 0.10 |
| E2 ubiquitin-conjugating protein |  | CAALFM\_C112650CA | A0A1D8PFF9 | 0.10 | 0.95 | 0.10 |
| Uncharacterized protein |  | CAALFM\_C207630CA | Q59U89 | 0.80 | 8.06 | 0.10 |
| Uncharacterized protein |  | CAALFM\_C111860WA | A0A1D8PF90 | 0.16 | 1.58 | 0.10 |
| Actin-related protein 3 | ARP3 | CAALFM\_C207320WA | Q59Z11 | 0.17 | 1.73 | 0.10 |
| Png2p | PNG2 | CAALFM\_C205660WA | A0A1D8PHH2 | 0.17 | 1.75 | 0.10 |
| S-methyl-5'-thioadenosine phosphorylase | MEU1 | CAALFM\_C303790WA | Q59ST1 | 0.16 | 1.61 | 0.10 |
| Ribosomal protein L19 | RPL19A | CAALFM\_C304500CA | A0A1D8PK40 | 0.17 | 1.77 | 0.10 |
| 60S ribosomal protein L13 | RPL13 | CAALFM\_C103020CA | O59931 | 0.15 | 1.78 | 0.09 |
| T-complex protein 1 subunit gamma | CCT3 | CAALFM\_C505120WA | Q5AK16 | 0.10 | 1.12 | 0.08 |
| Proteasome regulatory particle base subunit | RPN2 | CAALFM\_C112050WA | Q5A3L0 | 0.25 | 2.93 | 0.08 |
| Gst2p | GST2 | CAALFM\_C402990CA | Q5AFB4 | 0.17 | 2.09 | 0.08 |
| Histone acetyltransferase type B subunit 2 | HAT2 | CAALFM\_C604540CA | Q59RH5 | 0.08 | 0.95 | 0.08 |
| Putative hydrolase | NIT3 | CAALFM\_C110700CA | Q59WF0 | 0.23 | 2.92 | 0.08 |
| 40S ribosomal protein S1 (S3aE) | RPS1 | CAALFM\_C103090WA | P40910 | 0.56 | 7.12 | 0.08 |
| Uncharacterized protein |  | CAALFM\_CR06510WA | A0A1D8PT83 | 0.75 | 9.52 | 0.08 |
| Rct1p | RCT1 | CAALFM\_C305710WA | A0A1D8PKD1 | 0.16 | 2.06 | 0.08 |
| Rab family GTPase | VPS21 | CAALFM\_CR08060CA | Q59X89 | 0.16 | 2.08 | 0.08 |
| Ftr2p | FTR2 | CAALFM\_C114220CA | A0A1D8PFV2 | 0.15 | 2.09 | 0.07 |
| Transcription elongation factor | SPT6 | CAALFM\_C704300WA | Q3MNT0 | 0.10 | 1.32 | 0.07 |
| Uncharacterized protein |  | CAALFM\_C604410CA | A0A1D8PQE3 | 0.08 | 1.09 | 0.07 |
| Uncharacterized protein |  | CAALFM\_C108110WA | A0A1D8PEA9 | 0.10 | 1.40 | 0.07 |
| Dihydroxyacetone kinase | DAK2 | CAALFM\_C109190CA | A0A1D8PEI2 | 0.08 | 1.10 | 0.07 |
| Ribosomal 40S subunit protein S2 | RPS21 | CAALFM\_C101480CA | Q5A900 | 0.34 | 4.98 | 0.07 |
| Acetyl-CoA hydrolase | ACH1 | CAALFM\_C502000CA | P83773 | 2.14 | 31.60 | 0.07 |
| Adenosine kinase | ADO1 | CAALFM\_C603080CA | A0A1D8PQ26 | 0.39 | 5.88 | 0.07 |
| Threonine synthase | THR4 | CAALFM\_C502270WA | A0A1D8PNG9 | 0.16 | 2.39 | 0.07 |
| Mitogen-activated protein kinase | MKC1 | CAALFM\_CR00120CA | Q5AAG6 | 0.10 | 1.50 | 0.07 |
| Ribosomal 60S subunit protein L24A | RPL24A | CAALFM\_C404890CA | Q5A6A1 | 0.16 | 2.41 | 0.07 |
| Glutamine--fructose-6-phosphate aminotransferase | GFA1 | CAALFM\_C302280CA | P53704 | 0.33 | 5.13 | 0.06 |
| Malate dehydrogenase, cytoplasmic | MDH1 | CAALFM\_CR00540CA | P83778 | 0.42 | 6.66 | 0.06 |
| Uncharacterized protein |  | CAALFM\_C105160CA | A0A1D8PDH0 | 0.10 | 1.52 | 0.06 |
| Aspartate aminotransferase | AAT21 | CAALFM\_CR07620WA | Q59N40 | 0.70 | 11.31 | 0.06 |
| Dihydrolipoyl dehydrogenase | LPD1 | CAALFM\_CR07400CA | Q59RQ6 | 2.18 | 35.37 | 0.06 |
| Ran GTPase-binding protein | NTF2 | CAALFM\_C110100CA | A0A1D8PES3 | 0.49 | 8.15 | 0.06 |
| Replication protein A subunit | RFA1 | CAALFM\_C200380CA | Q5ACX4 | 0.10 | 1.62 | 0.06 |
| Histone H2B.2 | HTB2 | CAALFM\_C104180WA | Q59VP1 | 0.76 | 12.64 | 0.06 |
| Valine--tRNA ligase | VAS1 | CAALFM\_C206640CA | A0A1D8PHR0 | 0.16 | 2.62 | 0.06 |
| Uncharacterized protein |  | CAALFM\_C700630CA | A0A1D8PQM7 | 0.10 | 1.63 | 0.06 |
| Glutamate--tRNA ligase | GUS1 | CAALFM\_C700620WA | A0A1D8PQL8 | 0.16 | 2.67 | 0.06 |
| Carnitine O-acetyltransferase | CAT2 | CAALFM\_C402020WA | Q5AMQ5 | 0.58 | 9.83 | 0.06 |
| Uncharacterized protein |  | CAALFM\_C400410WA | Q59UQ1 | 0.08 | 1.32 | 0.06 |
| Uncharacterized protein |  | CAALFM\_C208100WA | A0A1D8PI22 | 0.10 | 1.64 | 0.06 |
| Eukaryotic translation initiation factor 3 subunit B (eIF3b) | PRT1 | CAALFM\_C701450CA | Q5AGV4 | 0.10 | 1.73 | 0.06 |
| Increased recombination centers protein 22-2 | IRC22-2 | CAALFM\_C210010CA | Q59XW9 | 0.08 | 1.36 | 0.06 |
| Protein transport protein SSO2 | SSO2 | CAALFM\_C209740WA | Q59YF0 | 0.17 | 3.10 | 0.06 |
| Oxidoreductase |  | CAALFM\_C401510WA | Q5AML3 | 0.25 | 4.55 | 0.05 |
| Threonine--tRNA ligase | THS1 | CAALFM\_C500110CA | A0A1D8PMV9 | 0.08 | 1.52 | 0.05 |
| Uncharacterized protein |  | CAALFM\_C304920CA | Q5ANE2 | 0.16 | 3.11 | 0.05 |
| Cullin-associated NEDD8-dissociated protein 1 | TIP120 | CAALFM\_C307610WA | Q5ADW3 | 0.10 | 1.98 | 0.05 |
| D-arabinose 1-dehydrogenase (NAD(P)(+)) | ARA1 | CAALFM\_C208130WA | A0A1D8PI24 | 0.16 | 3.39 | 0.05 |
| Heat shock protein 60, mitochondrial | HSP60 | CAALFM\_CR06490CA | O74261 | 0.25 | 5.56 | 0.05 |
| Type I HSP40 co-chaperone | YDJ1 | CAALFM\_CR04200WA | A0A1D8PSQ3 | 0.08 | 1.75 | 0.04 |
| Carnitine O-acetyltransferase | CTN1 | CAALFM\_C101740WA | Q59T80 | 0.08 | 1.80 | 0.04 |
| Uncharacterized protein |  | CAALFM\_C207650CA | A0A1D8PHY7 | 0.10 | 2.29 | 0.04 |
| Uncharacterized protein |  | CAALFM\_C504470CA | Q5AK88 | 0.39 | 9.33 | 0.04 |
| Nicotinate-nucleotide pyrophosphorylase [carboxylating] |  | CAALFM\_C107840WA | A0A1D8PE45 | 0.08 | 1.85 | 0.04 |
| Carnitine:acyl carnitine antiporter | CRC1 | CAALFM\_CR01980CA | Q5A967 | 0.17 | 4.14 | 0.04 |
| Ribosomal 40S subunit protein S11A |  | CAALFM\_C501540WA | A0A1D8PN83 | 0.08 | 1.90 | 0.04 |
| V-type proton ATPase subunit C | VMA5 | CAALFM\_C208190WA | Q5A2U9 | 0.08 | 1.97 | 0.04 |
| Aspartate transaminase | AAT1 | CAALFM\_C205250CA | A0A1D8PHC9 | 0.87 | 22.46 | 0.04 |
| Aspartate--tRNA ligase | DPS1-1 | CAALFM\_CR03170WA | Q59UF7 | 0.23 | 6.04 | 0.04 |
| Uncharacterized protein |  | CAALFM\_CR08990CA | A0A1D8PTU3 | 0.25 | 6.74 | 0.04 |
| Aldehyde dehydrogenase |  | CAALFM\_C100410CA | A0A1D8PC76 | 0.08 | 2.10 | 0.04 |
| Cytochrome c oxidase subunit 2 | COX2 | CaalfMp01 | Q9B8D8 | 0.10 | 2.70 | 0.04 |
| Uncharacterized protein |  | CAALFM\_C303410CA | Q5AED0 | 0.50 | 13.85 | 0.04 |
| Isocitrate dehydrogenase [NADP] | IDP1 | CAALFM\_C205890CA | A0A1D8PHH7 | 0.23 | 6.69 | 0.03 |
| V-type proton ATPase subunit a | VPH1 | CAALFM\_C405240CA | Q59R99 | 0.20 | 5.63 | 0.03 |
| Very-long-chain 3-oxoacyl-CoA reductase |  | CAALFM\_CR06070WA | Q59V93 | 0.17 | 5.07 | 0.03 |
| Ornithine carbamoyltransferase | ARG3 | CAALFM\_C603230WA | Q5ABU0 | 0.16 | 4.64 | 0.03 |
| Mlc1p | MLC1 | CAALFM\_CR03090CA | A0A1D8PSE1 | 0.08 | 2.28 | 0.03 |
| Serine hydroxymethyltransferase, cytosolic | SHM2 | CAALFM\_C603760CA | O13426 | 0.25 | 7.58 | 0.03 |
| V-type proton ATPase subunit |  | CAALFM\_C400020WA | A0A1D8PKX3 | 0.08 | 2.32 | 0.03 |
| Ribosomal 60S subunit protein L16A | RPL16A | CAALFM\_C100180WA | Q5AB87 | 0.10 | 2.93 | 0.03 |
| Calmodulin | CMD1 | CAALFM\_C406030WA | A0A1D8PMF8 | 0.18 | 5.78 | 0.03 |
| Coatomer subunit beta (Beta-coat protein) | SEC26 | CAALFM\_CR04380CA | Q5A6M6 | 0.08 | 2.58 | 0.03 |
| Ribosomal 60S subunit protein L10 | RPL10 | CAALFM\_C102460WA | Q5AIB8 | 0.16 | 5.39 | 0.03 |
| Heat shock protein homolog | MSI3 | CAALFM\_C106100CA | Q96VB9 | 0.56 | 19.62 | 0.03 |
| Thioredoxin reductase | TRR1 | CAALFM\_C502710WA | Q5AG89 | 0.17 | 6.07 | 0.03 |
| Dipeptidyl peptidase 3 |  | CAALFM\_C603960WA | A0A1D8PQB4 | 0.16 | 5.58 | 0.03 |
| Mdg1p | MDG1 | CAALFM\_C114290CA | A0A1D8PFV7 | 0.18 | 7.12 | 0.03 |
| Translation elongation factor 1 subunit beta | EFB1 | CAALFM\_C404480CA | A0A1D8PM35 | 0.08 | 3.03 | 0.03 |
| Uncharacterized protein |  | CAALFM\_C300850CA | A0A1D8PJ10 | 0.16 | 6.97 | 0.02 |
| Phm7p | PHM7 | CAALFM\_C208140CA | A0A1D8PI19 | 0.23 | 10.33 | 0.02 |
| Bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase | ADE17 | CAALFM\_CR04090CA | Q5A6R2 | 0.25 | 12.02 | 0.02 |
| Isoleucine biosynthesis protein | MMD1 | CAALFM\_C106900CA | A0A1D8PDX5 | 0.08 | 3.80 | 0.02 |
| D-arabinono-1,4-lactone oxidase | ALO1 | CAALFM\_CR09790WA | O93852 | 0.08 | 4.36 | 0.02 |
| Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited | ARO4 | CAALFM\_C105110CA | P79023 | 0.08 | 4.60 | 0.02 |
| Tfs1p | TFS1 | CAALFM\_C500930CA | Q5A1M1 | 0.16 | 9.81 | 0.02 |
| Type II HSP40 co-chaperone | SIS1 | CAALFM\_CR06080WA | Q59V92 | 0.08 | 4.93 | 0.02 |
| Long-chain fatty acid-CoA ligase | FAA4 | CAALFM\_CR10160WA | A0A1D8PU56 | 0.08 | 5.09 | 0.02 |
| Glycogen [starch] synthase | GSY1 | CAALFM\_CR00780CA | Q5A850 | 0.10 | 6.65 | 0.01 |
| Long-chain fatty acid transporter | ACB1 | CAALFM\_C700750WA | A0A1D8PQN3 | 0.08 | 5.51 | 0.01 |
| Heat shock protein | SSC1 | CAALFM\_C207380WA | P83784 | 0.31 | 22.62 | 0.01 |
| Ribosomal 60S subunit protein L3 | RPL3 | CAALFM\_C209430WA | Q59LS1 | 0.16 | 12.12 | 0.01 |
| Ribosomal 40S subunit protein S5 | RPS5 | CAALFM\_C503070WA | Q5AG43 | 0.16 | 12.41 | 0.01 |
| Ato1p | ATO1 | CAALFM\_C300920WA | A0A1D8PJ22 | 0.08 | 6.14 | 0.01 |
| Peptidyl-prolyl cis-trans isomerase | CPR3 | CAALFM\_C202320CA | Q5ALM6 | 0.08 | 6.95 | 0.01 |
| Aminopeptidase 2 | APE2 | CAALFM\_C104400CA | Q59KZ1 | 0.33 | 30.68 | 0.01 |
| V-type proton ATPase subunit B | VMA2 | CAALFM\_CR05780WA | Q59PT0 | 0.16 | 15.51 | 0.01 |
| Malate dehydrogenase | MDH1-1 | CAALFM\_C401900CA | Q5AMP4 | 0.17 | 24.00 | 0.01 |
| V-type proton ATPase catalytic subunit A | TFP1 | CAALFM\_C301630WA | Q5AJB1 | 0.10 | 13.78 | 0.01 |
| Heat shock protein SSA2 | SSA2 | CAALFM\_C104300CA | P46587 | 0.00 | 52.87 | matrix unique |
| Lipid-binding protein | LSP1 | CAALFM\_C206730WA | Q59KV8 | 0.08 | 20.37 | matrix unique |
| Slk19p | SLK19 | CAALFM\_C307310CA | Q5ADT0 | 0.00 | 19.81 | matrix unique |
| Aconitate hydratase, mitochondrial | ACO1 | CAALFM\_CR08210CA | P82611 | 0.00 | 17.28 | matrix unique |
| Small heat shock protein 21 | HSP21 | CAALFM\_C204010CA | Q5AHH4 | 0.00 | 16.20 | matrix unique |
| Glutathione-disulfide reductase | GLR1 | CAALFM\_C501520CA | Q59NQ5 | 0.00 | 14.82 | matrix unique |
| Bifunctional 4-alpha-glucanotransferase/amylo-alpha-1,6-glucosidase | GDB1 | CAALFM\_C405140CA | Q59MN2 | 0.00 | 12.24 | matrix unique |
| Pyruvate dehydrogenase E1 component subunit alpha | PDA1 | CAALFM\_C407110CA | Q5A0Z9 | 0.00 | 10.49 | matrix unique |
| Oligo-1,6-glucosidase IMA1 | MAL2 | CAALFM\_CR10790WA | A0A1D8PUB9 | 0.00 | 10.26 | matrix unique |
| Ribose-5-phosphate isomerase | RKI1 | CAALFM\_C301480CA | Q5AJ92 | 0.00 | 9.41 | matrix unique |
| Non-histone chromosomal protein 6 | NHP6 | CAALFM\_C401700CA | Q9UVL1 | 0.00 | 9.04 | matrix unique |
| Zuotin | ZUO1 | CAALFM\_C402870CA | Q5AF98 | 0.00 | 8.73 | matrix unique |
| Trifunctional formate-tetrahydrofolate ligase/methenyltetrahydrofolate cyclohydrolase/methylenetetrahydrofolate dehydrogenase | MIS11 | CAALFM\_CR07010WA | Q59SM8 | 0.00 | 8.72 | matrix unique |
| Trehalose-phosphatase | TPS2 | CAALFM\_C103380WA | Q5AI14 | 0.00 | 8.62 | matrix unique |
| Vacuolar protein 8 | VAC8 | CAALFM\_C405150WA | Q59MN0 | 0.00 | 8.47 | matrix unique |
| Lipid-binding protein | PIL1 | CAALFM\_C104680WA | A0A1D8PDD1 | 0.00 | 8.24 | matrix unique |
| 1-pyrroline-5-carboxylate dehydrogenase | PUT2 | CAALFM\_C504880CA | Q5AK46 | 0.00 | 7.73 | matrix unique |
| Alpha-ketoglutarate dehydrogenase | KGD1 | CAALFM\_C300880WA | A0A1D8PJ26 | 0.00 | 7.59 | matrix unique |
| Ribosomal 60S subunit protein L8B | RPL8B | CAALFM\_C305240CA | Q5ANA1 | 0.00 | 7.04 | matrix unique |
| Lysine--tRNA ligase | KRS1 | CAALFM\_C307410CA | Q5ADU2 | 0.00 | 6.74 | matrix unique |
| Phosphoribosylformylglycinamidine synthase | ADE6 | CAALFM\_CR04740CA | Q59MZ5 | 0.00 | 6.48 | matrix unique |
| Phosphoserine aminotransferase | SER1 | CAALFM\_C206210CA | Q59P52 | 0.00 | 6.16 | matrix unique |
| Heat shock protein 78, mitochondrial | HSP78 | CAALFM\_C203390CA | Q96UX5 | 0.00 | 6.07 | matrix unique |
| Carnitine O-acetyltransferase | CTN3 | CAALFM\_C304000CA | Q59MQ8 | 0.00 | 5.46 | matrix unique |
| Alanine--tRNA ligase | ALA1 | CAALFM\_C603720WA | Q5A8K2 | 0.00 | 5.41 | matrix unique |
| Ribosomal protein L15 | RPL15A | CAALFM\_CR04100CA | Q5A6R1 | 0.00 | 5.36 | matrix unique |
| Abp1p | ABP1 | CAALFM\_C402940WA | Q5AFA8 | 0.00 | 5.36 | matrix unique |
| Fumarase | FUM11 | CAALFM\_CR04530WA | Q5A6L1 | 0.00 | 5.31 | matrix unique |
| Putative phosphomutase |  | CAALFM\_C306920WA | Q5ADN2 | 0.00 | 5.26 | matrix unique |
| Ofr1p | OFR1 | CAALFM\_C108060WA | Q5A784 | 0.00 | 5.19 | matrix unique |
| Polyadenylate-binding protein, cytoplasmic and nuclear | PAB1 | CAALFM\_C103370WA | Q5AI15 | 0.00 | 5.19 | matrix unique |
| 40S ribosomal protein S8 | RPS8A | CAALFM\_C205610CA | Q59T44 | 0.00 | 5.17 | matrix unique |
| Tom40p | TOM40 | CAALFM\_C701970CA | Q5AH14 | 0.00 | 4.91 | matrix unique |
| Leucine--tRNA ligase | CDC60 | CAALFM\_CR01690CA | A0A1D8PS12 | 0.00 | 4.91 | matrix unique |
| Protein channel | TOM70 | CAALFM\_C702640WA | Q59LZ5 | 0.00 | 4.91 | matrix unique |
| Glycine--tRNA ligase | GRS1 | CAALFM\_C105290WA | Q5A2A5 | 0.00 | 4.90 | matrix unique |
| ATP-dependent 6-phosphofructokinase | PFK1 | CAALFM\_C504810WA | Q5AK53 | 0.00 | 4.87 | matrix unique |
| Cystathionine beta-synthase | CYS4 | CAALFM\_C101870CA | Q59T95 | 0.00 | 4.70 | matrix unique |
| Glycerol 2-dehydrogenase (NADP(+)) | GCY1 | CAALFM\_C307340WA | Q5ADT4 | 0.00 | 4.66 | matrix unique |
| AAA family ATPase | CDC48 | CAALFM\_C110790WA | Q59WG3 | 0.00 | 4.65 | matrix unique |
| Rim1p | RIM1 | CAALFM\_C105680CA | Q5AA01 | 0.00 | 4.62 | matrix unique |
| Etr1p | ETR1 | CAALFM\_C300200CA | A0A1D8PIW1 | 0.00 | 4.58 | matrix unique |
| Bfr1p | BFR1 | CAALFM\_C402270CA | Q5AMT7 | 0.00 | 4.56 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C103100WA | A0A1D8PCX0 | 0.00 | 4.56 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C100420WA | Q5ABA5 | 0.00 | 4.52 | matrix unique |
| Serine hydroxymethyltransferase | SHM1 | CAALFM\_C703330CA | A0A1D8PRB3 | 0.00 | 4.48 | matrix unique |
| Aldo-keto reductase superfamily protein |  | CAALFM\_C306860CA | Q5ADM5 | 0.00 | 4.36 | matrix unique |
| Protein transport protein SEC61 subunit alpha | SEC61 | CAALFM\_C307810CA | Q9P8E3 | 0.00 | 4.33 | matrix unique |
| Inosine-5'-monophosphate dehydrogenase | IMH3 | CAALFM\_C206390CA | Q59Q46 | 0.00 | 4.24 | matrix unique |
| Ribosomal 60S subunit protein L4B | RPL4B | CAALFM\_C114110CA | A0A1D8PFV1 | 0.00 | 4.22 | matrix unique |
| NADPH--cytochrome P450 reductase | NCP1 | CAALFM\_C403180WA | A0A1D8PLR7 | 0.00 | 4.20 | matrix unique |
| Hsp90 cochaperone | STI1 | CAALFM\_C501820WA | A0A1D8PN90 | 0.00 | 4.11 | matrix unique |
| FACT complex subunit SPT16 | CDC68 | CAALFM\_C406500WA | Q5A1D5 | 0.00 | 4.09 | matrix unique |
| Amino acid transporter | AGC1 | CAALFM\_C113400CA | Q5AL11 | 0.00 | 4.07 | matrix unique |
| Yhm2p | YHM2 | CAALFM\_C600600CA | Q59NH3 | 0.00 | 4.06 | matrix unique |
| Tricalbin |  | CAALFM\_C110680CA | A0A1D8PEY6 | 0.00 | 4.02 | matrix unique |
| 40S ribosomal protein S24 | RPS24 | CAALFM\_C300090WA | Q5A7K0 | 0.00 | 3.99 | matrix unique |
| Glutamine--tRNA ligase | GLN4 | CAALFM\_C700550CA | A0A1D8PQM9 | 0.00 | 3.92 | matrix unique |
| Adenosine 5'-monophosphoramidase | HNT1 | CAALFM\_C110780CA | Q59WG0 | 0.00 | 3.88 | matrix unique |
| Multiple drug resistance-associated protein-like transporter 1 | MLT1 | CAALFM\_C108210CA | Q5A762 | 0.00 | 3.84 | matrix unique |
| Ist2p | IST2 | CAALFM\_C107520CA | A0A1D8PE41 | 0.00 | 3.81 | matrix unique |
| Cysteine--tRNA ligase |  | CAALFM\_C113030CA | Q5AL46 | 0.00 | 3.79 | matrix unique |
| Vtc4p | VTC4 | CAALFM\_C403360CA | Q59PH5 | 0.00 | 3.71 | matrix unique |
| Ribosomal 40S subunit protein S20 | RPS20 | CAALFM\_CR08150WA | Q5A389 | 0.00 | 3.60 | matrix unique |
| Alpha-ketoglutarate dehydrogenase | KGD2 | CAALFM\_CR07420WA | A0A1D8PTH3 | 0.00 | 3.57 | matrix unique |
| GMP synthase [glutamine-hydrolyzing] | GUA1 | CAALFM\_C109490CA | Q5APF2 | 0.00 | 3.55 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR08050CA | Q59X88 | 0.00 | 3.53 | matrix unique |
| Tropomyosin | TPM2 | CAALFM\_CR08460WA | A0A1D8PTR7 | 0.00 | 3.47 | matrix unique |
| Pyruvate dehydrogenase E1 component subunit beta | PDB1 | CAALFM\_C404150CA | Q5A5V6 | 0.00 | 3.40 | matrix unique |
| Glyoxylate reductase |  | CAALFM\_C405390WA | Q59P08 | 0.00 | 3.38 | matrix unique |
| Cation-transporting ATPase | SPF1 | CAALFM\_C206540CA | Q59Q34 | 0.00 | 3.35 | matrix unique |
| Bifunctional carbamoylphosphate synthetase/aspartate transcarbamylase | URA2 | CAALFM\_CR07050CA | A0A1D8PTD1 | 0.00 | 3.33 | matrix unique |
| Pentafunctional AROM polypeptide | ARO1 | CAALFM\_C400890WA | Q5AME2 | 0.00 | 3.30 | matrix unique |
| Aspartate-semialdehyde dehydrogenase | HOM2 | CAALFM\_C202370CA | Q5ALM0 | 0.00 | 3.29 | matrix unique |
| Putative phosphotransferase |  | CAALFM\_C402620CA | Q5AF71 | 0.00 | 3.28 | matrix unique |
| Transcriptional regulator | HMO1 | CAALFM\_CR05670CA | Q59PR9 | 0.00 | 3.26 | matrix unique |
| Arc1p | ARC1 | CAALFM\_CR03060WA | A0A1D8PSC8 | 0.00 | 3.22 | matrix unique |
| Bifunctional hydroxyacyl-CoA dehydrogenase/enoyl-CoA hydratase | FOX2 | CAALFM\_C300810CA | A0A1D8PJ13 | 0.00 | 3.22 | matrix unique |
| Aminomethyltransferase | GCV1 | CAALFM\_C602500CA | A0A1D8PPW9 | 0.00 | 3.21 | matrix unique |
| Na(+)-exporting P-type ATPase | ENA2 | CAALFM\_C100390WA | Q5ABA1 | 0.00 | 3.17 | matrix unique |
| Serine--tRNA ligase, cytoplasmic | SES1 | CAALFM\_C302780WA | Q9HGT6 | 0.00 | 3.12 | matrix unique |
| Eukaryotic translation initiation factor 3 subunit C | NIP1 | CAALFM\_C401490WA | Q5AML1 | 0.00 | 3.07 | matrix unique |
| Pho88p | PHO88 | CAALFM\_CR09320CA | A0A1D8PTX9 | 0.00 | 3.05 | matrix unique |
| Ubiquinol--cytochrome-c reductase catalytic subunit | CYT1 | CAALFM\_C204950CA | A0A1D8PHA3 | 0.00 | 2.98 | matrix unique |
| Dihydroorotase | URA4 | CAALFM\_C500900CA | Q5A1L8 | 0.00 | 2.96 | matrix unique |
| Glycine cleavage system P protein | GCV2 | CAALFM\_C108400CA | A0A1D8PE97 | 0.00 | 2.96 | matrix unique |
| Glycine cleavage system H protein | GCV3 | CAALFM\_C113680CA | Q5AKX1 | 0.00 | 2.94 | matrix unique |
| Cytochrome b-c1 complex subunit 7 | QCR7 | CAALFM\_C603400CA | Q5ABS1 | 0.00 | 2.91 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C601560WA | Q5A4L1 | 0.00 | 2.91 | matrix unique |
| Kynureninase | BNA5 | CAALFM\_C108490WA | Q59QC4 | 0.00 | 2.87 | matrix unique |
| Calcium channel | YVC1 | CAALFM\_C207730WA | Q5A2J7 | 0.00 | 2.86 | matrix unique |
| Elongation factor Tu | TUF1 | CAALFM\_C100590WA | Q5ABC3 | 0.00 | 2.82 | matrix unique |
| Zn(2+) transporter |  | CAALFM\_C202180WA | A0A1D8PGH6 | 0.00 | 2.79 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C504950CA | A0A1D8PP33 | 0.00 | 2.79 | matrix unique |
| Ena21p | ENA21 | CAALFM\_C702910WA | Q5A5B0 | 0.00 | 2.77 | matrix unique |
| Putative Xaa-Pro dipeptidase |  | CAALFM\_C114450CA | A0A1D8PFY5 | 0.00 | 2.73 | matrix unique |
| Coatomer subunit alpha |  | CAALFM\_C301720CA | A0A1D8PJB0 | 0.00 | 2.73 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C102270CA | A0A1D8PCP4 | 0.00 | 2.65 | matrix unique |
| Phb1p | PHB1 | CAALFM\_C303730CA | Q59SS4 | 0.00 | 2.65 | matrix unique |
| Chaperonin-containing T-complex subunit | CCT2 | CAALFM\_C209520CA | Q59YC4 | 0.00 | 2.64 | matrix unique |
| Thioredoxin peroxidase | DOT5 | CAALFM\_C300480CA | Q5A7P9 | 0.00 | 2.63 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C200880WA | Q5AD31 | 0.00 | 2.63 | matrix unique |
| Galactokinase | GAL1 | CAALFM\_C102130CA | Q59VY8 | 0.00 | 2.55 | matrix unique |
| Pdx1p | PDX1 | CAALFM\_C113830CA | Q5AKV6 | 0.00 | 2.54 | matrix unique |
| Protein FMP52, mitochondrial | FMP52 | CAALFM\_C110280CA | Q5AP65 | 0.00 | 2.54 | matrix unique |
| Serine/threonine-protein phosphatase | GLC7 | CAALFM\_CR07650WA | Q59N42 | 0.00 | 2.53 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C210670WA | Q5A5Q4 | 0.00 | 2.52 | matrix unique |
| Glutamine-dependent NAD(+) synthetase |  | CAALFM\_C201530CA | Q5ALW6 | 0.00 | 2.51 | matrix unique |
| Myosin 2 | MYO2 | CAALFM\_C113780WA | Q5AKW2 | 0.00 | 2.50 | matrix unique |
| ATP-binding cassette family ATPase | KRE30 | CAALFM\_C208000CA | Q5A2T2 | 0.00 | 2.49 | matrix unique |
| Sorbose reductase | SOU1 | CAALFM\_C406390WA | P87219 | 0.00 | 2.48 | matrix unique |
| Histone H2A.2 | HTA2 | CAALFM\_C104170CA | Q59VP2 | 0.00 | 2.37 | matrix unique |
| Flavohemoprotein | YHB1 | CAALFM\_CR07790CA | Q59MV9 | 0.00 | 2.36 | matrix unique |
| Small COPII coat GTPase | SAR1 | CAALFM\_C602220WA | Q59S78 | 0.00 | 2.33 | matrix unique |
| Gcf1p | GCF1 | CAALFM\_C108550CA | Q59QB8 | 0.00 | 2.32 | matrix unique |
| 4-aminobutyrate transaminase | UGA1 | CAALFM\_C204190CA | A0A1D8PH55 | 0.00 | 2.30 | matrix unique |
| Translation initiation factor eIF2 subunit alpha | SUI2 | CAALFM\_C106960WA | Q5AAU7 | 0.00 | 2.29 | matrix unique |
| Dolichyl-phosphate-mannose--protein mannosyltransferase 1 | PMT1 | CAALFM\_C702890CA | O74189 | 0.00 | 2.26 | matrix unique |
| 40S ribosomal protein S6 | RPS6A | CAALFM\_C401270WA | A0A1D8PL99 | 0.00 | 2.25 | matrix unique |
| NADH-cytochrome b5 reductase 1 | CBR1 | CAALFM\_C405450CA | Q59P03 | 0.00 | 2.23 | matrix unique |
| Yhm1p | YHM1 | CAALFM\_C601930WA | A0A1D8PPR4 | 0.00 | 2.22 | matrix unique |
| Glycerol-3-phosphate dehydrogenase | GUT2 | CAALFM\_C406760WA | A0A1D8PMP1 | 0.00 | 2.21 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C112140WA | Q5A3M0 | 0.00 | 2.18 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C704210CA | A0A1D8PRJ1 | 0.00 | 2.18 | matrix unique |
| Sterol 24-C-methyltransferase | ERG6 | CAALFM\_C302150CA | O74198 | 0.00 | 2.13 | matrix unique |
| Transcription regulator | SSN6 | CAALFM\_C307020WA | Q5ADP3 | 0.00 | 2.11 | matrix unique |
| Nucleolar protein 58 | NOP58 | CAALFM\_C600370CA | Q59S06 | 0.00 | 2.11 | matrix unique |
| Proteasome regulatory particle base subunit | RPT1 | CAALFM\_C105240CA | Q5A2A0 | 0.00 | 2.10 | matrix unique |
| Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit | STT3 | CAALFM\_C201670CA | Q5ALU8 | 0.00 | 2.10 | matrix unique |
| ATP-dependent (S)-NAD(P)H-hydrate dehydratase |  | CAALFM\_C602030CA | Q59M69 | 0.00 | 2.10 | matrix unique |
| NADH-ubiquinone reductase (H(+)-translocating) | NDE1 | CAALFM\_C303420CA | Q5AEC9 | 0.00 | 2.10 | matrix unique |
| Sphingolipid transporter | NCR1 | CAALFM\_C114300CA | A0A1D8PFW9 | 0.00 | 2.05 | matrix unique |
| Myosin-5 | MYO5 | CAALFM\_C405100CA | Q59MQ0 | 0.00 | 2.03 | matrix unique |
| 40S ribosomal protein S26 | RPS26A | CAALFM\_C201610CA | Q5ALV6 | 0.00 | 2.00 | matrix unique |
| Actin-related protein 2/3 complex subunit 5 | ARC15 | CAALFM\_CR07210WA | Q59RN2 | 0.00 | 2.00 | matrix unique |
| Dolichyl-phosphate-mannose--protein mannosyltransferase 2 | PMT2 | CAALFM\_C306890WA | Q5ADM9 | 0.00 | 1.99 | matrix unique |
| Hsp30p | HSP30 | CAALFM\_C101990WA | Q59TA5 | 0.00 | 1.99 | matrix unique |
| rRNA methyltransferase | NOP1 | CAALFM\_C406720WA | Q5A0V9 | 0.00 | 1.98 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C701510WA | Q5AGW0 | 0.00 | 1.98 | matrix unique |
| Cytochrome c oxidase subunit IV | COX4 | CAALFM\_C201620WA | Q5ALV5 | 0.00 | 1.98 | matrix unique |
| D-lactate dehydrogenase | AIP2 | CAALFM\_C303040WA | A0A1D8PJK5 | 0.00 | 1.95 | matrix unique |
| S-formylglutathione hydrolase |  | CAALFM\_CR09670CA | A0A1D8PU04 | 0.00 | 1.88 | matrix unique |
| Protein SEY1 | SEY1 | CAALFM\_C604570WA | Q9C0L9 | 0.00 | 1.86 | matrix unique |
| tRNA (Cytosine-5-)-methyltransferase |  | CAALFM\_CR04300WA | A0A1D8PSR2 | 0.00 | 1.84 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C207010WA | A0A1D8PHU4 | 0.00 | 1.76 | matrix unique |
| Ribosomal 60S subunit protein L17B | RPL17B | CAALFM\_C204600CA | Q59TE0 | 0.00 | 1.73 | matrix unique |
| Hgt19p | HGT19 | CAALFM\_C300220WA | Q5A7L9 | 0.00 | 1.72 | matrix unique |
| RFX-like DNA-binding protein RFX2 | RFX2 | CAALFM\_C402030WA | Q5AMQ6 | 0.00 | 1.71 | matrix unique |
| Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial | SDH2 | CAALFM\_CR05180CA | Q59QN7 | 0.00 | 1.68 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C204370WA | Q59TB4 | 0.00 | 1.67 | matrix unique |
| Metacaspase-1 | MCA1 | CAALFM\_C305190CA | Q5ANA8 | 0.00 | 1.67 | matrix unique |
| Regulator of cytoskeleton and endocytosis RVS161 | RVS161 | CAALFM\_C700020CA | Q5AFE4 | 0.00 | 1.67 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C205570CA | Q59T48 | 0.00 | 1.66 | matrix unique |
| Cell growth-regulated gene 1 protein | CGR1 | CAALFM\_C402760CA | P56553 | 0.00 | 1.66 | matrix unique |
| Dihydroorotate dehydrogenase (quinone), mitochondrial | URA9 | CAALFM\_C109720WA | Q874I4 | 0.00 | 1.65 | matrix unique |
| Cytochrome c oxidase subunit VI | COX6 | CAALFM\_C203470CA | A0A1D8PH08 | 0.00 | 1.63 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C403770WA | A0A1D8PLW9 | 0.00 | 1.62 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C404160WA | Q5A5V8 | 0.00 | 1.62 | matrix unique |
| RuvB-like helicase 1 | RVB1 | CAALFM\_C406800WA | Q5A0W7 | 0.00 | 1.62 | matrix unique |
| Virulence protein | SSD1 | CAALFM\_C504730CA | Q5AK62 | 0.00 | 1.61 | matrix unique |
| Eukaryotic translation initiation factor 3 subunit A (eIF3a) | RPG1A | CAALFM\_C112770WA | Q59PL9 | 0.00 | 1.56 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR08920WA | A0A1D8PTU4 | 0.00 | 1.56 | matrix unique |
| Ribosome assembly factor mrt4 | MRT4 | CAALFM\_C602770WA | Q5AC00 | 0.00 | 1.55 | matrix unique |
| Dolichyl-phosphate beta-D-mannosyltransferase | DPM1 | CAALFM\_C108010WA | A0A1D8PEA2 | 0.00 | 1.55 | matrix unique |
| Guanine nucleotide-binding protein subunit alpha | GPA2 | CAALFM\_C302240CA | A0A1D8PJG1 | 0.00 | 1.55 | matrix unique |
| mRNA-binding protein | NPL3 | CAALFM\_C114280CA | A0A1D8PFV4 | 0.00 | 1.55 | matrix unique |
| Ssz1p | SSZ1 | CAALFM\_C404700WA | Q5A678 | 0.00 | 1.54 | matrix unique |
| Ribosomal 60S subunit protein L30 | RPL30 | CAALFM\_C404900WA | A0A1D8PM75 | 0.00 | 1.52 | matrix unique |
| Vacuolar transporter chaperone | VTC3 | CAALFM\_CR03610CA | A0A1D8PSJ6 | 0.00 | 1.52 | matrix unique |
| Histone H2A.1 | HTA1 | CAALFM\_C303910WA | Q59SU5 | 0.00 | 1.52 | matrix unique |
| Pst2p | PST2 | CAALFM\_C208640CA | Q59Y37 | 0.00 | 1.52 | matrix unique |
| Aldo-keto reductase superfamily protein |  | CAALFM\_C703350CA | A0A1D8PRB0 | 0.00 | 1.52 | matrix unique |
| Dynamin-like GTPase | VPS1 | CAALFM\_C501210WA | A0A1D8PN45 | 0.00 | 1.51 | matrix unique |
| Tyrosine--tRNA ligase | TYS1 | CAALFM\_C402980WA | Q5AFB3 | 0.00 | 1.50 | matrix unique |
| RuvB-like helicase 2 | RVB2 | CAALFM\_C701810WA | Q5AGZ9 | 0.00 | 1.50 | matrix unique |
| Ribosomal 60S subunit protein L2A | RPL2 | CAALFM\_C111060CA | A0A1D8PF08 | 0.00 | 1.49 | matrix unique |
| MICOS complex subunit MIC60 (Mitofilin) | MIC60 | CAALFM\_CR03530WA | Q5A044 | 0.00 | 1.49 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C405810WA | Q5A441 | 0.00 | 1.49 | matrix unique |
| Ras GTPase activating protein | IRA2 | CAALFM\_C112450CA | A0A1D8PFE8 | 0.00 | 1.48 | matrix unique |
| Translocation protein SEC62 | SEC62 | CAALFM\_C103340CA | Q5AI21 | 0.00 | 1.47 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C301420CA | Q5AJ84 | 0.00 | 1.47 | matrix unique |
| Phenylpyruvate decarboxylase | ARO10 | CAALFM\_CR06860CA | Q59MU3 | 0.00 | 1.46 | matrix unique |
| Xylulokinase | XKS1 | CAALFM\_C405300WA | A0A1D8PMB3 | 0.00 | 1.45 | matrix unique |
| L-aminoadipate-semialdehyde dehydrogenase | LYS2 | CAALFM\_C102820WA | A0A1D8PCV7 | 0.00 | 1.44 | matrix unique |
| Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 | OST1 | CAALFM\_C305530WA | A0A1D8PK87 | 0.00 | 1.44 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C302270WA | A0A1D8PJE5 | 0.00 | 1.44 | matrix unique |
| 3-hydroxy-3-methylglutaryl coenzyme A reductase (HMG-CoA reductase) | HMG1 | CAALFM\_C103780CA | A0A1D8PD39 | 0.00 | 1.42 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C111200WA | A0A1D8PF42 | 0.00 | 1.42 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C109430WA | A0A1D8PEK8 | 0.00 | 1.41 | matrix unique |
| ATP synthase subunit gamma | ATP3 | CAALFM\_CR01310WA | A0A1D8PRY3 | 0.00 | 1.40 | matrix unique |
| Prohibitin subunit | PHB2 | CAALFM\_C305030WA | Q5AND0 | 0.00 | 1.39 | matrix unique |
| Putative ATP-dependent permease | ADP1 | CAALFM\_CR05950CA | A0A1D8PT53 | 0.00 | 1.36 | matrix unique |
| Signal peptidase complex subunit | SPC2 | CAALFM\_C400620CA | Q59SJ1 | 0.00 | 1.35 | matrix unique |
| 60S ribosomal protein L20 | RPL20B | CAALFM\_C401520CA | A0A1D8PLC9 | 0.00 | 1.35 | matrix unique |
| Histidine--tRNA ligase | HTS1 | CAALFM\_C505490CA | Q5AJX0 | 0.00 | 1.33 | matrix unique |
| Vcx1p | VCX1 | CAALFM\_C108580CA | Q59QB4 | 0.00 | 1.33 | matrix unique |
| Mitochondrial 2-oxodicarboxylate carrier |  | CAALFM\_CR05480WA | A0A1D8PT04 | 0.00 | 1.33 | matrix unique |
| Uroporphyrinogen decarboxylase |  | CAALFM\_C210860CA | Q5A5N0 | 0.00 | 1.32 | matrix unique |
| Cullin | CDC53 | CAALFM\_C301700WA | Q5AJB7 | 0.00 | 1.32 | matrix unique |
| Proteasome regulatory particle base subunit | RPT5 | CAALFM\_C406870WA | A0A1D8PMQ4 | 0.00 | 1.32 | matrix unique |
| Mitogen-activated protein kinase | HOG1 | CAALFM\_C203330CA | Q92207 | 0.00 | 1.32 | matrix unique |
| Threonine dehydratase (EC 4.3.1.19) (Threonine deaminase) | ILV1 | CAALFM\_C206190WA | Q59P56 | 0.00 | 1.32 | matrix unique |
| Asr3p | ASR3 | CAALFM\_C203790CA | A0A1D8PH00 | 0.00 | 1.32 | matrix unique |
| Purine nucleoside phosphorylase (EC 2.4.2.1) (Inosine-guanosine phosphorylase) | PNP1 | CAALFM\_C303180CA | A0A1D8PJL8 | 0.00 | 1.31 | matrix unique |
| Single-stranded telomeric DNA-binding/mRNA-binding protein | GBP2 | CAALFM\_C700440CA | A0A1D8PQM1 | 0.00 | 1.31 | matrix unique |
| Maltose permease | MAL31 | CAALFM\_C504930CA | Q5AK39 | 0.00 | 1.31 | matrix unique |
| Tif11p | TIF11 | CAALFM\_C210710WA | Q5A5P8 | 0.00 | 1.30 | matrix unique |
| Bromodomain-containing factor 1 | BDF1 | CAALFM\_C500200CA | Q5A4W8 | 0.00 | 1.30 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C102650WA | A0A1D8PCU5 | 0.00 | 1.30 | matrix unique |
| Septation protein 7 | SEP7 | CAALFM\_C102230WA | Q59VX8 | 0.00 | 1.29 | matrix unique |
| Phospholipase | PLD1 | CAALFM\_C111590WA | A0A1D8PF62 | 0.00 | 1.25 | matrix unique |
| Zinc metalloprotease | STE24 | CAALFM\_C400280WA | A0A1D8PL01 | 0.00 | 1.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR03120WA | A0A1D8PSE0 | 0.00 | 1.22 | matrix unique |
| Sam51p | SAM51 | CAALFM\_C500640CA | A0A1D8PN01 | 0.00 | 1.21 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C209040WA | A0A1D8PIF1 | 0.00 | 1.20 | matrix unique |
| Alanine transaminase | ALT1 | CAALFM\_C303480CA | A0A1D8PJP4 | 0.00 | 1.20 | matrix unique |
| Tubulin-specific chaperone A |  | CAALFM\_CR04650WA | A0A1D8PST9 | 0.00 | 1.20 | matrix unique |
| Elongation factor G, mitochondrial (EF-Gmt) | MEF1 | CAALFM\_C113060CA | Q5AL45 | 0.00 | 1.19 | matrix unique |
| Snl1p | SNL1 | CAALFM\_C110530WA | Q59NB3 | 0.00 | 1.18 | matrix unique |
| Glucosamine 6-phosphate N-acetyltransferase | GNA1 | CAALFM\_C203870WA | Q5AHF9 | 0.00 | 1.17 | matrix unique |
| CTP synthase | URA7 | CAALFM\_C504570CA | Q5AK79 | 0.00 | 1.17 | matrix unique |
| Clustered mitochondria protein homolog | CLU1 | CAALFM\_C104970WA | Q59MA9 | 0.00 | 1.17 | matrix unique |
| Zinc finger-containing protein | ZPR1 | CAALFM\_C101110CA | Q5A934 | 0.00 | 1.17 | matrix unique |
| V-SNARE protein | VTI1 | CAALFM\_C303400CA | A0A1D8PJW1 | 0.00 | 1.14 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C700350CA | A0A1D8PQJ8 | 0.00 | 1.14 | matrix unique |
| Uridylate kinase | URA6 | CAALFM\_C104420CA | Q59KZ3 | 0.00 | 1.12 | matrix unique |
| Protein SDS23 | SDS24 | CAALFM\_C108370WA | Q5A744 | 0.00 | 1.12 | matrix unique |
| Proteasome regulatory particle lid subunit |  | CAALFM\_C208930WA | Q59SD0 | 0.00 | 1.12 | matrix unique |
| Carboxymethylenebutenolidase |  | CAALFM\_C102780WA | Q5AI87 | 0.00 | 1.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C203260WA | Q5AH92 | 0.00 | 1.11 | matrix unique |
| Bifunctional 4-hydroxy-4-methyl-2-oxoglutarate aldolase/oxaloacetate decarboxylase |  | CAALFM\_C110240CA | Q5AP69 | 0.00 | 1.11 | matrix unique |
| Phospholipid-transporting ATPase |  | CAALFM\_C303250WA | A0A1D8PJN3 | 0.00 | 1.11 | matrix unique |
| ATP-binding cassette transporter | SNQ2 | CAALFM\_C603840CA | A0A1D8PQ95 | 0.00 | 1.11 | matrix unique |
| Phosphatidylinositol 4,5-bisphosphate-binding protein | SLM2 | CAALFM\_C602060WA | A0A1D8PPT0 | 0.00 | 1.11 | matrix unique |
| Obg-like ATPase 1 | YBN5 | CAALFM\_C104890WA | A0A1D8PDE8 | 0.00 | 1.10 | matrix unique |
| Centromere/microtubule-binding protein | CBF5 | CAALFM\_C110620WA | O43101 | 0.00 | 1.10 | matrix unique |
| Aspartate aminotransferase | AAT22 | CAALFM\_C401200CA | A0A1D8PL85 | 0.00 | 1.09 | matrix unique |
| Ifg3p | IFG3 | CAALFM\_C500450CA | A0A1D8PMX7 | 0.00 | 1.09 | matrix unique |
| Methylglyoxal reductase (NADPH-dependent) |  | CAALFM\_C603240WA | Q5ABT9 | 0.00 | 1.09 | matrix unique |
| Pin3p | PIN3 | CAALFM\_C304880WA | Q5ANE7 | 0.00 | 1.09 | matrix unique |
| NADPH:quinone reductase |  | CAALFM\_C207070WA | Q59Z38 | 0.00 | 1.09 | matrix unique |
| Bifunctional farnesyl-diphosphate farnesyltransferase/squalene synthase | ERG9 | CAALFM\_C208610WA | A0A1D8PI71 | 0.00 | 1.09 | matrix unique |
| Ribosomal 40S subunit protein S17B | RPS17B | CAALFM\_C110870WA | A0A1D8PEY9 | 0.00 | 1.08 | matrix unique |
| Adenylate kinase isoenzyme 6 homolog | HBR1 | CAALFM\_C100340WA | Q8TG40 | 0.00 | 1.08 | matrix unique |
| Protein-transporting protein |  | CAALFM\_CR04080CA | A0A1D8PSM6 | 0.00 | 1.08 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C700250CA | A0A1D8PQJ1 | 0.00 | 1.06 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C500100CA | A0A1D8PMU2 | 0.00 | 1.03 | matrix unique |
| Ubiquitin carboxyl-terminal hydrolase |  | CAALFM\_C106390WA | A0A1D8PDR9 | 0.00 | 1.02 | matrix unique |
| Increased recombination centers protein 22-1 | IRC22-1 | CAALFM\_C209780CA | Q59YF4 | 0.00 | 1.02 | matrix unique |
| Glutathione synthetase | GSH2 | CAALFM\_CR08370WA | Q5A359 | 0.00 | 1.01 | matrix unique |
| Serine/threonine protein kinase |  | CAALFM\_C108540CA | Q59QB9 | 0.00 | 1.00 | matrix unique |
| Zn(2+) transporter |  | CAALFM\_C202200WA | A0A1D8PGL8 | 0.00 | 1.00 | matrix unique |
| Sedoheptulose-bisphosphatase |  | CAALFM\_C207420WA | A0A1D8PHW0 | 0.00 | 0.99 | matrix unique |
| Histone H3.3 | HHT3 | CAALFM\_C307090WA | Q5ADQ0 | 0.00 | 0.99 | matrix unique |
| Rax1p | RAX1 | CAALFM\_C304490WA | Q5ANJ8 | 0.00 | 0.99 | matrix unique |
| Chromatin-binding transcription coactivator |  | CAALFM\_C400390WA | Q59UQ4 | 0.00 | 0.99 | matrix unique |
| Regulator of cytoskeleton and endocytosis | RVS167 | CAALFM\_C604040CA | Q59LF3 | 0.00 | 0.99 | matrix unique |
| Lhp1p | LHP1 | CAALFM\_C107500CA | A0A1D8PE36 | 0.00 | 0.99 | matrix unique |
| 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial | EHD3 | CAALFM\_C103320CA | Q5AI24 | 0.00 | 0.98 | matrix unique |
| Chaperonin-containing T-complex subunit | CCT5 | CAALFM\_C207310WA | Q59Z12 | 0.00 | 0.98 | matrix unique |
| Trp99p | TRP99 | CAALFM\_C105410CA | A0A1D8PDN3 | 0.00 | 0.98 | matrix unique |
| Gre2p | GRE2 | CAALFM\_C206720WA | A0A1D8PHQ6 | 0.00 | 0.98 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C300470WA | Q5A7P8 | 0.00 | 0.98 | matrix unique |
| Autophagy-related protein 8 | ATG8 | CAALFM\_C105700WA | P0C075 | 0.00 | 0.98 | matrix unique |
| F1F0 ATP synthase subunit g | ATP20 | CAALFM\_C112590WA | Q59M30 | 0.00 | 0.97 | matrix unique |
| Translation termination factor GTPase eRF3 | SUP35 | CAALFM\_C209720WA | Q59YE8 | 0.00 | 0.96 | matrix unique |
| Septin | CDC12 | CAALFM\_C103210CA | A0A1D8PCY5 | 0.00 | 0.96 | matrix unique |
| Proteasome regulatory particle lid subunit | RPN8 | CAALFM\_C502030WA | A0A1D8PNA8 | 0.00 | 0.95 | matrix unique |
| Ribosomal 60S subunit protein L32 | RPL32 | CAALFM\_C601700WA | A0A1D8PPN6 | 0.00 | 0.93 | matrix unique |
| Cytochrome c oxidase subunit |  | CAALFM\_C604250WA | A0A1D8PQD5 | 0.00 | 0.92 | matrix unique |
| GTPase-activating protein | RNA1 | CAALFM\_C301990WA | A0A1D8PJD7 | 0.00 | 0.89 | matrix unique |
| Ribosomal 40S subunit protein S15 | RPS15 | CAALFM\_C304670CA | A0A1D8PK22 | 0.00 | 0.89 | matrix unique |
| Dolichyl-diphosphooligosaccharide-protein glycotransferase |  | CAALFM\_C103600WA | Q5AHZ2 | 0.00 | 0.89 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C206890CA | Q59Z55 | 0.00 | 0.89 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C206920CA | Q59Z54 | 0.00 | 0.89 | matrix unique |
| Phosphatidylinositol-3-phosphatase | SAC1 | CAALFM\_C109990WA | A0A1D8PEV5 | 0.00 | 0.89 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C400420CA | A0A1D8PL12 | 0.00 | 0.89 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C602530CA | Q5AC28 | 0.00 | 0.88 | matrix unique |
| 3'(2'),5'-bisphosphate nucleotidase 2 | HAL22 | CAALFM\_C601030WA | Q59XQ1 | 0.00 | 0.88 | matrix unique |
| Catabolic 3-dehydroquinase (cDHQase) | DQD1 | CAALFM\_C207260CA | Q59Z17 | 0.00 | 0.88 | matrix unique |
| Actin-related protein 2 | ARP2 | CAALFM\_CR08950WA | A0A1D8PTX1 | 0.00 | 0.88 | matrix unique |
| Acetyltransferase |  | CAALFM\_C306490WA | A0A1D8PKI3 | 0.00 | 0.88 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C202310WA | A0A1D8PGJ9 | 0.00 | 0.87 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR05860WA | Q59PT7 | 0.00 | 0.87 | matrix unique |
| Mrp8p | MRP8 | CAALFM\_C404430WA | Q5A646 | 0.00 | 0.87 | matrix unique |
| Coatomer subunit epsilon |  | CAALFM\_C500080CA | A0A1D8PMT6 | 0.00 | 0.87 | matrix unique |
| Ahp2p | AHP2 | CAALFM\_C702390WA | A0A1D8PR39 | 0.00 | 0.87 | matrix unique |
| Proteasome regulatory particle lid subunit | RPN3 | CAALFM\_C103520WA | A0A1D8PD15 | 0.00 | 0.86 | matrix unique |
| Cytochrome b-c1 complex subunit Rieske, mitochondrial | RIP1 | CAALFM\_C304430WA | A0A1D8PJX3 | 0.00 | 0.86 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C600250WA | A0A1D8PPA2 | 0.00 | 0.86 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C305150WA | Q5ANB5 | 0.00 | 0.85 | matrix unique |
| Presequence translocated-associated motor subunit | PAM17 | CAALFM\_C302500WA | Q5AEM8 | 0.00 | 0.85 | matrix unique |
| Prn4p | PRN4 | CAALFM\_C105880WA | Q5AA23 | 0.00 | 0.84 | matrix unique |
| Tom20p | TOM20 | CAALFM\_C102640CA | Q5AIA0 | 0.00 | 0.84 | matrix unique |
| Arp2/3 complex 34 kDa subunit | ARC35 | CAALFM\_C106080CA | Q5AA47 | 0.00 | 0.84 | matrix unique |
| Eukaryotic translation initiation factor 3 subunit I (eIF3i) | TIF34 | CAALFM\_C102790WA | Q5AI86 | 0.00 | 0.84 | matrix unique |
| Erp5p | ERP5 | CAALFM\_C110940CA | A0A1D8PF48 | 0.00 | 0.79 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C111670WA | A0A1D8PF63 | 0.00 | 0.79 | matrix unique |
| Serine/threonine protein kinase | YCK2 | CAALFM\_C305650WA | A0A1D8PKB4 | 0.00 | 0.79 | matrix unique |
| FACT complex subunit | POB3 | CAALFM\_C202380WA | Q5ALL8 | 0.00 | 0.78 | matrix unique |
| Ribosomal 40S subunit protein S13 | RPS13 | CAALFM\_C600650CA | A0A1D8PPE0 | 0.00 | 0.78 | matrix unique |
| Nrd1 complex RNA-binding subunit |  | CAALFM\_C500790CA | A0A1D8PN05 | 0.00 | 0.78 | matrix unique |
| Pyridoxal phosphate homeostasis protein |  | CAALFM\_C107510WA | A0A1D8PE30 | 0.00 | 0.77 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C504940WA | A0A1D8PP39 | 0.00 | 0.77 | matrix unique |
| C-22 sterol desaturase | ERG5 | CAALFM\_C702840CA | G1UB11 | 0.00 | 0.77 | matrix unique |
| Pyridoxamine-phosphate oxidase | PDX3 | CAALFM\_CR04590CA | A0A1D8PSU2 | 0.00 | 0.76 | matrix unique |
| Nucleotide exchange factor SIL1 | SIL1 | CAALFM\_CR08350WA | Q5A360 | 0.00 | 0.76 | matrix unique |
| Sterol-4-alpha-carboxylate 3-dehydrogenase (Decarboxylating) | ERG26 | CAALFM\_C406270CA | Q5A1B0 | 0.00 | 0.76 | matrix unique |
| ATP-dependent RNA helicase | DBP5 | CAALFM\_C301860CA | Q5AJD0 | 0.00 | 0.76 | matrix unique |
| 4a-hydroxytetrahydrobiopterin dehydratase | PHHB | CAALFM\_C200480CA | Q5ACY8 | 0.00 | 0.74 | matrix unique |
| Cysteine dioxygenase CDG1 | CDG1 | CAALFM\_CR09180WA | Q5A3Z5 | 0.00 | 0.74 | matrix unique |
| Clathrin light chain | CLC1 | CAALFM\_C401980CA | Q5AMQ2 | 0.00 | 0.74 | matrix unique |
| 60S ribosomal protein L27 | RPL27A | CAALFM\_C112390CA | A0A1D8PFG4 | 0.00 | 0.73 | matrix unique |
| Ubiquitin-specific protease |  | CAALFM\_C210050WA | A0A1D8PIM4 | 0.00 | 0.73 | matrix unique |
| Proline dehydrogenase | PUT1 | CAALFM\_C502600WA | A0A1D8PNH4 | 0.00 | 0.73 | matrix unique |
| Ribosomal 60S subunit protein L43A | RPL43A | CAALFM\_C504590CA | A0A1D8PP14 | 0.00 | 0.73 | matrix unique |
| snoRNP complex protein | SIK1 | CAALFM\_CR09950CA | A0A1D8PU46 | 0.00 | 0.71 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR09070CA | A0A1D8PTV5 | 0.00 | 0.68 | matrix unique |
| E3 ubiquitin-protein ligase | TOM1 | CAALFM\_C203180CA | A0A1D8PGT3 | 0.00 | 0.67 | matrix unique |
| Fe(2+) transporter | MRS4 | CAALFM\_C208070CA | Q5A2T7 | 0.00 | 0.67 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C703890CA | A0A1D8PRG7 | 0.00 | 0.67 | matrix unique |
| Enolase-phosphatase E1 | UTR4 | CAALFM\_C201860CA | Q5AM80 | 0.00 | 0.67 | matrix unique |
| Calmodulin-dependent protein kinase | CMK2 | CAALFM\_C210260CA | Q59XV1 | 0.00 | 0.66 | matrix unique |
| MICOS complex subunit MIC10 |  | CAALFM\_C404970CA | A0A1D8PM81 | 0.00 | 0.66 | matrix unique |
| E2 ubiquitin-conjugating protein |  | CAALFM\_C500560WA | Q5A513 | 0.00 | 0.66 | matrix unique |
| Protein transport protein sec16 |  | CAALFM\_C503140CA | A0A1D8PNM2 | 0.00 | 0.66 | matrix unique |
| Translation initiation factor eIF5B | FUN12 | CAALFM\_C108090CA | Q5A782 | 0.00 | 0.66 | matrix unique |
| Proteasome regulatory particle base subunit | RPT2 | CAALFM\_C300290WA | A0A1D8PIV7 | 0.00 | 0.66 | matrix unique |
| Arf family guanine nucleotide exchange factor | SEC7 | CAALFM\_C304820CA | Q5ANF9 | 0.00 | 0.66 | matrix unique |
| Proteasome regulatory particle lid subunit | RPN6 | CAALFM\_C403790WA | A0A1D8PLW8 | 0.00 | 0.66 | matrix unique |
| Uracil phosphoribosyltransferase | FUR1 | CAALFM\_C503390CA | Q59QT3 | 0.00 | 0.66 | matrix unique |
| Mitochondrial import inner membrane translocase subunit | TIM50 | CAALFM\_C111220CA | Q59W44 | 0.00 | 0.66 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C114320CA | A0A1D8PFV6 | 0.00 | 0.66 | matrix unique |
| Phosphomevalonate kinase | ERG8 | CAALFM\_C401870CA | A0A1D8PLH0 | 0.00 | 0.66 | matrix unique |
| Nif3p | NIF3 | CAALFM\_C405960WA | A0A1D8PMG0 | 0.00 | 0.66 | matrix unique |
| Mrv2p | MRV2 | CAALFM\_C504190WA | A0A1D8PNW4 | 0.00 | 0.66 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C108900WA | A0A1D8PEG9 | 0.00 | 0.65 | matrix unique |
| Branched-chain-amino-acid aminotransferase | BAT21 | CAALFM\_C204230WA | A0A1D8PH42 | 0.00 | 0.65 | matrix unique |
| Tryptophan--tRNA ligase | WRS1 | CAALFM\_C112380CA | Q5A3P4 | 0.00 | 0.65 | matrix unique |
| Phenylalanine--tRNA ligase subunit alpha | FRS2 | CAALFM\_C102710WA | A0A1D8PCT4 | 0.00 | 0.65 | matrix unique |
| Chaperonin-containing T-complex alpha subunit | TCP1 | CAALFM\_C108560WA | Q59QB7 | 0.00 | 0.65 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR09330CA | A0A1D8PTZ1 | 0.00 | 0.65 | matrix unique |
| Proteasome regulatory particle base subunit | RPT4 | CAALFM\_CR04000WA | Q5A6S2 | 0.00 | 0.65 | matrix unique |
| Peptidyl-prolyl cis-trans isomerase | ESS1 | CAALFM\_C104410CA | Q59KZ2 | 0.00 | 0.65 | matrix unique |
| Uricase |  | CAALFM\_C200180CA | Q5ACV3 | 0.00 | 0.65 | matrix unique |
| Vacuolar membrane protease |  | CAALFM\_C604650WA | Q59RF7 | 0.00 | 0.63 | matrix unique |
| Cytochrome c peroxidase, mitochondrial | CCP1 | CAALFM\_C302480CA | Q5AEN1 | 0.00 | 0.63 | matrix unique |
| Ribosomal 60S subunit protein L33A |  | CAALFM\_C205710CA | A0A1D8PHH4 | 0.00 | 0.62 | matrix unique |
| Non-specific serine/threonine protein kinase | SNF1 | CAALFM\_C501320WA | A0A1D8PN61 | 0.00 | 0.62 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C501410CA | A0A1D8PN56 | 0.00 | 0.62 | matrix unique |
| Translation initiation factor eIF2 subunit beta | SUI3 | CAALFM\_C704130CA | A0A1D8PRJ6 | 0.00 | 0.62 | matrix unique |
| Rab family GTPase | YPT52 | CAALFM\_C114100WA | A0A1D8PFT9 | 0.00 | 0.60 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C700520WA | A0A1D8PQM5 | 0.00 | 0.60 | matrix unique |
| Mam33p | MAM33 | CAALFM\_C703930CA | A0A1D8PRG4 | 0.00 | 0.60 | matrix unique |
| Glycerol-3-phosphate dehydrogenase [NAD(+)] | GPD1 | CAALFM\_C210240WA | Q59XU9 | 0.00 | 0.60 | matrix unique |
| tRNA ligase | LIG1 | CAALFM\_C702060WA | P43075 | 0.00 | 0.60 | matrix unique |
| Ubiquinol--cytochrome-c reductase subunit 8 | QCR8 | CAALFM\_C204590CA | A0A1D8PHA2 | 0.00 | 0.57 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C702450WA | A0A1D8PR36 | 0.00 | 0.57 | matrix unique |
| Dolichyl-phosphate beta-glucosyltransferase | ALG5 | CAALFM\_CR02790CA | A0A1D8PSA5 | 0.00 | 0.57 | matrix unique |
| Dolichyl-phosphate-mannose--protein mannosyltransferase 4 | PMT4 | CAALFM\_C206100WA | Q59X23 | 0.00 | 0.57 | matrix unique |
| V-type proton ATPase subunit G | VMA10 | CAALFM\_C207590WA | Q59U85 | 0.00 | 0.56 | matrix unique |
| NEDD8 family protein | RUB1 | CAALFM\_C303320WA | A0A1D8PJP6 | 0.00 | 0.56 | matrix unique |
| Karyopherin | MSN5 | CAALFM\_C403280WA | A0A1D8PLT4 | 0.00 | 0.56 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C100210CA | A0A1D8PC56 | 0.00 | 0.55 | matrix unique |
| Delta(24(24(1)))-sterol reductase | ERG4 | CAALFM\_C300760WA | A0A1D8PJ25 | 0.00 | 0.55 | matrix unique |
| Glucan 1\3-alpha-glucosidase ROT2 | ROT2 | CAALFM\_C500220WA | Q5A4X3 | 0.00 | 0.55 | matrix unique |
| Crg1p | CRG1 | CAALFM\_CR04960CA | A0A1D8PSY8 | 0.00 | 0.55 | matrix unique |
| Opt3p | OPT3 | CAALFM\_CR02220CA | A0A1D8PS61 | 0.00 | 0.55 | matrix unique |
| Serine/threonine-protein phosphatase | PPZ1 | CAALFM\_CR06420WA | Q59U06 | 0.00 | 0.55 | matrix unique |
| Frp6p | FRP6 | CAALFM\_C601430CA | Q5A4K0 | 0.00 | 0.54 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C604420WA | A0A1D8PQE6 | 0.00 | 0.54 | matrix unique |
| Glycogenin glucosyltransferase |  | CAALFM\_C101360CA | A0A1D8PCG4 | 0.00 | 0.54 | matrix unique |
| Proteasome regulatory particle base subunit | RPT6 | CAALFM\_C208780WA | A0A1D8PI93 | 0.00 | 0.54 | matrix unique |
| Ribosomal 40S subunit protein S25B | RPS25B | CAALFM\_C503540CA | A0A1D8PNQ6 | 0.00 | 0.54 | matrix unique |
| Phenylalanine--tRNA ligase subunit beta | FRS1 | CAALFM\_CR01760CA | A0A1D8PS16 | 0.00 | 0.54 | matrix unique |
| DNA-directed RNA polymerase subunit | RPO21 | CAALFM\_CR10680WA | A0A1D8PUA6 | 0.00 | 0.54 | matrix unique |
| Fructose-2,6-bisphosphatase |  | CAALFM\_CR08550WA | Q5A340 | 0.00 | 0.53 | matrix unique |
| Rab family GTPase | YPT72 | CAALFM\_C206910WA | A0A1D8PHR9 | 0.00 | 0.52 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C209600CA | Q59YD2 | 0.00 | 0.52 | matrix unique |
| NADH-ubiquinone oxidoreductase |  | CAALFM\_CR02620CA | Q5A222 | 0.00 | 0.52 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR01350CA | Q5A9E7 | 0.00 | 0.52 | matrix unique |
| Medium-chain fatty acid-CoA ligase | FAA21 | CAALFM\_C302810CA | A0A1D8PJI7 | 0.00 | 0.51 | matrix unique |
| Ctp1p | CTP1 | CAALFM\_C304270CA | A0A1D8PJV4 | 0.00 | 0.51 | matrix unique |
| Erv46p | ERV46 | CAALFM\_C500830CA | Q59X92 | 0.00 | 0.51 | matrix unique |
| Histone acetyltransferase type B catalytic subunit | HAT1 | CAALFM\_C104670WA | Q59VF4 | 0.00 | 0.51 | matrix unique |
| Transcription factor | NDT80 | CAALFM\_C200140WA | Q5ACU9 | 0.00 | 0.50 | matrix unique |
| Ribosomal protein P2A | RPP2A | CAALFM\_CR08360CA | A0A1D8PTS0 | 0.00 | 0.50 | matrix unique |
| Uga2p | UGA2 | CAALFM\_C101810CA | Q59T88 | 0.00 | 0.46 | matrix unique |
| Delta-aminolevulinic acid dehydratase | HEM2 | CAALFM\_C203300WA | A0A1D8PGU4 | 0.00 | 0.46 | matrix unique |
| Gtt11p | GTT11 | CAALFM\_C303720WA | A0A1D8PJR2 | 0.00 | 0.44 | matrix unique |
| Ald6p | ALD6 | CAALFM\_C405130CA | A0A1D8PM94 | 0.00 | 0.44 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C603310WA | A0A1D8PQ49 | 0.00 | 0.44 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C603380WA | A0A1D8PQ55 | 0.00 | 0.44 | matrix unique |
| Carbamoyl-phosphate synthase | CPA2 | CAALFM\_CR01330WA | Q5A8A6 | 0.00 | 0.44 | matrix unique |
| Cwh8p | CWH8 | CAALFM\_C102250WA | Q59VX6 | 0.00 | 0.44 | matrix unique |
| Ssh1p | SSH1 | CAALFM\_C105530CA | A0A1D8PDL0 | 0.00 | 0.44 | matrix unique |
| Acyl carrier protein | ACP1 | CAALFM\_C106060CA | A0A1D8PDT0 | 0.00 | 0.44 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C209650WA | A0A1D8PIF0 | 0.00 | 0.44 | matrix unique |
| Ato2p | ATO2 | CAALFM\_C300930WA | A0A1D8PJ42 | 0.00 | 0.44 | matrix unique |
| Casein kinase 2 catalytic subunit | CKA1 | CAALFM\_CR10660WA | A0A1D8PUA2 | 0.00 | 0.44 | matrix unique |
| Proteasome regulatory particle base subunit | PR26 | CAALFM\_C203060WA | Q5A0L8 | 0.00 | 0.44 | matrix unique |
| Phosphoribosylglycinamide formyltransferase | ADE8 | CAALFM\_C203090CA | A0A1D8PGS7 | 0.00 | 0.44 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C208390WA | Q59K70 | 0.00 | 0.44 | matrix unique |
| AP complex subunit beta | APL2 | CAALFM\_C302430WA | A0A1D8PJI6 | 0.00 | 0.44 | matrix unique |
| Superoxide dismutase [Cu-Zn] | SOD1 | CAALFM\_C402320CA | A0A1D8PLJ3 | 0.00 | 0.44 | matrix unique |
| Chaperonin-containing T-complex subunit | CCT6 | CAALFM\_C406830CA | A0A1D8PMN9 | 0.00 | 0.44 | matrix unique |
| Deoxyhypusine hydroxylase (DOHH) | LIA1 | CAALFM\_C207290WA | Q59Z14 | 0.00 | 0.44 | matrix unique |
| Actin-related protein 2/3 complex subunit | ARC40 | CAALFM\_CR06180WA | A0A1D8PT60 | 0.00 | 0.44 | matrix unique |
| Pex11p | PEX11 | CAALFM\_C604310WA | A0A1D8PQD7 | 0.00 | 0.44 | matrix unique |
| Kap120p | KAP120 | CAALFM\_C704030CA | A0A1D8PRI4 | 0.00 | 0.44 | matrix unique |
| Ribosome biogenesis protein | YTM1 | CAALFM\_C109510WA | Q5APF0 | 0.00 | 0.44 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C207540WA | A0A1D8PI37 | 0.00 | 0.43 | matrix unique |
| Acetylornithine transaminase | ARG8 | CAALFM\_C405070CA | A0A1D8PM83 | 0.00 | 0.43 | matrix unique |
| Malate dehydrogenase | MDH1-3 | CAALFM\_C210480WA | Q5A5S6 | 0.00 | 0.43 | matrix unique |
| Calcineurin regulatory subunit B | CNB1 | CAALFM\_C505160CA | A0A1D8PP58 | 0.00 | 0.43 | matrix unique |
| Ran guanyl-nucleotide exchange factor |  | CAALFM\_C702780WA | A0A1D8PR80 | 0.00 | 0.43 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C304630WA | Q5ANI2 | 0.00 | 0.39 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C404760CA | A0A1D8PM63 | 0.00 | 0.39 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C114030WA | A0A1D8PFU2 | 0.00 | 0.39 | matrix unique |
| Ribosomal protein P2B | RPP2B | CAALFM\_C304680WA | Q5ANH5 | 0.00 | 0.39 | matrix unique |
| DNA topoisomerase 1 | TOP1 | CAALFM\_C600950CA | A0A1D8PPI2 | 0.00 | 0.39 | matrix unique |
| Ribosomal 60S subunit protein L23B | RPL23A | CAALFM\_C602070CA | A0A1D8PPT5 | 0.00 | 0.39 | matrix unique |
| Protein transport protein Sec61 subunit beta |  | CAALFM\_CR01490CA | A0A1D8PRY9 | 0.00 | 0.39 | matrix unique |
| E2 SUMO-conjugating protein |  | CAALFM\_CR08560CA | Q5A339 | 0.00 | 0.39 | matrix unique |
| TATA-binding protein-associated factor | TAF14 | CAALFM\_C204220CA | A0A1D8PH31 | 0.00 | 0.35 | matrix unique |
| NEDD8-activating enzyme E1 regulatory subunit |  | CAALFM\_C501590WA | A0A1D8PN68 | 0.00 | 0.35 | matrix unique |
| Cwh43p | CWH43 | CAALFM\_CR01290CA | A0A1D8PRY4 | 0.00 | 0.35 | matrix unique |
| Kel1p | KEL1 | CAALFM\_C100140WA | Q5AB80 | 0.00 | 0.33 | matrix unique |
| Ribosomal protein L37 | RPL37B | CAALFM\_C111360WA | A0A1D8PF45 | 0.00 | 0.33 | matrix unique |
| Methylenetetrahydrofolate reductase | MET13 | CAALFM\_C302950CA | Q5AEI0 | 0.00 | 0.33 | matrix unique |
| Dolichyl-diphosphooligosaccharide--protein glycotransferase |  | CAALFM\_C505020CA | Q5AK26 | 0.00 | 0.33 | matrix unique |
| Apm1p | APM1 | CAALFM\_C505400WA | Q5AJY4 | 0.00 | 0.33 | matrix unique |
| Ayr2p | AYR2 | CAALFM\_C603270CA | A0A1D8PQ42 | 0.00 | 0.33 | matrix unique |
| Replication factor C subunit 2 | RFC2 | CAALFM\_C700820WA | A0A1D8PQP2 | 0.00 | 0.33 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C703610CA | Q59R27 | 0.00 | 0.33 | matrix unique |
| NAD(P)H-hydrate epimerase |  | CAALFM\_C102220CA | Q59VX9 | 0.00 | 0.33 | matrix unique |
| Adh5p | ADH5 | CAALFM\_CR02070CA | A0A1D8PS45 | 0.00 | 0.33 | matrix unique |
| Mitochondrial pyruvate carrier |  | CAALFM\_CR08610WA | Q5A328 | 0.00 | 0.33 | matrix unique |
| alpha-1,2-Mannosidase | MNS1 | CAALFM\_C103730CA | A0A1D8PD38 | 0.00 | 0.33 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C700920CA | A0A1D8PQP9 | 0.00 | 0.33 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR05030WA | A0A1D8PSW7 | 0.00 | 0.33 | matrix unique |
| Nicotinamidase | PNC1 | CAALFM\_C703520WA | A0A1D8PRE2 | 0.00 | 0.33 | matrix unique |
| Threonine aldolase |  | CAALFM\_CR04880WA | A0A1D8PSW2 | 0.00 | 0.33 | matrix unique |
| Chaperonin-containing T-complex subunit | CCT8 | CAALFM\_C100110WA | Q5AB74 | 0.00 | 0.32 | matrix unique |
| Serine/threonine-protein phosphatase | CMP1 | CAALFM\_C100730CA | A0A1D8PCA8 | 0.00 | 0.32 | matrix unique |
| DNA-directed RNA polymerase subunit beta |  | CAALFM\_C101590CA | Q5A8Y5 | 0.00 | 0.32 | matrix unique |
| C-5 sterol desaturase | ERG3 | CAALFM\_C104770CA | Q59VG6 | 0.00 | 0.32 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C106660WA | A0A1D8PDV1 | 0.00 | 0.32 | matrix unique |
| F1F0 ATP synthase subunit k | ATP19 | CAALFM\_C112320CA | A0A1D8PFD4 | 0.00 | 0.32 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C114240WA | A0A1D8PFW3 | 0.00 | 0.32 | matrix unique |
| Ribosomal 60S subunit protein L31B |  | CAALFM\_C205410WA | A0A1D8PHF5 | 0.00 | 0.32 | matrix unique |
| Cytochrome c oxidase subunit 7A | COX9 | CAALFM\_C205930WA | A0A1D8PHI5 | 0.00 | 0.32 | matrix unique |
| Siderophore transporter | SIT1 | CAALFM\_C208050CA | Q5A2T6 | 0.00 | 0.32 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C504640CA | A0A1D8PP04 | 0.00 | 0.32 | matrix unique |
| Vid27p | VID27 | CAALFM\_C600130CA | A0A1D8PP94 | 0.00 | 0.32 | matrix unique |
| Probable metalloprotease | ARX1 | CAALFM\_C103230CA | Q5AI37 | 0.00 | 0.32 | matrix unique |
| Histone chaperone | ASF1 | CAALFM\_CR07860CA | Q59MV1 | 0.00 | 0.32 | matrix unique |
| Phosphoribosylaminoimidazole carboxylase | ADE2 | CAALFM\_C304520CA | Q92210 | 0.00 | 0.32 | matrix unique |
| Actin cytoskeleton-regulatory complex protein | END3 | CAALFM\_C301400WA | Q5AJ82 | 0.00 | 0.32 | matrix unique |
| Cap-associated protein CAF20 | CAF20 | CAALFM\_C109350WA | Q5AQ12 | 0.00 | 0.32 | matrix unique |
| Type 2C protein phosphatase | PTC2 | CAALFM\_CR01520WA | A0A1D8PRZ8 | 0.00 | 0.32 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR00130CA | A0A1D8PRL8 | 0.00 | 0.32 | matrix unique |
| Succinate dehydrogenase [ubiquinone] cytochrome b small subunit |  | CAALFM\_C103940WA | A0A1D8PD61 | 0.00 | 0.29 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C110350CA | A0A1D8PEU9 | 0.00 | 0.29 | matrix unique |
| Djp1p | DJP1 | CAALFM\_C110480WA | A0A1D8PEX2 | 0.00 | 0.29 | matrix unique |
| 1-acyl-sn-glycerol-3-phosphate acyltransferase | SLC1 | CAALFM\_C302600CA | Q5AEL8 | 0.00 | 0.29 | matrix unique |
| Mitochondrial pyruvate carrier |  | CAALFM\_C302620CA | A0A1D8PJH2 | 0.00 | 0.29 | matrix unique |
| Fesur1p | FESUR1 | CAALFM\_C307060WA | Q5ADP7 | 0.00 | 0.29 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C403370CA | A0A1D8PLT3 | 0.00 | 0.29 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C600200CA | A0A1D8PPB2 | 0.00 | 0.29 | matrix unique |
| Tom22p | TOM22 | CAALFM\_C702680WA | Q59LZ9 | 0.00 | 0.29 | matrix unique |
| Alpha-1,3/1,6-mannosyltransferase | ALG2 | CAALFM\_C604030WA | Q59LF2 | 0.00 | 0.29 | matrix unique |
| Golgi to ER traffic protein 1 (Guided entry of tail-anchored proteins 1) | GET1 | CAALFM\_C200320WA | Q5ACW6 | 0.00 | 0.29 | matrix unique |
| Mitochondrial presequence protease | CYM1 | CAALFM\_C306230WA | Q5A301 | 0.00 | 0.29 | matrix unique |
| Mis12p | MIS12 | CAALFM\_CR00080WA | A0A1D8PRL4 | 0.00 | 0.29 | matrix unique |
| Mci4p | MCI4 | CAALFM\_CR01740WA | Q5A995 | 0.00 | 0.29 | matrix unique |
| Ubiquitin-binding protein | CUE5 | CAALFM\_C105170CA | A0A1D8PDI5 | 0.00 | 0.28 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C114090WA | A0A1D8PFU8 | 0.00 | 0.28 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C304810CA | A0A1D8PK71 | 0.00 | 0.28 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C405610CA | A0A1D8PMD5 | 0.00 | 0.28 | matrix unique |
| Transcriptional regulator CBF1 | CBF1 | CAALFM\_C406580WA | Q5A1E3 | 0.00 | 0.28 | matrix unique |
| Oxysterol-binding protein related protein |  | CAALFM\_C108180CA | A0A1D8PE79 | 0.00 | 0.22 | matrix unique |
| Mevalonate kinase | ERG12 | CAALFM\_C109460WA | A0A1D8PEL1 | 0.00 | 0.22 | matrix unique |
| RNA polymerase specificity factor |  | CAALFM\_C202120WA | Q5ALP7 | 0.00 | 0.22 | matrix unique |
| Meiotic recombination directing protein | MSC7 | CAALFM\_C207600CA | A0A1D8PHY1 | 0.00 | 0.22 | matrix unique |
| Replication factor C subunit 3 | RFC3 | CAALFM\_C504000WA | A0A1D8PNV1 | 0.00 | 0.22 | matrix unique |
| Cyb5p | CYB5 | CAALFM\_C700700WA | A0A1D8PQP7 | 0.00 | 0.22 | matrix unique |
| Respiratory supercomplex factor 1, mitochondrial | RCF1 | CAALFM\_C503800WA | Q59N74 | 0.00 | 0.22 | matrix unique |
| Mitochondrial 37S ribosomal protein | NAM9 | CAALFM\_CR04140WA | Q5A6Q6 | 0.00 | 0.22 | matrix unique |
| Cytochrome c lysine N-methyltransferase | CTM1 | CAALFM\_CR10360CA | A0A1D8PU71 | 0.00 | 0.22 | matrix unique |
| Dap1p | DAP1 | CAALFM\_CR04060CA | Q5A6R5 | 0.00 | 0.22 | matrix unique |
| Protein YOP1 |  | CAALFM\_C101610CA | A0A1D8PCI8 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C103310WA | A0A1D8PCZ5 | 0.00 | 0.22 | matrix unique |
| Sepiapterin reductase family protein |  | CAALFM\_C104430CA | A0A1D8PDA0 | 0.00 | 0.22 | matrix unique |
| Amidophosphoribosyltransferase (ATase) | ADE4 | CAALFM\_C107710CA | A0A1D8PE37 | 0.00 | 0.22 | matrix unique |
| E1 ubiquitin-activating protein | UBA2 | CAALFM\_C108020WA | A0A1D8PE77 | 0.00 | 0.22 | matrix unique |
| 5'-3' exoribonuclease 1 | KEM1 | CAALFM\_C113420CA | A0A1D8PFP3 | 0.00 | 0.22 | matrix unique |
| Rho family guanine nucleotide exchange factor | ROM2 | CAALFM\_C203240CA | Q5AH90 | 0.00 | 0.22 | matrix unique |
| Dck1p | DCK1 | CAALFM\_C204050CA | A0A1D8PH11 | 0.00 | 0.22 | matrix unique |
| Blm3p | BLM3 | CAALFM\_C208010WA | Q5A2T3 | 0.00 | 0.22 | matrix unique |
| Arp9p | ARP9 | CAALFM\_C301030WA | Q5A9X7 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C302090CA | A0A1D8PJC7 | 0.00 | 0.22 | matrix unique |
| Acetolactate synthase | ILV2 | CAALFM\_C302320WA | A0A1D8PJF9 | 0.00 | 0.22 | matrix unique |
| Phosphopantothenate--cysteine ligase |  | CAALFM\_C305760WA | A0A1D8PKB0 | 0.00 | 0.22 | matrix unique |
| Transcription initiation factor IIA subunit 2 | TOA2 | CAALFM\_C401680WA | Q5AMM1 | 0.00 | 0.22 | matrix unique |
| F-actin-capping protein subunit beta |  | CAALFM\_C401950WA | Q5AMP9 | 0.00 | 0.22 | matrix unique |
| Tryptophan synthase | TRP5 | CAALFM\_C406110CA | A0A1D8PMH6 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C500750CA | A0A1D8PN11 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C502690WA | A0A1D8PNH7 | 0.00 | 0.22 | matrix unique |
| Actin-related protein 2/3 complex subunit 3 | ARC18 | CAALFM\_C601140CA | Q59WT0 | 0.00 | 0.22 | matrix unique |
| CCR4-NOT core subunit | CDC39 | CAALFM\_C604270WA | A0A1D8PQD2 | 0.00 | 0.22 | matrix unique |
| Nicotinate phosphoribosyltransferase | NPT1 | CAALFM\_C704040CA | A0A1D8PRI0 | 0.00 | 0.22 | matrix unique |
| GDP-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase | ALG11 | CAALFM\_C602270CA | Q59S72 | 0.00 | 0.22 | matrix unique |
| tRNA (guanine-N(7)-)-methyltransferase | TRM8 | CAALFM\_C404810CA | A0A1D8PM52 | 0.00 | 0.22 | matrix unique |
| Glucosamine-6-phosphate isomerase | NAG1 | CAALFM\_C604590CA | Q04802 | 0.00 | 0.22 | matrix unique |
| Eukaryotic translation initiation factor 3 subunit J (eIF3j) | HCR1 | CAALFM\_CR10370WA | Q5ACM9 | 0.00 | 0.22 | matrix unique |
| Homoserine kinase | THR1 | CAALFM\_C500650CA | Q92209 | 0.00 | 0.22 | matrix unique |
| Homoisocitrate dehydrogenase | LYS12 | CAALFM\_CR01400WA | Q5A9D9 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR03950WA | Q5A6S7 | 0.00 | 0.22 | matrix unique |
| Ubiquinone biosynthesis protein |  | CAALFM\_CR09590WA | A0A1D8PU08 | 0.00 | 0.22 | matrix unique |
| Probable lysine/arginine permease | CAN2 | CAALFM\_C601060CA | Q59WU0 | 0.00 | 0.22 | matrix unique |
| Serine C-palmitoyltransferase |  | CAALFM\_CR08640CA | Q5A325 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR09920WA | A0A1D8PU37 | 0.00 | 0.22 | matrix unique |
| Nuo1p | NUO1 | CAALFM\_CR09550CA | A0A1D8PU10 | 0.00 | 0.22 | matrix unique |
| SnoRNA-binding protein | NHP2 | CAALFM\_CR04360CA | Q5A6M9 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C102750CA | A0A1D8PCV8 | 0.00 | 0.22 | matrix unique |
| Ifm3p | IFM3 | CAALFM\_C208080CA | A0A1D8PI81 | 0.00 | 0.22 | matrix unique |
| Slr1p | SLR1 | CAALFM\_C210290WA | A0A1D8PIP0 | 0.00 | 0.22 | matrix unique |
| Mitochondrial 37S ribosomal protein YmS18 |  | CAALFM\_C601980CA | A0A1D8PPR6 | 0.00 | 0.22 | matrix unique |
| Orotidine 5'-phosphate decarboxylase | URA3 | CAALFM\_C301350CA | P13649 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR06170WA | A0A1D8PT61 | 0.00 | 0.22 | matrix unique |
| DNA-directed RNA polymerase | RPO41 | CAALFM\_C100640CA | A0A1D8PCA4 | 0.00 | 0.22 | matrix unique |
| Transcriptional regulator | SIN3 | CAALFM\_C100930CA | A0A1D8PCC3 | 0.00 | 0.22 | matrix unique |
| Nma111p | NMA111 | CAALFM\_C100990CA | A0A1D8PCD2 | 0.00 | 0.22 | matrix unique |
| Protein-arginine omega-N methyltransferase | HMT1 | CAALFM\_C101030WA | Q5A943 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C101930WA | A0A1D8PCL8 | 0.00 | 0.22 | matrix unique |
| Rab geranylgeranyltransferase | BET4 | CAALFM\_C104070CA | A0A1D8PD57 | 0.00 | 0.22 | matrix unique |
| Putative ATP-binding cassette family ATPase | CAF16 | CAALFM\_C108430WA | Q59QD0 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C111890WA | Q5A3J2 | 0.00 | 0.22 | matrix unique |
| Ribokinase | RBK1 | CAALFM\_C112780WA | A0A1D8PFI3 | 0.00 | 0.22 | matrix unique |
| Polyamine acetyltransferase |  | CAALFM\_C114500CA | A0A1D8PFY0 | 0.00 | 0.22 | matrix unique |
| Replication factor C subunit 5 | RFC5 | CAALFM\_C200950CA | A0A1D8PG80 | 0.00 | 0.22 | matrix unique |
| Plc2p | PLC2 | CAALFM\_C203040WA | Q5A0L4 | 0.00 | 0.22 | matrix unique |
| Vacuolar protein sorting-associated protein 35 | VPS35 | CAALFM\_C205650WA | Q59T42 | 0.00 | 0.22 | matrix unique |
| Casein kinase |  | CAALFM\_C208270CA | A0A1D8PI35 | 0.00 | 0.22 | matrix unique |
| Methylenetetrahydrofolate reductase |  | CAALFM\_C210460CA | Q5A5S8 | 0.00 | 0.22 | matrix unique |
| Met18p (Fragment) | MET18 | CAALFM\_C301450CA | A0A1D8PJ95 | 0.00 | 0.22 | matrix unique |
| Uso6p | USO6 | CAALFM\_C305310WA | A0A1D8PK69 | 0.00 | 0.22 | matrix unique |
| Oxysterol-binding protein related protein | OSH3 | CAALFM\_C403590CA | Q59TM0 | 0.00 | 0.22 | matrix unique |
| Aspartokinase | HOM3 | CAALFM\_C405540WA | A0A1D8PMB8 | 0.00 | 0.22 | matrix unique |
| Gvp36p | GVP36 | CAALFM\_C405550CA | Q5A473 | 0.00 | 0.22 | matrix unique |
| Protein disulfide isomerase |  | CAALFM\_C504340WA | A0A1D8PNX4 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C600660CA | A0A1D8PPG2 | 0.00 | 0.22 | matrix unique |
| Ribosomal 60S subunit protein L25 | RPL25 | CAALFM\_C601970CA | A0A1D8PPS1 | 0.00 | 0.22 | matrix unique |
| Nab3p | NAB3 | CAALFM\_C602600WA | A0A1D8PPX7 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C604560WA | A0A1D8PQF9 | 0.00 | 0.22 | matrix unique |
| 3-isopropylmalate dehydrogenase | LEU2 | CAALFM\_C700400WA | A0A1D8PQK5 | 0.00 | 0.22 | matrix unique |
| Ubiquinone biosynthesis protein, mitochondrial | COQ4 | CAALFM\_C103160CA | Q5AI44 | 0.00 | 0.22 | matrix unique |
| Methylthioribulose-1-phosphate dehydratase | MDE1 | CAALFM\_C502820CA | Q5AG73 | 0.00 | 0.22 | matrix unique |
| Actin-related protein 4 | ARP4 | CAALFM\_C603350CA | Q5AC48 | 0.00 | 0.22 | matrix unique |
| F1F0 ATP synthase subunit delta | ATP16 | CAALFM\_CR10850CA | A0A1D8PUD2 | 0.00 | 0.22 | matrix unique |
| Ribosomal 60S subunit protein L28 | RPL28 | CAALFM\_CR03030CA | A0A1D8PSC5 | 0.00 | 0.22 | matrix unique |
| Nicotinamide-nucleotide adenylyltransferase |  | CAALFM\_CR00350WA | A0A1D8PRN2 | 0.00 | 0.22 | matrix unique |
| rRNA (Cytosine-C5-)-methyltransferase |  | CAALFM\_CR04170WA | A0A1D8PSN8 | 0.00 | 0.22 | matrix unique |
| Apl4p | APL4 | CAALFM\_CR02870WA | A0A1D8PSB0 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR01410CA | Q5A9D8 | 0.00 | 0.22 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C100160CA | Q5AB84 | 0.00 | 0.17 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C102000WA | A0A1D8PCP9 | 0.00 | 0.17 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C102970WA | A0A1D8PCX5 | 0.00 | 0.17 | matrix unique |
| CCR4-NOT core subunit | NOT5 | CAALFM\_C108300WA | A0A1D8PE87 | 0.00 | 0.17 | matrix unique |
| Frequenin |  | CAALFM\_C108680CA | A0A1D8PEF8 | 0.00 | 0.17 | matrix unique |
| CDP-diacylglycerol--serine O-phosphatidyltransferase | CHO1 | CAALFM\_C111240CA | A0A1D8PF32 | 0.00 | 0.17 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C200060CA | Q59L46 | 0.00 | 0.17 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C200360CA | A0A1D8PG26 | 0.00 | 0.17 | matrix unique |
| Protein phosphatase PP2A regulatory subunit B | CDC55 | CAALFM\_C201600CA | Q5ALV8 | 0.00 | 0.17 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C205760CA | Q59T30 | 0.00 | 0.17 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C208200WA | A0A1D8PI34 | 0.00 | 0.17 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C208620WA | A0A1D8PIB7 | 0.00 | 0.17 | matrix unique |
| Ccc1p | CCC1 | CAALFM\_C303710WA | Q59SS1 | 0.00 | 0.17 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C504380CA | A0A1D8PNZ2 | 0.00 | 0.17 | matrix unique |
| Phosphatidylinositol-binding protein |  | CAALFM\_C604100WA | A0A1D8PQC2 | 0.00 | 0.17 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C604180WA | A0A1D8PQC4 | 0.00 | 0.17 | matrix unique |
| Membrane insertase |  | CAALFM\_C701600WA | Q5AGX4 | 0.00 | 0.17 | matrix unique |
| Nuc2p | NUC2 | CAALFM\_C701900WA | Q5AH07 | 0.00 | 0.17 | matrix unique |
| NADH-ubiquinone oxidoreductase chain 5 | NAD5 | CaalfMp13 | Q9B8C9 | 0.00 | 0.17 | matrix unique |
| Mitochondrial fission 1 protein | FIS1 | CAALFM\_C700120WA | Q5AFF7 | 0.00 | 0.17 | matrix unique |
| Altered inheritance of mitochondria protein 24, mitochondrial | AIM24 | CAALFM\_C301170WA | Q59L25 | 0.00 | 0.17 | matrix unique |
| Golgi apparatus membrane protein | TVP18 | CAALFM\_C109800CA | Q5APC0 | 0.00 | 0.17 | matrix unique |
| Lanosterol synthase | ERG7 | CAALFM\_C202460WA | Q04782 | 0.00 | 0.17 | matrix unique |
| Septin | CDC11 | CAALFM\_C500070WA | G1UB61 | 0.00 | 0.17 | matrix unique |
| Ubiquitin-conjugating enzyme E2 2 | UBC2 | CAALFM\_C703870WA | O74201 | 0.00 | 0.17 | matrix unique |
| Non-specific serine/threonine protein kinase | KIN2 | CAALFM\_CR00260WA | A0A1D8PRN8 | 0.00 | 0.17 | matrix unique |
| 40S ribosomal protein S30 | RPS30 | CAALFM\_CR03770CA | A0A1D8PSK2 | 0.00 | 0.17 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR01300WA | A0A1D8PRX9 | 0.00 | 0.17 | matrix unique |
| Vacuolar protein sorting-associated protein 17 | VPS17 | CAALFM\_C101550WA | Q5A8Z0 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C101860WA | Q59T94 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C102700CA | A0A1D8PCT3 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C104910CA | A0A1D8PDG0 | 0.00 | 0.11 | matrix unique |
| MICOS complex subunit |  | CAALFM\_C105490CA | Q5A2C6 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C108080CA | A0A1D8PE69 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C109850CA | Q5APB5 | 0.00 | 0.11 | matrix unique |
| DNA-directed RNA polymerase subunit | RPA190 | CAALFM\_C110670CA | A0A1D8PEX3 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C111120CA | Q59WJ7 | 0.00 | 0.11 | matrix unique |
| MICOS complex subunit |  | CAALFM\_C111760CA | A0A1D8PF88 | 0.00 | 0.11 | matrix unique |
| Signal peptidase complex subunit | SPC3 | CAALFM\_C113020CA | Q5AL47 | 0.00 | 0.11 | matrix unique |
| Nicotinamide-nucleotide adenylyltransferase |  | CAALFM\_C113270WA | Q5AL24 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C113320CA | A0A1D8PFM7 | 0.00 | 0.11 | matrix unique |
| Serine C-palmitoyltransferase | LCB2 | CAALFM\_C113900CA | Q5AKV0 | 0.00 | 0.11 | matrix unique |
| Cytochrome c oxidase subunit 6A, mitochondrial (Cytochrome c oxidase polypeptide VIa) | COX13 | CAALFM\_C201590WA | Q5ALV9 | 0.00 | 0.11 | matrix unique |
| Amine oxidase | AMO1 | CAALFM\_C203120WA | Q5A0M7 | 0.00 | 0.11 | matrix unique |
| Protein-arginine N-methyltransferase |  | CAALFM\_C203130WA | A0A1D8PGT0 | 0.00 | 0.11 | matrix unique |
| Type 1 protein phosphatase-activating protein | SDS22 | CAALFM\_C204020CA | Q5AHH6 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C205160CA | A0A1D8PHC4 | 0.00 | 0.11 | matrix unique |
| Exopolyphosphatase |  | CAALFM\_C206110WA | Q59X24 | 0.00 | 0.11 | matrix unique |
| mRNA splicing protein | SMD2 | CAALFM\_C206240WA | A0A1D8PHP3 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C207100WA | A0A1D8PHT4 | 0.00 | 0.11 | matrix unique |
| Lysophospholipid acyltransferase | LPT1 | CAALFM\_C207480WA | A0A1D8PHX1 | 0.00 | 0.11 | matrix unique |
| Kis1p | KIS1 | CAALFM\_C209230CA | Q59X47 | 0.00 | 0.11 | matrix unique |
| Cu/Pi carrier |  | CAALFM\_C209590CA | Q59YD1 | 0.00 | 0.11 | matrix unique |
| Mitochondrial import inner membrane translocase subunit TIM23 | TIM23 | CAALFM\_C209900CA | Q59YG5 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C209910CA | A0A1D8PIL6 | 0.00 | 0.11 | matrix unique |
| Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit | OST2 | CAALFM\_C210200WA | A0A1D8PIN6 | 0.00 | 0.11 | matrix unique |
| Gcn1p | GCN1 | CAALFM\_C210550CA | A0A1D8PIR2 | 0.00 | 0.11 | matrix unique |
| Mitochondrial import inner membrane translocase subunit TIM44 | TIM44 | CAALFM\_C300250CA | Q5A7M2 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C300630WA | Q5A7S2 | 0.00 | 0.11 | matrix unique |
| Bifunctional glycerol-3-phosphate/glycerone-phosphate O-acyltransferase | SCT1 | CAALFM\_C300820WA | A0A1D8PJ38 | 0.00 | 0.11 | matrix unique |
| Calcium-transporting ATPase | PMC1 | CAALFM\_C301250WA | Q5AJ65 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C301610WA | A0A1D8PJA6 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C301690WA | A0A1D8PJA1 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C302820CA | A0A1D8PJM6 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C305880CA | A0A1D8PKD0 | 0.00 | 0.11 | matrix unique |
| Uracil-DNA glycosylase (UDG) | UNG1 | CAALFM\_C306400CA | A0A1D8PKH5 | 0.00 | 0.11 | matrix unique |
| GTPase-activating protein |  | CAALFM\_C307170CA | Q5ADQ8 | 0.00 | 0.11 | matrix unique |
| Choline-phosphate cytidylyltransferase | PCT1 | CAALFM\_C400570CA | Q59SI6 | 0.00 | 0.11 | matrix unique |
| rRNA-processing protein | PWP1 | CAALFM\_C401450WA | A0A1D8PLA3 | 0.00 | 0.11 | matrix unique |
| Ubiquitin-ubiquitin ligase |  | CAALFM\_C401560CA | A0A1D8PLC1 | 0.00 | 0.11 | matrix unique |
| Csh3p | CSH3 | CAALFM\_C403390WA | A0A1D8PLU5 | 0.00 | 0.11 | matrix unique |
| Ribose phosphate diphosphokinase subunit |  | CAALFM\_C500260WA | Q5A4X7 | 0.00 | 0.11 | matrix unique |
| 5-demethoxyubiquinone hydroxylase, mitochondrial | COQ7 | CAALFM\_C501290CA | A0A1D8PN46 | 0.00 | 0.11 | matrix unique |
| Nucleotidase |  | CAALFM\_C504360CA | Q5AK98 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C600560WA | A0A1D8PPE5 | 0.00 | 0.11 | matrix unique |
| Sec12p | SEC12 | CAALFM\_C601760WA | A0A1D8PPP9 | 0.00 | 0.11 | matrix unique |
| Mitochondrial 37S ribosomal protein | RSM23 | CAALFM\_C602370CA | A0A1D8PPW1 | 0.00 | 0.11 | matrix unique |
| Aminophospholipid translocase regulatory protein | CDC50 | CAALFM\_C603660CA | A0A1D8PQ78 | 0.00 | 0.11 | matrix unique |
| rRNA-binding ribosome biosynthesis protein | NOP15 | CAALFM\_C700690WA | A0A1D8PQN7 | 0.00 | 0.11 | matrix unique |
| FK506-binding protein 3 | FPR3 | CAALFM\_C103790CA | Q59VR3 | 0.00 | 0.11 | matrix unique |
| Signal peptidase complex catalytic subunit | SEC11 | CAALFM\_CR00990WA | Q5A869 | 0.00 | 0.11 | matrix unique |
| GDP-mannose transporter | VRG4 | CAALFM\_C107700CA | Q5A477 | 0.00 | 0.11 | matrix unique |
| CAP1-binding-protein | YBP1 | CAALFM\_C113960WA | Q5AKU3 | 0.00 | 0.11 | matrix unique |
| 37S ribosomal protein S9, mitochondrial | MRPS9 | CAALFM\_C112340CA | O94150 | 0.00 | 0.11 | matrix unique |
| Histone H2A.Z-specific chaperone | CHZ1 | CAALFM\_CR07230WA | Q59RN6 | 0.00 | 0.11 | matrix unique |
| Actin cytoskeleton-regulatory complex protein SLA1 | SLA1 | CAALFM\_C201640WA | Q5ALV2 | 0.00 | 0.11 | matrix unique |
| Lanosterol 14-alpha demethylase | ERG11 | CAALFM\_C500660CA | P10613 | 0.00 | 0.11 | matrix unique |
| 1-phosphatidylinositol 4-kinase | STT4 | CAALFM\_CR07090WA | A0A1D8PTE0 | 0.00 | 0.11 | matrix unique |
| DNA-directed RNA polymerase subunit beta |  | CAALFM\_CR05550CA | Q59M52 | 0.00 | 0.11 | matrix unique |
| Type 2C protein phosphatase | PTC5 | CAALFM\_CR08160WA | Q5A388 | 0.00 | 0.11 | matrix unique |
| Ife2p | IFE2 | CAALFM\_CR05340CA | A0A1D8PSZ0 | 0.00 | 0.11 | matrix unique |
| Glycerophosphocholine phosphodiesterase | GDE1 | CAALFM\_C504510WA | A0A1D8PNZ7 | 0.00 | 0.11 | matrix unique |
| Hgt3p | HGT3 | CAALFM\_CR03850WA | Q5A032 | 0.00 | 0.11 | matrix unique |
| Cu-binding protein | SCO1 | CAALFM\_CR09300CA | A0A1D8PTX2 | 0.00 | 0.11 | matrix unique |
| E2 ubiquitin-conjugating protein | UBC8 | CAALFM\_C101830CA | Q59T91 | 0.00 | 0.11 | matrix unique |
| Age1p | AGE1 | CAALFM\_C103480CA | A0A1D8PD25 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C104490WA | A0A1D8PDB1 | 0.00 | 0.11 | matrix unique |
| Fth1p | FTH1 | CAALFM\_C109400CA | A0A1D8PEK3 | 0.00 | 0.11 | matrix unique |
| Chorismate mutase | ARO7 | CAALFM\_C111500CA | Q59TS4 | 0.00 | 0.11 | matrix unique |
| Ribosome biosynthesis protein |  | CAALFM\_C112680WA | A0A1D8PFH2 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein (Fragment) |  | CAALFM\_C113370WA | A0A1D8PFN5 | 0.00 | 0.11 | matrix unique |
| Dos2p | DOS2 | CAALFM\_C113920WA | Q5AKU7 | 0.00 | 0.11 | matrix unique |
| Ddi1p | DDI1 | CAALFM\_C114420WA | A0A1D8PFX6 | 0.00 | 0.11 | matrix unique |
| Transcription factor IIF subunit |  | CAALFM\_C200220CA | A0A1D8PG13 | 0.00 | 0.11 | matrix unique |
| Acyl carrier protein | ACP12 | CAALFM\_C204030CA | Q5AHH7 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C204490WA | A0A1D8PH93 | 0.00 | 0.11 | matrix unique |
| DNA-binding ATPase |  | CAALFM\_C204500WA | A0A1D8PH70 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C205290CA | Q59ZG1 | 0.00 | 0.11 | matrix unique |
| F1F0 ATP synthase subunit h | ATP14 | CAALFM\_C206290CA | A0A1D8PHL7 | 0.00 | 0.11 | matrix unique |
| Divalent metal ion transporter | SMF12 | CAALFM\_C207160WA | A0A1D8PHV2 | 0.00 | 0.11 | matrix unique |
| Ribose phosphate diphosphokinase subunit | PRS5 | CAALFM\_C207890WA | Q5A2L2 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C208020CA | Q5A2T4 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C208910CA | A0A1D8PIA0 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C209050CA | A0A1D8PI97 | 0.00 | 0.11 | matrix unique |
| Hydroxyacylglutathione hydrolase | GLO2 | CAALFM\_C209260CA | A0A1D8PID4 | 0.00 | 0.11 | matrix unique |
| NEDD8-conjugating protein |  | CAALFM\_C300520WA | Q5A7Q5 | 0.00 | 0.11 | matrix unique |
| Retromer subunit | PEP8 | CAALFM\_C303880CA | A0A1D8PJS7 | 0.00 | 0.11 | matrix unique |
| Ubiquinol--cytochrome-c reductase subunit 6 |  | CAALFM\_C304080WA | A0A1D8PJT8 | 0.00 | 0.11 | matrix unique |
| Ribosomal 60S subunit protein L35A | RPL35 | CAALFM\_C304960WA | A0A1D8PK30 | 0.00 | 0.11 | matrix unique |
| Glg2p | GLG2 | CAALFM\_C306450WA | A0A1D8PKH2 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C401830CA | A0A1D8PLD9 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C402200CA | A0A1D8PLG7 | 0.00 | 0.11 | matrix unique |
| tRNA (Guanosine(18)-2'-O)-methyltransferase |  | CAALFM\_C403830WA | A0A1D8PLX4 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C406590WA | Q5A1E4 | 0.00 | 0.11 | matrix unique |
| Translation initiation factor eIF5 | TIF5 | CAALFM\_C502490CA | A0A1D8PNF5 | 0.00 | 0.11 | matrix unique |
| Nucleoporin |  | CAALFM\_C503550WA | A0A1D8PNP6 | 0.00 | 0.11 | matrix unique |
| Lap4p | LAP4 | CAALFM\_C503590WA | A0A1D8PNQ9 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C600360CA | A0A1D8PPE1 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C600910CA | A0A1D8PPH3 | 0.00 | 0.11 | matrix unique |
| Histone acetyltransferase | TRA1 | CAALFM\_C601320WA | A0A1D8PPL1 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C603300CA | A0A1D8PQ45 | 0.00 | 0.11 | matrix unique |
| Ribosomal 40S subunit protein S28B | RPS28B | CAALFM\_C700710WA | A0A1D8PQN0 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_C702100WA | A0A1D8PR11 | 0.00 | 0.11 | matrix unique |
| Bifunctional diacylglycerol cholinephosphotransferase/ethanolaminephosphotransferase |  | CAALFM\_C702690CA | Q59M00 | 0.00 | 0.11 | matrix unique |
| Imidazoleglycerol-phosphate synthase | HIS7 | CAALFM\_C703720CA | A0A1D8PRE9 | 0.00 | 0.11 | matrix unique |
| NADH-ubiquinone oxidoreductase chain 3 | NAD3 | CaalfMp10 | Q9B8D1 | 0.00 | 0.11 | matrix unique |
| V-type proton ATPase subunit D | VMA8 | CAALFM\_C406400CA | P87220 | 0.00 | 0.11 | matrix unique |
| Mitochondrial genome maintenance protein MGM101 | MGM101 | CAALFM\_C102660CA | Q5AI97 | 0.00 | 0.11 | matrix unique |
| IMP-specific 5'-nucleotidase 1 | ISN1 | CAALFM\_C101650WA | Q5A8X9 | 0.00 | 0.11 | matrix unique |
| Protein SIP5 | SIP5 | CAALFM\_C105910WA | Q5AA26 | 0.00 | 0.11 | matrix unique |
| Blood-induced peptide 1 | BLP1 | CAALFM\_C112850WA | P0CT51 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR01080WA | Q5A881 | 0.00 | 0.11 | matrix unique |
| Protein phosphatase regulator | SHP1 | CAALFM\_CR01610CA | A0A1D8PS15 | 0.00 | 0.11 | matrix unique |
| Acetyl-CoA C-acyltransferase | POT1 | CAALFM\_CR00150CA | A0A1D8PRL6 | 0.00 | 0.11 | matrix unique |
| Pex19p | PEX19 | CAALFM\_CR08600CA | Q5A330 | 0.00 | 0.11 | matrix unique |
| Triglyceride lipase |  | CAALFM\_CR02570CA | Q59LU6 | 0.00 | 0.11 | matrix unique |
| mRNA splicing protein |  | CAALFM\_CR10820WA | A0A1D8PUC1 | 0.00 | 0.11 | matrix unique |
| Ribosomal 40S subunit protein S29A |  | CAALFM\_CR08480CA | A0A1D8PTR4 | 0.00 | 0.11 | matrix unique |
| Uncharacterized protein |  | CAALFM\_CR05750WA | Q59PS7 | 0.00 | 0.11 | matrix unique |
| mRNA splicing protein |  | CAALFM\_CR07510WA | A0A1D8PTI0 | 0.00 | 0.11 | matrix unique |
| Putative ATP-dependent kinase |  | CAALFM\_CR09500CA | A0A1D8PTZ9 | 0.00 | 0.11 | matrix unique |
| Lysine/arginine permease | CAN1 | CAALFM\_C600960WA | A0A1D8PPI5 | 0.00 | 0.11 | matrix unique |
| SNAP receptor | SEC22 | CAALFM\_CR03970CA | A0A1D8PSL3 | 0.00 | 0.11 | matrix unique |
| Gef2p | GEF2 | CAALFM\_CR02350CA | A0A1D8PS75 | 0.00 | 0.11 | matrix unique |
| Hgt18p | HGT18 | CAALFM\_CR03040CA | A0A1D8PSC9 | 0.00 | 0.11 | matrix unique |

1Parameters used: minimum 95% peptide threshold, minimum 95% protein threshold and minimum of 2 peptides