| Query         | swissprot| swissprot| swissprot | swissprot| swissprot_evalue |
|---------------|----------|----------|-----------|----------|-----------------|
| TRINITY_sp| Q8W6WC4orf3 | Uncharacterized pro | 100.00 | 0.00 |
| TRINITY_sp| Q92SH1 | Histone H1x OS=Homo | 100.00 | 0.00 |
| TRINITY_sp| Q9Y33STARD10 | PCTP-like protein O | 100.00 | 0.00 |
| TRINITY_sp| Q1551ARPC5 | Actin-related prote | 100.00 | 0.00 |
| TRINITY_sp| Q1507TNIP1 | TNFAIP3-interacting | 100.00 | 0.00 |
| TRINITY_sp| P1418rpsA | 3OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp| Q9G7SLIRP | SRA stem-loop-inter | 100.00 | 0.00 |
| TRINITY_sp| Q9N2EPSENEN | Gamma-secretase sub | 100.00 | 0.00 |
| TRINITY_sp| P486PRRC2A | Protein PRRC2A OS=H | 100.00 | 0.00 |
| TRINITY_sp| Q054FABP7 | Fatty acid-binding | 100.00 | 0.00 |
| TRINITY_sp| Q5M9Iostc-b | Oligosaccharyltrans | 100.00 | 0.00 |
| TRINITY_sp| Q9Y51NAGED1 | Melanoma-associated | 100.00 | 0.00 |
| TRINITY_sp| Q279CAPN2 | Calpain-2 catalytic | 100.00 | 0.00 |
| TRINITY_sp| Q95LEIF4G2 | Eukaryotic translat | 100.00 | 0.00 |
| TRINITY_sp| P122Apcs | Serum amyloid P-com | 100.00 | 0.00 |
| TRINITY_sp| P008Odc1 | Ornithine decarboxy | 100.00 | 0.00 |
| TRINITY_sp| Q3UBTbbrg1 | Transforming growth | 100.00 | 0.00 |
| TRINITY_sp| P151GSPT1 | Eukaryotic peptide | 100.00 | 0.00 |
| TRINITY_sp| Q9H0MRPL18 | 39S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp| Q3S2F1AAMP | Angio-associated mi | 100.00 | 0.00 |
| TRINITY_sp| Q9UKVPS28 | Vacuolar protein so | 100.00 | 0.00 |
| TRINITY_sp| P438Plin2 | Perilipin-2 OS=Mus | 100.00 | 0.00 |
| TRINITY_sp| Q9W0MRXRA8 | Matrix-remodeling-a | 100.00 | 0.00 |
| TRINITY_sp| Q168ATP6V1F | V-type proton ATPas | 100.00 | 0.00 |
| TRINITY_sp| Q5E9MDNAJA1 | DnaJ homolog subfam | 100.00 | 0.00 |
| TRINITY_sp| Q3S2ERH | Enhancer of rudimen | 100.00 | 0.00 |
| TRINITY_sp| P102MYBL2 | Myb-related protein | 100.00 | 0.00 |
| TRINITY_sp| Q05P1RBM42 | RNA-binding protein | 100.00 | 0.00 |
| TRINITY_sp| Q9Y55SRPRB | Signal recognition | 100.00 | 0.00 |
| TRINITY_sp| P072Jsera | Serralysin OS=Serra | 100.00 | 0.00 |
| TRINITY_sp| P297VTn | Vitronectin OS=Mus | 100.00 | 0.00 |
| TRINITY_sp| P563Cox6b1 | Cytochrome c oxidas | 100.00 | 0.00 |
| TRINITY_sp| P148COX6B1 | Cytochrome c oxidas | 100.00 | 0.00 |
| TRINITY_sp| Q0MQDNDUFA1 | Acyl carrier protei | 100.00 | 0.00 |
| TRINITY_sp| P504Cs3p3 | Cysteine and glycin | 100.00 | 0.00 |
| TRINITY_sp| P412GARS | Glycine--tRNA ligas | 100.00 | 0.00 |
| TRINITY_sp| P102MYBL2 | Myb-related protein | 100.00 | 0.00 |
| TRINITY_sp| O002ATOX1 | Copper transport pr | 100.00 | 0.00 |
| TRINITY_sp| P079HSF90A | Heat shock protein | 100.00 | 0.00 |
| TRINITY_sp| P614PCBD1 | Pterin-4-alpha-carb | 100.00 | 0.00 |
| TRINITY_sp| Q3T1RPS23 | 40S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp| Q3T1RPS23 | 40S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp| P115MTHFD1 | C-1-tetrahydrofolat | 100.00 | 0.00 |
| TRINITY_sp| Q6ZWWRp135 | 60S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp| P427RLP35 | 60S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp| P616HSPE1 | 10 kDa heat shock p | 100.00 | 0.00 |
| TRINITY_sp| P614rpl36a | 60S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp| Q618Pzp | Pregnancy zone prote | 100.00 | 0.00 |
| TRINITY_sp| Q151NOM01 | Nodal modulator 1 O | 100.00 | 0.00 |
| TRINITY_sp| Q96AMRPL24 | 39S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp| O704Phl2 | Four and a half LIM | 100.00 | 0.00 |
| TRINITY_sp| Q56JJPFS13 | 40S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp| Q9R0Bcam | Basal cell adhesi | 100.00 | 0.00 |
| TRINITY_sp| P085PDHA1 | Pyruvate dehydrogen | 100.00 | 0.00 |
| TRINITY_sp| Q9CQRnaset2 | Ribonuclease T2 OS= | 100.00 | 0.00 |
| Accession   | Description                                    | Expression | ORF   |
|-------------|------------------------------------------------|------------|-------|
| TRINITY_sp| Histone deacetylase                            | 100.00     | 0.00  |
| TRINITY_sp| Serine--tRNA ligase                             | 100.00     | 0.00  |
| TRINITY_sp| CD63 antigen                                    | 100.00     | 0.00  |
| TRINITY_sp| Small acidic protein                            | 100.00     | 0.00  |
| TRINITY_sp| Telethonin                                      | 100.00     | 0.00  |
| TRINITY_sp| Peroxisomal bifunction                          | 100.00     | 0.00  |
| TRINITY_sp| SPARC-like protein                              | 100.00     | 0.00  |
| TRINITY_sp| Ubiquitin-like protein                          | 100.00     | 0.00  |
| TRINITY_sp| Ubiquitin-like protein                          | 100.00     | 0.00  |
| TRINITY_sp| THO complex subunit                             | 100.00     | 0.00  |
| TRINITY_sp| Aspartyl/asparaginy                             | 100.00     | 0.00  |
| TRINITY_sp| Sodium-dependent ph                             | 100.00     | 0.00  |
| TRINITY_sp| Selenoprotein W                                 | 100.00     | 0.00  |
| TRINITY_sp| Ubiquitin-like protein                          | 100.00     | 0.00  |
| TRINITY_sp| Ubiquitin-like protein                          | 100.00     | 0.00  |
| TRINITY_sp| Guanylate kinase OS=Homo sapi                  | 100.00     | 0.00  |
| TRINITY_sp| Protein cornichon h                             | 100.00     | 0.00  |
| TRINITY_sp| Photosystem I react                             | 100.00     | 0.00  |
| TRINITY_sp| Protein AMBP OS=Mus                             | 100.00     | 0.00  |
| TRINITY_sp| Protein AMBP OS=Mus                             | 100.00     | 0.00  |
| TRINITY_sp| Eukaryotic translat                             | 100.00     | 0.00  |
| TRINITY_sp| 5-aminolevulinate s                             | 100.00     | 0.00  |
| TRINITY_sp| ATP synthase-coupli                             | 100.00     | 0.00  |
| TRINITY_sp| Eukaryotic translat                             | 100.00     | 0.00  |
| TRINITY_sp| DNA polymerase deltal                          | 100.00     | 0.00  |
| TRINITY_sp| Cytochrome P450 4A1                              | 100.00     | 0.00  |
| TRINITY_sp| 39S ribosomal prote                             | 100.00     | 0.00  |
| TRINITY_sp| 60S ribosomal prote                             | 100.00     | 0.00  |
| TRINITY_sp| Polyadenylate-bindi                             | 100.00     | 0.00  |
| TRINITY_sp| U6 snRNA-associated                             | 100.00     | 0.00  |
| TRINITY_sp| Diamine acetyltrans                             | 100.00     | 0.00  |
| TRINITY_sp| Diamine acetyltrans                             | 100.00     | 0.00  |
| TRINITY_sp| ATP synthase subuni                             | 100.00     | 0.00  |
| TRINITY_sp| Cytochrome b-c1 com                             | 100.00     | 0.00  |
| TRINITY_sp| Selenium-binding pr                             | 100.00     | 0.00  |
| TRINITY_sp| Selenium-binding pr                             | 100.00     | 0.00  |
| TRINITY_sp| Cysteine and glycin                            | 100.00     | 0.00  |
| TRINITY_sp| Protein 1-antitrypsin                           | 100.00     | 0.00  |
| TRINITY_sp| Transmembrane prote                             | 100.00     | 0.00  |
| TRINITY_sp| Dolichyl-diphosphoo                             | 100.00     | 0.00  |
| TRINITY_sp| Putative uncharacte                            | 100.00     | 0.00  |
| TRINITY_sp| Protein NDRG2 OS=Mu                             | 100.00     | 0.00  |
| TRINITY_sp| Guanine nucleotide-                            | 100.00     | 0.00  |
| TRINITY_sp| Myosin regulatory l                             | 100.00     | 0.00  |
| TRINITY_sp| Hydroxyacyl-coenzym                             | 100.00     | 0.00  |
| TRINITY_sp| Protein phosphatase                             | 100.00     | 0.00  |
| TRINITY_sp| NADH dehydrogenase                             | 100.00     | 0.00  |
| TRINITY_sp| NADH dehydrogenase                             | 100.00     | 0.00  |
| TRINITY_sp| Protein disulfide-i                             | 100.00     | 0.00  |
| Gene Name                  | Description                           | Confidence | Score |
|---------------------------|---------------------------------------|------------|-------|
| TRINITY_sp|P087|RPS17 | 40S ribosomal protein | 100.00 | 0.00 |
| TRINITY_sp|P23I|CES1 | Liver carboxylester | 100.00 | 0.00 |
| TRINITY_sp|Q1JP|ARP6 | Actin-related protein | 100.00 | 0.00 |
| TRINITY_sp|P075|DCN  | Decorin OS=Homo sap | 100.00 | 0.00 |
| TRINITY_sp|Q9Y3I|STRAP | Serine-threonine ki | 100.00 | 0.00 |
| TRINITY_sp|P497|PSM2 | Proteosome subunit | 100.00 | 0.00 |
| TRINITY_sp|Q357|Cyp4a14| Cytochrome P450 4A1 | 100.00 | 0.00 |
| TRINITY_sp|Q1491|DRAF1 | Drl-associated core | 100.00 | 0.00 |
| TRINITY_sp|P460|RANGAP1| Ran GTPase-activati | 100.00 | 0.00 |
| TRINITY_sp|A3KN|UBE2M | NEDD8-conjugating e | 100.00 | 0.00 |
| TRINITY_sp|P117|FN1  | Fibronectin (Fragme | 100.00 | 0.00 |
| TRINITY_sp|P117|TCP1 | T-complex protein 1 | 100.00 | 0.00 |
| TRINITY_sp|P19O|Krt19 | Keratin, type I cyt | 100.00 | 0.00 |
| TRINITY_sp|P070|S100a4 | Protein S100-A4 OS= | 100.00 | 0.00 |
| TRINITY_sp|P264|S100A4 | Protein S100-A4 OS= | 100.00 | 0.00 |
| TRINITY_sp|P186|NELFE | Negative elongation | 100.00 | 0.00 |
| TRINITY_sp|Q644|Cyp3a11| Cytochrome P450 3A1 | 100.00 | 0.00 |
| TRINITY_sp|Q644|Cyp3a11| Cytochrome P450 3A1 | 100.00 | 0.00 |
| TRINITY_sp|Q8K0|Fgb  | Fibrinogen beta cha | 100.00 | 0.00 |
| TRINITY_sp|Q91X|Hpx  | Hemopexin OS=Mus mu | 100.00 | 0.00 |
| TRINITY_sp|Q91X|Hpx  | Hemopexin OS=Mus mu | 100.00 | 0.00 |
| TRINITY_sp|Q8K0|Fgb  | Fibrinogen beta cha | 100.00 | 0.00 |
| TRINITY_sp|Q91X|Hpx  | Hemopexin OS=Mus mu | 100.00 | 0.00 |
| TRINITY_sp|Q9JH|Cwc15 | Spliceosome-associa | 100.00 | 0.00 |
| TRINITY_sp|P050|APP  | Amyloid beta A4 pro | 100.00 | 0.00 |
| TRINITY_sp|Q354|Ech1 | Delta(3,-)-Delta(2, | 100.00 | 0.00 |
| TRINITY_sp|Q9UK|ACIN1 | Apoptotic chromatin | 100.00 | 0.00 |
| TRINITY_sp|Q32K|Protein C10 OS= | 100.00 | 0.00 |
| TRINITY_sp|Q32K|Protein C10 OS= | 100.00 | 0.00 |
| TRINITY_sp|P180|RPL35A | 60S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P678|CSNK2B | Casein kinase II su | 100.00 | 0.00 |
| TRINITY_sp|P149|UQCRB | Cytochrome b-c1 com | 100.00 | 0.00 |
| TRINITY_sp|Q56J|RPS13 | 40S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q56J|RPS13 | 40S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q56J|RPS13 | 40S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P005|PRKAR1A | cAMP-dependent prot | 100.00 | 0.00 |
| TRINITY_sp|A9JR|ppp4cb | Serine/threonine-pr | 100.00 | 0.00 |
| TRINITY_sp|Q149|UQCR11 | Cytochrome b-c1 com | 100.00 | 0.00 |
| TRINITY_sp|P565|EIF6  | Eukaryotic translat | 100.00 | 0.00 |
| TRINITY_sp|P495|SARS | Serine--tRNA ligase | 100.00 | 0.00 |
| TRINITY_sp|Q622|Sptbn1 | Spectrin beta chain | 100.00 | 0.00 |
| TRINITY_sp|P609|S100A10 | Protein S100-A10 OS | 100.00 | 0.00 |
| TRINITY_sp|Q9QX1|Egf17 | Epidermal growth fa | 100.00 | 0.00 |
| TRINITY_sp|P623|SNRPD3 | Small nuclear ribon | 100.00 | 0.00 |
| TRINITY_sp|Q150|KARS | Lysine--tRNA ligase | 100.00 | 0.00 |
| TRINITY_sp|Q3MI|RPL37A | 60S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q3MI|RPL37A | 60S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q3T1|DYNLRB1 | Dynein light chain | 100.00 | 0.00 |
| TRINITY_sp|P467|RPL28 | 60S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P411|Rpl128 | 60S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P042|H2-Eb1 | H-2 class II histoc | 100.00 | 0.00 |
| TRINITY_sp|P591|HTR4  | Histone H3.3 OS=Ara | 100.00 | 0.00 |
| TRINITY_sp|Q1RM|CTDNEP1 | CTD nuclear envelop | 100.00 | 0.00 |
| TRINITY_sp|P494|Hpd  | 4-hydroxyphenylpyru | 100.00 | 0.00 |
| Protein Name                          | Gene Name | Species     | Expression Score | Gene ID | Description               |
|---------------------------------------|-----------|-------------|------------------|---------|---------------------------|
| Histone H2A.V                         | H2AFV     | Bos taurus  | 100.00           |         |                           |
| 60S ribosomal protein                 | P0A9     | Mus musculus| 100.00           |         |                           |
| Peroxiredoxin-5, mi                   | P091     | Homo sapiens| 100.00           |         |                           |
| RNA-binding protein                   | P042     | Mus musculus| 100.00           |         |                           |
| 60S ribosomal protein                 | P042     | Mus musculus| 100.00           |         |                           |
| Peroxosomal acyl-co                   | P073     | Homo sapiens| 100.00           |         |                           |
| Cytochrome P450 2C2                   | P31949   | Homo sapiens| 100.00           |         |                           |
| Protein disulfide-i                   | P31949   | Homo sapiens| 100.00           |         |                           |
| E3 ubiquitin-protein                 | P31949   | Homo sapiens| 100.00           |         |                           |
| Protein regulator o                   | P31949   | Homo sapiens| 100.00           |         |                           |
| Myoglobin                            | Mb       | Mus musculus| 100.00           |         |                           |
| NADH dehydrogenase                    | NDUF566  | Homo sapiens| 100.00           |         |                           |
| Spermine synthase                     | SMS      | Mus musculus| 100.00           |         |                           |
| 40S ribosomal protein                 | CD81     | Homo sapiens| 100.00           |         |                           |
| Neudesin                             | CDP      | Homo sapiens| 100.00           |         |                           |
| Mesencephalic astro                   | CSDE1    | Homo sapiens| 100.00           |         |                           |
| ATP-dependent RNA h                  | Q68582   | Homo sapiens| 100.00           |         |                           |
| Transitional endopl                   | CB21     | Homo sapiens| 100.00           |         |                           |
| Cyclin-I                             | CCNB1    | Homo sapiens| 100.00           |         |                           |
| Electron transfer f                   | ETFB     | Homo sapiens| 100.00           |         |                           |
| CD81 antigen                          | ITB1     | Homo sapiens| 100.00           |         |                           |
| Heterogeneous nucle                   | HNRNPF   | Homo sapiens| 100.00           |         |                           |
| RING-box protein 2                    | S100A11  | Homo sapiens| 100.00           |         |                           |
| Vacuolar protein-so                   | S100A11  | Homo sapiens| 100.00           |         |                           |
| Rho-related GTP-bin                   | S100A11  | Homo sapiens| 100.00           |         |                           |
| 26S protease regula                   | S100A11  | Homo sapiens| 100.00           |         |                           |
| Small nuclear ribon                  | S100A11  | Homo sapiens| 100.00           |         |                           |
| NEDD8 OS=Bos taurus                   | NEDD8    | Homo sapiens| 100.00           |         |                           |
| DNA-directed RNA po                   | POLR2J   | Homo sapiens| 100.00           |         |                           |
| Nucleolysin TIAR OS                  | Q0108     | Homo sapiens| 100.00           |         |                           |
| 26S protease regula                   | S100A11  | Homo sapiens| 100.00           |         |                           |
| NADH dehydrogenase                    | NDUF566  | Homo sapiens| 100.00           |         |                           |
| DNA-directed RNA po                   | POLR2J   | Homo sapiens| 100.00           |         |                           |
| Nucleolysin TIAR OS                  | Q0108     | Homo sapiens| 100.00           |         |                           |
| 60S ribosomal prote                   | CD81     | Homo sapiens| 100.00           |         |                           |
| Insulin-like growth                   | P478b     | Homo sapiens| 100.00           |         |                           |
| Vitamin D-binding p                   | P2163     | Homo sapiens| 100.00           |         |                           |
| Cold shock domain-c                   | P291     | Homo sapiens| 100.00           |         |                           |
| Aspartate aminotrans                  | P052     | Homo sapiens| 100.00           |         |                           |
| Aspartate aminotrans                  | P052     | Homo sapiens| 100.00           |         |                           |
| Protein NDRG1 OS=Mu                   | NDRG1    | Homo sapiens| 100.00           |         |                           |
| Transcription inter                   | Q132     | Homo sapiens| 100.00           |         |                           |
| G2/mitotic-specific                   | P091     | Homo sapiens| 100.00           |         |                           |
| Protein S100-All OS                   | P505     | Homo sapiens| 100.00           |         |                           |
| Protein S100-All OS                   | P319     | Homo sapiens| 100.00           |         |                           |
| Bifunctional purine                   | ATIC     | Homo sapiens| 100.00           |         |                           |
| Guanine nucleotide-                   | P628     | Homo sapiens| 100.00           |         |                           |
| Coatomer subunit be                   | COPB1    | Homo sapiens| 100.00           |         |                           |
| Cold-inducible RNA-                   | Q1401    | Homo sapiens| 100.00           |         |                           |
| Integrin beta-1 OS                   | ITGB1    | Homo sapiens| 100.00           |         |                           |
| ADP-ribosylation fa                   | P840     | Homo sapiens| 100.00           |         |                           |
| E3 ubiquitin-protei                   | Q09H     | Homo sapiens| 100.00           |         |                           |
| Cathepsin D OS=Homo                   | CTSD     | Homo sapiens| 100.00           |         |                           |
| Accession     | Name                                      | Description                        | Value 1 | Value 2 |
|--------------|-------------------------------------------|------------------------------------|---------|---------|
| TRINITY_sp|P025|ASL1                             | Delta-1 crystallin                | 100.00  | 0.00    |
| TRINITY_sp|P106|Ctsb                             | Cathepsin B OS=Mus                | 100.00  | 0.00    |
| TRINITY_sp|Q56K|RPLP1                           | 60S acidic ribosomal               | 100.00  | 0.00    |
| TRINITY_sp|Q9DG6|Ndufv2                          | NADH dehydrogenase                | 100.00  | 0.00    |
| TRINITY_sp|P617|B2M                             | Beta-2-microglobulin              | 100.00  | 0.00    |
| TRINITY_sp|P352|RPL22                           | 60S ribosomal prote                | 100.00  | 0.00    |
| TRINITY_sp|Q4R5|RPL22                           | 60S ribosomal prote                | 100.00  | 0.00    |
| TRINITY_sp|O626|DES                             | Desmin OS=Bos tauri               | 100.00  | 0.00    |
| TRINITY_sp|Q9C72|Cs                              | Citrate synthase, m               | 100.00  | 0.00    |
| TRINITY_sp|P516|Myl2                            | Myosin regulatory l               | 100.00  | 0.00    |
| TRINITY_sp|P613|RPL27                           | 60S ribosomal prote                | 100.00  | 0.00    |
| TRINITY_sp|P188|ATF4                            | Cyclic AMP-dependen               | 100.00  | 0.00    |
| TRINITY_sp|P613|RPL27                           | 60S ribosomal prote                | 100.00  | 0.00    |
| TRINITY_sp|Q025|Myh6                            | Myosin-6 OS=Mus mus               | 100.00  | 0.00    |
| TRINITY_sp|Q2KJ|CDC42                           | Cell division contr              | 100.00  | 0.00    |
| TRINITY_sp|Q16Y|Cc42                            | Cdc42 homolog OS= Ae             | 100.00  | 0.00    |
| TRINITY_sp|O886|Psmc3                           | 26S protease regula               | 100.00  | 0.00    |
| TRINITY_sp|P412|IARS                            | Isoleucine--tRNA li               | 100.00  | 0.00    |
| TRINITY_sp|P563|Cyb5a                           | Cytochrome b5 OS=Mu               | 100.00  | 0.00    |
| TRINITY_sp|P206|COX5A                           | Cytochrome c oxidases             | 100.00  | 0.00    |
| TRINITY_sp|Q3ZC|PAIP2                           | Polyadenylate-bindi               | 100.00  | 0.00    |
| TRINITY_sp|P087|Gnia2                           | Guanine nucleotide-              | 100.00  | 0.00    |
| TRINITY_sp|Q3T0|RPS10                           | 40S ribosomal prote               | 100.00  | 0.00    |
| TRINITY_sp|Q999|Rtn4                            | Reticulon-4 OS=Mus                | 100.00  | 0.00    |
| TRINITY_sp|P514|Rpl19                           | 60S ribosomal prote               | 100.00  | 0.00    |
| TRINITY_sp|P329|Rpl9                            | 60S ribosomal prote               | 100.00  | 0.00    |
| TRINITY_sp|P319|UQCR1                           | Cytochrome b-c1 com              | 100.00  | 0.00    |
| TRINITY_sp|Q884|Capns1                          | Calpain small subun              | 100.00  | 0.00    |
| TRINITY_sp|Q3ZC|SKP1                            | S-phase kinase-asso               | 100.00  | 0.00    |
| TRINITY_sp|P276|APEX1                           | DNA-(apurinic or ap)              | 100.00  | 0.00    |
| TRINITY_sp|Q9UN|RPL26L1                          | 60S ribosomal prote               | 100.00  | 0.00    |
| TRINITY_sp|P213|FLNA                            | Filamin-A OS=Homo s              | 100.00  | 0.00    |
| TRINITY_sp|P223|NME2                            | Nucleoside diphosphh              | 100.00  | 0.00    |
| TRINITY_sp|P067|S100A6                          | Protein S100-A6 OS=              | 100.00  | 0.00    |
| TRINITY_sp|Q3T0|RPL23                           | 60S ribosomal prote               | 100.00  | 0.00    |
| TRINITY_sp|Q3T0|RPL23                           | 60S ribosomal prote               | 100.00  | 0.00    |
| TRINITY_sp|P321|PRDX2                           | Peroxiredoxin-2 OS=              | 100.00  | 0.00    |
| TRINITY_sp|P467|RPL21                           | 60S ribosomal prote               | 100.00  | 0.00    |
| TRINITY_sp|P436|PRC1                            | Protein regulator o              | 100.00  | 0.00    |
| TRINITY_sp|P438|CALU                            | Calumenin OS=Homo s              | 100.00  | 0.00    |
| TRINITY_sp|P048|RPN2                            | Dolichyl-diphosphoo               | 100.00  | 0.00    |
| TRINITY_sp|P048|RPN2                            | Dolichyl-diphosphoo               | 100.00  | 0.00    |
| TRINITY_sp|P363|U2AF2                           | Splicing factor U2A               | 100.00  | 0.00    |
| TRINITY_sp|Q3T0|RPS18                           | 40S ribosomal prote               | 100.00  | 0.00    |
| TRINITY_sp|Q3T0|RPS18                           | 40S ribosomal prote               | 100.00  | 0.00    |
| TRINITY_sp|P363|ARF1                            | ADP-ribosylation fa               | 100.00  | 0.00    |
| TRINITY_sp|P180|ARF4                            | ADP-ribosylation fa               | 100.00  | 0.00    |
| TRINITY_sp|Q3T0|RAN                            | GTP-binding nuclear               | 100.00  | 0.00    |
| Gene ID        | Description                          | Score 1  | Score 2  |
|---------------|--------------------------------------|----------|----------|
| TRINITY_sp|Q41|Rps5a  | 4OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q5E9|Rps5s | 4OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P05|Krt8  | Keratin, type II cy | 100.00 | 0.00 |
| TRINITY_sp|P606|Myl6  | Myosin light polype | 100.00 | 0.00 |
| TRINITY_sp|Q21|Nomo1 | Nodal modulator 1 O | 100.00 | 0.00 |
| TRINITY_sp|P612|Ppp1c  | Serine/threonine-pr | 100.00 | 0.00 |
| TRINITY_sp|P621|Ppplca | Serine/threonine-pr | 100.00 | 0.00 |
| TRINITY_sp|P0C|H2afz | Histone H2A.Z OS=Bo | 100.00 | 0.00 |
| TRINITY_sp|Q27|Igag  | Gag polyprotein OS= | 100.00 | 0.00 |
| TRINITY_sp|P033|Gag-pol | Gag-Pol polyprotein | 100.00 | 0.00 |
| TRINITY_sp|Q96|Rpl36al  | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q3S|Rpl36a | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q3Z|Eif3l  | Eukaryotic translat | 100.00 | 0.00 |
| TRINITY_sp|Q3S|Rpl36a | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q3Z|Actn2  | Alpha-actinin-2 OS= | 100.00 | 0.00 |
| TRINITY_sp|P043|Actn4  | Alpha-actinin-4 OS= | 100.00 | 0.00 |
| TRINITY_sp|Q5D|Actn4  | Alpha-actinin-4 OS= | 100.00 | 0.00 |
| TRINITY_sp|Q10|Ewsr1  | RNA-binding protein | 100.00 | 0.00 |
| TRINITY_sp|Q3T|Sec6l  | Protein transport p | 100.00 | 0.00 |
| TRINITY_sp|P624|Rpl7a  | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P129|Rpl17a | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P161|Lgals3 | Galectin-3 OS=Mus m | 100.00 | 0.00 |
| TRINITY_sp|Q93|Rpl36  | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q3S|Pgam1  | Phosphoglycerate mu | 100.00 | 0.00 |
| TRINITY_sp|Q93|Rpl36  | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q70|Rpl30  | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q70|Rpl30  | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q3M|Ubeb2l3 | Ubiquitin-conjugati | 100.00 | 0.00 |
| TRINITY_sp|Q5E|Eif1   | Eukaryotic translat | 100.00 | 0.00 |
| TRINITY_sp|Q9C|Atp5l  | ATP synthase subuni | 100.00 | 0.00 |
| TRINITY_sp|Q2N|Cct7   | T-complex protein l | 100.00 | 0.00 |
| TRINITY_sp|Q61|Psap   | Prosaposin OS=Mus m | 100.00 | 0.00 |
| TRINITY_sp|Q3M|Arfpc2 | Actin-related prote | 100.00 | 0.00 |
| TRINITY_sp|Q9Y|Nudc   | Nuclear migration p | 100.00 | 0.00 |
| TRINITY_sp|Q2Z|Mbd2  | Methyl-CpG-binding | 100.00 | 0.00 |
| TRINITY_sp|Q06|Pdx1   | Peroxisiredoxin-1 OS= | 100.00 | 0.00 |
| TRINITY_sp|P70|C3    | Complement C3 OS=Mu | 100.00 | 0.00 |
| TRINITY_sp|Q63|Scgb1al | Uteroglobin OS=Mus | 100.00 | 0.00 |
| TRINITY_sp|P01|C3    | Complement C3 OS=Mu | 100.00 | 0.00 |
| TRINITY_sp|E9P|Fga   | Fibrinogen alpha ch | 100.00 | 0.00 |
| TRINITY_sp|Q616|Hp    | Haptoglobin OS=Mus | 100.00 | 0.00 |
| TRINITY_sp|P077|Serpina3 | Serine protease inh | 100.00 | 0.00 |
| TRINITY_sp|Q07|Rpl18  | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q006|Apoal | Apolipoprotein A-I | 100.00 | 0.00 |
| TRINITY_sp|P077|Alb   | Serum albumin OS=Mu | 100.00 | 0.00 |
| TRINITY_sp|Q8V|Fgg   | Fibrinogen gamma ch | 100.00 | 0.00 |
| TRINITY_sp|P077|Serpina3 | Serine protease inh | 100.00 | 0.00 |
| TRINITY_sp|P082|Apoel | Apolipoprotein E OS | 100.00 | 0.00 |
| TRINITY_sp|P359|Rpl18  | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P020|Hbb-b1 | Hemoglobin subunit | 100.00 | 0.00 |
| TRINITY_sp|P519|Hnnna3 | Heterogeneous nuc1e | 100.00 | 0.00 |
| TRINITY_sp|P792|Rpl37  | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P390|Rpl37  | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q5A|Eif3e-a | Eukaryotic translat | 100.00 | 0.00 |
| TRINITY_sp|P792|Rpl37  | 6OS ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P053|Saal  | Serum amyloid A-1 p | 100.00 | 0.00 |
TRINITY_sp|P0491Saa3  Serum amyloid A-3 p 100.00 0.00
TRINITY_sp|Q352gLAMTOR5  Regulator complex p 100.00 0.00
TRINITY_sp|P6101P1n  Cardiac phospholamb 100.00 0.00
TRINITY_sp|O5512At2a2  Sarcoplasmic/endopl p 100.00 0.00
TRINITY_sp|E2RKRPL32  60S ribosomal prote 100.00 0.00
TRINITY_sp|P0CGUB111  Polyubiquitin OS=Ni 100.00 0.00
TRINITY_sp|P48Z2ATP5G3  ATP synthase F(0) c 100.00 0.00
TRINITY_sp|P213FLNA  Filamin-A OS=Homo s 100.00 0.00
TRINITY_sp|P235FL1  Cofilin-1 OS=Homo s 100.00 0.00
TRINITY_sp|P187Cf11  Cofilin-1 OS=Mus mu 100.00 0.00
TRINITY_sp|P610UBE2D3  Ubiquitin-conjugati 100.00 0.00
TRINITY_sp|P109Spp1  Osteopontin OS=Mus 100.00 0.00
TRINITY_sp|P109Spp1  Osteopontin OS=Mus 100.00 0.00
TRINITY_sp|Q013Apho  Beta-2-glycoprotein 100.00 0.00
TRINITY_sp|Q429APh  Phosphoglycerate ki 100.00 0.00
TRINITY_sp|P563ATP5E  ATP synthase subuniti 100.00 0.00
TRINITY_sp|Q5EAARPL15  60S ribosomal prote 100.00 0.00
TRINITY_sp|Q2NKWBLOC1S1  Biogenesis of lysos 100.00 0.00
TRINITY_sp|P365RPL4  60S ribosomal prote 100.00 0.00
TRINITY_sp|P631DYNLT1  Dynein light chain 100.00 0.00
TRINITY_sp|Q3T1RPS3  40S ribosomal prote 100.00 0.00
TRINITY_sp|Q3T1RPS3  40S ribosomal prote 100.00 0.00
TRINITY_sp|Q013Apho  HLA class I histoco 100.00 0.00
TRINITY_sp|Q76NRLPS4X  40S ribosomal prote 100.00 0.00
TRINITY_sp|Q76NRLPS4X  40S ribosomal prote 100.00 0.00
TRINITY_sp|Q3PHEEFL12  Elongation factor 1 100.00 0.00
TRINITY_sp|P2954-  Elongation factor 1 100.00 0.00
TRINITY_sp|P158RPS2  40S ribosomal prote 100.00 0.00
TRINITY_sp|P113gag  Retrovirus-related 100.00 0.00
TRINITY_sp|P254Rps2  40S ribosomal prote 100.00 0.00
TRINITY_sp|P113gag  Retrovirus-related 100.00 0.00
TRINITY_sp|P1284-  Probable Pol polypr 100.00 0.00
TRINITY_sp|P039Iap  IgE-binding protein 100.00 0.00
TRINITY_sp|P564Atp5b  ATP synthase subuniti 100.00 0.00
TRINITY_sp|Q753TBCA  Tubulin-specific ch 100.00 0.00
TRINITY_sp|H29PPTA  Peptidyl-prolyl cis 100.00 0.00
TRINITY_sp|P177PPia  Peptidyl-prolyl cis 100.00 0.00
TRINITY_sp|P5344-  Actin, cytoplasmic 100.00 0.00
TRINITY_sp|P5354-  Actin, cytoplasmic 100.00 0.00
TRINITY_sp|A5D7ACTN4  Alpha-actinin-4 OS= 100.00 0.00
TRINITY_sp|P136EEF2  Elongation factor 2 100.00 0.00
TRINITY_sp|P051SLC25A5  ADP/ATP translocase 100.00 0.00
TRINITY_sp|P1411Rp277a  60S ribosomal prote 100.00 0.00
TRINITY_sp|P146HS90B1  Endoplasmin OS=Homo 100.00 0.00
TRINITY_sp|P467RPL27a  60S ribosomal prote 100.00 0.00
TRINITY_sp|Q3T0RPL19  60S ribosomal prote 100.00 0.00
TRINITY_sp|P467RPL19  60S ribosomal prote 100.00 0.00
TRINITY_sp|P467RPL15  60S ribosomal prote 100.00 0.00
TRINITY_sp|P9ROEsd  S-formylglutathione 100.00 0.00
TRINITY_sp|P276RPL10  60S ribosomal prote 100.00 0.00
TRINITY_sp|P310SDHA  Succinate dehydroge 100.00 0.00
TRINITY_sp|Q8K2Sdha  Succinate dehydroge 100.00 0.00
TRINITY_sp|P147PDCD5  Programmed cell dea 100.00 0.00
TRINITY_sp|Q8K2Sdha  Succinate dehydroge 100.00 0.00
TRINITY_sp|P004SOD1  Superoxide dismutas 100.00 0.00
TRINITY_sp|P841RPS12  40S ribosomal prote 100.00 0.00
TRINITY_sp|P024COL1A1  Collagen alpha-1(I)  100.00  0.00
TRINITY_sp|P508RPSA  40S ribosomal prote  100.00  0.00
TRINITY_sp|Q96CPPP1R1f Protein phosphatase  100.00  0.00
TRINITY_sp|P142Rpsa  40S ribosomal prote  100.00  0.00
TRINITY_sp|Q4QYrpsa  40S ribosomal prote  100.00  0.00
TRINITY_sp|P119Tcp1  T-complex protein 1  100.00  0.00
TRINITY_sp|P094Ncl  Nucleolin OS=Mus mu  100.00  0.00
TRINITY_sp|P629Rps27a Ubiquitin-40S ribos  100.00  0.00
TRINITY_sp|P0CGUBL11 Polyubiquitin OS=NI  100.00  0.00
TRINITY_sp|P629RPS27A Ubiquitin-40S ribos  100.00  0.00
TRINITY_sp|A2QOHSPA8 Heat shock cognate  100.00  0.00
TRINITY_sp|P193HSPA8 Heat shock cognate  100.00  0.00
TRINITY_sp|P539Rpl12  60S ribosomal prote  100.00  0.00
TRINITY_sp|P612RPL12  60S ribosomal prote  100.00  0.00
TRINITY_sp|P178DDX5 Probable ATP-depend  100.00  0.00
TRINITY_sp|Q95LEIF4G2 Eukaryotic translat  100.00  0.00
TRINITY_sp|Q95LEIF4G2 Eukaryotic translat  100.00  0.00
TRINITY_sp|Q95LEIF4G2 Eukaryotic translat  100.00  0.00
TRINITY_sp|Q95LEIF4G2 Eukaryotic translat  100.00  0.00
TRINITY_sp|Q624Eif4g2 Eukaryotic translat  100.00  0.00
TRINITY_sp|P1271Fapbp1 Fatty acid-binding  100.00  0.00
TRINITY_sp|Q007Rbp4 Retinol-binding pro  100.00  0.00
TRINITY_sp|P511RAB7A Ras-related protein  100.00  0.00
TRINITY_sp|P235EIF4B Eukaryotic translat  100.00  0.00
TRINITY_sp|P086VIM Vimentin OS=Homo sa  100.00  0.00
TRINITY_sp|Q9CR5Rp114 60S ribosomal prote  100.00  0.00
TRINITY_sp|P098HNNRP1 Heterogeneous nucle  100.00  0.00
TRINITY_sp|Q2KHIU27A4 40S ribosomal prote  100.00  0.00
TRINITY_sp|Q969ERGIC1 Endoplasmic reticul  100.00  0.00
TRINITY_sp|P193NCL Nucleolin OS=Homo s  100.00  0.00
TRINITY_sp|Q95QC19orf4:Uncharacterized pro  100.00  0.00
TRINITY_sp|A144U2AF1 Splicing factor U2A  100.00  0.00
TRINITY_sp|Q150SNX17 Sorting nexin-17 OS  100.00  0.00
TRINITY_sp|P138RLc-a Myosin regulatory 1  100.00  0.00
TRINITY_sp|P240M Myosin regulatory 1  100.00  0.00
TRINITY_sp|P008Odc1 Ornithine decarboxy  100.00  0.00
TRINITY_sp|P973Rps3a 40S ribosomal prote  100.00  0.00
TRINITY_sp|Q56JRPS3A 40S ribosomal prote  100.00  0.00
TRINITY_sp|P601TP11 Triosephosphate iso  100.00  0.00
TRINITY_sp|Q9CQUqcrq Cytochrome b-1 com  100.00  0.00
TRINITY_sp|P135eef1as Elongation factor 1  100.00  0.00
TRINITY_sp|P135eef1as Elongation factor 1  100.00  0.00
TRINITY_sp|P215Eno3 Beta-enolase OS=Mus  100.00  0.00
TRINITY_sp|Q9CQUqcrq Cytochrome b-1 com  100.00  0.00
TRINITY_sp|Q149KPNB1 Importin subunit be  100.00  0.00
TRINITY_sp|P628RBX1 E3 ubiquitin-protei  100.00  0.00
TRINITY_sp|Q624Ndufa4 Cytochrome c oxidas  100.00  0.00
| TRINITY_sp|P181|RPL7 | 60S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q2HJ|HNRPAP2|Heterogeneous nucle | 100.00 | 0.00 |
| TRINITY_sp|Q165|CDC37| Hsp90 co-chaperone | 100.00 | 0.00 |
| TRINITY_sp|P141|Rpl17| 60S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q2KJ|CKS2| Cyclin-dependent ki | 100.00 | 0.00 |
| TRINITY_sp|P094|Pkg1| Phosphoglycerate ki | 100.00 | 0.00 |
| TRINITY_sp|Q921|Tf| Serotransferrin OS= | 100.00 | 0.00 |
| TRINITY_sp|Q921|Tf| Serotransferrin OS= | 100.00 | 0.00 |
| TRINITY_sp|Q133|EIF3I| Eukaryotic transl | 100.00 | 0.00 |
| TRINITY_sp|Q5E9|EIF3I| Eukaryotic transl | 100.00 | 0.00 |
| TRINITY_sp|P003|LDHA| L-lactate dehydroge | 100.00 | 0.00 |
| TRINITY_sp|Q3T0|RPL8| 60S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P061|UROD| Uroporphyrinogen de | 100.00 | 0.00 |
| TRINITY_sp|Q3T0|RPL8| 60S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P700|H4-VIII| Histone H4 type VII | 100.00 | 0.00 |
| TRINITY_sp|P700|H4-VIII| Histone H4 type VII | 100.00 | 0.00 |
| TRINITY_sp|P700|H4-VIII| Histone H4 type VII | 100.00 | 0.00 |
| TRINITY_sp|Q3T0|RPS11| 40S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q3T0|RPS11| 40S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q32P|EIF1A2| Elongation factor 1 | 100.00 | 0.00 |
| TRINITY_sp|P186|HSPD1| 60 kDa heat shock p | 100.00 | 0.00 |
| TRINITY_sp|P681|EIF1A1| Elongation factor 1 | 100.00 | 0.00 |
| TRINITY_sp|Q908|EIF1A1| Elongation factor 1 | 100.00 | 0.00 |
| TRINITY_sp|P077|PFN1| Profilin-1 OS=Homo | 100.00 | 0.00 |
| TRINITY_sp|P005|PES1| Pescadillo homolog | 100.00 | 0.00 |
| TRINITY_sp|P151|AKR1B1| Aldose reductase OS | 100.00 | 0.00 |
| TRINITY_sp|P018|−| Ig kappa chain C re | 100.00 | 0.00 |
| TRINITY_sp|Q761|RPS15A| 40S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|Q761|RPS15A| 40S ribosomal prote | 100.00 | 0.00 |
| TRINITY_sp|P053|RPLP0| 60S acidic ribosoma | 100.00 | 0.00 |
| TRINITY_sp|Q3S2|EIF4A1| Eukaryotic initiati | 100.00 | 0.00 |
| TRINITY_sp|P632|ACTG1| Actin, cytoplasmic | 100.00 | 0.00 |
| TRINITY_sp|Q3T1|EIF3D| Eukaryotic transl | 100.00 | 0.00 |
| TRINITY_sp|P819|−| Tubulin alpha-1B ch | 100.00 | 0.00 |
| TRINITY_sp|Q9Y2|POLR1D| DNA-directed RNA po | 100.00 | 0.00 |
| TRINITY_sp|P819|−| Tubulin alpha-1B ch | 100.00 | 0.00 |
| TRINITY_sp|P631|YWHAZ| 14-3-3 protein zeta | 100.00 | 0.00 |
| TRINITY_sp|Q3S2|SNRP2D| Small nuclear ribon | 100.00 | 0.00 |
| TRINITY_sp|Q9D3|Ephx1| Epoxide hydrolase 1 | 100.00 | 0.00 |
| TRINITY_sp|P0C6|OST4| Dolichyl-diphospho | 100.00 | 0.00 |
| TRINITY_sp|Q761|HSP90AB1| Heat shock protein | 100.00 | 0.00 |
| TRINITY_sp|P8VD|Atp1a1| Sodium/potassium-tr | 100.00 | 0.00 |
| TRINITY_sp|P050|ATP1A1| Sodium/potassium-tr | 100.00 | 0.00 |
| TRINITY_sp|P050|ATP1A1| Sodium/potassium-tr | 100.00 | 0.00 |
| TRINITY_sp|P151|GSPT1| Eukaryotic peptide | 100.00 | 0.00 |
| TRINITY_sp|Q060|YBX1| Nuclease-sensitive | 100.00 | 0.00 |
| TRINITY_sp|P678|YBX1| Nuclease-sensitive | 100.00 | 0.00 |
| TRINITY_sp|Q9M6|SAMDC| S-adenosylmethionin | 100.00 | 0.00 |
| TRINITY_sp|P168|Gapdh| Glyceraldehyde-3-ph | 100.00 | 0.00 |
| TRINITY_sp|P095|Fth1| Ferritin heavy chai | 100.00 | 0.00 |
| TRINITY_sp|P082|FTH| Ferritin heavy chai | 100.00 | 0.00 |
| TRINITY_sp|P027|FTH1| Ferritin heavy chai | 100.00 | 0.00 |
| TRINITY_sp|P044|GAPDH| Glyceraldehyde-3-ph | 100.00 | 0.00 |
| TRINITY_sp|P089|Lyz2| Lysozyme C-2 OS=Mus | 100.00 | 0.00 |
| TRINITY_sp|P0DN|Ndufbl| NADH dehydrogenase | 100.00 | 0.00 |
| Accession | Gene Symbol | Description | Log2 Fold Change | p-value |
|-----------|-------------|-------------|-----------------|---------|
| TRINITY_sp| P003| GAPDH | Glyceraldehyde-3-phosphate dehydrogenase | 100.00 | 0.00 |
| TRINITY_sp| P192| hsp-3 | Heat shock 70 kDa protein | 100.00 | 0.00 |
| TRINITY_sp| P064| PTMA | Prothymosin alpha | 100.00 | 0.00 |
| TRINITY_sp| P504| SERPINH1 | Serpin H1 | 100.00 | 0.00 |
| TRINITY_sp| Q016| SLC7A5 | Large neutral amino acid transporter | 100.00 | 0.00 |
| TRINITY_sp| Q132| SR5F5 | Serine/arginine-rich protein | 100.00 | 0.00 |
| TRINITY_sp| P511| RAB5C | Ras-related protein | 100.00 | 0.00 |
| TRINITY_sp| P511| RAB5C | Ras-related protein | 100.00 | 0.00 |
| TRINITY_sp| P176| CAPN2 | Calpain-2 catalytic | 100.00 | 0.00 |
| TRINITY_sp| A67| RPS7 | 40S ribosomal protein | 100.00 | 0.00 |
| TRINITY_sp| Q8IVK| MTN-RNR2 | Humanin | 100.00 | 0.00 |
| TRINITY_sp| A67| RPS7 | 40S ribosomal protein | 100.00 | 0.00 |
| TRINITY_sp| P619| SUMO2 | Small ubiquitin-related protein | 100.00 | 0.00 |
| TRINITY_sp| Q150| P16A | Protein disulfide isomerase | 100.00 | 0.00 |
| TRINITY_sp| Q9CX2| NDufs4 | NADH dehydrogenase | 100.00 | 0.00 |
| TRINITY_sp| P024| COL1A1 | Collagen alpha-1(I) | 100.00 | 0.00 |
| TRINITY_sp| P402| Cd9 | CD9 antigen | 100.00 | 0.00 |
| TRINITY_sp| Q3T1| TMED9 | Transmembraneemp24 | 100.00 | 0.00 |
| TRINITY_sp| Q9CQ7| Sdhb | Succinate dehydrogenase | 100.00 | 0.00 |
| TRINITY_sp| Q9CQ7| Sdhb | Succinate dehydrogenase | 100.00 | 0.00 |
| TRINITY_sp| Q8JHE| EIF4A2 | Eukaryotic initiation factor | 100.00 | 0.00 |
| TRINITY_sp| Q3S2| EIF4A2 | Eukaryotic initiation factor | 100.00 | 0.00 |
| TRINITY_sp| P397| FEN1 | Flap endonuclease 1 | 100.00 | 0.00 |
| TRINITY_sp| P479| Rpl16 | 60S ribosomal protein | 100.00 | 0.00 |
| TRINITY_sp| Q66P| ARL6IP4 | ADP-ribosylation factor | 100.00 | 0.00 |
| TRINITY_sp| O776| JUN | Transcription factor | 100.00 | 0.00 |
| TRINITY_sp| P128| ACTN1 | Alpha-actinin-1 | 100.00 | 0.00 |
| TRINITY_sp| P973| Psmel | Proteasome activator | 100.00 | 0.00 |
| TRINITY_sp| Q3V5| psbA | Photosystem II protein | 100.00 | 0.00 |
| TRINITY_sp| Q3V5| psbA | Photosystem II protein | 100.00 | 0.00 |
| TRINITY_sp| P114| Fabp3 | Fatty acid-binding protein | 100.00 | 0.00 |
| TRINITY_sp| Q6EWE| EIF5A | Eukaryotic translation initiation factor | 100.00 | 0.00 |
| TRINITY_sp| Q3ZC| SNRPD1 | Small nuclear ribonucleoprotein | 100.00 | 0.00 |
| TRINITY_sp| P453| Akr1b1 | Aldose reductase | 100.00 | 0.00 |
| TRINITY_sp| P055| ITGB1 | Integrin beta-1 | 100.00 | 0.00 |
| TRINITY_sp| O975| GD11 | Rab GDP dissociation inhibitor | 100.00 | 0.00 |
| TRINITY_sp| P132| SPARC | SPARC | 100.00 | 0.00 |
| TRINITY_sp| P783| TUBB | Tubulin beta chain | 100.00 | 0.00 |
| TRINITY_sp| P179| Pcn | Proliferating cell nuclear antigen | 100.00 | 0.00 |
| TRINITY_sp| P263| RPL13 | 60S ribosomal protein | 100.00 | 0.00 |
| TRINITY_sp| P160| Lgals1 | Galectin-1 | 100.00 | 0.00 |
| TRINITY_sp| P093| LGALSL1 | Galectin-1 | 100.00 | 0.00 |
| TRINITY_sp| P612| PABPC1 | Polyadenylate-bindin | 100.00 | 0.00 |
| TRINITY_sp| P263| RPL13 | 60S ribosomal protein | 100.00 | 0.00 |
| TRINITY_sp| Q4R7| GNB2L1 | Guanine nucleotide-binding protein | 100.00 | 0.00 |
| TRINITY_sp| P612| PABPC1 | Polyadenylate-bindin | 100.00 | 0.00 |
| TRINITY_sp| P122| CKB | Creatine kinase B-tropomyosin | 100.00 | 0.00 |
| TRINITY_sp| A6QLR| RPS9 | 40S ribosomal protein | 100.00 | 0.00 |
| TRINITY_sp| A6QLR| RPS9 | 40S ribosomal protein | 100.00 | 0.00 |
| TRINITY_sp| A6QLR| RPS9 | 40S ribosomal protein | 100.00 | 0.00 |
| TRINITY_sp| P032| E1A | Early E1A protein | 100.00 | 0.00 |
| TRINITY_sp| Q3ZBF| SHFM1 | 26S proteasome component | 100.00 | 0.00 |
| TRINITY_sp| Q3ZPF| SNRNP | U1 small nuclear ribonucleoprotein | 100.00 | 0.00 |
| TRINITY_sp| P067| ENO1 | Alpha-enolase | 100.00 | 0.00 |
| TRINITY_sp| P171| Eno1 | Alpha-enolase | 100.00 | 0.00 |
| TRINITY_sp| P293| Pabpc1 | Polyadenylate-bindin | 100.00 | 0.00 |
null
39S ribosomal protein L2, mitochondrial OS=Homo sapiens GN=MRPL2 PE=1 SV=2
40S ribosomal protein S29 OS=Bos taurus GN=RPS29 PE=3 SV=2
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform OS=Mus musculus GN=Ppp2r5a PE=1 SV=1
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial OS=Gorilla gorilla gorilla GN=NDUFB2 PE=3 SV=1
Granulins OS=Homo sapiens GN=GRN PE=1 SV=2
ATP synthase subunit e, mitochondrial OS=Mus musculus GN=Atp5i PE=1 SV=2
Protein PET100 homolog, mitochondrial OS=Homo sapiens GN=PET100 PE=1 SV=1
3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3
Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1
Translocator protein OS=Homo sapiens GN=TSPO PE=1 SV=3
Protein lifeguard 1 OS=Bos taurus GN=GRINA PE=2 SV=1
Coronin-1A OS=Mus musculus GN=Coro1a PE=1 SV=5
Protein S100-A9 OS=Mus musculus GN=S100a9 PE=1 SV=3
Gamma-interferon-inducible lysosomal thiol reductase OS=Homo sapiens GN=IFI30 PE=1 SV=3
26S protease regulatory subunit 7 OS=Bos taurus GN=PSMC2 PE=2 SV=3
Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1
Apolipoprotein C-I OS=Mus musculus GN=Apoc1 PE=1 SV=1
Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=1 SV=1
Glycoprotein hormones alpha chain OS=Homo sapiens GN=CGA PE=1 SV=1
Chemokine-like factor OS=Homo sapiens GN=CKLF PE=2 SV=1
Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2
OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=1 SV=1
Secretoglobin family 3A member 2 OS=Mus musculus GN=Scgb3a2 PE=2 SV=1
Proteasome activator complex subunit 2 OS=Mus musculus GN=Psme2 PE=1 SV=4
6.8 kDa mitochondrial proteolipid OS=Mus musculus GN=Mp68 PE=1 SV=1
Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3
40S ribosomal protein S26 OS=Bos taurus GN=RPS26 PE=3 SV=3
60S ribosomal protein L23a OS=Bos taurus GN=RPL23A PE=2 SV=1
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1
Troponin I, cardiac muscle OS=Mus musculus GN=Tnni3 PE=1 SV=2
HLA class II histoc OS=Homo sapiens GN=CD74 PE=1 SV=3
40S ribosomal protein S29 OS=Bos taurus GN=RPS29 PE=3 SV=2
| Description | Short Name | Name | OS | GN | PE | SV |
|-------------|------------|------|----|-----|----|----|
| ATP synthase subunit f, mitochondrial | ATP5J2 | ATP synthase subunit f, mitochondrial | Homo sapiens | ATP5J2 | 1 | 3 |
| 60S ribosomal protein | RPL13 | 60S ribosomal protein | Homo sapiens | MRPL52 | 1 | 2 |
| ATP-dependent 6-pho | PFKP | ATP-dependent 6-pho | Homo sapiens | ATP5J2 | 1 | 3 |
| Transmembrane prote | mem50a | Transmembrane prote | Homo sapiens | ATP5J2 | 1 | 3 |
| Four and a half LIM | FL2 | Four and a half LIM | Homo sapiens | CLU | 1 | 1 |
| Dynactin subunit 2 | DCTN2 | Dynactin subunit 2 | Homo sapiens | CLU | 1 | 1 |
| Aconitate hydratase | Aco2 | Aconitate hydratase | Mus musculus | Aco2 | 1 | 1 |
| ATPase inhibitor, mitochondrial | Atpif1 | ATPase inhibitor, mitochondrial | Mus musculus | Atpif1 | 1 | 2 |
| Clusterin | Clu | Clusterin | Mus musculus | Clu | 1 | 1 |
| 40S ribosomal protein | RPS21 | 40S ribosomal protein | Mus musculus | Rps21 | 1 | 1 |
| 40S ribosomal protein | RPS28 | 40S ribosomal protein | Bos taurus | Rps28 | 3 | 1 |
| CUE domain-containing protein 2 | CUEDC2 | CUE domain-containing protein 2 | Homo sapiens | CUEDC2 | 1 | 1 |
| APOBEC3G | COP | APOBEC3G | Homo sapiens | COP | 1 | 1 |
| 39S ribosomal protein | RPS16 | 39S ribosomal protein | Homo sapiens | RPL35a | 1 | 2 |
| 40S ribosomal protein | RPS28 | 40S ribosomal protein | Mus musculus | RPS28 | 1 | 1 |
| Calponin-3 | CNN3 | Calponin-3 | Bos taurus | CNN3 | 2 | 1 |
| Epidermal growth factor-like protein 7 | Egfl7 | Epidermal growth factor-like protein 7 | Mus musculus | Egfl7 | 2 | 2 |
| Apolipoprotein A-II | Apoa2 | Apolipoprotein A-II | Mus musculus | Apoa2 | 2 | 2 |
| 40S ribosomal protein | RPS28 | 40S ribosomal protein | Bos taurus | RPS28 | 3 | 1 |
| 39S ribosomal protein | RPL13 | 39S ribosomal protein | Gallus gallus | RPL13 | 2 | 2 |
| Medium-chain specific acyl-CoA dehydrogenase | Acadm | Medium-chain specific acyl-CoA dehydrogenase | Mus musculus | Acadm | 1 | 1 |
| NADP-dependent malic enzyme, chloroplastic | MOD1 | NADP-dependent malic enzyme, chloroplastic | Zea mays | MOD1 | 1 | 1 |
| Fibrinogen-like protein 1 | Fgl1 | Fibrinogen-like protein 1 | Mus musculus | Fgl1 | 2 | 2 |
| Transmembrane protein 50A | Tmem50a | Transmembrane protein 50A | Mus musculus | Tmem50a | 1 | 1 |
| 60S ribosomal protein | RPL13 | 60S ribosomal protein | Gallus gallus | RPL13 | 2 | 2 |
| Medium-chain specific acyl-CoA dehydrogenase | Acadm | Medium-chain specific acyl-CoA dehydrogenase | Mus musculus | Acadm | 1 | 1 |
| NADP-dependent malic enzyme, chloroplastic | MOD1 | NADP-dependent malic enzyme, chloroplastic | Zea mays | MOD1 | 1 | 1 |
| Fibrinogen-like protein 1 | Fgl1 | Fibrinogen-like protein 1 | Mus musculus | Fgl1 | 2 | 2 |
| Transmembrane protein 50A | Tmem50a | Transmembrane protein 50A | Mus musculus | Tmem50a | 1 | 1 |
| 60S ribosomal protein | RPL13 | 60S ribosomal protein | Gallus gallus | RPL13 | 2 | 2 |
| Alpha-crystallin B | CRYAB | Alpha-crystallin B | Bos taurus | CRYAB | 1 | 1 |
| Non-specific lipid-transfer protein | Scp2 | Non-specific lipid-transfer protein | Mus musculus | Scp2 | 3 | 1 |
TRINITY_sp|Q9H31PPDPF  Pancreatic progenitor cell differentiation and proliferation factor OS=Homo sapiens GN=PPDPF PE=1 SV=1 100.00 0.00
TRINITY_sp|Q32C1CCT8  T-complex protein 1 OS=Homo sapiens GN=TCP1 PE=1 SV=1 100.00 0.00
TRINITY_sp|P0411Fapb4  Fatty acid-binding protein OS=Homo sapiens GN=FABP4 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q0257Myh6  Myosin-6 OS=Mus musculus GN=Myh6 PE=2 SV=1 100.00 0.00
TRINITY_sp|P2231UBA1  Ubiquitin-like modifier OS=Homo sapiens GN=UBA1 PE=1 SV=1 100.00 0.00
TRINITY_sp|P4931NASP  Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=1 100.00 0.00
TRINITY_sp|P6327Crip1  Cysteine-rich protein OS=Homo sapiens GN=CRIP1 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q1287CDC20  Cell division cycle protein 20 OS=Homo sapiens GN=CDC20 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q96EIDA2AP1  DAZ-associated protein OS=Homo sapiens GN=DAZAP1 PE=1 SV=1 100.00 0.00
TRINITY_sp|P3786TALDO1  Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=1 100.00 0.00
TRINITY_sp|A8XYK-  T-complex protein 1 OS=Homo sapiens GN=TCP1 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q9Y41HYOU1  Hypoxia up-regulate OS=Homo sapiens GN=HYOU1 PE=1 SV=1 100.00 0.00
TRINITY_sp|P2433COX7B  Cytochrome c oxidase OS=Homo sapiens GN=CYCOX PE=1 SV=1 100.00 0.00
TRINITY_sp|P3527RFC2  Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q3T0FPPP1CA  Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP1CA PE=1 SV=1 100.00 0.00
TRINITY_sp|P6111Kap  Kidney androgen-regulated protein OS=Homo sapiens GN=KAP PE=1 SV=1 100.00 0.00
TRINITY_sp|P5095ANXA11  Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q6045APP  Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=1 100.00 0.00
TRINITY_sp|P07045Mybpc3  Myosin-binding protein OS=Homo sapiens GN=MYBPC3 PE=1 SV=1 100.00 0.00
TRINITY_sp|P0095ASS1  Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q6433Tm4sfl1  Transmembrane 4 L6 OS=Homo sapiens GN=TM4L6 PE=1 SV=1 100.00 0.00
TRINITY_sp|P0880RPSA  40S ribosomal protein OS=Homo sapiens GN=RPSA PE=1 SV=1 100.00 0.00
TRINITY_sp|Q0286RPL6  60S ribosomal protein OS=Homo sapiens GN=RPL6 PE=1 SV=1 100.00 0.00
TRINITY_sp|P0241COL3A1  Collagen alpha-1(II) OS=Homo sapiens GN=COL3A1 PE=1 SV=1 100.00 0.00
TRINITY_sp|P1487Rplp0  60S acidic ribosomal protein OS=Homo sapiens GN=RPLP0 PE=1 SV=1 100.00 0.00
TRINITY_sp|P1627MOD1  NADP-dependent malic enzyme OS=Homo sapiens GN=MAL PE=1 SV=1 100.00 0.00
TRINITY_sp|P5197E010  Alpha-1-acid glycoprotein OS=Homo sapiens GN=AAGCPE10 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q6057ORM1  Alpha-1-acid glycoprotein OS=Homo sapiens GN=AAGCPE10 PE=1 SV=1 100.00 0.00
TRINITY_sp|P0952Myl3  Myosin light chain OS=Homo sapiens GN=MYL3 PE=1 SV=1 100.00 0.00
TRINITY_sp|P9747Rps5  40S ribosomal protein OS=Homo sapiens GN=RPS5 PE=1 SV=1 100.00 0.00
TRINITY_sp|P2187SftpC  Pulmonary surfactant OS=Homo sapiens GN=SFTPC PE=1 SV=1 100.00 0.00
TRINITY_sp|P2767RPL10  60S ribosomal protein OS=Homo sapiens GN=RPL10 PE=1 SV=1 100.00 0.00
TRINITY_sp|P2937Ft11  Ferritin light chain OS=Homo sapiens GN=FTH1 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q1377NACA  Nascent polypeptide OS=Homo sapiens GN=NACA PE=1 SV=1 100.00 0.00
TRINITY_sp|P4797Rpl13  60S ribosomal protein OS=Homo sapiens GN=RPL13 PE=1 SV=1 100.00 0.00
TRINITY_sp|E9PVFga  Fibrinogen alpha chain OS=Homo sapiens GN=FGB PE=1 SV=1 100.00 0.00
TRINITY_sp|P5437OA21  Ornithine decarboxylase OS=Homo sapiens GN=ODC1 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q3T0FRPL8  60S ribosomal protein OS=Homo sapiens GN=RPL8 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q243JRPL23A  60S ribosomal protein OS=Homo sapiens GN=RPL23A PE=1 SV=1 100.00 0.00
TRINITY_sp|Q243JRPL23A  60S ribosomal protein OS=Homo sapiens GN=RPL23A PE=1 SV=1 100.00 0.00
TRINITY_sp|P0193Hba  Hemoglobin subunit OS=Homo sapiens GN=HBA1 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q3BBNBP8  Pulmonary surfactant OS=Homo sapiens GN=SFTPC PE=1 SV=1 100.00 0.00
TRINITY_sp|P1831DSTN  Destrin OS=Homo sapiens GN=DSTN PE=1 SV=1 100.00 0.00
TRINITY_sp|P4221GF1  Green fluorescent protein OS=Homo sapiens GN=GFP PE=1 SV=1 100.00 0.00
TRINITY_sp|P5357-Actin, cytoplasmic OS=Homo sapiens GN=ACTC1 PE=1 SV=1 100.00 0.00
TRINITY_sp|P2097-Actin OS=Volvox carteri GN=ACTC1 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q90YKRps23  40S ribosomal protein OS=Homo sapiens GN=RPS23 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q5657RPS25  40S ribosomal protein OS=Homo sapiens GN=RPS25 PE=1 SV=1 100.00 0.00
TRINITY_sp|P01882Bm  Beta-2-microglobulin OS=Homo sapiens GN=BM2M PE=1 SV=1 100.00 0.00
TRINITY_sp|P3287psaD  Photosystem I reaction centre OS=Homo sapiens GN=PSAD PE=1 SV=1 100.00 0.00
TRINITY_sp|Q7611RPS15A  40S ribosomal protein OS=Homo sapiens GN=RPS15A PE=1 SV=1 100.00 0.00
TRINITY_sp|Q0MQ1NDUFA6  NADH dehydrogenase OS=Homo sapiens GN=NADH PE=1 SV=1 100.00 0.00
TRINITY_sp|Q5EAKRPL15  60S ribosomal protein OS=Homo sapiens GN=RPL15 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q5657RPL31  60S ribosomal protein OS=Homo sapiens GN=RPL31 PE=1 SV=1 100.00 0.00
TRINITY_sp|Q6U2IRP13S  60S ribosomal protein OS=Homo sapiens GN=RPL31 PE=1 SV=1 100.00 0.00
TRINITY_sp|P026MYL6  Myosin light polypeptide OS=Homo sapiens GN=MYL6 PE=1 SV=1 100.00 0.00
| Gene ID | Description | Identity | E-Value |
|--------|-------------|----------|---------|
| TRINITY_sp|P097{rp1K| 50S ribosomal protein | 99.10 | 0.00 |
| TRINITY_sp|Q9SPC|CRT2| Beta-carotene 3-hyd | 99.10 | 0.00 |
| TRINITY_sp|Q008|SerpinA|Alpha-1-antitrypsin | 99.10 | 0.00 |
| TRINITY_sp|P111|CMO1| Calmodulin OS=Pleur | 99.10 | 0.00 |
| TRINITY_sp|Q750|WDR1| WD repeat-containin | 99.00 | 0.00 |
| TRINITY_sp|Q6621|RPL24| 40S ribosomal protein | 99.00 | 0.00 |
| TRINITY_sp|Q3T0|RPS10| 40S ribosomal protein | 99.00 | 0.00 |
| TRINITY_sp|Q6891|dh3B| Isocitrate dehydrog | 99.00 | 0.00 |
| TRINITY_sp|Q5E9|RPS6| 40S ribosomal protein | 99.00 | 0.00 |
| TRINITY_sp|P534| act10| Actin OS=Dictyos | 99.00 | 0.00 |
| TRINITY_sp|P483|CAT1| Catalase isozyme | 99.00 | 0.00 |
| TRINITY_sp|P002|PETE| Plastocyanin OS=Cuc | 98.90 | 0.00 |
| TRINITY_sp|Q1A7| Dimethyladenosine t | 98.90 | 0.00 |
| TRINITY_sp|Q791|UQCRH| Cytochrome b-c1 com | 98.90 | 0.00 |
| TRINITY_sp|Q015|CAP1| Adenyl cyclase | 98.90 | 0.00 |
| TRINITY_sp|P114|TUBB1| Tubulin beta chain | 98.90 | 0.00 |
| TRINITY_sp|Q3M1|RPL37A| 60S ribosomal protein | 98.80 | 0.00 |
| TRINITY_sp|P324|RPL7A| 60S ribosomal protein | 98.80 | 0.00 |
| TRINITY_sp|Q9NR|MRL17| 39S ribosomal protein | 98.80 | 0.00 |
| TRINITY_sp|P040|compA| Outer membrane prot | 98.80 | 0.00 |
| TRINITY_sp|P611|rsps19| 40S ribosomal protein | 98.80 | 0.00 |
| TRINITY_sp|P175|Selenbp|Selenium-binding pr | 98.80 | 0.00 |
| TRINITY_sp|Q410|PSQ1| Oxygen-evolving enh | 98.80 | 0.00 |
| TRINITY_sp|O223|TUBA1| Tubulin alpha-1 cha | 98.80 | 0.00 |
| TRINITY_sp|Q9MI|mt-co3| Cytochrome c oxidas | 98.80 | 0.00 |
| TRINITY_sp|P268|gag| Gag polyprotein OS= | 98.80 | 0.00 |
| TRINITY_sp|P492|PKC1| Phosphoenolpyruvate | 98.80 | 0.00 |
| TRINITY_sp|P684|-| Histone H3.1 OS=Bos | 98.80 | 0.00 |
| TRINITY_sp|O043|TUBB| Tubulin beta chain | 98.80 | 0.00 |
| TRINITY_sp|Q5E9|RPS8| 40S ribosomal protein | 98.80 | 0.00 |
| TRINITY_sp|Q7ZW|rp118a| 60S ribosomal protein | 98.80 | 0.00 |
| TRINITY_sp|A8G8|rp1J| 50S ribosomal protein | 98.80 | 0.00 |
| TRINITY_sp|P033|pol| Pol polyprotein OS= | 98.70 | 0.00 |
| TRINITY_sp|P025|-| Calmodulin OS=Tetra | 98.70 | 0.00 |
| TRINITY_sp|Q9M6|SAMDC| S-adenosylmethionin | 98.70 | 0.00 |
| TRINITY_sp|O043|TUBB| Tubulin beta chain | 98.70 | 0.00 |
| TRINITY_sp|Q019|TAGLN| Transgelin OS=Homo | 98.70 | 0.00 |
| TRINITY_sp|Q32S|BRD2| Bromodomain-contain | 98.60 | 0.00 |
| TRINITY_sp|Q9CR|Nsa2| Ribosome biogenesis | 98.60 | 0.00 |
| TRINITY_sp|Q24S|SAMDC| S-adenosylmethionin | 98.60 | 0.00 |
| TRINITY_sp|Q9FG|UBL5| Ubiquitin-like prot | 98.60 | 0.00 |
| TRINITY_sp|P087|RPS2| 40S ribosomal protein | 98.60 | 0.00 |
| TRINITY_sp|P612|RPL12| 60S ribosomal protein | 98.60 | 0.00 |
| TRINITY_sp|Q9M6|SAMDC| S-adenosylmethionin | 98.60 | 0.00 |
| TRINITY_sp|P233|-| Polyubiquitin (Frag | 98.60 | 0.00 |
| TRINITY_sp|Q2KH|RPS27| 40S ribosomal protein | 98.60 | 0.00 |
| TRINITY_sp|P563|ATP5I| ATP synthase subunit | 98.60 | 0.00 |
| TRINITY_sp|A7Z0|CLINT1| Clathrin interactor | 98.60 | 0.00 |
| TRINITY_sp|Q3S2|RPL13A| 60S ribosomal protein | 98.50 | 0.00 |
| TRINITY_sp|P700|rsps15| 40S ribosomal protein | 98.50 | 0.00 |
| TRINITY_sp|A8G8|Efuf1| Elongation factor T | 98.50 | 0.00 |
| TRINITY_sp|Q7ZW|rp127| 60S ribosomal protein | 98.50 | 0.00 |
| TRINITY_sp|P319|HNRNPH| Heterogeneous nucle | 98.50 | 0.00 |
| TRINITY_sp|A2XJ|OsI_012| Chlorophyll a-b bin | 98.50 | 0.00 |
| TRINITY_sp|P047|CAB25| Chlorophyll a-b bin | 98.50 | 0.00 |
| Accession     | Description                                 | Organism          | Score | E-value |
|--------------|---------------------------------------------|-------------------|-------|---------|
| TRINITY_sp|Catalase OS=Ipomoea                          | 97.40             | 0.00  |
| TRINITY_sp|Putative Pol polypr                          | 97.40             | 0.00  |
| TRINITY_sp|Polyubiquitin-B OS=                           | 97.40             | 0.00  |
| TRINITY_sp|Histone H3 OS=Acrop                         | 97.40             | 0.00  |
| TRINITY_sp|Histone H3 OS=Acrop                         | 97.40             | 0.00  |
| TRINITY_sp|Rho-related protein                          | 97.40             | 0.00  |
| TRINITY_sp|Histone H4 variant                          | 97.40             | 0.00  |
| TRINITY_sp|Myosin heavy chain,                          | 97.30             | 0.00  |
| TRINITY_sp|Phospho-2-dehydro-3                         | 97.30             | 0.00  |
| TRINITY_sp|40S ribosomal prote                         | 97.30             | 0.00  |
| TRINITY_sp|Cytochrome b6-f com                          | 97.30             | 0.00  |
| TRINITY_sp|Tubulin alpha chain                          | 97.30             | 0.00  |
| TRINITY_sp|Beta-crystallin B2                           | 97.30             | 0.00  |
| TRINITY_sp|Polyadenylate-bind                          | 97.20             | 0.00  |
| TRINITY_sp|60S ribosomal prote                          | 97.20             | 0.00  |
| TRINITY_sp|NADH-ubiquinone oxi                          | 97.20             | 0.00  |
| TRINITY_sp|72 kDa type IV coll                          | 97.20             | 0.00  |
| TRINITY_sp|Pol polyprotein OS=                          | 97.10             | 0.00  |
| TRINITY_sp|40S ribosomal prote                          | 97.10             | 0.00  |
| TRINITY_sp|Protein translation                          | 97.10             | 0.00  |
| TRINITY_sp|Inositol-3-phosphat                          | 97.10             | 0.00  |
| TRINITY_sp|40S ribosomal prote                          | 97.10             | 0.00  |
| TRINITY_sp|Actin, cytoplasmic                           | 97.10             | 0.00  |
| TRINITY_sp|Histone H3.1 OS=Bos                          | 97.10             | 0.00  |
| TRINITY_sp|Histone H3.2 OS=Bos                          | 97.10             | 0.00  |
| TRINITY_sp|Glyceraldehyde-3-ph                          | 97.00             | 0.00  |
| TRINITY_sp|60S ribosomal prote                          | 97.00             | 0.00  |
| TRINITY_sp|Interferon-induced                           | 97.00             | 0.00  |
| TRINITY_sp|60S acidic ribosoma                         | 97.00             | 0.00  |
| TRINITY_sp|Elongation factor 1                          | 97.00             | 0.00  |
| TRINITY_sp|Actin OS=Chlamydomo                          | 97.00             | 0.00  |
| TRINITY_sp|Green fluorescent p                          | 97.00             | 0.00  |
| TRINITY_sp|60S acidic ribosoma                         | 97.00             | 0.00  |
| TRINITY_sp|Aldo-keto reductase                          | 96.90             | 0.00  |
| TRINITY_sp|Enolase OS=Ricus                            | 96.90             | 0.00  |
| TRINITY_sp|Photosystem I react                          | 96.90             | 0.00  |
| TRINITY_sp|RNA-binding protein                          | 96.90             | 0.00  |
| TRINITY_sp|Heat shock cognate                          | 96.90             | 0.00  |
| TRINITY_sp|Glutamine synthetases                       | 96.90             | 0.00  |
| TRINITY_sp|Polyubiquitin-B OS=                           | 96.90             | 0.00  |
| TRINITY_sp|Polyubiquitin-B OS=                           | 96.90             | 0.00  |
| TRINITY_sp|Actin OS=Chlamydomo                          | 96.90             | 0.00  |
| TRINITY_sp|40S ribosomal prote                          | 96.80             | 0.00  |
| TRINITY_sp|Uncharacterized pro                          | 96.80             | 0.00  |
| TRINITY_sp|Ubiquitin-conjugati                          | 96.70             | 0.00  |
| TRINITY_sp|60S ribosomal prote                          | 96.70             | 0.00  |
| TRINITY_sp|LINE-1 retrotranspo                          | 96.70             | 0.00  |
| TRINITY_sp|NADH dehydrogenase                          | 96.70             | 0.00  |
| TRINITY_sp|Centromere protein                          | 96.70             | 0.00  |
| TRINITY_sp|NADP-dependent glyc                         | 96.60             | 0.00  |
| TRINITY_sp|Eukaryotic translat                          | 96.60             | 0.00  |
| TRINITY_sp|Pre-mRNA-processing                         | 96.60             | 0.00  |
| TRINITY_sp|40S ribosomal prote                          | 96.60             | 0.00  |
| TRINITY_sp|Polyubiquitin-B OS=                           | 96.60             | 0.00  |
| TRINITY_sp|Polyubiquitin-B OS=                           | 96.60             | 0.00  |
| TRINITY_sp|60S ribosomal prote                          | 96.50             | 0.00  |
Elongation factor 1-alpha OS=Manihot esculenta GN=EF1 PE=3 SV=1

60S ribosomal protein L18a OS=Ictalurus punctatus GN=rpl18a PE=2 SV=1

60S ribosomal protein L7a OS=Takifugu rubripes GN=rpl7a PE=3 SV=3

Elongation factor 2 OS=Beta vulgaris PE=2 SV=1

Phosphoglycerate kinase, chloroplastic OS=Nicotiana tabacum PE=2 SV=1

Oxygen-evolving enhancer protein 1, chloroplastic OS=Volvox carteri GN=PSBO PE=2 SV=1

60S ribosomal protein L8 OS=Danio rerio GN=rpl8 PE=2 SV=3

Gag-Pol polyprotein OS=Moloney murine leukemia virus (isolate Shinnick) GN=gag-pol PE=1 SV=4

Actin, plasmodial isoform OS=Physarum polycephalum GN=ARDA PE=1 SV=2

Tubulin beta chain OS=Tetrahymena thermophila GN=BTU1 PE=1 SV=1

Histone H4, major OS=Tetrahymena pyriformis PE=1 SV=2

40S ribosomal protein S3 OS=Ictalurus punctatus GN=rps3 PE=2 SV=1

60S ribosomal protein L44 OS=Chlamydomonas reinhardtii GN=RPL44 PE=3 SV=2

Alpha-actinin-2 OS=Bos taurus GN=ACTN2 PE=2 SV=1

ATP synthase subunit a OS=Gallus gallus GN=MT-ATP6 PE=3 SV=1

H-2 class I histocompatibility antigen, D-D alpha chain OS=Mus musculus GN=H2-D1 PE=1 SV=1

60S ribosomal protein L17 OS=Felis catus GN=RPL17 PE=2 SV=3

Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Mus musculus GN=Gnas PE=1 SV=1

Ubiquitin-like protein 5 OS=Arabidopsis thaliana GN=UBL5 PE=3 SV=1

Photosystem II protein D1 OS=Chlamydomonas moewusii GN=psbA PE=3 SV=1

Large T antigen OS=Simian virus 40 PE=1 SV=2

Heat shock protein 90 OS=Theileria annulata GN=TA12105 PE=3 SV=1

Chlorophyll a-b binding protein of LHCII type I, chloroplastic (Fragment) OS=Cucumis sativus PE=2 SV=1

Actin-1 OS=Pisum sativum PE=2 SV=1

60S ribosomal protein L10 OS=Solanum melongena GN=RPL10 PE=2 SV=1

60S ribosomal protein L18 OS=Oreochromis mossambicus GN=rpl18 PE=3 SV=2

Ubiquitin-NEDD8-like protein RUB1 OS=Arabidopsis thaliana GN=RUB1 PE=1 SV=3

Ribulose-phosphate 3-epimerase, chloroplastic OS=Spinacia oleracea GN=RPE PE=1 SV=1
| Accession | Description | E Value |
|-----------|-------------|---------|
| TRINITY_sp| Chlorophyll a-b bin | 95.00 |
| TRINITY_sp| Glycerate dehydroge | 95.00 |
| TRINITY_sp| Cytochrome c oxidas | 95.00 |
| TRINITY_sp| Photosystem I react | 94.90 |
| TRINITY_sp| 6OS ribosomal prote | 94.90 |
| TRINITY_sp| ATP-dependent zinc | 94.80 |
| TRINITY_sp| SPARC OS=Bos taurus | 94.80 |
| TRINITY_sp| Photosystem I P700 | 94.80 |
| TRINITY_sp| Cytochrome c oxidas | 94.70 |
| TRINITY_sp| Phosphate carrier p | 94.70 |
| TRINITY_sp| 6OS ribosomal prote | 94.70 |
| TRINITY_sp| Cilia- and flagella | 94.70 |
| TRINITY_sp| Elongation factor T | 94.70 |
| TRINITY_sp| Elongation factor 2 | 94.60 |
| TRINITY_sp| 6OS ribosomal prote | 94.60 |
| TRINITY_sp| Elongation factor 1 | 94.60 |
| TRINITY_sp| Photosystem I react | 94.50 |
| TRINITY_sp| Superoxide dismutas | 94.40 |
| TRINITY_sp| Fructose-bisphospha | 94.40 |
| TRINITY_sp| Chlorophyll a-b bin | 94.40 |
| TRINITY_sp| Glyceraldehyde-3-ph | 94.30 |
| TRINITY_sp| Elongation factor T | 94.30 |
| TRINITY_sp| Heterogeneous nucle | 94.30 |
| TRINITY_sp| Phosphoglycerate ki | 94.30 |
| TRINITY_sp| Cytochrome b6 OS=Ac | 94.30 |
| TRINITY_sp| Putative protein FA | 94.20 |
| TRINITY_sp| Chlorophyll a-b bin | 94.20 |
| TRINITY_sp| Triosephosphate iso | 94.20 |
| TRINITY_sp| 3OS ribosomal prote | 94.20 |
| TRINITY_sp| Photosystem II 22 k | 94.10 |
| TRINITY_sp| Ribulose-phosphate | 94.10 |
| TRINITY_sp| Photosystem II CP43 | 94.10 |
| TRINITY_sp| Syndecan-2 OS=Bos t | 94.10 |
| TRINITY_sp| NADH-ubiquinone oxi | 94.00 |
| TRINITY_sp| Enolase 1 OS=Hevea | 93.90 |
| TRINITY_sp| Caffeoyl-CoA O-meth | 93.80 |
| TRINITY_sp| Splicing factor 3B | 93.80 |
| TRINITY_sp| NADH-ubiquinone oxi | 93.80 |
| TRINITY_sp| 14-3-3-like protein | 93.80 |
| TRINITY_sp| ATP synthase subuni | 93.80 |
| TRINITY_sp| ADP/ATP translocase | 93.70 |
| TRINITY_sp| Cilia- and flagella | 93.70 |
| TRINITY_sp| Photosystem II 22 k protein | 93.70 |
| TRINITY_sp| Photosystem I react | 93.70 |
| TRINITY_sp| NADH-ubiquinone oxi | 93.70 |
| TRINITY_sp| Chlorophyll a-b bin | 93.60 |
| TRINITY_sp| Ribulose-phosphate | 93.60 |
| TRINITY_sp| Ferredoxin--NADP re | 93.60 |
| TRINITY_sp| Cytochrome c oxidas | 93.60 |
| TRINITY_sp| 6OS ribosomal prote | 93.50 |
| TRINITY_sp|Q9LRFGLO1 | Peroxisomal (S)-2-h | 93.50 | 0.00 |
| TRINITY_sp|Q9M38RPL| 50S ribosomal prote | 93.50 | 0.00 |
| TRINITY_sp|Q913\_eefg-b | Elongation factor I | 93.50 | 0.00 |
| TRINITY_sp|P0041MT-CO3 | Cytochrome c oxidase | 93.50 | 0.00 |
| TRINITY_sp|Q2F7\_gag-pol | Gag-Pol polyprotein | 93.50 | 0.00 |
| TRINITY_sp|Q006\_CHSP70 | Stromal 70 kDa heat | 93.50 | 0.00 |
| TRINITY_sp|Q9FU- | Elongation factor I | 93.50 | 0.00 |
| TRINITY_sp|Q914\_rp113a | 60S ribosomal prote | 93.40 | 0.00 |
| TRINITY_sp|P328\_psaD | Photosystem I react | 93.30 | 0.00 |
| TRINITY_sp|Q9X1\_PBC1 | Proteasome subunit | 93.30 | 0.00 |
| TRINITY_sp|P0C1- | Ubiquitin-60S ribos | 93.30 | 0.00 |
| TRINITY_sp|Q8DRIrAD | DNA repair protein | 93.30 | 0.00 |
| TRINITY_sp|Q412\_PSAE | Photosystem I react | 93.30 | 0.00 |
| TRINITY_sp|Q016\_LHCA1 | Chlorophyll a-b bin | 93.20 | 0.00 |
| TRINITY_sp|P275\_CA8 | Chlorophyll a-b bin | 93.20 | 0.00 |
| TRINITY_sp|Q087\_PIPI-3 | Aquaporin PIP1-3 OS | 93.20 | 0.00 |
| TRINITY_sp|P033\_gag-pol | Gag-Pol polyprotein | 93.20 | 0.00 |
| TRINITY_sp|Q5E9\_RPS6 | 40S ribosomal prote | 93.20 | 0.00 |
| TRINITY_sp|A5JS\_SERF2 | Small EDRK-rich fac | 93.20 | 0.00 |
| TRINITY_sp|Q4V1CALR | Calreticulin OS=Chl | 93.20 | 0.00 |
| TRINITY_sp|Q7ZW\_chmp2a | Charged multivesicu | 93.10 | 0.00 |
| TRINITY_sp|Q9SDFLHC | Chlorophyll a-b bin | 93.10 | 0.00 |
| TRINITY_sp|Q961\_mt-co3 | Cytochrome c oxidase | 93.10 | 0.00 |
| TRINITY_sp|Q5E9\_RPS6 | 40S ribosomal prote | 93.10 | 0.00 |
| TRINITY_sp|P372\_psbB | Photosystem II CP47 | 93.10 | 0.00 |
| TRINITY_sp|P499\_- | Ferritin, heavy sub | 93.10 | 0.00 |
| TRINITY_sp|P629\_PPIA | Peptidyl-prolyl cis | 93.10 | 0.00 |
| TRINITY_sp|P275\_CA215 | Chlorophyll a-b bin | 93.10 | 0.00 |
| TRINITY_sp|P456\_PA3623 | Lipoprotein NlpD/Lp | 93.10 | 0.00 |
| TRINITY_sp|P938\_- | Phosphoglcomutase, | 93.00 | 0.00 |
| TRINITY_sp|P274\_CA13 | Chlorophyll a-b bin | 92.90 | 0.00 |
| TRINITY_sp|P249\_MT-C01 | Cytochrome c oxidase | 92.90 | 0.00 |
| TRINITY_sp|Q431\_LOX1.5 | Probable linoleate | 92.80 | 0.00 |
| TRINITY_sp|P109\_PETH | Ferredoxin--NADP re | 92.80 | 0.00 |
| TRINITY_sp|P478\_RPS4 | 40S ribosomal prote | 92.80 | 0.00 |
| TRINITY_sp|P001\_MT-CYB | Cytochrome b OS=Hom | 92.80 | 0.00 |
| TRINITY_sp|P199\_- | 40S ribosomal prote | 92.80 | 0.00 |
| TRINITY_sp|P089\_HTA3 | Histone H2A.Z OS=Te | 92.80 | 0.00 |
| TRINITY_sp|P091\_psaB | Photosystem I P700 | 92.80 | 0.00 |
| TRINITY_sp|P0041mt-Co3 | Cytochrome c oxidase | 92.70 | 0.00 |
| TRINITY_sp|Q9FF\_PIP2-4 | Probable aquaporin | 92.60 | 0.00 |
| TRINITY_sp|P315\_CD4B | ATP-dependent Clp p | 92.60 | 0.00 |
| TRINITY_sp|P0485\_RPL17 | 60S ribosomal prote | 92.60 | 0.00 |
| TRINITY_sp|Q020\_PSBS | Photosystem II 22 k | 92.60 | 0.00 |
| TRINITY_sp|Q90YFrp6 | 40S ribosomal prote | 92.60 | 0.00 |
| TRINITY_sp|P142\_cabII-1 | Chlorophyll a-b bin | 92.60 | 0.00 |
| TRINITY_sp|P497\_petC | Cytochrome b6-f com | 92.60 | 0.00 |
| TRINITY_sp|P691\_- | Histone H3 OS=Tetra | 92.60 | 0.00 |
| TRINITY_sp|Q9S1IHXSP90-5 | Heat shock protein | 92.60 | 0.00 |
| TRINITY_sp|P398\_RPL3 | 60S ribosomal prote | 92.50 | 0.00 |
| TRINITY_sp|Q0486\_ARF1 | ADP-ribosylation fa | 92.50 | 0.00 |
| TRINITY_sp|Q1LZ\_DDRGK1 | DDRGK domain-contai | 92.50 | 0.00 |
| TRINITY_sp|Q395\_YPTC4 | GTP-binding protein | 92.40 | 0.00 |
| TRINITY_sp|P492\_RPS18 | 40S ribosomal prote | 92.30 | 0.00 |
| TRINITY_sp|P142\_cabII-1 | Chlorophyll a-b bin | 92.30 | 0.00 |
| TRINITY_sp|Q9FWXHAC12 | Histone acetyltrans | 92.30 | 0.00 |
TRINITY_sp|P038:MT-ND3  NADH-ubiquinone oxi  90.60  0.00
TRINITY_sp|P483:CAT1  Catalase isozyme 1  90.60  0.00
TRINITY_sp|Q9SMK-  V-type proton ATPases  90.60  0.00
TRINITY_sp|Q031:PM4A  Plasma membrane ATP  90.50  0.00
TRINITY_sp|Q486:GPX6  Probable phospholipid  90.50  0.00
TRINITY_sp|P514:Rpl19  60S ribosomal protein  90.40  0.00
TRINITY_sp|P039:Mtnd4  NADH-ubiquinone oxi  90.40  0.00
TRINITY_sp|P529:-  14-3-3-like protein  90.40  0.00
TRINITY_sp|Q7XJ:GAS8  Growth arrest-speci  90.40  0.00
TRINITY_sp|P411:Rps11  40S ribosomal protein  90.40  0.00
TRINITY_sp|Q7RT:HPFA  PHD finger-like dom  90.30  0.00
TRINITY_sp|Q9SL:PSBP  Oxygen-evolving enh  90.20  0.00
TRINITY_sp|Q8L:ABCE2  ABC transporter E  90.20  0.00
TRINITY_sp|O202:-  Transketolase, chlo  90.20  0.00
TRINITY_sp|Q8W1:Cyp1  Peptidyl-prolyl cis  90.10  0.00
TRINITY_sp|P505:H2B  Histone H2B.1 OS=Ch  90.10  0.00
TRINITY_sp|P089:HTB1  Histone H2B.1 OS=Te  90.10  0.00
TRINITY_sp|P3TO:RPL14  60S ribosomal protein  90.00  0.00
TRINITY_sp|P493:CAT1  Catalase isozyme 1  90.00  0.00
TRINITY_sp|P189:MT-ND2  NADH-ubiquinone oxi  90.00  0.00
TRINITY_sp|P235:-  2-methyl-6-phytyl-1  90.00  0.00
TRINITY_sp|Q7XJ:RCA2  Ribulose bisphospha  90.00  0.00
TRINITY_sp|Q6ZD:SDH1  Succinate dehydroge  90.00  0.00
TRINITY_sp|A0CCIPx4  Serine/threonine-pr  90.00  0.00
TRINITY_sp|O817:IDH3  Isocitrate dehydrog  90.00  0.00
TRINITY_sp|Q9MB:DH1C10  Dynein-1-beta heavy  90.00  0.00
TRINITY_sp|Q90Y:Rpl135a  60S ribosomal prote  90.00  0.00
TRINITY_sp|P0D1:At2g300P  PHD finger-like dom  89.90  0.00
TRINITY_sp|P478:Rpl127a  60S ribosomal prote  89.90  0.00
TRINITY_sp|Q9XF:PIP1-2  Aquaporin PIP1-2 OS  89.90  0.00
TRINITY_sp|P2651GAPC  Glyceraldehyde-3-ph  89.90  0.00
TRINITY_sp|Q032:RBG7  Glycine-rich RNA-bi  89.80  0.00
TRINITY_sp|P505:H2A-II  Histone H2A OS=Chla  89.80  0.00
TRINITY_sp|P287:-  Formate--tetrahydro  89.70  0.00
TRINITY_sp|P294:TPT  Triose phosphate/ph  89.70  0.00
TRINITY_sp|P096:CTSL  Cathepsin L1 (Fragm  89.70  0.00
TRINITY_sp|Q426:TKT3  Transketolase, chlo  89.70  0.00
TRINITY_sp|O246:AS  Asparagine syntheta  89.70  0.00
TRINITY_sp|P933:GAPN  NADP-dependent glyc  89.60  0.00
TRINITY_sp|Q412:PSAEA  Photosystem I react  89.60  0.00
TRINITY_sp|Q957:GGAT2  Glutamate--glyoxyla  89.60  0.00
TRINITY_sp|Q9SL:PSBP  Oxygen-evolving enh  89.60  0.00
TRINITY_sp|P8241:PSRP3  30S ribosomal prote  89.60  0.00
TRINITY_sp|P343:prp-8  Pre-mRNA-splicing f  89.50  0.00
TRINITY_sp|P3T0:RPL17  60S ribosomal prote  89.50  0.00
TRINITY_sp|P339:CO  Zinc finger protein  89.50  0.00
TRINITY_sp|P307:RPL9  60S ribosomal prote  89.40  0.00
TRINITY_sp|P485:APX1  L-ascorbate peroxid  89.40  0.00
TRINITY_sp|P365:RPL4  60S ribosomal prote  89.40  0.00
TRINITY_sp|Q9PV:c8b  Complement componen  89.40  0.00
TRINITY_sp|Q6VA:V  Tubulin alpha-4 cha  89.30  0.00
TRINITY_sp|P350:-  Histone H2B.1/H2B.2  89.30  0.00
TRINITY_sp|P503:GAPA  Glyceraldehyde-3-ph  89.30  0.00
TRINITY_sp|P680:RPS29A  40S ribosomal prote  89.30  0.00
TRINITY_sp|P496:-  Ubiquitin-60S ribos  89.30  0.00
TRINITY_sp|Q8W1:PK  Pyridoxal kinase OS  89.30  0.00
| Accession | Description                                                                 | Ortholog | Score |
|-----------|------------------------------------------------------------------------------|----------|-------|
| sp|Q8VZ|RPL35 |50S ribosomal protein|89.20 |0.00 |
| sp|Q9Z5|TCTP |Translationally-conorrelated|89.20 |0.00 |
| sp|Q9SA|YchF1 |Oglob-like ATPase 1|89.10 |0.00 |
| sp|P499| - |Ferritin, heavy subunit|89.00 |0.00 |
| sp|Q944|FBA2 |Fructose-bisphosphatase|88.90 |0.00 |
| sp|O648|At2g230|Uncharacterized protein|88.90 |0.00 |
| sp|P123|PSAG |Photosystem I reaction center|88.90 |0.00 |
| sp|Q6EU|PIP1-1 |Aquaporin PIP1-1 OS|88.90 |0.00 |
| sp|Q392| - |DNA-directed RNA polymerase|88.90 |0.00 |
| sp|P023| - |Histone H4, major O|88.90 |0.00 |
| sp|B7G8| PHATRDR|Translation factor|88.90 |0.00 |
| sp|P378|PFL |Formate acetyltransferase|88.90 |0.00 |
| sp|Q5XJ|gagd |Glyceraldehyde-3-phosphate dehydrogenase|88.80 |0.00 |
| sp|P113| - |Retrovirus-related|88.70 |0.00 |
| sp|P275|CAP10A |Chlorophyll a-b binding protein|88.70 |0.00 |
| sp|P691| - |Histone H3 OS=Tetra|88.70 |0.00 |
| sp|O786| - |Cytchrome b OS=Carotinoid|88.70 |0.00 |
| sp|O221|At2g4488|Putative ribosome biogenesis factor|88.70 |0.00 |
| sp|Q9SV|NIP5-1 |Probable aquaporin|88.60 |0.00 |
| sp|Q9AX| - |Eukaryotic translation initiation factor|88.60 |0.00 |
| sp|Q395|ODA2 |Dynein gamma chain, heavy polypeptide|88.60 |0.00 |
| sp|Q9FN|CHLH |Magnesium-chelatase|88.60 |0.00 |
| sp|Q58D|RPL7 |60S ribosomal protein|88.50 |0.00 |
| sp|Q56Y|AGT1 |Serine--glyoxylate aminotransferase|88.50 |0.00 |
| sp|Q386| - |V-type proton ATPase|88.50 |0.00 |
| sp|P557|mt-co3 |Cytochrome c oxidase|88.40 |0.00 |
| sp|P275|CAP10A |Chlorophyll a-b binding protein|88.30 |0.00 |
| sp|P0CH| - |Ubiquitin-60S ribosome|88.30 |0.00 |
| sp|P612|RPL12 |60S ribosomal protein|88.30 |0.00 |
| sp|Q9S9|HSP70-5 |Heat shock 70 kDa protein|88.30 |0.00 |
| sp|A8HS|CHLRE|40S ribosomal protein|88.30 |0.00 |
| sp|P0C2|crp-79 |Ubiquitin-60S ribosome|88.30 |0.00 |
| sp|P123|PSAF |Photosystem I reaction center|88.20 |0.00 |
| sp|P411|HSP90B1 |Endoplasmic reticulum OS=Cani|88.20 |0.00 |
| sp|O814|PAP1 |Probable plastid-linked protein|88.20 |0.00 |
| sp|Q5AD|HHHT3 |Histone H3.3 OS=Cani|88.20 |0.00 |
| sp|Q396|ODA11 |Dynein alpha chain|88.20 |0.00 |
| sp|Q9SU|PSAK |Photosystem I reaction center|88.20 |0.00 |
| sp|A2XK|OsI-012|Costar family protein|88.20 |0.00 |
| sp|P552|CGS1 |Cystathionine gamma synthase|88.10 |0.00 |
| sp|Q9AR|CHT1 |Magnesium-protoporphyrin|88.10 |0.00 |
| sp|Q934|actb |Actin, cytoplasmic|88.00 |0.00 |
| sp|Q9CA|CHLP |Geranylgeranyldiphosphate|88.00 |0.00 |
| sp|P975|Nptn |Neuroplastin OS=Rat|87.90 |0.00 |
| sp|P593|Eif5 |Eukaryotic translation initiation factor|87.90 |0.00 |
| sp|O890|Rbm3 |RNA-binding protein|87.80 |0.00 |
| sp|Q3S2|RPN2 |Dolichyl-diphosphooligosaccharide-peptide|87.80 |0.00 |
| sp|Q9SS|PRP8A |Pre-mRNA-processing factor|87.80 |0.00 |
| sp|Q9AR|CHT1 |Magnesium-protoporphyrin|87.80 |0.00 |
| sp|Q7KY|ch1N |Light-independent photometer|87.80 |0.00 |
| sp|Q8T0|ART2 |Putative uncharacterized protein|87.80 |0.00 |
| sp|Q9S1|CYP18-2 |Peptidyl-prolyl cis-trans isomerase|87.70 |0.00 |
| sp|P838|TXNL4A |Thioredoxin-like protein|87.70 |0.00 |
| sp|Q8RX|TYW1 |S-adenosyl-L-methionine synthase|87.60 |0.00 |
TRINITY_sp|Q9SZRPT2A | 26S proteasome regulatory subunit A | 87.60 | 0.00
TRINITY_sp|Q9LYCSP41A | Chloroplast stem-loop RNA-binding protein | 87.55 | 0.00
TRINITY_sp|Q9F1KHAC12 | Histone acetyltransferase | 87.50 | 0.00
TRINITY_sp|Q9SLATG8D | Autophagy-related protein 8d | 87.50 | 0.00
TRINITY_sp|P505fH2A-II | Histone H2A OS=Chlamydomonas reinhardtii | 87.50 | 0.00
TRINITY_sp|Q9H8METT17A | Methyltransferase-1 | 87.50 | 0.00
TRINITY_sp|O089fRPL36A | 60S ribosomal protein L40 | 87.40 | 0.00
TRINITY_sp|Q56Y7AGT1 | Serine--glyoxylate aminotransferase | 87.40 | 0.00
TRINITY_sp|Q54Lsmc4 | Structural maintena | 87.40 | 0.00
TRINITY_sp|P3222CYSK | Cysteine synthase, thiosulfate sulfurtransferase | 87.30 | 0.00
TRINITY_sp|Q8JJ6fapb1 | Fatty acid-binding protein | 87.20 | 0.00
TRINITY_sp|P038fMtnd2 | NADH-ubiquinone oxidoreductase chain 1 | 87.20 | 0.00
TRINITY_sp|Q3961psaD | Photosystem I reaction center subunit II | 87.20 | 0.00
TRINITY_sp|C1F9RthrS | Threonine--tRNA ligase | 87.10 | 0.00
TRINITY_sp|A2XJfOsI_012 | Chlorophyll a-b binding protein | 87.10 | 0.00
TRINITY_sp|P485fPPX2 | Serine/threonine-protein phosphatase PP-X isozyme 2 | 87.00 | 0.00
TRINITY_sp|Q9STIfCalreticulin | Calreticulin OS=Chlamydomonas reinhardtii | 87.00 | 0.00
TRINITY_sp|Q9C9HPR | Glycerate dehydrogenase | 87.00 | 0.00
TRINITY_sp|O655fCIPK6 | CBL-interacting serine/threonine-protein kinase 6 | 86.90 | 0.00
TRINITY_sp|P114fTUBA1 | Tubulin alpha-1 | 86.90 | 0.00
TRINITY_sp|P0C2fcrp-79 | Ubiquitin-60S ribosomal protein | 86.90 | 0.00
TRINITY_sp|Q401fCYP-3 | Cysteine protease | 86.80 | 0.00
TRINITY_sp|P4921RPL32A | 60S ribosomal protein L32A | 86.80 | 0.00
TRINITY_sp|P493fSerine hydroxymethyltransferase | Serine hydroxymethyltransferase | 86.80 | 0.00
TRINITY_sp|Q9MI1mt-c0l | Cytochrome c oxidase subunit II | 86.80 | 0.00
TRINITY_sp|P257fTRG-31 | Probable aquaporin | 86.70 | 0.00
TRINITY_sp|Q8LZ9mt-cyb | Cytochrome b OS=Arabidopsis thaliana | 86.70 | 0.00
TRINITY_sp|P0226fRPL5 | 60S ribosomal protein L5 | 86.70 | 0.00
TRINITY_sp|Q86Cfctor | Target of rapamycin | 86.70 | 0.00
TRINITY_sp|P168fHistone H2B.3 | Histone H2B.3 OS=Vigna radiata var. radiata | 86.70 | 0.00
TRINITY_sp|P427fRPS13 | 30S ribosomal protein L13 | 86.60 | 0.00
TRINITY_sp|P078fMajor actin | Major actin OS=Dictyostelium discoideum | 86.60 | 0.00
TRINITY_sp|P263fTFIID | TATA-box-binding protein | 86.60 | 0.00
TRINITY_sp|Q94Smt-cyb | Cytochrome b OS=Arabidopsis thaliana | 86.55 | 0.00
TRINITY_sp|P462fRPS23 | 40S ribosomal protein L23 | 86.50 | 0.00
TRINITY_sp|P293fRPS1 | 30S ribosomal protein L1 | 86.40 | 0.00
TRINITY_sp|Q9ARcCTH1 | Magnesium-protoporin | 86.30 | 0.00
TRINITY_sp|Q2QVfCLEPC2 | Chaperone protein C | 86.30 | 0.00
TRINITY_sp|P464fTBP1 | 26S protease-regulating subunit | 86.20 | 0.00
TRINITY_sp|O225fV-type proton ATPase | V-type proton ATPase | 86.20 | 0.00
TRINITY_sp|P542fGDCST | Aminomethyltransferase | 86.20 | 0.00
TRINITY_sp|P481fMT-ND1 | NADH-ubiquinone oxidoreductase chain 1 | 86.10 | 0.00
TRINITY_sp|F43CfCTPA3 | Carboxyl-terminal-peptidase | 86.10 | 0.00
TRINITY_sp|F6H7fTHI1-2 | Thiamine thiazole synthase | 86.10 | 0.00
TRINITY_sp|P226fChlorophyll a-b binding protein | Chlorophyll a-b binding protein | 86.10 | 0.00
TRINITY_sp|P316fENO | Enolase (Fragment) | 86.00 | 0.00
TRINITY_sp|Q8LG6TDT | Tonoplast dicarboxylate transporter | 85.90 | 0.00
TRINITY_sp|Q9SBfPER42 | Peroxidase-42 OS=Arabidopsis thaliana | 85.90 | 0.00
TRINITY_sp|Q6K6fOs02g075 | Leucine aminopeptidase | 85.90 | 0.00
TRINITY_sp|Q948IfFerritin-3, chloroplastic | Ferritin-3, chloroplastic | 85.80 | 0.00
TRINITY_sp|P482fRPS4 | 30S ribosomal protein L4 | 85.80 | 0.00
TRINITY_sp|Q9U7fHistone H3 | Histone H3 OS=Mastigamoeba balamuthia | 85.80 | 0.00
TRINITY_sp|P325fGLC7 | Serine/threonine-protein phosphatase PP-X | 85.80 | 0.00
TRINITY_sp|A0CCIffP4x4 | Serine/threonine-protein phosphatase PP-X | 85.80 | 0.00
TRINITY_sp|P018fH2-L | H-2 class I histocompatibility antigen | 85.80 | 0.00
TRINITY_sp|P384fATP2 | ATP synthase subunit | 85.80 | 0.00
| Accession | Description                                      | Score | E-value |
|-----------|--------------------------------------------------|-------|---------|
| TRINITY_sp| Ubiquitin-fold modifiers                        | 85.70 | 0.00    |
| TRINITY_sp| MICOS complex subunit                           | 85.70 | 0.00    |
| TRINITY_sp| Ubiquitin-60S ribosome                          | 85.70 | 0.00    |
| TRINITY_sp| Serum response factor                            | 85.70 | 0.00    |
| TRINITY_sp| Ubiquitin-conjugating protein                    | 85.70 | 0.00    |
| TRINITY_sp| 60S acidic ribosome                              | 85.70 | 0.00    |
| TRINITY_sp| Photosynthetic NDH                               | 85.70 | 0.00    |
| TRINITY_sp| Serine/threonine-protein                         | 85.60 | 0.00    |
| TRINITY_sp| Calmodulin OS=Tetra                             | 85.60 | 0.00    |
| TRINITY_sp| Polysubunit of 20                                  | 85.60 | 0.00    |
| TRINITY_sp| 60S ribosomal protein                            | 85.50 | 0.00    |
| TRINITY_sp| GTP-binding protein                              | 85.50 | 0.00    |
| TRINITY_sp| Putative uncharacterized protein                 | 85.40 | 0.00    |
| TRINITY_sp| Peptidyl-prolyl cis                               | 85.40 | 0.00    |
| TRINITY_sp| DNA-directed RNA polymer                         | 85.40 | 0.00    |
| TRINITY_sp| Heat shock protein                               | 85.40 | 0.00    |
| TRINITY_sp| Filalin-4 OS=Olea                                | 85.40 | 0.00    |
| TRINITY_sp| Protein CURVATURE T                              | 85.30 | 0.00    |
| TRINITY_sp| Glyceroldehyde-3-phosphate                       | 85.30 | 0.00    |
| TRINITY_sp| Hsp90 co-chaperone                               | 85.30 | 0.00    |
| TRINITY_sp| Glutamate--glyoxylal                               | 85.20 | 0.00    |
| TRINITY_sp| Acyl-CoA-binding protein                         | 85.20 | 0.00    |
| TRINITY_sp| Tryptophan synthase                              | 85.20 | 0.00    |
| TRINITY_sp| Serine/threonine-protein                         | 85.20 | 0.00    |
| TRINITY_sp| Pre-mRNA-processing                              | 85.20 | 0.00    |
| TRINITY_sp| Ubiquitin-conjugating protein                    | 85.10 | 0.00    |
| TRINITY_sp| Heat shock cognate                               | 85.10 | 0.00    |
| TRINITY_sp| Integrator complex                               | 85.10 | 0.00    |
| TRINITY_sp| Chlorophyll a-b bin                               | 85.10 | 0.00    |
| TRINITY_sp| Peroxiredoxin-2E-1                               | 85.10 | 0.00    |
| TRINITY_sp| Asparagine synthetental                          | 85.00 | 0.00    |
| TRINITY_sp| Histone H2A-IV OS=V                              | 85.00 | 0.00    |
| TRINITY_sp| Glyceroldehyde-3-phosphate                       | 84.90 | 0.00    |
| TRINITY_sp| 40S ribosomal protein                            | 84.90 | 0.00    |
| TRINITY_sp| Cell division contr                               | 84.90 | 0.00    |
| TRINITY_sp| Dynnein heavy chain                              | 84.80 | 0.00    |
| TRINITY_sp| Methionine aminopeptide                          | 84.80 | 0.00    |
| TRINITY_sp| Probable voltage-ga                              | 84.80 | 0.00    |
| TRINITY_sp| Complement component                             | 84.80 | 0.00    |
| TRINITY_sp| Photosystem II stabil                            | 84.70 | 0.00    |
| TRINITY_sp| Serine/threonine-protein                         | 84.70 | 0.00    |
| TRINITY_sp| Serine/threonine-protein                         | 84.60 | 0.00    |
| TRINITY_sp| Plasticid ATP/ADP-t                              | 84.60 | 0.00    |
| TRINITY_sp| Cytochrome c oxidases                            | 84.60 | 0.00    |
| TRINITY_sp| Betaine--homocystei                              | 84.60 | 0.00    |
| TRINITY_sp| Mitogen-activated p                              | 84.60 | 0.00    |
| TRINITY_sp| Chloroplast stem-lo                               | 84.50 | 0.00    |
| TRINITY_sp| ATP-dependent zinc                               | 84.50 | 0.00    |
| TRINITY_sp| ubiquitin-conjugatif                              | 84.50 | 0.00    |
| TRINITY_sp| Heat shock 70 kDa p                              | 84.50 | 0.00    |
| TRINITY_sp| Histone H2B.3 OS=Vo                              | 84.50 | 0.00    |
| TRINITY_sp| NADH-ubiquinone oxidase                          | 84.40 | 0.00    |
| TRINITY_sp| Tubulin alpha chain                              | 84.40 | 0.00    |
| TRINITY_sp| Sm-like protein LSM                               | 84.40 | 0.00    |
| TRINITY_sp| ATP-dependent zinc                               | 84.40 | 0.00    |
| Name                        | Description                      | Score | Old Score |
|-----------------------------|----------------------------------|-------|-----------|
| Ubiquitin-fold modifier 1  | OS=Chlamydomonas reinhardtii GN=PR46a PE=3 SV=1 | 84.40 | 0.00      |
| Target of rapamycin         | OS=Dictyostelium discoideum GN=tor PE=1 SV=1 | 84.40 | 0.00      |
| Elongation factor 2         | OS=Gallus gallus GN=EEF2 PE=1 SV=3 | 84.40 | 0.00      |
| Probable aquaporin PIP1-2   | OS=Oryza sativa subsp. japonica GN=PIP1-2 PE=2 SV=3 | 84.40 | 0.00      |
| Proteasome subunit beta type-7-A | OS=Arabidopsis thaliana GN=PBB1 PE=1 SV=2 | 84.40 | 0.00      |
| Chlorophyll a-b binding protein of LHCII type I, chloroplastic | OS=Dunaliella salina PE=2 SV=1 | 84.40 | 0.00      |
| Coiled-coil domain-containing protein 65 homolog (Fragment) | OS=Chlamydomonas reinhardtii GN=CCDC65 PE=1 SV=1 | 84.40 | 0.00      |
| Dynein gamma chain, flagellar outer arm | OS=Chlamydomonas reinhardtii GN=ODA2 PE=1 SV=1 | 84.40 | 0.00      |
| Glyceraldehyde-3-phosphate dehydrogenase GAPA1, chloroplastic | OS=Arabidopsis thaliana GN=GAPA1 PE=1 SV=3 | 84.40 | 0.00      |
| Biotinidase | OS=Takifugu rubripes GN=btd PE=3 SV=1 | 84.40 | 0.00      |
| Diphthamide biosynthesis protein 3 | OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) GN=DPH3 PE=3 SV=1 | 84.40 | 0.00      |
| Actin, cytoplasmic 1        | OS=Xenopus laevis GN=actb PE=2 SV=1 | 84.40 | 0.00      |
| 40S ribosomal protein S29   | OS=Drosophila melanogaster GN=RpS29 PE=1 SV=1 | 84.40 | 0.00      |
| Dynein-1-beta heavy chain, flagellar inner arm I1 complex | OS=Chlamydomonas reinhardtii GN=DHC10 PE=1 SV=1 | 84.40 | 0.00      |
| 60S ribosomal protein L39-1 | OS=Oryza sativa subsp. japonica GN=RPL39A PE=3 SV=1 | 84.40 | 0.00      |
| Keratin, type II cytoskeletal 8 | OS=Homo sapiens GN=KRT8 PE=1 SV=7 | 84.40 | 0.00      |
| Fructose-bisphosphate aldolase, cytoplasmic isozyme 1 | OS=Pisum sativum PE=2 SV=1 | 84.40 | 0.00      |
| 26S protease regulatory subunit 7A | OS=Oryza sativa subsp. japonica GN=RPT1A PE=2 SV=1 | 84.40 | 0.00      |
| 40S ribosomal protein S15a  | OS=Daucus carota GN=RPS15A PE=2 SV=3 | 84.40 | 0.00      |
| Glutathione reductase, cytosolic | OS=Pisum sativum PE=2 SV=1 | 84.40 | 0.00      |
| Peptidyl-prolyl cis-trans isomerase CYP71 | OS=Arabidopsis thaliana GN=CYP71 PE=1 SV=1 | 84.40 | 0.00      |
| Pre-mRNA-processing-splicing factor 8A | OS=Arabidopsis thaliana GN=PRP8A PE=1 SV=1 | 84.40 | 0.00      |
| Dynein-1-beta heavy chain, flagellar inner arm I1 complex | OS=Chlamydomonas reinhardtii GN=DHC10 PE=1 SV=1 | 84.40 | 0.00      |
| Thioredoxin-like protein 4A | OS=Homo sapiens GN=TXNL4A PE=1 SV=1 | 84.40 | 0.00      |
| Succinate dehydrogenase assembly factor 4, mitochondrial | OS=Drosophila melanogaster GN=Sirup PE=3 SV=1 | 84.40 | 0.00      |
| Delta-aminolevulinic acid dehydratase, chloroplastic | OS=Chlamydomonas reinhardtii GN=HEMB PE=2 SV=1 | 84.40 | 0.00      |
| Peptidyl-prolyl cis-trans isomerase | OS=Catharanthus roseus GN=PCKR1 PE=1 SV=1 | 84.40 | 0.00      |
| Ribulose bisphosphate carboxylase/oxygenase activase 1, chloroplastic | OS=Nicotiana tabacum PE=1 SV=1 | 84.40 | 0.00      |
| 60S ribosomal protein L39-1 | OS=Oryza sativa subsp. japonica GN=RPL39A PE=3 SV=2 | 84.40 | 0.00      |
| Peptidyl-prolyl cis-trans isomerase | OS=Arabidopsis thaliana GN=CYP71 PE=1 SV=1 | 84.40 | 0.00      |
| Pre-mRNA-processing-splicing factor 8A | OS=Arabidopsis thaliana GN=PRP8A PE=1 SV=1 | 84.40 | 0.00      |
| Dynein-1-beta heavy chain, flagellar inner arm I1 complex | OS=Chlamydomonas reinhardtii GN=DHC10 PE=1 SV=1 | 84.40 | 0.00      |
| Thioredoxin-like protein 4A | OS=Homo sapiens GN=TXNL4A PE=1 SV=1 | 84.40 | 0.00      |
| Succinate dehydrogenase assembly factor 4, mitochondrial | OS=Drosophila melanogaster GN=Sirup PE=3 SV=1 | 84.40 | 0.00      |
| Delta-aminolevulinic acid dehydratase, chloroplastic | OS=Chlamydomonas reinhardtii GN=HEMB PE=2 SV=1 | 84.40 | 0.00      |
| Peptidyl-prolyl cis-trans isomerase | OS=Catharanthus roseus GN=PCKR1 PE=1 SV=1 | 84.40 | 0.00      |
| Ribulose bisphosphate carboxylase/oxygenase activase 1, chloroplastic | OS=Nicotiana tabacum PE=1 SV=1 | 84.40 | 0.00      |
| 60S ribosomal protein L39-1 | OS=Oryza sativa subsp. japonica GN=RPL39A PE=3 SV=1 | 84.40 | 0.00      |
TRINITY_sp|Q2NL|CLPTM1  Cleft lip and palate  82.90  0.00
TRINITY_sp|Q0741-LHCBA.4.1 Chlorophyll a-b bin  82.80  0.00
TRINITY_sp|Q8RWFVTC2 GDP-L-galactose pho  82.80  0.00
TRINITY_sp|P0CGubb Polyubiquitin-B OS=  82.80  0.00
TRINITY_sp|Q9264-DHX38 Pre-mRNA-splicing f  82.70  0.00
TRINITY_sp|Q9CS7RPT5A 26S protease regula  82.70  0.00
TRINITY_sp|Q9UD7-Histone H3 OS=Masti  82.70  0.00
TRINITY_sp|Q9FNN5o585 NADH dehydrogenase  82.60  0.00
TRINITY_sp|Q9M4RPT4B 26S protease regula  82.60  0.00
TRINITY_sp|Q2326-CKS1 Cyclin-dependent ki  82.50  0.00
TRINITY_sp|Q9V58RPL38 60S ribosomal prote  82.50  0.00
TRINITY_sp|Q0153rpsL 30S ribosomal prote  82.40  0.00
TRINITY_sp|P2156CYP Peptidyl-yl cis  82.40  0.00
TRINITY_sp|P3616HSC80 Heat shock cognate  82.40  0.00
TRINITY_sp|Q9U99ripp6c Serine/threonine-pr  82.30  0.00
TRINITY_sp|Q0484C31A 31 kDa ribonucleopr  82.20  0.00
TRINITY_sp|P1286GAPB Glyceraldehyde-3-ph  82.20  0.00
TRINITY_sp|Q3691psaD Photosystem I react  82.20  0.00
TRINITY_sp|Q541YdhkJ Hybrid signal trans  82.20  0.00
TRINITY_sp|P3616HSC80 Heat shock cognate  82.20  0.00
TRINITY_sp|Q9441GLYK D-glycerate 3-kinas  82.20  0.00
TRINITY_sp|Q9AXSSNLSL Photosynthetic NDH  82.10  0.00
TRINITY_sp|Q9Y24EIF3L Eukaryotic translat  82.10  0.00
TRINITY_sp|O6031AQR Intron-binding prot  82.10  0.00
TRINITY_sp|Q9M31rps6 40S ribosomal prote  82.10  0.00
TRINITY_sp|P2586UBC2 Ubiquitin-conjugati  82.10  0.00
TRINITY_sp|P2866CLKR27 3-oxoacyl-[acyl-car  82.10  0.00
TRINITY_sp|Q4266SODA Superoxide dismutas  82.10  0.00
TRINITY_sp|Q541YdhkK Hybrid signal trans  82.10  0.00
TRINITY_sp|Q9FG2UBL5 Ubiquitin-like prot  82.10  0.00
TRINITY_sp|P0841rpl14-a 60S ribosomal prote  82.00  0.00
TRINITY_sp|P9291KIN11 SNF1-related protei  82.00  0.00
TRINITY_sp|Q9MBHDHC10 Dynein-1-beta heavy  82.00  0
TRINITY_sp|Q9LYZRPL1 50S ribosomal prot  81.90  0.00
TRINITY_sp|Q3955TUBG Tubulin gamma chain  81.90  0.00
TRINITY_sp|O4946AAC3 ADP,ATP carrier prot  81.80  0.00
TRINITY_sp|Q9ST7HSP70-6 Heat shock 70 kDa p  81.80  0.00
TRINITY_sp|Q5XXIMSH2 DNA mismatch repair  81.80  0.00
TRINITY_sp|O2686msrB Peptide methionin  81.80  0.00
TRINITY_sp|P3641hspB Heat shock cognate  81.80  0.00
TRINITY_sp|P1606GDCSH Glycine cleavage sy  81.80  0.00
TRINITY_sp|P4646-Malate dehydrogenas  81.80  0.00
TRINITY_sp|P8327hb2 Hemoglobin subunit  81.70  0.00
TRINITY_sp|O8051RAB1B Ras-related protein  81.70  0.00
TRINITY_sp|P2346-Ribulose bisphospha  81.70  0.00
TRINITY_sp|P3124ACO 1-aminocyclopropane  81.60  0.00
TRINITY_sp|Q7X59RCA1 Ribulose bisphospha  81.60  0.00
TRINITY_sp|A2XMRPP22A Serine/threonine-pr  81.60  0.00
TRINITY_sp|P2837TBP2 TATA-box-binding pr  81.60  0.00
TRINITY_sp|Q8LPA-BCE2 ABC transporter E f  81.60  0.00
TRINITY_sp|P0847RBCS Ribulose bisphospha  81.60  0.00
TRINITY_sp|P0614-40S ribosomal prot  81.60  0.00
TRINITY_sp|P4112Rpl128 60S ribosomal prot  81.50  0.00
TRINITY_sp|Q9XHRPL37A 60S ribosomal prot  81.50  0.00
TRINITY_sp|P0495Fn1 Fibronectin OS=Ratt  81.50  0.00
TRINITY_sp|P5921RPS13B 40S ribosomal prot  81.50  0.00
| Gene Accession Name | Description                                      | Identity % | Similarity % |
|---------------------|--------------------------------------------------|------------|-------------|
| TRINITY_sp|Q9C9\At1g527|Probable histone H2 | 81.50 | 0.00 |
| TRINITY_sp|Q9C8\At1g334|PHD finger protein | 81.50 | 0.00 |
| TRINITY_sp|Q405\PSBR|Photosystem II 10 k | 81.50 | 0.00 |
| TRINITY_sp|Q430\H2|Histone H4 OS=Pyren | 81.40 | 0.00 |
| TRINITY_sp|Q6ZR\(DNAH12|Dynemin heavy chain | 81.30 | 0.00 |
| TRINITY_sp|Q405\PSBR|Photosystem II 10 k | 81.30 | 0.00 |
| TRINITY_sp|Q9FR\TOR|Serine/threonine-pr | 81.30 | 0.00 |
| TRINITY_sp|P301\(act-1a|Actin-1 OS=Onchocer | 81.30 | 0.00 |
| TRINITY_sp|P503\GAPA|Glyceraldehyde-3-ph | 81.30 | 0.00 |
| TRINITY_sp|P314\VHA55|V-type proton ATPas | 81.30 | 0.00 |
| TRINITY_sp|P229\MED37D|Probable mediator o | 81.20 | 0.00 |
| TRINITY_sp|P028\H2|Heat shock 70 kDa p | 81.20 | 0.00 |
| TRINITY_sp|Q655\FTSH2|ATP-dependent zinc | 81.20 | 0.00 |
| TRINITY_sp|Q9S\At4g302|Probable small nucl | 81.20 | 0.00 |
| TRINITY_sp|P226\ARG7|Argininosuccinate l | 81.20 | 0.00 |
| TRINITY_sp|P571\MDH2|Malate dehydrogenas | 81.20 | 0.00 |
| TRINITY_sp|P488\HSPA1L|Heat shock 70 kDa p | 81.20 | 0.00 |
| TRINITY_sp|Q032\MYBL2|Myb-related protein | 81.10 | 0.00 |
| TRINITY_sp|Q3T0\IPPP1CA|Serine/threonine-pr | 81.10 | 0.00 |
| TRINITY_sp|Q8C\tor|Target of rapamycin | 81.10 | 0.00 |
| TRINITY_sp|Q233\NYFB3|Nuclear transcripti | 81.10 | 0.00 |
| TRINITY_sp|P055\Cd8b|T-cell surface glyc | 81.00 | 0.00 |
| TRINITY_sp|Q9LY\RPL1|50S ribosomal prote | 81.00 | 0.00 |
| TRINITY_sp|Q2K3\RPS27|40S ribosomal prote | 81.00 | 0.00 |
| TRINITY_sp|P137\oprF|Outer membrane pori | 81.00 | 0.00 |
| TRINITY_sp|Q9SP\CRTZ|Beta-carotene 3-hyd | 81.00 | 0.00 |
| TRINITY_sp|Q9SM\DHC1|Dynemin-1-alpha heav | 81.00 | 0.00 |
| TRINITY_sp|Q9Y2\POMP|Proteasome maturati | 80.90 | 0.00 |
| TRINITY_sp|Q8JH\aldob|Fructose-bisphospha | 80.90 | 0.00 |
| TRINITY_sp|Q080\RPS8|40S ribosomal prote | 80.90 | 0.00 |
| TRINITY_sp|P074\BETA|Tubulin beta-1 chai | 80.90 | 0.00 |
| TRINITY_sp|P677\PPP2CA|Serine/threonine-pr | 80.90 | 0.00 |
| TRINITY_sp|Q215\M28.5|NHP2-like protein l | 80.80 | 0.00 |
| TRINITY_sp|Q92R\YKT61|VAMP-like protein Y | 80.80 | 0.00 |
| TRINITY_sp|P548\|26S protease regula | 80.80 | 0.00 |
| TRINITY_sp|P496\RPL19C|60S ribosomal prote | 80.70 | 0.00 |
| TRINITY_sp|Q9FK\LSM5|Sm-like protein LSM | 80.70 | 0.00 |
| TRINITY_sp|Q8TG\ART2|Putative uncharacte | 80.70 | 0.00 |
| TRINITY_sp|Q397\-|Acyl-CoA-binding pr | 80.60 | 0.00 |
| TRINITY_sp|P808\petM|Cytochrome b6-f com | 80.60 | 0.00 |
| TRINITY_sp|P692\UB\EP52|Ubiquitin-60S ribos | 80.60 | 0.00 |
| TRINITY_sp|Q54Y\dhkJ|Hybrid signal trans | 80.60 | 0.00 |
| TRINITY_sp|Q395\GSA|Glutamate-1-semiald | 80.60 | 0.00 |
| TRINITY_sp|Q852\HD16|Casein kinase 1-lik | 80.60 | 0.00 |
| TRINITY_sp|Q9AR\CTH1|Magnesium-protoporp | 80.60 | 0.00 |
| TRINITY_sp|Q9SJ\VHA-a2|V-type proton ATPas | 80.60 | 0.00 |
| TRINITY_sp|Q9ZR\FH|Frataxin, mitochond | 80.60 | 0.00 |
| TRINITY_sp|Q2RB\Os11g01|Clathrin heavy chai | 80.60 | 0.00 |
| TRINITY_sp|A8J\MDRC7|Dynemin regulatory c | 80.50 | 0.00 |
| TRINITY_sp|Q7F9\CLPC1|Chaperone protein C | 80.50 | 0.00 |
| TRINITY_sp|P547\RAN1A|GTP-binding nuclear | 80.40 | 0.00 |
| TRINITY_sp|Q54G\nsa2|Ribosome biogenesis | 80.40 | 0.00 |
| TRINITY_sp|P547\CDC48|Cell division cycle | 80.40 | 0.00 |
| TRINITY_sp|Q54Y\dhkJ|Hybrid signal trans | 80.40 | 0.00 |
| TRINITY_sp|P120\CAB37|Chlorophyll a-b bin | 80.30 | 0.00 |
| TRINITY_sp|P150\env|Envelope glycoprote | 80.30 | 0.00 |
TRINITY_sp|Q6P2X|PRPF8  Pre-mRNA-processing  79.50  0
TRINITY_sp|Q8WXM|DNAH7  Dynein heavy chain  79.50  0.00
TRINITY_sp|Q9S2U|RPT2A  26S proteasome regul  79.40  0.00
TRINITY_sp|P2976|~  60S acidic ribosoma  79.40  0.00
TRINITY_sp|Q9S7T|ITS1  Threonine synthase  79.40  0.00
TRINITY_sp|O826|GATA9  GATA transcription  79.40  0.00
TRINITY_sp|O650|SB62  60S ribosomal prote  79.40  0.00
TRINITY_sp|Q9Y2U|UBE2D4  Ubiquitin-conjugati  79.30  0.00
TRINITY_sp|P350|SAHH  Adenosylhomocystein  79.30  0.00
TRINITY_sp|Q329|ATPD  ATP synthase delta  79.20  0.00
TRINITY_sp|P221|PSAH  Photosystem I react  79.20  0.00
TRINITY_sp|Q8LP|LACS6  Long chain acyl-CoA  79.20  0.00
TRINITY_sp|P123|PSAE  Photosystem I react  79.20  0.00
TRINITY_sp|Q6P1Y|PGN1L1  Fidgetin-like prote  79.10  0.00
TRINITY_sp|P111|HSP70  Heat shock 70 kDa p  79.10  0.00
TRINITY_sp|O026|mdh-2  Probable malate deh  79.10  0.00
TRINITY_sp|B9DG|ACS  Acetyl-coenzyme A s  79.10  0.00
TRINITY_sp|P462|CSBP  Sedoheptulose-1,7-b  79.00  0.00
TRINITY_sp|P563|minD  Putative septum sit  79.00  0.00
TRINITY_sp|Q2QV|CLPC2  Chaperone protein C  79.00  0.00
TRINITY_sp|P289|~  Elongation factor 2  78.90  0.00
TRINITY_sp|P361|HSC80  Heat shock cognate  78.90  0.00
TRINITY_sp|Q9W8|pph-3  Serine/threonine-pr  78.90  0.00
TRINITY_sp|Q9MB|DHC10  Dynein-1-beta heavy  78.90  0.00
TRINITY_sp|A1Z0|hamp  Hepcidin OS=Larimic  78.80  0.00
TRINITY_sp|P344|mog-1  Probable pre-mRNA-s  78.80  0.00
TRINITY_sp|O649|RPT1  26S protease regul  78.80  0.00
TRINITY_sp|P0C8|CCRP1  Probable serine/thr  78.80  0.00
TRINITY_sp|Q86A|polr3a  DNA-directed RNA po  78.70  0.00
TRINITY_sp|Q9X1|ELF5A-1  Eukaryotic translat  78.70  0.00
TRINITY_sp|P0C5|PP2A4  Putative serine/thr  78.70  0.00
TRINITY_sp|Q9SH|RUB1  Ubiquitin-NEDD8-lik  78.70  0.00
TRINITY_sp|P239|PSAL  Photosystem I react  78.60  0.00
TRINITY_sp|P112|Fn1  Fibronectin OS=Mus  78.60  0.00
TRINITY_sp|P350|~  Histone H2A OS=Acro  78.60  0.00
TRINITY_sp|P350|~  Histone H2A OS=Acro  78.60  0.00
TRINITY_sp|A8JF|NCS6  Cytoplasmic tRNA 2-  78.60  0.00
TRINITY_sp|P022|HTA1  Histone H2AX OS=Tet  78.60  0.00
TRINITY_sp|P206|bimG  Serine/threonine-pr  78.60  0.00
TRINITY_sp|Q9SL|PGR5  Protein PROTON GRAD  78.40  0.00
TRINITY_sp|P061|PSBR  Photosystem II 10 k  78.40  0.00
TRINITY_sp|Q32P|LSM3  U6 snRNA-associated  78.40  0.00
TRINITY_sp|Q93Y|ppal  Soluble inorganic p  78.40  0.00
TRINITY_sp|Q9LD|CBP5  HACA ribonucleop  78.40  0.00
TRINITY_sp|Q8LK|DME  Transcriptional act  78.40  0.00
TRINITY_sp|Q377|mt-co2  Cytochrome c oxidas  78.40  0.00
TRINITY_sp|A41J|mms1  Meiosis-specific nu  78.40  0.00
TRINITY_sp|P277|ODA6  Dynein, 70 kDa inte  78.40  0.00
TRINITY_sp|Q395|ODA4  Dynein beta chain,  78.40  0.00
TRINITY_sp|Q6QJ|SULP2  Sulfate permease 2,  78.30  0.00
TRINITY_sp|O650|SB62  60S ribosomal prote  78.30  0.00
TRINITY_sp|Q8LP|AFABC2  ABC transporter B f  78.30  0.00
TRINITY_sp|Q9H6|TAS1P1  Threonine aspartase  78.30  0.00
TRINITY_sp|Q6ZR|DNAH12  Dynein heavy chain  78.30  0.00
TRINITY_sp|Q3T0|RPL14  60S ribosomal prote  78.20  0.00
TRINITY_sp|A4QNI|nip7  60S ribosome subunit  78.20  0.00
| Accession   | Description                             | Value 1 | Value 2 |
|-------------|-----------------------------------------|---------|---------|
| TRINITY_sp|Serine/threonine-protein phosphatase PP1 isozyme 2 OS=Acetabularia peniculus PE=3 SV=1| 78.20   | 0.00    |
| TRINITY_sp|DNA helicase INO80 OS=Tetrahymena pyriformis GN=HTA1 PE=1 SV=2| 78.10   | 0.00    |
| TRINITY_sp|50S ribosomal protein L23 OS=Arabidopsis thaliana GN=RPL23A PE=2 SV=3| 78.10   | 0.00    |
| TRINITY_sp|Elongation factor 1| 78.10   | 0.00    |
| TRINITY_sp|Dynein-1-beta heavy OS=Arabidopsis thaliana GN=TRAPPC6B PE=2 SV=1| 78.60   | 0.00    |
| TRINITY_sp|Ferredoxin-1, chloro| 78.60   | 0.00    |
| TRINITY_sp|Intron-binding prote OS=Arabidopsis thaliana GN=TRAPPC6B PE=2 SV=1| 78.60   | 0.00    |
| TRINITY_sp|60S ribosomal protein L23 OS=Arabidopsis thaliana GN=RPL23A PE=2 SV=3| 78.10   | 0.00    |
| TRINITY_sp|Integrator complex 0.00| 78.00   | 0.00    |
| TRINITY_sp|Ras-related protein OS=Arabidopsis thaliana GN=CYP20-1 PE=1 SV=1| 78.00   | 0.00    |
| TRINITY_sp|Oxygen-evolving enh OS=Tetrahymena pyriformis PE=3 SV=2| 78.00   | 0.00    |
| TRINITY_sp|40S ribosomal protein OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) GN=rps-28 PE=1 SV=1| 78.00   | 0.00    |
| TRINITY_sp|Galactinol synthase OS=Arabidopsis thaliana GN=GOLS2 PE=1 SV=1| 78.00   | 0.00    |
| TRINITY_sp|Probable elongator OS=Dictyostelium discoideum GN=elp3 PE=3 SV=1| 78.00   | 0.00    |
| TRINITY_sp|Elongation factor 1-alpha, oocyte form OS=Xenopus laevis GN=eef1ao PE=1 SV=1| 78.00   | 0.00    |
| TRINITY_sp|Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Bos taurus GN=PPP1CA PE=2 SV=1| 78.00   | 0.00    |
| TRINITY_sp|Ferredoxin, chloro OS=Chlamydomonas reinhardtii GN=PETF PE=1 SV=2| 78.00   | 0.00    |
| TRINITY_sp|Galactinol synthase OS=Arabidopsis thaliana GN=GOLS2 PE=1 SV=1| 78.00   | 0.00    |
TRINITY_sp|P505|H2A-II  Histone H2A OS=Chla  77.50  0.00
TRINITY_sp|P427|RPS11  4OS ribosomal prote  77.50  0.00
TRINITY_sp|P341|racB  Rho-related protein  77.50  0.00
TRINITY_sp|Q426|ATPD  ATP synthase delta  77.50  0.00
TRINITY_sp|Q027|RPL24  5OS ribosomal prote  77.40  0.00
TRINITY_sp|Q9SM|DHC1  Dynein-1-alpha heav  77.40  0.00
TRINITY_sp|P286|  28 kDa ribonucleop  77.40  0.00
TRINITY_sp|F4KG|RVE1  Protein REVEILLE 1  77.40  0.00
TRINITY_sp|O500|AP-17  AP-2 complex subuni  77.40  0.00
TRINITY_sp|Q8H5|Os07g062  Manganese-dependent  77.40  0.00
TRINITY_sp|A22C|SC34  6OS ribosomal prote  77.40  0.00
TRINITY_sp|Q631|Dnah7  Dynein heavy chain  77.40  0.00
TRINITY_sp|Q396|ODA11  Dynein alpha chain,  77.40  0.00
TRINITY_sp|Q9R0|ctsf  Cathepsin F OS=Mus  77.30  0.00
TRINITY_sp|Q2S0|pckA2  Phosphoenolpyruvate  77.30  0.00
TRINITY_sp|P341|ck5  Cyclin-dependent ki  77.30  0.00
TRINITY_sp|A8HY|METM  S-adenosylmethionin  77.30  0.00
TRINITY_sp|Q9SE|RPT3  26S protease regula  77.30  0.00
TRINITY_sp|Q9S|SHMs  Serine hydroxymethy  77.30  0.00
TRINITY_sp|Q655|FTSH2  ATP-dependent zinc  77.30  0.00
TRINITY_sp|P0DL|DRC1  Dynein regulatory c  77.20  0.00
TRINITY_sp|P492|RPS20A  4OS ribosomal prote  77.20  0.00
TRINITY_sp|Q9ST|R  Calreticulin OS=Chl  77.20  0.00
TRINITY_sp|Q9MRIN1  RuvB-like protein 1  77.20  0.00
TRINITY_sp|P215|CYP  Peptidyl-prolyl cis  77.20  0.00
TRINITY_sp|P929|APR1  5'-adenylylsulfate  77.10  0.00
TRINITY_sp|Q3BA|  Uncharacterized pro  77.10  0.00
TRINITY_sp|Q430|Os06g02  Asparagine syntheta  77.10  0.00
TRINITY_sp|Q271|DHC-8  Dynein heavy chain,  77.10  0.00
TRINITY_sp|Q7F9|CLPC1  Chaperone protein C  77.00  0.00
TRINITY_sp|Q5Y8|MAP2B  Methionine aminopep  77.00  0.00
TRINITY_sp|A8LP|hs1U  ATP-dependent prote  77.00  0.00
TRINITY_sp|Q6ZD|SDH1  Succinate dehydroge  77.00  0.00
TRINITY_sp|P628|RAB1A  Ras-related protein  77.00  0.00
TRINITY_sp|Q761|RPS15A  4OS ribosomal prote  76.90  0.00
TRINITY_sp|Q963|ARP1  ADP-ribosylation fa  76.90  0.00
TRINITY_sp|O650|SB62  6OS ribosomal prote  76.90  0.00
TRINITY_sp|Q54U|dnapkc  DNA-dependent prote  76.90  0.00
TRINITY_sp|Q8LQ|FTSH5  ATP-dependent zinc  76.90  0.00
TRINITY_sp|P222|fb1  rRNA 2'-O-methylitra  76.90  0.00
TRINITY_sp|Q54J|pdx1  Probable pyridoxal  76.90  0.00
TRINITY_sp|P179|FSMC3  26S protease regula  76.90  0.00
TRINITY_sp|P539|PETH  Ferredoxin--NADP re  76.90  0.00
TRINITY_sp|Q9LCA|3g123  Nascent polypeptide  76.90  0.00
TRINITY_sp|P462|RPL8A  6OS ribosomal prote  76.90  0.00
TRINITY_sp|Q9VHe|IF4AI1  Eukaryotic initiati  76.90  0.00
TRINITY_sp|P493|  Glycine-rich RNA-bi  76.90  0.00
TRINITY_sp|Q9SF|PAH1  Phosphatidate phosph  76.90  0.00
TRINITY_sp|Q9CY|SerB1  Plasminogen activat  76.80  0.00
TRINITY_sp|P838|  Histone H2B (Fragme  76.80  0.00
TRINITY_sp|P518|  ADP-ribosylation fa  76.80  0.00
TRINITY_sp|P518|  ADP-ribosylation fa  76.80  0.00
TRINITY_sp|P518|  ADP-ribosylation fa  76.80  0.00
TRINITY_sp|Q9LK|RPS9B  4OS ribosomal prote  76.80  0.00
TRINITY_sp|P413|FTRC  Ferredoxin-thioredo  76.80  0.00
TRINITY_sp|Q9LRL|RPL13AB  6OS ribosomal prote  76.80  0.00
| Accession | Description |
|-----------|-------------|
| TRINITY_sp| 5141RPL18AB | 60S ribosomal protein L18a-2 |
| TRINITY_sp| P793FCCB   | Propionyl-CoA carboxylase |
| TRINITY_sp| Q0VU9SmD1  | Probable small nucleolar protein |
| TRINITY_sp| P378PFL    | Formate acetyltransferase |
| TRINITY_sp| P458RPL31  | 60S ribosomal protein L31 |
| TRINITY_sp| P485pph-1  | Serine/threonine-protein kinase |
| TRINITY_sp| Q9YG2SUCGL | Succinate-CoA ligase |
| TRINITY_sp| Q599trpB   | Tryptophan synthetase |
| TRINITY_sp| Q9ST1tAt2g402 | Eukaryotic translation initiation factor |
| TRINITY_sp| O603AQR    | Intron-binding protein |
| TRINITY_sp| P2641HSP70 | Heat shock 70 kDa protein |
| TRINITY_sp| Q31KmmMmG  | tRNA uridine 5-carboxymethyltransferase |
| TRINITY_sp| P0CT1HTB1  | Histone H2B |
| TRINITY_sp| P0CYRPS23A | 40S ribosomal protein RPS23A |
| TRINITY_sp| Q395YPTC5  | GTP-binding protein |
| TRINITY_sp| Q4G2DER2.1 | Dynein gamma chain, flagellar outer arm |
| TRINITY_sp| Q2W89argG  | Argininosuccinate synthase |
| TRINITY_sp| P462RPL8A  | 60S ribosomal protein L8-1 |
| TRINITY_sp| Q8VZIAASK5 | Shaggy-related protein |
| TRINITY_sp| Q650SB62   | 60S ribosomal protein L6 |
| TRINITY_sp| Q395ODA2   | Dynein gamma chain, flagellar outer arm |
| TRINITY_sp| Q9P2IDNAH1 | Dynein heavy chain |
| TRINITY_sp| P9WQ1treS  | Trehalose synthetase |
| TRINITY_sp| P426GLN1   | Glutamine synthetase |
| TRINITY_sp| Q9AUF0s3g07 | Coatamer subunit |
| TRINITY_sp| Q9LDRCBF5  | H/ACA ribonucleoprotein |
| TRINITY_sp| P843ACTB   | Actin, cytoplasmic |
| TRINITY_sp| Q425At1g7901 | NADH dehydrogenase |
| TRINITY_sp| Q9TWcyPB   | Peptidyl-prolyl cis-trans isomerase |
| TRINITY_sp| Q9FFRPL12C | 60S ribosomal protein |
| TRINITY_sp| P490Os12g02 | Protein mago nashi |
| TRINITY_sp| Q9ZWAt2g430 | Isopropylmalate dehydrogenase |
| TRINITY_sp| P492RPS17  | 40S ribosomal protein |
| TRINITY_sp| Q9LVBOB1   | Protein BOBER 1 |
| TRINITY_sp| P327RCB8.3 | Ribulose bisphosphate carboxylase |
| TRINITY_sp| Q425At1g7901 | NADH dehydrogenase |
| TRINITY_sp| Q431LOX1.5 | Probable linoleate synthase |
| TRINITY_sp| Q9SJM1BF1A | Multifunctional bridging protein |
| TRINITY_sp| Q94F1CHL1  | Magnesium-chelatase |
| TRINITY_sp| Q8G7SCOA   | Succinate-CoA ligase |
| TRINITY_sp| Q2331NYB3  | Nuclear transcriptase |
| TRINITY_sp| Q321PCP1   | rRNA-processing protein |
| TRINITY_sp| Q321H2AFV  | Histone H2A.V |
| TRINITY_sp| P0CC0UBB   | Polyubiquitin-B |
| TRINITY_sp| P484Pp1alpha | Serine/threonine-protein kinase |
| TRINITY_sp| Q9NITcypE  | Peptidyl-prolyl cis-trans isomerase |
| TRINITY_sp| Q541fragA  | Ras-related GTP-binding protein |
| TRINITY_sp| Q9SBPGK    | Phosphoglycerate kinase |
| TRINITY_sp| Q9UFDNAH17 | Dynein heavy chain |
| TRINITY_sp| P0C8CCRP1  | Probable serine/threonine-protein kinase |
| TRINITY_sp| Q6C01SNU13 | 13 kDa ribonucleoprotein |
| TRINITY_sp| Q59LCSE4   | Histone H3-like centromere protein |
| TRINITY_sp| P229INMED37D | Probable mediator of development |
| TRINITY_sp| C1M1MICPUCDF | tRNA-splicing ligase |
| TRINITY_sp| Q9AXDH     | Deoxyhypusine synthase |
| TRINITY_sp| H3JUGTGT1  | Peptidyl-serine aldehyde |
| Gene Name          | Description                              | ORF    | Start Position | End Position |
|-------------------|------------------------------------------|--------|----------------|--------------|
| Pad1              | RuvB-like 2 OS=Xenopus laevis            | ruvbl2 | 76.00          | 0.00         |
| Pad1              | Protein translation                      | 94J     | 75.90          | 0.00         |
| Pad1              | Lysozyme C, spleen                      | P817    | 75.90          | 0.00         |
| Pad1              | Uncharacterized pro                     | Q3BA1   | 75.90          | 0.00         |
| Pad1              | Succinate dehydroge                      | Q9YH7   | 75.90          | 0.00         |
| Pad1              | Activating signal c                     | Q5C      | 75.90          | 0.00         |
| Pad1              | Eukaryotic translat                       | Q245EI | 75.90          | 0.00         |
| Pad1              | Ethylene-responsive                      | O803ERF | 75.90          | 0.00         |
| Pad1              | Dynein gamma chain, serine/threonine-pr | O395ODA | 75.90          | 0.00         |
| Pad1              | Calmodulin-2 OS=Oryza sativa             | O2Y6CAM | 75.90          | 0.00         |
| Pad1              | H-2 class II histoc                      | P044Cd7 | 75.80          | 0.00         |
| Pad1              | Histone deacetylase                      | Q325RPD | 75.80          | 0.00         |
| Pad1              | Extracellular signa                      | Q54QerK | 75.80          | 0.00         |
| Pad1              | 40S ribosomal prote                      | Q5E98RPS | 75.80         | 0.00         |
| Pad1              | Splicing factor 3B                       | O576sf3b | 75.80        | 0.00         |
| Pad1              | Serine/threonine-pr                      | P206bimG | 75.80          | 0.00         |
| Pad1              | Glutamine synthetas                      | Q426GLN | 75.80          | 0.00         |
| Pad1              | 60S ribosomal prote                      | Q496RPL | 75.80          | 0.00         |
| Pad1              | Uncharacterized pro                      | Q3BA1   | 75.70          | 0.00         |
| Pad1              | 40S ribosomal prote                      | Q086RPS | 75.70          | 0.00         |
| Pad1              | Ras-related C3 botu                      | P629RAC | 75.70          | 0.00         |
| Pad1              | COP9 signalosome co                      | Q8W2CSN | 75.60          | 0.00         |
| Pad1              | Deoxyhypusine synth                      | P387DY5 | 75.60          | 0.00         |
| Pad1              | Putative uncharacter                      | Q96CC8orf4 | 75.60   | 0.00         |
| Pad1              | ATP synthase subunit                     | P502ALTA | 75.60        | 0.00         |
| Pad1              | Chlorophyll a-b bin                      | Q039L18 | 75.60          | 0.00         |
| Pad1              | RuvB-like 1 OS=Homo                     | Q9Y2RUV | 75.60          | 0.00         |
| Pad1              | UDP-sulfoquinovose                      | Q84KISQ | 75.60          | 0.00         |
| Pad1              | Dynein alpha chain, serine/threonine-pr | Q396ODA | 75.60          | 0.00         |
| Pad1              | Phosphomannomutase                      | Q080PMM | 75.60          | 0.00         |
| Pad1              | Pyrophosphate-energ                      | P3141AVP | 75.60        | 0.00         |
| Pad1              | 14-3-3-like protein                     | P546fttB | 75.50          | 0.00         |
| Pad1              | Guanine nucleotide                        | P364gpB | 75.50           | 0.00        |
| Pad1              | 50S ribosomal prote                      | Q2IIfpIL | 75.50         | 0.00         |
| Pad1              | Histone H3 type 2 O                      | Q6LCh3-II | 75.50       | 0.00         |
| Pad1              | Phytoene dehydrogen                     | P285PDS | 75.50          | 0.00         |
| Pad1              | Pancreatic progenit                      | Q6PPDPfa | 75.40        | 0.00         |
| Pad1              | 60S ribosomal prote                      | Q6PBripL | 75.40        | 0.00         |
| Pad1              | Cilia- and flagella                      | A8HUFCAP | 75.40        | 0.00         |
| Pad1              | Actin-1 OS=Pismus sa                     | P301   | 75.30          | 0.00         |
| Pad1              | Oryzain alpha chain                     | P257Os49 | 75.30          | 0.00         |
| Pad1              | Actin-related prote                      | O966arcD | 75.30         | 0.00         |
| Pad1              | Ubiquitin-conjugati                      | P258UBC | 75.30          | 0.00         |
| Pad1              | Sodium/potassium-tr                      | Q137ATP | 75.30          | 0.00         |
| Pad1              | Phytochrome-associia                    | Q8LSFYP | 75.30          | 0.00         |
| Pad1              | Sulfate permease 1,                      | Q8RVSUL | 75.30          | 0.00         |
| Pad1              | Eukaryotic initiati                      | Q9VHeIF4 | 75.20          | 0.00         |
| Pad1              | Sec-independent pro                     | C4IZ2TAT | 75.20          | 0.00         |
| Pad1              | 40S ribosomal prote                      | Q9SCRPS | 75.20          | 0.00         |
| Pad1              | Proteasome subunit                      | Q9SXIPAD | 75.20        | 0.00         |
| Gene ID | Description                                      | Start | End   |
|--------|--------------------------------------------------|-------|-------|
| PPP2CA | Serine/threonine-protein phosphatase 2A          | 75.10 | 0.00  |
| TBP1   | TATA-box-binding protein                         | 75.10 | 0.00  |
| 1G4    | Deoxyuridine 5'-triphosphate                    | 75.00 | 0.00  |
| DNAJA1 | DnaJ homolog subfamily A                        | 75.00 | 0.00  |
| dhcA   | Dynein heavy chain                              | 75.00 | 0.00  |
| Calreticulin OS=Chl |                             | 75.00 | 0.00  |
| PRPF8  | Pre-mRNA-processing protein                     | 75.00 | 0.00  |
| HGO    | Homogentisate 1,2-diketo acid                    | 75.00 | 0.00  |
| PRPF8  | H/ACA ribonucleoprotein                          | 75.00 | 0.00  |
| PRPF8  | Probable mediator                                | 75.00 | 0.00  |
| Dxs    | 1-deoxy-D-xylulose-lyase                         | 75.00 | 0.00  |
| IIL1   | 3-isopropylmalate d                              | 75.00 | 0.00  |
| PRPF8  | 60S ribosomal protease                           | 75.00 | 0.00  |
| Q0QHI  | Probable citrate synthetase                      | 75.00 | 0.00  |
| Os10g050| DEAD-box ATP-dependent helicase                   | 74.90 | 0.00  |
| ARL2   | ADP-riboseylation factor                         | 74.90 | 0.00  |
| PRPF8  | Heat shock 70 kDa protein                         | 74.90 | 0.00  |
| Rac1   | Ras-related C3 botanical protein                 | 74.90 | 0.00  |
| PRPF8  | Lysozyme C OS=Sperl                          | 74.80 | 0.00  |
| PRPF8  | Cysteine proteinase                              | 74.80 | 0.00  |
| FttB   | 14-3-3-like protein                              | 74.80 | 0.00  |
| PRPF8  | 40S ribosomal protease                           | 74.80 | 0.00  |
| PRPF8  | Autophagy-related protein                        | 74.80 | 0.00  |
| PRPF8  | Dynein 11 kDa light                             | 74.80 | 0.00  |
| GLN2   | Glutamine synthetase                             | 74.80 | 0.00  |
| Q32L   | Betaine--homocysteili                           | 74.80 | 0.00  |
| Q426   | RuBiSCO large subunit                           | 74.80 | 0.00  |
| UBC1   | Ubiquitin-conjugating activity                   | 74.70 | 0.00  |
| CBP5   | H/ACA ribonucleoprotein                          | 74.70 | 0.00  |
| RPL37A | 60S ribosomal protease                           | 74.70 | 0.00  |
| HD10   | Dynamin-1-beta heavy                            | 74.70 | 0.00  |
| PE11D  | Peroxisomal membrane                            | 74.70 | 0.00  |
| PAP5   | Serine/threonine-protein                         | 74.60 | 0.00  |
| PAB1   | Proteasome subunit                              | 74.60 | 0.00  |
| ino80  | Putative DNA helicase                            | 74.60 | 0.00  |
| Rpl7b  | Ras-related protein                              | 74.60 | 0.00  |
| HD6    | Casein kinase II subunit                         | 74.60 | 0.00  |
| tf     | Serotransferrin OS=                              | 74.60 | 0.00  |
| RAD51  | DNA repair protein                               | 74.60 | 0.00  |
| TEF    | Elongation factor 1                              | 74.60 | 0.00  |
| Rps2   | 40S ribosomal proteome                           | 74.60 | 0.00  |
| RdP1   | Dihydrolipoyle dehydrogen                        | 74.60 | 0.00  |
| hba1   | Hemoglobin subunit                               | 74.60 | 0.00  |
| ATP synthase subunit |                               | 74.60 | 0.00  |
| TIRE   | Probable serine/threonine-protein                | 74.60 | 0.00  |
| Prad1  | ADP-riboseylation factor                         | 74.60 | 0.00  |
| RAB1A  | Ras-related protein                              | 74.60 | 0.00  |
| Carbonic anhydrase, mitochondrial |                               | 74.60 | 0.00  |
| RPL27A | 60S ribosomal proteome                           | 74.50 | 0.00  |
| KIF17  | Kinesin-like protein                             | 74.50 | 0.00  |
| RPL17  | 60S ribosomal proteome                           | 74.50 | 0.00  |
| PSAF   | Photosystem I reaction                           | 74.50 | 0.00  |
| HD6    | Casein kinase II subunit                         | 74.50 | 0.00  |
| CHR11  | ISWI chromatin-remodeling factor                 | 74.50 | 0.00  |
| HD16   | Casein kinase 1-like                            | 74.50 | 0.00  |
TRINITY_sp|Q557ffpab-1  SCF ubiquitin ligase  74.40  0.00
TRINITY_sp|Q54f:narf1  Probable cytosolic  74.40  0.00
TRINITY_sp|P629s:RAC1  Ras-related C3 botu  74.40  0.00
TRINITY_sp|P446:moq  Molybdopterin adeny  74.40  0.00
TRINITY_sp|B0C0mibab  tRNA-2-methylthio-N  74.40  0.00
TRINITY_sp|A7MB:RQCD1  Cell differentiation  74.40  0.00
TRINITY_sp|Q54r:ar18  ADP-ribosylation fa  74.40  0.00
TRINITY_sp|P520cyn-7  Peptidyl-prolyl cis  74.40  0.00
TRINITY_sp|P598:SPCC550.1  Putative ATP-depend  74.30  0.00
TRINITY_sp|Q54f:ascc3  Activating signal c  74.30  0.00
TRINITY_sp|Q007:-  Histone H2A type 4  74.30  0.00
TRINITY_sp|Q8LAl:GATA1  GATA transcription  74.30  0.00
TRINITY_sp|A8IEI:PRMT1  Protein arginine N-  74.30  0.00
TRINITY_sp|Q256:VAPB  V-type proton ATPas  74.20  0.00
TRINITY_sp|P490:-  Vacuolar-processing  74.20  0.00
TRINITY_sp|Q54f:dim1  Probable dimethylad  74.20  0.00
TRINITY_sp|Q9LS:EN01  Enolase 1 OS=Hevea  74.20  0.00
TRINITY_sp|P094:CLTA  Clathrin light chai  74.20  0.00
TRINITY_sp|Q9BZ:DPH1  Diphthamide biosynt  74.20  0.00
TRINITY_sp|Q395:ODA4  Dynein beta chain,  74.20  0.00
TRINITY_sp|Q8L3:FZRP2  Protein FIZZY-RELAT  74.20  0.00
TRINITY_sp|P049:CLTB  Clathrin light chai  74.20  0.00
TRINITY_sp|Q9DC:Ndufs7  NADH dehydrogenase  74.10  0.00
TRINITY_sp|Q9DC:Ndufs7  NADH dehydrogenase  74.10  0.00
TRINITY_sp|Q3BA:-  Uncharacterized pro  74.10  0.00
TRINITY_sp|P368:YPTV3  GTP-binding protein  74.10  0.00
TRINITY_sp|Q9MA:SDC  Serine decarboxylas  74.10  0.00
TRINITY_sp|Q226:RPS16  40S ribosomal prote  74.10  0.00
TRINITY_sp|P818:Ppc1  Phosphoenolpyruvate  74.10  0.00
TRINITY_sp|Q9M0:AUR1  Serine/threonine-pr  74.10  0.00
TRINITY_sp|Q62D:SDH1  Succinate dehydroge  74.10  0.00
TRINITY_sp|Q425:At5g117:NADH dehydrogenase  74.10  0.00
TRINITY_sp|P559:-  Probable cyclin-dep  74.00  0.00
TRINITY_sp|P340:dhcA  Dynein heavy chain,  74.00  0.00
TRINITY_sp|P611:RAB2A  Ras-related protein  74.00  0.00
TRINITY_sp|Q5R5:ATP5A1  ATP synthase subuni  74.00  0.00
TRINITY_sp|O650:SB62  60S ribosomal prote  74.00  0.00
TRINITY_sp|Q6H5:Os09g02:Enoyl-acyl-carrier  74.00  0.00
TRINITY_sp|Q390:CPK11  Calcium-dependent p  74.00  0.00
TRINITY_sp|O818:PUMP1  Mitochondrial uncou  74.00  0.00
TRINITY_sp|Q9SE1:RPT4A  26S protease regula  74.00  0.00
TRINITY_sp|Q54:aco1  Probable cytoplasm  74.00  0.00
TRINITY_sp|Q401:HSF8  Heat shock factor p  74.00  0.00
TRINITY_sp|Q9CP:Cox6c  Cytochrome c oxidas  74.00  0.00
TRINITY_sp|O477:-  Tubulin beta chain  73.90  0.00
TRINITY_sp|Q2451EIF6  Eukaryotic translant  73.90  0.00
TRINITY_sp|Q945:RPS15  40S ribosomal prote  73.90  0.00
TRINITY_sp|Q3T0:RPL30  60S ribosomal prote  73.90  0.00
TRINITY_sp|Q9DE1:ruvb11  RuvB-like 1 OS=Xeno  73.90  0.00
TRINITY_sp|Q940:TMN2  Transmembrane 9 sup  73.90  0.00
TRINITY_sp|Q918:fabp10a  Fatty acid-binding  73.80  0.00
TRINITY_sp|Q86C:tor  Target of rapamycin  73.80  0.00
TRINITY_sp|Q54H:mybQ  Myb-like protein Q  73.80  0.00
TRINITY_sp|Q1W3:-  Phosphomannomutase  73.80  0.00
TRINITY_sp|P1211:ATPC  ATP synthase gamma  73.80  0.00
TRINITY_sp|Q9FM:PI4KB1  Phosphatidylinosito  73.80  0.00
| Accession | Description | Organism | Signal Peptide | Mw/Charge |
|-----------|-------------|----------|----------------|-----------|
| TRINITY_sp| Calmodulin  | OS=Paramecium tetraurelia |  | 73.80 0.00 |
| TRINITY_sp| Cytosolic Fe-S cluster | |  | 73.80 0.00 |
| TRINITY_sp| Pre-mRNA-processing | |  | 73.80 0.00 |
| TRINITY_sp| Uncharacterized protein | |  | 73.70 0.00 |
| TRINITY_sp| Thiamine thiazole synthase | |  | 73.70 0.00 |
| TRINITY_sp| 40S ribosomal protein S5 | |  | 73.70 0.00 |
| TRINITY_sp| Uncharacterized protein | |  | 73.70 0.00 |
| TRINITY_sp| Heat shock protein | |  | 73.70 0.00 |
| TRINITY_sp| Peptidyl-prolyl cis-Thr protein | |  | 73.70 0.00 |
| TRINITY_sp| Threonine--tRNA ligase | |  | 73.70 0.00 |
| TRINITY_sp| Pre-mRNA-splicing factor 8A | |  | 73.70 0.00 |
| TRINITY_sp| Multidrug resistance protein | |  | 73.70 0.00 |
| TRINITY_sp| 40S ribosomal protein S25-2 | |  | 73.70 0.00 |
| TRINITY_sp| UDP-arabinopyranose mutase | |  | 73.70 0.00 |
| TRINITY_sp| Cytosolic Fe-S cluster assembly factor | |  | 73.70 0.00 |
| TRINITY_sp| Small nuclear ribonucleoprotein Sm D2 | |  | 73.70 0.00 |
| TRINITY_sp| Thiamine thiazole synthase | |  | 73.70 0.00 |
| TRINITY_sp| ATP-citrate synthase beta chain | |  | 73.70 0.00 |
| TRINITY_sp| Lipoyl synthase | |  | 73.70 0.00 |
| TRINITY_sp| Ubiquitin-conjugating enzyme E2 | |  | 73.70 0.00 |
| TRINITY_sp| Ras-related protein Rab-14 | |  | 73.70 0.00 |
| TRINITY_sp| 40S ribosomal protein S4 | |  | 73.70 0.00 |
| TRINITY_sp| Cysteine proteinase inhibitor | |  | 73.70 0.00 |
| TRINITY_sp| Protein PROTON GRAD | |  | 73.70 0.00 |
| TRINITY_sp| Alcohol dehydrogenase | |  | 73.70 0.00 |
| TRINITY_sp| ATP synthase subunit | |  | 73.70 0.00 |
| TRINITY_sp| Lipoyl synthase, mitochondrial | |  | 73.70 0.00 |
| TRINITY_sp| 40S ribosomal protein | |  | 73.70 0.00 |
| TRINITY_sp| Pre-mRNA-splicing factor | |  | 73.70 0.00 |
| TRINITY_sp| Multidrug resistance protein | |  | 73.70 0.00 |
| TRINITY_sp| Uncharacterized protein | |  | 73.70 0.00 |
| TRINITY_sp| Protein PROTON GRAD | |  | 73.70 0.00 |
| TRINITY_sp| Alcohol dehydrogenase | |  | 73.70 0.00 |
| TRINITY_sp| ABC transporter F family | |  | 73.70 0.00 |
| TRINITY_sp| Small nuclear ribonucleoprotein | |  | 73.70 0.00 |
| TRINITY_sp| Oxygen-evolving enhancer | |  | 73.70 0.00 |
| TRINITY_sp| Probable mediator of RNA polymerase II transcription | |  | 73.70 0.00 |
| TRINITY_sp| Probable mediator of RNA polymerase II transcription | |  | 73.70 0.00 |
| TRINITY_sp| Protein PROTON GRAD | |  | 73.70 0.00 |
| TRINITY_sp| Ubiquitin-60S ribosomal protein | |  | 73.70 0.00 |
| TRINITY_sp| Mitochondrial import inner membrane translocase subunit | |  | 73.70 0.00 |
| TRINITY_sp| Threonine--tRNA ligase, mitochondrial | |  | 73.70 0.00 |
| TRINITY_sp| 40S ribosomal protein | |  | 73.70 0.00 |
| Gene ID | Description                                                                 | ORG | Score |
|-------|-----------------------------------------------------------------------------|-----|-------|
| TRINITY_sp| P221:ACTA  | Actin-1 OS=Phytopht | 73.10 | 0.00 |
| TRINITY_sp| Q9M0EIF6-2  | Eukaryotic translat | 73.10 | 0.00 |
| TRINITY_sp| Q4AGGPX4  | Phospholipid hydrop | 73.00 | 0.00 |
| TRINITY_sp| Q7ZUcsnrpe  | Small nuclear ribon | 73.00 | 0.00 |
| TRINITY_sp| P544(-  | T-complex protein l | 72.90 | 0.00 |
| TRINITY_sp| P42S4arpC  | Actin-related prote  | 72.90 | 0.00 |
| TRINITY_sp| Q9LXAt3g6231  | Probable pre-mRNA-s | 72.90 | 0.00 |
| TRINITY_sp| Q4JQJNT-D2  | NADH-ubiquinone oxi | 72.90 | 0.00 |
| TRINITY_sp| A2T21FT46  | Intraflagellar tran | 72.80 | 0.00 |
| TRINITY_sp| Q9STCUT  | Deoxyuridine 5'-tri | 72.80 | 0.00 |
| TRINITY_sp| O611savka  | Serine/threonine-pr | 72.80 | 0.00 |
| TRINITY_sp| Q395:YPTC6  | Ras-related protein | 72.80 | 0.00 |
| TRINITY_sp| Q4081MPK1  | Mitogen-activated p | 72.80 | 0.00 |
| TRINITY_sp| Q425:FTS21  | Cell division prote | 72.80 | 0.00 |
| TRINITY_sp| Q5711GFBP4  | Insulin-like growth | 72.70 | 0.00 |
| TRINITY_sp| A8JBECHLREDR  | Pescadillo homolog | 72.70 | 0.00 |
| TRINITY_sp| Q3SZ2RPL32  | 60S ribosomal prote | 72.70 | 0.00 |
| TRINITY_sp| Q9LR:RPL27AB  | 60S ribosomal prote | 72.70 | 0.00 |
| TRINITY_sp| Q8LECHMP1A  | ESCRT-related prote | 72.70 | 0.00 |
| TRINITY_sp| F0C8C3CRP1  | Probable serine/thr | 72.70 | 0.00 |
| TRINITY_sp| Q6F2KPRF8  | Pre-mRNA-processing | 72.70 | 0.00 |
| TRINITY_sp| Q9FLNRPB12  | DNA-directed RNA po | 72.70 | 0.00 |
| TRINITY_sp| Q6WWUPL3  | E3 ubiquitin-protei | 72.70 | 0.00 |
| TRINITY_sp| Q6684rbab4b  | Ras-related protein | 72.70 | 0.00 |
| TRINITY_sp| P479: rps27  | 40S ribosomal prote | 72.70 | 0.00 |
| TRINITY_sp| P390(-  | Dynemin beta chain, | 72.70 | 0.00 |
| TRINITY_sp| Q9BSNAA11  | N-alpha-acetyltrans | 72.70 | 0.00 |
| TRINITY_sp| Q12XKelp3  | Probable elongator | 72.60 | 0.00 |
| TRINITY_sp| Q279:HSRA1A  | Heat shock 70 kDa p | 72.60 | 0.00 |
| TRINITY_sp| Q1KV1nfa  | Translation initiat | 72.60 | 0.00 |
| TRINITY_sp| Q9Y3:LSM2  | U6 snRNA-associated | 72.60 | 0.00 |
| TRINITY_sp| P492:PKC1  | Phosphoenolpyruvate | 72.60 | 0.00 |
| TRINITY_sp| Q9F2IDNAH1  | Dynemin heavy chain | 72.50 | 0.00 |
| TRINITY_sp| Q6F4Rpl39  | 60S ribosomal prote | 72.50 | 0.00 |
| TRINITY_sp| Q6F4Rpl39  | 60S ribosomal prote | 72.50 | 0.00 |
| TRINITY_sp| P420NDUS7  | NADH dehydrogenase | 72.50 | 0.00 |
| TRINITY_sp| P502:ALTA  | Tubulin alpha-1A ch | 72.50 | 0.00 |
| TRINITY_sp| Q2HJ1LSM5  | U6 snRNA-associated | 72.50 | 0.00 |
| TRINITY_sp| Q54KmanG  | Alpha-mannosidase G | 72.50 | 0.00 |
| TRINITY_sp| Q044CTT5  | T-complex protein l | 72.50 | 0.00 |
| TRINITY_sp| Q56YMAPP2B  | Methionine aminopep | 72.50 | 0.00 |
| TRINITY_sp| A55D8sbds  | Ribosome maturation | 72.50 | 0.00 |
| TRINITY_sp| Q949MPC1  | Mitochondrial pyruv | 72.50 | 0.00 |
| TRINITY_sp| Q751Aos05g01  | Isovaleryl-CoA dehy | 72.50 | 0.00 |
| TRINITY_sp| Q271:EIF2A  | Elongation factor l | 72.50 | 0.00 |
| TRINITY_sp| Q8L4ZCDKB1-1  | Cyclin-dependent ki | 72.50 | 0.00 |
| TRINITY_sp| A8JFNC56  | Cytoplasmic tRNA 2- | 72.50 | 0.00 |
| TRINITY_sp| Q9Z5CCHLPL  | Geranylgeranyl diph | 72.50 | 0.00 |
| TRINITY_sp| Q419:PSBQ2  | Oxygen-evolving enh | 72.40 | 0.00 |
| TRINITY_sp| Q9M0E1IF6-2  | Eukaryotic translat | 72.40 | 0.00 |
| TRINITY_sp| P4191-  | GTP-binding nuclear | 72.40 | 0.00 |
| TRINITY_sp| Q8LAMATA1  | GATA transcription | 72.40 | 0.00 |
| TRINITY_sp| Q7X91FIE1  | Protein PHOTOPERIOD | 72.40 | 0.00 |
| TRINITY_sp| P544(-  | T-complex protein l | 72.40 | 0.00 |
| TRINITY_sp| Q823:THIC  | Phosphomethylpyrimi | 72.40 | 0.00 |
| TRINITY_sp| Q9SIIAt2g299  | Presenilin-like pro | 72.40 | 0.00 |
Actin-related protein 2 OS=Acanthamoeba castellanii GN=arp2 PE=2 SV=1

Serine/threonine-pr OS=Rattus norvegicus GN=arp2 PE=2 SV=1

Ribose-phosphate py OS=Dictyostelium discoideum GN=rnrA PE=3 SV=1

Enolase OS=Arabidopsis thaliana GN=enol-1 PE=1 SV=3

Dynein heavy chain OS=Caenorhabditis elegans GN=enol-1 PE=1 SV=3

Formate--tetrahydro OS=Arabidopsis thaliana GN=ARP2 PE=2 SV=1

Enolase OS=Caenorhabditis elegans GN=enol-1 PE=2 SV=2

Ribonucleoside-diphosphate reductase large subunit OS=Arabidopsis thaliana GN=RPN11 PE=1 SV=1

Ras protein let-60 OS=Caenorhabditis elegans GN=let-60 PE=1 SV=1

Ribose-phosphate pyrophosphokinase 2, chloroplastic OS=Spinacia oleracea GN=PRS2 PE=2 SV=1

Ribonucleoside-diphosphate reductase large subunit OS=Arabidopsis thaliana GN=RNR1 PE=1 SV=1

Vacuolar cation/proton exchanger 1 OS=Arabidopsis thaliana GN=CAX1 PE=1 SV=3

40S ribosomal protein S30-A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rps3001 PE=3 SV=1

Glutaryl-CoA dehydrogenase, mitochondrial OS=Dictyostelium discoideum GN=gcdh PE=3 SV=1

SNF1-related protein kinase catalytic subunit alpha KIN10 OS=Arabidopsis thaliana GN=KIN10 PE=1 SV=2

Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Bos taurus GN=PPP2CA PE=1 SV=1

Sperm-associated antigen 6 OS=Mus musculus GN=Spag6 PE=1 SV=1

Ras-related C3 botulinum toxin substrate 1 OS=Bos taurus GN=RAC1 PE=1 SV=1

Cation-transporting ATPase CA1 OS=Dunaliella bioculata GN=CA1 PE=2 SV=1

Ferritin-1, chloroplastic OS=Zea mays GN=FER1 PE=1 SV=2

14-3-3-like protein GF14 upsilon OS=Arabidopsis thaliana GN=GRF5 PE=1 SV=2

Ras-related protein RABB1c OS=Arabidopsis thaliana GN=RABB1C PE=1 SV=1

Dynein heavy chain 1, axonemal OS=Homo sapiens GN=DNAH1 PE=2 SV=4

Major actin OS=Dictyostelium discoideum GN=act1 PE=1 SV=2

Myosin ID heavy chain OS=Dictyostelium discoideum GN=myoD PE=1 SV=2

26S protease regulatory subunit 6B homolog OS=Arabidopsis thaliana GN=RPT3 PE=1 SV=1

Ribonucleoside-diphosphate reductase large subunit OS=Arabidopsis thaliana GN=RNR1 PE=1 SV=1

Vacuolar protein-sorting-associated protein 11 homolog OS=Arabidopsis thaliana GN=VPS11 PE=1 SV=1

Envelope glycoprotein OS=Rauscher mink cell focus-inducing virus GN=env PE=3 SV=1
| Accession | Description                                                                 | Start | End  |
|-----------|------------------------------------------------------------------------------|-------|------|
| TRINITY_sp| Heat shock protein HSP81-3                                                   | 71.20 | 0.00 |
| TRINITY_sp| 50S ribosomal proteasome                                                    | 71.20 | 0.00 |
| TRINITY_sp| GTP-binding protein                                                         | 71.20 | 0.00 |
| TRINITY_sp| 40S ribosomal proteasome                                                    | 71.20 | 0.00 |
| TRINITY_sp| Cyclin-dependent kinase                                                     | 71.20 | 0.00 |
| TRINITY_sp| Acidic endochitinase                                                        | 71.10 | 0.00 |
| TRINITY_sp| Ubiquitin-conjugating enzyme                                                 | 71.10 | 0.00 |
| TRINITY_sp| Uncharacterized protein                                                      | 71.10 | 0.00 |
| TRINITY_sp| ABC transporter Ff                                                           | 71.10 | 0.00 |
| TRINITY_sp| Diaminopimelate epimerase                                                   | 71.10 | 0.00 |
| TRINITY_sp| FACT complex subunit                                                        | 71.10 | 0.00 |
| TRINITY_sp| Pyruvate, phosphate                                                         | 71.10 | 0.00 |
| TRINITY_sp| Malate dehydrogenase                                                        | 71.10 | 0.00 |
| TRINITY_sp| RING-box protein 1                                                           | 71.10 | 0.00 |
| TRINITY_sp| Ras-like protein                                                             | 71.10 | 0.00 |
| TRINITY_sp| Photosystem I subunit                                                        | 71.10 | 0.00 |
| TRINITY_sp| T-complex protein 1                                                          | 71.10 | 0.00 |
| TRINITY_sp| Pyrroline, phosphate                                                         | 71.10 | 0.00 |
| TRINITY_sp| Quercetin 2,3-dioxy                                                           | 71.00 | 0.00 |
| TRINITY_sp| 26S protease regulus                                                         | 71.00 | 0.00 |
| TRINITY_sp| 60S ribosomal proteasome                                                    | 71.00 | 0.00 |
| TRINITY_sp| S-adenosylmethionin                                                         | 71.00 | 0.00 |
| TRINITY_sp| Glutaryl-CoA dehydrogenase                                                  | 71.00 | 0.00 |
| TRINITY_sp| 40S ribosomal proteasome                                                    | 71.00 | 0.00 |
| TRINITY_sp| Cyclin-dependent kinase                                                     | 71.00 | 0.00 |
| TRINITY_sp| Cytoplasmic tRNA 2                                                          | 71.00 | 0.00 |
| TRINITY_sp| 2-amino-3-ketobutyryl                                                       | 71.00 | 0.00 |
| TRINITY_sp| Ribonucleoside-diph                                                        | 71.00 | 0.00 |
| TRINITY_sp| GATA transcription                                                          | 71.00 | 0.00 |
| TRINITY_sp| Heat shock 70 kDa p                                                          | 71.00 | 0.00 |
| TRINITY_sp| Chaperonin CPN60-2                                                           | 71.00 | 0.00 |
| TRINITY_sp| Actin OS=Cyanidioscormus                                                     | 71.00 | 0.00 |
| TRINITY_sp| H/ACA ribonucleoprotein                                                     | 71.00 | 0.00 |
| TRINITY_sp| Eukaryotic translation                                                      | 71.00 | 0.00 |
| TRINITY_sp| DNA topoisomerase 6                                                          | 71.00 | 0.00 |
| TRINITY_sp| Mediator of RNA pol                                                          | 70.90 | 0.00 |
| TRINITY_sp| NifU-like protein 2                                                          | 70.90 | 0.00 |
| TRINITY_sp| 60S ribosomal proteasome                                                    | 70.90 | 0.00 |
| TRINITY_sp| Ornithine aminotransfere                                                     | 70.90 | 0.00 |
| TRINITY_sp| Dynein heavy chain                                                          | 70.90 | 0.00 |
| TRINITY_sp| Ribose-phosphate pyrolysin                                                  | 70.90 | 0.00 |
| TRINITY_sp| Serine/threonine-pr                                                          | 70.90 | 0.00 |
| TRINITY_sp| ATP-dependent 6-phosphorine                                                  | 70.90 | 0.00 |
| TRINITY_sp| 3-methyl-2-oxobutano                                                        | 70.90 | 0.00 |
| TRINITY_sp| Pre-mRNA-splicing factor                                                    | 70.90 | 0.00 |
| TRINITY_sp| 3-oxoacyl-[acyl-carbonyl]                                                   | 70.90 | 0.00 |
| TRINITY_sp| Magnesium-protoporposine                                                    | 70.90 | 0.00 |
| TRINITY_sp| Serine/threonine-pr                                                          | 70.90 | 0.00 |
| TRINITY_sp| Glycogen synthase k                                                         | 70.80 | 0.00 |
| TRINITY_sp| tRNA uridine 5-carb                                                         | 70.80 | 0.00 |
TRINITY_sp|P797t|c9  Complement component C9 70.80 0.00
TRINITY_sp|P905t|- Tubulin gamma-2 cha 70.80 0.00
TRINITY_sp|Q5QM|Os01g01|DEAD-box ATP-depend 70.80 0.00
TRINITY_sp|Q8JFI|FK506A2  Eukaryotic initiat 70.80 0.00
TRINITY_sp|Q3E8J|YL154C- Uncharacterized pro 70.80 0.00
TRINITY_sp|P344| mog-1  Probable pre-mRNA-s 70.80 0.00
TRINITY_sp|P483|FK506-b 12 kDa FK506-bindin 70.80 0.00
TRINITY_sp|P436|drg1  Developmentally-reg 70.80 0.00
TRINITY_sp|Q755t|SF3B1  Splicing factor 3B 70.80 0.00
TRINITY_sp|Q9M3|NP8.F  Protein NRT1/ PTR F 70.70 0.00
TRINITY_sp|P546|piKA  Phosphatidylinosito 70.70 0.00
TRINITY_sp|P496|RPL19C  60S ribosomal prote 70.70 0.00
TRINITY_sp|Q9S1|WRKY1  WRKY transcription 70.70 0.00
TRINITY_sp|Q388|CHLG  Chlorophyll synthas 70.70 0.00
TRINITY_sp|O426|smad1  Small nuclear ribon 70.70 0.00
TRINITY_sp|Q416|CDC2  Cell division contr 70.70 0.00
TRINITY_sp|Q2R|GME-2  GDP-mannose 3,5-epi 70.70 0.00
TRINITY_sp|Q9FN|MRRB1  PsbB mRNA maturatio 70.70 0.00
TRINITY_sp|Q54K|rbxl1  RING-box protein 1 70.70 0.00
TRINITY_sp|P427|PAB2  Polyadenylate-bindi 70.70 0.00
TRINITY_sp|Q9SM|DHC1  Dynein-1-alpha heav 70.70 0.00
TRINITY_sp|Q3Ba| Uncharacterized pro 70.70 0.00
TRINITY_sp|P168| Histone H2A-III OS= 70.70 0.00
TRINITY_sp|P222|fb1  rRNA 2'-O-methyltra 70.60 0.00
TRINITY_sp|P524|Ubc2  Ubiquitin-conjugati 70.60 0.00
TRINITY_sp|Q54I|acad8  Isobutyryl-CoA dehy 70.60 0.00
TRINITY_sp|Q426|SAMDC  S-adenosylmethionin 70.60 0.00
TRINITY_sp|Q243| Plastidic ATP/ADP-t 70.60 0.00
TRINITY_sp|P736|mutS2  Endonuclease MutS2 70.60 0.00
TRINITY_sp|Q9SA|BCDH  2-oxoisovalerate de 70.60 0.00
TRINITY_sp|Q0E2|UVR3  (6-4)DNA photolyase 70.50 0.00
TRINITY_sp|Q55F|bkdB  2-oxoisovalerate de 70.50 0.00
TRINITY_sp|P491|RAB2A  Ras-related protein 70.50 0.00
TRINITY_sp|O157|vacA  Vacuolin-A OS=Dicty 70.50 0.00
TRINITY_sp|Q9AR|HD6  Casein kinase II su 70.50 0.00
TRINITY_sp|P800|GGPS1  Geranylgeranyl pyro 70.50 0.00
TRINITY_sp|Q8RY|PEX6  Peroxisome biogenes 70.50 0.00
TRINITY_sp|P804|PSBY  Photosystem II core 70.50 0.00
TRINITY_sp|B041|apls2  AP-1 complex subuni 70.50 0.00
TRINITY_sp|Q428|RBP2  DNA-directed RNA po 70.50 0.00
TRINITY_sp|P0C8|CCRP1  Probable serine/thr 70.50 0.00
TRINITY_sp|Q9HB|ATP6V0A/V-type proton ATPas 70.50 0.00
TRINITY_sp|P341|mvpA  Major vault protein 70.50 0.00
TRINITY_sp|Q9SL|RAD50  DNA repair protein 70.50 0.00
TRINITY_sp|Q84J|B" EPSII Probable serine/thr 70.50 0.00
TRINITY_sp|A4FU|SNRPE  Small nuclear ribon 70.40 0.00
TRINITY_sp|Q9XG|PAA1  Proteasome subunit 70.40 0.00
TRINITY_sp|Q281|pocla  POC1 centriolar pro 70.40 0.00
TRINITY_sp|P207|MAK  Serine/threonine-pr 70.40 0.00
TRINITY_sp|Q922|Dyrk3  Dual specificity ty 70.40 0.00
TRINITY_sp|O225|CLA1  1-deoxy-D-xylulose- 70.40 0.00
TRINITY_sp|Q9C5|MSRB2  Peptide methionine 70.30 0.00
TRINITY_sp|Q182|rap-1  Ras-related protein 70.30 0.00
TRINITY_sp|P331|IDH2  Isocitrate dehydrog 70.30 0.00
TRINITY_sp|Q8HI|ABC110  ABC transporter I f 70.30 0.00
TRINITY_sp|Q7Z|rap1b  Ras-related protein 70.30 0.00
| Accession   | Description                                      | Score | Value |
|-------------|-------------------------------------------------|-------|-------|
| TRINITY_sp| P542| Cation-transporting ATPase CA1 | 70.30 | 0.00  |
| TRINITY_sp| Q529| ATP-dependent zinc | 70.30 | 0.00  |
| TRINITY_sp| Q9T6| Protein yippee-like | 70.30 | 0.00  |
| TRINITY_sp| P06| Plasminogen OS=Bos | 70.20 | 0.00  |
| TRINITY_sp| O228| Probable pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH3 | 69.80 | 0.00  |
| TRINITY_sp| P50| Ribonucleoside-diphosphate cyclohydrolase | 70.20 | 0.00  |
| TRINITY_sp| A2XUC| Cyclin-dependent kinase | 70.20 | 0.00  |
| TRINITY_sp| P427| 60S ribosomal protein | 70.20 | 0.00  |
| TRINITY_sp| P557| Heat shock protein | 70.20 | 0.00  |
| TRINITY_sp| Q8LSN| Phytochrome-association protein | 70.20 | 0.00  |
| TRINITY_sp| Q8RW| Transketolase-1, ch | 70.20 | 0.00  |
| TRINITY_sp| O822| Probable small nucleolar RNA protein | 70.20 | 0.00  |
| TRINITY_sp| P008| Ribulose bisphosphate carboxylase | 70.20 | 0.00  |
| TRINITY_sp| Q676| DNA repair protein | 70.20 | 0.00  |
| TRINITY_sp| Q9Z| ER lumen protein-retaining receptor | 70.20 | 0.00  |
| TRINITY_sp| A8XJ| 60S ribosomal protein | 70.20 | 0.00  |
| TRINITY_sp| P943| Structural maintenance protein | 70.10 | 0.00  |
| TRINITY_sp| P623| U6 snRNA-associated protein | 70.10 | 0.00  |
| TRINITY_sp| P087| Histone H3 OS=Caeno | 70.10 | 0.00  |
| TRINITY_sp| Q9XFL| Chlorophyll a-b bin | 70.10 | 0.00  |
| TRINITY_sp| Q8T2| Cytosolic Fe-S cluster | 70.10 | 0.00  |
| TRINITY_sp| Q148| Chromodomain-helicase | 70.10 | 0.00  |
| TRINITY_sp| O813| Bifunctional dihydrolipoamide acetyltransferase | 70.10 | 0.00  |
| TRINITY_sp| P490| Protein mago nashi | 70.10 | 0.00  |
| TRINITY_sp| Q396| Protochlorophyllide | 70.10 | 0.00  |
| TRINITY_sp| Q9LV| Thylakoid lumenal protein | 70.10 | 0.00  |
| TRINITY_sp| P55C| Vacuolar protein sorting-associated protein | 70.10 | 0.00  |
| TRINITY_sp| Q8LK| NADP-dependent glyceraldehyde-3-phosphate dehydrogenase | 70.10 | 0.00  |
| TRINITY_sp| Q2JS| Uridylyl kinase OS=Caeno | 70.10 | 0.00  |
| TRINITY_sp| P364| Heat shock cognate | 70.10 | 0.00  |
| TRINITY_sp| P479| 40S ribosomal protein | 70.10 | 0.00  |
| TRINITY_sp| P806| Ferredoxin-thioredoxin | 70.00 | 0.00  |
| TRINITY_sp| Q401| Metallothionein-lik | 70.00 | 0.00  |
| TRINITY_sp| Q8VY| Casein kinase 1-lik | 70.00 | 0.00  |
| TRINITY_sp| P348| 10 kDa chaperonin, chaperonin OS=Caeno | 70.00 | 0.00  |
| TRINITY_sp| Q385| Tubulin gamma-2 chain | 70.00 | 0.00  |
| TRINITY_sp| Q9LV| T-complex protein | 70.00 | 0.00  |
| TRINITY_sp| A7MB| Cell differentiation | 70.00 | 0.00  |
| TRINITY_sp| Q9U| Dynein heavy chain | 70.00 | 0.00  |
| TRINITY_sp| Q437| Granule-bound starch | 70.00 | 0.00  |
| TRINITY_sp| Q9QX| Activating signal c | 70.00 | 0.00  |
| TRINITY_sp| Q154| Splicing factor 3B | 69.90 | 0.00  |
| TRINITY_sp| Q9NZ| Ferredoxin-dependent | 69.90 | 0.00  |
| TRINITY_sp| Q93V| GDP-mannose 3,5-epimerase | 69.90 | 0.00  |
| TRINITY_sp| Q8AV| Biotinidase | 69.80 | 0.00  |
| TRINITY_sp| P0CG| Polyubiquitin OS=Taki | 69.80 | 0.00  |
| TRINITY_sp| P518| Pyruvate decarboxylase | 69.80 | 0.00  |
| TRINITY_sp| Q462| Formate acetyltransferase | 69.80 | 0.00  |
| TRINITY_sp| Q392| SKP1-like protein | 69.80 | 0.00  |
| TRINITY_sp| B3QP| 2,3-bisphosphoglycerate | 69.80 | 0.00  |
| TRINITY_sp| A1JH| Homogentisate solanesyltransferase | 69.80 | 0.00  |
| TRINITY_sp| Q9SE| 26S protease regulatory subunit | 69.80 | 0.00  |
| TRINITY_sp| Q8WX| Dynein heavy chain | 69.80 | 0.00  |
| TRINITY_sp| Q9LV| Dihydropyrimidinase d | 69.80 | 0.00  |
| TRINITY_sp| Q8LS| Phytochrome-association protein | 69.80 | 0.00  |
| TRINITY_sp| P296| Cyclin-dependent kinase | 69.80 | 0.00  |
| TRINITY_sp|Q387;PDH2 | Pyruvate dehydrogen | 69.30 | 0.00 |
| TRINITY_sp|Q91L1DHAD | Dihydroxy-acid dehy | 69.30 | 0.00 |
| TRINITY_sp|O039HSP90-4 | Heat shock protein | 69.30 | 0.00 |
| TRINITY_sp|Q080f- | Malate dehydrogenas | 69.30 | 0.00 |
| TRINITY_sp|O352;Nsmaf | Protein FAN OS=Mus | 69.20 | 0.00 |
| TRINITY_sp|Q3B7;CH1D1L | Chromodomain-helica | 69.20 | 0.00 |
| TRINITY_sp|Q018; | Heat shock 70 kDa p | 69.20 | 0.00 |
| TRINITY_sp|Q7XR;RFC4 | Replication factor | 69.20 | 0.00 |
| TRINITY_sp|O444;SmD3 | Small nuclear ribon | 69.20 | 0.00 |
| TRINITY_sp|Q8L94At4g137; | Inosine triphospha | 69.20 | 0.00 |
| TRINITY_sp|O048;NPP5 | Serine/threonine-pr | 69.20 | 0.00 |
| TRINITY_sp|O8241At3g461; | Histidine--tRNA lig | 69.20 | 0.00 |
| TRINITY_sp|L7HUI;ICL1 | Isocitrate lyase OS | 69.20 | 0.00 |
| TRINITY_sp|Q6VNW;Wdfy3 | WD repeat and FYVE | 69.20 | 0.00 |
| TRINITY_sp|Q8RY;DEGP7 | Protease Do-like 7 | 69.20 | 0.00 |
| TRINITY_sp|O860;bdhA | D-beta-hydroxybutyrm | 69.20 | 0.00 |
| TRINITY_sp|O018;acbp-1 | Acyl-CoA-binding pr | 69.20 | 0.00 |
| TRINITY_sp|Q7XZ;SAC9 | Probable phosphoino | 69.20 | 0.00 |
| TRINITY_sp|O422;gnb211 | Guanine nucleotide- | 69.20 | 0.00 |
| TRINITY_sp|Q631;Dnah7 | Dynein heavy chain | 69.20 | 0.00 |
| TRINITY_sp|Q8TD;DNAH3 | Dynein heavy chain | 69.10 | 0.00 |
| TRINITY_sp|Q17QUBE2G2 | Ubiquitin-conjugati | 69.10 | 0.00 |
| TRINITY_sp|Q54K;csyS | Cysteine--tRNA liga | 69.10 | 0.00 |
| TRINITY_sp|P462;RPL38 | 60S ribosomal prote | 69.10 | 0.00 |
| TRINITY_sp|O0241; | Dynein light chain | 69.10 | 0.00 |
| TRINITY_sp|P109; | Actin, macronuclear | 69.10 | 0.00 |
| TRINITY_sp|Q55F;pyd1 | Dihydropyrimidin d | 69.10 | 0.00 |
| TRINITY_sp|Q9SS;RAP2-12 | Ethylene-responsive | 69.10 | 0.00 |
| TRINITY_sp|B8ANICHLH | Magnesium-chelatase | 69.10 | 0.00 |
| TRINITY_sp|Q9D1;Ube2c | Ubiquitin-conjugati | 69.00 | 0.00 |
| TRINITY_sp|O2261;DRM1 | Dormancy-associated | 69.00 | 0.00 |
| TRINITY_sp|Q9SS;PRP8A | Pre-mRNA-processing | 69.00 | 0.00 |
| TRINITY_sp|B9L9;rpmM | 50S ribosomal prote | 69.00 | 0.00 |
| TRINITY_sp|Q8LG;PEX4 | Protein PEROXIN-4 O | 69.00 | 0.00 |
| TRINITY_sp|A8J7;ATPG | ATP synthase subuni | 69.00 | 0.00 |
| TRINITY_sp|Q8HO;At1g0811 | Lactoylglutathione | 69.00 | 0.00 |
| TRINITY_sp|Q4P7;DED1 | ATP-dependent RNA h | 69.00 | 0.00 |
| TRINITY_sp|Q6ZI;YchF1 | Obg-like ATPase 1 O | 69.00 | 0.00 |
| TRINITY_sp|Q3BA; | Uncharacterized pro | 69.00 | 0.00 |
| TRINITY_sp|Q9H2;etfA | Electron transfer f | 69.00 | 0.00 |
| TRINITY_sp|P341HmvpA | Major vault protein | 69.00 | 0.00 |
| TRINITY_sp|Q9L3;ABCB19 | ABC transporter B f | 68.90 | 0.00 |
| TRINITY_sp|Q54K;mobA | MOB kinase activato | 68.90 | 0.00 |
| TRINITY_sp|Q86H;pdhB | Pyruvate dehydrogen | 68.90 | 0.00 |
| TRINITY_sp|Q8T2;mcob | Methylcrotonoyl-CoA | 68.90 | 0.00 |
| TRINITY_sp|Q9CA;ABCI6 | ABC transporter I f | 68.90 | 0.00 |
| TRINITY_sp|P3681YPT2 | GTP-binding protein | 68.90 | 0.00 |
| TRINITY_sp|Q5DM;IFT172 | Intraflagellar tran | 68.90 | 0.00 |
| TRINITY_sp|Q9FN;PEX1 | Peroxisome biogenes | 68.90 | 0.00 |
| TRINITY_sp|P0D1;RPL37 | 60S ribosomal prote | 68.90 | 0.00 |
| TRINITY_sp|Q8WX;DNAH7 | Dynein heavy chain | 68.90 | 0.00 |
| TRINITY_sp|Q0P5;PPIH | Peptidyl-prolyl cis | 68.80 | 0.00 |
| TRINITY_sp|Q401;MTB | Metallothionein-lik | 68.80 | 0.00 |
| TRINITY_sp|P258;chCA | Clathrin heavy chai | 68.80 | 0.00 |
| TRINITY_sp|Q569;selectenbp1 | Selenium-binding pr | 68.80 | 0.00 |
| TRINITY_sp|Q8GX;CFIS2 | Pre-mRNA cleavage f | 68.80 | 0.00 |
| Accession   | Description                          | Score | Probability |
|-------------|--------------------------------------|-------|-------------|
| sp|Q8W4HML1|Protein MEI2-like 1|68.80|0.00|
| sp|Q54IDDB_U02|Probable serine/thr|68.80|0.00|
| sp|Q2299THERM_1|POC1 centriolar pro|68.80|0.00|
| sp|Q9F1DEGP9|Protease Do-like 9|68.80|0.00|
| sp|F4KD_NRPC2|DNA-directed RNA po|68.80|0.00|
| sp|Q9UWpph-3|Serine/threonine-pr|68.80|0.00|
| sp|Q036BIP4|Luminal-binding pro|68.80|0.00|
| sp|Q495_NIFS1|Cysteine desulfurases|68.80|0.00|
| sp|P2222_Pyruvate kinase, cy|68.80|0.00|
| sp|P5201cyn-7|Peptidyl-prolyl cis|68.80|0.00|
| sp|P6144rpl36a|60S ribosomal prote|68.80|0.00|
| sp|A2Q8ncs6|Cytoplasmic tRNA 2-|68.80|0.00|
| sp|Q9C0CDNAH6|Dynnein heavy chain|68.80|0.00|
| sp|Q8S8TET8|Tetraspanin-8 OS=Ar|68.80|0.00|
| sp|A2XCIK51|Cyclin-dependent ki|68.70|0.00|
| sp|Q9KLKATATA|Sec-independent pro|68.70|0.00|
| sp|Q5NAMDH|Histidinol dehydrog|68.70|0.00|
| sp|Q9CA_A1g777|Ubiquitin-fold modi|68.60|0.00|
| sp|P36991|Protein AMBP (Fragm|68.60|0.00|
| sp|P1712_P|Actin, non-muscl|68.60|0.00|
| sp|P816(-)|Alcohol dehydrogena|68.60|0.00|
| sp|P8697TEF1|Elongation factor 1|68.60|0.00|
| sp|Q4312_P|Proliferating cell|68.60|0.00|
| sp|A2YP1CARM1|Probable histone-ar|68.60|0.00|
| sp|Q8RY1PEX6|Peroxisome biogenes|68.60|0.00|
| sp|O045FAD4L1|Fatty acid desatura|68.60|0.00|
| sp|Q550TskA|Transcription facto|68.60|0.00|
| sp|O2466AS|Asparagine synthet|68.60|0.00|
| sp|Q274his-41|Probable histone H2|68.60|0.00|
| sp|Q86Auuroc1|Probable urocanate|68.60|0.00|
| sp|B1K<lepA|Elongation factor 4|68.60|0.00|
| sp|F4K2CUV|Pre-mRNA-splicing f|68.50|0.00|
| sp|Q102rcp2|DNA-directed RNA po|68.50|0.00|
| sp|Q9MOUGT80A2|Sterol 3-beta-gluco|68.50|0.00|
| sp|P114PSBP|Oxygen-evolving enh|68.50|0.00|
| sp|P929AATP2|ADP,ATP carrier pro|68.50|0.00|
| sp|Q9DGhtpt1|Translationally-con|68.50|0.00|
| sp|Q76NhavP|V-type proton ATPas|68.50|0.00|
| sp|Q7S7cpr2|Peptidyl-prolyl cis|68.50|0.00|
| sp|A4QNMip7|60S ribosome subuni|68.50|0.00|
| sp|P0D2RPL37|60S ribosomal prote|68.50|0.00|
| sp|P0C2ACX3|Acyl-coenzyme A oxi|68.40|0.00|
| sp|E29O2Acidic endo|68.40|0.00|
| sp|Q91rlrpl1b01|60S ribosomal prote|68.40|0.00|
| sp|P1300acPA|F-actin-capping pro|68.40|0.00|
| sp|Q044IDH2|Isocitrade dehydrog|68.40|0.00|
| sp|P540Td2h2|Isocitrade dehydrog|68.40|0.00|
| sp|P870spg1|Septum-promoting GT|68.40|0.00|
| sp|Q395YPTC4|GTP-binding protein|68.40|0.00|
| sp|F4HXXNUP155|Nuclear pore comple|68.40|0.00|
| sp|Q084CCKA2|Casein kinase II su|68.40|0.00|
| sp|Q7SDawrgt-1|tRNA(His) guanylyl|68.40|0.00|
| sp|Q395ODA9|Dynein, 78 kDa inte|68.40|0.00|
| sp|P3499gap3|Glyceraldehyde-3-ph|68.40|0.00|
| sp|Q044IDH2|Isocitrade dehydrog|68.30|0.00|
TRINITY_sp|Q9SUU4at4g3022: Probable small nucl cell 67.90 0.00
TRINITY_sp|Q418:RPS21 4OS ribosomal protein 67.90 0.00
TRINITY_sp|Q54Ktpncod RNA-binding protein 67.90 0.00
TRINITY_sp|Q9LPCYP18-1 Peptidyl-prolyl cis-trans isomerase 67.90 0.00
TRINITY_sp|P737:s1r1251 Peptidyl-prolyl cis-trans isomerase 67.90 0.00
TRINITY_sp|Q9VCIime4 Probable N6-adenosine-methyltransferase 67.90 0.00
TRINITY_sp|Q9LJjdvpe Vacuolar-processing peptidase 67.90 0.00
TRINITY_sp|A9LNCPSF30 30-kDa cleavage and polyadenylation specificity factor 67.90 0.00
TRINITY_sp|Q8CDIAgbp12 Cytosolic carboxypeptidase 67.90 0.00
TRINITY_sp|Q9LFBOALA4 Protein BOLA4, chloplast 67.90 0.00
TRINITY_sp|Q9M2IRH52 DEAD-box ATP-dependant helicase 67.90 0.00
TRINITY_sp|Q8Y1LmsrA Peptide methionine sulfoxidase 67.90 0.00
TRINITY_sp|Q9CRU9Cfs1 Ubiquitin-fold modifier conjugating enzyme 67.80 0.00
TRINITY_sp|P136:ATP1A3 Sodium/potassium-translocating ATPase 67.80 0.00
TRINITY_sp|Q939:pyrABC Protein pyrABC OS=Arabidopsis thaliana 67.80 0.00
TRINITY_sp|Q8HXISOD2 Superoxide dismutase 67.80 0.00
TRINITY_sp|Q151:HEETN3 Centrin-3 OS=Homo sapiens 67.80 0.00
TRINITY_sp|Q8LE1AAP19-1 AP-1 complex subunit 67.80 0.00
TRINITY_sp|Q9C8IAtig523 Coatamer subunit beta 67.80 0.00
TRINITY_sp|Q1W3:jcdk1 Cyclin-dependent kinase 67.70 0.00
TRINITY_sp|P487:CDK1 Cyclin-dependent kinase 67.70 0.00
TRINITY_sp|Q970:PCA Phosphoenolpyruvate carboxykinase 67.70 0.00
TRINITY_sp|B9DGLC8 Acetyl-CoA carboxylase 67.70 0.00
TRINITY_sp|Q395:clpB1 ClpB chaperone 67.70 0.00
TRINITY_sp|Q425:SCE1 SUMO-conjugating enzyme 67.70 0.00
TRINITY_sp|Q559:ppsa Phosphoenolpyruvate carboxykinase 67.70 0.00
TRINITY_sp|P341:psma7 Proteasome subunit 67.70 0.00
TRINITY_sp|P008:RBCS-1 Ribulose bisphosphate carboxylase 67.70 0.00
TRINITY_sp|P341:mvpa Major vault protein 67.70 0.00
TRINITY_sp|P479:zfsl Zinc finger protein 67.70 0.00
TRINITY_sp|P479:zfsl Zinc finger protein 67.70 0.00
TRINITY_sp|P462:ASP5 Aspartate aminotransferase 67.70 0.00
TRINITY_sp|P614:rp136a 60S ribosomal proteins 67.70 0.00
TRINITY_sp|Q5YGGLEY DNA gyrase subunit 67.70 0.00
TRINITY_sp|Q8W44:XPQ DNA repair helicase 67.70 0.00
TRINITY_sp|Q2W2htuf1 Elongation factor T 67.70 0.00
TRINITY_sp|Q631:Dnah7 Dynein heavy chain 67.70 0.00
TRINITY_sp|Q0P5:CKS1B Cyclin-dependent kinase 67.60 0.00
TRINITY_sp|Q598:RPL14 Ribosomal proteins 67.60 0.00
TRINITY_sp|P491:PSAN Photosystem I reaction center subunit 67.60 0.00
TRINITY_sp|Q963:ARP1 ADP-ribosylation factor 67.60 0.00
TRINITY_sp|Q9BYIACRT3 Actin-related protein 67.60 0.00
TRINITY_sp|Q425:Atig7901 NADH dehydrogenase 67.60 0.00
TRINITY_sp|Q6F2:STT3A Dolichyl-diphosphooligosaccharide protein 67.60 0.00
TRINITY_sp|Q101:Os03g05 DEAD-box ATP-dependant helicase 67.60 0.00
TRINITY_sp|Q9U99pppp6c Serine/threonine-protein kinase 67.60 0.00
TRINITY_sp|Q9XFRPPL4 Ribosomal proteins 67.60 0.00
TRINITY_sp|Q9Z41ifcA Fumarate reductase 67.60 0.00
TRINITY_sp|P427:UBC4 Ubiquitin-conjugating enzyme 67.60 0.00
TRINITY_sp|Q8D3cclpB1 Chaperone protein C 67.60 0.00
TRINITY_sp|Q032:MYBL2 Myb-related protein 67.60 0.00
TRINITY_sp|A5UWnf1 Endonuclease V OS=Arabidopsis thaliana 67.60 0.00
TRINITY_sp|O650:PPBC1 Proteasome subunit 67.60 0.00
TRINITY_sp|P542:PPMA1 Plasma membrane ATPase 67.60 0.00
TRINITY_sp|Q9SO11hcAP-A Chlorophyll a-b binding protein 67.60 0.00
| Protein Name                          | Gene Name   | Species            | Function                                      | Expression Level |
|--------------------------------------|-------------|--------------------|-----------------------------------------------|------------------|
| Chromosome transmission fidelity     | ctf18       | Xenopus laevis     | DNA polymerase kapp                           | 67.50 ± 0.00     |
| DNA polymerase                        | Polk        | Arabidopsis thaliana | D-hydantoinase/dihy  | 67.50 ± 0.00     |
| DNA-directed RNA po                   | ftsh2       | Drosophila melanogaster | RNA polymerase II subunit | 67.50 ± 0.00     |
| ATP-dependent Clp p                   | rpc1        | Arabidopsis thaliana | Mitochondrial porphobilinogen dea               | 67.50 ± 0.00     |
| Ras-related GTP-bin                   | RRAGD       | Arabidopsis thaliana | Ras-related GTP-bin | 67.50 ± 0.00     |
| Probable ATP-dependent               | ddx17       | Dictyostelium discoideum | ATP-dependent helicase | 67.50 ± 0.00     |
| Dynein heavy chain                    | prof1-1B    | Arabidopsis thaliana | Dynein heavy chain | 67.50 ± 0.00     |
| UDP-sulfoquinovose                    | udpA        | Arabidopsis thaliana | UDP-sulfoquinovose | 67.50 ± 0.00     |
| Protein transport                     | sec61       | Drosophila melanogaster | Protein transport | 67.50 ± 0.00     |
| Fructose-bisphosphate aldolase       | fba4        | Arabidopsis thaliana | Fructose-bisphosphate aldolase | 67.50 ± 0.00     |
| Ubiquinol oxidase 4                   | aox4        | Arabidopsis thaliana | Ubiquinol oxidase 4 | 67.50 ± 0.00     |
| Dynein heavy chain                    | prof1-1B    | Arabidopsis thaliana | Dynein heavy chain | 67.50 ± 0.00     |
| UDP-glucose 6-dehyd                     | ugd1        | Arabidopsis thaliana | UDP-glucose 6-dehyd | 67.50 ± 0.00     |
| Ubiquinol oxidase 4                   | aox4        | Arabidopsis thaliana | Ubiquinol oxidase 4 | 67.50 ± 0.00     |
| Calmodulin                           | calmodulin  | Triticum aestivum  | Calmodulin                                     | 67.50 ± 0.00     |
| 40S ribosomal protein                 | rps16c      | Arabidopsis thaliana | 40S ribosomal protein | 67.40 ± 0.00     |
| DNA-directed RNA polymerase II subunit| nrbp1       | Arabidopsis thaliana | DNA-directed RNA polymerase II subunit | 67.40 ± 0.00     |
| ATP-dependent zinc                    | p340         | Arabidopsis thaliana | ATP-dependent zinc | 67.30 ± 0.00     |
| Acetyl-coenzyme A c                   | accD         | Arabidopsis thaliana | Acetyl-coenzyme A c | 67.30 ± 0.00     |
| 60S ribosomal prote                   | rpl30       | Arabidopsis thaliana | 60S ribosomal prote | 67.30 ± 0.00     |
| Splicing factor 3B                    | splicing2   | Arabidopsis thaliana | Splicing factor 3B | 67.20 ± 0.00     |
| Regulator of telome                   | rtel1       | Arabidopsis thaliana | Regulator of telome | 67.20 ± 0.00     |
| Gene ID | Description | Domain | E-value | Identity |
|--------|-------------|--------|---------|----------|
| TRINITY_sp|Q3BA1| Uncharacterized protein | ORF91 | Phalaenopsis aphrodite subsp. formosana | 0.00 |
| TRINITY_sp|Q8GY9RH10| DEAD-box ATP-dependent | DExH | 0.00 |
| TRINITY_sp|0485CAT4| Catalase-4 | OS=Glyci | 67.20 |
| TRINITY_sp|Q9SMHDHC1B| Cytoplasmic dynein | 67.20 |
| TRINITY_sp|Q2Q51UGD4| UDP-glucose 6-dehydrogenase | 67.20 |
| TRINITY_sp|Q9D01Rfc5| Replication factor | 67.10 |
| TRINITY_sp|P225| Polyubiquitin | OS=Ph | 67.10 |
| TRINITY_sp|P2750Act79B| Chlorophyll a-b binding | Actin, larval muscle | 67.10 |
| TRINITY_sp|Q425SCE1| SUMO-conjugating enzyme | 67.10 |
| TRINITY_sp|P534CN| Caltractin | OS=Naegleri | 67.10 |
| TRINITY_sp|P485PPX2| Serine/threonine-protein kinase | 67.10 |
| TRINITY_sp|Q9P27IFT80| Intraflagellar transport protein | 67.10 |
| TRINITY_sp|P1395-| G2/mitotic-specific | 67.10 |
| TRINITY_sp|Q9Y3ISF3B6| Splicing factor 3B | 67.00 |
| TRINITY_sp|Q2HH6GAR1| H/ACA ribonucleoprotein | 67.00 |
| TRINITY_sp|Q9LHFYYPP3| Phytochrome-associated | 67.00 |
| TRINITY_sp|Q55FrbdB| 2-oxoisovalerate dehydratase | 67.00 |
| TRINITY_sp|P0899Ymel11| ATP-dependent zinc metalloprotease | 67.00 |
| TRINITY_sp|P0410TK1| Thymidine kinase | 66.90 |
| TRINITY_sp|Q3SHEIcl1e| Caltractin ICl1 cytoplasmic | 66.90 |
| TRINITY_sp|Q433VAP| V-type proton ATPase | 66.90 |
| TRINITY_sp|Q9FN6BRR2C| DEAH-box ATP-dependent helicase | DEXH | 66.90 |
| TRINITY_sp|Q8NK1rpl3| 6OS ribosomal protein | 66.90 |
| TRINITY_sp|Q9U71-| Histone H3 | Os=Masti | 66.90 |
| TRINITY_sp|Q10G6MSI1| Histone-binding protein | 66.90 |
| TRINITY_sp|P546vatA| V-type proton ATPase | 66.90 |
| TRINITY_sp|P519UBE2E1| Ubiquitin-conjugating enzyme | 66.90 |
| TRINITY_sp|Q8VZGPY1P32| Syntaxin-132 | 66.90 |
| TRINITY_sp|Q488RPN2A| 26S proteasome non-ATPase | 66.90 |
| TRINITY_sp|Q558uprt| Uracil phosphoribosyltransferase | 66.80 |
| TRINITY_sp|Q54Qdmt1| Probable dimethyladenylation | 66.80 |
| TRINITY_sp|Q8S33ALB3| Inner membrane protein | 66.80 |
| TRINITY_sp|P937-| Acid beta-fructofuranosidase | 66.80 |
| TRINITY_sp|Q8RKXOVA4| Tryptophan--tRNA ligase | 66.80 |
| TRINITY_sp|Q54Gns2a| Ribosome biogenesis | 66.80 |
| TRINITY_sp|Q9CAXCL2| Casein kinase 1-like | 66.70 |
| TRINITY_sp|Q861hnat9| N-acetyltransferase | 66.70 |
| TRINITY_sp|A8ISNARL3| ADP-ribosylation factor | 66.70 |
| TRINITY_sp|Q54carbon| CLPTM1-like membrane | 66.70 |
| TRINITY_sp|Q962-| Protein BUD31 homolog | 66.70 |
| TRINITY_sp|P4277UBC5| Ubiquitin-conjugating enzyme | 66.70 |
| TRINITY_sp|P5466fimA| Fimbrin | 66.70 |
| TRINITY_sp|Q54Hiap2s1| AP-2 complex subunit | 66.70 |
| TRINITY_sp|Q6UXC16orf8| UPF0764 protein | C16 | 66.70 |
| TRINITY_sp|Q9NQ1KIF13B| Kinesin-like protein | 66.70 |
| TRINITY_sp|Q54Yetf| Electron transfer factor | 66.70 |
| TRINITY_sp|Q9BMderf1| Eukaryotic peptide | 66.70 |
| TRINITY_sp|Q56J0RPS26| 40S ribosomal protein | 66.70 |
| TRINITY_sp|Q8HX2MUT| Methylmalonyl-CoA mutase | 66.70 |
| TRINITY_sp|Q8BJClChdh| Choline dehydrogenase | 66.70 |
| TRINITY_sp|Q416FKBP15| FK506-binding protein | 66.70 |
| TRINITY_sp|Q9M2VPGPS2| CDP-diacylglycerol-phosphatidylinositol transferase | 66.70 |
| TRINITY_sp|Q8RUINLP3| Omega-amidase, chloroplast | 66.70 |
| Accession | Gene Name                      | Protein Name                        | E Value | 66.70 | 0.00 |
|-----------|--------------------------------|-------------------------------------|---------|-------|------|
| TRINITY_sp| O0384-| MT-CO2  | Cytochrome c oxidase         | 0.00   | 66.70|
| TRINITY_sp| Q9LFW| VAMP713 | Vesicle-associated           | 0.00   | 66.70|
| TRINITY_sp| Q9V13| Sm2D2   | Probable small nucl          | 0.00   | 66.70|
| TRINITY_sp| O0841| AMPD    | AMP deaminase OS=Ar          | 0.00   | 66.70|
| TRINITY_sp| Q96NC| ZMAT2   | Zinc finger matrin-          | 0.00   | 66.70|
| TRINITY_sp| Q9DAF| Pacrg   | Parkin coregulated          | 0.00   | 66.70|
| TRINITY_sp| Q9K95| aceA    | Isocitrate lyase OS         | 0.00   | 66.70|
| TRINITY_sp| P2941| PGK1    | Phosphoglycerate ki         | 0.00   | 66.70|
| TRINITY_sp| Q71UR| RPS27L  | 40S ribosomal prote          | 0.00   | 66.70|
| TRINITY_sp| Q941I| PM51    | DNA mismatch repair         | 0.00   | 66.70|
| TRINITY_sp| Q54U8| kif3    | Kinesin-related pro         | 0.00   | 66.70|
| TRINITY_sp| Q9I05| purB    | Adenylosuccinate ly         | 0.00   | 66.70|
| TRINITY_sp| Q8471| CDKE1   | Cyclin-dependent ki         | 0.00   | 66.70|
| TRINITY_sp| Q8LPR| At5g145 | Isocitrate dehydrog         | 0.00   | 66.70|
| TRINITY_sp| Q2LR4| rpmA    | 50S ribosomal prote          | 0.00   | 66.70|
| TRINITY_sp| B82R1| proS    | Proline--tRNA ligas         | 0.00   | 66.70|
| TRINITY_sp| A8ID4| CHLRED  | Ribosome biogenesis         | 0.00   | 66.70|
| TRINITY_sp| P0875| mhcA    | Myosin-2 heavy chai         | 0.00   | 66.70|
| TRINITY_sp| Q7RYF| cys-17  | Cysteine synthase l         | 0.00   | 66.60|
| TRINITY_sp| A2YI3| OsI_250 | Glutamine-dependent         | 0.00   | 66.60|
| TRINITY_sp| P3316| IDH2    | Isocitrate dehydrog         | 0.00   | 66.50|
| TRINITY_sp| P5474| RAN1A   | GTP-binding nuclear         | 0.00   | 66.50|
| TRINITY_sp| Q7726| catA    | Catalase-A OS=Dicty         | 0.00   | 66.50|
| TRINITY_sp| Q0434| B'BETA  | Serine/threonine pr         | 0.00   | 66.50|
| TRINITY_sp| Q54W9| ino1    | Inositol-3-phosphat         | 0.00   | 66.50|
| TRINITY_sp| Q015C| Ot07g01 | Probable alanine--t         | 0.00   | 66.50|
| TRINITY_sp| Q3SW1| dnaK    | Chaperone protein D         | 0.00   | 66.40|
| TRINITY_sp| Q86A4| uroc1   | Probable urocanate          | 0.00   | 66.40|
| TRINITY_sp| Q93V8| RPS51   | 30S ribosomal prote         | 0.00   | 66.40|
| TRINITY_sp| Q9SVD| DRG3    | Developmentally-reg         | 0.00   | 66.40|
| TRINITY_sp| Q9VHG| Gie     | ADP-ribosylation fa         | 0.00   | 66.40|
| TRINITY_sp| Q5551| trpC    | Indole-3-glycerol p         | 0.00   | 66.40|
| TRINITY_sp| Q8DJ5| clpB1   | Chaperone protein C         | 0.00   | 66.40|
| TRINITY_sp| Q0811| 811l    | Cysteine synthase,          | 0.00   | 66.40|
| TRINITY_sp| Q9FJ1| ABCA9   | ABC transporter A f          | 0.00   | 66.30|
| TRINITY_sp| Q54W4| abcB4   | ABC transporter B f          | 0.00   | 66.30|
| TRINITY_sp| Q54M4| dhps    | Probable deoxyhypus         | 0.00   | 66.30|
| TRINITY_sp| Q9CA1| CKL2    | Casein kinase 1-lik         | 0.00   | 66.30|
| TRINITY_sp| Q4911| RAB2A   | Ras-related protein         | 0.00   | 66.30|
| TRINITY_sp| Q9K95| aceA    | Isocitrate lyase OS         | 0.00   | 66.30|
| TRINITY_sp| Q6421| Serpind | Heparin cofactor 2           | 0.00   | 66.30|
| TRINITY_sp| P0C81| CCRP1   | Probable serine/thr         | 0.00   | 66.30|
| TRINITY_sp| B9N84| POPTR_0 | Biotin carboxylase          | 0.00   | 66.30|
| TRINITY_sp| A0CXF| FEN1-1 | Flap endonuclease 1         | 0.00   | 66.30|
| TRINITY_sp| Q7T26| csnk1da | Casein kinase I iso         | 0.00   | 66.30|
| TRINITY_sp| Q9DJO| ADA7    | Leucine-rich repeat         | 0.00   | 66.30|
| TRINITY_sp| Q6DH9| prpf38a | Pre-mRNA-splicing f         | 0.00   | 66.30|
| TRINITY_sp| Q55C6| CmekA   | Dual specificity mi         | 0.00   | 66.30|
| TRINITY_sp| O4266| smd1    | Small nuclear ribon         | 0.00   | 66.30|
| TRINITY_sp| Q9FHT| TMN4    | Transmembrane 9 sup         | 0.00   | 66.30|
| TRINITY_sp| P2751| CBR     | Carotene biosynthes         | 0.00   | 66.30|
| TRINITY_sp| A4IHF| ttc30a  | Tetratricopeptide r         | 0.00   | 66.30|
| TRINITY_sp| P0801| Mgst1   | Microsomal glutathi         | 0.00   | 66.20|
| TRINITY_sp| Q3B81| katnal2 | Katanin p60 ATPase-         | 0.00   | 66.20|
| TRINITY_sp| Q8IYF| FANCM   | Fanconi anemia grou         | 0.00   | 66.20|
| TRINITY_sp| Q86I7| pex4    | Ubiquitin-conjugati         | 0.00   | 66.20|
TRINITY_sp|Q6F99|msbA Lipid A export ATP-binding/permease protein MsbA OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) GN=msbA PE=3 SV=1

TRINITY_sp|Q9LS5|ETFB Electron transfer f OS=Dictyostelium discoideum GN=ETFB PE=1 SV=3

TRINITY_sp|Q6P51|hsd12 Hydroxysteroid dehydrogenase OS=Arabidopsis thaliana GN=HS3PE=1 SV=1

TRINITY_sp|G5EG1|let-92 Serine/threonine-protein kinase Let-92 OS=Caenorhabditis elegans GN=LET-92 PE=3 SV=1

TRINITY_sp|Q8LG1|CUL4 Cullin-4 OS=Arabidopsis thaliana GN=CUL4 PE=3 SV=1

TRINITY_sp|Q8KZ2|Nat10 RNA cytidine acetyltransferase OS=Mus musculus GN=NAT10 PE=1 SV=1

TRINITY_sp|Q9SUAA|4g302 Probable small nucleolar protein 4g302 OS=Arabidopsis thaliana GN=4G302 PE=2 SV=1

TRINITY_sp|Q0264|Atg20420 Succinate--CoA ligase OS=Arabidopsis thaliana GN=SUCB_ARATH PE=3 SV=1

TRINITY_sp|P0DJD|RPL18 60S ribosomal protein OS=Arabidopsis thaliana GN=RPL23A PE=1 SV=1

TRINITY_sp|B7K9|miaB tRNA-2-methylthio-N OS=Arabidopsis thaliana GN=MIAB PE=1 SV=1

TRINITY_sp|Q2371|Elongation factor 2 OS=Arabidopsis thaliana GN=E2FOSPE=1 SV=1

TRINITY_sp|B0GI|apls2 AP-1 complex subunit OS=Arabidopsis thaliana GN=AP1S2PE=3 SV=1

TRINITY_sp|Q087|myb Transcriptional activator OS=Arabidopsis thaliana GN=MYB PE=3 SV=1

TRINITY_sp|Q86Cttor Target of rapamycin OS=Arabidopsis thaliana GN=TOR1PE=1 SV=1

TRINITY_sp|P233|WARS Tryptophan--tRNA ligase OS=Arabidopsis thaliana GN=WARS PE=1 SV=1

TRINITY_sp|Q57A|dnaK Chaperone protein D OS=Arabidopsis thaliana GN=DNAK PE=1 SV=1

TRINITY_sp|Q0J0|Os09g05 Pyruvate dehydrogenase OS=Arabidopsis thaliana GN=PDHPE=1 SV=1

TRINITY_sp|A0BD|GSPATT0 Adenylosuccinate synthetase OS=Arabidopsis thaliana GN=GSPATT0 PE=3 SV=1

TRINITY_sp|P818|Ppc1 Phosphoenolpyruvate carboxykinase OS=Arabidopsis thaliana GN=PPCK PE=1 SV=1

TRINITY_sp|Q8LFAABC2|ABC transporter B f OS=Arabidopsis thaliana GN=ABCB2 PE=1 SV=1

TRINITY_sp|Q804|ADK-B Adenylate kinase OS=Arabidopsis thaliana GN=ADK-B PE=1 SV=1

TRINITY_sp|A9NK|mitotic-spindle organelles OS=Arabidopsis thaliana GN=MITOSPE=1 SV=1

TRINITY_sp|Q6J9|ERF086 Ethylene-responsive transcription factor OS=Arabidopsis thaliana GN=ERF086 PE=1 SV=1

TRINITY_sp|Q4CUMTc00.10 Major vault protein OS=Arabidopsis thaliana GN=MVPPE=1 SV=1

TRINITY_sp|Q3961|DA11 Dynein alpha chain OS=Arabidopsis thaliana GN=DNYNPE=1 SV=1

TRINITY_sp|P116|UOX Uricase OS=Oryza sativa subsp. japonica GN=UOX PE=1 SV=1

TRINITY_sp|Q147|NAA30 N-alpha-acetyltransferase OS=Arabidopsis thaliana GN=NTasePE=1 SV=1

TRINITY_sp|Q86K|ube2n Probable ubiquitin-activating enzyme OS=Arabidopsis thaliana GN=UBA2PE=1 SV=1

TRINITY_sp|A7RP|pno1 RNA-binding protein OS=Arabidopsis thaliana GN=PNO1PE=1 SV=1

TRINITY_sp|Q54L|acmsd 2-amino-3-carboxymuconate decarboxylase OS=Arabidopsis thaliana GN=ACMSDPE=1 SV=1

TRINITY_sp|Q090|Slc25a5 ADP/ATP translocase OS=Arabidopsis thaliana GN=SLC25A5PE=1 SV=1

TRINITY_sp|Q54|rfc2 Probable replication factor C subunit OS=Arabidopsis thaliana GN=RFC2PE=1 SV=1

TRINITY_sp|Q54Q|rab32A Ras-related protein OS=Arabidopsis thaliana GN=RAB32APE=1 SV=1

TRINITY_sp|Q3HV|CPA N-carbamoylputrescine amidase OS=Arabidopsis thaliana GN=CPA PE=1 SV=1

TRINITY_sp|Q94AK|STR6 Rhodanese-like OS=Arabidopsis thaliana GN=STR6PE=1 SV=1

TRINITY_sp|P0CO|HIS3 Imidazoleglycerol-3-phosphate dehydratase OS=Arabidopsis thaliana GN=HIS3PE=1 SV=1

TRINITY_sp|Q9CA|NIFU5 NifU-like protein OS=Arabidopsis thaliana GN=NIFU5PE=1 SV=1

TRINITY_sp|Q244|RPL23A 60S ribosomal protein OS=Arabidopsis thaliana GN=RPL23APE=1 SV=1

TRINITY_sp|P087|mhcA Myosin-2 heavy chain OS=Arabidopsis thaliana GN=MYOSIN-2PE=1 SV=1

TRINITY_sp|P056| Serine-threonine-protein phosphatase OS=Arabidopsis thaliana GN=PP2ACPE=1 SV=1

TRINITY_sp|Q932|DAP LL-diaminopimelate OS=Arabidopsis thaliana GN=LLDAPPE=1 SV=1

TRINITY_sp|P340|manA Lysosomal alpha-mannosidase OS=Arabidopsis thaliana GN=MANAPE=1 SV=1

TRINITY_sp|A8GW|iscS Cysteine desulfurase OS=Arabidopsis thaliana GN=CYSDESCPE=1 SV=1

TRINITY_sp|Q8RE|malaS Alanine--tRNA ligase OS=Arabidopsis thaliana GN=MALAPE=1 SV=1

TRINITY_sp|Q23M|tt116 A Probable beta-tubulin OS=Arabidopsis thaliana GN=BTUBPE=1 SV=1

TRINITY_sp|P229|MED37D Probable mediator OS=Arabidopsis thaliana GN=MED37DPE=1 SV=1

TRINITY_sp|Q9XS|Atg1275 Ubiquitin-fold modulator OS=Arabidopsis thaliana GN=UFB1PE=1 SV=1

TRINITY_sp|Q9ZV|HEN2 DEP domain OS=Arabidopsis thaliana GN=DEP1PE=1 SV=1

TRINITY_sp|Q6E71|DDB1 DNA damage-binding OS=Arabidopsis thaliana GN=DDB1PE=1 SV=1

TRINITY_sp|F4J3|CTPA3 Carboxyl-terminal OS=Arabidopsis thaliana GN=CTPA3PE=1 SV=1

TRINITY_sp|Q9LM|MPK8 Mitogen-activated protein kinase OS=Arabidopsis thaliana GN=MPK8PE=1 SV=1

TRINITY_sp|Q9SG|RPS19A 40S ribosomal protein OS=Arabidopsis thaliana GN=RPS19APE=1 SV=1

TRINITY_sp|Q9P6|ppk15 Serine/threonine-protein phosphatase OS=Arabidopsis thaliana GN=PPK15PE=1 SV=1

TRINITY_sp|Q6Z8|Os02g01 L-aspartate oxidase OS=Arabidopsis thaliana GN=LDOPE=1 SV=1

TRINITY_sp|Q9RY|f01E GTP cyclohydrolase OS=Arabidopsis thaliana GN=GYHPE=1 SV=1

TRINITY_sp|Q9P4|B1122 (E3 ubiquitin-protein ligase OS=Arabidopsis thaliana GN=UBAPPE=1 SV=1
| Gene Symbol | Description                                      | Value 1 | Value 2 |
|-------------|--------------------------------------------------|---------|---------|
| ACYP2       | Acylphosphatase-2 O                              | 65.80   | 0.00    |
| RPL34       | 60S ribosomal protein                            | 65.80   | 0.00    |
| RNK1        | Nucleoside diphosphokinase                      | 65.80   | 0.00    |
| RER1A       | Protein RER1A OS=Ar                              | 65.80   | 0.00    |
| PFD20       | Nuclear cap-binding                              | 65.80   | 0.00    |
| eef-2       | Elongation factor 2                              | 65.80   | 0.00    |
| ndk         | Nucleoside diphosphokinase                      | 65.80   | 0.00    |
| PPD2K2      | Pyruvate, phosphate                              | 65.80   | 0.00    |
| PvrK        | UMP-CMP kinase OS=D                              | 65.80   | 0.00    |
| CYP49A      | Peptidyl-prolyl cis                              | 65.80   | 0.00    |
| PP2AA1      | Serine/threonine-pr                              | 65.80   | 0.00    |
| pckG        | Phosphoenolpyruvate                              | 65.80   | 0.00    |
| awd         | Nucleoside diphosphokinase                      | 65.80   | 0.00    |
| RH21        | DEAD-box ATP-depend                              | 65.80   | 0.00    |
| TYN1        | S-adenosyl-L-methio                             | 65.80   | 0.00    |
| PHYPADR     | ATP-dependent (S)-N                              | 65.80   | 0.00    |
| CDC48E      | Ras-related protein                              | 65.70   | 0.00    |
| CDC48E      | Ras-related protein                              | 65.70   | 0.00    |
| QAOX1P1      | 5-oxygenolase OS=A                               | 65.70   | 0.00    |
| arocC       | Chorismate synthase                              | 65.70   | 0.00    |
| Icl1e       | Caltractin ICL1e OS                              | 65.70   | 0.00    |
| erkB        | Extracellular signal                             | 65.70   | 0.00    |
| MPC4        | Mitochondrial pyruv                              | 65.70   | 0.00    |
| ABCCC9      | ABC transporter C f                              | 65.70   | 0.00    |
| Pplp2       | 60S acidic ribosoma                              | 65.70   | 0.00    |
| Dspi        | Ribonucleoside-diphosphokinase                   | 65.70   | 0.00    |
| PDS         | 15-cis-phytoene des                              | 65.70   | 0.00    |
| CBP5        | H/ACA ribonucleoprotein                         | 65.70   | 0.00    |
| RPS3C       | 40S ribosomal prote                              | 65.70   | 0.00    |
| RPL26A      | 60S ribosomal prote                              | 65.70   | 0.00    |
| RER1A       | Protein ORANGE-LIKE                             | 65.70   | 0.00    |
| Os03g05     | Elongation factor G                             | 65.70   | 0.00    |
| RFC2        | Replication factor                               | 65.70   | 0.00    |
| RPS9B       | 40S ribosomal prote                              | 65.60   | 0.00    |
| FK506-binding | 12 kDa FK506-bindin                      | 65.60   | 0.00    |
| po13        | DNA polymerase delta                             | 65.60   | 0.00    |
| RPS2D       | 40S ribosomal prote                              | 65.60   | 0.00    |
| LICDC48E    | Cell division contr                             | 65.60   | 0.00    |
| urml1       | Ubiquitin-related m                              | 65.60   | 0.00    |
| CCRP1       | Probable serine/thr                             | 65.60   | 0.00    |
| PSBR        | Photosystem II 10 k                              | 65.60   | 0.00    |
| PIN4        | Peptidyl-prolyl cis                              | 65.60   | 0.00    |
| Casein kinase I OS=                           | 65.60   | 0.00    |
| IVD         | Isovaleryl-CoA dehy                             | 65.60   | 0.00    |
| FOVA6       | Proline--tRNA ligas                              | 65.60   | 0.00    |
| IyChF       | Ribosome-binding AT                              | 65.50   | 0.00    |
| SUC5        | Sucrose transport p                              | 65.50   | 0.00    |
| SAM1        | S-adenosylmethionin                             | 65.50   | 0.00    |
| INO80       | Putative DNA helica                             | 65.50   | 0.00    |
| UBC5        | Ubiquitin-conjugat                              | 65.50   | 0.00    |
| hbx10       | Homeobox protein 10                              | 65.50   | 0.00    |
| ubc15       | Ubiquitin-conjugat                              | 65.50   | 0.00    |
| clec3a      | C-type lectin domai                             | 65.50   | 0.00    |
| UGD5        | UDP-glucose 6-dehyd                              | 65.50   | 0.00    |
| VNG2        | Chromatin modificat                             | 65.50   | 0.00    |
| FTS1        | Threonine synthase                              | 65.50   | 0.00    |
TRINITY_sp|Q6Z44|PL10B   DEAD-box ATP-dependent   65.50 0.00
TRINITY_sp|Q9SP1|psbW    Photosystem II reac   65.50 0.00
TRINITY_sp|A4PB1RAD54 DNA repair and reco   65.50 0.00
TRINITY_sp|P0DJ3|RPL7    60S ribosomal prote   65.50 0.00
TRINITY_sp|Q397|PPDK Pyruvate, phosphate   65.50 0.00
TRINITY_sp|Q431|LOX1.5 Probable linoleate   65.50 0.00
TRINITY_sp|Q70G0|Os07g06\Ti redoxin reducta   65.50 0.00
TRINITY_sp|A0JMk|katna12 Katanin p60 ATPase-   65.40 0.00
TRINITY_sp|Q6PK1|ias Lipoyl synthase, mi   65.40 0.00
TRINITY_sp|A8JJ|CHLRREDR Molybdopterin synth   65.40 0.00
TRINITY_sp|Q8TG7|TAR1 Protein TAR1 OS=Sac   65.40 0.00
TRINITY_sp|Q9FJH|UPF1 Regulator of nonsen   65.40 0.00
TRINITY_sp|Q246|RPO3 DNA-directed RNA po   65.40 0.00
TRINITY_sp|Q54C1|Kct4 T-complex protein 1   65.40 0.00
TRINITY_sp|Q5B5|cpsf2 Cleavage and polyad   65.40 0.00
TRINITY_sp|B1LUn|nuoC NADH-quinone oxid   65.40 0.00
TRINITY_sp|Q9LQD|RG1 Developmentally-reg   65.40 0.00
TRINITY_sp|Q570|ELF4 Protein ELF4-LIKE 4   65.40 0.00
TRINITY_sp|Q9SWZ|RPL10A 60S ribosomal prote   65.40 0.00
TRINITY_sp|A7RXz|amhdh1 Probable imidazolon   65.40 0.00
TRINITY_sp|Q8S94|At2g33838 Tyrosine--tRNA liga   65.40 0.00
TRINITY_sp|P43S|cpr-4 Cathepsin B-like cy   65.30 0.00
TRINITY_sp|P268|FKBP2 Peptidyl-prolyl cis   65.30 0.00
TRINITY_sp|B9K81|rpmA 50S ribosomal prote   65.30 0.00
TRINITY_sp|Q9M7J|SEP1 Stress enhanced pro   65.30 0.00
TRINITY_sp|Q0VDG|VPSB Vacuolar protein so   65.30 0.00
TRINITY_sp|Q3M6f|lipB Octanoyltransferase   65.30 0.00
TRINITY_sp|Q9UKC|CNOT11 CCR4-NOT transcript   65.30 0.00
TRINITY_sp|P341|myoD Myosin ID heavy cha   65.30 0.00
TRINITY_sp|P268|ALDH2 Aldehyde dehydrogen   65.30 0.00
TRINITY_sp|Q406|KO1 Probable voltage-ga   65.30 0.00
TRINITY_sp|Q087f|myb Transcriptional act   65.30 0.00
TRINITY_sp|P466|ASP1 Aspartate aminotran   65.30 0.00
TRINITY_sp|Q9PHM|MOB1A MOB kinase activato   65.30 0.00
TRINITY_sp|Q8LSF|FYPP Phytochrome-associ   65.30 0.00
TRINITY_sp|P268|ATP9 ATP synthase subuni   65.30 0.00
TRINITY_sp|P268|ATP9 ATP synthase subuni   65.30 0.00
TRINITY_sp|Q9V3K|RPS1 30S ribosomal prote   65.30 0.00
TRINITY_sp|P056| Myosin-2 heavy cha   65.30 0.00
TRINITY_sp|P534|CTN Caltractin OS=Naegi   65.30 0.00
TRINITY_sp|Q051|Rac2 Ras-related C3 botu   65.20 0.00
TRINITY_sp|Q402F|FI51 Probable aldehyde d   65.20 0.00
TRINITY_sp|P519|NEK2 Serine/threonine-pr   65.20 0.00
TRINITY_sp|Q54D|fcbA Eukaryotic translat   65.20 0.00
TRINITY_sp|Q6QN| Casein kinase I OS=   65.20 0.00
TRINITY_sp|B8JHb|A2cp1_1 Maf-like protein A2   65.20 0.00
TRINITY_sp|P478| Eukaryotic translat   65.20 0.00
TRINITY_sp|Q5RKS|sirt2 NAD-dependent prote   65.20 0.00
TRINITY_sp|Q5XK|nfsl Probable cysteine d   65.20 0.00
TRINITY_sp|Q5TC|cct5 T-complex protein 1   65.20 0.00
TRINITY_sp|Q3MH1|RRBP4 Histone-binding pro   65.20 0.00
TRINITY_sp|P091J|ALS Acetolactate syntha   65.20 0.00
TRINITY_sp|Q5Cpg|Glucose-6-phosphate   65.20 0.00
TRINITY_sp|Q039|L1818 Chlorophyll a-b bin   65.20 0.00
TRINITY_sp|O609|cuA Cullin-1 OS=Dictyos   65.20 0.00
TRINITY_sp|Q23F|RPL26 60S ribosomal prote   65.20 0.00
TRINITY_sp|Q23F57|RPL26   60S ribosomal protein L26 65.20 0.00
TRINITY_sp|Q54D1MrkA Probable serine/threonine-protein kinase 65.20 0.00
TRINITY_sp|P4966- Ubiquitin-60S ribosomal protein 65.20 0.00
TRINITY_sp|Q97UL80s2899 Uncharacterized protein 65.10 0.00
TRINITY_sp|Q97Y2U|UBE2D4 Ubiquitin-conjugating enzyme E2D 65.10 0.00
TRINITY_sp|Q54Q7psmB7 Proteasome subunit 65.10 0.00
TRINITY_sp|Q2264CYTb Cytochrome c oxidase subunit 65.10 0.00
TRINITY_sp|P423185MTOR Serine/threonine-protein kinase 65.10 0.00
TRINITY_sp|Q9SXZ|CPLS1 ATP-dependent Clp protease 65.10 0.00
TRINITY_sp|P1465|EchS1 Enoyl-CoA hydratase 65.10 0.00
TRINITY_sp|P3400|PAP1 Proteasome subunit 65.10 0.00
TRINITY_sp|Q8SSN|nat5 N-alpha-acetyltransferase 65.10 0.00
TRINITY_sp|Q55CsdhB Succinate dehydrogenase 65.10 0.00
TRINITY_sp|Q92F|At2g0366 Ubiquinone biosynthesis 65.10 0.00
TRINITY_sp|Q8L73|RPL18AA 60S ribosomal protein L18a 65.10 0.00
TRINITY_sp|P632186PS17 40S ribosomal protein 65.10 0.00
TRINITY_sp|Q939M|Pccbi Propionyl-CoA carboxylase subunit 65.10 0.00
TRINITY_sp|Q88M1PaxB Paxillin-B 65.10 0.00
TRINITY_sp|P5157|AFC1 Serine/threonine-protein kinase 65.10 0.00
TRINITY_sp|Q54T|rio2 Serine/threonine-protein kinase 65.00 0.00
TRINITY_sp|Q9W4f|rg Neurobeachin 65.00 0.00
TRINITY_sp|Q9SN8|At3g4752 Malate dehydrogenase 65.00 0.00
TRINITY_sp|Q8608|bdhA D-beta-hydroxybutyryl CoA dehydratase 65.00 0.00
TRINITY_sp|Q6ZL1V|ETE4 Propionate-CoA carboxylase subunit 65.00 0.00
TRINITY_sp|Q9FN5|CLP2 ATP-dependent Clp protease 65.00 0.00
TRINITY_sp|A4X0|dnaJ Chaperone protein DnaJ 65.00 0.00
TRINITY_sp|Q91H29|FOLD2 Bifunctional protein 65.00 0.00
TRINITY_sp|Q4307|PYRB1 Aspartate carboxypeptidase 65.00 0.00
TRINITY_sp|P3783|KARS Lysine-tRNA synthetase 65.00 0.00
TRINITY_sp|P4600|NOP2 Probable 28S ribosomal protein NOP2 65.00 0.00
TRINITY_sp|P2364|MT-CYB Cytochrome c oxidase subunit 65.00 0.00
TRINITY_sp|Q0313|AAEL0061 Lysosomal aspartic proteinase 65.00 0.00
TRINITY_sp|Q68R|IFT81 Intraflagellar transport protein 65.00 0.00
TRINITY_sp|Q9L12|NIFU4 NifU-like protein 4 64.90 0.00
TRINITY_sp|Q17966|rnn-1 GDP-binding nuclear protein 64.90 0.00
TRINITY_sp|Q8B99|RPL10A 60S ribosomal protein L10a 64.90 0.00
TRINITY_sp|A4S65|OSTLU_41620 Lon protease homolog 64.90 0.00
TRINITY_sp|Q9EH4|UPF1 Regulator of nonsense-mediated decay 64.90 0.00
TRINITY_sp|Q54D0|mdhB Probable malate dehydrogenase 64.90 0.00
TRINITY_sp|C6TB1AKR1 Probable aldo-keto reductase 64.90 0.00
TRINITY_sp|Q8E99|hs1V ATP-dependent protease 64.90 0.00
TRINITY_sp|Q66L1|mak16-a Protein MAK16 homolog 64.90 0.00
TRINITY_sp|Q32P|FCF1 rRNA-processing associate 64.90 0.00
TRINITY_sp|Q9321STT3A Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 64.90 0.00
TRINITY_sp|Q7T31|ccdc25 Coiled-coil domain-containing protein 64.90 0.00
TRINITY_sp|Q97Y3|RBXM2 RNA-binding motif protein 64.90 0.00
TRINITY_sp|Q8RWA|At4g31390 Uncharacterized aarF domain-containing protein kinase 64.90 0.00
TRINITY_sp|Q5F33EFTUD2 116 kDa U5 small nuclear RNA processing 64.90 0.00
TRINITY_sp|Q92Z|CCT1 Proline-rich coiled-coil domain-containing protein 64.90 0.00
TRINITY_sp|Q9SKC|CAF1-7 Probable CCR4-associating factor 64.90 0.00
| Accession     | Description                                                                 | Score | Domain |
|--------------|-----------------------------------------------------------------------------|-------|--------|
| TRINITY_sp|P383\|Os02g01| Protein transport protein | 64.60 | 0.00   |
| TRINITY_sp|Q553\|cs | Citrate synthase, m | 64.50 | 0.00   |
| TRINITY_sp|Q3ZC\|CNOT7 | CCR4-NOT transcript | 64.50 | 0.00   |
| TRINITY_sp|Q94J\|RIDA | Reactive Intermedia | 64.50 | 0.00   |
| TRINITY_sp|Q54E\|shmt2 | Serine hydroxymethyltransferase | 64.50 | 0.00   |
| TRINITY_sp|P234\|TRXM | Thioredoxin M-type | 64.50 | 0.00   |
| TRINITY_sp|P545\|yqjY | Uncharacterized protein | 64.50 | 0.00   |
| TRINITY_sp|O226\|DEGP1 | Protease Do-like 1 | 64.50 | 0.00   |
| TRINITY_sp|Q9ZV\|HEN2 | DEH-box ATP-depend | 64.50 | 0.00   |
| TRINITY_sp|Q9SN\|UGE5 | UDP-glucose 4-epimerase | 64.50 | 0.00   |
| TRINITY_sp|Q7GR\|Os01g03| Probable chromatin- | 64.50 | 0.00   |
| TRINITY_sp|P293\|Fructose-bisphosphatase | 64.50 | 0.00   |
| TRINITY_sp|P403\|RIC2 | Ras-related protein | 64.50 | 0.00   |
| TRINITY_sp|A8HS\|CHLREDRA | 40S ribosomal protein | 64.50 | 0.00   |
| TRINITY_sp|P5241\|AGPC | Glucose-1-phosphate dehydrogenase | 64.50 | 0.00   |
| TRINITY_sp|Q9AB\|mdh | Malate dehydrogenase | 64.50 | 0.00   |
| TRINITY_sp|Q56W\|PED1 | 3-ketoacyl-CoA thiolesterase | 64.50 | 0.00   |
| TRINITY_sp|Q7XT\|Os04g01| Pyruvate dehydrogenase | 64.50 | 0.00   |
| TRINITY_sp|Q9ZN\|SKD1 | Protein SUPPRESSOR | 64.50 | 0.00   |
| TRINITY_sp|Q546\|fimA | Fimbrin OS=Dictyostelium | 64.50 | 0.00   |
| TRINITY_sp|Q7ZV\|vps29 | Vacuolar protein | 64.50 | 0.00   |
| TRINITY_sp|O226\|DEGP1 | Protease Do-like 1 | 64.50 | 0.00   |
| TRINITY_sp|Q9MO\|NSF | Vesicle-fusing ATPase | 64.50 | 0.00   |
| TRINITY_sp|Q215\|M28.5 | NHP2-like protein | 64.40 | 0.00   |
| TRINITY_sp|P577\|EFSEC | Selenocysteine-specific | 64.40 | 0.00   |
| TRINITY_sp|Q9SE\|tdef3 | Elongation factor 3 | 64.40 | 0.00   |
| TRINITY_sp|Q4K4\|LSM4 | Sm-like protein LSM | 64.40 | 0.00   |
| TRINITY_sp|Q6MV\|dut-1 | Deoxyuridine 5'-triphosphatase | 64.40 | 0.00   |
| TRINITY_sp|Q9Z1\|Vars | Valine--tRNA ligase | 64.40 | 0.00   |
| TRINITY_sp|O149\|BTAF1 | TATA-binding protein | 64.40 | 0.00   |
| TRINITY_sp|O1371\|smc5 | Structural maintainance | 64.40 | 0.00   |
| TRINITY_sp|Q388\|CRT2 | Calreticulin-2 OS=A | 64.40 | 0.00   |
| TRINITY_sp|P428\|ZBP14 | 14 kDa zinc-binding protein | 64.40 | 0.00   |
| TRINITY_sp|Q9CS\|RPS7A | 40S ribosomal protein | 64.40 | 0.00   |
| TRINITY_sp|Q55B\|raptor | Protein raptor homolog | 64.40 | 0.00   |
| TRINITY_sp|Q9HG\|BiP | 78 kDa glucose-regul | 64.40 | 0.00   |
| TRINITY_sp|P929\|APR3 | 5'-adenylylsulfate | 64.40 | 0.00   |
| TRINITY_sp|P305\|CAT2 | Catalase isozyme 2 | 64.40 | 0.00   |
| TRINITY_sp|Q7VA\|infB | Translation initiation | 64.40 | 0.00   |
| TRINITY_sp|P0A\|fseA | Anti-sigma-E factor | 64.30 | 0.00   |
| TRINITY_sp|Q9UW\|pph-3 | Serine/threonine-protein phosphatase | 64.30 | 0.00   |
| TRINITY_sp|Q9HD\|vpl12 | Probable N-acetylglutamate synthase | 64.30 | 0.00   |
| TRINITY_sp|Q90Y\|rps4 | 40S ribosomal protein | 64.30 | 0.00   |
| TRINITY_sp|P458\|prpD | 2-methylcitrate dehydratase | 64.30 | 0.00   |
| TRINITY_sp|Q54W\|drq2 | Developmentally-regulated | 64.30 | 0.00   |
| TRINITY_sp|Q9MA\|NOP5-5 | Probable nucleolar | 64.30 | 0.00   |
| TRINITY_sp|Q6H7\|Os02g06 | DEAD-box ATP-depend | 64.30 | 0.00   |
| TRINITY_sp|Q437\|ROA1 | DNA replication lic | 64.30 | 0.00   |
| TRINITY_sp|Q918\|auruka-a | Aurora kinase A-A | 64.30 | 0.00   |
| TRINITY_sp|Q84W\|CCT3 | T-complex protein 1 | 64.30 | 0.00   |
| TRINITY_sp|Q275\|psmA1 | Proteasome subunit | 64.30 | 0.00   |
| TRINITY_sp|A8J7\|ATPG | ATP synthase subunit | 64.30 | 0.00   |
| TRINITY_sp|Q14L\|adc | Probable acetateacetyltransferase | 64.30 | 0.00   |
| TRINITY_sp|Q034\| | Glutamate synthase | 64.30 | 0.00   |
| TRINITY_sp|Q9XI\|PLT1 | Putative polyol transporter | 64.30 | 0.00   |
Beta-amylase 3, chloroplastic OS=Arabidopsis thaliana GN=BAM3 PE=1 SV=3
Dynein-1-beta heavy chain, flagellar inner arm I1 complex OS=Chlamydomonas reinhardtii GN=DHC10 PE=1 SV=1
Ras-related protein YPTC6 OS=Chlamydomonas reinhardtii GN=YPTC6 PE=3 SV=1
Probable pancreatic secretory proteinase inhibitor OS=Anguilla anguilla PE=1 SV=1
Cysteine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=SYCO PE=2 SV=1
N-acetylmuramic acid 6-phosphate etherase OS=Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343) GN=murQ PE=3 SV=1
40S ribosomal protein S18 OS=Argopecten irradians GN=RPS18 PE=2 SV=1
1,4-alpha-glucan-branching enzyme 2-1, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=SBE2.1 PE=1 SV=1
Alanine--glyoxylate aminotransferase 2 homolog 1, mitochondrial OS=Arabidopsis thaliana GN=AGT2 PE=1 SV=1
KRR1 small subunit processome component homolog OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=mis3 PE=3 SV=1
Peptidyl-prolyl cis-trans isomerase H OS=Bos taurus GN=PPIH PE=2 SV=1
Plastid 30S ribosomal protein S14 OS=Euglena longa GN=rps14 PE=3 SV=1
Probable beta-tubulin polyglutamylase OS=Tetrahymena thermophila (strain SB210) GN=Ttll6a PE=3 SV=2
Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Drosophila melanogaster GN=CG4933 PE=2 SV=1
Malate dehydrogenase [NADP], chloroplastic OS=Medicago sativa GN=MDH1 PE=2 SV=1
DNA-directed RNA polymerase II subunit RPB2 OS=Solanum lycopersicum GN=RPB2 PE=2 SV=1
60S ribosomal protein L22 OS=Macaca fascicularis GN=RPL22 PE=2 SV=3
Diphthamide biosynthesis protein 1 OS=Mus musculus GN=Dph1 PE=1 SV=1
40S ribosomal protein S11 OS=Dunaliella tertiolecta GN=RPS11 PE=2 SV=1
Splicing factor 3B subunit 6 OS=Homo sapiens GN=SF3B6 PE=1 SV=1
60S ribosomal protein L24-2 OS=Arabidopsis thaliana GN=RPL24B PE=1 SV=2
Probable serine/threonine-protein kinase CCRP1 OS=Zea mays GN=CCRP1 PE=1 SV=1
Dihydrolipoyl dehydrogenase, mitochondrial OS=Dictyostelium discoideum GN=lpd PE=3 SV=1
Casein kinase 1-like protein 2 OS=Arabidopsis thaliana GN=CKL2 PE=1 SV=1
DNA replication ATP-dependent helicase/nuclease DNA2 OS=Xenopus tropicalis GN=dna2 PE=3 SV=1
Probable choline-phosphate cytidylyltransferase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPCC1827.02c PE=1 SV=3
Probable magnesium transporter NIPA3 OS=Arabidopsis thaliana GN=At1g34470 PE=2 SV=1
Probable NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Caenorhabditis elegans GN=F53F4.10 PE=3 SV=1
Multifunctional methyltransferase subunit TRM112-like protein At1g22270 OS=Arabidopsis thaliana GN=At1g22270 PE=2 SV=1
Probable pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH3 OS=Arabidopsis thaliana GN=At2g47250 PE=2 SV=1
| Protein Name                                      | Organism          | Accession Number | Description                        | Value  |
|--------------------------------------------------|-------------------|------------------|------------------------------------|--------|
| Serine hydroxymethyltransferase, mitochondrial   | Solanum tuberosum | PE=2 SV=1        | N-glycosylase/DNA l                | 63.90  |
| Cystathionine gamma                              | Arabidopsis thaliana | GN=OGG1 PE=1 SV=1 | GATA transcription                   | 63.90  |
| Intraflagellar transport protein                 | Arabidopsis thaliana | GN=SFC1 PE=2 SV=1 | Mitochondrial succi                 | 63.90  |
| ATP synthase subunit                            | Homo sapiens      | PE=2 SV=1        | 6OS ribosomal protein               | 63.90  |
| Probable serine/thr                             | Arabidopsis thaliana | GN=Ppil2 PE=1 SV=2 | Peptidyl-prolyl cis-trans isomerase-like 2 | 63.90  |
| Photosystem II 10 kDa polypeptide, chloroplastic| Hordeum vulgare   | GN=PSBR PE=3 SV=1 | 40S ribosomal protein               | 63.90  |
| Acyl-CoA-binding protein                        | Dictyostelium discoideum | GN=acbA PE=1 SV=1 | -                                  | 63.90  |
| Protein SDE2 homolog                            | Mus musculus      | GN=Sde2 PE=1 SV=1 | Complement factor I                 | 63.90  |
| NADH dehydrogenase                              | Pseudomonas aeruginosa | GN=sodB PE=3 SV=3 | 40S ribosomal protein               | 63.90  |
| NADH dehydrogenase                              | Cucumis sativus    | GN=HPR-A PE=2 SV=1 | -                                  | 63.90  |
| Aconitate hydratase, cytoplasmic                | Cucurbita maxima   | PE=2 SV=1        | 40S ribosomal protein               | 63.90  |
| Translation machinery-associated protein         | Tetraodon nigroviridis | GN=tma7 PE=3 SV=1 | -                                  | 63.90  |
| CTP synthase                                    | Dictyostelium discoideum | GN=ctps PE=3 SV=1 | -                                  | 63.90  |
| Manganese-transporting ATPase                   | Mus musculus      | GN=Atp13a1 PE=1 SV=2 | -                                  | 63.90  |
| Ubiquitin-related modifier                      | Chlamydomonas reinhardtii | GN=URM1 PE=3 SV=1 | -                                  | 63.90  |
| Fumarate hydratase, mitochondrial               | Rhizopus oryzae   | GN=FUMR PE=3 SV=1 | -                                  | 63.90  |
| Aminocycle hydratase                            | Dictyostelium discoideum | GN=cysA PE=1 SV=1 | -                                  | 63.90  |
| Protein pleiotropic regulator                   | Arabidopsis thaliana | GN=PRL2 PE=2 SV=2 | -                                  | 63.90  |
| Polyadenylate-binding protein                   | Homo sapiens      | GN=PABPC1L PE=2 SV=1 | -                                  | 63.90  |
| Imidazoleglycerol-phosphate dehydratase         | Arabidopsis thaliana | GN=HISN5B PE=1 SV=2 | -                                  | 63.90  |
| Intraflagellar transport protein                 | Chlamydomonas reinhardtii | GN=IFT27 PE=1 SV=1 | -                                  | 63.90  |
| Germinal center kin                              | Caenorhabditis elegans | GN=gck-1 PE=1 SV=1 | -                                  | 63.90  |
| Proteasome subunit                              | Petunia hybrida    | GN=PBF1 PE=2 SV=1 | -                                  | 63.90  |
| Acyl-CoA-binding protein                        | Dictyostelium discoideum | GN=acbA PE=1 SV=1 | -                                  | 63.90  |
| Acyl-CoA-binding protein                        | Arabidopsis thaliana | GN=ACOC PE=1 SV=1 | -                                  | 63.90  |
| Ribosome biogenesis protein                     | Chlamydomonas reinhardtii | GN=CHLREDRAFT_128420 PE=3 SV=2 | - | 63.90 |
| Dynein regulatory c                              | Arabidopsis thaliana | GN=AT131_MOUSE PE=1 SV=1 | - | 63.90 |
| Zeta-carotene desat                              | Arabidopsis thaliana | GN=AFCT3_MOUSE PE=1 SV=1 | - | 63.90 |
| Photosystem II 10 k protease                    | Arabidopsis thaliana | GN=P46869_CHLRE PE=1 SV=1 | - | 63.90 |
| Acyl-CoA-binding protein                        | Arabidopsis thaliana | GN=ACOC PE=1 SV=1 | -                                  | 63.90  |
| Polyadenylate-binding protein                   | Arabidopsis thaliana | GN=P4VXR_MOUSE PE=1 SV=1 | - | 63.90 |
| Protein translocase                             | Plasmodium knowlesi | GN=P410_MOUSE PE=1 SV=1 | - | 63.90 |
| ADP-ribosylation fa                             | Arabidopsis thaliana | GN=ADP_MOUSE PE=1 SV=1 | - | 63.90 |
| Serine/threonine-pr                             | Arabidopsis thaliana | GN=SER_MOUSE PE=1 SV=1 | - | 63.90 |
| Ras-related protein                             | Arabidopsis thaliana | GN=ARL3_MOUSE PE=1 SV=1 | - | 63.90 |
| Proteasome subunit                              | Arabidopsis thaliana | GN=P9051_MOUSE PE=1 SV=1 | - | 63.90 |
| 40S ribosomal protein                           | Arabidopsis thaliana | GN=PSBR_MOUSE PE=1 SV=1 | - | 63.90 |
| Probable enoyl-CoA                              | Arabidopsis thaliana | GN=FLA10_MOUSE PE=1 SV=1 | - | 63.90 |
| Alanine--glyoxylate                             | Arabidopsis thaliana | GN=AGT2_MOUSE PE=1 SV=1 | - | 63.90 |
| COP9 signalosome co                              | Arabidopsis thaliana | GN=CSN2_MOUSE PE=1 SV=1 | - | 63.90 |
| Probable threonine--                            | Arabidopsis thaliana | GN=THR MOUSE PE=1 SV=1 | - | 63.90 |
| Homogentisate 1,2-d                             | Arabidopsis thaliana | GN=Q45Q_MOUSE PE=1 SV=1 | - | 63.90 |
| Glycerate dehydroge                            | Arabidopsis thaliana | GN=HPR-A_MOUSE PE=1 SV=1 | - | 63.90 |
| 3-isopropylmalate d                             | Arabidopsis thaliana | GN=PSBR_MOUSE PE=1 SV=1 | - | 63.90 |
| Superoxide dismutas                             | Arabidopsis thaliana | GN=Q39L_MOUSE PE=1 SV=1 | - | 63.90 |
| Protein pleiotropic                            | Arabidopsis thaliana | GN=PRL2_MOUSE PE=1 SV=1 | - | 63.90 |
| 2-methylisocitrate                              | Arabidopsis thaliana | GN=EJP_MOUSE PE=1 SV=1 | - | 63.90 |
| Kinesin-like protein                            | Arabidopsis thaliana | GN=FLA10_MOUSE PE=1 SV=1 | - | 63.90 |
| Uracil-DNA glycosyl                            | Arabidopsis thaliana | GN=UGLA_MOUSE PE=1 SV=1 | - | 63.90 |
| Ubiquitin carboxylase--                         | Arabidopsis thaliana | GN=USP47_MOUSE PE=1 SV=1 | - | 63.90 |
| Complement factor I                             | Arabidopsis thaliana | GN=CFI_MOUSE PE=1 SV=1 | - | 63.90 |
| Translation machine                           | Arabidopsis thaliana | GN=Q45Q_MOUSE PE=1 SV=1 | - | 63.90 |
| Iron-sulfur cluster                            | Arabidopsis thaliana | GN=ISU1_MOUSE PE=1 SV=1 | - | 63.90 |
| Ubiquitin-related m                             | Arabidopsis thaliana | GN=URM1_MOUSE PE=1 SV=1 | - | 63.90 |
| Manganese-transport                            | Arabidopsis thaliana | GN=ATP_MOUSE PE=1 SV=1 | - | 63.90 |
| NADH dehydrogenase                              | Arabidopsis thaliana | GN=ATP_MOUSE PE=1 SV=1 | - | 63.90 |
| Protein SDE2 homolo                             | Arabidopsis thaliana | GN=SDE2_MOUSE PE=1 SV=1 | - | 63.90 |
| Accession | Description | Score | E-Value |
|-----------|-------------|-------|---------|
| TRINITY_sp| Protease subunit | 63.60 | 0.00 |
| TRINITY_sp| 60S ribosomal prote | 63.60 | 0.00 |
| TRINITY_sp| Photosystem I react | 63.60 | 0.00 |
| TRINITY_sp| ABC transporter B f | 63.60 | 0.00 |
| TRINITY_sp| Extracellular signa | 63.60 | 0.00 |
| TRINITY_sp| Extracellular signa | 63.60 | 0.00 |
| TRINITY_sp| ABC transporter 60S ribosomal prote | 63.60 | 0.00 |
| TRINITY_sp| Hybrid signal trans | 63.60 | 0.00 |
| TRINITY_sp| MAPK/MAK/MAKK overl | 63.60 | 0.00 |
| TRINITY_sp| Cysteine synthase, | 63.60 | 0.00 |
| TRINITY_sp| Methionine aminopep | 63.60 | 0.00 |
| TRINITY_sp| Ferritin-3, chlorop | 63.60 | 0.00 |
| TRINITY_sp| Cell division contr | 63.60 | 0.00 |
| TRINITY_sp| ABC transporter I f | 63.60 | 0.00 |
| TRINITY_sp| Chaperone protein C | 63.60 | 0.00 |
| TRINITY_sp| ABC transporter A f | 63.60 | 0.00 |
| TRINITY_sp| T-complex protein 1 | 63.60 | 0.00 |
| TRINITY_sp| Phosphoglycolate ph | 63.60 | 0.00 |
| TRINITY_sp| Nuclear transcripti | 63.50 | 0.00 |
| TRINITY_sp| Probable short/bran | 63.50 | 0.00 |
| TRINITY_sp| Multidrug resistanc | 63.50 | 0.00 |
| TRINITY_sp| Probable phospholip | 63.50 | 0.00 |
| TRINITY_sp| Death-inducer oblit | 63.50 | 0.00 |
| TRINITY_sp| Lissencephaly-1 hom | 63.50 | 0.00 |
| TRINITY_sp| Ubiquitin-NEDD8-lik | 63.50 | 0.00 |
| TRINITY_sp| Ras-like protein ra | 63.50 | 0.00 |
| TRINITY_sp| T-complex protein 1 | 63.50 | 0.00 |
| TRINITY_sp| Chloride transport | 63.50 | 0.00 |
| TRINITY_sp| GDP-L-fucose syntha | 63.50 | 0.00 |
| TRINITY_sp| Copine-4 OS=Homo sa | 63.50 | 0.00 |
| TRINITY_sp| ABC transporter B f | 63.50 | 0.00 |
| TRINITY_sp| SNF1-related protei | 63.50 | 0.00 |
| TRINITY_sp| Cyclin-dependent ki | 63.50 | 0.00 |
| TRINITY_sp| Dynein gamma chain, | 63.50 | 0.00 |
| TRINITY_sp| Kinesin-like protei | 63.50 | 0.00 |
| TRINITY_sp| Protein TAR1 OS=Klu | 63.50 | 0.00 |
| TRINITY_sp| Angiopoietin-relate | 63.40 | 0.00 |
| TRINITY_sp| Peptidyl-prolyl cis | 63.40 | 0.00 |
| TRINITY_sp| Alpha-1-antitrypsin | 63.40 | 0.00 |
| TRINITY_sp| Putative DNA helica | 63.40 | 0.00 |
| TRINITY_sp| AP-2 complex subuni | 63.40 | 0.00 |
| TRINITY_sp| Nuclear cap-binding | 63.40 | 0.00 |
| TRINITY_sp| ABC transporter G f | 63.40 | 0.00 |
| TRINITY_sp| Ras-related protein | 63.40 | 0.00 |
| TRINITY_sp| N-alpha-acetyltrans | 63.40 | 0.00 |
| TRINITY_sp| Myosin IB heavy cha | 63.40 | 0.00 |
| TRINITY_sp| S-adenosylmethionin | 63.40 | 0.00 |
| TRINITY_sp| Phosphatase IMP1, | 63.40 | 0.00 |
| TRINITY_sp| Glycogen synthase k | 63.40 | 0.00 |
| TRINITY_sp| Protein pirA OS=Dic | 63.40 | 0.00 |
| TRINITY_sp| Histone H3 OS=Crypt | 63.40 | 0.00 |
| TRINITY_sp| ATPase ASNA1 homolo | 63.40 | 0.00 |
| TRINITY_sp| Calmodulin OS=Triti | 63.40 | 0.00 |
| TRINITY_sp| Glutathione S-trans | 63.40 | 0.00 |
| TRINITY_sp| Calcium-dependent p | 63.40 | 0.00 |
| Accession | Description | Percent Identity | Percentage Similarity |
|-----------|-------------|------------------|-----------------------|
| TRINITY_sp| Glyoxylate/succinic semialdehyde reductase 1 | 63.40 | 0.00 |
| TRINITY_sp| Chaperone protein C | 63.40 | 0.00 |
| TRINITY_sp| Calcium-dependent protein kinase C | 63.40 | 0.00 |
| TRINITY_sp| Dynamin heavy chain | 63.40 | 0.00 |
| TRINITY_sp| Carboxylic-phosphatase | 63.40 | 0.00 |
| TRINITY_sp| Cullin-3A | 63.40 | 0.00 |
| TRINITY_sp| N-alpha-acetyltransferase 20 | 63.40 | 0.00 |
| TRINITY_sp| 50S ribosomal protein L6 | 63.40 | 0.00 |
| TRINITY_sp| Phosphoglucomutase | 63.40 | 0.00 |
| TRINITY_sp| Tubulin glycylase 3E | 63.40 | 0.00 |
| TRINITY_sp| Succinate-CoA ligase [ADP-forming]: mitochondrial | 63.40 | 0.00 |
| TRINITY_sp| N-alpha-acetyltransferase 10 | 63.40 | 0.00 |
| TRINITY_sp| Pre-mRNA-splicing factor 38 | 63.40 | 0.00 |
| TRINITY_sp| Nuclear cap-binding protein subunit 2 | 63.40 | 0.00 |
| TRINITY_sp| Acetyl-coenzyme A carboxylase | 63.40 | 0.00 |
| TRINITY_sp| RNA replication polyprotein | 63.40 | 0.00 |
| TRINITY_sp| Peptidyl-prolyl cis-trans isomerase | 63.40 | 0.00 |
| TRINITY_sp| Chaperone protein ClpB1 | 63.40 | 0.00 |
| TRINITY_sp| 40S ribosomal protein S8-2 | 63.40 | 0.00 |
| TRINITY_sp| Uncharacterized GTP-binding protein | 63.40 | 0.00 |
| TRINITY_sp| Casein kinase I | 63.40 | 0.00 |
| TRINITY_sp| Photosystem II | 63.40 | 0.00 |
| TRINITY_sp| Inosine triphosphatase | 63.40 | 0.00 |
| TRINITY_sp| Thioredoxin reductase | 63.40 | 0.00 |
| TRINITY_sp| DNA replication lic | 63.40 | 0.00 |
| TRINITY_sp| Glyoxalase ElbB | 63.40 | 0.00 |
| TRINITY_sp| Dynein heavy chain | 63.40 | 0.00 |
| TRINITY_sp| 40S ribosomal prote | 63.40 | 0.00 |
| TRINITY_sp| Tubulin glycylase | 63.40 | 0.00 |
| TRINITY_sp| Calcium-transportin | 63.40 | 0.00 |
| TRINITY_sp| Pre-mRNA-splicing f | 63.40 | 0.00 |
| TRINITY_sp| 50S ribosomal prote | 63.40 | 0.00 |
| TRINITY_sp| 7-hydroxymethyl chl | 63.40 | 0.00 |
| TRINITY_sp| Probable tRNA N6-ad | 63.40 | 0.00 |
| TRINITY_sp| Acetyl-coenzyme A c | 63.40 | 0.00 |
| TRINITY_sp| Thioredoxin reducta | 63.40 | 0.00 |
| TRINITY_sp| Chaperonin CPN60-1 | 63.40 | 0.00 |
| TRINITY_sp| protein At3 | 63.40 | 0.00 |
| TRINITY_sp| Phenylalanine--tRNA | 63.40 | 0.00 |
| TRINITY_sp| Protein ORANGE-GREE | 63.40 | 0.00 |
| TRINITY_sp| Protein ORANGE-GREE | 63.40 | 0.00 |
| TRINITY_sp| Probable chromatin- | 63.40 | 0.00 |
| TRINITY_sp| Valine--tRNA ligase | 63.40 | 0.00 |
| TRINITY_sp| RNA-binding protein | 63.40 | 0.00 |
| TRINITY_sp| N-alpha-acetyltransferase | 63.40 | 0.00 |
| TRINITY_sp| Nuclear cap-binding | 63.40 | 0.00 |
| TRINITY_sp| Casein kinase 1-lik | 63.40 | 0.00 |
| TRINITY_sp| Mitotic spindle ass | 63.40 | 0.00 |
| TRINITY_sp| 60S ribosomal prote | 63.40 | 0.00 |
| TRINITY_sp| Acetate permease A | 63.40 | 0.00 |
| TRINITY_sp| Protein kinase 2 OS | 63.40 | 0.00 |
TRINITY_sp|Q569Iselenbpl Selenium-binding protein 63.10 0.00
TRINITY_sp|Q9FD2RPL21E 60S ribosomal protein L21e 63.10 0.00
TRINITY_sp|P207\_MAK Serine/threonine-protein kinase MAK 63.10 0.00
TRINITY_sp|P509\_CCT4 T-complex protein 1 63.10 0.00
TRINITY_sp|O615\_gch GTP cyclohydrolase 63.10 0.00
TRINITY_sp|O500\_OTC Ornithine carbamoyltransferase 63.10 0.00
TRINITY_sp|P2161- Pyrophosphate-energized vacuolar membrane proton pump 63.10 0.00
TRINITY_sp|Q9RO\_Lgmn Legumain OS=Rattus norvegicus 63.10 0.00
TRINITY_sp|Q9VA\_CG11837 Probable dimethyladenosine transferase 63.10 0.00
TRINITY_sp|Q9ZW\_CKL19 Casein kinase 1-like protein 9 63.10 0.00
TRINITY_sp|C0US1\_Mj16 Putative lysine-specific histone deacetylase 63.10 0.00
TRINITY_sp|O825\_PTSZ2-1 Cell division protein 63.10 0.00
TRINITY_sp|Q9HG\_NAT10 RNA cytidine acetyltransferase 63.10 0.00
TRINITY_sp|Q3MH\_RBBP4 Histone-binding protein 63.00 0.00
TRINITY_sp|P118\_- High mobility group protein 63.00 0.00
TRINITY_sp|Q764\_- Casein kinase II subunit alpha 63.00 0.00
TRINITY_sp|Q91\_tif213 Eukaryotic translation initiation factor 2 subunit gamma 63.00 0.00
TRINITY_sp|Q54K\_auh Methylglutaconyl-CoA oxidase 63.00 0.00
TRINITY_sp|Q9SM\_DHC1 Dynein-1-alpha heavy chain 63.00 0.00
TRINITY_sp|Q86X\_CFS2 Pre-mRNA cleavage factor Im 25 kDa subunit 63.00 0.00
TRINITY_sp|Q76M\_hpd 4-hydroxyphenylpyruvate dioxygenase 63.00 0.00
TRINITY_sp|P930\_- 60S ribosomal protein L37a 63.00 0.00
TRINITY_sp|Q999\_TEP1 Telomerase protein 63.00 0.00
TRINITY_sp|Q154\_SF3B4 Splicing factor 3B 63.00 0.00
TRINITY_sp|Q9BV\_RFN126 E3 ubiquitin-protein ligase 63.00 0.00
TRINITY_sp|Q995\_yakc Aldo-keto reductase 63.00 0.00
TRINITY_sp|Q430\_- Granule-bound starch degradation protein 63.00 0.00
TRINITY_sp|Q8C3\_Guf1 Translation factor 63.00 0.00
TRINITY_sp|Q9Y3\_NALAD2 N-acetylated-alpha-aminoacyl-tRNA synthetase 63.00 0.00
TRINITY_sp|Q9C5\_SMC2-1 Structural maintenance of chromosomes protein 63.00 0.00
TRINITY_sp|Q9SY1\_PEX10 Peroxisome biogenesis factor 63.00 0.00
TRINITY_sp|Q9LN\_CLO 110 kDa U5 small nuclear RNA binding protein 63.00 0.00
TRINITY_sp|P320\_RPL37A 60S ribosomal protein L37a 63.00 0.00
TRINITY_sp|P320\_RPL37A 60S ribosomal protein L37a 63.00 0.00
TRINITY_sp|P231\_CDC2 Cell division control protein 2 homolog 63.00 0.00
TRINITY_sp|P283\_acuE Malate synthase, gluconate-6-phosphate dehydrogenase 63.00 0.00
TRINITY_sp|P209\_aarA Citrate synthase OS=Lactobacillus casei 62.90 0.00
TRINITY_sp|P372\_PIGA Phosphatidylinositol-4-phosphate 62.90 0.00
TRINITY_sp|Q9US\_gpi10 GPI mannosyltransferase 62.90 0.00
TRINITY_sp|C1D6\_pyrC Dihydroorotate dehydrogenase OS=Lactobacillus casei 62.90 0.00
TRINITY_sp|P0DK\_RFPS10-1 40S ribosomal protein L24 62.90 0.00
TRINITY_sp|Q8TF\_DYNL2 Dynein light chain 62.90 0.00
TRINITY_sp|Q9C8\_At1g6333 Putative flavin-containing oxidoreductase 62.90 0.00
TRINITY_sp|Q9LY\_RGLG2 E3 ubiquitin-protein ligase RGLG2 62.90 0.00
TRINITY_sp|Q9LR\_CLO Polyadenylate-binding protein-interacting protein 9 62.90 0.00
TRINITY_sp|Q54W\_pex7 Peroxisomal targeting signal 2 receptor 62.90 0.00
TRINITY_sp|O603\_AQR Intron-binding protein aquarius 62.90 0.00
TRINITY_sp|Q84M\_ABC1 ABC transporter A family member 1 62.80 0.00
TRINITY_sp|P931\_CDC2 Cell division control protein 2 homolog 62.80 0.00
TRINITY_sp|D4BO\_ARB_02077 Probable glucan endohydrolase 62.80 0.00
TRINITY_sp|Q7MX\_gpl1 ATP-dependent Clp protease 62.80 0.00
TRINITY_sp|Q55G\_psmA5 Proteasome subunit alpha 62.80 0.00
TRINITY_sp|Q861\_dst1 Serine/threonine-protein kinase DST1 62.80 0.00
TRINITY_sp|Q91M\_- Inositol-3-phosphatase 62.80 0.00
TRINITY_sp|Q9CA\_DRG2 Developmentally-regulated protein 62.80 0.00
TRINITY_sp|Q9B2\_CRNL1 Crooked neck-like protein 62.80 0.00
TRINITY_sp|Q2KJ:PRPF6  Pre-mRNA-processing  62.80  0.00
TRINITY_sp|O0461ADNT1  Mitochondrial aden i  62.80  0.00
TRINITY_sp|O2381SIR  Sulfite reductase [  62.80  0.00
TRINITY_sp|P234f-  Ribulose bisphospha 62.80  0.00
TRINITY_sp|Q8T6fabcF2  ABC transporter F  f  62.80  0.00
TRINITY_sp|P0ACfumA  Fumarate hydratase 62.80  0.00
TRINITY_sp|Q9LSUbUC32  Ubiquitin-conjugati 62.70  0.00
TRINITY_sp|P024Rplp2  60S acidic ribosoma 62.70  0.00
TRINITY_sp|Q228bEME2  Uroporphyrinogen de 62.70  0.00
TRINITY_sp|Q541polr3b  DNA-directed RNA po 62.70  0.00
TRINITY_sp|Q6QNN-  Casein kinase I OS= 62.70  0.00
TRINITY_sp|Q8GWAt1g184  Peptidyl-tRNA hyd 62.70  0.00
TRINITY_sp|A8GKcatD  3'-5' ssDNA/RNA exo 62.70  0.00
TRINITY_sp|Q8LPAbCE2  ABC transporter E  f  62.70  0.00
TRINITY_sp|O646fURT1  UTP:RNA uridylyltra 62.70  0.00
TRINITY_sp|Q9SEI-  Pirin-like protein 62.70  0.00
TRINITY_sp|Q9S1At2g402  Eukaryotic translat 62.70  0.00
TRINITY_sp|Q655PFTSH2  ATP-dependent zinc 62.70  0.00
TRINITY_sp|Q224fHDA19  Histone deacetylase 62.70  0.00
TRINITY_sp|F496f-  Aconitate hydratase 62.70  0.00
TRINITY_sp|Q9SEfAAA1  Katanin p60 ATPase- 62.70  0.00
TRINITY_sp|Q9SMDHIC1B  Cytoplasmic dynein 62.70  0.00
TRINITY_sp|Q652fPHT4;4  Probable anion tran 62.70  0.00
TRINITY_sp|A5P3fSF3A2  Splicing factor 3A 62.70  0.00
TRINITY_sp|C5D4deoC  Deoxyribose-phospha 62.60  0.00
TRINITY_sp|P534f-  Actin OS=Chlamydomo 62.60  0.00
TRINITY_sp|Q55Cfamhd1  Probable imidazolon 62.60  0.00
TRINITY_sp|Q6QNI-  Casein kinase I OS= 62.60  0.00
TRINITY_sp|P2641HSP70  Heat shock 70 kDa p 62.60  0.00
TRINITY_sp|Q414fPCM3  Putative calmodulin 62.60  0.00
TRINITY_sp|Q964f-  Meiotic recombinati 62.60  0.00
TRINITY_sp|Q9SVfUEV1D  Ubiquitin-conjugati 62.60  0.00
TRINITY_sp|Q6AVfOs03g06  Probable N-acetyl-g 62.60  0.00
TRINITY_sp|O005fNOP56  Nucleolar protein 5 62.60  0.00
TRINITY_sp|Q229fRH24  DEAD-box ATP-depend 62.60  0.00
TRINITY_sp|Q9D2fDnaaf1  Dynein assembly fac 62.60  0.00
TRINITY_sp|Q9MBfDHC10  Dynein-1-beta heavy 62.60  0.00
TRINITY_sp|Q9QYfAbcc5  Multidrug resistanc 62.60  0.00
TRINITY_sp|P465fubc4  Ubiquitin-conjugati 62.50  0.00
TRINITY_sp|Q7KWfprp19  Pre-mRNA-processing 62.50  0.00
TRINITY_sp|E2KRfRPL32  60S ribosomal prote 62.50  0.00
TRINITY_sp|P306fcdc-25. M-phase inducer pho 62.50  0.00
TRINITY_sp|Q54Yfmrpl33  Probable 39S riboso 62.50  0.00
TRINITY_sp|Q46EmrskB  Peptide methionine 62.50  0.00
TRINITY_sp|Q2H3fPKNOX1  Homeobox protein PK 62.50  0.00
TRINITY_sp|P623fCPK1  Calcium-dependent p 62.50  0.00
TRINITY_sp|B8AMEfCHLD  Magnesium-chelatase 62.50  0.00
TRINITY_sp|O830fpip  Probable proline im 62.50  0.00
TRINITY_sp|Q2K1fTCEB1  Transcription elong 62.50  0.00
TRINITY_sp|Q540fekerB  Extracellular signa 62.50  0.00
TRINITY_sp|P316fparpl  Poly [ADP-ribose] p 62.50  0.00
TRINITY_sp|Q9FVCfDHDPS2  4-hydroxy-tetrahydr 62.50  0.00
TRINITY_sp|Q56KfCF3B5  Splicing factor 3B 62.50  0.00
TRINITY_sp|Q922fPlrg1  Pleiotropic regulat 62.50  0.00
TRINITY_sp|Q8MQfcsA  Citrate synthase, p 62.50  0.00
TRINITY_sp|A4K4fRTET1  Regulator of telome 62.50  0.00
| Accession | Description | Expression | Score |
|-----------|-------------|------------|-------|
| TRINITY_sp|Q388tXPB1   | DNA repair helicase | 62.50 |
| TRINITY_sp|P489tCYP97B2| Cytochrome P450 97B| 62.50 |
| TRINITY_sp|B9DiACS     | Acetyl-coenzyme A s| 62.50 |
| TRINITY_sp|Q93IF3B6    | Splicing factor 3B| 62.50 |
| TRINITY_sp|A8J0tCHLRDRJ| 1-acyl-sn-glycerol-| 62.50 |
| TRINITY_sp|Q8VYfCKLl2  | Casein kinase 1-lik| 62.50 |
| TRINITY_sp|Q742tAGR231C| Lipoyl synthase, mi| 62.50 |
| TRINITY_sp|Q5DM3FT7172 | Intraflagellar tran| 62.50 |
| TRINITY_sp|Q52J2NLGY1  | Peptide-N(4)-(N-ace| 62.50 |
| TRINITY_sp|Q1ZX1DBB_G02| Probable serine/thr| 62.50 |
| TRINITY_sp|P027tSLC25A4 | ADP/ATP translocase| 62.40 |
| TRINITY_sp|P524tPAC1   | Proteasome subunit| 62.40 |
| TRINITY_sp|P168tH2A5II | Histone H2A-III OS=| 62.40 |
| TRINITY_sp|Q54S0nfyA   | Acetyl-coenzyme A s| 62.40 |
| TRINITY_sp|Q54SNFYA    | Nuclear transcripti| 62.40 |
| TRINITY_sp|P025tAct79B | Actin, larval muscl| 62.40 |
| TRINITY_sp|Q237tElong2 | Elongation factor 2| 62.40 |
| TRINITY_sp|Q54J4oatA   | Probable ornithine| 62.40 |
| TRINITY_sp|Q6YS0Os7g03 | DEAD-box ATP-depend| 62.40 |
| TRINITY_sp|Q827tHISN3  | 1-(5-phosphoribosyl| 62.40 |
| TRINITY_sp|Q4K7tRPL5   | 60S ribosomal prote| 62.40 |
| TRINITY_sp|P111tDLST   | Dihydrolipoyllysine| 62.40 |
| TRINITY_sp|Q0W4tALDH6B2| Methylmalonate-semi| 62.40 |
| TRINITY_sp|A8IB1CHLRDRJ| 40S ribosomal prote| 62.40 |
| TRINITY_sp|Q08D7PANK3  | Pantothenate kinase| 62.30 |
| TRINITY_sp|Q8GWGFA2    | Chaperone protein d| 62.30 |
| TRINITY_sp|P0CC0DDB_G02| Enolase superfami| 62.30 |
| TRINITY_sp|Q240tMT2    | Metallothionein-lik| 62.30 |
| TRINITY_sp|Q86AtpsmB1  | Proteasome subunit| 62.30 |
| TRINITY_sp|Q86Ktrappc3 | Trafficking protein| 62.30 |
| TRINITY_sp|Q55DtpsmB3  | Proteasome subunit| 62.30 |
| TRINITY_sp|Q9LHFYPP3  | Phytochrome-associa| 62.30 |
| TRINITY_sp|Q75J1pckA   | Phosphoenolpyruvate| 62.30 |
| TRINITY_sp|Q059tRAB1A  | Ras-related protein| 62.30 |
| TRINITY_sp|P423tMTOR   | Serine/threonine-pr| 62.30 |
| TRINITY_sp|P460tNOP2   | Probable 28S rRNA (| 62.30 |
| TRINITY_sp|Q9XYfcpA    | Probable C-terminal| 62.30 |
| TRINITY_sp|P067tTOP2   | DNA topoisomerase 2| 62.30 |
| TRINITY_sp|A8JA1DYF13  | Intraflagellar tran| 62.30 |
| TRINITY_sp|Q3EDtABCI19 | ABC transporter I f| 62.30 |
| TRINITY_sp|P503tGdi1   | Rab GDP dissociatio| 62.30 |
| TRINITY_sp|O654tXCP1   | Cysteine protease X| 62.30 |
| TRINITY_sp|A1WZ3rpmG   | 50S ribosomal prote| 62.30 |
| TRINITY_sp|Q243tIswi   | Chromatin-remodelin| 62.30 |
| TRINITY_sp|Q8K0t0plah  | 5-oxoproline OS=M  | 62.30 |
| TRINITY_sp|Q392tPP2AB2 | Serine/threonine pr| 62.30 |
| TRINITY_sp|Q8RWtRVE8   | Protein REVEILLE 8 | 62.30 |
| TRINITY_sp|A8HTVtuf1   | Elongation factor T| 62.20 |
| TRINITY_sp|Q2S3JmrsB   | Peptide methionine| 62.20 |
| TRINITY_sp|P511tMSK-2  | Glycogen synthase k| 62.20 |
| TRINITY_sp|Q9URtACT    | Actin, gamma OS=Pen| 62.20 |
| TRINITY_sp|P297tACTB   | Actin, cytoplasmic| 62.20 |
| TRINITY_sp|Q1tVMQC5S1  | Molybdenum cofactor| 62.20 |
| TRINITY_sp|Q91OtpurB   | Adenylosuccinate ly| 62.20 |
| TRINITY_sp|Q8D7tclpB1  | Chaperone protein C| 62.20 |
| TRINITY_sp|Q54QFERkB   | Extracellular signa| 62.20 |
TRINITY_sp|P107(CAB7) Chlorophyll a-b binding protein 7, chloroplastic OS=Solanum lycopersicum GN=CAB7 PE=3 SV=1
TRINITY_sp|Q86J1lvsB BEACH domain-containing protein OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q92G1ACX1.2 Putative peroxisomal protein OS=Arabidopsis thaliana GN=PRDX2 PE=2 SV=1
TRINITY_sp|Q59XRAS1 Ras-like protein 1 OS=Arabidopsis thaliana GN=PRDX2 PE=2 SV=1
TRINITY_sp|P2431- Proliferating cell nuclear antigen OS=Catharanthus roseus GN=PRDX2 PE=2 SV=1
TRINITY_sp|P8231- Non-specific lipid-transfer protein OS=Prunus armeniaca GN=PRDX2 PE=2 SV=1
TRINITY_sp|Q31Q8g1qC Glucose-1-phosphate dehydrogenase OS=Rickettsia conorii (strain ATCC VR-613 / Malish 7) GN=fdxB PE=3 SV=1
TRINITY_sp|Q9S2ILIP5 Protein HOMOLOG OF MAMMALIAN LYST-INTERACTING PROTEIN 5 OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|P0AFmog Molybdopterin adenyltransferase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q065*: Pyrophosphatase-energizer OS=Bos taurus GN=PRDX2 PE=2 SV=1
TRINITY_sp|P1977(MIB) Myosin heavy chain OS=Arabidopsis thaliana GN=PRDX2 PE=2 SV=1
TRINITY_sp|Q9SU4ATR2 NADPH-cytochrome P450 reductase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q92H1clpB Chaperone protein OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q0598RAB1A Ras-related protein OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q0598UTP13 U3 small nucleolar OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q7477mis3 KRR1 small subunit OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q499GCDCSP Glycine dehydrogenase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|P2002ATP2B1 Plasma membrane calcium ATPase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q3ZBFASPN Asporin OS=Bos taurus GN=PRDX2 PE=2 SV=1
TRINITY_sp|P5425PGIC1 Glucose-6-phosphate dehydrogenase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q8R32Rfc3 Replication factor OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q92JfBfxd2B 2Fe-2S ferredoxin OXOS10010000021 OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q6NScdk11 Threonylcarbamoyladenylosyltransferase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q56KXHRH15 DEAD-box ATP-dependant helicase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q6TBPCYP97C1 Carotene epsilon-monoxygenase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q9LJM3KE1 MAP3K epsilon protease OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q99C0RPL6C 6OS ribosomal prote OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|P6004RPL7B 6OS ribosomal prote OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q3U7Cdk15 Cyclin-dependent kinases OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q9BW8CCDC94 Coiled-coil domain-containing protein OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q45F7S Serine/threonine-protein kinase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q6YU0Os02g01 Putative multidrug resistance protein OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q54DiamedA AMP deaminase OS=Dictyostelium discoideum GN=PRDX2 PE=2 SV=1
TRINITY_sp|Q9C6At4g178 Acetylornithine deaminase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q600ubp12 Probable ubiquitin OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q7477mis3 KRR1 small subunit OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q9AXOOs01g06 Uroporphyrinogen dehydratase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q0021DH1S2 Phospho-2-dehydrogenase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q9Muint4g3621 Proline--tRNA ligase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|F4KEEMB2247 Valine--tRNA ligase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q4285WAXY Granule-bound starchy endosperm protein OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q4V8fSteap4 Metallochaperone OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q9BG1PRDX2 Peroxiredoxin-2 OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|Q655CIPK6 CBL-interacting protein kinase OS=Arabidopsis thaliana GN=LIP5 PE=1 SV=1
TRINITY_sp|P109* Actin, macronuclear OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|P357Prdx1 Peroxiredoxin-1 OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|P347ARF ADP-ribosylation factor OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|Q8KuvalS1 Probable valine--tRNA ligase OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|P114* Actin OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|Q9ZWOCAO Chlorophyllide a oxidase OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|Q6YU0Os08g01 Putative aconitase OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|P0DJRPL13A 60S ribosomal prote OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|Q54PlabcC8 ABC transporter C family OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|P4041 T-complex protein OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|Q9UL1RAB21 Ras-related protein OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|Q9KNtrpS Tryptophan--tRNA ligase OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|Q6YU0Os08g01 Putative aconitase OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|P0DJRPL13A 60S ribosomal prote OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|Q54PlabcC8 ABC transporter C family OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|P4041 T-complex protein OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|Q9UL1RAB21 Ras-related protein OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
TRINITY_sp|Q9KNtrpS Tryptophan--tRNA ligase OS=Dictyostelium discoideum GN=LIP5 PE=1 SV=1
| Accession      | Description                                                                 | Identity | Similarity |
|----------------|-----------------------------------------------------------------------------|----------|------------|
| TRINITY_sp|Q75I0|Histidine triad nucleotide-binding protein 1 OS=Bos taurus GN=HINT1 PE=1 SV=2 | 61.60    | 0.00       |
| TRINITY_sp|Q039L|Chlorophyll a-b bin | 61.60    | 0.00       |
| TRINITY_sp|P0765|Uncharacterized oxi | 61.60    | 0.00       |
| TRINITY_sp|F4JLA|Isoleucine--tRNA li | 61.60    | 0.00       |
| TRINITY_sp|Q243T|Proteasome subunit | 61.60    | 0.00       |
| TRINITY_sp|Q9YFI|DEXH-box ATP-depend | 61.60    | 0.00       |
| TRINITY_sp|P320|SPBc2 prophase-deri | 61.60    | 0.00       |
| TRINITY_sp|E9L7I|Bifunctional aspart | 61.60    | 0.00       |
| TRINITY_sp|Q54U|DNA-dependent prote | 61.60    | 0.00       |
| TRINITY_sp|Q9X2E|Leucine--tRNA ligas | 61.60    | 0.00       |
| TRINITY_sp|Q94A0|Organellar oligopep | 61.60    | 0.00       |
| TRINITY_sp|Q6JD|Probable cysteine-- | 61.50    | 0.00       |
| TRINITY_sp|Q8NKG|1,4-alpha-gluca-br | 61.50    | 0.00       |
| TRINITY_sp|Q6NRH|mcm9 | 61.50    | 0.00       |
| TRINITY_sp|Q154A|Multidrug resistanc | 61.50    | 0.00       |
| TRINITY_sp|P905|Histone H3 OS=Euplo | 61.50    | 0.00       |
| TRINITY_sp|Q28H|Queuine tRNA-riboys | 61.50    | 0.00       |
| TRINITY_sp|Q963|Acyl-coenzyme A oxi | 61.50    | 0.00       |
| TRINITY_sp|Q75I|Zinc finger CCCH-ty | 61.50    | 0.00       |
| TRINITY_sp|Q2HFI|ATP-dependent RNA h | 61.50    | 0.00       |
| TRINITY_sp|B8AL|Arginine biosynthes | 61.50    | 0.00       |
| TRINITY_sp|P150|Ras-like protein ra | 61.50    | 0.00       |
| TRINITY_sp|Q395|YPTC6 | 61.50    | 0.00       |
| TRINITY_sp|P301|DNA topoisomerase 2 | 61.50    | 0.00       |
| TRINITY_sp|Q99M|Lysine--tRNA ligase | 61.50    | 0.00       |
| TRINITY_sp|P629|RAC1 | 61.50    | 0.00       |
| TRINITY_sp|Q9FE0|Elongation factor G | 61.50    | 0.00       |
| TRINITY_sp|O220|Mitogen-activated p | 61.50    | 0.00       |
| TRINITY_sp|Q63L|Dnah1 | 61.50    | 0.00       |
| TRINITY_sp|Q9F|DEXH-box ATP-depend | 61.50    | 0.00       |
| TRINITY_sp|P332|4OS ribosomal prote | 61.50    | 0.00       |
| TRINITY_sp|Q222|Endoplasmin homolog | 61.40    | 0.00       |
| TRINITY_sp|A9NK|Mitotic-spindle org | 61.40    | 0.00       |
| TRINITY_sp|F4K2I|Pre-mRNA-splicing f | 61.40    | 0.00       |
| TRINITY_sp|Q9SL|Importin subunit al | 61.40    | 0.00       |
| TRINITY_sp|P629|Histidine triad nuc | 61.40    | 0.00       |
| TRINITY_sp|Q425|Threonyl synthase | 61.40    | 0.00       |
| TRINITY_sp|Q55A|V-type proton ATPas | 61.40    | 0.00       |
| TRINITY_sp|P320|ADP/ATP translocase | 61.40    | 0.00       |
| TRINITY_sp|Q8T2|Serine/threonine-pr | 61.40    | 0.00       |
| TRINITY_sp|Q55BH|Histone deacetylase | 61.40    | 0.00       |
| TRINITY_sp|Q9SL|Protein TAR1 OS=Klu | 61.40    | 0.00       |
| TRINITY_sp|Q9SW1|U-box domain-contai | 61.40    | 0.00       |
| TRINITY_sp|P356|RPL7A-1 | 61.40    | 0.00       |
| TRINITY_sp|Q243|DNA topoisomerase 2 | 61.40    | 0.00       |
| TRINITY_sp|Q6T4|rbrA | 61.40    | 0.00       |
| TRINITY_sp|P1261|T-complex protein 1 | 61.40    | 0.00       |
| TRINITY_sp|P437|Chaperone protein D | 61.40    | 0.00       |
| Accession     | Description                                                   | Score | Difference |
|--------------|---------------------------------------------------------------|-------|------------|
| TRINITY_sp|K0754132E Guanylate cyclase 3                                  | 61.40 | 0.00       |
| TRINITY_sp|Q61547CDK1 Cyclin-dependent kinase                             | 61.40 | 0.00       |
| TRINITY_sp|Q7XP0404g0661 Kinesin-like calmodulin                          | 61.40 | 0.00       |
| TRINITY_sp|Q9LR4GGAT1 Glutamate--glyoxylate                               | 61.40 | 0.00       |
| TRINITY_sp|Q9M45PGM1 Phosphoglucomutase                                   | 61.40 | 0.00       |
| TRINITY_sp|Q81T1kif5 Kinesin-related protein                              | 61.40 | 0.00       |
| TRINITY_sp|Q9COCDNAH6 Dynein heavy chain                                  | 61.40 | 0.00       |
| TRINITY_sp|P2771TTR Transthyretin OS=Ga                                    | 61.30 | 0.00       |
| TRINITY_sp|Q131FPRKA1 5'-AMP-activated protein                            | 61.30 | 0.00       |
| TRINITY_sp|Q54pppal Inorganic pyrophosphatase                             | 61.30 | 0.00       |
| TRINITY_sp|Q9DAFPacrg Parkin coregulated                                  | 61.30 | 0.00       |
| TRINITY_sp|Q9C81EMB3003 Dihydrolipooyllysine                              | 61.30 | 0.00       |
| TRINITY_sp|Q9495GLY1 Glycerol-3-phosphatase                               | 61.30 | 0.00       |
| TRINITY_sp|Q5ZKS2PAST Spastin OS=Gallus g                                 | 61.30 | 0.00       |
| TRINITY_sp|Q489CMMDH Malate dehydrogenas                                  | 61.30 | 0.00       |
| TRINITY_sp|P2745GRP-2 Glycine-rich protein                               | 61.30 | 0.00       |
| TRINITY_sp|Q9WUM5P1 Dolichol-phosphate                                    | 61.30 | 0.00       |
| TRINITY_sp|Q743sSPBC3H7 Uncharacterized met                               | 61.30 | 0.00       |
| TRINITY_sp|B1XJipra Peptide chain release                                 | 61.30 | 0.00       |
| TRINITY_sp|B0G12pip5k3 1-phosphatidylinositol                             | 61.30 | 0.00       |
| TRINITY_sp|Q8W2ISAT4 Serine acetyltransfer                               | 61.30 | 0.00       |
| TRINITY_sp|P6781SECIIA Signal peptidase co                               | 61.30 | 0.00       |
| TRINITY_sp|B3VMKBADH2 betaine aldehyde de                                 | 61.30 | 0.00       |
| TRINITY_sp|Q6DC3eisenb Selenium-binding protein                           | 61.30 | 0.00       |
| TRINITY_sp|P484tCNAG_001Actin OS=Cryptococcus                            | 61.30 | 0.00       |
| TRINITY_sp|Q8W11SMU1 Suppressor of mec-8                                   | 61.20 | 0.00       |
| TRINITY_sp|Q429sec27 Probable coatomer s                                  | 61.20 | 0.00       |
| TRINITY_sp|Q9W41krg Neurobeachin OS=Dro                                   | 61.20 | 0.00       |
| TRINITY_sp|P5088RPL12A 6OS ribosomal prote                                  | 61.20 | 0.00       |
| TRINITY_sp|Q9HHE2E4.130 Regulator of nonsense                             | 61.20 | 0.00       |
| TRINITY_sp|Q8IXZ2C3H3 Zinc finger CCCH do                                 | 61.20 | 0.00       |
| TRINITY_sp|Q9D8Dnajb4 DnaJ homolog subfam                                 | 61.20 | 0.00       |
| TRINITY_sp|Q8202HPA Histidinol-phosphat                                   | 61.20 | 0.00       |
| TRINITY_sp|Q2435P4H5 Prolyl 4-hydroxylas                                  | 61.20 | 0.00       |
| TRINITY_sp|Q3YWHAL Histidine ammonia-1                                    | 61.20 | 0.00       |
| TRINITY_sp|Q9SBPPDK [Pyruvate dehydrogena]                                | 61.20 | 0.00       |
| TRINITY_sp|Q8CS5Cwcc22 Pre-mRNA-splicing factors                          | 61.20 | 0.00       |
| TRINITY_sp|P323sPPH3 Serine/threonine-pr                                  | 61.20 | 0.00       |
| TRINITY_sp|Q75COCLPB2 Chaperone protein C                                 | 61.20 | 0.00       |
| TRINITY_sp|B0C6prfC Peptide chain release                                 | 61.20 | 0.00       |
| TRINITY_sp|Q623sAtm Serine-protein kinase                                | 61.20 | 0.00       |
| TRINITY_sp|Q9SL1Atg200 Protein phosphatase                                | 61.20 | 0.00       |
| TRINITY_sp|B8A2MNC6 DNA replication lic                                   | 61.20 | 0.00       |
| TRINITY_sp|F41KE8m2761 Threonine--tRNA lig                                  | 61.20 | 0.00       |
| TRINITY_sp|Q6NYICMA16 Protein MAK16 homol                                | 61.10 | 0.00       |
| TRINITY_sp|Q9TU1RAC2 Ras-related C3 botu                                  | 61.10 | 0.00       |
| TRINITY_sp|Q8S41AAT1 Acetyl-CoA acetyltransfer                            | 61.10 | 0.00       |
| TRINITY_sp|Q9BRWDR83 WD repeat domain-co                                  | 61.10 | 0.00       |
| TRINITY_sp|Q8XS2Atg2g338 Tyrrosine--tRNA lig                               | 61.10 | 0.00       |
| TRINITY_sp|P464tVps4b Vacuolar protein so                                 | 61.10 | 0.00       |
| TRINITY_sp|Q55F1galbT 4-aminobutyrate ami                                 | 61.10 | 0.00       |
| TRINITY_sp|A3KPDufaf5 Arginine-hydroxylas                                 | 61.10 | 0.00       |
| TRINITY_sp|Q0295SLC25A1 Mitochondrial 2-oxo                               | 61.10 | 0.00       |
| TRINITY_sp|J9R1VDR Divinyl chlorophyll                                   | 61.10 | 0.00       |
| TRINITY_sp|P5496mp2 Inositol monophosphate                               | 61.10 | 0.00       |
| TRINITY_sp|Q9UHENDOR1 NADPH-dependent dif                                 | 61.10 | 0.00       |
| TRINITY_sp| Q5UP\_MIMI\_R2 (DnaJ-like protein R) | 60.40 | 0.00 |
| TRINITY_sp| Q916\_aad-a (Alpha-aspartyl dipeptide synthetase) | 60.40 | 0.00 |
| TRINITY_sp| B0BNEsd (S-formylglutathione synthetase) | 60.40 | 0.00 |
| TRINITY_sp| Q9410\_os01g08\_Probable mannose-1-phosphate 5'-epimerase-like protein | 60.40 | 0.00 |
| TRINITY_sp| Q93W\_SBP2 (Selenium-binding protein) | 60.40 | 0.00 |
| TRINITY_sp| Q142\_mtr4 (ATP-dependent RNA helicase) | 60.40 | 0.00 |
| TRINITY_sp| Q93X\_CPA (N-carboxamidoputrescine decarboxylase) | 60.40 | 0.00 |
| TRINITY_sp| Q392\_TOUSLED (Serine/threonine-protein kinase) | 60.40 | 0.00 |
| TRINITY_sp| Q8244\_At3g461 (Histidine-tRNA ligase) | 60.40 | 0.00 |
| TRINITY_sp| Q489\_CMDH (Malate dehydrogenase) | 60.40 | 0.00 |
| TRINITY_sp| Q232\_SHM4 (Serine hydroxymethyltransferase) | 60.40 | 0.00 |
| TRINITY_sp| Q611\_Abcb7 (ATP-binding cassette protein) | 60.40 | 0.00 |
| TRINITY_sp| Q9SC1\_DHS1 (Deoxyhypusine synthase) | 60.40 | 0.00 |
| TRINITY_sp| Q9SF\_RPL4A (60S ribosomal protein) | 60.40 | 0.00 |
| TRINITY_sp| B6D5\_Dnaaf1 (Dynein assembly factor) | 60.40 | 0.00 |
| TRINITY_sp| Q5K5\_os07g06 (DEAD-box ATP-dependent RNA helicase) | 60.40 | 0.00 |
| TRINITY_sp| Q9SR\_FKBP16 (Peptidyl-prolyl cis-trans isomerase) | 60.40 | 0.00 |
| TRINITY_sp| Q9FI\_RPS8B (40S ribosomal protein) | 60.40 | 0.00 |
| TRINITY_sp| P073\_JACYP1 (Acylphosphatase-1) | 60.30 | 0.00 |
| TRINITY_sp| F126\_MLYCD (Malonyl-CoA decarboxylase) | 60.30 | 0.00 |
| TRINITY_sp| P423\_CBN1 (Calcineurin subunit) | 60.30 | 0.00 |
| TRINITY_sp| Q9SL\_TCX6 (Protein TESMIN/TSO1) | 60.30 | 0.00 |
| TRINITY_sp| Q9MQ\_NDUF6 (NADH dehydrogenase) | 60.30 | 0.00 |
| TRINITY_sp| Q9CW\_Rph5 (Diphthine methyl ester) | 60.30 | 0.00 |
| TRINITY_sp| Q97Y\_msrA (Peptide methionine) | 60.30 | 0.00 |
| TRINITY_sp| Q9FW\_HAC12 (Histone acetyltrans) | 60.30 | 0.00 |
| TRINITY_sp| P515\_AFC2 (Serine/threonine-protein kinase) | 60.30 | 0.00 |
| TRINITY_sp| Q5X4\_purC (Phosphoribosylaminoimidazole) | 60.30 | 0.00 |
| TRINITY_sp| Q3BA\_1 (Uncharacterized protein) | 60.30 | 0.00 |
| TRINITY_sp| Q9FL\_NLE1 (Notchless protein) | 60.30 | 0.00 |
| TRINITY_sp| P348\_ (Serine hydroxymethyltransferase) | 60.30 | 0.00 |
| TRINITY_sp| Q5UP\_MIMI\_R2 (DnaJ-like protein R) | 60.30 | 0.00 |
| TRINITY_sp| P496\_WAN2A2 (Alpha-mannosidase) | 60.30 | 0.00 |
| TRINITY_sp| Q6L4\_DBB1 (DNA damage-binding protein) | 60.30 | 0.00 |
| TRINITY_sp| F419\_GLYR2 (Glyoxylate/succinic semialdehyde reductase) | 60.30 | 0.00 |
| TRINITY_sp| Q9Y7\_tor2 (Serine/threonine-protein kinase) | 60.30 | 0.00 |
| TRINITY_sp| P352\_Rab6a (Ras-related protein) | 60.30 | 0.00 |
| TRINITY_sp| Q71U\_RPS27L (40S ribosomal protein) | 60.30 | 0.00 |
| TRINITY_sp| P056\_sacC (Levanase OS=Bacillus subtilis) | 60.30 | 0.00 |
| TRINITY_sp| Q9SP\_RRP41 (Exosome complex component) | 60.30 | 0.00 |
| TRINITY_sp| Q7KQ\_PF10_00 (Tubulin beta chain) | 60.30 | 0.00 |
| TRINITY_sp| P114\_PSBP (Oxygen-evolving enhancer) | 60.30 | 0.00 |
| TRINITY_sp| Q54Q\_erkB (Extracellular signal receptor) | 60.30 | 0.00 |
| TRINITY_sp| P493\_CCT3 (T-complex protein 1) | 60.30 | 0.00 |
| TRINITY_sp| Q96S\_ADH2 (Alcohol dehydrogenase) | 60.30 | 0.00 |
| TRINITY_sp| Q5K5\_gcvP (Glycine dehydrogenase) | 60.30 | 0.00 |
| TRINITY_sp| Q9MA\_ERCC1 (DNA excision repair component) | 60.30 | 0.00 |
| TRINITY_sp| B0R0\_chd8 (Chromodomain-helicase) | 60.30 | 0.00 |
| TRINITY_sp| Q9MO\_At1g742 (Probable phosphatase) | 60.20 | 0.00 |
| TRINITY_sp| P217\_rps-26 (40S ribosomal protein) | 60.20 | 0.00 |
| TRINITY_sp| P953\_mls (Malate synthase OS=Oryza sativa subsp. japonica) | 60.20 | 0.00 |
| TRINITY_sp| P462\_ (Fructose-1,6-bisphosphatase) | 60.20 | 0.00 |
| TRINITY_sp| P0DJ\_RPL18 (60S ribosomal protein) | 60.20 | 0.00 |
| TRINITY_sp| P314\_AVP1 (Pyrophosphate-energized vacuolar membrane proton pump) | 60.20 | 0.00 |
| TRINITY_sp| Q9SU\_Rab7a (Ras-related protein) | 60.20 | 0.00 |
| TRINITY_sp| A7HW\_RecA (Protein RecA OS=Parasolan) | 60.20 | 0.00 |
TRINITY_sp|Q8VX7|AGAL3  Alpha-galactosidase 3 60.20 0.00
TRINITY_sp|Q1674|MAN2A1  Alpha-mannosidase 2 60.20 0.00
TRINITY_sp|Q1008|SPAC3H11  Glutathione gamma-g 60.20 0.00
TRINITY_sp|Q9ZQ2|U2AF35A  Splicing factor U2a 60.20 0.00
TRINITY_sp|Q8616|dst1  Serine/threonine-pr 60.20 0.00
TRINITY_sp|Q6DFC|chmp2a  Charged multivesicu 60.20 0.00
TRINITY_sp|Q54X3|etfdh  Electron transfer f 60.20 0.00
TRINITY_sp|Q54M6|fkd  Probable serine/thr 60.20 0.00
TRINITY_sp|Q9SC4|G0212  5-formyltetrahydrof 60.20 0.00
TRINITY_sp|Q69TPX|1I1  Peroxiredoxin-2E-1, 60.20 0.00
TRINITY_sp|P3684|NITA  Nitratreductase [ 60.20 0.00
TRINITY_sp|P0C07|NUDT24  Nudix hydrolase 24, 60.20 0.00
TRINITY_sp|Q4254|ASB1  Anthranilate synth 60.20 0.00
TRINITY_sp|Q8LG6|CUL4  Cullin-4 OS=Arabido 60.20 0.00
TRINITY_sp|Q2229|CTY1  Mannose-1-phosphate 60.20 0.00
TRINITY_sp|Q5684|gmd  GDP-mannose 4,6-deh 60.20 0.00
TRINITY_sp|Q54V5|ctps  CTP synthase OS=Dic 60.20 0.00
TRINITY_sp|P9404|HAL3B  Probable phosphopan 60.20 0.00
TRINITY_sp|Q8H11|PGRL1A  PGR5-like protein 1 60.20 0.00
TRINITY_sp|Q54P6|mtr  Methionine synthase 60.20 0.00
TRINITY_sp|Q6AV7|PPDK1  Pyruvate, phosphate 60.20 0.00
TRINITY_sp|Q8HOA|ABCFC3  ABC transporter F 60.20 0.00
TRINITY_sp|Q9655|SAMDC  S-adenosylmethionin 60.20 0.00
TRINITY_sp|O9662|arcC  Actin-related protei 60.10 0.00
TRINITY_sp|Q93Vf|At3g0265  WAT1-related protei 60.10 0.00
TRINITY_sp|Q8W4F|RH30  DEAD-box ATP-depend 60.10 0.00
TRINITY_sp|P481t|trpl27a  60S ribosomal prote 60.10 0.00
TRINITY_sp|P0817|At4g31790  Probable diphthine 60.10 0.00
TRINITY_sp|Q6SOX|kif6  Kinesin-related pro 60.10 0.00
TRINITY_sp|Q95Yv|ckk8  Probable cyclin-dep 60.10 0.00
TRINITY_sp|P0DJI|RPL17  60S ribosomal prote 60.10 0.00
TRINITY_sp|Q86A4|gltA  Citrate synthase OS 60.10 0.00
TRINITY_sp|Q3Y8I|DAW1  Dynine assembly fac 60.10 0.00
TRINITY_sp|Q9625|GD11  Guanosine nucleotid 60.10 0.00
TRINITY_sp|Q4292|Os12g06  Malate dehydrogenas 60.10 0.00
TRINITY_sp|P1788|crn  Protein crooked nec 60.10 0.00
TRINITY_sp|Q2YD4|ARL1  ADP-ribosylation fa 60.10 0.00
TRINITY_sp|P1777|FBA1  Fructose-bisphospha 60.10 0.00
TRINITY_sp|A8IEI|PRMT1  Protein arginine N- 60.10 0.00
TRINITY_sp|Q5LAl|hisS  Histidine--tRNA lig 60.00 0.00
TRINITY_sp|Q8LT7|AGD11  Probable ADP-ribo 60.00 0.00
TRINITY_sp|P1761|ypt3  GTP-binding protein 60.00 0.00
TRINITY_sp|B8AEI|MCM5  DNA replication lic 60.00 0.00
TRINITY_sp|Q217t|rskn1  Putative ribosomal 60.00 0.00
TRINITY_sp|Q54J7|purL  Phosphoribosylformy 60.00 0.00
TRINITY_sp|P366W|rad8  DNA repair protein 60.00 0.00
TRINITY_sp|Q9VHC1G11985  Probable splicing f 60.00 0.00
TRINITY_sp|Q93Vf|GIF3  GRFL-interacting fa 60.00 0.00
TRINITY_sp|Q6ERV|CAD8B  Probable cinnamyl a 60.00 0.00
TRINITY_sp|Q8T6r|arsA  ATPase ASNA1 homolo 60.00 0.00
TRINITY_sp|Q4QW7|adhfe1  Hydroxyacid-oxoacid 60.00 0.00
TRINITY_sp|Q9VDI|Ino80  Putative DNA helica 60.00 0.00
TRINITY_sp|Q9LH4|At5g0601  Tropinone reductase 60.00 0.00
TRINITY_sp|Q29Af|GA17800  Leishmanolysin-like 60.00 0.00
TRINITY_sp|Q9UE1|FTSJ1  Putative tRNA (cyti 60.00 0.00
TRINITY_sp|Q84SIO|os07g05  Zinc finger CCCH do 60.00 0.00
| Accession | Description                                           | Value 1 | Value 2 |
|-----------|-------------------------------------------------------|---------|---------|
| TRINITY_sp| 50S ribosomal protein L4                               | 60.00   | 0.00    |
| TRINITY_sp| Diphthamide biosynth                                    | 60.00   | 0.00    |
| TRINITY_sp| Equilibrative nuclear protein                           | 60.00   | 0.00    |
| TRINITY_sp| Pre-rRNA-processing protein                            | 60.00   | 0.00    |
| TRINITY_sp| Serine/threonine-protein kinase                         | 60.00   | 0.00    |
| TRINITY_sp| Serine/threonine-protein kinase                         | 60.00   | 0.00    |
| TRINITY_sp| GTP-binding nuclear protein Ran                        | 60.00   | 0.00    |
| TRINITY_sp| Bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT | 60.00   | 0.00    |
| TRINITY_sp| Pre-rRNA-processing protein PNO1                      | 60.00   | 0.00    |
| TRINITY_sp| Indole-3-acetic acid-induced protein ARG2              | 60.00   | 0.00    |
| TRINITY_sp| Probable plastid-lid                                    | 60.00   | 0.00    |
| TRINITY_sp| ADP-ribosylation factor                                 | 59.90   | 0.00    |
| TRINITY_sp| GTP-loop GTPase 1 O                                    | 59.90   | 0.00    |
| TRINITY_sp| Probable serine/thr                                     | 59.90   | 0.00    |
| TRINITY_sp| SKP1-like protein 1                                      | 59.90   | 0.00    |
| TRINITY_sp| 50S ribosomal protein                                  | 59.80   | 0.00    |

### Additional Entries

- **TRINITY_sp|Q80346**: 50S ribosomal protein L4
- **TRINITY_sp|Q6C0CD**: Diphthamide biosynth
- **TRINITY_sp|Q8VXENT**: Equilibrative nuclear
- **TRINITY_sp|Q6BJ7P**: Pre-rRNA-processing
- **TRINITY_sp|Q048Mak**: Serine/threonine-protein kinase
- **TRINITY_sp|P09444**: U1 small nuclear ribonuclease
- **TRINITY_sp|Q8VZVC**: Vacuolar protein sorting
- **TRINITY_sp|Q5B1P**: Peptidyl-prolyl cis-trans isomerase
- **TRINITY_sp|Q9M1LMP**: Mitogen-activated protein kinase
- **TRINITY_sp|Q8VZUXX**: UDP-glucuronic acid glucuronyltransferase
- **TRINITY_sp|P2751-**: Chlorophyll a-b binding protein
- **TRINITY_sp|P6014EL**: Nuclear ribonucleasen
- **TRINITY_sp|P2002pyr1-3**: Protein PYR1-3
- **TRINITY_sp|P5924RPS27AA**: Ubiquitin-40S ribosomal protein
- **TRINITY_sp|Q9S2PFAD4**: Fatty acid desaturase
- **TRINITY_sp|Q861IVDDB_G02**: Uncharacterized protein
- **TRINITY_sp|Q7U6EDNA**: Chaperone protein D
- **TRINITY_sp|Q7057Srpk1**: SRSF protein kinase
- **TRINITY_sp|Q2864ABCC2**: Canalicular multispanning protein
- **TRINITY_sp|F8083ydA**: General stress protein
- **TRINITY_sp|Q9LVAABCBC25**: ABC transporter B family
- **TRINITY_sp|P108FPLCD1**: 1-phosphatidylinositol transferase
- **TRINITY_sp|F4KEFFHIT**: Bifunctional biotinyltransferase
- **TRINITY_sp|Q5SPSechac1**: Glutathione-specific protein
- **TRINITY_sp|Q9SLTRAD50**: DNA repair protein
- **TRINITY_sp|Q9QY1Rdh11**: Retinol dehydrogenase
- **TRINITY_sp|Q9Z2RH28**: DEAD-box ATP-dependent helicase
- **TRINITY_sp|Q5G5Cdst2**: Serine/threonine-protein kinase
- **TRINITY_sp|Q4F1IP4H13**: Prolyl 4-hydroxylase
- **TRINITY_sp|Q9X7FPREP**: Prolyl endopeptidase
- **TRINITY_sp|Q2FKQf1B**: Formate acetyltransferase
- **TRINITY_sp|Q7Z2rran**: GTP-binding nuclear protein
- **TRINITY_sp|Q9NP1NMRK2**: Nicotinamide ribosyltransferase
- **TRINITY_sp|Q0MXICSE4**: Histone H3-like cenin
- **TRINITY_sp|Q0041TPRP-F1**: 36.4 kDa proline-rich protein
- **TRINITY_sp|Q8CEERdh13**: Retinol dehydrogenase
- **TRINITY_sp|Q8691pakF**: Serine/threonine-protein kinase
- **TRINITY_sp|Q54YVpolr2h**: DNA-directed RNA polymerase
- **TRINITY_sp|Q6504EGR1**: NEDD8-activating enzyme
- **TRINITY_sp|Q9FFCKL7**: Casein kinase 1-like
- **TRINITY_sp|P5241PUR5**: Phosphoribosylformyltransferase
- **TRINITY_sp|O59801**: Putative ATP-dependant enzyme
- **TRINITY_sp|O499DADK**: Adenosine kinase OS
- **TRINITY_sp|Q8K2ZNAT10**: RNA cytidine acetyltransferase
- **TRINITY_sp|Q9LUMBAP4**: Probable plastid-like
- **TRINITY_sp|Q96KARL5B**: ADP-ribosylation factor
- **TRINITY_sp|Q9HCQPN1**: GTPase
- **TRINITY_sp|Q54HddrkA**: Probable serine/threonine kinase
- **TRINITY_sp|Q3925SKP1A**: SKP1-like protein
- **TRINITY_sp|O8178BETAC-AL**: Beta-adaptin-like protein
- **TRINITY_sp|P3225ARG2**: Indole-3-acetic acid
- **TRINITY_sp|P136ECp**: Ceruloplasmin
- **TRINITY_sp|Q54Qurm1**: Ubiquitin-related modifier
- **TRINITY_sp|Q53NMPK15**: Mitogen-activated protein kinase
- **TRINITY_sp|Q6IVUJA5**: Ubiquitin-like modifier
- **TRINITY_sp|Q2GHFrp1T**: 50S ribosomal protein L20
| Gene Name                        | Description                                      | Score | E-Value |
|---------------------------------|--------------------------------------------------|-------|---------|
| TRINITY_sp|Q9JI1Stk3                                  | Serine/threonine-protein kinase 3 OS=Mus musculus | 59.80 | 0.00    |
| TRINITY_sp|P872(RPL3A4)                               | 60S ribosomal protein OS=Arabidopsis thaliana | 59.80 | 0.00    |
| TRINITY_sp|Q8VVLMSM                                  | Sm-like protein LSM OS=Arabidopsis thaliana | 59.80 | 0.00    |
| TRINITY_sp|Q9MBIFKFBP                                | 6-phosphofructo-2-k OS=Arabidopsis thaliana | 59.80 | 0.00    |
| TRINITY_sp|Q2TAKIF19                                 | Kinesin-like protein OS=Arabidopsis thaliana | 59.80 | 0.00    |
| TRINITY_sp|P583JttaE                                 | Low specificity L-t OS=Arabidopsis thaliana | 59.80 | 0.00    |
| TRINITY_sp|Q9COCDNAH6                                | Dynein heavy chain OS=Arabidopsis thaliana | 59.80 | 0.00    |
| TRINITY_sp|A2YGISUSP                                 | UDP-sugar pyrophosphorylase OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|P217Psp26                                 | 40S ribosomal protein OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|O150SYN2J2                                 | Synaptotagmin-2 OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|Q9HTURAC2                                 | Ras-related C3 botulin OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|Q9H5DHX35                                 | Probable ATP-dependence OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|Q9LXHAM2                                  | Histone acetyltransf. OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|P127RSP3                                  | Flagellar radial sp OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|Q940ZTP29                                 | Zinc transporter ZT OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|Q2UESPSYN1                                | Spermidine synthase OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|Q9ATGTGD3                                 | Protein TRIGALACTOS OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|P372PSY1                                   | Phytoene synthase, OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|Q1JPD2HGDH                                 | D-2-hydroxyglutarate OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|P468KRP95                                 | Kinesin-II 95 kDa OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|B9FMKIN13A                                 | Kinesin-like protein OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|P0C8CCRP1                                 | Probable serine/thr OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|Q9FIAT5g478                               | Adenylate kinase 2, OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|Q9F1IRP88B                                | 40S ribosomal prote OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|P231ABC4                                  | Phosphatidylcholine OS=Arabidopsis thaliana | 59.70 | 0.00    |
| TRINITY_sp|P187Pila1                                  | Fimbrial protein OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q9SCKALA5                                 | Probable phospholipid OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q54Icox17                                 | Cytochrome c oxidase OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|P0822At2g197AP4                          | Complex subunit OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q5R4CPNE6                                 | Copine-6 OS=Pongo abelii | 59.60 | 0.00    |
| TRINITY_sp|P828fbdxr                                 | NADPH:adrenodoxin oxidoreductase OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q8BYUsp47                                 | Ubiquitin carboxyl-terminal OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q54G3act10                                | Actin-10 OS=Dictyostelium discoideum | 59.60 | 0.00    |
| TRINITY_sp|Q75HSAPK10                                | Serine/threonine-pr OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q5Kcdh1                                   | Anaphase-promoting OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q9C7ATE2                                  | Arginyl-t-RNA--prote OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|A2XFPRR73                                 | Two-component respo OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q54Jhal1                                  | Probable histidine OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|P465POL3                                  | DNA polymerase delta OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q54DIVDBB_G02                             | Protein unc-50 homo OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|B6TRHPYRD                                 | Riboflavin biosynthesis OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q54Vdxx47                                 | Probable ATP-dependence OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q8S2FTSH3                                 | ATP-dependent zinc OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q039TM30                                  | Membrane-associated OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|P391YCP1                                  | Metal resistance pr OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q9C9JKAS2                                 | 3-oxoacyl-[acyl-car OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q9FTTRECQL3                               | ATP-dependent DNA h OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|P356RPS20                                 | 40S ribosomal prote OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|P8031Cct6a                                 | T-complex protein 1 OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|P116ND1                                   | NADH-ubiquinone oxi OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q145DHX8                                  | ATP-dependent RNA h OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|Q54XDDB_G02                               | Probable serine/thr OS=Arabidopsis thaliana | 59.60 | 0.00    |
| TRINITY_sp|A8FIprfA                                   | Peptide chain relea OS=Arabidopsis thaliana | 59.50 | 0.00    |
| TRINITY_sp|Q932At4g116E3                              | Ubiquitin-prote OS=Arabidopsis thaliana | 59.50 | 0.00    |
| TRINITY_sp|D4A5Dmgc111                               | 3-hydroxymethyl-3-m OS=Arabidopsis thaliana | 59.50 | 0.00    |
| TRINITY_sp|Q1PFEDA2                                  | Probable serine pro OS=Arabidopsis thaliana | 59.50 | 0.00    |
| Gene Symbol | Description | MIPS Score | Eukaryotic Score |
|-------------|-------------|------------|-----------------|
| vha-2       | V-type proton ATPase | 59.50 | 0.00 |
| pkgB        | Protein kinase 2 OS | 59.50 | 0.00 |
| CIPK1       | CBL-interacting pro | 59.50 | 0.00 |
| nubp2       | Cytosolic Fe-Sclus | 59.50 | 0.00 |
| gnptab      | N-acetylglucosamine | 59.50 | 0.00 |
| yptc6       | Ras-related protein | 59.50 | 0.00 |
| gpn1        | GPN-loop GTase 1 O | 59.50 | 0.00 |
| hmgcl       | Hydroxymethylglutar | 59.50 | 0.00 |
| Cbs         | Cystathionine beta- | 59.50 | 0.00 |
| agps1       | Glucose-1-phosphate | 59.50 | 0.00 |
| mpped1      | Metallophosphoester | 59.50 | 0.00 |
| mak3        | N-alpha-acetyltrans | 59.50 | 0.00 |
| 4ps17       | 4OS ribosomal prote | 59.50 | 0.00 |
| dpkplipa    | Phosphoglycolate ph | 59.50 | 0.00 |
| sae2        | SUMO-activating enz | 59.50 | 0.00 |
| odhB        | Dihydrolipoyleysine | 59.50 | 0.00 |
| smnR1       | Malate dehydrogenas | 59.50 | 0.00 |
| pol         | Retrovirus-related | 59.50 | 0.00 |
| lanapc8     | Anaphase-promoting | 59.50 | 0.00 |
| DDB_G02     | Putative aldehyde d | 59.50 | 0.00 |
| DDB_G02     | Putative aldehyde d | 59.50 | 0.00 |
| ATG7        | Ubiquitin-like modi | 59.50 | 0.00 |
| SPH4112      | Glycerol kinase OS= | 59.50 | 0.00 |
| SPH4112      | Glycerol kinase OS= | 59.50 | 0.00 |
| SPH4112      | Histone-lysine N-me | 59.40 | 0.00 |
| msh6        | DNA mismatch repair | 59.40 | 0.00 |
| ycf1        | Metal resistance pr | 59.40 | 0.00 |
| ABCA1       | ABC transporter A f | 59.40 | 0.00 |
| ATG7        | Ubiquitin-like modi | 59.40 | 0.00 |
| ARF1A        | Guanine nucleotide- | 59.40 | 0.00 |
| ISPCA4      | Transcription activ | 59.40 | 0.00 |
| urod        | Uroporphyrinogen de | 59.40 | 0.00 |
| TOE2        | AP2-like ethylene-r | 59.40 | 0.00 |
| DDB_G02     | Putative aldehyde d | 59.40 | 0.00 |
| P2332       | Thymidine kinase OS | 59.40 | 0.00 |
| DDB_G02     | Putative aldehyde d | 59.40 | 0.00 |
| arfa        | ADP-ribsylation fa | 59.40 | 0.00 |
| TXN         | Thioredoxin OS=Homo | 59.40 | 0.00 |
| yheh        | Probable multidrug | 59.40 | 0.00 |
| PRPF18      | Pre-mRNA-splicing f | 59.40 | 0.00 |
| Q37t-       | Glutamate--tRNA lig | 59.40 | 0.00 |
| ade6        | Phosphoribosylamino | 59.40 | 0.00 |
| HDA9        | Histone deacetylase | 59.40 | 0.00 |
| GIPK        | GPI-anchor transami | 59.40 | 0.00 |
| DDB_G02     | Probable serine/thr | 59.40 | 0.00 |
| RKP         | E3 ubiquitin-protei | 59.40 | 0.00 |
| MPK2        | Mitogen-activated p | 59.40 | 0.00 |
| atg022      | E3 ubiquitin-protei | 59.40 | 0.00 |
| SUMO01      | Small ubiquitin-rel | 59.30 | 0.00 |
| QHMOB1A     | MOB kinase activato | 59.30 | 0.00 |
| SDPR        | Serum deprivation-r | 59.30 | 0.00 |
| 16orf8      | UF0764 protein C16 | 59.30 | 0.00 |
| snrpb       | Small nuclear ribon | 59.30 | 0.00 |
| PAP7        | Probable plastid-li | 59.30 | 0.00 |
| canA        | Calcineurin subunit | 59.30 | 0.00 |
| psmd4       | 26S proteasome non- | 59.30 | 0.00 |
| ISU1        | Suppressor of mec-8 | 59.30 | 0.00 |
| TTTLL3C     | Tubulin glycylase 3 | 59.30 | 0.00 |
| Gene Name                     | Protein Name                  | Organism          | Accession   | Description                            | Score | Value |
|------------------------------|--------------------------------|-------------------|-------------|----------------------------------------|-------|-------|
| TRINITY_sp|P549BI02  | Biotin synthase      | Arabidopsis thaliana | sp|O22609|DEGP1_ARATH | 59.30 | 0.00  |
| TRINITY_sp|Q8LAUBP4  | Ubiquitin carboxyl-  | OS=Dictyostelium discoideum | sp|P10272|POL_BAEVM | 59.10 | 0.00  |
| TRINITY_sp|A2XUCDBGK2 | Cyclin-dependent ki | Arabidopsis thaliana | sp|Q95C57|SMC21_ARATH | 59.30 | 0.00  |
| TRINITY_sp|P361{-}   | Endoplasmin homolog  | Homo sapiens     | sp|Q1JQB2|BUB3_BOVIN | 59.30 | 0.00  |
| TRINITY_sp|Q3BKSNU13 | NHP2-like protein 1 | Dictyostelium discoideum | sp|Q54673|D2HDH_ARATH | 59.30 | 0.00  |
| TRINITY_sp|Q6P8SNU13 | NHP2-like protein 1 | Arabidopsis thaliana | sp|Q90398|RH14 | 59.30 | 0.00  |
| TRINITY_sp|Q9JSNRPB6B | DNA-directed RNA po | Homo sapiens     | sp|Q80914|Prcp | 59.30 | 0.00  |
| TRINITY_sp|P7072act18 | Actin-18          | Dictyostelium discoideum | sp|Q847P3|POLIB_ARATH | 59.30 | 0.00  |
| TRINITY_sp|Q9YYESTK24 | Serine/threonine-pr | Arabidopsis thaliana | sp|Q88WUPF1L4 | Peptidyl-prolyl cis | 59.30 | 0.00  |
| TRINITY_sp|Q9HCCHD8  | Chromodomain-helica | Homo sapiens     | sp|Q915PURB | Adenylosuccinate ly | 59.20 | 0.00  |
| TRINITY_sp|Q54WEglnA3 | Type-3 glutamine sy | Homo sapiens     | sp|Q9349RAB1BV | Ras-related protein | 59.20 | 0.00  |
| TRINITY_sp|O266msRA  | Peptide methionine | Homo sapiens     | sp|Q9349RAB1BV | Ras-related protein | 59.20 | 0.00  |
| TRINITY_sp|A6VNIinfB | Translation initiat | Homo sapiens     | sp|Q9349RAB1BV | Ras-related protein | 59.20 | 0.00  |
| TRINITY_sp|Q9295BRP1 | Transcription facto | Homo sapiens     | sp|Q9349RAB1BV | Ras-related protein | 59.20 | 0.00  |
| TRINITY_sp|Q9XXmyoK  | Myosin-K heavy chai | Arabidopsis thaliana | sp|Q9349RAB1BV | Ras-related protein | 59.20 | 0.00  |
| TRINITY_sp|B7PXspas  | Spastin OS=IXodes s | Dictyostelium discoideum | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q1INTasc3 | Activating signal c | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q24FRP1L36 | 6OS ribosomal prote | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q232D2HGHD | D-2-hydroxyglutarat | homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q387CDC2A | Cell division contr | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q54P11vaF | BEACH domain-contai | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|P119IScp2 | Non-specific lipid- | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|A2YVFAB1 | Proteasome subunit  | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|P0C1cyp15 | Peptidyl-prolyl cis | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q95Gislbp2 | Oocyte-specific his | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q2VVVhs1V | ATP-dependent prote | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q550DDBG02 | Probable serine/thr | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q9H1JANAPC1 | Anaphase-promoting | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|P239VMA16 | V-type proton ATPas | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|P491RAB2B | Ras-related protein | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|P403RIC2 | Ras-related protein | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q84NPOLIB | DNA polymerase I B  | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q54Npophah | 5-oxoprolinase OS=D | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q7SYFgttrt1 | Queuine tRNA-ribozy | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q6Z1YchF1 | Obg-like ATPase 1 O | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q555aatA | Aspartate aminotran | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q866GCys | Crustapain OS=Panda | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|O648Acx  | Acyl-coenzyme A oxi | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q0PSIGCAT | 2-amino-3-ketobutyry | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|P102pol  | Pol polyprotein OS= | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q557ig6pd-1 | Glucose-6-phosphate | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q5ZIIDOHH | Deoxyhypusine hydro | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q7TMFrcp | Lysosomal Pro-X car | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q8BY5SEC11C | Signal peptidase co | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q8H1RH14 | DEAD-box ATP-depend | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q8GWCOX11 | Cytochrome c oxidas | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q9C5S1SMC2-1 | Structural maintena | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|A2CDIrp1A | 50S ribosomal prote | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q1JCQBUB3 | Mitotic checkpoint | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q399- | Beta-carotene ketol | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
| TRINITY_sp|Q526DEGP1 | Protease Do-like 1, | Homo sapiens     | sp|Q850F3|Pcb15 | 59.20 | 0.00  |
TRINITY_sp|Q9LK:UKL2  Uridine kinase-like 59.10 0.00
TRINITY_sp|Q9C8:ABCC11  ABC transporter C f 59.10 0.00
TRINITY_sp|Q386:-  V-type proton ATPase 59.10 0.00
TRINITY_sp|Q54\yakA  Probable serine/thr 59.10 0.00
TRINITY_sp|Q94J\NLP2  Nitrilase-like prot 59.10 0.00
TRINITY_sp|Q425:PIMT1  Protein-L-isoaspart 59.10 0.00
TRINITY_sp|P496\GAPC  Glyceraldehyde-3-ph 59.10 0.00
TRINITY_sp|Q9M0\IB1  Aspartate--tRNA lig 59.10 0.00
TRINITY_sp|Q94G\AAS1  Anthranilate synth 59.10 0.00
TRINITY_sp|Q8LI:Os07g06:  Probable MYST-like 59.10 0.00
TRINITY_sp|Q5Bh:spb1  AdoMet-dependent rR 59.10 0.00
TRINITY_sp|Q9NR:UBQLN4  Ubiquilin-4 OS=Homo 59.10 0.00
TRINITY_sp|Q6UW:PCSK4  Proprotein converta 59.10 0.00
TRINITY_sp|Q6CN:ASF1  Histone chaperone A 59.00 0.00
TRINITY_sp|Q54D:abcA9  ABC transporter A f 59.00 0.00
TRINITY_sp|P3641:rab11A  Ras-related protein 59.00 0.00
TRINITY_sp|Q23F:FTLL3C  Tubulin glycyrase 59.00 0.00
TRINITY_sp|Q613:1f88  Intraflagellar tran 59.00 0.00
TRINITY_sp|Q22J:rpmE  50S ribosomal prote 59.00 0.00
TRINITY_sp|P524:PUR3  Phosphoribosylglyc 59.00 0.00
TRINITY_sp|Q54S:ps11  40S ribosomal prote 59.00 0.00
TRINITY_sp|Q92Q:VHA-F  V-type proton ATPase 59.00 0.00
TRINITY_sp|Q8S2:GRELIP  Protein GRIP OS=Ara 59.00 0.00
TRINITY_sp|P144:FGA  Fibrinogen alpha ch 59.00 0.00
TRINITY_sp|Q77T:Rrm1  Ribonucleoside-diph 59.00 0.00
TRINITY_sp|Q84K:ABCA2  ABC transporter A f 59.00 0.00
TRINITY_sp|Q9NP:EXOSC4  Exosome complex com 59.00 0.00
TRINITY_sp|Q54U:serA  D-3-phosphoglycerat 59.00 0.00
TRINITY_sp|P392:EL13  Probable mannitol d 59.00 0.00
TRINITY_sp|Q997:MTR  Methionine synthase 59.00 0.00
TRINITY_sp|Q8KA:clpB2  Probable chaperone 59.00 0.00
TRINITY_sp|O741:SPCC122  Chorismate synthase 58.90 0.00
TRINITY_sp|Q56r:At5g5877:  Dehydrodolichyl dip 58.90 0.00
TRINITY_sp|Q08D:DNM1  Dynamin-1 OS=Bos ta 58.90 0.00
TRINITY_sp|P023:mps7  40S ribosomal prote 58.90 0.00
TRINITY_sp|Q54U:kif3  Kinesin-related pro 58.90 0.00
TRINITY_sp|Q84K:ABCA2  ABC transporter A f 59.00 0.00
TRINITY_sp|Q9FNT:OM9-2  Mitochondrial impor 58.90 0.00
TRINITY_sp|P102:MYBL1  Myb-related protein 58.90 0.00
TRINITY_sp|Q75H:SPK10  Serine/threonine-pr 58.90 0.00
TRINITY_sp|P326:FBP26  Fructose-2,6-bispho 58.90 0.00
TRINITY_sp|P056:sacC  Levanase OS=Bacillu 58.90 0.00
TRINITY_sp|Q5B0:ccw15  Pre-mRNA-splicing f 58.90 0.00
TRINITY_sp|Q9LX:RLF  Cytochrome b5 domain 58.90 0.00
TRINITY_sp|Q9FL:At5g399(Translation factor 58.90 0.00
TRINITY_sp|Q9LM:SMD3B  Small nuclear ribon 58.90 0.00
TRINITY_sp|Q9S7:PKL  CHD3-type chromatin 58.90 0.00
TRINITY_sp|Q831:mpd1  AMP deaminase 1 OS= 58.90 0.00
TRINITY_sp|Q931:-  Actin, muscle OS=Br 58.90 0.00
TRINITY_sp|P462:-  DNA-directed RNA po 59.00 0.00
TRINITY_sp|Q9UK:CNOT11  CCR4-NOT transcript 58.90 0.00
TRINITY_sp|P078:Acac1b  3-ketoacyl-Coa thio 58.90 0.00
TRINITY_sp|Q652:KEA2  K(+) efflux antipor 58.90 0.00
TRINITY_sp|Q55D:DDB_G02:KIN17-like protein 58.90 0.00
TRINITY_sp|Q9L2:PPS2  Phosphopantothen 58.90 0.00
TRINITY_sp|Q69R:GLU  Ferredoxin-depen 58.90 0.00
TRINITY_sp|Q9SF1CCT7  T-complex protein 1  58.90  0.00
TRINITY_sp|Q9SMXPO1  Protein EXPORTIN 1A  58.90  0.00
TRINITY_sp|O823THIC  Phosphomethylpyrimi  58.90  0.00
TRINITY_sp|Q9BYSEC11C  Signal peptidase co  58.80  0.00
TRINITY_sp|Q4P2IUMAG_05  Tubulin beta chain  58.80  0.00
TRINITY_sp|Q9Z37Top3b  DNA topoisomerase 3  58.80  0.00
TRINITY_sp|Q96RBBBS4  Bardet-Biedl syndro  58.80  0.00
TRINITY_sp|B6IP2gatB  Aspartyl/glutamyl-t  58.80  0.00
TRINITY_sp|Q942Ispt16  FACT complex subuni  58.80  0.00
TRINITY_sp|P4921RPL9  60S ribosomal prote  58.80  0.00
TRINITY_sp|Q8WVI6SNRNP27  U4/U6.U5 small nucl  58.80  0.00
TRINITY_sp|P411trpl1  50S ribosomal prote  58.80  0.00
TRINITY_sp|Q86KCDDB_G02  Probable GH family  58.80  0.00
TRINITY_sp|P4781Eukaryotic transit  58.80  0.00
TRINITY_sp|P499SRP-54C  Signal recognition  58.80  0.00
TRINITY_sp|Q8RXIOVA4  Tryptophan--tRNA li  58.80  0.00
TRINITY_sp|Q9PYIDNAH2  Dynein heavy chain  58.80  0.00
TRINITY_sp|Q55DIDDB_G02  Putative methylster  58.80  0.00
TRINITY_sp|A4IFMPOLR3A  DNA-directed RNA po  58.80  0.00
TRINITY_sp|Q55GglcS  Glycogen [starch] s  58.80  0.00
TRINITY_sp|Q059myb1l  Myb-related protein  58.80  0.00
TRINITY_sp|O1498BTAFA1  TATA-binding protei  58.80  0.00
TRINITY_sp|Q54MEasns  Probable asparagine  58.80  0.00
TRINITY_sp|Q55Closgep  Probable tRNA N6-ad  58.80  0.00
TRINITY_sp|Q21C1dnaJ  Chaperone protein D  58.80  0.00
TRINITY_sp|Q8H0PFLSP1  Chloroplast process  58.80  0.00
TRINITY_sp|Q8MS2  Physarolisin OS=Phy  58.80  0.00
TRINITY_sp|Q8RHFlon  Lon protease OS=Fus  58.80  0.00
TRINITY_sp|Q9MIABCDF4  ABC transporter F  58.80  0.00
TRINITY_sp|Q8VXORFC3  Replication factor  58.80  0.00
TRINITY_sp|Q92T9Os06g05  Probable methionine  58.80  0.00
TRINITY_sp|O231HCF164  Thioredoxin-like pr  58.80  0.00
TRINITY_sp|P215-  Malate dehydrogenas  58.80  0.00
TRINITY_sp|Q31Ktsf  Elongation factor T  58.80  0.00
TRINITY_sp|O153PMM2  Phosphomannomutase  58.80  0.00
TRINITY_sp|P010C4  Complement C4 (Frag  58.70  0.00
TRINITY_sp|Q55ADDB_G02  PH and Rap-GAP doma  58.70  0.00
TRINITY_sp|P546pikA  Phosphatidylinosito  58.70  0.00
TRINITY_sp|P399DLD3  D-lactate dehydroge  58.70  0.00
TRINITY_sp|A1L2fd2hgdh  D-2-hydroxyglutarat  58.70  0.00
TRINITY_sp|Q6FLFASFI  Histone chaperone A  58.70  0.00
TRINITY_sp|Q9BMDRPS6  40S ribosomal prote  58.70  0.00
TRINITY_sp|Q6Z1JML2  Protein MEI2-like  58.70  0.00
TRINITY_sp|P0CNWCWC26  Pre-mRNA-splicing f  58.70  0.00
TRINITY_sp|Q3BAl-  Uncharacterized pro  58.70  0.00
TRINITY_sp|Q414PCM3  Putative calmodulin  58.70  0.00
TRINITY_sp|P200pyr1-3  Protein PYR1-3 OS=D  58.70  0.00
TRINITY_sp|Q60BygloB  Hydroxyacylglutathi  58.70  0.00
TRINITY_sp|P265hemA  5-aminoolvinate s  58.70  0.00
TRINITY_sp|Q8LF1DH1  Isocitrate dehydrog  58.70  0.00
TRINITY_sp|Q8LGCCDC27B  Cell division cycle  58.70  0.00
TRINITY_sp|P4IRWATG1C  Serine/threonine-pr  58.70  0.00
TRINITY_sp|Q6GPFdrbr1-a  Lariat debranching  58.70  0.00
TRINITY_sp|Q8RXWIN2  Probable protein ph  58.70  0.00
TRINITY_sp|Q88J1UM1  UDP-arabinopyranose  58.70  0.00
TRINITY_sp|P205CAH1  Carbonic anhydrase  58.70  0.00
| Accession | Description                                      | Ar. thaliana | Mus. musculus | Dictyostelium discoideum | Homo sapiens | Rattus norvegicus | T. thermophila | Zea mays | Rahnella sp. (strain Y9602) | X. laevis | G. moniliformis | D. discoideum | C. elegans | R. norvegicus | T. rubens | A. thaliana | A. thaliana |
|-----------|--------------------------------------------------|--------------|---------------|--------------------------|--------------|------------------|---------------|----------|-----------------------------|-----------|-------------------|---------------|-------------|--------------|-----------|-------------|-------------|
| sp|Q9C7:OER01| Endoplasmic reticul 58.70 0.00 |
| sp|Q9M8:SN31| Guanine nucleotide- 58.70 0.00 |
| sp|Q54I1:izic| Protein LZIC OS=Dic 58.70 0.00 |
| sp|Q666:Rs124d1| Probable ribosome b 58.60 0.00 |
| sp|P3471:pgp-1| Multidrug resistanc 58.60 0.00 |
| sp|Q96D:SNRNP40| US small nuclear ri 58.60 0.00 |
| sp|A0AT:-| Non-specific lipid- 58.60 0.00 |
| sp|Q23MT:tt116a| Probable beta-tubul 58.60 0.00 |
| sp|Q942:ilys1| Homocitrate synthas 58.60 0.00 |
| sp|Q11Q:rfps0| 3OS ribosomal prote 58.60 0.00 |
| sp|Q68W:DNAH7| Dynein heavy chain 58.60 0.00 |
| sp|Q150:EFTUD2| 116 kDa U5 small nu 58.60 0.00 |
| sp|P085:CYC1| Cytochrome c1, heme 58.60 0.00 |
| sp|Q9V6:CG6066| NKP family protein 58.60 0.00 |
| sp|Q535:il/vX| Putative acetolacta 58.60 0.00 |
| sp|Q545:shkC| Dual specificity pr 58.60 0.00 |
| sp|Q821:GDH2| Glycine cleavage sy 58.60 0.00 |
| sp|Q8V2:RIBF2| FAD synthetase 2, c 58.60 0.00 |
| sp|Q862:KLP1| Kinesin heavy chain 58.60 0.00 |
| sp|Q705:ALDH6A1| Methylmalonate-semi 58.60 0.00 |
| sp|O224:HDA19| Histone deacetylase 58.60 0.00 |
| sp|Q9S1:RPS25B| 4OS ribosomal prote 58.60 0.00 |
| sp|Q631:Dnah7| Dynein heavy chain 58.60 0.00 |
| sp|P201:CSY4| Citrate synthase 4, 58.50 0.00 |
| sp|Q8LP:ABCA8| ABC transporter A f 58.50 0.00 |
| sp|Q9VR:G01| Inositol hexakispho 58.50 0.00 |
| sp|Q66P:Cdc14b| Dual specificity pr 58.50 0.00 |
| sp|Q7NB:dnalJ| Chaperone protein D 58.50 0.00 |
| sp|A2YKO:623| Probable histone H2 58.50 0.00 |
| sp|Q54U:ucpC| Probable mitochondr 58.50 0.00 |
| sp|Q7ZV:vps29| Vacuolar protein so 58.50 0.00 |
| sp|Q8TD:HELQ| Helicase POLQ-like 58.50 0.00 |
| sp|Q9VP:C1lp| Cleavage and polyad 58.50 0.00 |
| sp|P207:MAK| Serine/threonine-pr 58.50 0.00 |
| sp|P52S:myb12| Myb-related protein 58.50 0.00 |
| sp|Q94C:Atg271| DDRGK domain-contai 58.50 0.00 |
| sp|Q869:Imdn1| Midsasin OS=Dictyost 58.50 0.00 |
| sp|O492:PPD4| PsbP domain-contain 58.50 0.00 |
| sp|H9BW:rab7| Ras-related protein 58.50 0.00 |
| sp|B0KK:cbpA| Curved DNA-binding 58.50 0.00 |
| sp|A4SM:ebp| Fructose-1,6-bispho 58.50 0.00 |
| sp|Q9SHRR:44A| Exosome complex exo 58.50 0.00 |
| sp|Q087:myb| Transcriptional act 58.50 0.00 |
| sp|Q9ZR:ABC1| ABC transporter B f 58.50 0.00 |
| sp|Q6K6:Os02g05| Ubiquitin-like modi 58.50 0.00 |
| sp|Q56A:abc8| ATP-binding cassett 58.50 0.00 |
| sp|E8XY:ttatD| 3'-'5' ssDNA/RNA exo 58.50 0.00 |
| sp|B2SAR:rlmE| Ribosomal RNA large 58.50 0.00 |
| sp|P929:APR2| 5'-adenyllysulfate 58.50 0.00 |
| sp|Q9ST1:34g83| Probable Ufmi-speci 58.50 0.00 |
| sp|Q080:At1g228| Putative methyltran 58.50 0.00 |
| sp|Q95L:CSE4| Histone H3-like cen 58.50 0.00 |
| sp|P612:DYNL1| Dynein light chain 58.40 0.00 |
| sp|P491:PH11| Glucose-6-phosphate 58.40 0.00 |
| sp|Q9CR:RPL6C| 6OS ribosomal prote 58.40 0.00 |
| sp|Q4U4:Xirp2| Xin actin-binding r 58.40 0.00 |
| Gene Name | Description | Accession | Value |
|-----------|-------------|-----------|-------|
| CYP19-2  | Peptidyl-prolyl cis-trans isomerase | sp|P93375| 58.40 |
| KAT2A    | Histone acetyltransferase | sp|Q6R2V6| 58.40 |
| AOX4     | Ubiquinol oxidase | sp|Q941Q3| 58.40 |
| GLPD     | Glycogen phosphorylase | sp|Q54XJ4| 58.40 |
| HOP      | Hsp70-Hsp90 organizing protein | sp|Q28C5| 58.40 |
| BOLA2    | Protein BOLA2 | sp|Q75JG8| 58.40 |
| DPH5     | Diphthine methyl ester synthase | sp|Q8VX3| 58.40 |
| RBN      | Ribonuclease | sp|Q9DAF| 58.40 |
| PKB      | Protein PKB | sp|Q546| 58.40 |
| PACRG    | Protein PACRG | sp|Q8LFL8| 58.40 |
| CP12     | Calvin cycle protein | sp|Q8LFL8| 58.40 |
| DDB1     | Serine/threonine protein phosphatase 2A | sp|Q86KI1| 58.40 |
| AP2A1    | Uncharacterized protein | sp|Q8LFL8| 58.40 |
| FAM49    | Protein FAM49 | sp|Q86KI1| 58.40 |
| AGAL3    | Alpha-galactosidase | sp|Q803S3| 58.40 |
| AB5F     | Alcohol dehydrogenase | sp|Q8LFL8| 58.40 |
| MEMO1    | Uncharacterized protein | sp|Q8LFL8| 58.40 |
| NB5R4    | Ribonuclease | sp|Q8LFL8| 58.40 |
| CP12     | Calvin cycle protein | sp|Q8LFL8| 58.40 |
| STT3B    | Dolichyl-diphosphoo | sp|Q8LFL8| 58.40 |
| ABCF5    | ABC transporter | sp|Q8LFL8| 58.40 |
| FPC2     | Phosphoenolpyruvate carboxykinase | sp|Q8LFL8| 58.40 |
| P289     | Elongation factor 2 | sp|Q8LFL8| 58.40 |
| ACT104   | Actin-104 | sp|Q8LFL8| 58.40 |
| ATP9b    | Probable phospholipid transfer protein | sp|Q8LFL8| 58.40 |
TRINITY_sp|P3354ABCC1 Multidrug resistance-associated protein 1 (ABCC1) 58.20 0.00
TRINITY_sp|Q0CFVATEG_0686 Leukotriene A-4 hydrolase (LTA4H) 58.20 0.00
TRINITY_sp|Q8TDWDNAH3 Dynein heavy chain 58.20 0.00
TRINITY_sp|P3789KARS Lysine--tRNA ligase 58.20 0.00
TRINITY_sp|P208l- Chlorophyll a-b bin 58.20 0.00
TRINITY_sp|Q55FtRab6 Ras-related protein 58.20 0.00
TRINITY_sp|Q54BPsmB5 Proteasome subunit 58.20 0.00
TRINITY_sp|B0G1pip5k3 1-phosphatidylinositol 58.20 0.00
TRINITY_sp|B0JXiFabH 3-oxoacyl-[acyl-carrier-protein] synthase (FABH) 58.20 0.00
TRINITY_sp|P5921HTR2 Histone H3.2 OS=Ara 58.20 0.00
TRINITY_sp|Q9FNMMBR1 PsbB mRNA maturation 58.20 0.00
TRINITY_sp|Q9M8WIN1 Acetylornithine amidohydrolase 58.20 0.00
TRINITY_sp|Q1491DRAPI Drl-1-associated core protein 58.20 0.00
TRINITY_sp|Q9LHTVHA-d2 V-type proton ATPase 58.20 0.00
TRINITY_sp|Q9UQ(MOK MAPK/MAK/MRK overla 58.20 0.00
TRINITY_sp|Q54YugpB UTP-glucose-1-phosphotransferase 58.20 0.00
TRINITY_sp|P2271Gucy1b2 Guanylate cyclase C 58.20 0.00
TRINITY_sp|Q56XAOX4 Ubiquinol oxidase 58.20 0.00
TRINITY_sp|Q6I5DCDK-1 Cyclin-dependent kinase 58.20 0.00
TRINITY_sp|Q144Ktfu1 Elongation factor Tu 58.20 0.00
TRINITY_sp|Q2XY5SPL15 Squamosa promoter-binding protein-like 58.20 0.00
TRINITY_sp|Q54Mpgc Putative phosphatidylcholine (PC) receptor 58.10 0.00
TRINITY_sp|P4171PGK Phosphoglycerate kinase 58.10 0.00
TRINITY_sp|P558SUMO1 Small ubiquitin-related modifier 58.10 0.00
TRINITY_sp|P3511UBC2 Ubiquitin-conjugating enzyme E2 58.10 0.00
TRINITY_sp|A2VE5TTC30A Tetrameric peptide transporter 58.10 0.00
TRINITY_sp|Q54Kwdr5 WD repeat-containing protein 58.10 0.00
TRINITY_sp|P3854Bm1_4472 GTP-binding nuclear protein (Ran) 58.10 0.00
TRINITY_sp|P9091djr-1.1 1-glutathione-independent glutathione reductase 58.10 0.00
TRINITY_sp|A9UNby51 Bystin OS=Monosiga brevicollis (Byslin) 58.10 0.00
TRINITY_sp|Q64MML4 Protein MEI2-like 4 58.10 0.00
TRINITY_sp|Q56KCRIP1 Cysteine-rich protease (CRIP1) 58.10 0.00
TRINITY_sp|Q54NbcA Branched-chain-amino acid transaminase (BCAT) 58.10 0.00
TRINITY_sp|Q429fkh1 Peptidyl-prolyl cis-trans isomerase (PPI) 58.10 0.00
TRINITY_sp|Q388PP2A1 Serine/threonine-protein kinase 58.10 0.00
TRINITY_sp|P153rpal DNA-directed RNA polymerase II subunit B 58.10 0.00
TRINITY_sp|Q907EEF2 Elongation factor 2 58.10 0.00
TRINITY_sp|Q9LMSMD3B Small nuclear ribonucleoprotein (SNR) 58.10 0.00
TRINITY_sp|Q8LD2PA1 Proteasome subunit 58.10 0.00
TRINITY_sp|Q54Dlstan8 Protein LST8 homolog 58.10 0.00
TRINITY_sp|Q494PGDH1 D-3-phosphoglycerate dehydrogenase 58.10 0.00
TRINITY_sp|P0770trfA General transcriptase (TRF) 58.10 0.00
TRINITY_sp|Q654Os06g0204 Pyruvate dehydrogenase 58.10 0.00
TRINITY_sp|Q1560Rsd2 Radical S-adenosyl-l-methionine (SAM) methyltransferase 58.10 0.00
TRINITY_sp|Q6DWDDG1 Digalactosyldiacylglycerol (DG) synthase 58.10 0.00
TRINITY_sp|F4ICISEC31A Protein transport system (PTS) 58.10 0.00
TRINITY_sp|Q8BGWdr2 WD repeat-containing protein 58.10 0.00
TRINITY_sp|B2RX1Abcc3 Canalicular multispecific organic anion transporter (ABCC3) 58.10 0.00
TRINITY_sp|F41VCHR10 Probable helicase C 58.10 0.00
TRINITY_sp|Q5A51NIK1 Histidine protein kinase (Hpk) 58.00 0.00
TRINITY_sp|Q9VCIIme4 Probable N6-adenosine deaminase 58.00 0.00
TRINITY_sp|Q55Bnek2 Probable serine/threonine protein kinase (PPK) 58.00 0.00
TRINITY_sp|A2VDdxx1 ATP-dependent RNA helicase (DDX1) 58.00 0.00
TRINITY_sp|Q8STabcC10 ABC transporter C family (ABC) 58.00 0.00
TRINITY_sp|Q6FJASFP Histone chaperone A 58.00 0.00
TRINITY_sp|Q60E05g03 Putative NAD kinase 58.00 0.00
| Accession | Description                                                                 | Score | E-value |
|-----------|------------------------------------------------------------------------------|-------|---------|
| sp|Q9401CCT2| T-complex protein 1 | 57.80 | 0.00    |
| sp|P052(Su(var):Heterochromatin protein) | 57.80 | 0.00    |
| sp|Q341| ATP-dependent Clp proteasome subunit | 57.80 | 0.00    |
| sp|Q226| Cyanate hydratase | 57.80 | 0.00    |
| sp|Q541| Probable methylmalonyl-CoA mutase | 57.80 | 0.00    |
| sp|Q0DL| Dynein regulatory chain | 57.80 | 0.00    |
| sp|Q744| Pyridoxine/pyridoxamine 5'-phosphate oxidase | 57.80 | 0.00    |
| sp|Q655| Molybdenum cofactor | 57.80 | 0.00    |
| sp|Q851| Probable GTF-binding factor | 57.80 | 0.00    |
| sp|Q801| DEAD-box ATP-dependent helicase | 57.80 | 0.00    |
| sp|Q803| Endoplasmic reticulum transmembrane protein | 57.80 | 0.00    |
| sp|Q8DG| Aspartyl/glutamyl-tRNA-synthetase | 57.80 | 0.00    |
| sp|Q241| Protoporphyrinogen oxidase | 57.80 | 0.00    |
| sp|Q3CL| 50S ribosomal protein L10a-2 | 57.80 | 0.00    |
| sp|Q1L2| U11/U12 small nucleolar RNA | 57.80 | 0.00    |
| sp|Q72K| Inorganic pyrophosphatase | 57.80 | 0.00    |
| sp|Q0WJ| Clathrin heavy chain | 57.80 | 0.00    |
| sp|Q9UR| Protein arginine N-methyltransferase | 57.80 | 0.00    |
| sp|Q66| DNAJ homolog subfamily B | 57.80 | 0.00    |
| sp|Q8LP| E3 ubiquitin-protein ligase | 57.80 | 0.00    |
| sp|Q55B| Probable serine/threonine-protein kinase | 57.80 | 0.00    |
| sp|Q084| Ras-like protein 3 | 57.80 | 0.00    |
| sp|Q9VF| 60S ribosomal protein L10a | 57.70 | 0.00    |
| sp|Q152| Ras-related protein | 57.70 | 0.00    |
| sp|Q54Q| Extracellular signal-regulatory protein kinase | 57.70 | 0.00    |
| sp|Q2WL| 50S ribosomal protein L25 | 57.70 | 0.00    |
| sp|Q7U0| Fructose-1,6-bisphosphatase | 57.70 | 0.00    |
| sp|Q541| Probable ATP-dependent factor | 57.70 | 0.00    |
| sp|Q66S| Kinesin-related protein | 57.70 | 0.00    |
| sp|Q54G| Coiled-coil domain | 57.70 | 0.00    |
| sp|P551| UDP-glucose 4-epimerase | 57.70 | 0.00    |
| sp|Q9W7| Cleavage and polyadenylation factor | 57.70 | 0.00    |
| sp|Q962| Phosphoserine aminotransferase | 57.70 | 0.00    |
| sp|Q8L7| THO complex subunit | 57.70 | 0.00    |
| sp|Q54J| Probable succinyl-CoA synthetase | 57.70 | 0.00    |
| sp|Q5NV| Thioredoxin reductase | 57.70 | 0.00    |
| sp|Q429| 2,3-bisphosphoglycerate kinase | 57.70 | 0.00    |
| sp|F4IA| Starch synthase 3 | 57.70 | 0.00    |
| sp|Q429| N-acetyltransferase | 57.70 | 0.00    |
| sp|P934| Histidine-5'-DNA ligase | 57.70 | 0.00    |
| sp|Q6K5| Cyclin-dependent kinase | 57.70 | 0.00    |
| sp|Q55B| Ethanolamine-phosphatase | 57.70 | 0.00    |
| sp|P629| Ras-related C3 botulinum toxin | 57.70 | 0.00    |
| sp|A819| Cilia- and flagella associated protein | 57.70 | 0.00    |
| sp|Q54P| Stromal cell-derived factor | 57.70 | 0.00    |
| sp|Q54N| NADH-cytochrome b5 reductase | 57.60 | 0.00    |
| sp|A6TU| tRNA-specific 2-thioredoxin | 57.60 | 0.00    |
| sp|Q9VL| Probable small nucleolar RNA | 57.60 | 0.00    |
| sp|Q9D| 60S acidic ribosomale | 57.60 | 0.00    |
| sp|Q9NU| Midasins | 57.60 | 0.00    |
| sp|P464| Vacuolar protein sorting protein | 57.60 | 0.00    |
| sp|P318| RNA-directed DNA polymerase | 57.60 | 0.00    |
| sp|Q54W| Density-regulated protein | 57.60 | 0.00    |
| sp|Q126| Phospholipid-translocase | 57.60 | 0.00    |
| sp|Q54F| Xanthine dehydrogenase | 57.60 | 0.00    |
| Accession | Description | Score | Value |
|-----------|-------------|-------|-------|
| TRINITY_sp|Replication factor Rfc5|57.00|0.00|
| TRINITY_sp|Vacuolar-processing|57.00|0.00|
| TRINITY_sp|Obg-like ATPase 1 O|57.00|0.00|
| TRINITY_sp|Anaphase-promoting|57.00|0.00|
| TRINITY_sp|Peptidyl-prolyl cis|57.00|0.00|
| TRINITY_sp|5OS ribosomal prote|57.00|0.00|
| TRINITY_sp|2-amino-3-ketobutyryr|57.00|0.00|
| TRINITY_sp|Malignant T-cell-am|57.00|0.00|
| TRINITY_sp|Target of rapamycin|57.00|0.00|
| TRINITY_sp|Cell differentia|57.00|0.00|
| TRINITY_sp|Probable ubiquitin-con|57.00|0.00|
| TRINITY_sp|0.00|0.00|0.00|
| TRINITY_sp|0.00|0.00|0.00|
| TRINITY_sp|Glutamyl-tRNA reductase 1, chloroplastic|56.90|0.00|
| TRINITY_sp|NHP2-like protein 1|56.90|0.00|
| TRINITY_sp|Gastric triacylglyc|56.90|0.00|
| TRINITY_sp|Cytochrome c OS=Tet|56.90|0.00|
| TRINITY_sp|Putative maltooligo|56.90|0.00|
| TRINITY_sp|Superoxide dismutas|56.90|0.00|
| TRINITY_sp|Mitotic-spindle org|56.90|0.00|
| TRINITY_sp|Pyruvate kinase OS=|56.90|0.00|
| TRINITY_sp|Rho GTPase-activati|56.90|0.00|
| TRINITY_sp|Ras-related protein|56.90|0.00|
| TRINITY_sp|Ras-related protein|56.90|0.00|
| TRINITY_sp|Serine/threonine-pr|56.90|0.00|
| TRINITY_sp|Mannitol dehydrogen|56.90|0.00|
| TRINITY_sp|Histone H2A.2 OS=Me|56.90|0.00|
| TRINITY_sp|Iron-sensing transc|56.90|0.00|
| TRINITY_sp|Splicing factor U2a|56.90|0.00|
| TRINITY_sp|Protein TabA OS=Pse|56.90|0.00|
| TRINITY_sp|Auxin transport pro|56.90|0.00|
| TRINITY_sp|Serine/threonine-pr|56.90|0.00|
| TRINITY_sp|RING-H2 finger prot|56.90|0.00|
| TRINITY_sp|Intraflagellar tran|56.90|0.00|
| TRINITY_sp|Phosphoribosylamine|56.90|0.00|
| TRINITY_sp|Probable 3',5'-cycl|56.90|0.00|
| TRINITY_sp|Probable nucleolar|56.90|0.00|
| TRINITY_sp|SKP1-like protein 1|56.90|0.00|
| TRINITY_sp|Glutamyl-tRNA reduc|56.90|0.00|
| TRINITY_sp|Dicarboxylate trans|56.90|0.00|
| TRINITY_sp|Chaperone protein D|56.90|0.00|
| TRINITY_sp|Hypersensitive-indu|56.90|0.00|
| TRINITY_sp|ATP-dependent zinc|56.90|0.00|
| TRINITY_sp|Peptidyl-prolyl cis|56.80|0.00|
| TRINITY_sp|Probable 3'-hydroxyli|56.80|0.00|
| TRINITY_sp|6OS ribosomal prote|56.80|0.00|
| TRINITY_sp|AFG3-like protein 2|56.80|0.00|
| Gene Symbol | Description | Detail Information |
|-------------|-------------|--------------------|
| myoD        | Myosin ID heavy chain | Dictyostelium discoideum |
| GFA1        | Glutamine--fructose 6-phosphate amidotransferase |  |
| SNRPD2      | Small nuclear ribonucleoprotein Sm D2 | Bos taurus |
| FTSH8       | ATP-dependent zinc metalloprotease | Arabidopsis thaliana |
| secA        | Protein translocase subunit SecA | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| get3        | ATPase get3 | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| SNRPD2      | Small nuclear ribonucleoprotein Sm D2 | Bos taurus |
| FTSH8       | ATP-dependent zinc metalloprotease | Arabidopsis thaliana |
| secA        | Protein translocase subunit SecA | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| get3        | ATPase get3 | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| SNRPD2      | Small nuclear ribonucleoprotein Sm D2 | Bos taurus |
| FTSH8       | ATP-dependent zinc metalloprotease | Arabidopsis thaliana |
| secA        | Protein translocase subunit SecA | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| get3        | ATPase get3 | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| SNRPD2      | Small nuclear ribonucleoprotein Sm D2 | Bos taurus |
| FTSH8       | ATP-dependent zinc metalloprotease | Arabidopsis thaliana |
| secA        | Protein translocase subunit SecA | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| get3        | ATPase get3 | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| SNRPD2      | Small nuclear ribonucleoprotein Sm D2 | Bos taurus |
| FTSH8       | ATP-dependent zinc metalloprotease | Arabidopsis thaliana |
| secA        | Protein translocase subunit SecA | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| get3        | ATPase get3 | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| SNRPD2      | Small nuclear ribonucleoprotein Sm D2 | Bos taurus |
| FTSH8       | ATP-dependent zinc metalloprotease | Arabidopsis thaliana |
| secA        | Protein translocase subunit SecA | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| get3        | ATPase get3 | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| SNRPD2      | Small nuclear ribonucleoprotein Sm D2 | Bos taurus |
| FTSH8       | ATP-dependent zinc metalloprotease | Arabidopsis thaliana |
| secA        | Protein translocase subunit SecA | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| get3        | ATPase get3 | Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) |
| Accession | Protein Name/Description                                      | E-value | Score |
|-----------|-------------------------------------------------------------|---------|-------|
| TRINITY_sp| Methionine gamma-lyase                                      |         |       |
| TRINITY_sp| Arogenate dehydratase                                      |         |       |
| TRINITY_sp| Succinate dehydroge                                       |         |       |
| TRINITY_sp| Dihydropyrimidinase                                       |         |       |
| TRINITY_sp| 40S ribosomal prote                                       |         |       |
| TRINITY_sp| ABC transporter D f                                        |         |       |
| TRINITY_sp| Ubiquitin-2 OS=Mus                                         |         |       |
| TRINITY_sp| Thioredoxin reducta                                       |         |       |
| TRINITY_sp| Ribulose-phosphate                                        |         |       |
| TRINITY_sp| tRNA(His) guanylylt                                      |         |       |
| TRINITY_sp| Chlorophyll a-b bin                                        |         |       |
| TRINITY_sp| Photosystem II reac                                        |         |       |
| TRINITY_sp| DNA replication lic                                       |         |       |
| TRINITY_sp| Malate synthase OS=                                       |         |       |
| TRINITY_sp| Dynein beta chain,                                        |         |       |
| TRINITY_sp| 5'-AMP-activated se                                       |         |       |
| TRINITY_sp| Phosphoribosylformy                                        |         |       |
| TRINITY_sp| ADP/ATP translocase                                        |         |       |
| TRINITY_sp| Peptide methionine                                        |         |       |
| TRINITY_sp| ADP-ribosylation fa                                       |         |       |
| TRINITY_sp| Glutathione peroxid                                        |         |       |
| TRINITY_sp| Protein ref(2)P OS=                                        |         |       |
| TRINITY_sp| Ras-related protein                                        |         |       |
| TRINITY_sp| 40S ribosomal prote                                        |         |       |
| TRINITY_sp| Asparagine--tRNA li                                       |         |       |
| TRINITY_sp| Ras-like protein 2                                         |         |       |
| TRINITY_sp| 60S ribosomal prote                                        |         |       |
| TRINITY_sp| Threonine--tRNA lig                                       |         |       |
| TRINITY_sp| NEDD8-conjugating e                                       |         |       |
| TRINITY_sp| Aspartokinase 2, ch                                        |         |       |
| TRINITY_sp| Protein URA2 OS=Sac                                        |         |       |
| TRINITY_sp| ER lumen protein-re                                       |         |       |
| TRINITY_sp| Nuclear/nucleolar G                                        |         |       |
| TRINITY_sp| Glutaminate--fructose                                      |         |       |
| TRINITY_sp| Cytosolic carboxyype                                       |         |       |
| TRINITY_sp| Trafficking protein                                        |         |       |
| TRINITY_sp| Glycogen synthase k                                       |         |       |
| TRINITY_sp| Threonine--tRNA lig                                       |         |       |
| TRINITY_sp| Extracellular signa                                       |         |       |
| TRINITY_sp| Methylmalonyl-CoA e                                       |         |       |
| TRINITY_sp| Protein SEC13 homol                                       |         |       |
| TRINITY_sp| Leishmanolysin-like                                       |         |       |
| TRINITY_sp| Actin, cytoplasmian                                        |         |       |
| TRINITY_sp| 60S ribosomal prote                                        |         |       |
| TRINITY_sp| Inosine-5'-monophos                                       |         |       |
| TRINITY_sp| Proline--tRNA ligas                                       |         |       |
| TRINITY_sp| Serine/threonine-pr                                       |         |       |
| TRINITY_sp| Protein SEC13 homol                                       |         |       |
| TRINITY_sp| DNA-directed DNA po                                       |         |       |
| TRINITY_sp| Thioredoxin OS=Egu                                        |         |       |
| TRINITY_sp| DNA replication lic                                       |         |       |
| TRINITY_sp| UDP-glucose:glycopr                                       |         |       |
| TRINITY_sp| 50S ribosomal prote                                        |         |       |
| Accession       | Protein Name                                      | Description                                      | Score | E-value |
|-----------------|---------------------------------------------------|--------------------------------------------------|-------|---------|
| Q5631-          | Eukaryotic translation factor                     | 56.20                                            |       |         |
| Q532X-FKBP53    | Peptidyl-prolyl cis PE-diesterase                 | 56.20                                            |       |         |
| Q345J-papA      | Poly(A) polymerase                                | 56.20                                            |       |         |
| Q5971-dph1      | Diphthamide biosynth                             | 56.20                                            |       |         |
| Q6Y2Y-RFC3      | Replication factor                               | 56.20                                            |       |         |
| Q9123-Smarca5   | SWI/SNF-related mat                 | 56.20                                            |       |         |
| Q6R3-Poli       | DNA polymerase iota                               | 56.20                                            |       |         |
| Q8754-myb       | Transcriptional act                               | 56.20                                            |       |         |
| Q9455-sua5      | Threonylcarbamoyl-A                              | 56.30                                            |       |         |
| Q6315-Dnah1     | Dynein heavy chain                               | 56.30                                            |       |         |
| Q807q-glplv     | Glycogen phosphoryl dehyd                        | 56.30                                            |       |         |
| Q9479-PMP2      | Myelin P2 protein O                              | 56.20                                            |       |         |
| Q5456-POL3      | DNA polymerase delta                             | 56.20                                            |       |         |
| Q7564-SNRP20    | US small nuclear ribosomes                        | 56.20                                            |       |         |
| Q9544-SAR1      | Small COPII coat GT                              | 56.20                                            |       |         |
| Q972P-NEK1      | Serine/threonine-propylase                       | 56.20                                            |       |         |
| Q5841-lpd       | Dihydrolipoyl dehyd                              | 56.20                                            |       |         |
| Q9479-PMP2      | Myelin P2 protein O                              | 56.20                                            |       |         |
| Q9544-SAR1      | Small COPII coat GT                              | 56.20                                            |       |         |
| Q9544-SAR1      | Small COPII coat GT                              | 56.20                                            |       |         |
| Q9544-SAR1      | Small COPII coat GT                              | 56.20                                            |       |         |
| Gene/ID | Protein Name                          | Species                  | Accession | Score |
|--------|---------------------------------------|--------------------------|-----------|-------|
| TRINITY_sp| Q84Q1| Phosphoenolpyruvate phosphate translocator 2 | Oryza sativa subsp. japonica | PPT2  | 56.20 |
| TRINITY_sp| Q141| Probable ATP-dependent protein | Oryza sativa subsp. japonica | MEI2-like 3 | 56.20 |
| TRINITY_sp| Q5PQ4- | Uncharacterized protein | Oryza sativa subsp. japonica | Structural maintena | 56.20 |
| TRINITY_sp| Q54F1 | NADH dehydrogenase | Oryza sativa subsp. japonica | PTP2  | 56.20 |
| TRINITY_sp| Q704F | Methionine synthase | Oryza sativa subsp. japonica | MTR  | 56.20 |
| TRINITY_sp| Q8BDJ3 | Chaperone protein C | Oryza sativa subsp. japonica | Multidrug resistant | 56.20 |
| TRINITY_sp| Q5F3 | Multidrug resistance protein | Oryza sativa subsp. japonica | ABC1 | 56.20 |
| TRINITY_sp| Q75S | RNAaseH2 ribonuclease H2 | Oryza sativa subsp. japonica | Autophagy-related | 56.20 |
| TRINITY_sp| Q44 | Endoribonuclease YS | Oryza sativa subsp. japonica | ADP-ribosylation factor | 56.20 |
| TRINITY_sp| Q74Z | Protein FIZZY-RELATED | Oryza sativa subsp. japonica | URA3 | 56.20 |
| TRINITY_sp| Q96B | ADP-ribosylation factor | Oryza sativa subsp. japonica | ARS1  | 56.20 |
| TRINITY_sp| Q4N5 | V-type proton ATPase | Oryza sativa subsp. japonica | FYH1  | 56.20 |
| TRINITY_sp| Q4V1 | 40S ribosomal protein | Oryza sativa subsp. japonica | Subunit 21 | 56.20 |
| TRINITY_sp| Q23F | Tubulin | Oryza sativa subsp. japonica | Glycylated | 56.20 |
| TRINITY_sp| Q9X7 | Protein FZB | Oryza sativa subsp. japonica | FZB | 56.20 |
| TRINITY_sp| Q34L | Major vault protein | Oryza sativa subsp. japonica | Major vault protein | 56.20 |
| TRINITY_sp| Q4G2 | Glutathionyl-hydroquinone reductase | Oryza sativa subsp. japonica | GLY | 56.20 |
| TRINITY_sp| Q182 | Chaperone protein D | Oryza sativa subsp. japonica | Chaperone protein D | 56.20 |
| TRINITY_sp| Q9BL | Ammonium transporter | Oryza sativa subsp. japonica | AMT1  | 56.20 |
| TRINITY_sp| Q341 | 3-hydroxy-3-methylglutaryl CoA | Oryza sativa subsp. japonica | Reductase | 56.20 |
| TRINITY_sp| Q9SS1 | 40S ribosomal protein | Oryza sativa subsp. japonica | 24A  | 56.20 |
| TRINITY_sp| Q5A4 | Transcriptional regulator | Oryza sativa subsp. japonica | SMC3 | 56.20 |
| TRINITY_sp| Q59 | Peptidyl-prolyl cis-trans isomerase | Oryza sativa subsp. japonica | FZR1  | 56.20 |
| TRINITY_sp| Q459 | ATP phosphoribosyltransferase | Oryza sativa subsp. japonica | ATP | 56.20 |
| TRINITY_sp| P468 | Kinesin-like protein | Oryza sativa subsp. japonica | KINESIN | 56.20 |
| TRINITY_sp| P104 | Phosphatidylinositol transferase | Oryza sativa subsp. japonica | PI3K | 56.20 |
| TRINITY_sp| Q9SJ | Ubiquitin-conjugating enzyme | Oryza sativa subsp. japonica | UBC10 | 56.20 |
| TRINITY_sp| Q791 | Cleavage and polyadenylation specificity factor subunit 3 | Oryza sativa subsp. japonica | PPS21 | 56.20 |
| TRINITY_sp| P114 | Superoxide dismutase | Oryza sativa subsp. japonica | 1  | 56.20 |
| TRINITY_sp| Q9LZ | Ras-related protein | Oryza sativa subsp. japonica | Ras-related protein | 56.20 |
| TRINITY_sp| Q076 | Small nuclear ribonucleoprotein | Oryza sativa subsp. japonica | SnRNP | 56.20 |
| TRINITY_sp| Q93W | Protein S6 kinase | Oryza sativa subsp. japonica | 421 | 56.20 |
| TRINITY_sp| P56 | Eukaryotic translation initiation factor 4E | Oryza sativa subsp. japonica | EEF1 | 56.20 |
| TRINITY_sp| Q6C4 | ATP-dependent RNA helicase | Oryza sativa subsp. japonica | RABE1D | 56.20 |
| TRINITY_sp| Q387 | Thiamine thiazole synthase | Oryza sativa subsp. japonica | THIAMINE | 56.20 |
| TRINITY_sp| Q3M1 | Putative tRNA synthetase | Oryza sativa subsp. japonica | 10 | 56.20 |
| TRINITY_sp| B7 | ATP-dependent zinc metalloprotease | Oryza sativa subsp. japonica | 1 | 56.20 |
| TRINITY_sp| Q126 | Phospholipid-transfer protein | Oryza sativa subsp. japonica | 4 | 56.20 |
| TRINITY_sp| Q943 | Structural maintenance protein | Oryza sativa subsp. japonica | PSMA1 | 56.20 |
| TRINITY_sp| Q9DA | Parkin coregulator | Oryza sativa subsp. japonica | PARKIN | 56.20 |
| TRINITY_sp| Q395 | GTP-binding protein | Oryza sativa subsp. japonica | GTP-binding protein | 56.20 |
| TRINITY_sp| Q75M | Protein ME2-like | Oryza sativa subsp. japonica | ME2 | 56.20 |
| TRINITY_sp| Q396 | 5-methyltetrahydrofolate | Oryza sativa subsp. japonica | FH4 | 56.20 |
| TRINITY_sp| Q099 | Aldo-keto reductase | Oryza sativa subsp. japonica | AKR | 56.20 |
| TRINITY_sp| Q6BV | Plasma membrane protein | Oryza sativa subsp. japonica | PM | 56.20 |
| TRINITY_sp| Q12X | Guanine exchange factor | Oryza sativa subsp. japonica | GEF | 56.20 |
| TRINITY_sp| Q54M | 2-oxoisovalerate dehydrogenase | Oryza sativa subsp. japonica | 2OXID | 56.20 |
| TRINITY_sp| Q8HL | Os07g01010 | Oryza sativa subsp. japonica | DFR | 56.20 |
| TRINITY_sp| Q154 | Multidrug resistance protein | Oryza sativa subsp. japonica | ABCC4 | 56.20 |
| Protein Name | Description | Score | Identity |
|--------------|-------------|-------|----------|
| Pyruvate dehydrogen | 56.00 | 0.00 |
| TRINITY_sp|529(- | Protein DEFECTIVE | 56.00 | 0.00 |
| TRINITY_sp|F4IA|DEX1 | 56.00 | 0.00 |
| TRINITY_sp|Q0PG|AKR4C9 | 56.00 | 0.00 |
| TRINITY_sp|O489|POD1 | 56.00 | 0.00 |
| TRINITY_sp|Q8RW|NAPRT1 | 56.00 | 0.00 |
| TRINITY_sp|Q056|dnaJ | 56.00 | 0.00 |
| TRINITY_sp|O22|GCP1 | 56.00 | 0.00 |
| TRINITY_sp|Q23F|TTLL3C | 56.00 | 0.00 |
| TRINITY_sp|Q9S5|SYNC1 | 56.00 | 0.00 |
| TRINITY_sp|Q8W4|ICYP71 | 56.00 | 0.00 |
| TRINITY_sp|A40Q|VITIF1 | 56.00 | 0.00 |
| TRINITY_sp|F4K5|RVE2 | 56.00 | 0.00 |
| TRINITY_sp|Q5W9|USP | 56.00 | 0.00 |
| TRINITY_sp|P162|F9 | 55.90 | 0.00 |
| TRINITY_sp|Q6ZW|Ube2d2b | 55.90 | 0.00 |
| TRINITY_sp|Q946|- | 55.90 | 0.00 |
| TRINITY_sp|Q5U8|dhkA | 55.90 | 0.00 |
| TRINITY_sp|Q86C|tor | 55.90 | 0.00 |
| TRINITY_sp|Q5RJ|DDB_G02| Probable iron/ascor | 55.90 | 0.00 |
| TRINITY_sp|P456|piK | 55.90 | 0.00 |
| TRINITY_sp|P623|CPK4 | 55.90 | 0.00 |
| TRINITY_sp|P252|NFYB | 55.90 | 0.00 |
| TRINITY_sp|O665|aq_141 | 55.90 | 0.00 |
| TRINITY_sp|Q9DA|Pacrg | 55.90 | 0.00 |
| TRINITY_sp|P484|CNAG_00 | Actin OS=Cryptococcus | 55.90 | 0.00 |
| TRINITY_sp|P412|Abca2 | 55.90 | 0.00 |
| TRINITY_sp|O8K6|Kap2al-1 | AP-2 complex subunit | 55.90 | 0.00 |
| TRINITY_sp|Q0PS|RBMB42 | RNA-binding protein | 55.90 | 0.00 |
| TRINITY_sp|Q452|hbdA | 3-hydroxybutyryl-Co | 55.90 | 0.00 |
| TRINITY_sp|Q653|SPS1 | Solanesyl-diphospha | 55.90 | 0.00 |
| TRINITY_sp|Q557|s110608 | Ycf49-like protein | 55.90 | 0.00 |
| TRINITY_sp|Q54VI|riol | Serine/threonine-pr | 55.90 | 0.00 |
| TRINITY_sp|Q94I|GGPS | Geranylgeranyl pyro | 55.90 | 0.00 |
| TRINITY_sp|Q2Q|PYGK1 | Guanylate kinase 1 | 55.90 | 0.00 |
| TRINITY_sp|Q405|AOX2 | Ubiquinol oxidase 2 | 55.90 | 0.00 |
| TRINITY_sp|P328|IMP3 | U3 small nucleolar | 55.90 | 0.00 |
| TRINITY_sp|P932| |- | Zeaxanthin epoxidases | 55.90 | 0.00 |
| TRINITY_sp|Q5R4|XRN2 | 5'-3' exoribonuclea | 55.90 | 0.00 |
| TRINITY_sp|Q8PF|IdusA | tRNA-dihydouridine | 55.90 | 0.00 |
| TRINITY_sp|Q9MM|MPT3 | Mitochondrial phosph | 55.90 | 0.00 |
| TRINITY_sp|O181|gqt-1 | UDP-N-acetylglucosa | 55.90 | 0.00 |
| TRINITY_sp|P402|CKB1 | Casein kinase II su | 55.90 | 0.00 |
| TRINITY_sp|Q93V|RPS1 | 3OS ribosomal prote | 55.90 | 0.00 |
| TRINITY_sp|Q54X|ap1b1 | AP-1 complex subunit | 55.90 | 0.00 |
| TRINITY_sp|Q8DI|hemC | Porphobilinogen dea | 55.90 | 0.00 |
| TRINITY_sp|Q6P8|Capsl | Calcypohsin-like pr | 55.90 | 0.00 |
| TRINITY_sp|Q9FR|AM11 | Amidase 1 OS=Arabid | 55.90 | 0.00 |
| TRINITY_sp|Q550|rheb | GTP-binding protein | 55.90 | 0.00 |
| TRINITY_sp|Q5R6|RPP1 | Ribosome production | 55.90 | 0.00 |
| TRINITY_sp|Q8HI|PYD3 | Beta-ureidopropionia | 55.90 | 0.00 |
| TRINITY_sp|G0S8|CTHT_00 | Eukaryotic translat | 55.90 | 0.00 |
| TRINITY_sp|Q045|SNL4 | Paired amphipathic | 55.90 | 0.00 |
| TRINITY_sp|Q3S6|CDKE-1 | Cyclin-dependent ki | 55.90 | 0.00 |
| TRINITY_sp|Q2Q4|BSL2 | Serine/threonine-pr | 55.90 | 0.00 |
| TRINITY_sp|P281|RABD2A | Ras-related protein | 55.90 | 0.00 |
| TRINITY_sp|Q9SHE|PSAF | Photosystem I react | 55.80 | 0.00 |
| Gene ID         | Description                                      | Protein Name | Accession | Value 1 | Value 2 |
|----------------|--------------------------------------------------|--------------|-----------|---------|---------|
| TRINITY_sp|ADP-ribosylation factor 2 Drosophila melanogaster| Arf102F      | Q9A7J9    | 55.80   | 0.00    |
| TRINITY_sp|Serine/threonine-protein kinase 34 Arabidopsis thaliana| CPK34       | Q66K55    | 55.80   | 0.00    |
| TRINITY_sp|Target of rapamycin Dictyostelium discoideum| Tor         | A2P220    | 55.80   | 0.00    |
| TRINITY_sp|Cilia-and flagella-associated protein 206 Tetrahymena thermophila| CFAP206    | Q9Y4Q4    | 55.80   | 0.00    |
| TRINITY_sp|Ubiquitin-conjugating enzyme E2-16 kDa Colletotrichum gloeosporioides| UBC1        | Q8XSW0    | 55.80   | 0.00    |
| TRINITY_sp|Long chain acyl-CoA synthetase 3 Arabidopsis thaliana| LACS3      | Q5O059    | 55.80   | 0.00    |
| TRINITY_sp|Cyclin-dependent kinase-like 5 Homo sapiens| CDKL5      | P46412    | 55.80   | 0.00    |
| TRINITY_sp|Probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase Mus musculus| Alg8       | Q9W6V9    | 55.80   | 0.00    |
| TRINITY_sp|Dynein heavy chain 1, axonemal Rattus norvegicus| Dnah1     | P46412    | 55.80   | 0.00    |
| TRINITY_sp|Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial Dictyostelium discoideum| MCCA       | Q9W6V9    | 55.80   | 0.00    |
| TRINITY_sp|Methylated-DNA-protein-cysteine methyltransferase Mycobacterium paratuberculosis| Ogt       | Q9W6V9    | 55.80   | 0.00    |
| TRINITY_sp|Calcium-transporting ATPase 2, endoplasmic reticulum-type Arabidopsis thaliana| ECA2       | Q9W6V9    | 55.80   | 0.00    |
| TRINITY_sp|Glutamine--tRNA ligase Lupinus luteus| GalK       | Q9W6V9    | 55.80   | 0.00    |
| TRINITY_sp|Putative phospholipase A2 Schizosaccharomyces pombe| PLG7      | Q9W6V9    | 55.80   | 0.00    |
| TRINITY_sp|Putative vacuolar protein sorting-associated protein 13A Dictyostelium discoideum| VPS13A    | Q9W6V9    | 55.80   | 0.00    |
| TRINITY_sp|Hydroxymethylglutaryl-CoA synthase A Dictyostelium discoideum| HGS A      | Q9W6V9    | 55.80   | 0.00    |
| TRINITY_sp|Aspartate--tRNA ligase Schizosaccharomyces pombe| DPS1      | Q9W6V9    | 55.80   | 0.00    |
| TRINITY_sp|25S rRNA (cytosine-C(5))-methyltransferase Schizosaccharomyces pombe| Nop2      | Q9W6V9    | 55.80   | 0.00    |
TRINITY_sp|Q9FJ7|TOP1B  DNA topoisomerase 1  55.70  0.00
TRINITY_sp|Q86ZK|klp1     Kinesin heavy chain     55.70  0.00
TRINITY_sp|Q860;bhdA  D-beta-hydroxybutyryl 55.70  0.00
TRINITY_sp|Q963;SPY   Probable UDP-N-acetyl 55.70  0.00
TRINITY_sp|Q266;+      Thioredoxin peroxidase  55.60  0.00
TRINITY_sp|A5D7;DDX52  Probable ATF-depend  55.60  0.00
TRINITY_sp|Q9CO;DNAH6  Dynein heavy chain   55.60  0.00
TRINITY_sp|Q92Q;IMBR1  E3 ubiquitin-protein  55.60  0.00
TRINITY_sp|Q9LD;DFP5   7-dehydrocholesterol 55.60  0.00
TRINITY_sp|Q54X;DDB_G02 DEP domain-contain  55.60  0.00
TRINITY_sp|A8EX;mmnG  tRNA uridine 5-carb  55.60  0.00
TRINITY_sp|Q94K;At3g581 Phenylalanine--tRNA 55.60  0.00
TRINITY_sp|Q9FF;UBC22  Ubiquitin-conjugat  55.60  0.00
TRINITY_sp|Q9SB;AP4M   AP-4 complex subuni  55.60  0.00
TRINITY_sp|Q54D;gcvT   Aminomethyltransferase 55.60  0.00
TRINITY_sp|Q944;ubCB   Ubiquitin conjugat  55.60  0.00
TRINITY_sp|Q9NP;UBE2T  Ubiquitin-conjugat  55.60  0.00
TRINITY_sp|Q9WV;Mok    MAPK/MAK/MRK overla  55.60  0.00
TRINITY_sp|O141;lys12  Homoisoisocitrate dehy 55.60  0.00
TRINITY_sp|Q5Z8;Os06g055 Probable inositol o 55.60  0.00
TRINITY_sp|P534;CYTA  Actin, cytoskeletal    55.60  0.00
TRINITY_sp|Q54E;rpc19  DNA-directed RNA po  55.60  0.00
TRINITY_sp|Q0VD;VPS4B  Vacuolar protein so  55.60  0.00
TRINITY_sp|Q753;VPS4B  Vacuolar protein so  55.60  0.00
TRINITY_sp|Q9UQ;MOK    MAPK/MAK/MRK overla  55.60  0.00
TRINITY_sp|Q926;GCN1  eIF-2-alpha kinase     55.60  0.00
TRINITY_sp|P139;G2+    G2/mitotic-specific   55.60  0.00
TRINITY_sp|P529;14-3-3 Probable beta-tubul  55.60  0.00
TRINITY_sp|Q23M;Ttl16a Probable beta-tubul  55.60  0.00
TRINITY_sp|Q9SB;AP4M   AP-4 complex subuni  55.60  0.00
TRINITY_sp|Q75M;ML3   Protein MEI2-like 3   55.60  0.00
TRINITY_sp|P141;AAC4  AAC-rich mRNA clone   55.60  0.00
TRINITY_sp|Q10N;V2  Guanylate kinase 2,  55.60  0.00
TRINITY_sp|Q54G;nsa2  Ribosome biogenesis   55.60  0.00
TRINITY_sp|Q54S;sf3b3  Probable splicing f  55.60  0.00
TRINITY_sp|Q9SB;ABC1  Protein ABC transpo  55.60  0.00
TRINITY_sp|Q275;thyB   Thymidine kinase 1  55.60  0.00
TRINITY_sp|Q9SY;RHM1  Trifunctional UDP-g  55.60  0.00
TRINITY_sp|Q9FL;NRPB12 DNA-directed RNA po  55.60  0.00
TRINITY_sp|Q9P7;ras2   Probable DNA-direct  55.60  0.00
TRINITY_sp|Q9FS;MD1  Malate dehydrogenas  55.60  0.00
TRINITY_sp|Q5VQ;Os06g013 Translation factor  55.60  0.00
TRINITY_sp|P548;P5CSB  Delta-1-pyruvino  55.60  0.00
TRINITY_sp|Q3V0;Dna12  Dynein heavy chain  55.60  0.00
TRINITY_sp|Q9ZQ;IMBR1  E3 ubiquitin-protein  55.60  0.00
TRINITY_sp|Q9D7;Acad8  Isobutyryl-CoA dehy  55.60  0.00
TRINITY_sp|Q7X8;GATA  Glutamyl-tRNA(Gln)  55.60  0.00
TRINITY_sp|Q54T;rio2   Serine/threonine-pr  55.60  0.00
TRINITY_sp|Q059;gpx1   Glutathione peroxid  55.60  0.00
TRINITY_sp|Q9CG;ABC14  ABC transporter G f  55.60  0.00
TRINITY_sp|P427;CLBP1  Chaperone protein C  55.60  0.00
TRINITY_sp|Q8NB;RDH13  Retinol dehydrogena  55.50  0.00
TRINITY_sp|D4BQ;ARB_020 Probable glucan end  55.50  0.00
TRINITY_sp|P039;rasD  Ras-like protein ra  55.50  0.00
TRINITY_sp|Q631;Abcc2  Canalicular multis  55.50  0.00
TRINITY_sp|P372;dis3   Exosome complex exo  55.50  0.00
| Accession       | Description                                                                 | Homo sapiens | Homo sapiens |
|----------------|-----------------------------------------------------------------------------|--------------|--------------|
| TRINITY_sp|O226|DEGP1|Protease Do-like 1, chloroplastic OS=Arabidopsis thaliana GN=DEGP1 PE=1 SV=2|55.50|0.00|
| TRINITY_sp|P499|Ctsh|Pro-cathepsin H OS=|55.50|0.00|
| TRINITY_sp|Q8BWK|Kdm4a|Lysine-specific dem|55.50|0.00|
| TRINITY_sp|Q8BUH|Tnnl14b|Thioredoxin-like pr|55.50|0.00|
| TRINITY_sp|Q6ZHO|Os02g07|Putative D-cysteine|55.50|0.00|
| TRINITY_sp|P9196|ADP-ribosylation fa|55.50|0.00|
| TRINITY_sp|Q328I|IMP3|U3 small nucleolar|55.50|0.00|
| TRINITY_sp|Q4361|ADP-ribosylation fa|55.50|0.00|
| TRINITY_sp|Q007g1lpV|Glycogen phosphoryl|55.50|0.00|
| TRINITY_sp|Q7SYt|qtrtt1|Queine tRNA-ribosy|55.50|0.00|
| TRINITY_sp|P247S|ATP1A2|Sodium/potassium-tr|55.50|0.00|
| TRINITY_sp|A8IEI|PRMT1|Protein arginine N-|55.50|0.00|
| TRINITY_sp|P312U|UBA2|Ubiquitin-activatin|55.50|0.00|
| TRINITY_sp|Q6506|PBC1|Proteasome subunit|55.50|0.00|
| TRINITY_sp|Q961F|PYURF|Protein preY, mitoc|55.40|0.00|
| TRINITY_sp|P403R|RIC1|Ras-related protein|55.40|0.00|
| TRINITY_sp|P4061|F01G4.6|Phosphate carrier|55.40|0.00|
| TRINITY_sp|P365S|rpb6|DNA-directed RNA po|55.40|0.00|
| TRINITY_sp|Q917g1gsk3b|Glycogen synthase k|55.40|0.00|
| TRINITY_sp|P1322|PCT1|Choline-phosphate c|55.40|0.00|
| TRINITY_sp|Q54Xkbrk1|Protein BRICK1 OS=D|55.40|0.00|
| TRINITY_sp|Q552vcch1|Probable cytochrome|55.40|0.00|
| TRINITY_sp|P5514|Glutaredoxin OS=Ric|55.40|0.00|
| TRINITY_sp|P176f|fgg|Fibrinogen gamma ch|55.40|0.00|
| TRINITY_sp|Q7T31ccdc25|Coiled-coil domain-|55.40|0.00|
| TRINITY_sp|P341lmpvA|Major vault protein|55.40|0.00|
| TRINITY_sp|Q059g|GRP10|Glycine-rich RNA-bi|55.40|0.00|
| TRINITY_sp|Q5RGjgnptab|N-acetylglucosamine|55.40|0.00|
| TRINITY_sp|P128P|Triosephosphate iso|55.40|0.00|
| TRINITY_sp|Q8LParah3|Protein FIZZY-RELAT|55.40|0.00|
| TRINITY_sp|P114P|PSBP|Oxygen-evolving enh|55.40|0.00|
| TRINITY_sp|B6JK|acsA|Acetyl-coenzyme A s|55.40|0.00|
| TRINITY_sp|A4IIlttc26|Intraflagellar tran|55.40|0.00|
| TRINITY_sp|A2XY|PRMT6.1|Probable protein ar|55.40|0.00|
| TRINITY_sp|Q54Rjddd|G02|Delta-1-pyrroline-5|55.40|0.00|
| TRINITY_sp|B9RARCOM15|Probable aspartyl a|55.40|0.00|
| TRINITY_sp|Q1JP|farsa|Phenylalanine--tRNA|55.40|0.00|
| TRINITY_sp|P0AF|mog|Molybdopterin adeny|55.40|0.00|
| TRINITY_sp|Q9LYF|PKBP19|Peptidyl-prolyl cis|55.40|0.00|
| TRINITY_sp|O677jasd|Aspartate-semialdeh|55.40|0.00|
| TRINITY_sp|Q0088|repB|TFIH basal transcr|55.40|0.00|
| TRINITY_sp|Q134SSF3|B2|Splicing factor 3B|55.40|0.00|
| TRINITY_sp|Q5RFALDH2|Aldehyde dehydrogen|55.40|0.00|
| TRINITY_sp|Q2QMKMCCA|Methylcrotonoyl-CoA|55.40|0.00|
| TRINITY_sp|P334g|SOD1|Superoxide dismutas|55.40|0.00|
| TRINITY_sp|O044U|UCH2|Ubiquitin carboxyb-|55.40|0.00|
| TRINITY_sp|Q9ZM4RH28|DEAD-box ATP-depend|55.40|0.00|
| TRINITY_sp|P459AP|DNA-(apurinic or ap|55.40|0.00|
| TRINITY_sp|P0D3JRPL18A|60S ribosomal prote|55.30|0.00|
| TRINITY_sp|Q020P|rad3|Protein kinase rad3|55.30|0.00|
| TRINITY_sp|Q23MT|Ttl116a|Probable beta-tubul|55.30|0.00|
| TRINITY_sp|Q9L2RABE1D|Ras-related protein|55.30|0.00|
| TRINITY_sp|Q219RA1F4.1|Probable glycerol k|55.30|0.00|
| TRINITY_sp|Q9USkklp3|Kinesin-like protei|55.30|0.00|
| TRINITY_sp|Q9ZSA4ts492|Probable 3-hydroxyi|55.30|0.00|
| TRINITY_sp|Q86A_cpsf3|Cleavage and polyad|55.30|0.00|
| Gene Name                | Description                      | Accession | E Value | Bit Score |
|-------------------------|----------------------------------|-----------|---------|-----------|
| TRINITY_sp|P0C8H|CCRP1 | Probable serine/threonine-protein kinase | 55.30 | 0.00 |
| TRINITY_sp|Q940F|SRK2E | Serine/threonine-protein kinase | 55.30 | 0.00 |
| TRINITY_sp|Q554E|slr0537 | Uncharacterized sugar kinase | 55.30 | 0.00 |
| TRINITY_sp|Q54D|comG | Aldehyde dehydrogenase | 55.30 | 0.00 |
| TRINITY_sp|Q8WXW|DNAH7 | Dynein heavy chain | 55.30 | 0.00 |
| TRINITY_sp|A5N69|dnaJ | Chaperone protein D | 55.30 | 0.00 |
| TRINITY_sp|Q6S0|kif6 | Kinesin-related protein | 55.30 | 0.00 |
| TRINITY_sp|Q9LJ3|MAPK3 | MAPK3 epsilon protease | 55.30 | 0.00 |
| TRINITY_sp|O236A|At1g29880 | Glycine--tRNA ligase | 55.30 | 0.00 |
| TRINITY_sp|Q9FXF|STT3B | Dolichyl-diphosphooligosaccharide-protein N-acetylglucosaminyltransferase | 55.30 | 0.00 |
| TRINITY_sp|P056|CTS2 | Cathepsin Z | 55.30 | 0.00 |
| TRINITY_sp|Q55B|sod2 | Superoxide dismutase | 55.30 | 0.00 |
| TRINITY_sp|O353|Abcc1 | Multidrug resistance protein | 55.30 | 0.00 |
| TRINITY_sp|Q9VDB|CG6353 | Protein archease-like | 55.20 | 0.00 |
| TRINITY_sp|Q54N|derl2 | Probable derlin-2 | 55.20 | 0.00 |
| TRINITY_sp|Q55G|ChLim | Calponin homology a | 55.20 | 0.00 |
| TRINITY_sp|Q9SZI|HISN4 | Imidazole glycerol kinase | 55.20 | 0.00 |
| TRINITY_sp|Q91VJ|Duufs1 | NADH-ubiquinone oxidoreductase | 55.20 | 0.00 |
| TRINITY_sp|Q3MFr|fpsQ | 3OS ribosomal protein | 55.20 | 0.00 |
| TRINITY_sp|P395|DRS2 | Probable phospholipid-transferase | 55.20 | 0.00 |
| TRINITY_sp|P265|At2g3067 | Histone H1.2 | 55.20 | 0.00 |
| TRINITY_sp|Q9FGF|PUB50 | Putative U-box domain | 55.20 | 0.00 |
| TRINITY_sp|Q112|PARP2 | Poly [ADP-ribose] polymerase | 55.20 | 0.00 |
| TRINITY_sp|Q54I|ndrB | Probable serine/threonine-protein kinase | 55.20 | 0.00 |
| TRINITY_sp|Q4IH5|SYD | Chromatin structure | 55.20 | 0.00 |
| TRINITY_sp|Q097F|pan2 | PAB-dependent poly(A) binding protein | 55.20 | 0.00 |
| TRINITY_sp|Q8PVV|ubc15 | Ubiquitin-conjugating enzyme | 55.20 | 0.00 |
| TRINITY_sp|P266|VARS | Valine--tRNA ligase | 55.20 | 0.00 |
| TRINITY_sp|Q8WW7|ICYP71 | Peptidyl-prolyl cis-trans isomerase | 55.20 | 0.00 |
| TRINITY_sp|Q271|KIN11D | Kinesin-like protein | 55.20 | 0.00 |
| TRINITY_sp|P283|acuE | Malate synthase | 55.20 | 0.00 |
| TRINITY_sp|Q54N|gnp3 | GTPase | 55.20 | 0.00 |
| TRINITY_sp|Q84W1|SHM7 | Serine hydroxymethyltransferase | 55.20 | 0.00 |
| TRINITY_sp|Q52Q|AIL6 | AP2-like ethylene-responsive transcription factor | 55.20 | 0.00 |
| TRINITY_sp|Q6PB1|rps3a | 40S ribosomal protein | 55.20 | 0.00 |
| TRINITY_sp|Q9LYA|AK1 | Aspartokinase | 55.20 | 0.00 |
| TRINITY_sp|P243|al-3 | Geranylgeranyl pyrophosphate synthase | 55.20 | 0.00 |
| TRINITY_sp|Q9SZF|ABC9 | ABC transporter G family | 55.20 | 0.00 |
| TRINITY_sp|Q102|SPAC56F5 | Eukaryotic translation initiation factor 5 | 55.20 | 0.00 |
| TRINITY_sp|A2Y9O|OsI_021 | Soluble starch synthase | 55.20 | 0.00 |
| TRINITY_sp|Q0VD1|MP4 | U3 small nucleolar RNA | 55.20 | 0.00 |
| TRINITY_sp|P566|KNOX1 | Homeobox protein | 55.20 | 0.00 |
| TRINITY_sp|Q8VC9|Acscf2 | Acyl-CoA synthetase | 55.20 | 0.00 |
| TRINITY_sp|Q4HYA|At1g4886 | ATP-dependent DExH-box helicase | 55.20 | 0.00 |
| TRINITY_sp|Q8WXW|DNAH7 | Dynein heavy chain | 55.20 | 0.00 |
| TRINITY_sp|P872|RPL34A | 60S ribosomal protein | 55.20 | 0.00 |
| TRINITY_sp|Q947|ALG2 | Alpha-1,3/1,6-mannosyltransferase | 55.20 | 0.00 |
| TRINITY_sp|Q9Y8C|TOP2 | DNA topoisomerase | 55.10 | 0.00 |
| TRINITY_sp|A6Q4R|dnaJ | Chaperone protein D | 55.10 | 0.00 |
| TRINITY_sp|F4IGB|BCHC2 | BEACH domain-containing protein | 55.10 | 0.00 |
| TRINITY_sp|Q4IS9|At2g3200 | DNA topoisomerase | 55.10 | 0.00 |
| TRINITY_sp|Q920|IMycld | Malonyl-CoA decarboxylase | 55.10 | 0.00 |
| TRINITY_sp|Q101|SPAC26A5 | Hydrolase | 55.10 | 0.00 |
Cysteine desulfurase 1 OS=Anabaena variabilis (strain ATCC 29413 / PCC 7937) GN=nifS1 PE=3 SV=2
Guanylate kinase 1 OS=Oryza sativa subsp. japonica GN=GK1 PE=2 SV=2
Probable ATP-dependent RNA helicase ddx49 OS=Dictyostelium discoideum GN=ddx49 PE=3 SV=1
Ubiquitin-conjugating enzyme E2 D4 OS=Homo sapiens GN=UBE2D4 PE=1 SV=1
AMSH-like ubiquitin thioesterase 3 OS=Arabidopsis thaliana GN=AMSH3 PE=1 SV=2
ATP-dependent zinc metalloprotease FTSH 8, mitochondrial OS=Oryza sativa subsp. japonica GN=FTSH8 PE=3 SV=1
Acyl-CoA synthetase short-chain family member B, mitochondrial OS=Dictyostelium discoideum GN=aslB PE=3 SV=1
Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4
Extracellular signal-regulated kinase 1 OS=Dictyostelium discoideum GN=erkA PE=2 SV=2
ABC transporter C family member 12 OS=Dictyostelium discoideum GN=abcC12 PE=3 SV=1
Probable ADP-ribosylation factor GTPase-activating protein AGD9 OS=Arabidopsis thaliana GN=AGD9 PE=1 SV=1
Protein COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B CCB3, chloroplastic OS=Arabidopsis thaliana GN=CCB3 PE=1 SV=1
NADP-dependent malic enzyme OS=Dictyostelium discoideum GN=malA PE=2 SV=1
GPN-loop GTPase 3 OS=Dictyostelium discoideum GN=gpn3 PE=3 SV=1
Coronin-like protein crn1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=crn1 PE=1 SV=1
Protein PYR1-3 OS=Dictyostelium discoideum GN=pyr1-3 PE=1 SV=3
Elongation factor G, mitochondrial OS=Dictyostelium discoideum GN=gfm1 PE=3 SV=1
Sulfite oxidase, mitochondrial OS=Rattus norvegicus GN=Suox PE=1 SV=2
C-Myc-binding protein homolog OS=Dictyostelium discoideum GN=mycbp PE=3 SV=1
ABC transporter B family member 9 OS=Arabidopsis thaliana GN=ABCB9 PE=3 SV=2
Serine/threonine-protein kinase tousled-like 2 OS=Danio rerio GN=tlk2 PE=2 SV=2
Myosin ID heavy chain OS=Dictyostelium discoideum GN=myoD PE=1 SV=2
Probable NOT transcription complex subunit VIP2 (Fragment) OS=Nicotiana benthamiana GN=VIP2 PE=1 SV=1
Periodic tryptophan protein 2 homolog OS=Dictyostelium discoideum GN=pwp2 PE=3 SV=1
Probable serine/thr
| TRINITY_sp|Q8L7HHSK  | Homoserine kinase O  | 55.00  | 0.00    |
| TRINITY_sp|Q1L2iID11  | Isopenetyl-diphosph | 55.00  | 0.00    |
| TRINITY_sp|F4KIJAt5g108 | Protein RRC1-like O | 55.00  | 0.00    |
| TRINITY_sp|Q4291-      | Glucose-6-phosphate | 55.00  | 0.00    |
| TRINITY_sp|A5D8sbdts  | Ribosome maturation | 55.00  | 0.00    |
| TRINITY_sp|P226DEG1   | Protease Do-like 1, | 55.00  | 0.00    |
| TRINITY_sp|Q54GeCtsp12 | CTD small phosphata| 55.00  | 0.00    |
| TRINITY_sp|P025+-      | Actin-1 OS=Acantham | 55.00  | 0.00    |
| TRINITY_sp|F4IUUPF2    | Regulator of nonsen | 55.00  | 0.00    |
| TRINITY_sp|B0S6eral1   | GTPase Era, mitoch | 55.00  | 0.00    |
| TRINITY_sp|Q4233CPK12  | Calcium-dependent p | 55.00  | 0.00    |
| TRINITY_sp|A8J6sSULTR2 | Proton/sulfate cotr | 55.00  | 0.00    |
| TRINITY_sp|A5H0sDUR1,2 | Urea amidolyase OS= | 55.00  | 0.00    |
| TRINITY_sp|P3642ALATS  | Alanine--tRNA ligas | 55.00  | 0.00    |
| TRINITY_sp|Q9SGUMGL    | Methionine gamma-ly | 55.00  | 0.00    |
| TRINITY_sp|Q9ST1VPS29  | Vacuolar protein so | 55.00  | 0.00    |
| TRINITY_sp|A4FP3PPE1   | Peptidyl-prolyl cis | 55.00  | 0.00    |
| TRINITY_sp|O049sUMK3   | UMP-CMP kinase 3 OS | 54.90  | 0.00    |
| TRINITY_sp|Q86J6trmt61a| tRNA (adenine(58)-N | 54.90  | 0.00    |
| TRINITY_sp|Q8J1+-      | Type-4 ice-structur | 54.90  | 0.00    |
| TRINITY_sp|Q9KV1lysA   | Diaminopimelate dec | 54.90  | 0.00    |
| TRINITY_sp|Q66Kcuta    | Protein CtuA homolo | 54.90  | 0.00    |
| TRINITY_sp|Q1333TARBP1 | Probable methyltran | 54.90  | 0.00    |
| TRINITY_sp|Q9F19DEGP10 | Protease Do-like 10 | 54.90  | 0.00    |
| TRINITY_sp|Q9CSsTIF3H1 | Eukaryotic translat | 54.90  | 0.00    |
| TRINITY_sp|O221sGCP1   | Probable tRNA N6-ad | 54.90  | 0.00    |
| TRINITY_sp|B0R0sidikey-von Willebrand fact | 54.90 | 0.00 |
| TRINITY_sp|Q9TV1cdk-9  | Probable cyclin-dep | 54.90  | 0.00    |
| TRINITY_sp|Q7KW3iunH   | Inosine-uridine-pre | 54.90  | 0.00    |
| TRINITY_sp|Q7Y2erf3   | Eukaryotic peptide | 54.90  | 0.00    |
| TRINITY_sp|Q96NKXMAT2  | Zinc finger matrin- | 54.90  | 0.00    |
| TRINITY_sp|Q0JC1ZEP    | Zeaxanthin epoxid | 54.90  | 0.00    |
| TRINITY_sp|Q94B8Atig718| Uncharacterized aar | 54.90  | 0.00    |
| TRINITY_sp|P197sMIB    | Myosin heavy chain | 54.90  | 0.00    |
| TRINITY_sp|Q2K2CCDC5L  | Cell division cycle | 54.90  | 0.00    |
| TRINITY_sp|Q92SSOMR1   | Threonine dehydrata | 54.90  | 0.00    |
| TRINITY_sp|Q32LCNN3    | Calponin-3 OS=Bos t | 54.90  | 0.00    |
| TRINITY_sp|P0CG5RUB3   | Ubiquitin-like prot | 54.90  | 0.00    |
| TRINITY_sp|Q9ATsRPL23A | 60S ribosomal prote | 54.90  | 0.00    |
| TRINITY_sp|Q8RCpsuG    | Pseudouridine-5'-ph | 54.90  | 0.00    |
| TRINITY_sp|Q7DMFSAS1   | Peptidyl-prolyl cis | 54.90  | 0.00    |
| TRINITY_sp|M1C2EBP1    | ERBB-3 BINDING PROT | 54.90  | 0.00    |
| TRINITY_sp|Q8W55KIN7D  | Kinesin-like protei | 54.90  | 0.00    |
| TRINITY_sp|O809sAGD7   | ADP-ribosylation fa | 54.90  | 0.00    |
| TRINITY_sp|Q0VFskctd7  | BTB/POZ domain-cont | 54.90  | 0.00    |
| TRINITY_sp|Q91VAbca7   | ATP-binding cassett | 54.90  | 0.00    |
| TRINITY_sp|Q54JabcC3   | ABC transporter C f | 54.90  | 0.00    |
| TRINITY_sp|P4223Dbi    | Acyl-CoA-binding pr | 54.80  | 0.00    |
| TRINITY_sp|Q95KC1G11412| N-alpha-acetyltetr | 54.80  | 0.00    |
| TRINITY_sp|O818sPUM1   | Mitochondrial uncou | 54.80  | 0.00    |
| TRINITY_sp|P301fTOP2   | DNA topoisomerase 2 | 54.80  | 0.00    |
| TRINITY_sp|Q86B1lanapc8| Anaphase-promoting | 54.80  | 0.00    |
| TRINITY_sp|Q907spiml   | Lon protease homolo | 54.80  | 0.00    |
| TRINITY_sp|Q22R1RFC1   | Replication factor | 54.80  | 0.00    |
| TRINITY_sp|P527trs-1   | Threonine--tRNA lig | 54.80  | 0.00    |
| TRINITY_sp|Q2PQfAGL    | Glycogen debranchi | 54.80  | 0.00    |
TRINITY_sp|Q9ZQVU2AF35A Splicing factor U2a 54.80 0.00
TRINITY_sp|Q54T7gpn2 GP1-loop GTPase 2 h 54.80 0.00
TRINITY_sp|Q9S17RKP E3 ubiquitin-protein 54.80 0.00
TRINITY_sp|P1521PCMT1 Protein-L-isoadap 54.80 0.00
TRINITY_sp|Q9FMIDIT2-1 Dicarboxylate trans 54.80 0.00
TRINITY_sp|Q6Q4Atp2b4 Plasma membrane cal 54.80 0.00
TRINITY_sp|Q05B1shq1 Protein SHQ1 homolo 54.80 0.00
TRINITY_sp|Q6WWUPL3 E3 ubiquitin-protein 54.80 0.00
TRINITY_sp|F4IVCH5 Protein CHROMATIN R 54.80 0.00
TRINITY_sp|Q631Dnah1 Dynein heavy chain 54.80 0.00
TRINITY_sp|Q0366BIP4 Luminal-binding pro 54.80 0.00
TRINITY_sp|Q6NYIs1c25a2 Calcium-binding mit 54.80 0.00
TRINITY_sp|B3P0tal Transaldolase OS=Ce 54.80 0.00
TRINITY_sp|P0CA8vccpr1 Probable serine/thr 54.80 0.00
TRINITY_sp|Q8U0Xpol Exportin-1 OS=Rattu 54.80 0.00
TRINITY_sp|P283SMARCA1 Probable global tra 54.80 0.00
TRINITY_sp|Q5DM1IFT172 Intraflagellar tran 54.80 0.00
TRINITY_sp|Q5XAOX4 Ubiquinol oxidase 4 54.80 0.00
TRINITY_sp|Q408EMB8 Embryogenesis-assoc 54.80 0.00
TRINITY_sp|Q84SNOL Chlorophyll(ide) b 54.80 0.00
TRINITY_sp|Q7F2ICSB DNA excision repair 54.80 0.00
TRINITY_sp|Q9BX1GTPBP2 GDP-binding protein 54.80 0.00
TRINITY_sp|Q154ABCC4 Multidrug resistanc 54.80 0.00
TRINITY_sp|Q28Gtma7 Translation machine 54.70 0.00
TRINITY_sp|Q9M5PEAMT Phosphoethanolamine 54.70 0.00
TRINITY_sp|Q9UPCEP16 Centrosomal protein 54.70 0.00
TRINITY_sp|Q5SI1TTHA156 DNA base-flipping p 54.70 0.00
TRINITY_sp|Q541mycbp C-Myc-binding prote 54.70 0.00
TRINITY_sp|Q015facA Acetyl-coenzyme A s 54.70 0.00
TRINITY_sp|Q54D1DDL_G02 Down syndrome criti 54.70 0.00
TRINITY_sp|Q86AXvamp7B Vesicle-associated 54.70 0.00
TRINITY_sp|Q019-t Serine--tRNA ligase 54.70 0.00
TRINITY_sp|Q6K1CAX3 Vacuolar cation/pro 54.70 0.00
TRINITY_sp|P3211PRDX2 Peroxiredoxin-2 OS= 54.70 0.00
TRINITY_sp|Q8H1NBP35 Cytosolic Fe-S clus 54.70 0.00
TRINITY_sp|P312pab1 Polyadenylate-bind 54.70 0.00
TRINITY_sp|Q9P7SPBC170 Probable mitochondr 54.70 0.00
TRINITY_sp|Q9UVMMRE11 Double-strand break 54.70 0.00
TRINITY_sp|P170crtD Hydroxyneurosporene 54.70 0.00
TRINITY_sp|Q940CCT2 T-complex protein 1 54.70 0.00
TRINITY_sp|Q9C81FAS4 ATP-dependent RNA h 54.70 0.00
TRINITY_sp|P078Acaalb 3-ketoacyl-CoA thio 54.70 0.00
TRINITY_sp|Q351Copb2 Coatomer subunit be 54.70 0.00
TRINITY_sp|Q9SYMTPS1 Alpha, alpha-trehalo 54.70 0.00
TRINITY_sp|Q54YIileS Probable isoleucine 54.70 0
TRINITY_sp|P343ced-7 ABC transporter ced 54.70 0.00
TRINITY_sp|P150rasG Ras-like protein ra 54.70 0.00
TRINITY_sp|Q67XCSBD5UF1 DUF21 domain-contai 54.70 0.00
TRINITY_sp|P402hp2 Casein kinase I hom 54.70 0.00
TRINITY_sp|O756SNRNP20U5 small nuclear ri 54.70 0
TRINITY_sp|P489-beta-galactosidase 54.60 0.00
TRINITY_sp|Q141MORC3 MORC family CW-type 54.60 0.00
TRINITY_sp|Q809PGFS1 CDP-diacylglycerol- 54.60 0.00
TRINITY_sp|Q929BRF1 Transcription facto 54.60 0.00
TRINITY_sp|Q93YUBP9 Ubiquitin carboxyl- 54.60 0.00
TRINITY_sp|Q552Cct8 T-complex protein 1 54.60 0.00
| Protein Name                        | Organism                  | Gene Symbol | Protein ID | Description                               | p-value | e-value |
|-------------------------------------|---------------------------|-------------|------------|-------------------------------------------|---------|---------|
| ATP-dependent RNA helicase DBP4    | Ustilago maydis           | AT2B1       | P20020     | DNA topoisomerase 3                        | 54.60   | 0.00    |
| Putative tRNA pseudouridine synthase Pus10 | Mus musculus             | PUS10       | P37841     | Hypothetical protein                       | 54.60   | 0.00    |
| DEAD-box ATP-dependent protease Q5 | Arabidopsis thaliana     | Q5        | P34099     | DEAD-box ATP-dependent protease            | 54.60   | 0.00    |
| DNA topoisomerase 3                 | Ustilago maydis           | AT2B1       | P20020     | DNA topoisomerase 3                        | 54.60   | 0.00    |
| Uridine-cytidine ki                | Arabidopsis thaliana     | EBCC11      | Q6RF66     | Uridine-cytidine ki                        | 54.60   | 0.00    |
| Putative DNA helicase              | Arabidopsis thaliana     | EBCC11      | Q6RF66     | Putative DNA helicase                      | 54.60   | 0.00    |
| Kinesin-like protein               | Arabidopsis thaliana     | KIF3C       | P0265     | Kinesin-like protein                       | 54.60   | 0.00    |
| Kinesin-like protein               | Arabidopsis thaliana     | KIF3C       | P0265     | Kinesin-like protein                       | 54.60   | 0.00    |
| Ras-related C3 botulin            | Arabidopsis thaliana     | P607       | P0265     | Ras-related C3 botulin                     | 54.60   | 0.00    |
| Fibrinogen beta chain             | Homo sapiens              | FGB         | P4285     | Fibrinogen beta chain                     | 54.60   | 0.00    |
| Plasma membrane calmodulin        | Arabidopsis thaliana     | Rab2a       | P34099     | Plasma membrane calmodulin                 | 54.60   | 0.00    |
| Dihydropyrimidinase              | Arabidopsis thaliana     | rpsI        | P34099     | Dihydropyrimidinase                       | 54.60   | 0.00    |
| Short integuments 2               | Arabidopsis thaliana     | RPL3       | P34099     | Short integuments 2                        | 54.60   | 0.00    |
| Putative DNA helicase              | Arabidopsis thaliana     | EBCC11      | Q6RF66     | Putative DNA helicase                      | 54.60   | 0.00    |
| Delta(12)-acyl-lipid desaturase    | Punica granatum           | FAD12       | P34099     | Delta(12)-acyl-lipid desaturase            | 54.60   | 0.00    |
| Putative glucose-6-phosphatase C2 | Dictyostelium discoideum | FGB         | P4285     | Putative glucose-6-phosphatase C2          | 54.60   | 0.00    |
| Lysosomal catalase                | Arabidopsis thaliana     | RPL3       | P34099     | Lysosomal catalase                         | 54.60   | 0.00    |
| Accession          | Description                                      | E-value | Score |
|--------------------|--------------------------------------------------|---------|-------|
| TRINITY_sp|A6GY|dapF | Diaminopimelate epimerase | Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511) | 54.50 |
| TRINITY_sp|P0DJ3RPL27 | | 60S ribosomal protein | 54.40 |
| TRINITY_sp|Q631|Abcc2 | Canalicular multi-sp | 54.40 |
| TRINITY_sp|Q54H|drkA | Probable serine/threonine kinase | 54.40 |
| TRINITY_sp|O763|dco | Discs overgrown protein | 54.40 |
| TRINITY_sp|Q6DJ|cars2 | Probable cysteine-tRNA ligase | 54.40 |
| TRINITY_sp|Q182|rap-1 | Ras-related protein | 54.40 |
| TRINITY_sp|Q86KD|GB2 | Probable GH family | 54.40 |
| TRINITY_sp|Q390|CKI1 | Casein kinase 1-like | 54.40 |
| TRINITY_sp|Q993|TY3B-G | Transposon Ty3-Ga | 54.40 |
| TRINITY_sp|O075|yhdW | Putative glycerophosphate dehydratase | 54.40 |
| TRINITY_sp|P361|Endo | Endoplasmic reticulum | 54.40 |
| TRINITY_sp|Q99J|Mlycd | Malonyl-CoA decarboxylase | 54.40 |
| TRINITY_sp|B2GU|Man1b1 | Endoplasmic reticulum | 54.40 |
| TRINITY_sp|P103|ND6 | NADH-ubiquinone oxidoreductase | 54.40 |
| TRINITY_sp|P072|URA2 | Protein URA2 | 54.40 |
| TRINITY_sp|Q8WX|DNAH7 | Dynein heavy chain | 54.40 |
| TRINITY_sp|P068|Myb | Transcriptional activator | 54.40 |
| TRINITY_sp|P0DO|PpSQ1_03 | 3-sulfolactaldehyde dehydrogenase | 54.40 |
| TRINITY_sp|Q6FC|ACIAD12 | Adenine deaminase | 54.40 |
| TRINITY_sp|O750|mcm7 | DNA replication licensing factor | 54.40 |
| TRINITY_sp|Q55G|cpnD | Copine-D | 54.40 |
| TRINITY_sp|P0501|PARP2 | Poly [ADP-ribose] polymerase | 54.40 |
| TRINITY_sp|Q8WX|DNAH7 | Dynein heavy chain | 54.40 |
| TRINITY_sp|Q6CQ|TAR1-A | Protein TAR1 | 54.40 |
| TRINITY_sp|P558|sgA | Serine/threonine kinase | 54.40 |
| TRINITY_sp|P118| | High mobility group | 54.40 |
| TRINITY_sp|Q9HC|XAB2 | Pre-mRNA-splicing factor | 54.40 |
| TRINITY_sp|Q9UE|FTSJ1 | Putative RNA (cytoplasmic) | 54.40 |
| TRINITY_sp|P048| | Actin, cytoplasmic | 54.40 |
| TRINITY_sp|Q7NH|mnmE | tRNA modification GTPase | 54.40 |
| TRINITY_sp|Q55F|acrA | Adenylate cyclase | 54.40 |
| TRINITY_sp|Q5W|Jmem2 | Transmembrane protein | 54.40 |
| TRINITY_sp|A8FJ|CFAP65 | Cilia- and flagella | 54.40 |
| TRINITY_sp|Q7SD|ccp-1 | Cytochrome c peroxidase | 54.40 |
| TRINITY_sp|P519|Nek1 | Serine/threonine-protein kinase | 54.40 |
| TRINITY_sp|P049|TATB | Sec-independent protein translocase | 54.40 |
| TRINITY_sp|P785|FCA1 | Cytosine deaminase | 54.40 |
| TRINITY_sp|Q5X3|dnaJ | Chaperone protein | 54.40 |
| TRINITY_sp|Q9VW|1(1)|G01 | Probable isocitrate dehydrogenase | 54.30 |
| TRINITY_sp|P469|RPE1 | Ribulose-phosphate kinase | 54.30 |
| TRINITY_sp|Q131|PRKA1 | 5'-AMP-activated protein kinase | 54.30 |
| TRINITY_sp|Q54I|arpA | Centrosomin | 54.30 |
| TRINITY_sp|Q32P|DYNLRB2 | Dynein light chain | 54.30 |
| TRINITY_sp|P619|DCAF7 | DDB1- and CDC48-associating factor | 54.30 |
| TRINITY_sp|Q007|glpV | Glycogen phosphorylase | 54.30 |
| TRINITY_sp|O308|HD_0322 | Reticulon family protein | 54.30 |
| TRINITY_sp|Q952|MBD4 | Methyl-CpG-binding protein | 54.30 |
| TRINITY_sp|Q997|ABCA3 | ATP-binding cassette A3 | 54.30 |
| TRINITY_sp|Q9FM|RD21 | Probable cysteine protease | 54.30 |
| TRINITY_sp|Q6CS|CERT1-1 | Transcription activator | 54.30 |
| TRINITY_sp|P347|ARF | ADP-ribosylation factor | 54.30 |
| TRINITY_sp|P296|CDKAK-2 | Cyclin-dependent kinase | 54.30 |
| TRINITY_sp|Q1ZK|fah | Fumarate-lactate oxidoreductase | 54.30 |
| TRINITY_sp|O627|SCP2 | Non-specific lipid-transfer protein | 54.30 |
| TRINITY_sp|Q5ZK|METTL14 | N6-adenosine-methyltransferase | 54.30 |
| Protein ID       | Description                             | Percent Identity | E-Value |
|-----------------|-----------------------------------------|------------------|---------|
| trinity_dn37332_c0_g9 | Probable adenylate DNA mismatch repair DNA | 54.10             | 0.00    |
| trinity_dn37780_c0_g4 | Histone H1-I                            | 54.10             | 0.00    |
| trinity_dn34877_c0_g1 | Mitochondrial import inner membrane translocase subunit TIM17-1 | 54.10             | 0.00    |
| trinity_dn32420_c0_g1 | Transmembrane and TPR repeat-containing protein CG5038 | 54.10             | 0.00    |
| trinity_dn31439_c0_g2 | Ubiquitin carboxyl-terminal hydrolase 44-B | 54.10             | 0.00    |
| trinity_dn30380_c1_g1 | Long chain acyl-CoA synthetase 2         | 54.10             | 0.00    |
| trinity_dn29772_c0_g2 | Frataxin, mitochondrial                  | 54.10             | 0.00    |
| trinity_dn26988_c0_g1 | NADH nitrate reductase                  | 54.10             | 0.00    |
| trinity_dn24215_c0_g1 | Bifunctional dihydrofolate reductase-thymidylate synthase | 54.10             | 0.00    |
| trinity_dn19725_c0_g1 | Coatomer subunit alpha                  | 54.10             | 0.00    |
| trinity_dn52315_c0_g1 | FHA domain-containing protein DDL        | 54.10             | 0.00    |
| trinity_dn49075_c0_g4 | Probable succinyl-CoA:3-ketoacid coenzyme A transferase, mitochondrial | 54.10             | 0.00    |
| trinity_dn49940_c0_g2 | Probable serine/threonine-protein kinase pkgA | 54.10             | 0.00    |
| trinity_dn46878_c1_g6 | OBG-like ATPase 1                       | 54.10             | 0.00    |
| trinity_dn46867_c0_g1 | Myb family transcrip | 54.10             | 0.00    |
| trinity_dn46393_c0_g4 | Actin, cytoplasmic                  | 54.10             | 0.00    |
| trinity_dn45672_c1_g2 | Probable adenylate DNA mismatch repair DNA | 54.10             | 0.00    |
| trinity_dn44893_c0_g7 | Histone H1-I                            | 54.10             | 0.00    |
| trinity_dn44549_c0_g2 | Probable adenylate DNA mismatch repair DNA | 54.10             | 0.00    |
| trinity_dn42980_c0_g2 | Myb family transcrip | 54.10             | 0.00    |
| TRINITY_sp|Q10P1ADIPOR3 | Heptahelical transm | 53.80 | 0.00 |
| TRINITY_sp|Q9M80FTSHI3 | Probable inactive A | 53.80 | 0.00 |
| TRINITY_sp|Q2QPGYK1 | Guanylate kinase 1 | 53.80 | 0.00 |
| TRINITY_sp|Q3S21WDR18 | WD repeat-containin | 53.80 | 0.00 |
| TRINITY_sp|Q6FRGSP1 | GTP-binding nuclear | 53.80 | 0.00 |
| TRINITY_sp|Q747SPBC170 | 4,5-DOPA dioxygenas | 53.80 | 0.00 |
| TRINITY_sp|P1321LCP1 | Digestive cysteine | 53.80 | 0.00 |
| TRINITY_sp|Q54EeepnA | Epsin OS=Dictyostel | 53.80 | 0.00 |
| TRINITY_sp|P9379NUTD23 | Nudix hydrolase 23, | 53.80 | 0.00 |
| TRINITY_sp|P5481cddc-48 | Transitional endop | 53.80 | 0.00 |
| TRINITY_sp|Q4205ABCC2 | ABC transporter C | 53.80 | 0.00 |
| TRINITY_sp|O485POLD2 | DNA polymerase delt | 53.80 | 0.00 |
| TRINITY_sp|Q62RDNHAH12 | Dynein heavy chain | 53.80 | 0.00 |
| TRINITY_sp|Q2TEPCS2 | Glutathione gamma-g | 53.80 | 0.00 |
| TRINITY_sp|A2RVdph6 | Diphthine--ammonia | 53.80 | 0.00 |
| TRINITY_sp|Q54Wmetap1 | Methionine aminopep | 53.80 | 0.00 |
| TRINITY_sp|Q8VXUESP3 | Pre-mRNA-splicing f | 53.80 | 0.00 |
| TRINITY_sp|Q1PDSCSCL28 | Serine/arginine-ric | 53.80 | 0.00 |
| TRINITY_sp|Q7XTtRNA-dihydouridin | 53.80 | 0.00 |
| TRINITY_sp|Q55Enat10 | RNA cytidine acetyl | 53.80 | 0.00 |
| TRINITY_sp|Q5F3EFTUD2 | 116 kDa U5 small nu | 53.80 | 0.00 |
| TRINITY_sp|A8HMFAP9 | Intraflagellar tran | 53.80 | 0.00 |
| TRINITY_sp|P567PSMD2 | 26S proteasome non- | 53.80 | 0.00 |
| TRINITY_sp|Q8NKN1scon-3 | E3 ubiquitin ligase | 53.80 | 0.00 |
| TRINITY_sp|Q7TMWnarf1 | Cytosolic Fe-S clus | 53.80 | 0.00 |
| TRINITY_sp|Q2RBOs11g01 | Clathrin heavy chai | 53.80 | 0.00 |
| TRINITY_sp|A2XVUCDKG2 | Cyclin-dependent ki | 53.70 | 0.00 |
| TRINITY_sp|Q9SFSTIM14 | Mitochondrial impor | 53.70 | 0.00 |
| TRINITY_sp|Q024Sfri_36 | Uncharacterized pro | 53.70 | 0.00 |
| TRINITY_sp|P0ABElbB | Glyoxalase ElbB OS= | 53.70 | 0.00 |
| TRINITY_sp|Q9FKILSM5 | Sm-like protein LSM | 53.70 | 0.00 |
| TRINITY_sp|P092(Tubulin beta-1 chai | 53.70 | 0.00 |
| TRINITY_sp|P044(Calmodulin OS=Triti | 53.70 | 0.00 |
| TRINITY_sp|P322rasS | Ras-like protein ra | 53.70 | 0.00 |
| TRINITY_sp|O808MTACP2 | Acyl carrier protei | 53.70 | 0.00 |
| TRINITY_sp|Q2RKrsgA | Putative ribosome b | 53.70 | 0.00 |
| TRINITY_sp|Q6T3Spata20 | Spermatogenesis-ass | 53.70 | 0.00 |
| TRINITY_sp|Q9H4WNK1 | Serine/threonine-pr | 53.70 | 0.00 |
| TRINITY_sp|Q99yakc | Aldo-keto reductase | 53.70 | 0.00 |
| TRINITY_sp|Q64J1PIMT2 | Protein-L-isoaspar | 53.70 | 0.00 |
| TRINITY_sp|Q8HXMUT | Methylmalonyl-CoA m | 53.70 | 0.00 |
| TRINITY_sp|Q479l-dehydro | 53.70 | 0.00 |
| TRINITY_sp|Q9C5TIF3E1 | Eukaryotic translat | 53.70 | 0.00 |
| TRINITY_sp|Q8EJpprPC | 2-methylcitrate syn | 53.70 | 0.00 |
| TRINITY_sp|P3566RPL7A-1 | 60S ribosomal prote | 53.70 | 0.00 |
| TRINITY_sp|Q9HCPNEN5 | Copine-5 OS=Homo sa | 53.70 | 0.00 |
| TRINITY_sp|P6299RAC1 | Ras-related C3 botu | 53.70 | 0.00 |
| TRINITY_sp|Q395l-Dynein 18 kDa light | 53.70 | 0.00 |
| TRINITY_sp|Q9Y6ARL5A | ADP-ribovlation fa | 53.70 | 0.00 |
| TRINITY_sp|Q5SN1ISP | 2-C-methyl-D-erythr | 53.70 | 0.00 |
| TRINITY_sp|D3ZALchd6 | Chromomadin-helica | 53.70 | 0.00 |
| TRINITY_sp|Q8S2ISPE | 4-diphosphocytidyl- | 53.70 | 0.00 |
| TRINITY_sp|B8NY1bx1B | Probable exo-1,4-be | 53.70 | 0.00 |
| TRINITY_sp|P087ND5 | NADH-ubiquinone oxi | 53.70 | 0.00 |
| TRINITY_sp|Q861xstdt1 | Serine/threonine-pr | 53.70 | 0.00 |
| TRINITY_sp|Q150EFTUD2 | 116 kDa U5 small nu | 53.70 | 0.00 |
TRINITY_sp|P524|GPDH  Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Cuphea lanceolata GN=GPDH PE=2 SV=1
TRINITY_sp|Q553|DAFA  Diflavin flavoprotein OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|A2XVI0sI_016  DEAD-box ATP-depend OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|COSUJ3MJL6  Putative lysine-spe OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|P871|TRZ2  Ribonuclease Z 2, m OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q94AOOP  Organellar oligopep OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q6OL|CPY57  Peptidyl-prolyl cis OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9984G  Cyclin-G-associated OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9983TY3B-G  Transposon Ty3-G Ga OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q6DGKsupt4h1  Transcription elong OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9HS5DHX35  Probable ATP-depend OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|A7IP|rp10  50S ribosomal prote OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q183|Rab6  Ras-related protein OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q032|CED-10  Ras-related protein OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|O049|UMK3  UMP-CMP kinase 3 OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q918IMY6  Unconventional myos OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q84KIP5  Serine/threonine-pr OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q91XDCXR  L-xylulose reducta OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9ZVIIAPHX  Phytanoyl-CoA dioxy OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|F742|Gpxl  Hydroperoxy fatty a OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q6I5|CDCK1  Cyclin-dependent ki OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q7VG1RMN  Dual-specificity RN OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|P600|RPL7C  60S ribosomal prote OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q1411SPAC31G  Uncharacterized AAA OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9L2|ABC14C  ABC transporter C f OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q54Q|LDG1039  Probable ubiquitin OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9JSJGC1  Epimerase family pr OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9MB8GLPK  Glycerol kinase OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9MRHHSU  DEAD-box ATP-depend OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9SCFKBP13  Peptidyl-prolyl cis OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9CAERF013  Ethylene-responsive OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q6V5FZnf474  Zinc finger protein OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q5F3|EFTUD2  116 kDa U5 small nu OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q6FPPICL1  Isocitrate lyase OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|P283|RPA2  DNA-directed RNA po OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9FPIUBP12  Ubiquitin carboxyl OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q8W4VRHA-a3  V-type proton ATPas OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q0WVMCM4  DNA replication lic OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|C6E5|rnhB  Ribonuclease HII OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q5VQ|Os01g01  DEAD-box ATP-depend OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|P519|Nek1  Serine/threonine-pr OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|A8JGLILP1  Lipoyl synthase, mi OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q851|GRS7X  Monothiol glutared OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9P2LDNAH1  Dynein heavy chain OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9ZVAt2g387U  Uncharacterized pro OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q8BP3Fra10acc1  Protein FRA10AC1 ho OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q6CU|SMP3  GPI mannosyltransf OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9LP|RN4  26S proteasome non- OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q9UBMBD2  Methyl-CpG-binding OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|B0T6mm9G  tRNA uridine 5-carb OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q1PFCPKL9  Calcium-dependent p OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q6DH1lgd15  Cytosolic carboxype OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|P051|FRKACB  cAMP-dependent prot OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|Q923trp1  Multifunctional try OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|B8ARESRT1  NAD-dependent prote OS=Mus musculus GN=DAFA PE=1 SV=2
TRINITY_sp|P409|Arfl02F  ADP-ribosylation fa OS=Mus musculus GN=DAFA PE=1 SV=2
| Protein Name | Gene Name | Organism | Function | Accession | E-values | Bit-scores | Number of Features | Description |
|--------------|-----------|----------|----------|-----------|----------|------------|------------------|-------------|
| NAD(P)H-hydrate epimerase | NAXE | Sus scrofa |  |  |  | 53.50 | 0.00 | NAD(P)H-hydrate epimerase | |
| 4-hydroxybutyrate c | Cat2 | Aplysia californica |  |  |  | 53.50 | 0.00 | 4-hydroxybutyrate c | |
| Probable proline im | Pip | Homo sapiens |  |  |  | 53.50 | 0.00 | Probable proline im | |
| Probable plasma mem | PatB | Dictyostelium discoideum |  |  |  | 53.50 | 0.00 | Probable plasma membrane | |
| Putative calcium-transporting ATPase 7, plasma membrane-type | ACA7 | Arabidopsis thaliana |  |  |  | 53.50 | 0.00 | Putative calcium-transporting ATPase 7, plasma membrane-type | |
| 3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ | FabZ | Clostridium botulinum |  |  |  | 53.50 | 0.00 | 3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ | |
| Temptin | Temptin | Aplysia californica |  |  |  | 53.50 | 0.00 | Temptin | |
| Structural maintenance of chromosomes protein 6 | SMC6 | Dictyostelium discoideum |  |  |  | 53.50 | 0.00 | Structural maintenance of chromosomes protein 6 | |
| Dynein assembly factor 1, axonemal | DNAAF1 | Bos taurus |  |  |  | 53.50 | 0.00 | Dynein assembly factor 1, axonemal | |
| ADP-ribosylation factor-like protein 5A | Arl5a | Mus musculus |  |  |  | 53.50 | 0.00 | ADP-ribosylation factor-like protein 5A | |
| Putative 12-oxophytodienoate reductase 3 | OPR3 | Oryza sativa subsp. japonica |  |  |  | 53.50 | 0.00 | Putative 12-oxophytodienoate reductase 3 | |
| Mitogen-activated protein kinase kinase kinase NPK1 | NPK1 | Nicotiana tabacum |  |  |  | 53.50 | 0.00 | Mitogen-activated protein kinase kinase kinase NPK1 | |
| Protein ref(2)P | Ref(2)P | Drosophila simulans |  |  |  | 53.50 | 0.00 | Protein ref(2)P | |
| 3-hydroxyanthranilate 3,4-dioxygenase | Haao | Dictyostelium discoideum |  |  |  | 53.50 | 0.00 | 3-hydroxyanthranilate 3,4-dioxygenase | |
| 4-hydroxybutyrate coenzyme A transferase | Cat2 | Clostridium kluyveri |  |  |  | 53.50 | 0.00 | 4-hydroxybutyrate coenzyme A transferase | |
| Mitogen-activated protein kinase 8 | MPK8 | Oryza sativa subsp. japonica |  |  |  | 53.50 | 0.00 | Mitogen-activated protein kinase 8 | |
| Acyl-coenzyme A synthetase ACSM2, mitochondrial | Acsm2 | Mus musculus |  |  |  | 53.50 | 0.00 | Acyl-coenzyme A synthetase ACSM2, mitochondrial | |
| ATP-dependent RNA helicase DHX8 | DHX8 | Homo sapiens |  |  |  | 53.50 | 0.00 | ATP-dependent RNA helicase DHX8 | |
| Dynein heavy chain 7, axonemal | DNAH7 | Homo sapiens |  |  |  | 53.50 | 0.00 | Dynein heavy chain 7, axonemal | |
| Probable proline iminopeptidase | Pip | Leptolyngbya boryana |  |  |  | 53.50 | 0.00 | Probable proline iminopeptidase | |
| Catalase | KatA | Pseudomonas putida |  |  |  | 53.50 | 0.00 | Catalase | |
| Probable plasma membrane ATPase | PatB | Dictyostelium discoideum |  |  |  | 53.50 | 0.00 | Probable plasma membrane ATPase | |
| Choline-phosphate cytidylyltransferase B | PCYT1B | Homo sapiens |  |  |  | 53.50 | 0.00 | Choline-phosphate cytidylyltransferase B | |
| U4/U6.U5 tri-snRNP-associated protein 2 | Usp39 | Mus musculus |  |  |  | 53.50 | 0.00 | U4/U6.U5 tri-snRNP-associated protein 2 | |
| Transcription initiation factor TFIID subunit 12 | TAF12 | Arabidopsis thaliana |  |  |  | 53.50 | 0.00 | Transcription initiation factor TFIID subunit 12 | |
| Dynein heavy chain 1, axonemal | DNAH1 | Rattus norvegicus |  |  |  | 53.50 | 0.00 | Dynein heavy chain 1, axonemal | |

**Additional Information:**

- The table lists various proteins with their associated gene names, organisms, and functions.
- Each row corresponds to a different protein with its respective information.
- The table also includes columns for E-values and bit-scores, which are measures of similarity between sequences.
- The number of features per protein is also listed.
| Gene ID     | Gene Name | Protein Description                                                                 | ID       | Description                     |
|------------|-----------|--------------------------------------------------------------------------------------|----------|----------------------------------|
| TRINITY_sp| Q9LYvAt3g558| Protein yippee-like                                                                  | 53.30    | 0.00                            |
| TRINITY_sp| Q54JcJvcrn| Phosphatidylinosito                                                                  | 53.30    | 0.00                            |
| TRINITY_sp| A0A81lm14ar| Protein LSM14 homol                                                                  | 53.30    | 0.00                            |
| TRINITY_sp| P070v0C0060| Cytochrome b-c1                                                                      | 53.30    | 0.00                            |
| TRINITY_sp| Q54Kvccbl| Kynurenine--oxoglutar              | 53.30    | 0.00                            |
| TRINITY_sp| A2WNv01307| Glucosidase 2 subunit                                                            | 53.30    | 0.00                            |
| TRINITY_sp| Q54Mvmsun2| SUN domain-containin                                                                | 53.30    | 0.00                            |
| TRINITY_sp| Q395yYptc6| Ras-related protein                                                                 | 53.30    | 0.00                            |
| TRINITY_sp| P341fFhkc| Probable serine/thr                                                             | 53.30    | 0.00                            |
| TRINITY_sp| P320sSc2| Non-specific lipid-                               | 53.30    | 0.00                            |
| TRINITY_sp| Q32Lsvsml| Stomatin-like prote                                                             | 53.30    | 0.00                            |
| TRINITY_sp| Q2Rkv0Obg| GTPase Obg OS=Moore                                                                | 53.30    | 0.00                            |
| TRINITY_sp| Q8vylvLTD| Protein LHCP TRANSL                                                               | 53.30    | 0.00                            |
| TRINITY_sp| Q95Tv0Yyy| Riboflavin biosynth                                                                | 53.30    | 0.00                            |
| TRINITY_sp| P391Yyw1| Threonylcarbamoyl-A                                                             | 53.30    | 0.00                            |
| TRINITY_sp| Q612vPc2a| Propionyl-CoA carbo                                                                | 53.30    | 0.00                            |
| TRINITY_sp| Q9P6v4en4| Endocytosis protein                                                               | 53.30    | 0.00                            |
| TRINITY_sp| P078vPETF| Ferredoxin, chlorop                                                               | 53.30    | 0.00                            |
| TRINITY_sp| Q75Kvncsa| Calcium-binding pro                                                                | 53.30    | 0.00                            |
| TRINITY_sp| Q37Sv0O8g7| Aspartate aminotran                                                                | 53.30    | 0.00                            |
| TRINITY_sp| Q54wDDBG02| Delta-1-pyrroline-5                                                                | 53.30    | 0.00                            |
| TRINITY_sp| Q869vPakb| Serine/threonine-pr                                                                | 53.30    | 0.00                            |
| TRINITY_sp| Q9E0vIgmp2| DNA-binding protein                                                                | 53.30    | 0.00                            |
| TRINITY_sp| Q7K KwserS| Serine--tRNA ligase                                                                 | 53.30    | 0.00                            |
| TRINITY_sp| Q9LuvRh35| DEAD-box ATP-depend                                                                | 53.30    | 0.00                            |
| TRINITY_sp| Q9C7vRpn8b| 26S proteasome non-                                                               | 53.30    | 0.00                            |
| TRINITY_sp| Q31LwleuS| Leucine--tRNA ligas                                                                | 53.30    | 0.00                            |
| TRINITY_sp| Q9XfSsr30| Serine/arginine-ric                                                               | 53.30    | 0.00                            |
| TRINITY_sp| P424vCobA| Uroporphyrinogen-II                                                              | 53.30    | 0.00                            |
| TRINITY_sp| Q9LyvRlgl2| E3 ubiquitin-protein                                                              | 53.30    | 0.00                            |
| TRINITY_sp| Q32PvEml3| Echinoderm microtub                                                               | 53.30    | 0.00                            |
| TRINITY_sp| Q6C3vAlg13| UDP-N-acetylglucosa                                                                | 53.30    | 0.00                            |
| TRINITY_sp| Q6N2vPtpdc| Protein tyrosine ph                                                                | 53.30    | 0.00                            |
| TRINITY_sp| Q2HJvFahd1| Acylypyruvase FAHD1,                                                             | 53.30    | 0.00                            |
| TRINITY_sp| Q5VvVem29| Proteasome-associated                                                             | 53.30    | 0.00                            |
| TRINITY_sp| Q86Cvtorr| Target of rapamycin                                                               | 53.30    | 0.00                            |
| TRINITY_sp| Q817vAt4g317| Probable diphthine                                                                 | 53.30    | 0.00                            |
| TRINITY_sp| A41ivsfp3612| mRNA decay activator                                                              | 53.20    | 0.00                            |
| TRINITY_sp| Q969vRab24| Ras-related protein                                                                | 53.20    | 0.00                            |
| TRINITY_sp| Q416vAnt-g1| ADP,ATP carrier pro                                                               | 53.20    | 0.00                            |
| TRINITY_sp| Q227vAt4g025| NADH dehydrogenase                                                               | 53.20    | 0.00                            |
| TRINITY_sp| Q154vAbcc5| Multidrug resistanc                                                                | 53.20    | 0.00                            |
| TRINITY_sp| Q9Y7vset1| Histidine-lysine N-me                                                             | 53.20    | 0.00                            |
| TRINITY_sp| P146vFd4e| cAMP-specific 3',5'                                                               | 53.20    | 0.00                            |
| TRINITY_sp| Q11Evr1mN| Dual-specificity RN                                                                | 53.20    | 0.00                            |
| TRINITY_sp| Q04wPurh| Bifunctional purine                                                                | 53.20    | 0.00                            |
| TRINITY_sp| Q54vEtdt| D-tyrosyl-tRNA(Tyr)                                                                | 53.20    | 0.00                            |
| TRINITY_sp| Q9F1vSpp| Stromal processing                                                               | 53.20    | 0.00                            |
| TRINITY_sp| A2XvVcdxg-2| Cyclin-dependent ki                                                               | 53.20    | 0.00                            |
| TRINITY_sp| Q0P5vAnkrd39| Ankyrin repeat doma                                                               | 53.20    | 0.00                            |
| TRINITY_sp| Q5R8vUba5| Ubiquitin-like modi                                                                | 53.20    | 0.00                            |
| TRINITY_sp| Q31Lvpob| Glutamate 5-kinase                                                                | 53.20    | 0.00                            |
| TRINITY_sp| Q55FvKrsb| Serine/threonine-pr                                                                | 53.20    | 0.00                            |
| TRINITY_sp| Q8VvOrth2| E3 ubiquitin-protein                                                              | 53.20    | 0.00                            |
| TRINITY_sp| O44vUch2| Ubiquitin carboxyl-                                                               | 53.20    | 0.00                            |
| TRINITY_sp| Q99JvTaf11| Transcription initii                                                               | 53.20    | 0.00                            |
| Gene ID          | Description                                                        | Score | P-value |
|------------------|--------------------------------------------------------------------|-------|---------|
| VATF             | V-type proton ATPase                                                | 53.20 | 0.00    |
| A4IFKCD7         | BTB/POZ domain-containing protein                                  | 53.20 | 0.00    |
| P312RAD16        | DNA repair protein                                                  | 53.20 | 0.00    |
| Q5Z02fmdA        | Formamidase OS=Meth                                               | 53.20 | 0.00    |
| Q54Kcdk5rap1     | CDK5RAP1-like protein                                              | 53.20 | 0.00    |
| B3EM2gatA        | Glutamy-A-tRNA(Gln)                                                | 53.20 | 0.00    |
| D2XKFLOT2        | Flotillin-like protein                                             | 53.20 | 0.00    |
| Q7KRGCG1646      | Pre-mRNA-processing protein                                        | 53.20 | 0.00    |
| P509sadal       | AMP deaminase OS=Sc                                                | 53.20 | 0.00    |
| Q8GYXSR          | Sulfiredoxin, chlor                                                | 53.20 | 0.00    |
| Q8YH2ndvA        | Beta-(1--->2)glucan                                                | 53.20 | 0.00    |
| P493XYL1         | NAD(P)H-dependent D                                                | 53.10 | 0.00    |
| Q5XT1RPL17       | 60S ribosomal protein                                              | 53.10 | 0.00    |
| P1364HOM2        | Aspartate-semialdehyde                                            | 53.10 | 0.00    |
| Q94AODLD         | D-lactate dehydroge                                                | 53.10 | 0.00    |
| Q54Ddralp1       | Drl-associated core                                                | 53.10 | 0.00    |
| Q54Fmrho1        | Maestro heat-like r                                                | 53.10 | 0.00    |
| Q8R7rp            | Ribose-phosphate py                                                | 53.10 | 0.00    |
| Q9ST7ABA7        | ABC transporter A f                                                | 53.10 | 0.00    |
| Q8LPF4ABA8       | ABC transporter A f                                                | 53.10 | 0.00    |
| P496-             | Ubiquitin-60S ribos                                                | 53.10 | 0.00    |
| Q4121Acs11       | Long-chain-fatty-ac                                                | 53.10 | 0.00    |
| Q72BgluQ         | Glutamy-Q tRNA(Asp)                                                | 53.10 | 0.00    |
| P3421rab-6.1     | Ras-related protein                                                | 53.10 | 0.00    |
| Q4931Atg332     | NADH dehydrogenase                                                 | 53.10 | 0.00    |
| Q519Nek1         | Serine/threonine-pr                                                | 53.10 | 0.00    |
| Q9C7RPN8B        | 26S proteasome non-                                                | 53.10 | 0.00    |
| P462-             | TATA-box-binding protein                                           | 53.10 | 0.00    |
| Q9SGABC10        | ABC transporter B f                                                | 53.10 | 0.00    |
| Q6P1FIGNL1       | Fidgetin-like prote                                                | 53.10 | 0.00    |
| P0D7RPL24        | 60S ribosomal protein                                              | 53.10 | 0.00    |
| Q9FGIRERI1       | Protein RETICULATINA-                                              | 53.10 | 0.00    |
| Q8RWWTM10       | Transmembrane 9 sup                                                | 53.10 | 0.00    |
| Q5M7Atg542      | Dihydrolipooyllysine                                              | 53.10 | 0.00    |
| A3DJpck6        | Phosphoenolpyruvate                                                | 53.10 | 0.00    |
| Q4R6BB5S        | Bardet-Biedl syndro                                               | 53.10 | 0.00    |
| Q55Ax1dpC       | Dynamin-like protel                                                | 53.10 | 0.00    |
| Q963ACX4        | Acyl-coenzyme A oxi                                                | 53.10 | 0.00    |
| Q54YfDDB_G02    | DNA-binding protein                                                | 53.10 | 0.00    |
| O808CPFTSY      | Cell division prote                                                | 53.10 | 0.00    |
| D7SP1LRK10L     | Protein SUPPRESSOR                                                | 53.10 | 0.00    |
| Q7XZc1lpB       | Chaperone protein C                                                | 53.10 | 0.00    |
| Q014SBE1        | 1,4-alpha-glucan-br                                                | 53.10 | 0.00    |
| Q9SUIPS1K       | Photosystem I react                                                | 53.10 | 0.00    |
| Q56Y1Atg5p587   | Dehydrodolichyl dip                                               | 53.00 | 0.00    |
| A8PTCDUS3       | tRNA-dihydouridine                                                | 53.00 | 0.00    |
| Q1WCCcript      | Cysteine-rich PDZ-b                                                | 53.00 | 0.00    |
| P454fths22      | Cell division prote                                                | 53.00 | 0.00    |
| Q8K2A2ML1       | Alpha-2-macroglobulin                                              | 53.00 | 0.00    |
| Q541cox19       | Cytochrome c oxidas                                                | 53.00 | 0.00    |
| Q6P9hagh        | Hydroxyacylglutathione                                            | 53.00 | 0.00    |
| Q4WVlsb1        | AdoMet-dependent rR                                                | 53.00 | 0.00    |
| QBBMDlat        | Dihydrolipooyllysine                                              | 53.00 | 0.00    |
| Q9LR2RPL36C     | 60S ribosomal prote                                                | 53.00 | 0.00    |
| Q861Idst1       | Serine/threonine-pr                                                | 53.00 | 0.00    |
| Q5Z1VEPO1       | Twinkle protein, mi                                                | 53.00 | 0.00    |
| Accession      | Description                                      | Expression | Localised |
|---------------|--------------------------------------------------|------------|-----------|
| TRINITY_sp|541fragA  | Ras-related GTP-binding protein A | 52.90 | 0.00 |
| TRINITY_sp|Q9JJAAbcb9 | ATP-binding cassette | 52.90 | 0.00 |
| TRINITY_sp|Q137TARBP1 | Probable methyltransferase | 52.90 | 0.00 |
| TRINITY_sp|Q5SN0S6g01 | Zinc finger CCCH do | 52.90 | 0.00 |
| TRINITY_sp|Q275psmA1 | Proteasome subunit | 52.90 | 0.00 |
| TRINITY_sp|Q37DHRS7 | Dehydrogenase/reductase | 52.90 | 0.00 |
| TRINITY_sp|Q432PCNA | Proliferating cell | 52.90 | 0.00 |
| TRINITY_sp|Q405NPK1 | Mitogen-activated protein | 52.80 | 0.00 |
| TRINITY_sp|Q5A5NIK1 | Histidine protein k | 52.80 | 0.00 |
| TRINITY_sp|P324GBP1 | Guanylate-binding protein p | 52.80 | 0.00 |
| TRINITY_sp|Q395ODA4 | Dynemin beta chain | 52.80 | 0.00 |
| TRINITY_sp|Q9NEFrsp-3 | Probable splicing factor | 52.80 | 0.00 |
| TRINITY_sp|Q69KHAL3 | Phosphopantetheinylase | 52.80 | 0.00 |
| TRINITY_sp|Q170Cdc42 | Cdc42 homolog OS=An | 52.80 | 0.00 |
| TRINITY_sp|Q9FKIABCA11 | ABC transporter A f | 52.80 | 0.00 |
| TRINITY_sp|Q9NR1DYRK4 | Dual specificity tyrosine phosphorylation kinase | 52.80 | 0.00 |
| TRINITY_sp|Q9SSRGRLG1 | E3 ubiquitin-protein ligase | 52.80 | 0.00 |
| TRINITY_sp|A6QRAbA6B | Ras-related protein | 52.80 | 0.00 |
| TRINITY_sp|Q9C5PFK7 | ATP-dependent 6-phosphatase | 52.80 | 0.00 |
| TRINITY_sp|Q9LT2RD21C | Probable cysteine protein | 52.80 | 0.00 |
| TRINITY_sp|P151lefBA | Elongation factor 2 | 52.80 | 0.00 |
| TRINITY_sp|Q0WWAtg343 | Coatamer subunit ga | 52.80 | 0.00 |
| TRINITY_sp|Q82CRYZ | Quinone oxidoreductase | 52.80 | 0.00 |
| TRINITY_sp|Q7DLFPGB1 | Proteasome subunit | 52.80 | 0.00 |
| TRINITY_sp|Q14DHX34 | Probable ATP-dependent protein | 52.80 | 0.00 |
| TRINITY_sp|P236IWAR5 | Tryptophan--tRNA ligase | 52.80 | 0.00 |
| TRINITY_sp|Q95URab7a | Ras-related protein | 52.80 | 0.00 |
| TRINITY_sp|B4FH15-cis-zeta-carotenoid | 52.80 | 0.00 |
| TRINITY_sp|G0SERLI1 | Translation initiation factor | 52.80 | 0.00 |
| TRINITY_sp|Q8L3FZ2R2 | Protein FIZZY-RELATED | 52.80 | 0.00 |
| TRINITY_sp|Q8CFQAr | Intron-binding protein | 52.80 | 0.00 |
| TRINITY_sp|P41MAAt2g011 | DExH-box ATP-dependent | 52.80 | 0.00 |
| TRINITY_sp|Q9ZT1ERD2 | ER lumen protein-receptor | 52.80 | 0.00 |
| TRINITY_sp|Q7T3rab13 | Ras-related protein | 52.80 | 0.00 |
| TRINITY_sp|Q956FZ2 | Zinc finger FYVE domain | 52.80 | 0.00 |
| TRINITY_sp|Q11J1cd | Isocitrate dehydrogenase | 52.80 | 0.00 |
| TRINITY_sp|Q54Snlv | Putative ribosome binding protein | 52.80 | 0.00 |
| TRINITY_sp|Q9FMHRD21B | Probable cysteine protease | 52.80 | 0.00 |
| TRINITY_sp|Q9FY7BCAT5 | Branched-chain-aminotransferase | 52.80 | 0.00 |
| TRINITY_sp|Q9LY1AK1 | Aspartokinase 1, choline | 52.80 | 0.00 |
| TRINITY_sp|Q9WXrbpA | Putative RNA-binding protein | 52.80 | 0.00 |
| TRINITY_sp|Q8H1LTE20.3 | Thylakoid luminal protein | 52.80 | 0.00 |
| TRINITY_sp|P056Actin-2 heavy chain | 52.80 | 0.00 |
| TRINITY_sp|P536Actin | 52.80 | 0.00 |
| TRINITY_sp|A8MSLPD1 | Dihydrolipoyl dehydrogenase | 52.80 | 0.00 |
| TRINITY_sp|Q9SFPAH1 | Phosphatidate phosphatase | 52.80 | 0.00 |
| TRINITY_sp|Q8WIKPK | Pyridoxal kinase OS | 52.80 | 0.00 |
| TRINITY_sp|Q9PDNAH2 | Dynemin heavy chain | 52.80 | 0.00 |
| TRINITY_sp|Q9FItg477 | Probable acetyl-CoA transferase | 52.80 | 0.00 |
| TRINITY_sp|Q6AVAXDH | Xanthine dehydrogenase | 52.80 | 0.00 |
| TRINITY_sp|Q9MFDSPT1B | Dual specificity protein phosphatase | 52.70 | 0.00 |
| TRINITY_sp|P533NUTD6 | Nucleoside diphosphate kinase | 52.70 | 0.00 |
| TRINITY_sp|Q9SKOABC3 | ABC transporter C family | 52.70 | 0.00 |
| TRINITY_sp|Q9ZRICAD | Probable mannitol diphosphatase | 52.70 | 0.00 |
TRINITY_sp|Q5U2!usp47 Ubiquitin carboxyl- 52.70 0.00
TRINITY_sp|Q9M8D1D Protein DJ-1 homolo 52.70 0.00
TRINITY_sp|Q1Q003303921 Putative cysteine p 52.70 0.00
TRINITY_sp|Q8BY9Rdhd12 Retinol dehydrogena 52.70 0.00
TRINITY_sp|Q86Kfghi Bis(5'-adenosyl)-tr 52.70 0.00
TRINITY_sp|Q0VFkctd7 BtB/POZ domain-cont 52.70 0.00
TRINITY_sp|Q9NRkDXX21 Nucleolar RNA helic 52.70 0.00
TRINITY_sp|Q9LVKBOB1 Protein BOB1 OS 52.70 0.00
TRINITY_sp|O60t1limE LIM domain-containi 52.70 0.00
TRINITY_sp|Q54Ytrappc5 Trafficking protein 52.70 0.00
TRINITY_sp|Q32PMZL1 Myelin protein zero 52.70 0.00
TRINITY_sp|O356Abtrappc7 Retinol-specific AT 52.70 0.00
TRINITY_sp|P0944snrnp70 U1 small nuclear ri 52.70 0.00
TRINITY_sp|P04772ubu Glutamine synthetas 52.70 0.00
TRINITY_sp|Q640tatd1 Putative deoxyribon 52.70 0.00
TRINITY_sp|P790rhp16 ATP-dependent helic 52.70 0.00
TRINITY_sp|Q1DDkynU Kynureninase OS=Myx 52.70 0.00
TRINITY_sp|Q9MBIDHC10 Dynein-1-beta heavy 52.70 0.00
TRINITY_sp|Q3SZPMPCB Mitochondrial-proce 52.70 0.00
TRINITY_sp|P407Rac1 Ras-related protein 52.70 0.00
TRINITY_sp|Q165CAMK4 Calcium/calmodulin- 52.70 0.00
TRINITY_sp|P2976 60S acidic ribosoma 52.70 0.00
TRINITY_sp|Q52KSP1 Spingosine-1-phosp 52.70 0.00
TRINITY_sp|Q9CSRFC1 Replication factor 52.70 0.00
TRINITY_sp|P1147ubb1 Tubulin beta chain 52.70 0.00
TRINITY_sp|Q8GYfAt2g432CMP-sialic acid tra 52.70 0.00
TRINITY_sp|O810NRFPA DNA-directed RNA po 52.70 0.00
TRINITY_sp|Q190pho-1 Intestinal acid pho 52.70 0.00
TRINITY_sp|O959TOB3 DNA topoisomerase 3 52.70 0.00
TRINITY_sp|Q9LUNRAP2-2 Ethylene-responsive 52.70 0.00
TRINITY_sp|Q9NWUCC1 Uridine-cytidine ki 52.70 0.00
TRINITY_sp|P543eas Ethanolamine kinase 52.70 0.00
TRINITY_sp|Q8VFHCC1 Protein SC01 homolo 52.70 0.00
TRINITY_sp|O645STR1 Thiosulfate/3-merca 52.70 0.00
TRINITY_sp|A7HTrpmA 50S ribosomal prote 52.70 0.00
TRINITY_sp|P965gtFB Vancomycin glycone 52.70 0.00
TRINITY_sp|Q027RPL24 50S ribosomal prote 52.70 0.00
TRINITY_sp|P0DJRLP6 60S ribosomal prote 52.70 0.00
TRINITY_sp|Q2HJFAHD1 Acylpyruvase FAHD1, 52.60 0.00
TRINITY_sp|O805CYCU4-1 Cyclin-U4-1 OS=Arab 52.60 0.00
TRINITY_sp|Q9FVE2FC Transcription facto 52.60 0.00
TRINITY_sp|Q6PKhp Hemopexin OS=Danio 52.60 0.00
TRINITY_sp|Q54REDB G02 Probable serine/thr 52.60 0.00
TRINITY_sp|Q210kin-29 Serine/threonine-pr 52.60 0.00
TRINITY_sp|P518PRKX cAMP-dependent prot 52.60 0.00
TRINITY_sp|Q86Aerh Enhancer of rudimen 52.60 0.00
TRINITY_sp|Q9UCN1NOT8 CCR4-NOT transcript 52.60 0.00
TRINITY_sp|Q710spp2 Secreted phosphopro 52.60 0.00
TRINITY_sp|Q8RXNNDK4 Nucleoside diphosph 52.60 0.00
TRINITY_sp|Q5KWDnaJ Chaperone protein D 52.60 0.00
TRINITY_sp|Q23MTtl16a Probable beta-tubul 52.60 0.00
TRINITY_sp|P23F2TLLC Tubulin glycolase 3 52.60 0.00
TRINITY_sp|P386RPL24 60S ribosomal prote 52.60 0.00
TRINITY_sp|Q86GCys Crustapain OS=Panda 52.60 0.00
TRINITY_sp|A9WSglpG Glycerol kinase OS= 52.60 0.00
TRINITY_sp|Q99JRfc4 Replication factor 52.60 0.00
| Accession | Gene Name       | Description                              | Gene Symbol | Confidence |
|-----------|----------------|------------------------------------------|-------------|------------|
| TRINITY_sp| Q54H5srr       | Probable serine racemase                | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q861\DDB_G02 | PH domain-containing                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q9R1EB9d1      | B9 domain-containing                    | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q54Fnetfa      | Electron transfer factor                | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| P470\VTC4      | Vacuolar transport factor               | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q54Ehaox       | Hydroxyacid oxidase                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q6F3CPK10      | Calcium-dependent phosphatase           | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q6EE:CCT8      | T-complex protein                        | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q2331NYFB3     | Nuclear transcript                      | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q8691pakF      | Serine/threonine protein                | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q9C6\ABC14     | ABC transporter Gf                      | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q6EVFBRM       | ATP-dependent helicase                  | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| A2C4rznz       | Ribonuclease Z                          | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q5KQCAX2       | Vacuolar cation/proton                  | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| P182\-         | Tubulin beta-1 chain                    | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| H3JUSGT1       | Peptidyl serine aldehyde                | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q2444ARBE1A    | Ras-related protein                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q818LGLALDH    | L-galactose dehydrogenase               | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q8IQC5G021     | Uncharacterized Gol                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q9FGKS20       | 3-ketoacyl-CoA synthase                 | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| B1WVhem         | Uroporphyrinogen dehydratase            | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| P286(\SYNPCC7 | Uncharacterized protein                 | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q6ZMKIF6       | Kinesin-like protein                    | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q7ZXnle1       | Notchless protein h                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| P107\-sevA     | Severin OS=Dictyost                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q6D3ublcp1     | Ubiquitin-like domain                   | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q6F7mak16      | Protein MAK16 homolog                   | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q9FPLAGD5      | Probable ADP-ribosyltransferase         | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| QWLUUGGT       | UDP-glucose:glycoprotein                | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q9UTKSPAC109   | Putative CCA tRNA n                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q5ZIXXR2       | 5'-3' exoribonuclease                   | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q9STICEP2      | KDEL-tailed cysteine                    | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q5ZIXTBCD      | Tubulin-specific chd                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q86Ctor        | Target of rapamycin                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q54YDDB_G02    | DNA-binding protein                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| A8P5AMP4       | Probable Xaa-Pro am                      | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q9LT\At3g128  | Peroxisomal 2,4-dienoyl-CoA synthase    | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q0791PAM18     | Mitochondrial import                    | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| O026\HSD17B1c | 3-hydroxyacyl-CoA dehydrogenase         | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q4IAACYM1      | Mitochondrial presequence               | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q54Wccdc94     | Coiled-coil domain                      | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q86AcmcfX      | Mitochondrial subunit                   | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| B4JHG18624     | Lateral signaling t                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q5Q4Lig3       | DNA ligase 3 OS=Dicotyledon            | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| B1LXapaG       | Protein ApaG OS=Monocotyledon          | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q5Z8I06g07|RNA pseudouridinase                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q6D3ric8b      | Synembryon-B OS=Danio rerio             | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| B7LS\treF      | Cytoplasmic trehalase                   | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| F4KC\FBA4      | Fructose-bisphosphatase                | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q4U4Xirp2      | Xin actin-binding protein               | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q9FK\RABA1C    | Ras-related protein                     | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q9NEcpph-5     | Serine/threonine-phosphatase           | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| P511apE        | DNA-(apurinic or apyrimidinic) repair    | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| Q9SK\At2g320|Folate-biopterin trimer                 | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| 0784\ycf19     | Uncharacterized protein                 | OS=Dictyostelium discoideum | 0.00 |
| TRINITY_sp| P0C8\CCRP1     | Probable serine/threonine phosphatase   | OS=Dictyostelium discoideum | 0.00 |
| Accession | Description |
|-----------|-------------|
| sp|Q54YS0|Y8111_DICDI |
| sp|Q1K9C4|YFK7_SCHPO |
| sp|Q5FGQ8|DNAJ_EHRRG |
| sp|Q8S6N5|ACC1_ORYSJ |
| sp|Q7TXL9|PPSB_MYCBO |
| sp|Q9SV07|ASAT1_ARATH |
| sp|Q8WXX0|DYH7_HUMAN |
| sp|A8ICS9|CFAP46_CHLRE |
| sp|P43333|RU2A_ARATH |
| sp|Q9ZUP4|CKL5_ARATH |
| sp|Q8SKU2|TIC62_PEA |
| sp|B7KHF1|Y2224_CYAP7 |
| sp|F4KFV7|SUV3L_ARATH |
| sp|Q40477|ERF4_TOBAC |
| sp|Q8LDR3|CYP23_ARATH |
| sp|Q1EB31|DBP4_COCIM |
| sp|P28011|AAT1_MEDSA |
| sp|E9PU17|ABCAH_RAT |
| sp|O81884|GALDH_ARATH |
| sp|Q9M8K7|DUS1B_ARATH |
| sp|P18961|YPK2_YEAST |
| sp|Q9MLpdeD|cGMP-dependent 3',5 |
| sp|O359\Neck2|Serine/threonine-pr |
| sp|Q7ZWalg11|GDP-Man:Man(3)GlcNA |
| sp|P189\YPK2|Serine/threonine-pr |
| sp|Q5V\CDKAL1|Threonylcarbamoyladyl |
| sp|Q9MB\FKFBP|6-phosphofructo-2-k |
| sp|Q9M8D\DSPTP1B|Dual specificity pr |
| sp|Q0818\LGALDH|L-galactose dehydro |
| sp|Q995_yakc|Aldo-keto reductase |
| sp|E9PU1Abca17|ATP-binding casset |
| sp|P2801AAT-1|Aspartate aminotran |
| sp|Q1EB\DBP4|ATP-dependent RNA h |
| sp|Q8LD\CYP23|Peptidyl-prolyl cis |
| sp|Q404\ERF4|Ethylene-responsive |
| sp|Q6PF1ndor1|NADPH-dependent dif |
| sp|F4KF\At5g3989|DExH-box ATP-depend |
| sp|B7KHZ\PCC7424_Nucleoid-associated |
| sp|A7YE\ttc30a|Tetratricopeptide r |
| sp|Q8SK\TIC62|Protein TIC 62, chl |
| sp|Q9ZUIC\KL5|Casein kinase 1-lik |
| sp|P433\Atlg97\U2 small nuclear ri |
| sp|A8IC\CFAP46|Cilia- and flagella |
| sp|Q8XM\DNAH7|Dynemin heavy chain |
| sp|O085\Gtpbp1|GTP-binding protein |
| sp|Q9SV\ASAT1|Acy-CoA---sterol 0- |
| sp|Q7TXi\ppsB|Phthiocerol/phenolp |
| sp|Q8S6\ACC1|Acetyl-CoA carboxyl |
| sp|Q0HA\Ttc21b|Tetratricopeptide r |
| sp|Q5FQ\dnaJ|Chaperone protein D |
| sp|Q1K9\SPAC167.Probable E3 ubiquit |
| sp|Q8IU\CAMK1D|Calcium/calmodulin- |
| sp|Q54Y\DDB_G02\DNA-binding protein |
| TRINITY_sp|B6SF7MAA3 | Probable helicase M | 52.40 | 0.00 |
| TRINITY_sp|Q7T3Ikvat3 | Kynurenine--oxoglutarate hydroxylase subfamily | 52.40 | 0.00 |
| TRINITY_sp|Q9DKCselo | Selenoprotein O | 52.40 | 0.00 |
| TRINITY_sp|A2Y4CDKD-1 | Cyclin-dependent kinase | 52.40 | 0.00 |
| TRINITY_sp|Q8MY1DDB_GO2 | Probable serine/threonine protein kinase | 52.30 | 0.00 |
| TRINITY_sp|P868(-) | Non-specific lipid-transfer protein | 52.30 | 0.00 |
| TRINITY_sp|Q9UBgDNAJb11 | DnaJ homolog subfam | 52.30 | 0.00 |
| TRINITY_sp|P512iycf45 | Uncharacterized protein | 52.30 | 0.00 |
| TRINITY_sp|Q93V1PABN1 | Polyadenylate-binding protein | 52.30 | 0.00 |
| TRINITY_sp|F4HP1IRE4 | Probable serine/threonine protein kinase | 52.30 | 0.00 |
| TRINITY_sp|P465ubc4 | Ubiquitin-conjugating enzyme | 52.30 | 0.00 |
| TRINITY_sp|A7RPv1q2284 | NAD(P)H-hydratase epimerase | 52.30 | 0.00 |
| TRINITY_sp|Q5ZjIGARNL3 | GTPase-activating RAS GRB domain | 52.30 | 0.00 |
| TRINITY_sp|P375iaaA | Isoaspartyl peptidase | 52.30 | 0.00 |
| TRINITY_sp|Q99JAActr3 | Actin-related protein | 52.30 | 0.00 |
| TRINITY_sp|P047lamp | Glutamine synthetase | 52.30 | 0.00 |
| TRINITY_sp|Q7ZVsmu1 | WD40 repeat-containing protein | 52.30 | 0.00 |
| TRINITY_sp|Q177trxr-1 | Thioredoxin reductase | 52.30 | 0.00 |
| TRINITY_sp|P264ePARP1 | Poly ADP-ribose polymerase | 52.30 | 0.00 |
| TRINITY_sp|Q8LSPANK2 | Pantothenate kinase | 52.30 | 0.00 |
| TRINITY_sp|Q08Cznrf2 | E3 ubiquitin-protein ligase | 52.30 | 0.00 |
| TRINITY_sp|B3EFinfB | Translation initiation factor | 52.30 | 0.00 |
| TRINITY_sp|P078Acox1 | Peroxisomal acyl-coenzyme A oxidase | 52.30 | 0.00 |
| TRINITY_sp|Q8L9RPL21M | 50S ribosomal protein L21 | 52.30 | 0.00 |
| TRINITY_sp|P364trab2A | Ras-related protein | 52.30 | 0.00 |
| TRINITY_sp|P546patA | Calcium-transporting protein | 52.30 | 0.00 |
| TRINITY_sp|Q6GN6adml-a | Proteasomal ubiquitin-conjugating enzyme | 52.30 | 0.00 |
| TRINITY_sp|Q96DEDAC11 | Histone deacetylase | 52.30 | 0.00 |
| TRINITY_sp|Q55iube2w | Probable ubiquitin-conjugating enzyme | 52.30 | 0.00 |
| TRINITY_sp|P538JJJ1 | J protein JJJ1 OS=S. cerevisiae | 52.30 | 0.00 |
| TRINITY_sp|P044fcalmodulin | Calmodulin OS=T. menthae | 52.30 | 0.00 |
| TRINITY_sp|P451iettA | Energy-dependent transporter | 52.30 | 0.00 |
| TRINITY_sp|Q9SXRROA2 | DNA replication lic | 52.30 | 0.00 |
| TRINITY_sp|Q154MMPED1 | Metallophosphoesterase | 52.30 | 0.00 |
| TRINITY_sp|B5X8brc3 | Lys-63-specific deubiquitylase | 52.30 | 0.00 |
| TRINITY_sp|Q0947ALG2 | Alpha-1,3,1,6-mannosyltransferase | 52.30 | 0.00 |
| TRINITY_sp|P432Abcb1 | Multidrug resistance protein | 52.30 | 0.00 |
| TRINITY_sp|Q311ipanB | 3-methyl-2-oxobutanal dehydrogenase | 52.30 | 0.00 |
| TRINITY_sp|Q049PRF6 | Pre-mRNA-processing factor | 52.30 | 0.00 |
| TRINITY_sp|B2RWfCfap58 | Cilia- and flagella-associated protein | 52.30 | 0.00 |
| TRINITY_sp|A9UNbyisan | Bystin OS=Monosiga | 52.30 | 0.00 |
| TRINITY_sp|Q9STALDH10A | Betaine aldehyde dehydrogenase | 52.30 | 0.00 |
| TRINITY_sp|P1241vinraft | Vignain OS=Vigna mungo | 52.30 | 0.00 |
| TRINITY_sp|Q23FETTL1L3C | Tubulin glycolyase 3 | 52.30 | 0.00 |
| TRINITY_sp|POCAATTL1L3B | Tubulin glycolyase 3 | 52.30 | 0.00 |
| TRINITY_sp|Q6TEIfam91al | Protein FAM91Al OS=Populus | 52.30 | 0.00 |
| TRINITY_sp|Q8TAMTTCC8 | Tetratricopeptide repeat domain | 52.30 | 0.00 |
| TRINITY_sp|C4LAcme | Hydroxylamine dehydrogenase | 52.30 | 0.00 |
| TRINITY_sp|Q55decas1 | Cycloartenol synthase | 52.30 | 0.00 |
| TRINITY_sp|P598RDH12 | Retinol dehydrogenase | 52.30 | 0.00 |
| TRINITY_sp|A7E3PTPD1 | Protein tyrosine phosphatase | 52.30 | 0.00 |
| TRINITY_sp|P142PSAK | Photosystem I reaction center | 52.30 | 0.00 |
| TRINITY_sp|Q1PFAAL1 | AP2-like ethylene-responsive factor | 52.30 | 0.00 |
| TRINITY_sp|Q54Jrcagd | 2-oxoglutarate dehydrogenase | 52.30 | 0.00 |
| TRINITY_sp|Q9SS3SDP6 | Glycerol-3-phosphate dehydrogenase | 52.30 | 0.00 |
| TRINITY_sp|Q755IPL1 | Spindle assembly checkpoint protein | 52.30 | 0.00 |
| Gene ID     | Description                                      | Score | E-value |
|------------|--------------------------------------------------|-------|---------|
| P298c_cysE | Serine acetyltransferase                         | 52.30 | 0.00    |
| P0758c_CAPN15 | Calpain-15 OS=Homo                               | 52.20 | 0.00    |
| P999F_PFP-ALPI | Pyrophosphate--fructokinase                      | 52.20 | 0.00    |
| P5X8c_Atp13a3 | Probable cation-traporter                        | 52.20 | 0.00    |
| P0DJc_RPL13  | 60S ribosomal protein                            | 52.20 | 0.00    |
| P9S1c_DSK2B  | Ubiquitin domain-coat                           | 52.20 | 0.00    |
| P172c_unch-119 | Protein unc-119 OS=                           | 52.20 | 0.00    |
| P0141c_SPAC4A8,UPF0047 protein C4A |                                   | 52.20 | 0.00    |
| P0141c_SPAC4A8,UPF0047 protein C4A |                                   | 52.20 | 0.00    |
| P6COc_COF1   | Coflin OS=Yarrowia                               | 52.20 | 0.00    |
| P22Xc_FSM    | Chromatin assembly                               | 52.20 | 0.00    |
| P3501yfkJ    | Low molecular weight                             | 52.20 | 0.00    |
| P5141c_RPL26A | 60S ribosomal protein                           | 52.20 | 0.00    |
| P54Fc_nubpl  | Iron-sulfur protein                              | 52.20 | 0.00    |
| P9Y6c_ARL5A  | ADP-riboseylation afa                            | 52.20 | 0.00    |
| P091c_Amacr  | Alpha-methylacyl-Co                              | 52.20 | 0.00    |
| P4L1c_SH2450 | Uncharacterized epi                               | 52.20 | 0.00    |
| P0U3c_DD1    | DNA damage-inducible                             | 52.20 | 0.00    |
| P3411c_mvpA  | Major vault protein                              | 52.20 | 0.00    |
| P6T3c_Spata20 | Spermatogenesis-ass                              | 52.20 | 0.00    |
| P9D8c_Tex9   | Testis-expressed seed                            | 52.20 | 0.00    |
| P812cNALCN   | Sodium leak channel                              | 52.20 | 0.00    |
| P00Lc_0s01g062 | Neutral ceramidase                            | 52.20 | 0.00    |
| P395c_ODA4   | Dynnein beta chain                               | 52.20 | 0.00    |
| P048cTpl1A   | Triosephosphate iso                              | 52.20 | 0.00    |
| P491c_RAB2A  | Ras-related protein                              | 52.20 | 0.00    |
| P6E7c_gpsA   | Glycerol-3-phosphat                              | 52.20 | 0.00    |
| P87Ac_b1h    | Beta-lactamase hydr                              | 52.20 | 0.00    |
| P6N2c_rbm22  | Pre-mRNA-splicing factors                        | 52.20 | 0.00    |
| P0PGc_AKR4C9 | Aldo-keto reductase                              | 52.20 | 0.00    |
| P9CS5c RH5   | DEAD-box ATP-dependal                            | 52.20 | 0.00    |
| P5BPc_LOG2   | Cytokinin riboside                               | 52.20 | 0.00    |
| P54Sc_all1B1 | Probable allantoina                              | 52.20 | 0.00    |
| P318cRNA      | RNA-directed DNA polymer                        | 52.20 | 0.00    |
| P5XF1kdm8    | Lysine-specific dem                              | 52.20 | 0.00    |
| P52Nc_RAB1A  | Ras-related protein                              | 52.20 | 0.00    |
| P222cNDT1    | Nicotinamide adenin                              | 52.20 | 0.00    |
| P9BFCtropinone reductase |                             | 52.20 | 0.00    |
| P08DcRNA      | Probable tRNA methy                              | 52.20 | 0.00    |
| P431cRPE     | Ribulose-phosphate                               | 52.20 | 0.00    |
| P949cMPC1    | Mitochondrial pyruv                              | 52.20 | 0.00    |
| P9NBc_hiw    | E3 ubiquitin-protein                             | 52.20 | 0.00    |
| P9LS2PBD1    | Proteosome subunit                               | 52.20 | 0.00    |
| P905cElongation factor 1 |                            | 52.20 | 0.00    |
| P459cARP     | DNA-(apurinic or apyrimidinic) nucleotide excision | 52.10 | 0.00    |
| P12XGxGx [cytosine deaminase] |        | 52.10 | 0.00    |
| P2R7MYO9A    | Unconventional myosin                            | 52.10 | 0.00    |
| P065cGPN3    | GPN-loop GTPase 3                                | 52.10 | 0.00    |
| P54JaabcC3   | ABC transporter C                               | 52.10 | 0.00    |
| P99MnKars    | Lysine--tRNA ligase                              | 52.10 | 0.00    |
| Accession     | Description                                      | Value 1 | Value 2 | Value 3 |
|---------------|--------------------------------------------------|---------|---------|---------|
| TRINITY_sp|Ataxin-10 homolog OS=Dictyostelium discoideum GN=atxn10 PE=3 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Ras-related protein OS=Arabidopsis thaliana GN=NRPB1 PE=1 SV=3 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Sm-like protein LSM2 OS=Arabidopsis thaliana GN=LSM2 PE=1 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|O-phosphoseryl-tRNA(Sec) selenium transferase OS=Dictyostelium discoideum GN=sepsecs PE=3 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Centrosomal protein of 164 kDa OS=Mus musculus GN=Cep164 PE=1 SV=2 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|60S ribosomal protein L35 OS=Tetrahymena thermophila (strain SB210) GN=RPL35 PE=1 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|ABC transporter C family member 3 OS=Dictyostelium discoideum GN=abcC3 PE=3 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Ras-related protein RHN1 OS=Nicotiana plumbaginifolia GN=RHN1 PE=2 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Protein NLP5 OS=Arabidopsis thaliana GN=NLP5 PE=2 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|ATP-dependent Clp protease proteolytic subunit OS=Ralstonia solanacearum (strain GMI1000) GN=clpP PE=3 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Cytosolic purine 5'-nucleotidase OS=Dictyostelium discoideum GN=nt5c2 PE=3 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|RNA-binding protein 42 OS=Bos taurus GN=RBM42 PE=2 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial OS=Bos taurus GN=NDUFS8 PE=1 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Trehalose synthase OS=Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129) GN=treT PE=1 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Protein-glutamate O-methyltransferase OS=Danio rerio GN=armt1 PE=2 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|1,4-dihydroxy-2-naphthoyl-CoA synthase OS=Bacillus subtilis (strain 168) GN=menB PE=1 SV=2 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Kinesin-like protein KIF6 OS=Homo sapiens GN=KIF6 PE=1 SV=3 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Ras-related protein Rab-6.1 OS=Caenorhabditis elegans GN=rab-6.1 PE=3 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Prolyl 4-hydroxylase 5 OS=Arabidopsis thaliana GN=P4H5 PE=2 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Retrovirus-related Pol polyprotein from transposon 297 OS=Drosophila melanogaster GN=pol PE=3 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Exonuclease 1 OS=Dictyostelium discoideum GN=exo1 PE=3 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Kinesin-related protein 3 OS=Dictyostelium discoideum GN=kif3 PE=1 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=1 SV=2 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Mitotic checkpoint protein BUB3.2 OS=Arabidopsis thaliana GN=BUB3.2 PE=2 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|ABC transporter C family member 2 OS=Arabidopsis thaliana GN=ABCC2 PE=1 SV=2 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|ATP-binding cassette sub-family A member 1 OS=Mus musculus GN=Abca1 PE=1 SV=4 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Serine/threonine-protein phosphatase BSU1 OS=Arabidopsis thaliana GN=BSU1 PE=1 SV=2 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|RAC family serine/threonine-protein kinase homolog OS=Dictyostelium discoideum GN=pkbA PE=1 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|GTP-binding protein ypt1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ypt1 PE=1 SV=2 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|Heat stress transcription factor A-4b OS=Oryza sativa subsp. japonica GN=HSFA4B PE=2 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|60S ribosomal protein L23A OS=Tetrahymena thermophila (strain SB210) GN=RPL23A PE=1 SV=1 | 52.10   | 0.00    | 0.00    |
| TRINITY_sp|DNA (cytosine-5)-methyltransferase 1 OS=Gallus gallus GN=DNMT1 PE=1 SV=1 | 52.10   | 0.00    | 0.00    |
| Accession | Description | Expression | Function |
|------------|-------------|------------|----------|
| TRINITY_sp| 26S proteasome non- | 52.00 | 0.00 |
| TRINITY_sp| 26S proteasome non-ATPase regulatory subunit 12 homolog A | 52.00 | 0.00 |
| TRINITY_sp| Target of rapamycin | 52.00 | 0.00 |
| TRINITY_sp| N-terminal acetyltransferase B complex catalytic subunit naa20 | 52.00 | 0.00 |
| TRINITY_sp| Probable RNA-binding protein 19 | 52.00 | 0.00 |
| TRINITY_sp| Aldo-keto reductase yakc [NADP(+)] | 52.00 | 0.00 |
| TRINITY_sp| AP-1 complex subunit gamma | 52.00 | 0.00 |
| TRINITY_sp| Histone chaperone asf1 | 52.00 | 0.00 |
| TRINITY_sp| E3 ubiquitin-protein ligase UPL3 | 52.00 | 0.00 |
| TRINITY_sp| ATP-dependent RNA helicase dhx8 | 52.00 | 0.00 |
| TRINITY_sp| Probable cation-transporting ATPase 13A3 | 52.00 | 0.00 |
| TRINITY_sp| 30S ribosomal protein S16 | 52.00 | 0.00 |
| TRINITY_sp| Cathepsin L | 52.00 | 0.00 |
| TRINITY_sp| tRNA modification GTPase GTPBP3, mitochondrial | 52.00 | 0.00 |
| TRINITY_sp| Bile salt export pump | 52.00 | 0.00 |
| TRINITY_sp| Myosin IC heavy chain | 52.00 | 0.00 |
| TRINITY_sp| ABC transporter G family member 7 | 52.00 | 0.00 |
| TRINITY_sp| Methyltransferase-like protein 6 | 52.00 | 0.00 |
| TRINITY_sp| 30S ribosomal protein S16 | 52.00 | 0.00 |
| TRINITY_sp| Cathepsin L | 52.00 | 0.00 |
TRINITY_sp|Q6L5C0s05g05: Zinc finger CCCH domain-containing protein 1 51.90 0.00
TRINITY_sp|P0C88C4RF1: Probable serine/threonine-protein kinase 51.90 0.00
TRINITY_sp|P505s0m04: Structural maintenance of chromosomes (SMC) complex 51.90 0.00
TRINITY_sp|Q9I81: Heat shock 70 kDa protein 1 51.90 0.00
TRINITY_sp|C0QTprfA: Peptide transferase 51.90 0.00
TRINITY_sp|Q428RPB2: DNA-directed RNA polymerase 51.90 0.00
TRINITY_sp|P406t: Aldo-keto reductase 51.90 0.00
TRINITY_sp|P0AG1purF: Amidophosphoribosyltransferase 51.90 0.00
TRINITY_sp|Q940dymA: Dynamin-A 51.90 0.00
TRINITY_sp|Q2NSgrol2: 60 kDa chaperonin 2 51.90 0.00
TRINITY_sp|Q9LDUUPS1: Uridine 5'-monophosphatase 51.90 0.00
TRINITY_sp|Q4U2agtpbpl: Cytosolic carboxypeptidase 51.90 0.00
TRINITY_sp|Q92GpikxAI: Narbonolide/10-deoxyechinolide synthase 51.90 0.00
TRINITY_sp|Q025yK2: Probable serine/threonine-protein kinase 51.90 0.00
TRINITY_sp|P086tR: Ras-like protein 3 51.90 0.00
TRINITY_sp|Q9M6CP1: Cycloleucalenol cyclase 51.90 0.00
TRINITY_sp|Q809tFTSH4: ATP-dependent zinc endonuclease 51.90 0.00
TRINITY_sp|A4FUHRPL22L1: 60S ribosomal protein L22 51.80 0.00
TRINITY_sp|Q55E1ubub2: Putative mitotic checkpoint protein 51.80 0.00
TRINITY_sp|Q9LTFN1MT1: Glycylpeptide N-tetrahydropyrimidinetransferase 51.80 0.00
TRINITY_sp|Q9P407tp7: Probable U3 small nuclear RNA-processing protein 51.80 0.00
TRINITY_sp|Q8NHEPK13C3: Phosphatidylinositol-4-phosphate 51.80 0.00
TRINITY_sp|Q54J3alg5: Dolichyl-phosphate synthase 51.80 0.00
TRINITY_sp|P930tRH21: DEAD-box ATP-dependent helicase 51.80 0.00
TRINITY_sp|Q4Z4petM: Cytochrome b6-f complex protein 51.80 0.00
TRINITY_sp|P562tGfer: FAD-linked sulfhydryl oxidase 51.80 0.00
TRINITY_sp|P2715CBR: Carotene biosynthesis protein 51.80 0.00
TRINITY_sp|Q134tRca-1: Myb-like DNA-binding protein 51.80 0.00
TRINITY_sp|Q93VPABN1: Polyadenylate-binding protein 51.80 0.00
TRINITY_sp|P237t1txB: Leukotoxin export protein 51.80 0.00
TRINITY_sp|P0AFtjyjq: UPF0047 protein YjD 51.80 0.00
TRINITY_sp|Q9M0tKEA3: K(+) efflux antiporter 51.80 0.00
TRINITY_sp|Q9SRtDML2: DEMETER-like protein 51.80 0.00
TRINITY_sp|Q827tPSTP: Phosphoserine phosphatase 51.80 0.00
TRINITY_sp|B2I6tmnetE: 5-methyltetrahydrofolate reductase 51.80 0.00
TRINITY_sp|B9Sq1RCPM05: Probable bifunctional enzyme 51.80 0.00
TRINITY_sp|Q9Z2tVAC14: Protein VAC14 homolog 51.80 0.00
TRINITY_sp|P519tNek1: Serine/threonine-protein kinase 51.80 0.00
TRINITY_sp|P490tGPI8: GPI-anchored protein 51.80 0.00
TRINITY_sp|Q54Vtdans56: Probable ATP-dependent helicase 51.80 0.00
TRINITY_sp|Q86Gtgcg-28: Receptor-type guanylyl cyclase 51.80 0.00
TRINITY_sp|Q8LFCAMY2: Probable alpha-amylase 51.80 0.00
TRINITY_sp|O491tTIF3C1: Eukaryotic translation initiation factor 3 51.80 0.00
TRINITY_sp|F411tELP2: Elongator complex protein 51.80 0.00
TRINITY_sp|Q9T0tLACS4: Long chain acyl-CoA dehydrogenase 51.80 0.00
TRINITY_sp|Q3V0tDnah12: Dynein heavy chain 51.70 0.00
TRINITY_sp|Q9M7tRPL29A: 60S ribosomal protein L29 51.70 0.00
TRINITY_sp|Q7Z6HUWE1: E3 ubiquitin-protein ligase 51.70 0.00
TRINITY_sp|Q6NWype13: Protein yippee-like 51.70 0.00
TRINITY_sp|Q9C71NTP2: Nuclear transport factor 51.70 0.00
TRINITY_sp|Q9YHtnncapd2: Condensin complex subunit 51.70 0.00
TRINITY_sp|E1BB2RANB3: DNA annealing helicase 51.70 0.00
TRINITY_sp|Q54Nku70: ATP-dependent DNA helicase 51.70 0.00
TRINITY_sp|Q410tSBE1: 1,4-alpha-glucan-branching enzyme 51.70 0.00
TRINITY_sp|E1VB1HELO_23: Putative glutathione S-transferase 51.70 0.00
TRINITY_sp|Q008tMAPK: Mitogen-activated protein kinase 51.70 0.00
TRINITY_sp|Q0KI|CG9801 PP2C-like domain-containing protein CG9801 0.00
TRINITY_sp|Q9FR|TAP14B Transcription initiation factor 0.00
TRINITY_sp|Q545|midA Protein arginine methyltransferase 0.00
TRINITY_sp|Q8BM|Lipk Lipase member K OS= 0.00
TRINITY_sp|P341|pkgC Protein kinase 3 OS= 0.00
TRINITY_sp|Q8H1|ALEU Thiol protease aleu 0.00
TRINITY_sp|P98I|Atp9b Probable phospholipid-transporting ATPase IIB 0.00
TRINITY_sp|Q008|MAPK Mitogen-activated protein kinase 0.00
TRINITY_sp|A7HT|rplA 50S ribosomal protein L9 0.00
TRINITY_sp|Q9C0|DNAH6 Dynein heavy chain 0.00
TRINITY_sp|Q94Z|PDIL2-2 Protein disulfide isomerase 0.00
TRINITY_sp|Q9JK|Myg1 UPP0160 protein MYG1 0.00
TRINITY_sp|Q6GL|desi1 Desumoylating isopeptidase 1 0.00
TRINITY_sp|Q7V2|FZ1 Protein FIZZY-RELAT 0.00
TRINITY_sp|Q008|MAPK Mitogen-activated protein kinase 0.00
TRINITY_sp|Q207|atad-3 ATPase family AAA d 0.00
TRINITY_sp|Q8TG|TAR1 Protein TAR1 OS=Saccharomyces cerevisiae 0.00
TRINITY_sp|Q6NZ|SDG40 Protein SET DOMAIN GROUP 40 0.00
TRINITY_sp|Q9Y6|ARL5A ADP-ribosylation factor GTPase 0.00
TRINITY_sp|Q8RT|PRP31 U4/U6 small nuclear ribonucleoprotein 0.00
TRINITY_sp|Q8LG|COL6 Zinc finger protein 0.00
TRINITY_sp|Q323|ybiA N-glycosidase YbiA 0.00
TRINITY_sp|Q8Y2|RSc0270 ATPase family AAA d 0.00
TRINITY_sp|P0AG|trmH tRNA (guanosine(18)) 0.00
TRINITY_sp|Q6MD|clpb Chaperone protein C 0.00
TRINITY_sp|Q6PF|jmjd6 Bifunctional arginine methyltransferase 0.00
TRINITY_sp|Q8KA|pckG Phosphoenolpyruvate carboxykinase [GTP] 0.00
TRINITY_sp|Q00W|EUE1 Thymidylate kinase 0.00
TRINITY_sp|Q9C5|CM3 Chorismate mutase 0.00
TRINITY_sp|Q926|EDEM1 ER degradation-enhancing protein EDEM1 0.00
TRINITY_sp|Q323|ybiA N-glycosidase YbiA 0.00
TRINITY_sp|A8I4|FAP100 Cilia- and flagella associated protein 0.00
TRINITY_sp|Q9UB|HDAC6 Histone deacetylase 0.00
TRINITY_sp|Q748|cafl Poly(A) ribonuclease 0.00
TRINITY_sp|Q7XX|PYRD Dihydroorotate dehydrogenase 0.00
TRINITY_sp|Q286|ABCC2 Canalicular multispecific organic anion transporter 0.00
TRINITY_sp|Q711|CCL4 C-C motif chemokine 0.00
TRINITY_sp|P492|RPL9 60S ribosomal protein L9 0.00
TRINITY_sp|Q9LS|PAE1 Proteasome subunit 0.00
TRINITY_sp|Q817|coq-2 4-hydroxybenzoate CoA ligase 0.00
TRINITY_sp|Q6NV|decr2 Peroxisomal 2,4-dienoyl-CoA reductase 0.00
TRINITY_sp|Q9VH|GstZ2 Probable maleylacetate racemase 0.00
TRINITY_sp|Q86A|polr3a DNA-directed RNA polymerase III subunit 0.00
TRINITY_sp|Q7T3|dbr1 Larval debranching enzyme 0.00
TRINITY_sp|Q7YS|canA Calcineurin subunit 0.00
| Accession     | Description                                                                 | Eukaryotic ortholog | Name  | Score |
|--------------|------------------------------------------------------------------------------|---------------------|-------|-------|
| TRINITY_sp|O644(BMY1) | Beta-amylase OS=Vig | 51.60 | 0.00 |
| TRINITY_sp|Q9P7.gad8 | Serine/threonine-pr | 51.60 | 0.00 |
| TRINITY_sp|Q9C5.ELF5A-3 | Eukaryotic translat | 51.60 | 0.00 |
| TRINITY_sp|Q6Z5.SAP12 | Zinc finger A20 and | 51.60 | 0.00 |
| TRINITY_sp|P231.ABCB4 | Phosphatidylcholine | 51.60 | 0.00 |
| TRINITY_sp|Q9BU.TRMO | tRNA (adenine(37)-N) | 51.60 | 0.00 |
| TRINITY_sp|Q9F2.SMGL | Protein SMGL OS=Ar | 51.60 | 0.00 |
| TRINITY_sp|P485~ | Cytochrome b-c1 com | 51.60 | 0.00 |
| TRINITY_sp|G5DB.CPP1 | Protein CHAPERONE-L | 51.60 | 0.00 |
| TRINITY_sp|O499.TLP40 | Peptidyl-prolyl cis | 51.60 | 0.00 |
| TRINITY_sp|Q5W1.lsm1 | Probable U6 snRNA-a | 51.60 | 0.00 |
| TRINITY_sp|Q5G1DDB_G02 | PXMP2/4 family prot | 51.60 | 0.00 |
| TRINITY_sp|Q86A.purF | Amidophosphoribosyl | 51.60 | 0.00 |
| TRINITY_sp|Q54K.Macc | Methylcrotonyl-CoA | 51.60 | 0.00 |
| TRINITY_sp|Q7ZV.fsirt2 | NAD-dependent prote | 51.60 | 0.00 |
| TRINITY_sp|Q9SH1.UBC34 | Ubiquitin-conjugati | 51.60 | 0.00 |
| TRINITY_sp|P078.SUOX | Sulfite oxidase OS= | 51.60 | 0.00 |
| TRINITY_sp|P524.PAC1 | Proteasome subunit | 51.60 | 0.00 |
| TRINITY_sp|Q568.igtoc1 | Glycosyltransferase | 51.60 | 0.00 |
| TRINITY_sp|Q54S.sf3b3 | Probable splicing f | 51.60 | 0.00 |
| TRINITY_sp|Q9F1i.UBC27 | Ubiquitin-conjugati | 51.60 | 0.00 |
| TRINITY_sp|Q018.YPT1 | Ras-like GTP-bindin | 51.60 | 0.00 |
| TRINITY_sp|Q9BZ1.TPBPF4 | Nucleolar GTP-bindi | 51.60 | 0.00 |
| TRINITY_sp|Q9C9RPL6B | 60S ribosomal prote | 51.60 | 0.00 |
| TRINITY_sp|Q2NCJ.ELI_029 | Blue-light-activate | 51.60 | 0.00 |
| TRINITY_sp|F4IE6.RID1 | Pre-mRNA-splicing f | 51.60 | 0.00 |
| TRINITY_sp|Q8NDI.PAPD5 | Non-canonical poly( | 51.60 | 0.00 |
| TRINITY_sp|Q99y.yakc | Aldo-keto reductase | 51.60 | 0.00 |
| TRINITY_sp|F4KA.MCM6 | DNA replication lic | 51.60 | 0.00 |
| TRINITY_sp|F1Q4s.atp9b | Probable phospholip | 51.60 | 0.00 |
| TRINITY_sp|P347.RAS1 | Ras-like protein 1 | 51.60 | 0.00 |
| TRINITY_sp|P153.RpS27A | Ubiquitin-40S ribos | 51.60 | 0.00 |
| TRINITY_sp|Q54R.mkkA | Mitogen-activated p | 51.60 | 0.00 |
| TRINITY_sp|Q9LXAt5g128 | Zinc finger CCH do | 51.60 | 0.00 |
| TRINITY_sp|Q9C5.SMCC2-1 | Structural maintena | 51.60 | 0.00 |
| TRINITY_sp|Q86A.spkA-1 | Stress-activated pr | 51.60 | 0.00 |
| TRINITY_sp|P518.lig1 | DNA ligase 1 OS=Xen | 51.60 | 0.00 |
| TRINITY_sp|Q551.purU | Formyltetrahydrofol | 51.60 | 0.00 |
| TRINITY_sp|A3QKr.elin2 | Erlin-2 OS=Danio re | 51.60 | 0.00 |
| TRINITY_sp|B7ZC.KIF28P | Kinesin-like protei | 51.50 | 0.00 |
| TRINITY_sp|P051.CFI | Complement factor I | 51.50 | 0.00 |
| TRINITY_sp|Q3S47.AHK5 | Histidine kinase 5 | 51.50 | 0.00 |
| TRINITY_sp|F1Q4q.atp9b | Probable phospholip | 51.50 | 0.00 |
| TRINITY_sp|Q9LE1.GPXC1 | Probable phospholip | 51.50 | 0.00 |
| TRINITY_sp|P521.kpna1 | Importin subunit al | 51.50 | 0.00 |
| TRINITY_sp|Q9XGB."ALPH| Serine/threonine pr | 51.50 | 0.00 |
| TRINITY_sp|Q54S.pemtA | Phosphatidylethanol | 51.50 | 0.00 |
| TRINITY_sp|Q55C.rasU | Ras-like protein ra | 51.50 | 0.00 |
| TRINITY_sp|P981.ATP8B2 | Phospholipid-transp | 51.50 | 0.00 |
| TRINITY_sp|Q5XJ.fip111 | Pre-mRNA 3'-end-pro | 51.50 | 0.00 |
| TRINITY_sp|Q230.eca2 | Calcium-transportin | 51.50 | 0.00 |
| TRINITY_sp|P229.let-60 | Ras protein let-60 | 51.50 | 0.00 |
| TRINITY_sp|A0Q34.ribBA | Riboflavin biosynth | 51.50 | 0.00 |
| TRINITY_sp|Q8L77.RPL18AA | 60S ribosomal prote | 51.50 | 0.00 |
| TRINITY_sp|Q2K1T.2DH | L-threonine 3-dehyd | 51.50 | 0.00 |
| TRINITY_sp|Q9FJH.UPF1 | Regulator of nonsen | 51.50 | 0.00 |
| Gene ID         | Description                                      | Chromosome | Strain | Organism | Organism ID | Chromosome | Strain | Organism | Organism ID | Log2 Fold Change |
|----------------|--------------------------------------------------|------------|--------|----------|-------------|------------|--------|----------|-------------|-----------------|
| TRINITY_sp|Q082:REX4 | RNA exonuclease 4 | O | S. cerevisiae | S288c | 2 | ATCC 204508 | 0.00 |
| TRINITY_sp|P525:myb12 | Myb-related protein | 51.50 | 0.00 |
| TRINITY_sp|P142:PSAG | Photosystem I | 51.50 | 0.00 |
| TRINITY_sp|P519:Nek1 | Serine/threonine-protein kinase | 51.50 | 0.00 |
| TRINITY_sp|Q8C0:Agps | Alkyldihydroxyacetone | 51.50 | 0.00 |
| TRINITY_sp|P102:MYB | Transcriptional activator | 51.50 | 0.00 |
| TRINITY_sp|Q9PT:kcnab2 | Voltage-gated potassium channel | 51.50 | 0.00 |
| TRINITY_sp|B0G1:mecFC | Mitochondrial electron transfer | 51.50 | 0.00 |
| TRINITY_sp|Q138:EXOSC2 | Exosome complex component | 51.50 | 0.00 |
| TRINITY_sp|P918:Mo25 | Protein Mo25 | 51.50 | 0.00 |
| TRINITY_sp|P351:UBC11 | Ubiquitin-conjugating enzyme | 51.50 | 0.00 |
| TRINITY_sp|Q8NG:GTP | Tubulin--tyrosine ligase | 51.50 | 0.00 |
| TRINITY_sp|Q6DE:etnppl | Ethanolamine-phosphate biosynthesis | 51.50 | 0.00 |
| TRINITY_sp|B2RX:Jabc3 | Canalicular multispacer | 51.50 | 0.00 |
| TRINITY_sp|Q9ST:ABC | ABC transporter A family | 51.50 | 0.00 |
| TRINITY_sp|A8IB:CFAP77 | Cilia- and flagella-associated protein | 51.50 | 0.00 |
| TRINITY_sp|Q389:KIN10 | SNF1-related protein kinase | 51.50 | 0.00 |
| TRINITY_sp|Q6NMA:8g597 | UDP-galactose/UDP-glucose transporter | 51.50 | 0.00 |
| TRINITY_sp|Q5ZLG:GFPAT3 | Glycerol-3-phosphate dehydrogenase | 51.50 | 0.00 |
| TRINITY_sp|Q9SW:DHC1 | Dynactin-1 alpha | 51.50 | 0.00 |
| TRINITY_sp|Q64I:ublc1p | Ubiquitin-like domain | 51.50 | 0.00 |
| TRINITY_sp|Q8NB:RDH13 | Retinol dehydrogenase | 51.50 | 0.00 |
| TRINITY_sp|Q6KU:ube2z | Ubiquitin-conjugating enzyme | 51.50 | 0.00 |
| TRINITY_sp|Q8TI:kip5 | Kinesin-related protein | 51.50 | 0.00 |
| TRINITY_sp|P467:cysB | Cystathionine beta-synthase | 51.50 | 0.00 |
| TRINITY_sp|P860:bdhA | D-beta-hydroxybutyrate dehydrogenase | 51.50 | 0.00 |
| TRINITY_sp|Q54P:csnk2b | Casein kinase II | 51.50 | 0.00 |
| TRINITY_sp|Q103:CYCB2-1 | Cyclin-B2-1 | 51.50 | 0.00 |
| TRINITY_sp|P411:At1g0962 | Leucine--tRNA ligase | 51.50 | 0.00 |
| TRINITY_sp|Q9CS:AXT1 | Histone-lysine N-methyltransferase | 51.50 | 0.00 |
| TRINITY_sp|P467:KIN10 | DNA-directed RNA polymerase | 51.50 | 0.00 |
| TRINITY_sp|P240:GluS | Glu S. griseus protease | 51.50 | 0.00 |
| TRINITY_sp|Q9VQ:CG3326 | Fidgetin-like protein | 51.40 | 0.00 |
| TRINITY_sp|P529:VPS4 | Vacuolar protein sorting | 51.40 | 0.00 |
| TRINITY_sp|Q55E:Vps13E | Putative vacuolar protein | 51.40 | 0.00 |
| TRINITY_sp|Q5E9:NFYA | Nuclear transcript | 51.40 | 0.00 |
| TRINITY_sp|Q9SB:RPN7 | 26S proteasome non-ATPase | 51.40 | 0.00 |
| TRINITY_sp|Q338:ECN5 | Histone acetyltransferase | 51.40 | 0.00 |
| TRINITY_sp|Q9CB:RAB1 | Ras-related protein | 51.40 | 0.00 |
| TRINITY_sp|Q9SL:TCX6 | Protein tesmin/TSO1 | 51.40 | 0.00 |
| TRINITY_sp|Q9UN:CD14A | Dual specificity protein kinase | 51.40 | 0.00 |
| TRINITY_sp|O349:ypsA | Probable NAD-dependence | 51.40 | 0.00 |
| TRINITY_sp|Q588:TEB | Helicase and polymerase | 51.40 | 0.00 |
| TRINITY_sp|P0C6:DNAh2 | Dynein heavy chain | 51.40 | 0.00 |
| TRINITY_sp|Q9NR:HELLS | Lymphoid-specific helicase | 51.40 | 0.00 |
| TRINITY_sp|P241:CDKA-1 | Cyclin-dependent kinase | 51.40 | 0.00 |
| TRINITY_sp|Q7ZU:stk3 | Serine/threonine-protein kinase | 51.40 | 0.00 |
| TRINITY_sp|P832:CBR2 | NADH-cytochrome b5 reductase | 51.40 | 0.00 |
| TRINITY_sp|G5EC:let-92 | Serine/threonine-protein kinase | 51.40 | 0.00 |
| TRINITY_sp|P777:ajO | Uncharacterized oxidoreductase | 51.40 | 0.00 |
| TRINITY_sp|Q40T:RGP2 | Ras-related protein | 51.40 | 0.00 |
| TRINITY_sp|Q9CS:SUP4 | Protein SUPPRESSOR | 51.40 | 0.00 |
| TRINITY_sp|Q0DJ:Os5g03 | Coatomer subunit | 51.40 | 0.00 |
| TRINITY_sp|Q11K:gluQ | Glutamyl-Q tRNA synthetase | 51.40 | 0.00 |
| TRINITY_sp|B0F9:IGC6 | Golgin candidate | 51.40 | 0.00 |
TRINITY_sp|A8JF:ODA1  Outer dynein arm pr  51.10  0.00
TRINITY_sp|Q54GWDDB_G02:Coiled-coil domain-  51.10  0.00
TRINITY_sp|Q869NDBB_G02:3-hydroxybutyryl-Co  51.10  0.00
TRINITY_sp|Q54RIpyk  Pyruvate kinase OS=  51.10  0.00
TRINITY_sp|A2ARIPip5k1  Inositol hexakispho  51.10  0.00
TRINITY_sp|Q9P2IWKD35  WD repeat-containin  51.10  0.00
TRINITY_sp|Q86Cctor  Target of rapamycin  51.10  0.00
TRINITY_sp|A5D9:SPRTN  SprT-like domain-co  51.10  0.00
TRINITY_sp|Q9U7TUBE1  Tubulin epsilon cha  51.10  0.00
TRINITY_sp|Q049:GDHA  Glutamate dehydrote  51.10  0.00
TRINITY_sp|Q54RIyif6  Protein YIPF6 homol  51.10  0.00
TRINITY_sp|Q68O1COX10  Protein root UVB spec  51.10  0.00
TRINITY_sp|Q9S1IRPN1A  26S proteasome non-  51.10  0.00
TRINITY_sp|P290TIV1  Acid beta-fructofur  51.10  0.00
TRINITY_sp|Q3UTCCdk15  Cyclin-dependent ki  51.10  0.00
TRINITY_sp|Q751CNOT3  CCR4-NOT transcript  51.10  0.00
TRINITY_sp|Q9NWRL1M  E3 ubiquitin-protein  51.10  0.00
TRINITY_sp|Q5M7:TH1  Thiamine biosynthet  51.10  0.00
TRINITY_sp|Q8231At2g258:Probable transcript  51.10  0.00
TRINITY_sp|Q93Y1RUS6  Protein root UVB se  51.10  0.00
TRINITY_sp|P109:R-  Retrovirus-related  51.10  0.00
TRINITY_sp|Q647At2g348:Coatomer subunit ep  51.10  0.00
TRINITY_sp|Q6DGXkcd6  BTB/POZ domain-cont  51.10  0.00
TRINITY_sp|Q68E1amdh1  Probable imidazol  51.10  0.00
TRINITY_sp|Q9BRRIOK1  Serine/threonine-pr  51.10  0.00
TRINITY_sp|F736s111770  Uncharacterized pro  51.10  0.00
TRINITY_sp|Q6522ACX2  Acyl-coenzyme A oxi  51.10  0.00
TRINITY_sp|P5653HDAC3  Histone deacetylase  51.10  0.00
TRINITY_sp|Q9C92SPPA  Serine protease SPP  51.10  0.00
TRINITY_sp|Q4KDUR3  Urea-proton symport  51.10  0.00
TRINITY_sp|Q9SM7AAE3  Oxalate--CoA ligase  51.10  0.00
TRINITY_sp|P1141CRYZ  Quinone oxidoreduct  51.00  0.00
TRINITY_sp|Q9COCDNAH6  Dynein heavy chain  51.00  0.00
TRINITY_sp|Q120TSRS3  Ribosome biogenesis  51.00  0.00
TRINITY_sp|P509upp  Uracil phosphoribos  51.00  0.00
TRINITY_sp|Q9C5GRF12  14-3-3-like protein  51.00  0.00
TRINITY_sp|Q55Epats1  Probable serine/th  51.00  0.00
TRINITY_sp|Q54Qphr2aB  Serine/threonine-pr  51.00  0.00
TRINITY_sp|Q9LE1At5g0816:ACA ribonucleop  51.00  0.00
TRINITY_sp|Q9J1Istk3  Serine/threonine-pr  51.00  0.00
TRINITY_sp|Q8RXRH8  DEAD-box ATP-depend  51.00  0.00
TRINITY_sp|Q038MSH6  DNA mismatch repair  51.00  0.00
TRINITY_sp|Q54RcnrB  CLPTM1-like membran  51.00  0.00
TRINITY_sp|Q9LXYHMM2  Histone acetyltrans  51.00  0.00
TRINITY_sp|P2644PARP1  Poly [ADP-ribose] p  51.00  0.00
TRINITY_sp|Q96PINSUN5  Probable 28S rRNA (  51.00  0.00
TRINITY_sp|Q9RHsssb2  Single-stranded DNA  51.00  0.00
TRINITY_sp|Q7ZXkif19  Kinesin-like protei  51.00  0.00
TRINITY_sp|BOD2IAMPP  Probable Xaa-Pro am  51.00  0.00
TRINITY_sp|Q8LTHDHA18  Histone deacetylase  51.00  0.00
TRINITY_sp|Q8T2mccb  Methylenecrotonoyl-CoA  51.00  0.00
TRINITY_sp|Q8AVsyf2  Pre-mRNA-splicing f  51.00  0.00
TRINITY_sp|Q8BZc25a2Mitochondrial 2-oxo  51.00  0.00
TRINITY_sp|B3PFdnaK  Chaperone protein D  51.00  0.00
TRINITY_sp|O046ICURT1A  Protein CURVATURE T  51.00  0.00
TRINITY_sp|Q9LZfRPL36C  60S ribosomal prote  51.00  0.00
| Protein Name | Description | Start | End |
|--------------|-------------|-------|-----|
| TRINITY_sp|Q9FT09MED34 | Mediator of RNA pol | 50.30 0.00 |
| TRINITY_sp|B0G1ucpB | Mitochondrial subst | 50.30 0.00 |
| TRINITY_sp|Q63SprrmB | 50S ribosomal prote | 50.30 0.00 |
| TRINITY_sp|P4320MSH2 | DNA mismatch repair | 50.30 0.00 |
| TRINITY_sp|Q9LF0XPT | Xylulose 5-phosphat | 50.30 0.00 |
| TRINITY_sp|P3740hprT | Hypoxanthine-guanin | 50.30 0.00 |
| TRINITY_sp|O8S0TAt2g4400 | 6,7-dimethyl-8-ribo | 50.30 0.00 |
| TRINITY_sp|Q9X0cui1B | Cullin-2 OS=Dictyos | 50.30 0.00 |
| TRINITY_sp|Q8AK0ABC2A | ABC transporter A f | 50.30 0.00 |
| TRINITY_sp|P5240UBA1 | Ubiquitin-activatin | 50.30 0.00 |
| TRINITY_sp|Q4380SS3 | Soluble starch synt | 50.30 0.00 |
| TRINITY_sp|P5111RAB22A | Ras-related protein | 50.30 0.00 |
| TRINITY_sp|P4030RIC1 | Ras-related protein | 50.30 0.00 |
| TRINITY_sp|P4030RIC1 | Ras-related protein | 50.30 0.00 |
| TRINITY_sp|Q9FG0QS | Quinolate synthas | 50.30 0.00 |
| TRINITY_sp|Q9650CAT1 | Catalase-1 OS=Arabi | 50.30 0.00 |
| TRINITY_sp|Q3R0CNX1 | Molybdopterin biosy | 50.30 0.00 |
| TRINITY_sp|Q6312Abcc | Canalicular multisp | 50.30 0.00 |
| TRINITY_sp|A6N6Wdr35 | WD repeat-containin | 50.30 0.00 |
| TRINITY_sp|P5370GFA1 | Glutamine--fructose | 50.30 0.00 |
| TRINITY_sp|Q5E90BCS1L | Mitochondrial chape | 50.20 0.00 |
| TRINITY_sp|Q9VP0IC13690 | Ribonuclease H2 sub | 50.20 0.00 |
| TRINITY_sp|Q5K0qluD | Glutamate dehydroge | 50.20 0.00 |
| TRINITY_sp|O3221yvgN | Glyoxal reductase O | 50.20 0.00 |
| TRINITY_sp|O1540ABC4 | Multidrug resistanc | 50.20 0.00 |
| TRINITY_sp|Q5E1EpypA | Pyridoxal kinase OS | 50.20 0.00 |
| TRINITY_sp|Q8AO0asnS | Asparagene--tRNA li | 50.20 0.00 |
| TRINITY_sp|Q8BVWMet16 | Methyltransferase-1 | 50.20 0.00 |
| TRINITY_sp|Q7YSvcanA | Calcineurin subunit | 50.20 0.00 |
| TRINITY_sp|Q0560US4L | tRNA-dihydrouridine | 50.20 0.00 |
| TRINITY_sp|P1590acu-8 | Acetyl-CoA hydrolas | 50.20 0.00 |
| TRINITY_sp|O8240At5g267 | Glutamate--tRNA lig | 50.20 0.00 |
| TRINITY_sp|P4110svkA | Serine/threonine-pr | 50.20 0.00 |
| TRINITY_sp|P4670cysB | Cystathionine beta- | 50.20 0.00 |
| TRINITY_sp|Q7K0serS | Serine--tRNA ligase | 50.20 0.00 |
| TRINITY_sp|Q9CR0RH5 | DEAD-box ATP-depend | 50.20 0.00 |
| TRINITY_sp|Q3R80At3g265 | Probable pre-mRNA-s | 50.20 0.00 |
| TRINITY_sp|P8TD0DNAH3 | Dynin heavy chain | 50.20 0.00 |
| TRINITY_sp|Q8XIFdeoC | Deoxyribose-phospha | 50.20 0.00 |
| TRINITY_sp|Q8HE0LLL8 | IAA-amino acid hydr | 50.20 0.00 |
| TRINITY_sp|P2580RPL15 | 50S ribosomal prote | 50.20 0.00 |
| TRINITY_sp|P5460pkbA | RAC family serine/t | 50.20 0.00 |
| TRINITY_sp|Q54Twro2 | Serine/threonine-pr | 50.20 0.00 |
| TRINITY_sp|Q55B0md3 | 60S ribosomal expor | 50.20 0.00 |
| TRINITY_sp|P1550ade6 | Phosphoribosylamino | 50.20 0.00 |
| TRINITY_sp|Q5630TM_0019 | Uncharacterized oxi | 50.20 0.00 |
| TRINITY_sp|Q9Y60FARP3 | Poly [ADP-ribose] p | 50.20 0.00 |
| TRINITY_sp|Q54Swde3 | WD repeat-containin | 50.20 0.00 |
| TRINITY_sp|P7360mutS2 | Endonuclease MutS2 | 50.20 0.00 |
| TRINITY_sp|O0410ISA1 | Isoamylase 1, chlor | 50.20 0.00 |
| TRINITY_sp|B9DH0ARIA | ARM REPEAT PROTEIN | 50.20 0.00 |
| TRINITY_sp|Q0840ADK-B | Adenylate kinase 4 | 50.20 0.00 |
| TRINITY_sp|Q10W0Os03g03 | DEAD-box ATP-depend | 50.10 0.00 |
| TRINITY_sp|Q103gd11 | Probable secretory | 50.10 0.00 |
| TRINITY_sp|E1BNKascc3 | Activating signal c | 50.10 0.00 |
| TRINITY_sp|Q9Z00Txnr2d | Thioredoxin reducta | 50.10 0.00 |
| TRINITY_sp|F4JY{TCX7 | Protein tesmin/TSO1 |
| TRINITY_sp|Q9UKIMR| mRNA turnover prote |
| TRINITY_sp|Q145DH8 | ATP-dependent RNA h |
| TRINITY_sp|Q294MAN2B1 | Lysosomal alpha-man |
| TRINITY_sp|Q9XF1DDM1 | ATP-dependent DNA h |
| TRINITY_sp|Q54WbzbP | Probable basic-leuc |
| TRINITY_sp|Q94KFAF2 | Plastid lipid-associ |
| TRINITY_sp|P277JTRP1 | Multifunctional try |
| TRINITY_sp|Q099nhtl | Endonuclease III ho |
| TRINITY_sp|Q86Ctor | Target of rapamycin |
| TRINITY_sp|Q99P1psn3 | Phosphatidate phos |
| TRINITY_sp|Q9SNJATL59 | E3 ubiquitin-protei |
| TRINITY_sp|A819CFPA45 | Cilia- and flagella |
| TRINITY_sp|Q9D8Dnajb4 | DnaJ homolog subfam |
| TRINITY_sp|Q3ZB1-UPF0235 | protein C15 |
| TRINITY_sp|Q6DBIAat5g058 | Probable sugar phos |
| TRINITY_sp|Q005CDK11 | Cyclin-dependent ki |
| TRINITY_sp|Q93VIATG18A | Autophagy-related p |
| TRINITY_sp|P267lvbqS | Virulence sensor pr |
| TRINITY_sp|P512ycf36 | Uncharacterized pro |
| TRINITY_sp|Q54QLDDB-G02 | Probable zinc trans |
| TRINITY_sp|Q9FGGCP3 | Gamma-tubulin compl |
| TRINITY_sp|A2YXSPL15 | Squamosa promoter-b |
| TRINITY_sp|Q8V2JRMR2 | Receptor homology r |
| TRINITY_sp|Q9NZ5E1F2AK3 | Eukaryotic translat |
| TRINITY_sp|Q9Y3EXOSC1 | Exosome complex com |
| TRINITY_sp|Q135SQSTM1 | Sequestosome-1 OS=H |
| TRINITY_sp|Q104gsk3 | Protein kinase gsk3 |
| TRINITY_sp|P368XPTV2 | GTP-binding protein |
| TRINITY_sp|Q9NW1RBM2 | RNA-binding protein |
| TRINITY_sp|Q926NUP205 | Nuclear pore comple |
| TRINITY_sp|Q203ppt-1 | Palmitoyl-protein t |
| TRINITY_sp|B1X1glgC | Glucose-1-phosphate |
| TRINITY_sp|P980c3 | Complement C3 (Frag |
| TRINITY_sp|Q154ABCC4 | Multidrug resistanc |
| TRINITY_sp|A5H0DUR1,2 | Urea amidolyase OS= |
| TRINITY_sp|Q8BW1Dnaha3 | Dynein heavy chain |
| TRINITY_sp|Q9H2letfB | Electron transfer f |
| TRINITY_sp|P929MDAR5 | Monodehydroascorbat |
| TRINITY_sp|Q93VRPS1 | 3OS ribosomal prote |
| TRINITY_sp|A3KMJRANBP10 | Ran-binding protein |
| TRINITY_sp|Q929RANBP1C | Ran-binding protein |
| TRINITY_sp|P943ycQL | Uncharacterized pro |
| TRINITY_sp|Q3S2ETRHD1 | Putative peptidyl-t |
| TRINITY_sp|Q92RMLHL1 | DNA mismatch repair |
| TRINITY_sp|Q54Peif2b4 | Translation initiat |
| TRINITY_sp|P502Su(var);Heterochromatin pro |
| TRINITY_sp|P919co- | ADP-ribosylation fa |
| TRINITY_sp|Q955HISN8 | Histidinol dehydrol |
| TRINITY_sp|Q727TMED4 | Transmembrane emp24 |
| TRINITY_sp|Q597gyp1 | GTPase-activating p |
| TRINITY_sp|Q5RBPRCP | Lysosomal Pro-X car |
| TRINITY_sp|Q545vps15 | Probable serine/thr |
| TRINITY_sp|Q9NEvrsp-3 | Probable splicing f |
| TRINITY_sp|Q9N1EPEK | Eukaryotic translat |
| TRINITY_sp|A2BD\Nocs3 | Adenyllytransferase |
| Protein Name                                      | Description                                                                 | Accession | Score | E-value |
|--------------------------------------------------|-----------------------------------------------------------------------------|-----------|-------|---------|
| mRNA export factor                               | 14-3-3-like protein                                                        | 49.90     | 0.00  |         |
| Inositol hexakisphosphate kinase 1                | DEAD-box ATP-depend                                                        | 49.80     | 0.00  |         |
| Calmodulin                                       | Adenine kinase OS                                                          | 49.80     | 0.00  |         |
| 4-hydroxyphenylpyruvate dioxygenase               | Serine/threonine-pr                                                        | 49.80     | 0.00  |         |
| Dihydroorotate dehydrogenase (quinone), mitochondrial | Urea-proton symport                                                        | 49.80     | 0.00  |         |
| Probable serine/thr                             | Photosystem I reac                                                           | 49.80     | 0.00  |         |
| Probable serine/thr                             | Squalene methyltran                                                        | 49.80     | 0.00  |         |
| Probable myosin lig                               | cAMP-dependent prot                                                         | 49.80     | 0.00  |         |
| Protein FIZZY-RELATED 2                          | Probable serine/thr                                                        | 49.80     | 0.00  |         |
| DNA repair and reco                              | Nuclear control of                                                         | 49.70     | 0.00  |         |
| Probable serine/thr                             | Calmodulin OS=Triti                                                         | 49.70     | 0.00  |         |
| Probable myosin lig                               | Ras-related protein                                                        | 49.80     | 0.00  |         |
| U2 small nuclear ri                               | RNA polymerase II                                                         | 49.70     | 0.00  |         |
| U2 small nuclear ri                               | tRNA-dihydrouridine                                                        | 49.70     | 0.00  |         |
| Probable myosin lig                               | Oxygen-dependent co                                                       | 49.70     | 0.00  |         |
| Probable serine/thr                             | Calcineurin subunit                                                        | 49.70     | 0.00  |         |
| Probable serine/thr                             | DNA mismatch repair                                                        | 49.70     | 0.00  |         |
| Probable serine/thr                             | 4-hydroxyphenylpyru                                                       | 49.70     | 0.00  |         |
| Splicing factor 3B                                | Probable low-specific                                                       | 49.70     | 0.00  |         |
| Probable serine/thr                             | Probable low-specific                                                       | 49.70     | 0.00  |         |
| Probable serine/thr                             | 60S acidic ribosoma                                                         | 49.70     | 0.00  |         |
| ATP-dependent RNA h                              | 49.70                                                                         | 0.00  |         |
| DNA repair and reco                              | 49.70                                                                         | 0.00  |         |
| Probable serine/thr                             | Dihydrolipoyllysine                                                        | 49.70     | 0.00  |         |
| Serine/threonine-pr                              | Ornithine decarboxy                                                        | 49.70     | 0.00  |         |
| Gene ID | Gene Name | Description |
|---------|------------|-------------|
| Atbca7  | ATP-binding cassette sub-family A member 7 | OS=Mus musculus |
| Q86A>Fpolr3a | DNA-directed RNA polymerase III subunit rpc1 | OS=Dictyostelium discoideum |
| Q9XInm7 | Nucleoside diphosphokinase | OS=Arabidopsis thaliana |
| Q54B>UNP02G020000 | Acetolactate synthase-like protein | OS=Mus musculus |
| Q8BU>I1vbl | Flagellar radial spoke protein 1 | OS=Arabidopsis thaliana |
| Q9MA>SCPL4 | ATP-dependent helicase BRM | OS=Arabidopsis thaliana |
| Q27Y>RSPl | Flagellar radial spoke protein 1 | OS=Arabidopsis thaliana |
| Q6EV>BRM | S-adenosyl-L-methionine-dependent tRNA 4-demethylwyosine synthase | OS=Arabidopsis thaliana |
| Q27Y>RSPl | Probable coatomer subunit beta' | OS=Caenorhabditis elegans |
| Q9FN>SS1 | DNA-directed RNA polymerase 2, chloroplastic/mitochondrial | OS=Arabidopsis thaliana |
| Q9LF>RPT2 | Ubiquitin carboxyl-terminal hydrolase 22 | OS=Arabidopsis thaliana |
| Q84K>GAMMA-AP-1 complex subunit | DNA-directed RNA polymerase III subunit rpc1 | OS=Dictyostelium discoideum |
| Q758>SC5D | Probable serine/threonine-protein kinase nek3 | OS=Schizosaccharomyces pombe |
| Q431>~ | Non-specific lipid-binding protein | OS=Arabidopsis thaliana |
| P136>HM2 | Probable serine/threonine-protein kinase nek3 | OS=Schizosaccharomyces pombe |
| Q8VI>Abcc2 | Probable thymidylate kinase | OS=Homo sapiens |
| Q860>bdhA | Probable thymidylate kinase | OS=Homo sapiens |
| Q54K>gluD | Probable thymidylate kinase | OS=Homo sapiens |
| Q91W>Hdac11 | Probable thymidylate kinase | OS=Homo sapiens |
| Q7F8>CYCA1-1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q9M3>NPF8.1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q323>ybiA | Probable thymidylate kinase | OS=Homo sapiens |
| Q91L>Aat5g128 | Probable thymidylate kinase | OS=Homo sapiens |
| Q8W>WCANT1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q54K>gluD | Probable thymidylate kinase | OS=Homo sapiens |
| Q94E>Aat5g022 | Probable thymidylate kinase | OS=Homo sapiens |
| Q139>crn1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q8RXT>TYW1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q8W>WCANT1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q8K1>MetAll5 | Probable thymidylate kinase | OS=Homo sapiens |
| Q8CGXElac2 | Probable thymidylate kinase | OS=Homo sapiens |
| P498>DLD | Probable thymidylate kinase | OS=Homo sapiens |
| P318>XYL1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q9ZW>PCS2 | Probable thymidylate kinase | OS=Homo sapiens |
| Q68W>gxrC2 | Probable thymidylate kinase | OS=Homo sapiens |
| P502>TUBB1 | Probable thymidylate kinase | OS=Homo sapiens |
| P347>RAS1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q9CD>DNAT6 | Probable thymidylate kinase | OS=Homo sapiens |
| A2YFP>OBGC1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q091>krp1 | Probable thymidylate kinase | OS=Homo sapiens |
| A6NKS>SR42E2 | Probable thymidylate kinase | OS=Homo sapiens |
| Q55E>psmB4-1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q8K1>MetAll5 | Probable thymidylate kinase | OS=Homo sapiens |
| Q8CGXElac2 | Probable thymidylate kinase | OS=Homo sapiens |
| P498>DLD | Probable thymidylate kinase | OS=Homo sapiens |
| P318>XYL1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q9ZW>PCS2 | Probable thymidylate kinase | OS=Homo sapiens |
| Q68W>gxrC2 | Probable thymidylate kinase | OS=Homo sapiens |
| P502>TUBB1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q3T1>BOLA1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q8LD>A1tig5622 | Probable thymidylate kinase | OS=Homo sapiens |
| B1ZG>glpK | Probable thymidylate kinase | OS=Homo sapiens |
| Q612>Lcp1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q94>SPBC660 | Probable thymidylate kinase | OS=Homo sapiens |
| P2391>DTYMK | Probable thymidylate kinase | OS=Homo sapiens |
| Q99>Corasp2 | Probable thymidylate kinase | OS=Homo sapiens |
| Q54V>hdaC | Probable thymidylate kinase | OS=Homo sapiens |
| Q201>copb-2 | Probable thymidylate kinase | OS=Homo sapiens |
| Q8MX>DDB_G020000 | Probable thymidylate kinase | OS=Homo sapiens |
| Q91F>CONST1 | Probable thymidylate kinase | OS=Homo sapiens |
| Q9L>EYUBP22 | Probable thymidylate kinase | OS=Homo sapiens |
| Protein ID | Name                                                        | Description                                          | Log2Fold Change |
|-----------|-------------------------------------------------------------|------------------------------------------------------|-----------------|
| TRINITY_sp|M0ZYINDA1                                                   | Internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mitochondrial | 49.50 |
| TRINITY_sp|Q91YFMett113                                               | Methyltransferase-1                                   | 49.50 |
| TRINITY_sp|Q9XVRpb-12                                                 | Probable DNA-direct                                    | 49.50 |
| TRINITY_sp|Q54qphpB                                                  | Prohibitin-2 OS=Dic                                    | 49.50 |
| TRINITY_sp|Q230JKAB1                                                 | Probable voltage-gama                                  | 49.50 |
| TRINITY_sp|Q0IIIDUSP10                                               | Dual specificity pr                                   | 49.50 |
| TRINITY_sp|P484PPP3CC                                                | Serine/threonine-pr                                   | 49.50 |
| TRINITY_sp|Q8GXCFSTS2                                                | Pre-mRNA cleavage f                                   | 49.50 |
| TRINITY_sp|D0NLCPITG_12tRNA (guanine(37)-N)                         | RNA exonuclease 4 O                                   | 49.50 |
| TRINITY_sp|Q6BIKREX4                                                 | Pre-mRNA cleavage f                                   | 49.50 |
| TRINITY_sp|Q9UNHCDC1A2                                               | Dual specificity pr                                   | 49.50 |
| TRINITY_sp|Q127pab1                                                  | Protein phosphatase                                   | 49.50 |
| TRINITY_sp|Q8VYDJ1C                                                  | Protein DJ-1 homolo                                   | 49.50 |
| TRINITY_sp|O355Pfkb3                                                 | 6-phosphofructo-2-k                                    | 49.50 |
| TRINITY_sp|Q165CAMK4                                                 | Calcium/calmodulin-                                   | 49.50 |
| TRINITY_sp|Q9ESUbe4b                                                 | Ubiquitin conjugati                                   | 49.50 |
| TRINITY_sp|Q5TOCFAP70                                                | Cilia- and flagella                                   | 49.50 |
| TRINITY_sp|P2951UUBB7                                               | Tubulin beta-7 chain,                                  | 49.50 |
| TRINITY_sp|Q3ZBIPIRTH2                                               | Peptidyl-tRNA hydro                                   | 49.50 |
| TRINITY_sp|P929RS31                                                  | Serine/arginine-ric                                   | 49.50 |
| TRINITY_sp|Q9LTAtg128                                                 | Peroxisomal 2,4-die                                   | 49.50 |
| TRINITY_sp|Q151NPC1                                                  | Niemann-Pick C1 pro                                   | 49.50 |
| TRINITY_sp|Q6AYAlg14                                                 | UDP-N-acetylglucosa                                   | 49.50 |
| TRINITY_sp|Q395ODA4                                                  | Dynein beta chain,                                    | 49.50 |
| TRINITY_sp|Q9SYIBRR2A                                                | DExH-box ATP-depend                                   | 49.50 |
| TRINITY_sp|Q12KpXi                                                   | Probable serine/thr                                   | 49.50 |
| TRINITY_sp|Q9SDRCE1                                                  | NEDD8-conjugating e                                   | 49.50 |
| TRINITY_sp|Q9CS5DTC                                                  | Mitochondrial dicar                                   | 49.50 |
| TRINITY_sp|Q9NKmfeA                                                  | Peroxisomal multiflu                                  | 49.50 |
| TRINITY_sp|Q389LCY1                                                 | Lycopene beta cycla                                   | 49.50 |
| TRINITY_sp|Q455LIG1                                                  | DNA ligase 1 OS=Ara                                    | 49.50 |
| TRINITY_sp|P320f-                                                   | Stearoyl-[acyl-carr]                                  | 49.50 |
| TRINITY_sp|Q631Dnahl                                                  | Dynein heavy chain                                    | 49.50 |
| TRINITY_sp|Q54DiamA                                                  | AMP deaminase OS=Di                                   | 49.50 |
| TRINITY_sp|Q437WAXY                                                  | Granule-bound starc                                   | 49.50 |
| TRINITY_sp|P563EIF5A4                                                | Eukaryotic translat                                   | 49.50 |
| TRINITY_sp|Q5RHDcun1d4                                               | DCN1-like protein 4                                  | 49.50 |
| TRINITY_sp|Q8INGyc88B                                               | Soluble guanylate c                                   | 49.50 |
| TRINITY_sp|Q93YAtg318                                                 | Acetolactate syntha                                   | 49.50 |
| TRINITY_sp|Q94BDIGA                                                  | Phosphatidylinosito                                   | 49.40 |
| TRINITY_sp|Q8CHTtl15                                                 | Tubulin polyglutamy                                   | 49.40 |
| TRINITY_sp|Q547drkC                                                  | Probable serine/thr                                   | 49.40 |
| TRINITY_sp|Q266f-                                                   | 33 kDa inner dynein                                   | 49.40 |
| TRINITY_sp|P196f-                                                   | Non-specific lipid-                                   | 49.40 |
| TRINITY_sp|Q9SRCHIP                                                  | E3 ubiquitin-protei                                   | 49.40 |
| TRINITY_sp|A6LTrapt                                                  | Adenine phosphoribo                                   | 49.40 |
| TRINITY_sp|Q2V2infB                                                  | Translation initiat                                   | 49.40 |
| TRINITY_sp|P518pdcA                                                  | Pyruvate decarboxyl                                   | 49.40 |
| TRINITY_sp|Q3SEHc1le                                                 | Caltractin ICL1e OS                                   | 49.40 |
| TRINITY_sp|Q0DHFPTS8H8                                               | ATP-dependent zinc                                    | 49.40 |
| TRINITY_sp|Q8YMc1pB2                                                 | Chaperone protein C                                   | 49.40 |
| TRINITY_sp|Q9GZFREX04                                                | RNA exonuclease 4 O                                   | 49.40 |
| TRINITY_sp|Q952MB0                                                   | Methyl-CpG-binding                                    | 49.40 |
| TRINITY_sp|Q54Spd2                                                   | Phospholipase D Z O                                   | 49.40 |
| TRINITY_sp|Q8J1nifk                                                  | MKI67 FHA domain-in                                   | 49.40 |
| TRINITY_sp|A7SLCnat9                                                 | N-acetyltransferase                                   | 49.40 |
TRINITY_sp|Q8BR4Man2a2 Alpha-mannosidase 2 49.40 0.00
TRINITY_sp|P167vUBI Ubiquitin-like protein 49.40 0.00
TRINITY_sp|A9V2C Probable nitrile hydrolase 49.40 0.00
TRINITY_sp|O65GH2 Gamma-glutamyltransferase 49.40 0.00
TRINITY_sp|B9F1logL2 Probable cytokinin receptor 49.40 0.00
TRINITY_sp|Q9C8UN50A Nuclear pore complex protein 49.40 0.00
TRINITY_sp|Q9BRRI0K1 Serine/threonine-protein kinase 49.40 0.00
TRINITY_sp|Q9SU4At4g3234 Probable sugar phosphatase 49.40 0.00
TRINITY_sp|Q5RKSbdsc Ribosome maturation factor 49.40 0.00
TRINITY_sp|F454CSN1 COP9 signalsome complex subunit 49.40 0.00
TRINITY_sp|A6LMValaS Alanine--tRNA ligase 49.40 0.00
TRINITY_sp|Q8STabcC10 ABC transporter C family member 49.40 0.00
TRINITY_sp|Q0QILTA3 Dihydropyrimidinase 49.40 0.00
TRINITY_sp|Q056CTR1 Serine/threonine-protein kinase 49.40 0.00
TRINITY_sp|Q2XNFPUT1 Polyamine transporter 49.40 0.00
TRINITY_sp|Q2301KAB1 Probable voltage-gated potassium channel 49.40 0.00
TRINITY_sp|Q7YSycanA Calcineurin subunit 49.40 0.00
TRINITY_sp|Q99M9UTR3 UDP-galactose/UDP-glucose transporter 49.40 0.00
TRINITY_sp|Q8I8lap1g1 AP-1 complex subunit 49.40 0.00
TRINITY_sp|Q9C2Fopn1 LisH domain-containing protein 49.40 0.00
TRINITY_sp|Q8L76SDN5 Small RNA degrading protein 49.40 0.00
TRINITY_sp|Q0WRPBL7 Probable serine/threonine-protein kinase 49.40 0.00
TRINITY_sp|Q96THBB4 Bardet-Biedl syndrome protein 49.40 0.00
TRINITY_sp|Q86Hpolr1a DNA-directed RNA polymerase 49.40 0.00
TRINITY_sp|P109Rap1g1 Retrovirus-related protein 49.40 0.00
TRINITY_sp|Q9M34ATG6 Bcl-1-like protein 49.40 0.00
TRINITY_sp|P479AP2 Floral homeotic protein 49.40 0.00
TRINITY_sp|Q138GNL2 Nucleolar GTP-binding protein 49.30 0.00
TRINITY_sp|Q9SB6ABC1 Protein ABC transporter 49.30 0.00
TRINITY_sp|Q6DCI3ch3 E3 ubiquitin-protein ligase 49.30 0.00
TRINITY_sp|Q39JcdnaJ Chaperone protein D 49.30 0.00
TRINITY_sp|Q54Liints4 Integrator complex subunit 49.30 0.00
TRINITY_sp|Q54CtraPP2 Trafficking protein 49.30 0.00
TRINITY_sp|A0P2NNT01CX_1 Putative 3-methyladenine phosphoribosyltransferase 49.30 0.00
TRINITY_sp|Q5MB1ABC2 ATP-binding cassette transporter 49.30 0.00
TRINITY_sp|Q9BR1CBW1 COB4 domain-containing protein 49.30 0.00
TRINITY_sp|Q9SKAt2g2029 Zinc finger CCHC domain-containing protein 49.30 0.00
TRINITY_sp|Q550S1c35c1 GDP-fucose transporter 49.30 0.00
TRINITY_sp|Q8NCACYN2H1 Cytoplasmic dynein 49.30 0.00
TRINITY_sp|Q8L4WEEL Wee1-like protein kinase 49.30 0.00
TRINITY_sp|P396tmirA Ferredoxin--nitrite reductase 49.30 0.00
TRINITY_sp|Q9M21RPS27B 40S ribosomal protein S27 49.30 0.00
TRINITY_sp|Q8IUCCM1K1 Calcium/calmodulin-dependent protein kinase 49.30 0.00
TRINITY_sp|Q940CTM1 Transmembrane 9 superfamily protein 49.30 0.00
TRINITY_sp|Q55Edhak Probable dihydroxy acid dehydrogenase 49.30 0.00
TRINITY_sp|Q75JaspS1 Aspartate--tRNA ligase 49.30 0.00
TRINITY_sp|Q9LN4F4H3 Probable prolyl 4-hydroxylase 49.30 0.00
TRINITY_sp|Q4QEGMPP GMP reductase OS=Le 49.30 0.00
| Gene Name                                      | Description                                          | Score 1 | Score 2 | Score 3 |
|-----------------------------------------------|------------------------------------------------------|---------|---------|---------|
| Ras-like protein 1                            | OS=Saccharomyces cerevisiae                         | 49.30   | 0.00    |         |
| GTP-binding protein                           | OS=Danio rerio                                       | 49.30   | 0.00    |         |
| Cilia- and flagella                           | OS=Streptomyces avermitilis                         | 49.30   | 0.00    |         |
| Low-affinity phosphatase                      | OS=Schizosaccharomyces pombe                        | 49.30   | 0.00    |         |
| Acidic endochitinase                          | OS=Nicotiana tabacum                                 | 49.30   | 0.00    |         |
| Acetyl-coenzyme A synthetase                  | OS=Streptomyces avermitilis                         | 49.30   | 0.00    |         |
| Guanylate cyclase soluble subunit beta-2      | OS=Homo sapiens                                      | 49.30   | 0.00    |         |
| Vesicle transport protein GOT1B               | OS=Mus musculus                                      | 49.30   | 0.00    |         |
| GTP-binding protein At2g22870                 | OS=Arabidopsis thaliana                             | 49.30   | 0.00    |         |
| Probable prolyl 4-hydroxylase 9               | OS=Arabidopsis thaliana                             | 49.30   | 0.00    |         |
| Protein RKD3                                   | OS=Arabidopsis thaliana                             | 49.30   | 0.00    |         |
| DnaJ homolog subfamily C member 5B            | OS=Bos taurus                                        | 49.30   | 0.00    |         |
| Mitochondrial substrate carrier family protein E | OS=Dictyostelium discoideum                       | 49.30   | 0.00    |         |
| Ras-related C3 botulinum substrate 1          | OS=Bos taurus                                        | 49.30   | 0.00    |         |
| GPI mannosyltransferase                       | OS=Mus musculus                                      | 49.30   | 0.00    |         |
| Low-affinity phosphate transporter PHO91      | OS=Saccharomyces cerevisiae                         | 49.30   | 0.00    |         |
| Ras-related protein Rab-32                   | OS=Homo sapiens                                      | 49.30   | 0.00    |         |
| ABC transporter G family member 1             | OS=Dictyostelium discoideum                       | 49.30   | 0.00    |         |
| Sm-like protein LSM4                          | OS=Arabidopsis thaliana                             | 49.30   | 0.00    |         |
| Subtilisin inhibitor CLSI-I                   | OS=Canavalia lineata                                 | 49.30   | 0.00    |         |
| 26S proteasome non-ATPase regulatory subunit 6 | OS=Homo sapiens                                      | 49.30   | 0.00    |         |
| Protease Do-like 9                            | OS=Arabidopsis thaliana                             | 49.30   | 0.00    |         |
| Major vault protein alpha                     | OS=Dictyostelium discoideum                       | 49.30   | 0.00    |         |
| E3 ubiquitin-protein ligase UPL7              | OS=Arabidopsis thaliana                             | 49.30   | 0.00    |         |
| cAMP-dependent protein kinase catalytic subunit alpha | OS=Bos taurus                                      | 49.30   | 0.00    |         |
| Cilia- and flagella-associated protein 52     | OS=Chlamydomonas reinhardtii                       | 49.30   | 0.00    |         |
| Protease Dc-like 9                            | OS=Arabidopsis thaliana                             | 49.30   | 0.00    |         |
| ABC transporter G family member 1             | OS=Dictyostelium discoideum                       | 49.30   | 0.00    |         |
| Sm-like protein LSM4                          | OS=Arabidopsis thaliana                             | 49.30   | 0.00    |         |
| Subtilisin inhibitor CLSI-I                   | OS=Canavalia lineata                                 | 49.30   | 0.00    |         |
| 26S proteasome non-ATPase regulatory subunit 6 | OS=Homo sapiens                                      | 49.30   | 0.00    |         |
| Protease Do-like 9                            | OS=Arabidopsis thaliana                             | 49.30   | 0.00    |         |
| Major vault protein alpha                     | OS=Dictyostelium discoideum                       | 49.30   | 0.00    |         |
| E3 ubiquitin-protein ligase UPL7              | OS=Arabidopsis thaliana                             | 49.30   | 0.00    |         |
| cAMP-dependent protein kinase catalytic subunit alpha | OS=Bos taurus                                      | 49.30   | 0.00    |         |
| Cilia- and flagella-associated protein 52     | OS=Chlamydomonas reinhardtii                       | 49.30   | 0.00    |         |
| Protease Dc-like 9                            | OS=Arabidopsis thaliana                             | 49.30   | 0.00    |         |
| ABC transporter G family member 1             | OS=Dictyostelium discoideum                       | 49.30   | 0.00    |         |
| Accession     | Description                                                                 | Score | E-value |
|--------------|-----------------------------------------------------------------------------|-------|---------|
| TRINITY_sp|Q409\^\text{-}\text{\text{-}} | Monodehydroascorbate reductase | 49.10 | 0.00    |
| TRINITY_sp|P454:CSN1 | COP9 signalosome co | 49.10 | 0.00    |
| TRINITY_sp|Q54WglnA3 | Type-3 glutamine synthetase | 49.10 | 0.00    |
| TRINITY_sp|Q54V:maf1 | Repressor of RNA polymerase III transcription | 49.10 | 0.00    |
| TRINITY_sp|Q6JQ:ACAD10 | Acyl-CoA dehydrogenase | 49.10 | 0.00    |
| TRINITY_sp|Q1OMOs3g02\text{-}\text{\text{-}} | Asparagine synthetase | 49.10 | 0.00    |
| TRINITY_sp|P801\^\text{-}\text{\text{-}} | Extracellular serine protease | 49.10 | 0.00    |
| TRINITY_sp|Q803:ergic3 | Endoplasmic reticulum | 49.10 | 0.00    |
| TRINITY_sp|Q152:FPW2 | Periodic tryptophan | 49.10 | 0.00    |
| TRINITY_sp|Q9LE8:RANGAP1 | RAN GTPase-activating protein | 49.10 | 0.00    |
| TRINITY_sp|P425\^\text{-}\text{\text{-}} | Soma ferritin OS=Ly | 49.10 | 0.00    |
| TRINITY_sp|Q9C5:HAC1 | Histone acetyltransferase | 49.10 | 0.00    |
| TRINITY_sp|Q389:FTB | Protein farnesyltransferase subunit beta | 49.10 | 0.00    |
| TRINITY_sp|Q963:ACX4 | Acyl-coenzyme A oxidase | 49.10 | 0.00    |
| TRINITY_sp|P871:not1 | General negative regulator | 49.10 | 0.00    |
| TRINITY_sp|B0D6:LABIDR | Pentafunctional ARO | 49.10 | 0.00    |
| TRINITY_sp|P258:chCA | Clathrin heavy chain | 49.10 | 0.00    |
| TRINITY_sp|Q9SG:ATL72 | RING-H2 finger protein | 49.10 | 0.00    |
| TRINITY_sp|Q32P:DYNLRB2 | Dynein light chain | 49.00 | 0.00    |
| TRINITY_sp|C1F1:MICPUN\_ | Inosine triphosphatase | 49.00 | 0.00    |
| TRINITY_sp|Q0WV:RPP6L | Protein RPP6-like | 49.00 | 0.00    |
| TRINITY_sp|Q66K:TBC1D9B | TBC1 domain family | 49.00 | 0.00    |
| TRINITY_sp|O1421:trm10 | tRNA (guanine)-N1 | 49.00 | 0.00    |
| TRINITY_sp|Q9CG:COMMd4 | COMM domain-containing protein | 49.00 | 0.00    |
| TRINITY_sp|Q86A1:DDB-G02\^\text{-}\text{\text{-}} | Probable myosin ligand | 49.00 | 0.00    |
| TRINITY_sp|Q541:eif2b1 | Translation initiation factor | 49.00 | 0.00    |
| TRINITY_sp|Q158:CPK2 | Calcium-dependent protein | 49.00 | 0.00    |
| TRINITY_sp|Q932:E5DP2 | Stromal cell-derived factor | 49.00 | 0.00    |
| TRINITY_sp|Q58:D:SORD | Sorbitol dehydrogenase | 49.00 | 0.00    |
| TRINITY_sp|F4HY:IRE3 | Probable serine/threonine protein kinase | 49.00 | 0.00    |
| TRINITY_sp|O227:PXG3 | Probable peroxigenase | 49.00 | 0.00    |
| TRINITY_sp|Q86A1:spkA-1 | Stress-activated protein | 49.00 | 0.00    |
| TRINITY_sp|Q5UP:MIMI_R5 | Uncharacterized protein | 49.00 | 0.00    |
| TRINITY_sp|Q9YS:OARDI | O-acetyl-ADP-ribose transferase | 49.00 | 0.00    |
| TRINITY_sp|Q8C9:Sef2 | Sperm flagellar protein | 49.00 | 0.00    |
| TRINITY_sp|A5GW:rp5J | 3OS ribosomal protein | 49.00 | 0.00    |
| TRINITY_sp|Q2M2:ALKBH7 | Alpha-ketoglutarate | 49.00 | 0.00    |
| TRINITY_sp|Q8LF:DRP3B | Dynamin-related protein | 49.00 | 0.00    |
| TRINITY_sp|Q08D:AP2B1 | AP-1 complex subunit | 49.00 | 0.00    |
| TRINITY_sp|Q9XF:LHCb5 | Chlorophyll a-b binding protein | 49.00 | 0.00    |
| TRINITY_sp|P46B:KRP95 | Kinesin-II 95 kDa | 49.00 | 0.00    |
| TRINITY_sp|Q9XG:VHA-D | V-type proton ATPase | 49.00 | 0.00    |
| TRINITY_sp|Q9XF:DEE76 | Degreening-related protein | 49.00 | 0.00    |
| TRINITY_sp|Q54J:h2 | Probable histidine | 49.00 | 0.00    |
| TRINITY_sp|F4J6:IREH1 | Probable serine/threonine protein kinase | 49.00 | 0.00    |
| TRINITY_sp|P223:SODB | Superoxide dismutase | 49.00 | 0.00    |
| TRINITY_sp|A4S6:OSTLU\_ | Lon protease | 49.00 | 0.00    |
| TRINITY_sp|Q31V:treF | Cytoplasmic trehalase | 49.00 | 0.00    |
| TRINITY_sp|Q655:FMCU3 | Molybdenum cofactor | 49.00 | 0.00    |
| TRINITY_sp|Q86A:DDB-G02\^\text{-}\text{\text{-}} | Probable acetyl-CoA ligase | 49.00 | 0.00    |
| TRINITY_sp|P272:ahr | Aldehyde reductase | 49.00 | 0.00    |
| TRINITY_sp|Q993:TY3B-G | Transposon Ty3-G | 49.00 | 0.00    |
| TRINITY_sp|P0AB:dedA | Protein DedA OS=E. coli | 49.00 | 0.00    |
| TRINITY_sp|Q8GY:PGM | Phosphoglycerate mutase | 49.00 | 0.00    |
| TRINITY_sp|Q2NK:DPY30 | Protein dpy-30 homolog | 49.00 | 0.00    |
| TRINITY_sp|Q9SF:RABE1E | Ras-related protein | 49.00 | 0.00    |
| ID                  | Gene Name          | Description                        | Score | Details |
|---------------------|--------------------|-------------------------------------|-------|---------|
| TRINITY_sp|Q08D2|PRPF4B | Serine/threonine-protein kinase PRP4 homolog | 48.90 | 0.00 |
| TRINITY_sp|Q9FP1|UBP12 | Ubiquitin carboxyl-terminal peptidase | 48.90 | 0.00 |
| TRINITY_sp|Q9VH3|DppIII | Dipeptidyl peptidase III | 48.90 | 0.00 |
| TRINITY_sp|P592|RPS27AA | Ubiquitin-40S ribosomal protein | 48.80 | 0.00 |
| TRINITY_sp|Q9FG6|EB1C | Microtubule-associated protein EB1 | 48.80 | 0.00 |
| TRINITY_sp|Q9P76|mit1 | Chromatin remodelin | 48.80 | 0.00 |
| TRINITY_sp|Q86Kh|fhit | Binds (5'-adenosyl)-triphosphate | 48.80 | 0.00 |
| TRINITY_sp|B6EK|cutC | Copper homeostasis | 48.80 | 0.00 |
| TRINITY_sp|Q640|tadtn1 | Putative deoxyribonuclease | 48.80 | 0.00 |
| TRINITY_sp|A0D5EGS|SPAT0 | Probable protein phosphatase | 48.80 | 0.00 |
| TRINITY_sp|Q8BV3|Dpp9 | Dipeptidyl peptidase IX | 48.80 | 0.00 |
| TRINITY_sp|Q2KH2|HBS1L | HBS1-like protein | 48.80 | 0.00 |
| TRINITY_sp|Q59G|Slc25a4 | ADP/ATP translocase | 48.80 | 0.00 |
| TRINITY_sp|Q6EPF|FACE1 | CAAX prenyl proteasome | 48.80 | 0.00 |
| TRINITY_sp|Q9WX3|rpBF | Putative RNA-binding protein | 48.80 | 0.00 |
| TRINITY_sp|Q9C66|GAMMACA | Gamma carbonic anhydrase | 48.80 | 0.00 |
| TRINITY_sp|Q9FG1|ARR18 | Two-component response protein | 48.80 | 0.00 |
| TRINITY_sp|Q8699|pakF | Serine/threonine-protein kinase | 48.80 | 0.00 |
| TRINITY_sp|Q541|indrB | Probable serine/threonine-protein kinase | 48.80 | 0.00 |
| TRINITY_sp|Q743S|SPBC15D | COBW domain-containing protein | 48.80 | 0.00 |
| TRINITY_sp|Q55G|DDB_G02 | Probable mitochondrial protein | 48.80 | 0.00 |
| TRINITY_sp|Q7S26|sec23a | Protein transport | 48.80 | 0.00 |
| TRINITY_sp|F4JGK|KIN14D | Kinesin-like protein | 48.80 | 0.00 |
| TRINITY_sp|Q2531|PRKACA | cAMP-dependent protein kinase | 48.80 | 0.00 |
| TRINITY_sp|Q54D|polr2c | DNA-directed RNA polymerase | 48.80 | 0.00 |
| TRINITY_sp|F4HX1|PLA1 | Phospholipase A1 | 48.80 | 0.00 |
| TRINITY_sp|P046t|tyrB | Aromatic-amino-acid synthase | 48.80 | 0.00 |
| TRINITY_sp|P703U|Ufd11 | Ubiquitin fusion protein | 48.80 | 0.00 |
| TRINITY_sp|Q29R|FPWD1 | Peptidylprolyl isomerase | 48.80 | 0.00 |
| TRINITY_sp|Q8HL1|MNS2 | Mannosyl-oligosaccharide transferase | 48.80 | 0.00 |
| TRINITY_sp|B2RW5|Cfap58 | Cilia- and flagella-associated protein | 48.80 | 0.00 |
| TRINITY_sp|Q8LF4|At1g222 | Multifunctional metacaspase | 48.80 | 0.00 |
| TRINITY_sp|Q8RI3|Nfx1 | NFX1-type zinc finger | 48.80 | 0.00 |
| TRINITY_sp|Q9AS3|At1g324 | Vacuolar protein sorting associated protein | 48.80 | 0.00 |
| TRINITY_sp|Q8AV1|rpf1 | Ribosome production | 48.80 | 0.00 |
| TRINITY_sp|Q54J|JabcC3 | ABC transporter C family member | 48.80 | 0.00 |
| TRINITY_sp|Q809F|FTSH4 | ATP-dependent zinc protease | 48.80 | 0.00 |
| TRINITY_sp|Q9SEE|GAL1 | Galactokinase OS=Araport | 48.80 | 0.00 |
| TRINITY_sp|Q8JF7|dat3 | Probable inactive transporter | 48.80 | 0.00 |
| TRINITY_sp|Q6579|EX2 | Protein EXECUTER 2 | 48.80 | 0.00 |
| TRINITY_sp|Q54X|DDB_G02 | Glucose-induced degradation | 48.80 | 0.00 |
| TRINITY_sp|Q617K|Kif3b | Kinesin-like protein | 48.80 | 0.00 |
| TRINITY_sp|Q9FU4|At3g071 | Protein transport | 48.80 | 0.00 |
| TRINITY_sp|Q6PC9|htf314 | Transcription factor | 48.70 | 0.00 |
| TRINITY_sp|O7566|SNRNP20 | U5 small nuclear ribonucleoprotein | 48.70 | 0.00 |
| TRINITY_sp|P7271|typA | GTP-binding protein | 48.70 | 0.00 |
| TRINITY_sp|Q18C3|rpl1M | 50S ribosomal protein | 48.70 | 0.00 |
| TRINITY_sp|Q102p|plal | Poly(A) polymerase | 48.70 | 0.00 |
| TRINITY_sp|Q9QX1|Nme7 | Nucleoside diphosphate | 48.70 | 0.00 |
| TRINITY_sp|Q540t|treh | Trehalase OS=Dictyostelium | 48.70 | 0.00 |
| TRINITY_sp|O246P|PBD2 | Proteasome subunit | 48.70 | 0.00 |
| TRINITY_sp|P2811|pkgB | Protein kinase 2 | 48.70 | 0.00 |
| TRINITY_sp|C4YK1|RAS1 | Ras-like protein | 48.70 | 0.00 |
| TRINITY_sp|Q86AD|DDB_G02 | Probable myosin ligand | 48.70 | 0.00 |
| TRINITY_sp|Q55D9|DDB_G02 | Probable 18S rRNA | 48.70 | 0.00 |
| TRINITY_sp|Q0CC8|gedE | Glutathione S-transferase | 48.70 | 0.00 |
| Gene Name | Protein Name | Function | Score |
|-----------|--------------|----------|-------|
| TRINITY_sp| P187| Vesicle-fusing ATPase | 48.60 |
| TRINITY_sp| Q389| Acetyl-CoA carboxyl | 48.60 |
| TRINITY_sp| Q8WX| Dynein heavy chain | 48.60 |
| TRINITY_sp| Q5M9| Diphthine--ammonia | 48.60 |
| TRINITY_sp| Q165| Mitogen-activated p | 48.60 |
| TRINITY_sp| Q235| Beta-amylase 3, chl | 48.60 |
| TRINITY_sp| Q9FL| DEAD-box ATP-depend | 48.60 |
| TRINITY_sp| Q8CG| Zinc phosphodiester | 48.60 |
| TRINITY_sp| Q6PI| tRNA-dihydouridine | 48.60 |
| TRINITY_sp| P496| Ubiquitin-60S ribos | 48.60 |
| TRINITY_sp| P98Z| Phospholipid-transp | 48.60 |
| TRINITY_sp| Q99M| Methylcrotonoyl-CoA | 48.60 |
| TRINITY_sp| P434| Cyclin-dependent k | 48.60 |
| TRINITY_sp| P525| Myb-related protein | 48.60 |
| TRINITY_sp| Q075| Guanylate cyclase 3 | 48.60 |
| TRINITY_sp| Q9SN| Metal transporter N | 48.60 |
| TRINITY_sp| B2GK| Malate dehydrogenas | 48.50 |
| TRINITY_sp| O942| Putative phospholip | 48.50 |
| TRINITY_sp| Q98E| Putative pterin-4-a | 48.50 |
| TRINITY_sp| F4JY| Protein tesmin/TSO1 | 48.50 |
| TRINITY_sp| P710| Putative multidrug | 48.50 |
| TRINITY_sp| Q9Y3| Protein MEMO1 OS=Ho | 48.50 |
| TRINITY_sp| Q8RX| ABC transporter G f | 48.50 |
| TRINITY_sp| Q1ZX| Guanine exchange fa | 48.50 |
| TRINITY_sp| O975| Thioredoxin OS=Equu | 48.50 |
| TRINITY_sp| Q84N| Probable AMP deamin | 48.50 |
| TRINITY_sp| Q9H6| ATP-dependent DNA h | 48.50 |
| TRINITY_sp| Q922| Ubiquitin carboxyl- | 48.50 |
| TRINITY_sp| Q0DH| ATP-dependent zinc | 48.50 |
| TRINITY_sp| Q7RX| Probable imidazolon | 48.50 |
| TRINITY_sp| P736| Putative quercetin | 48.50 |
| TRINITY_sp| A7MK| Methylthioribose-1- | 48.50 |
| TRINITY_sp| Q9XF| ATP-dependent DNA h | 48.50 |
| TRINITY_sp| Q6P9| Cytochrome b5 domai | 48.50 |
| TRINITY_sp| P519| Serine/threonine-pr | 48.50 |
| TRINITY_sp| Q8VI| Canaliculic multisp | 48.50 |
| TRINITY_sp| Q93V| Autophagy-related p | 48.50 |
| TRINITY_sp| Q1ZX| Guanine exchange fa | 48.50 |
| TRINITY_sp| B1ZX| tRNA pseudouridine | 48.50 |
| TRINITY_sp| Q5N4| Branched-chain-amin | 48.50 |
| TRINITY_sp| Q644| Cytochrome P450 3A1 | 48.50 |
| TRINITY_sp| P466| Glutamate--tRNA lig | 48.50 |
| TRINITY_sp| P251| 6-phosphofructo-2-k | 48.50 |
| TRINITY_sp| Q9NY| TBC1 domain family | 48.50 |
| TRINITY_sp| Q67S| Chaperone protein D | 48.50 |
| TRINITY_sp| Q94K| Nucleosome assembly | 48.50 |
| TRINITY_sp| Q9FT| ATP-dependent DNA h | 48.50 |
| TRINITY_sp| Q8CO| Elongation factor-l | 48.50 |
| TRINITY_sp| Q9PD| Octanoyltransferase | 48.50 |
| TRINITY_sp| Q8TB| DEPTOR | 48.50 |
| TRINITY_sp| Q9SE| Galactokinase OS=Ar | 48.50 |
| TRINITY_sp| P271| Ornithine decarboxy | 48.50 |
| TRINITY_sp| Q7NB| Chaperone protein D | 48.50 |
| TRINITY_sp| Q9D6| Calmodulin-like pro | 48.50 |
| TRINITY_sp| Q9SG| High mobility group | 48.50 |
| TRINITY_sp| Q9S2| Putative glutathion | 48.50 |
| Protein Name | Description | p-value | q-value |
|--------------|-------------|---------|---------|
| LIM domain-containing protein B | Dictyostelium discoideum | 48.50 | 0.00 |
| Autophagy-related p | Arabidopsis thaliana | 48.50 | 0.00 |
| tRNA (cytosine(34)- | Dictyostelium discoideum | 48.50 | 0.00 |
| Starch synthase 3, | Arabidopsis thaliana | 48.50 | 0.00 |
| Protein CHROMATIN R | Arabidopsis thaliana | 48.50 | 0.00 |
| 5'-nucleotidase dom | Xenopus laevis | 48.50 | 0.00 |
| 10 kDa chaperonin, | Arabidopsis thaliana | 48.50 | 0.00 |
| cAMP-dependent prot | Arabidopsis thaliana | 48.40 | 0.00 |
| Ethylene receptor O | Arabidopsis thaliana | 48.40 | 0.00 |
| Dual specificity pr | Arabidopsis thaliana | 48.40 | 0.00 |
| Periodic tryptophan | Arabidopsis thaliana | 48.40 | 0.00 |
| Phenylacetone monoo | Mus musculus | 48.40 | 0.00 |
| Proliferation-assoc | Arabidopsis thaliana | 48.40 | 0.00 |
| Polyubiquitin | Arabidopsis thaliana | 48.40 | 0.00 |
| Putative nudix hydr | Arabidopsis thaliana | 48.40 | 0.00 |
| Protein SDE2 homolo | Arabidopsis thaliana | 48.40 | 0.00 |
| Serine--pyruvate am | Arabidopsis thaliana | 48.40 | 0.00 |
| Protein kinase 2 OS | Arabidopsis thaliana | 48.40 | 0.00 |
| Calcium/calmodulin- | Arabidopsis thaliana | 48.40 | 0.00 |
| Cytochrome b-c1 com | Arabidopsis thaliana | 48.40 | 0.00 |
| Putative mitochondr | Arabidopsis thaliana | 48.40 | 0.00 |
| Protein STIP1 homol | Arabidopsis thaliana | 48.40 | 0.00 |
| Eukaryotic translat | Arabidopsis thaliana | 48.40 | 0.00 |
| Endo-1,3(4)-beta-gl | Arabidopsis thaliana | 48.40 | 0.00 |
| Eukaryotic translat | Arabidopsis thaliana | 48.40 | 0.00 |
| Cilia- and flagella | Arabidopsis thaliana | 48.40 | 0.00 |
| Vacuolar protein so | Arabidopsis thaliana | 48.40 | 0.00 |
| Myosin light chain | Arabidopsis thaliana | 48.40 | 0.00 |
| 6-phosphofructo-2-k | Arabidopsis thaliana | 48.40 | 0.00 |
| Copine-9 OS=Mus mus | Arabidopsis thaliana | 48.40 | 0.00 |
| Probable serine/thr | Arabidopsis thaliana | 48.40 | 0.00 |
| Ornithine decarboxy | Arabidopsis thaliana | 48.40 | 0.00 |
| Cilia- and flagella | Arabidopsis thaliana | 48.40 | 0.00 |
| Sterol 3-beta-gluco | Arabidopsis thaliana | 48.40 | 0.00 |
| Aprataxin (Fragment | Arabidopsis thaliana | 48.40 | 0.00 |
| Kinesin-like protei | Arabidopsis thaliana | 48.40 | 0.00 |
| Protein THYLAKOID F | Arabidopsis thaliana | 48.40 | 0.00 |
| 2,3-bisphosphoglyce | Arabidopsis thaliana | 48.40 | 0.00 |
| ATP-dependent DNA h | Arabidopsis thaliana | 48.40 | 0.00 |
| Serine/threonine-pr | Arabidopsis thaliana | 48.40 | 0.00 |
| Cysteine--tRNA liga | Arabidopsis thaliana | 48.40 | 0.00 |
| ATP-dependent prote | Arabidopsis thaliana | 48.40 | 0.00 |
| Eukaryotic translat | Arabidopsis thaliana | 48.40 | 0.00 |
| Aspartate--tRNA lig | Arabidopsis thaliana | 48.40 | 0.00 |
| Heat shock factor p | Arabidopsis thaliana | 48.40 | 0.00 |
| 3-hydroxybutyril-Co | Arabidopsis thaliana | 48.40 | 0.00 |
| MORN repeat-contain | Arabidopsis thaliana | 48.40 | 0.00 |
| Accession     | Description                                                                 | Similarity | E-value |
|--------------|------------------------------------------------------------------------------|------------|---------|
| TRINITY_sp|A1Z9Emip120 | Protein lin-54 homo | 48.40 | 0.00 |
| TRINITY_sp|Q8GZ2lPLA2-BE | Phospholipase A2-be | 48.40 | 0.00 |
| TRINITY_sp|Q9SEI- | Pirin-like protein | 48.40 | 0.00 |
| TRINITY_sp|Q54YdhkB | Hybrid signal trans | 48.40 | 0.00 |
| TRINITY_sp|C0QKgroS | 10 kDa chaperonin O | 48.40 | 0.00 |
| TRINITY_sp|P4265- | 14-3-3-like protein | 48.30 | 0.00 |
| TRINITY_sp|Q9XY1fcpA | Probable C-terminal | 48.30 | 0.00 |
| TRINITY_sp|Q9U7xnp-1 | Transcriptional reg | 48.30 | 0.00 |
| TRINITY_sp|Q86c6tor | Target of rapamycin | 48.30 | 0.00 |
| TRINITY_sp|Q294MAN2B1 | Lysosomal alpha-man | 48.30 | 0.00 |
| TRINITY_sp|Q991HIS1 | ATP phosphoribosylt | 48.30 | 0.00 |
| TRINITY_sp|Q91WAs3mt | Arsenical methyltran | 48.30 | 0.00 |
| TRINITY_sp|Q9LZABC14 | ABC transporter C f | 48.30 | 0.00 |
| TRINITY_sp|Q6DJrccdc130 | Coiled-coil domain- | 48.30 | 0.00 |
| TRINITY_sp|Q7XA6mTN2 | 5'-methylthioadenos | 48.30 | 0.00 |
| TRINITY_sp|Q55cmasS | Aspartate--tRNA lig | 48.30 | 0.00 |
| TRINITY_sp|Q9H61PIF1 | ATP-dependent DNA h | 48.30 | 0.00 |
| TRINITY_sp|P527f- | Glutamine--tRNA lig | 48.30 | 0.00 |
| TRINITY_sp|P905f- | 66 kDa stress prote | 48.30 | 0.00 |
| TRINITY_sp|P0277PARG | Poly(ADP-ribose) gl | 48.30 | 0.00 |
| TRINITY_sp|P044f- | Calmodulin OS=Triti | 48.30 | 0.00 |
| TRINITY_sp|O494fPHB1 | Prohibitin-1, mitoc | 48.30 | 0.00 |
| TRINITY_sp|Q5RI9P6P6 | Poly [ADP-ribose] p | 48.30 | 0.00 |
| TRINITY_sp|P1624MOD1 | NADP-dependent mali | 48.30 | 0.00 |
| TRINITY_sp|P490POLD2 | DNA polymerase delt | 48.30 | 0.00 |
| TRINITY_sp|Q5VREHGO | Homogentisate 1,2-d | 48.30 | 0.00 |
| TRINITY_sp|Q91YCamkl | Calcium/calmodulin-- | 48.30 | 0.00 |
| TRINITY_sp|Q176lypt3 | GTP-binding protein | 48.30 | 0.00 |
| TRINITY_sp|Q9C6LHCA5 | Photosystem I chlor | 48.30 | 0.00 |
| TRINITY_sp|Q547mrKc | Probable serine/thr | 48.30 | 0.00 |
| TRINITY_sp|A41Hbop1 | Ribosome biogenesis | 48.30 | 0.00 |
| TRINITY_sp|Q9LNRRA3 | Arabinosyltransfera | 48.30 | 0.00 |
| TRINITY_sp|Q6Z8Os02g01 | L-aspartate oxidase | 48.30 | 0.00 |
| TRINITY_sp|Q8LG1DH6 | Isocitrater dehydrog | 48.30 | 0.00 |
| TRINITY_sp|Q5U2Fbnox9 | F-box only protein | 48.30 | 0.00 |
| TRINITY_sp|P465pip | Proline iminopeptid | 48.30 | 0.00 |
| TRINITY_sp|Q053schC | Putative polyketide | 48.30 | 0.00 |
| TRINITY_sp|Q5XiEci2 | Enolyl-CoA delta iso | 48.30 | 0.00 |
| TRINITY_sp|Q168TXRD1 | Thioredoxin reducta | 48.30 | 0.00 |
| TRINITY_sp|A1A5Prpf6 | Pre-mRNA-processing | 48.30 | 0.00 |
| TRINITY_sp|Q96JDNAH8 | Dynein heavy chain | 48.30 | 0.00 |
| TRINITY_sp|Q9BU1TRM0 | tRNA (adenine(37)-N | 48.30 | 0.00 |
| TRINITY_sp|Q5M9arl6 | ADP-riboylation fa | 48.30 | 0.00 |
| TRINITY_sp|Q9218Sf3b3 | Splicing factor 3B | 48.30 | 0.00 |
| TRINITY_sp|Q125AO-I | Copper amine oxidas | 48.30 | 0.00 |
| TRINITY_sp|Q5SUmeis3a | Homeobox protein me | 48.30 | 0.00 |
| TRINITY_sp|Q9Y3IAK6 | Adenylate kinase is | 48.20 | 0.00 |
| TRINITY_sp|Q9FSRABBE1E | Ras-related protein | 48.20 | 0.00 |
| TRINITY_sp|Q54XIDDB G02 | Glucose-induced deg | 48.20 | 0.00 |
| TRINITY_sp|B3DNAPC6 | Anaphase-promoting | 48.20 | 0.00 |
| TRINITY_sp|Q54Flmup1 | Iron-sulfur protein | 48.20 | 0.00 |
| TRINITY_sp|O140mak2 | Peroxide stress-act | 48.20 | 0.00 |
| TRINITY_sp|Q2KJPGS1 | CDP-diacylglycerol- | 48.20 | 0.00 |
| TRINITY_sp|Q8TIfamd1 | S-adenosylmethionin | 48.20 | 0.00 |
| TRINITY_sp|Q55Fme2A | Transcription facto | 48.20 | 0.00 |
| TRINITY_sp|Q0WW2Atg434 | Coatamer subunit ga | 48.20 | 0.00 |
| Gene Name | Description | Accession | Bit Score |
|-----------|-------------|-----------|-----------|
| TRINITY_sp| Pantoate-β-alan | 48.10 | 0.00 |
| TRINITY_sp| RNA polymerase II | 48.10 | 0.00 |
| TRINITY_sp| Pyruvate kinase | 48.10 | 0.00 |
| TRINITY_sp| Serine/arginine-rich | 48.10 | 0.00 |
| TRINITY_sp| Probable ATP-dependent | 48.10 | 0.00 |
| TRINITY_sp| Ras-related protein | 48.10 | 0.00 |
| TRINITY_sp| Riboflavin biosynthesis | 48.10 | 0.00 |
| TRINITY_sp| Serine/threonine-protein | 48.10 | 0.00 |
| TRINITY_sp| Probable phospholipid transferase | 48.10 | 0.00 |
| TRINITY_sp| Dynein heavy chain | 48.10 | 0.00 |
| TRINITY_sp| Ubiquitin carboxyl-terminal hydrolase | 48.10 | 0.00 |
| TRINITY_sp| Calcium/calmodulin-dependent | 48.10 | 0.00 |
| TRINITY_sp| Probable serine/threonine-protein | 48.10 | 0.00 |
| TRINITY_sp| Probable multidrug transporter | 48.10 | 0.00 |
| TRINITY_sp| Thylakoid membrane | 48.10 | 0.00 |
| TRINITY_sp| Uncharacterized protein | 48.10 | 0.00 |
| TRINITY_sp| Methylthioribulose transferase | 48.10 | 0.00 |
| TRINITY_sp| UFP0235 protein | 48.10 | 0.00 |
| TRINITY_sp| Nucleolar protein 56 | 48.10 | 0.00 |
| TRINITY_sp| Peptidyl-tRNA hydroxylase | 48.10 | 0.00 |
| TRINITY_sp| Nuclear pore complex protein | 48.10 | 0.00 |
| TRINITY_sp| Purine-uracil permease | 48.10 | 0.00 |
| TRINITY_sp| Bromodomain adjacent | 48.10 | 0.00 |
| TRINITY_sp| COP9 signalosome complex subunit | 48.10 | 0.00 |
| TRINITY_sp| Methylthioribose kinase | 48.10 | 0.00 |
| TRINITY_sp| Beta-lactamase | 48.10 | 0.00 |
| TRINITY_sp| Ubiquitin-like modifier | 48.10 | 0.00 |
| TRINITY_sp| Intraflagellar transport protein | 48.10 | 0.00 |
| TRINITY_sp| Retrovirus-related | 48.10 | 0.00 |
| TRINITY_sp| Cysteine synthase | 48.10 | 0.00 |
| TRINITY_sp| Alpha-tubulin N-acetyltransferase | 48.10 | 0.00 |
| TRINITY_sp| GTP-binding protein | 48.10 | 0.00 |
| TRINITY_sp| Vacuolar protein | 48.10 | 0.00 |
| TRINITY_sp| Ubiquitin-like protein | 48.10 | 0.00 |
| TRINITY_sp| Oligosaccharyltransferase | 48.10 | 0.00 |
| TRINITY_sp| Cytochrome b5 OS=Os | 48.10 | 0.00 |
| TRINITY_sp| Probable steroid-binding protein | 48.10 | 0.00 |
| TRINITY_sp| E3 ubiquitin-protein ligase | 48.10 | 0.00 |
| TRINITY_sp| Adenine phosphoribosyltransferase | 48.10 | 0.00 |
| TRINITY_sp| ABC transporter | 48.10 | 0.00 |
| TRINITY_sp| ATP-binding cassette | 48.10 | 0.00 |
| TRINITY_sp| Probable NOT protein | 48.10 | 0.00 |
| TRINITY_sp| Microtubule-associated | 48.10 | 0.00 |
| TRINITY_sp| GPI mannosyltransferase | 48.10 | 0.00 |
| TRINITY_sp| Nuclear export mediator | 48.10 | 0.00 |
| TRINITY_sp| 50S ribosomal protein | 48.10 | 0.00 |
| TRINITY_sp| Probable serine/threonine-protein | 48.10 | 0.00 |
| TRINITY_sp| NAD-dependent protein | 48.10 | 0.00 |
| TRINITY_sp| 50S ribosomal protein | 48.10 | 0.00 |
| TRINITY_sp| KDEL-tailed cysteine | 48.10 | 0.00 |
| TRINITY_sp| Threonine-β-tRNA ligase | 48.10 | 0.00 |
| Gene   | Protein Name                   | Function/Description                                                                 | Coverage | Identity | Score |
|--------|--------------------------------|-------------------------------------------------------------------------------------|----------|----------|-------|
| TRINITY_sp| O599pkaR                      | cAMP-dependent protein                                                              | 48.00    | 0.00     |       |
| TRINITY_sp| O0011AGPS                     | Alkylidihydroxyacetate                                                             | 48.00    | 0.00     |       |
| TRINITY_sp| Q7U2Mbo150                    | Putative S-adenosylmethionine                                                       | 48.00    | 0.00     |       |
| TRINITY_sp| P0400FUCAC                    | Tissue alpha-L-fuco                                                                 | 48.00    | 0.00     |       |
| TRINITY_sp| Q9R17Ctsz                      | Cathepsin Z OS=Ratt                                                                 | 48.00    | 0.00     |       |
| TRINITY_sp| Q389pkaR                       | Calnexin homolog OS                                                                | 48.00    | 0.00     |       |
| TRINITY_sp| Q7L2KCTD9                      | BTB/POZ domain-cont                                                                 | 48.00    | 0.00     |       |
| TRINITY_sp| Q389RABB1B                     | Ras-related protein                                                                | 48.00    | 0.00     |       |
| TRINITY_sp| Q6QNI                        | Nascent polypeptide                                                                | 48.00    | 0.00     |       |
| TRINITY_sp| P2881PA3568                    | Uncharacterized protein                                                            | 48.00    | 0.00     |       |
| TRINITY_sp| O574f                          | Voltage-dependent L                                                                | 48.00    | 0.00     |       |
| TRINITY_sp| E0X9At3g635                   | Zinc finger CCCH do                                                                 | 48.00    | 0.00     |       |
| TRINITY_sp| P1277RFS3                      | Flagellar radial sp                                                                | 48.00    | 0.00     |       |
| TRINITY_sp| P760TM7SF2                     | Delta(14)-sterol re                                                                | 48.00    | 0.00     |       |
| TRINITY_sp| P8W0COCR4-1                    | Carbon catabolite r                                                                 | 48.00    | 0.00     |       |
| TRINITY_sp| P541MSR4                      | Peptide methionine                                                                 | 48.00    | 0.00     |       |
| TRINITY_sp| B9DGQACS                      | Acetyl-coenzyme A s                                                                | 48.00    | 0.00     |       |
| TRINITY_sp| Q54BmncfG                      | Mitochondrial subunit                                                              | 48.00    | 0.00     |       |
| TRINITY_sp| Q84RFARI7                     | Probable E3 ubiquitin                                                              | 48.00    | 0.00     |       |
| TRINITY_sp| B5FYBAMTOR2                    | Regulator complex p                                                                 | 48.00    | 0.00     |       |
| TRINITY_sp| P546DAB1                      | Dynein assembly fac                                                                | 48.00    | 0.00     |       |
| TRINITY_sp| Q2JMWaspers                    | Aspartate--tRNA (Asp)                                                              | 48.00    | 0.00     |       |
| TRINITY_sp| Q3ZCCNOT7                      | CCR4-NOT transcript                                                               | 48.00    | 0.00     |       |
| TRINITY_sp| P315XPTV1                      | GTP-binding protein                                                               | 48.00    | 0.00     |       |
| TRINITY_sp| Q8088ARASP                     | Membrane metalloprotease                                                          | 48.00    | 0.00     |       |
| TRINITY_sp| A2CEcyb5d2                     | Neuфрerricin OS=Dani                                                               | 48.00    | 0.00     |       |
| TRINITY_sp| P546FCA                        | Phosphoenolpyruvate                                                                | 48.00    | 0.00     |       |
| TRINITY_sp| P2222FCA                       | Pyruvate kinase, cytoplasm                                                         | 48.00    | 0.00     |       |
| TRINITY_sp| P944tElt3                      | Elongation factor 3                                                                | 48.00    | 0.00     |       |
| TRINITY_sp| Q15KPHYLL0                     | Protein PHYLLO, chl                                                                 | 48.00    | 0.00     |       |
| TRINITY_sp| P007F2                         | Prothrombin OS=Homo                                                                 | 47.90    | 0.00     |       |
| TRINITY_sp| Q9MB1DHC10                     | Dynein-1-beta heavy                                                                 | 47.90    | 0.00     |       |
| TRINITY_sp| P501L2Rdh3                     | Retinol dehydrogenase                                                              | 47.90    | 0.00     |       |
| TRINITY_sp| O006FCN1                       | Ficolin-1-OS=Homo s                                                                | 47.90    | 0.00     |       |
| TRINITY_sp| Q9FL1ABC9A                     | ABC transporter A f                                                                | 47.90    | 0.00     |       |
| TRINITY_sp| Q5VJIdgt9                      | Probable serine/thr                                                               | 47.90    | 0.00     |       |
| TRINITY_sp| Q547mrp117                     | Probable 39S ribosome                                                             | 47.90    | 0.00     |       |
| TRINITY_sp| Q545eerkB                      | Extracellular signal                                                               | 47.90    | 0.00     |       |
| TRINITY_sp| Q999salxA                      | Alternative oxidase                                                                | 47.90    | 0.00     |       |
| TRINITY_sp| Q9Z21Mtmr2                     | Myotubularin-relate                                                               | 47.90    | 0.00     |       |
| TRINITY_sp| Q54WDDB02                      | DEP domain-containi                                                               | 47.90    | 0.00     |       |
| TRINITY_sp| E9PVGcn1                       | eIF-2-alpha kinase                                                                | 47.90    | 0.00     |       |
| TRINITY_sp| Q54Gxppep1                     | Xaa-Pro aminopeptidase                                                            | 47.90    | 0.00     |       |
| TRINITY_sp| Q96GlSDSL                      | Serine dehydratase                                                                | 47.90    | 0.00     |       |
| TRINITY_sp| Q54Wbud32                      | EKC/KEOPS complex s                                                               | 47.90    | 0.00     |       |
| TRINITY_sp| Q5VJIdgt9                      | Probable serine/thr                                                               | 47.90    | 0.00     |       |
| TRINITY_sp| Q54VDDB02                      | Probable serine/thr                                                               | 47.90    | 0.00     |       |
| TRINITY_sp| Q4G3                  | Peptidyl-prolyl cis                                                               | 47.90    | 0.00     |       |
| TRINITY_sp| P736wal1773                    | Putative quercetin                                                                | 47.90    | 0.00     |       |
| TRINITY_sp| Q76NNE2D2                      | ER lumen protein-re                                                               | 47.90    | 0.00     |       |
TRINITY_sp|Q2KI|TMEM256 Transmembrane protein 256 OS=Bos taurus GN=TMEM256 PE=3 SV=1 47.90 0.00
TRINITY_sp|Q62J|alc1 Probable allantoic acid 47.90 0.00
TRINITY_sp|Q2SS|UMP Uridine 5'-monophosphoribosyltransferase 47.90 0.00
TRINITY_sp|A7R2|bloc1s2 Biogenesis of lysosomes OS=Dictyostelium discoideum GN=report PE=2 SV=1 47.90 0.00
TRINITY_sp|Q54H|DDDB_G02{CBS domain-containment} OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|A146|NSRA Nuclear speckle RNA binding protein A 47.90 0.00
TRINITY_sp|Q6CK|me1 GrpE protein homolog OS=Dictyostelium discoideum GN=orf2 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q54T|ypdKA Probable serine/threonine protein kinase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q6O5|NEMF Nuclear export mediator factor A 47.90 0.00
TRINITY_sp|P546|apm2 AP-2 complex subunit 2 47.90 0.00
TRINITY_sp|Q3B4|zupT Zinc transporter ZupT 47.90 0.00
TRINITY_sp|Q9FI|At5g4772 Probable acetyl-CoA acetyltransferase 47.90 0.00
TRINITY_sp|Q8S0|Os01g0801 Probable membrane-associated protein OS=Os01g0801 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q9M9|RKD1 Protein RKD1 OS=Ara PE=2 SV=1 47.90 0.00
TRINITY_sp|Q426|SODA Superoxide dismutase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q726|RBBP6 E3 ubiquitin-protein ligase BBP6 47.90 0.00
TRINITY_sp|A7SW|vgl1942 Pescadillo homolog OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|P470|PRY3 Cell wall protein P 47.90 0.00
TRINITY_sp|P32O|mutT 8-oxo-dGTP diphosphatase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q66H|ft80 Intraflagellar transport protein OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q94E|PR46b Coiled-coil domain-containing protein OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q75L|ADA2 Transcriptional activator A2 47.90 0.00
TRINITY_sp|Q6QF|atg3 Ubiquitin-like-conjugating enzyme OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q929|bsaA Glutathione peroxidase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q9FV|AMT1-3 Ammonium transporter 47.90 0.00
TRINITY_sp|Q9WU|Ctsz Cathepsin Z OS=Mus 47.90 0.00
TRINITY_sp|Q9V3|Catsup Protein catecholamine O-methyltransferase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q9U1|gcV Glycine cleavage system H protein OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q391|FSBW Photosystem II reductase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q54L|abcC5 ABC transporter C family member C5 OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q235|RAB1A Ras-related protein OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q96P|AGAP3 Arf-GAP with GTPase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q8WNC|CST3A Cystatin-A OS=Felis 47.90 0.00
TRINITY_sp|Q9GL|ITIH3 Inter-alpha-trypsin inhibitor chain OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q54J|DDDB_G02{Probable iron/ascorbate oxidase} OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q5PQ|scl30a9 Zinc transporter OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q9SR|PEX13 Peroxisomal membrane OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|A77T|nmnt2 Glycylpeptide N-tetradecanoyltransferase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q54V|ecoq7 5-demethoxyubiquinone oxidoreductase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q944|SPBC660. Uncharacterized RNA OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q58D|MMAB Cob(I)inhydrin acid OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|C5CG|glgA Glycogen synthase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|P3641|rab7A Ras-related protein OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q0VC|OXSM 3-oxoacyl-[acyl-carrier]-protein reductase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q286|ABCC2 Canalicular multispanning protein OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q9Y4|AFG3L2 AFG3-like protein OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|C0Q7|rps0 30S ribosomal protein OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q54K|geFA Ras guanine nucleotide OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q8RW|UPL6 E3 ubiquitin-protein ligase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|P0CG|UBB Polyubiquitin-B OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q07G|sde2 Protein SDE2 homolog OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q54N|uch2 Ubiquitin carboxyl-terminal hydrolase OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q9M1|At3g5444 F-box protein OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q9QC|Immp11 Mitochondrial inner membrane protein OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|O614|O614.0 60S acidic ribosom OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|P084|Dlat Dihydrolipooyllysine OS=Dictyostelium discoideum GN=orf9 PE=2 SV=1 47.90 0.00
TRINITY_sp|Q9SY2LIL3.1  Light-harvesting complex-like protein 3 isoform 1, chloroplastic
TRINITY_sp|O882|Aspg  60 kDa lysophospholipase
TRINITY_sp|Q9BIB0464.9  Probable protein phosphatase 2a, ubiquitin-domain-containing
TRINITY_sp|Q54P|cwc2  Pre-mRNA-splicing factor
TRINITY_sp|Q9AS6FREE1  Protein FREE1 isoform OS=Arabidopsis thaliana
TRINITY_sp|Q52JNGLY1  Peptide-N(4)-acetyl-protein
TRINITY_sp|Q058|Dusp2  Dual specificity phosphatase
TRINITY_sp|Q54Q|tceb1  Transcription elongator
TRINITY_sp|P005VYES  Tyrosine-protein kinase
TRINITY_sp|Q9VNCCG12163  Putative cysteine protease
TRINITY_sp|A24H0Jsi023  Serine/threonine-protein kinase
TRINITY_sp|Q8KZ2Manba  Beta-mannosidase OS=Arabidopsis thaliana
TRINITY_sp|Q9KTTPro-pol  Pro-Pol polyprotein
TRINITY_sp|Q2N27  Probable phytol kinase
TRINITY_sp|Q6ZRDNAH12  Dynamin heavy chain
TRINITY_sp|P0A3ccspLA  Cold shock-like protein CspLA
TRINITY_sp|Q459ARP  DNA-(apurinic or apyrimidinic) glycosylase
TRINITY_sp|Q6D4ITt119  Probable tubulin alpha
TRINITY_sp|Q0087  Cysteine synthase O
TRINITY_sp|Q099yakc  Aldo-keto reductase
TRINITY_sp|Q9LKIUVH1  DNA repair endonuclease
TRINITY_sp|P536CLTCL1  Clathrin heavy chain
TRINITY_sp|Q9SHRRP44A  Exosome complex exosome
TRINITY_sp|Q9SNLULUX  Transcription factor
TRINITY_sp|Q5Clubal1  Ubiquitin-like modifier
TRINITY_sp|Q9LDITIF3A1  Eukaryotic translation initiation factor 3A
TRINITY_sp|Q81YDIS3L2  DIS3-like exonuclease
TRINITY_sp|Q3965  5-methyltetrahydrofolate hydrolase
TRINITY_sp|Q9CSMDPL1  Sphingosine-1-phosphatase
TRINITY_sp|P255chcA  Clathrin heavy chain
TRINITY_sp|Q9BX1GTPBP2  GTP-binding protein
TRINITY_sp|Q7Z7FCENPV  Centromere protein
TRINITY_sp|Q9SAJAKHSD1  Bifunctional aspartate transcarbamoylase
TRINITY_sp|P7065Mapk14  Mitogen-activated protein kinase
TRINITY_sp|Q088twy5  tRNA-lysine synthetase
TRINITY_sp|Q54Jatg6B  Beclin-1-like protein
TRINITY_sp|Q6NLIABPB9A  DNA-directed RNA polymerase
TRINITY_sp|Q5R1tat2  tRNA-specific adenylate
TRINITY_sp|Q59(s1r0305  TVP38/TEMEM64 family
TRINITY_sp|Q8L6EXO1  Exonuclease 1
TRINITY_sp|Q9UFPARPG  Poly [ADP-ribose] polymerase
TRINITY_sp|P087tND2  NADH-ubiquinone oxidoreductase
TRINITY_sp|Q1HDCX16  Cation/H (+) antiporter
TRINITY_sp|Q220tANP3  Mitogen-activated protein kinase
TRINITY_sp|A5DNY1P11  Type I phosphatases
TRINITY_sp|Q154MPMPD1  Metallophosphoesterase
TRINITY_sp|Q5HRpf1B  Formate acetyltransferase
TRINITY_sp|Q94AMKK1  Mitogen-activated protein kinase
TRINITY_sp|Q6Z6WMADS57  MADS-box family protein
TRINITY_sp|Q9AR1HAC1  Histone acetyltransferase
TRINITY_sp|Q9S1IDSK2B  Ubiquitin domain-containing protein
TRINITY_sp|P2216-  Pyrophosphate-energized ATPase
TRINITY_sp|Q6AKdhnA  Chaperone protein
TRINITY_sp|Q54SdhkD  Hybrid signal transducer
TRINITY_sp|Q8BYFIRdh12  Retinol dehydrogenase
TRINITY_sp|B9RAjRCOM_15  Probable aspartyl aminopeptidase
TRINITY_sp|Q9FKVAt5g661|Probable alpha-mann 47.70 0.00
TRINITY_sp|B3N4Trip1  Eukaryotic translat 47.70 0.00
TRINITY_sp|Q9GLwPRDX5  Peroxiredoxin-5, mi 47.70 0.00
TRINITY_sp|Q9NRHABC10  ATP-binding casset 47.70 0.00
TRINITY_sp|Q84JIAAt5g093|2-oxoisovalerate de 47.70 0.00
TRINITY_sp|A5FN1rpsK  30S ribosomal prote 47.70 0.00
TRINITY_sp|Q9M0IPFK1  ATP-dependent 6-pho 47.70 0.00
TRINITY_sp|P505sasp1  Serine/threonine-pr 47.70 0.00
TRINITY_sp|Q9XEXALG11  GDP-Man:Man(3)GlcNA 47.70 0.00
TRINITY_sp|F4HPILIG6  DNA ligase 6 OS=Ara 47.70 0.00
TRINITY_sp|Q9XYTfcpA  Probable C-terminal 47.70 0.00
TRINITY_sp|Q9FJIKPNB1  Importin subunit be 47.70 0.00
TRINITY_sp|Q9LVDEPE1  4-alpha-glucanotran 47.70 0.00
TRINITY_sp|O663sigA  RNA polymerase sigm 47.70 0.00
TRINITY_sp|Q9L5ARPD2  Actin-related prote 47.70 0.00
TRINITY_sp|Q67XAt5g065|F-box protein At5g0 47.70 0.00
TRINITY_sp|Q9SMILKRSDH  Alpha-aminoacidip s 47.70 0.00
TRINITY_sp|P2271Gucylb2  Guanylate cyclase s 47.70 0.00
TRINITY_sp|P370Por  NADPH--cytochrome P 47.70 0.00
TRINITY_sp|Q645Atp1a4  Sodium/potassium-tr 47.70 0.00
TRINITY_sp|P390Dynein beta chain, 47.70 0.00
TRINITY_sp|Q9MORPL28C  60S ribosomal prote 47.70 0.00
TRINITY_sp|Q9CG6MTK  Methylthioribose ki 47.70 0.00
TRINITY_sp|Q86sDHDDS  Dehydrodolichyl dip 47.70 0.00
TRINITY_sp|Q8WXDDNAH7  Dynein heavy chain 47.70 0.00
TRINITY_sp|Q9CSHAC1  Histone acetyltrans 47.70 0.00
TRINITY_sp|Q8WXDDNAH7  Dynein heavy chain 47.70 0.00
TRINITY_sp|Q414Putative calmodulin 47.60 0.00
TRINITY_sp|Q4551-D-hydantoinase OS=G 47.60 0.00
TRINITY_sp|F0NBhSiRe_14'Protein-lysine N-me 47.60 0.00
TRINITY_sp|Q918hspa5  78 kDa glucose-regu 47.60 0.00
TRINITY_sp|Q55Epats1  Probable serine/thr 47.60 0.00
TRINITY_sp|P570NMA0194  Uncharacterized pro 47.60 0.00
TRINITY_sp|Q54NVpsa28  Vacuolar protein so 47.60 0.00
TRINITY_sp|Q5A1Sdr16c6  Short-chain dehydro 47.60 0.00
TRINITY_sp|Q54Bggps1  Geranylgeranyl pyro 47.60 0.00
TRINITY_sp|Q386PPE3  Proteasome subunit 47.60 0.00
TRINITY_sp|Q7RAACP3  Calcium-dependent p 47.60 0.00
TRINITY_sp|Q9ATFAD2  Delta(12) fatty aci 47.60 0.00
TRINITY_sp|Q9P2HIIF17  Kinesin-like protei 47.60 0.00
TRINITY_sp|Q9XTPDE6D  Retinal rod rhodops 47.60 0.00
TRINITY_sp|O227FRP19B  Pre-mRNA-processing 47.60 0.00
TRINITY_sp|Q9LPVPN6  26S proteasome non- 47.60 0.00
TRINITY_sp|Q154MPPED1  Metallophosphoester 47.60 0.00
TRINITY_sp|Q86KicpnB-1  Copine-B OS=Dictyos 47.60 0.00
TRINITY_sp|P707Atp7a  Copper-transporting 47.60 0.00
TRINITY_sp|Q152SPTLC1  Serine palmitoylta 47.60 0.00
TRINITY_sp|P451ettA  Energy-dependent tr 47.60 0.00
TRINITY_sp|Q5Z8Ios06g071RNA pseudouridine s 47.60 0.00
TRINITY_sp|P0COREX4  RNA exonuclease 4 O 47.60 0.00
TRINITY_sp|Q6P3NEK5  Serine/threonine-pr 47.60 0.00
TRINITY_sp|C0QRigatA  Glutamyl-tRNA(Gln) 47.60 0.00
TRINITY_sp|O009Lysosomal acid alph 47.60 0.00
TRINITY_sp|Q8W2GCN5  Histone acetyltrans 47.60 0.00
TRINITY_sp|F13xddaXX11  ATP-dependent DNA h 47.60 0.00
TRINITY_sp|A7MGpepB  Peptidase B OS=Cron 47.60 0.00
| Accession       | Description                                      | Future   | Bacteria  |
|-----------------|--------------------------------------------------|----------|-----------|
| sp|O94489|EF3_SCHPO |47.60|0.00 |
| sp|Q8GWT4|ANM15_ARATH|47.60|0.00 |
| sp|Q69U49|RMR2_ORYSJ|47.60|0.00 |
| sp|Q3ZCE0|LSM8_BOVIN|47.60|0.00 |
| sp|Q8L6J5|RPO1B_TOBAC|47.60|0.00 |
| sp|A0AVT1|UBA6_HUMAN|47.60|0.00 |
| sp|Q9VXY0|CP4S3_DROME|47.60|0.00 |
| sp|Q6FS54|DBP3_CANGA|47.60|0.00 |
| sp|O04331|PHB3_ARATH|47.60|0.00 |
| sp|O22715|AP1M2_ARATH|47.60|0.00 |
| sp|P30839|AL3A2_RAT|47.60|0.00 |
| sp|Q24629|REF2P_DROSI|47.60|0.00 |
| sp|Q2RBN7|CLH1_ORYSJ|47.60|0.00 |
| sp|Q9AST3|SBH2_ARATH|47.60|0.00 |
| sp|Q8TCQ1|MARCH1_HUMAN|47.60|0.00 |
| sp|Q3MG79|RSGA_ANAVT|47.60|0.00 |
| sp|A8IZG4|CIAO1_CHLRE|47.60|0.00 |
| sp|Q8BXK_Cdssp2|Carboxy-terminal do|47.60|0.00 |
| sp|G0Y2{SSL-2|Botryococcus squale|47.50|0.00 |
| sp|A1ZKCHLREDR|Probable cytosolic|47.50|0.00 |
| sp|Q3MG:rsqA|Putative ribosome b|47.50|0.00 |
| sp|Q2UGG:ctg1|Serine/threonine-pr|47.50|0.00 |
| sp|Q625:ift52|Intraflagellar tran|47.50|0.00 |
| sp|Q087:Ube3a|Ubiquitin-protein l|47.50|0.00 |
| sp|Q8TC(MARCH1|E3 ubiquitin-protei|47.50|0.00 |
| sp|Q9AS1SBH2|Sphinganine C4-mono|47.50|0.00 |
| sp|Q2RB0s11g01|Clathrin heavy cha|47.50|0.00 |
| sp|Q4V7:nsun2|tRNA (cytosine(34)|47.50|0.00 |
| sp|Q246:ref(2)P|Protein ref(2)P OS|=47.50|0.00 |
| sp|Q8RW:PUX4|Plant UBX domain-co|47.50|0.00 |
| sp|Q91V:Memo1|Protein MEMO1 OS=Mu|47.50|0.00 |
| sp|Q8BXK_Cdssp2|Carboxy-terminal do|47.50|0.00 |
| sp|P308:Aldh3a2|Fatty aldehyde dehy|47.50|0.00 |
| sp|Q2271AP1M2|AP-1 complex subuni|47.50|0.00 |
| sp|O043:PHB3|Prohibitin-3, mitoc|47.50|0.00 |
| sp|Q6FS:DBP3|ATP-dependent RNA h|47.50|0.00 |
| sp|Q9VX:Ycyp4s3|Probable cytochrome|47.50|0.00 |
| sp|A0AV7UBA6|Ubiquitin-like modi|47.50|0.00 |
| sp|Q9F2I_PEX11A|Peroxialosomal membran|47.50|0.00 |
| sp|Q6EUF:PUB4|U-box domain-contai|47.50|0.00 |
| sp|Q7TXIppsC|Phthiocerol/phenolp|47.50|0.00 |
| sp|Q54T:gtaI|GATA zinc finger do|47.50|0.00 |
| sp|Q7XR:YSL6|Probable metal-nico|47.50|0.00 |
| sp|Q9D2`Mmab|Cob(I)yrinic acid a|47.50|0.00 |
| sp|Q8L6:RROT1-T|DNA-directed RNA po|47.50|0.00 |
| sp|Q6EKL:phospho:Probable phosphatases|47.50|0.00 |
| sp|Q3ZCELSM8|U6 snRNA-associated|47.50|0.00 |
| sp|Q6DUR:RMR1|Receptor homology r|47.50|0.00 |
| sp|Q8GW1PMRT15|Protein arginine N-|47.50|0.00 |
| sp|Q9444tef3|Elongation factor 3|47.50|0.00 |
| sp|Q5E91ARF3|ADP-ribosylation fa|47.50|0.00 |
| Accession | Description | Fold | Helix |
|-----------|-------------|------|-------|
| TRINITY_sp| Dynein light chain| 47.50| 0.00 |
| TRINITY_sp| Histone deacetylase| 47.40| 0.00 |
| TRINITY_sp| MAPK epsilon prote| 47.40| 0.00 |
| TRINITY_sp| DNA replication com| 47.40| 0.00 |
| TRINITY_sp| Aldose reductase A| 47.40| 0.00 |
| TRINITY_sp| Adenine DNA glycosy| 47.40| 0.00 |
| TRINITY_sp| AP-1 complex subunit| 47.40| 0.00 |
| TRINITY_sp| Fructokinase OS=Lac| 47.40| 0.00 |
| TRINITY_sp| Calcium-dependent p| 47.40| 0.00 |
| TRINITY_sp| Actin-like protein| 47.40| 0.00 |
| TRINITY_sp| Talin-B OS=Dictyost| 47.40| 0.00 |
| TRINITY_sp| PMS1 protein homolo| 47.40| 0.00 |
| TRINITY_sp| Heptahelical transm| 47.40| 0.00 |
| TRINITY_sp| Peroxisome biogenes| 47.40| 0.00 |
| TRINITY_sp| Eukaryotic translat| 47.40| 0.00 |
| TRINITY_sp| Proteasome subunit| 47.40| 0.00 |
| TRINITY_sp| Peptide methionine| 47.40| 0.00 |
| TRINITY_sp| Transposon Ty3-G Ga| 47.40| 0.00 |
| TRINITY_sp| ABC transporter A f| 47.40| 0.00 |
| TRINITY_sp| Ribosomal RNA small| 47.40| 0.00 |
| TRINITY_sp| NADH-cytochrome b5| 47.40| 0.00 |
| TRINITY_sp| putative RNA methyl| 47.40| 0.00 |
| TRINITY_sp| Glutaredoxin-3 OS=X| 47.40| 0.00 |
| TRINITY_sp| Protein ZGRF1| 47.40| 0.00 |
| TRINITY_sp| NADP-reducing hydro| 47.40| 0.00 |
| TRINITY_sp| DEAD-box ATP-depend| 47.40| 0.00 |
| TRINITY_sp| Calcium/calmodulin-| 47.40| 0.00 |
| TRINITY_sp| Cyclin-G-associated| 47.40| 0.00 |
| TRINITY_sp| Probable caffeoyl-C| 47.40| 0.00 |
| TRINITY_sp| NAD-dependent prote| 47.40| 0.00 |
| TRINITY_sp| ABC transporter F f| 47.40| 0.00 |
| TRINITY_sp| NEDD8-activating en| 47.40| 0.00 |
| TRINITY_sp| Cytochrome c oxidas| 47.40| 0.00 |
| TRINITY_sp| Probable pyridoxal| 47.40| 0.00 |
| TRINITY_sp| Uncharacterized pro| 47.40| 0.00 |
| TRINITY_sp| DDB1- and CUL4-associated| 47.40| 0.00 |
| TRINITY_sp| Trafficking protein| 47.40| 0.00 |
| TRINITY_sp| Nipped-B-like prote| 47.40| 0.00 |
| TRINITY_sp| Flagellar radial sp| 47.40| 0.00 |
| TRINITY_sp| Mitogen-activated p| 47.40| 0.00 |
| TRINITY_sp| ABC transporter F f| 47.40| 0.00 |
| TRINITY_sp| DNA gyrase subunit| 47.40| 0.00 |
| TRINITY_sp| Heterochromatin pro| 47.40| 0.00 |
| TRINITY_sp| Glutamate decarboxy| 47.40| 0.00 |
| TRINITY_sp| Dual specificity ty| 47.40| 0.00 |
| TRINITY_sp| Beta-lactamase hydr| 47.40| 0.00 |
| TRINITY_sp| Putative DEAH-box A| 47.40| 0.00 |
| TRINITY_sp| Actin, gamma OS=Acr| 47.30| 0.00 |
| TRINITY_sp| 40S ribosomal prote| 47.30| 0.00 |
| TRINITY_sp| L-methionine gamma-| 47.30| 0.00 |
| TRINITY_sp| F-box protein At5g065| 47.30| 0.00 |
| TRINITY_sp| NEDD8-conjugating e| 47.30| 0.00 |
| TRINITY_sp| Myb-like protein L| 47.30| 0.00 |
| TRINITY_sp| Stromal membrane-as| 47.30| 0.00 |
| TRINITY_sp| Protein RKD5 OS=Ara| 47.30| 0.00 |
| TRINITY_sp| Uncharacterized pro| 47.30| 0.00 |
| Gene ID | Description | Transcripts | Protein ID  |
|---------|-------------|-------------|------------|
| TRINITY_sp| 3-hydroxyisobutyryl | 47.20 0.00 | sp|Q5ZJH|
| TRINITY_sp| Glutamyl-tRNA(Gln) | 47.20 0.00 | sp|Q54L|
| TRINITY_sp| Glycine-tRNA ligas | 47.20 0.00 | sp|Q100|
| TRINITY_sp| Kinesin-like protei | 47.20 0.00 | sp|F4K4|
| TRINITY_sp| Phosphatidate cytid | 47.20 0.00 | sp|Q1PE|
| TRINITY_sp| Calmodulin-interact | 47.20 0.00 | sp|Q9LE|
| TRINITY_sp| Hormone-sensitive l | 47.20 0.00 | sp|Q054|
| TRINITY_sp| Diacylglycerol O-ac | 47.20 0.00 | sp|Q9SL|
| TRINITY_sp| Thioredoxin F1, chl | 47.20 0.00 | sp|Q9XF|
| TRINITY_sp| Protein farnesytra | 47.20 0.00 | sp|F493|
| TRINITY_sp| Cryptochrome-1 | 47.20 0.00 | sp|Q431|
| TRINITY_sp| GTP-binding protein | 47.20 0.00 | sp|P176|
| TRINITY_sp| Putative glucosamin | 47.20 0.00 | sp|Q8AB|
| TRINITY_sp| Protein zntB | 47.20 0.00 | sp|Q54L|
| TRINITY_sp| Mitogen-activated protein kinase kinase kinase 2 | 47.20 0.00 | sp|Q9SF|
| TRINITY_sp| DNA topoisomerase 1 | 47.20 0.00 | sp|Q499|
| TRINITY_sp| AP-3 complex subunit delta | 47.20 0.00 | sp|Q54RN|
| TRINITY_sp| Glutathione peroxidase | 47.20 0.00 | sp|Q9UR|
| TRINITY_sp| Protein transport p | 47.20 0.00 | sp|Q9M2|
| TRINITY_sp| Ras-related protein | 47.20 0.00 | sp|F257|
| TRINITY_sp| Transcription facto | 47.20 0.00 | sp|Q9FG|
| TRINITY_sp| Protease Do-like 1 | 47.20 0.00 | sp|Q226|
| TRINITY_sp| Serine carboxypepti | 47.20 0.00 | sp|P378|
| TRINITY_sp| DNA topoisomerase 1 | 47.20 0.00 | sp|Q54K|
| TRINITY_sp| Mitochondrial uncou | 47.20 0.00 | sp|Q9X|
| TRINITY_sp| Neutral alpha-gluco | 47.20 0.00 | sp|Q94S|
| TRINITY_sp| Acyl-CoA synthetase | 47.20 0.00 | sp|Q3UR|
| TRINITY_sp| AP-3 complex subuni | 47.20 0.00 | sp|Q54W|
| TRINITY_sp| Mitogen-activated p | 47.20 0.00 | sp|Q9F2|
| TRINITY_sp| Probable chromatin- | 47.20 0.00 | sp|Q7G8|
| TRINITY_sp| Cytochrome b5 domai | 47.20 0.00 | sp|Q6P9|
| TRINITY_sp| Nuclear valosin-con | 47.20 0.00 | sp|Q9DB|
| TRINITY_sp| High-affinity nitra | 47.20 0.00 | sp|P0DK|
| TRINITY_sp| Uncharacterized aar | 47.20 0.00 | sp|Q9MA|
| TRINITY_sp| Copper homeostasis | 47.20 0.00 | sp|Q89Z|
| TRINITY_sp| NADH-cytochrome b5 | 47.20 0.00 | sp|Q54N|
| TRINITY_sp| Glutathione peroxid | 47.20 0.00 | sp|Q9CF|
| TRINITY_sp| Vacuolar cation-tra | 47.10 0.00 | sp|Q126|
| TRINITY_sp| Anhydro-N-acetylmur | 47.10 0.00 | sp|Q15R|
| TRINITY_sp| Signal transduction | 47.10 0.00 | sp|P0A|
| TRINITY_sp| Tubulin beta chain | 47.10 0.00 | sp|Q081|
| TRINITY_sp| Putative tricarboxy | 47.10 0.00 | sp|P345|
| TRINITY_sp| M-phase inducer pho | 47.10 0.00 | sp|P303|
| TRINITY_sp| Ras-like GTF-bindin | 47.10 0.00 | sp|Q018|
| TRINITY_sp| Dynein heavy chain | 47.10 0.00 | sp|Q9C0|
| TRINITY_sp| M-phase inducer pho | 47.10 0.00 | sp|P303|
| TRINITY_sp| Probable serine/thr | 47.10 0.00 | sp|Q55E|
| TRINITY_sp| Importin subunit al | 47.10 0.00 | sp|F4JL|
| TRINITY_sp| CDP-diacylglycerol- | 47.10 0.00 | sp|Q147|
| TRINITY_sp| Serine/arginine-ric | 47.10 0.00 | sp|Q9FY|
| TRINITY_sp| Cytochrome c oxidas | 47.10 0.00 | sp|Q9SU|
| TRINITY_sp| Polycytochrome fmp | 47.10 0.00 | sp|B4SQ|
| TRINITY_sp| PAB-dependent poly( | 47.10 0.00 | sp|P0CD|
| TRINITY_sp| Importin subunit al | 47.10 0.00 | sp|O042|
| TRINITY_sp| F-box-like/WD repea | 47.10 0.00 | sp|Q9B2|
| TRINITY_sp| WD repeat-containin | 47.10 0.00 | sp|Q54J|
| Accession     | Name                                      | Description                                                      | Score | Description       |
|--------------|-------------------------------------------|------------------------------------------------------------------|-------|-------------------|
| sp|P54442|Akr1b8| Uncharacterized protein | 47.10| 0.00 |
| sp|Q54850|Akr1b8| Long-chain-fatty-ac | 47.10| 0.00 |
| sp|Q77822|Akr1b8| Tyrosine decarboxyl | 47.10| 0.00 |
| sp|P55471|Akr1b8| Geranylgeranyl tran | 47.10| 0.00 |
| sp|Q50338|Akr1b8| Integrator complex | 47.10| 0.00 |
| sp|Q7RA6|Akr1b8| Calcium-dependent p | 47.10| 0.00 |
| sp|Q5ZK42|Akr1b8| Choline/ethanolamin | 47.10| 0.00 |
| sp|Q9MA29|Akr1b8| Protein disulfide-i | 47.10| 0.00 |
| sp|Q3ZI27|Akr1b8| Microtubule-associa | 47.10| 0.00 |
| sp|Q9FQ6|Akr1b8| 5'-3' exoribonuclea | 47.10| 0.00 |
| sp|Q5CC2|Akr1b8| B3 domain-containin | 47.10| 0.00 |
| sp|Q8ABBT|Akr1b8| Putative glucosamin | 47.10| 0.00 |
| sp|Q77822|Akr1b8| Mitochondrial impor | 47.10| 0.00 |
| sp|Q9FP8|Akr1b8| Photosystem II 22 k | 47.10| 0.00 |
| sp|Q9Z1|Akr1b8| Valine--tRNA ligase | 47.10| 0.00 |
| sp|66NN|Akr1b8| Tubulin polyglutam | 47.10| 0.00 |
| sp|P15431|Akr1b8| Isopentenyl-diphosp | 47.10| 0.00 |
| sp|Q6PD|Akr1b8| RNA polymerase-asso | 47.10| 0.00 |
| sp|Q9LZ|Akr1b8| DnaJ protein ERDJ3B | 47.10| 0.00 |
| sp|A8P\|Akr1b8| Acylyphosphatase OS= | 47.10| 0.00 |
| sp|Q7SH|Akr1b8| Cysteine synthase 2 | 47.10| 0.00 |
| sp|A4FV|Akr1b8| RNA-binding protein | 47.10| 0.00 |
| sp|Q4K2|Akr1b8| Polyolpolyglutamate | 47.10| 0.00 |
| sp|Q8K4|Akr1b8| Endonuclease 8-like | 47.10| 0.00 |
| sp|P380|Akr1b8| Putative urea carbo | 47.10| 0.00 |
| sp|P099|Akr1b8| Leukotriene A-4 hyd | 47.10| 0.00 |
| sp|Q579|Akr1b8| ATPase family AAA d | 47.10| 0.00 |
| sp|Q9EQ\|Akr1b8| Tripeptidyl-peptida | 47.10| 0.00 |
| sp|Q8M2|Akr1b8| Physarolisin OS=Phy | 47.10| 0.00 |
| sp|Q7F|Akr1b8| Probable calcium-bi | 47.10| 0.00 |
| sp|Q828|Akr1b8| Histidine biosynthe | 47.10| 0.00 |
| sp|A8JF|Akr1b8| Cilia- and flagella | 47.10| 0.00 |
| sp|P0AG|Akr1b8| Amido phosphoribosyl | 47.10| 0.00 |
| sp|Q8BG|Akr1b8| PAB-dependent poly( | 47.10| 0.00 |
| sp|Q8KO|Akr1b8| Intraflagellar tran | 47.10| 0.00 |
| sp|Q396|Akr1b8| Dynine alpha chain | 47.10| 0.00 |
| sp|Q54r|Akr1b8| Mitogen-activated p | 47.10| 0.00 |
| sp|Q9FX|Akr1b8| BELL-like homeodoma | 47.10| 0.00 |
| sp|Q1PF|Akr1b8| BELL-like homeodoma | 47.10| 0.00 |
| sp|Q7XQ|Akr1b8| Serine/threonine-pr | 47.10| 0.00 |
| sp|P526|Akr1b8| D-lactate dehydroge | 47.10| 0.00 |
| sp|Q9SH|Akr1b8| Translation initiat | 47.10| 0.00 |
| sp|Q62|Akr1b8| Cullin-associated N | 47.10| 0.00 |
| sp|F4KO|Akr1b8| Myosin-2 OS=Arabido | 47.10| 0.00 |
| sp|Q54P|Akr1b8| Oxysterol-binding p | 47.10| 0.00 |
| sp|Q92E|Akr1b8| Probable dual-speci | 47.10| 0.00 |
| sp|Q54J|Akr1b8| Phosphatidylinosito | 47.10| 0.00 |
| sp|P517|Akr1b8| H(+)/Cl(-) exchange | 47.10| 0.00 |
| sp|QOP4|Akr1b8| Protein DPCD OS=Dan | 47.10| 0.00 |
| sp|Q9SP|Akr1b8| Hybrid signal trans | 47.10| 0.00 |
| sp|Q7TM|Akr1b8| ATP-binding cassett | 47.10| 0.00 |
| sp|P339|Akr1b8| Blasticidin-S deami | 47.10| 0.00 |
| sp|Q54Q|Akr1b8| NAD-dependent deace | 47.10| 0.00 |
| sp|Q9D8|Akr1b8| Actin-related prote | 47.10| 0.00 |
| sp|Q5RG|Akr1b8| Histone H2A deubiqu | 47.10| 0.00 |
| sp|P453|Akr1b8| Aldose reductase-re | 47.10| 0.00 |
| Gene Name         | Description                                      | Score | Format |
|-------------------|--------------------------------------------------|-------|--------|
| Bile pigment transporter 1 | OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) | 47.00 | 0.00   |
| 40S ribosomal protein 12 | OS=Dictyostelium discoideum | 47.00 | 0.00   |
| Proteasome subunit | OS=Rattus norvegicus | 47.00 | 0.00   |
| Methylthioribose kinase | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Cytochrome b-c1 complex subunit 7-2 | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Protein tyrosine phosphatase domain-containing protein 1 | OS=Danio rerio | 47.00 | 0.00   |
| SOSS complex subunit B1 | OS=Mus musculus | 47.00 | 0.00   |
| Probable prefoldin subunit 4 | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Transcription factor MYB98 | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Dynein heavy chain 12 | OS=Mus musculus | 47.00 | 0.00   |
| Probable anion transporter 4, chloroplastic | OS=Oryza sativa subsp. japonica | 47.00 | 0.00   |
| ATP-binding cassette sub-family A member 2 | OS=Rattus norvegicus | 47.00 | 0.00   |
| 40S ribosomal protein S12 | OS=Caenorhabditis elegans | 47.00 | 0.00   |
| 5-methylthioadenosine/S-adenosylhomocysteine deaminase | OS=Teredinibacter turnerae (strain ATCC 39867 / T7901) | 47.00 | 0.00   |
| Protein S-acyltransferase 24 | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Glycerol-3-phosphate dehydrogenase SDP6, mitochondrial | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Putative synaptobrevin homolog YKT6 | OS=Dictyostelium discoideum | 47.00 | 0.00   |
| Proteasome subunit alpha type-3 | OS=Mus musculus | 47.00 | 0.00   |
| Ras-related protein Rab-2A | OS=Dictyostelium discoideum | 47.00 | 0.00   |
| Nucleolar protein 10 | OS=Homo sapiens | 47.00 | 0.00   |
| Formamidopyrimidine-DNA glycosylase | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Cilia- and flagella-associated protein 52 | OS=Chlamydomonas reinhardtii | 47.00 | 0.00   |
| Exosome complex component RRP45B | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Bile pigment transporter 1 | OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) | 47.00 | 0.00   |
| 40S ribosomal protein 12 | OS=Dictyostelium discoideum | 47.00 | 0.00   |
| Proteasome subunit | OS=Rattus norvegicus | 47.00 | 0.00   |
| Methylthioribose kinase | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Cytochrome b-c1 complex subunit 7-2 | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Protein tyrosine phosphatase domain-containing protein 1 | OS=Danio rerio | 47.00 | 0.00   |
| SOSS complex subunit B1 | OS=Mus musculus | 47.00 | 0.00   |
| Probable prefoldin subunit 4 | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Transcription factor MYB98 | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Dynein heavy chain 12 | OS=Mus musculus | 47.00 | 0.00   |
| Probable anion transporter 4, chloroplastic | OS=Oryza sativa subsp. japonica | 47.00 | 0.00   |
| ATP-binding cassette sub-family A member 2 | OS=Rattus norvegicus | 47.00 | 0.00   |
| 40S ribosomal protein S12 | OS=Caenorhabditis elegans | 47.00 | 0.00   |
| 5-methylthioadenosine/S-adenosylhomocysteine deaminase | OS=Teredinibacter turnerae (strain ATCC 39867 / T7901) | 47.00 | 0.00   |
| Protein S-acyltransferase 24 | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Glycerol-3-phosphate dehydrogenase SDP6, mitochondrial | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Putative synaptobrevin homolog YKT6 | OS=Dictyostelium discoideum | 47.00 | 0.00   |
| Proteasome subunit alpha type-3 | OS=Mus musculus | 47.00 | 0.00   |
| Ras-related protein Rab-2A | OS=Dictyostelium discoideum | 47.00 | 0.00   |
| Nucleolar protein 10 | OS=Homo sapiens | 47.00 | 0.00   |
| Formamidopyrimidine-DNA glycosylase | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Cilia- and flagella-associated protein 52 | OS=Chlamydomonas reinhardtii | 47.00 | 0.00   |
| Exosome complex component RRP45B | OS=Arabidopsis thaliana | 47.00 | 0.00   |
| Accession | Description | OS          | ID      |
|-----------|-------------|-------------|---------|
| TRINITY_sp| Protein kinase 2 OS | Dictyostelium discoideum pkgB | OS=Dictyostelium discoideum GN=pkgB PE=1 SV=2 |
| TRINITY_sp| Protein DGS1, mitoc | Rattus norvegicus Prep | OS=Rattus norvegicus GN=Prep PE=1 SV=1 |
| TRINITY_sp| Transmembrane prote | Arabidopsis thaliana RRA2 | OS=Arabidopsis thaliana GN=RRA2 PE=2 SV=1 |
| TRINITY_sp| Serine/threonine-protein phosphatase BSL1 | Arabidopsis thaliana BSL1 | OS=Arabidopsis thaliana GN=BSL1 PE=1 SV=2 |
| TRINITY_sp| Dynein heavy chain 6, axonemal | Homo sapiens DNAH6 | OS=Homo sapiens GN=DNAH6 PE=2 SV=3 |
| TRINITY_sp| ATP-dependent RNA helicase DDX3Y | Mus musculus Ddx3y | OS=Mus musculus GN=Ddx3y PE=1 SV=2 |
| TRINITY_sp| MAPK/MAK/MRK overlapping kinase | Homo sapiens MOK | OS=Homo sapiens GN=MOK PE=2 SV=1 |
| TRINITY_sp| V-type proton ATPases | Arabidopsis thaliana VHA-C | OS=Arabidopsis thaliana GN=VHA-C PE=1 SV=1 |
| TRINITY_sp| Dual-functional monooxygenase/methyltransferase psoF | Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) psoF | OS=Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) GN=psoF PE=1 SV=1 |
| TRINITY_sp| ATP-binding cassette sub-family B member 7, mitochondrial | Homo sapiens ABCB7 | OS=Homo sapiens GN=ABCB7 PE=1 SV=2 |
| TRINITY_sp| Transmembrane protein 222 | Homo sapiens TMEM222 | OS=Homo sapiens GN=TMEM222 PE=1 SV=2 |
| TRINITY_sp| Rubrerythrin | Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / DSM 644 / NCIMB 8303) rbr | OS=Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / DSM 644 / NCIMB 8303) GN=rbr PE=1 SV=1 |
| TRINITY_sp| DNA polymerase delta small subunit | Arabidopsis thaliana POLD2 | OS=Arabidopsis thaliana GN=POLD2 PE=2 SV=2 |
| TRINITY_sp| Fatty aldehyde dehydrogenase | Rattus norvegicus Aldh3a2 | OS=Rattus norvegicus GN=Aldh3a2 PE=1 SV=1 |
| TRINITY_sp| Protein DGS1, mitochondrial | Arabidopsis thaliana DGS1 | OS=Arabidopsis thaliana GN=DGS1 PE=1 SV=1 |
| TRINITY_sp| m7GpppN-mRNA hydrolase | Mus musculus Dcp2 | OS=Mus musculus GN=Dcp2 PE=1 SV=2 |
| TRINITY_sp| Trafficking protein | Homo sapiens trappc4 | OS=Homo sapiens GN=trappc4 PE=3 SV=1 |
| TRINITY_sp| Lactation elevated protein 1 homolog B | Danio rerio lace1b | OS=Danio rerio GN=lace1b PE=2 SV=1 |
| TRINITY_sp| Palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, chloroplastic | Arabidopsis thaliana ADS3 | OS=Arabidopsis thaliana GN=ADS3 PE=1 SV=2 |
| TRINITY_sp| Protein TAR1 | Saccharomyces cerevisiae (strain ATCC 204508 / S288c) TAR1 | OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAR1 PE=2 SV=1 |
| TRINITY_sp| FACT complex subunit SSRP1 | Zea mays SSRP1 | OS=Zea mays GN=SSRP1 PE=1 SV=1 |
| TRINITY_sp| Dynein alpha chain, flagellar outer arm | Chlamydomonas reinhardtii ODA11 | OS=Chlamydomonas reinhardtii GN=ODA11 PE=3 SV=2 |
| TRINITY_sp| Zinc finger protein 593 | Xenopus tropicalis znf593 | OS=Xenopus tropicalis GN=znf593 PE=2 SV=1 |
| TRINITY_sp| CHD3-type chromatin-remodeling factor PICKLE | Arabidopsis thaliana PKL | OS=Arabidopsis thaliana GN=PKL PE=1 SV=1 |
| TRINITY_sp| Multidrug resistance-associated protein 4 | Homo sapiens ABCC4 | OS=Homo sapiens GN=ABCC4 PE=1 SV=3 |
| TRINITY_sp| Fatty aldehyde dehy | Homo sapiens SLBP2 | OS=Homo sapiens GN=SLBP2 PE=2 SV=1 |
| TRINITY_sp| Palmitoyl-monogalac | Homo sapiens ADS3 | OS=Homo sapiens GN=ADS3 PE=1 SV=2 |
| TRINITY_sp| Multidrug resistance-associated protein 4 | Homo sapiens ABCC4 | OS=Homo sapiens GN=ABCC4 PE=1 SV=3 |
| TRINITY_sp| Lactation elevated protein 1 homolog B | Danio rerio lace1b | OS=Danio rerio GN=lace1b PE=2 SV=1 |
| TRINITY_sp| Palmitoyl-monogalac | Homo sapiens ADS3 | OS=Homo sapiens GN=ADS3 PE=1 SV=2 |
| TRINITY_sp| Multidrug resistance-associated protein 4 | Homo sapiens ABCC4 | OS=Homo sapiens GN=ABCC4 PE=1 SV=3 |
| TRINITY_sp| Lactation elevated protein 1 homolog B | Danio rerio lace1b | OS=Danio rerio GN=lace1b PE=2 SV=1 |
| Accession       | Gene Information                                      | FPKM | Pearson   |
|-----------------|-------------------------------------------------------|------|-----------|
| TRINITY_sp|tRNA (guanine-N(7))-methyltransferase OS=Yarrowia lipolytica (strain CLIB 122 / E 150) GN=TRM8 PE=3 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Cycloeucalenol cycloisomerase OS=Arabidopsis thaliana GN=CPI1 PE=2 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|ERI1 exoribonuclease 3 OS=Bos taurus GN=ERI3 PE=2 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Mediator of RNA polymer II transcription subunit 10 OS=Xenopus tropicalis GN=med10 PE=2 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|E3 ubiquitin-protein ligase RNF13 OS=Mus musculus GN=Rnf13 PE=1 SV=2 | 46.20 | 0.00 |
| TRINITY_sp|Cyclin-P3-1 OS=Oryza sativa subsp. japonica GN=CYCP3-1 PE=3 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Hormone-sensitive lipase OS=Sus scrofa GN=LIPE PE=2 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|WW domain-containing oxidoreductase OS=Drosophila melanogaster GN=Wwox PE=2 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|E3 ubiquitin-protein ligase HACE1 OS=Gallus gallus GN=HACE1 PE=2 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Centromere protein V OS=Homo sapiens GN=CENPV PE=1 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Ras-related protein Rab-2-A OS=Zea mays GN=RAB2A PE=2 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Hormone-sensitive lipase OS=Sus scrofa GN=LIPE PE=2 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|WW domain-containing oxidoreductase OS=Drosophila melanogaster GN=Wwox PE=2 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|E3 ubiquitin-protein ligase HACE1 OS=Gallus gallus GN=HACE1 PE=2 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Centromere protein V OS=Homo sapiens GN=CENPV PE=1 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Ras-related protein Rab-1A OS=Canis lupus familiaris GN=RAB1A PE=1 SV=3 | 46.20 | 0.00 |
| TRINITY_sp|Copine-5 OS=Mus musculus GN=Cpne5 PE=1 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Serine/threonine-protein kinase ppk15 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ppk15 PE=1 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Countin-1 OS=Dictyostelium discoideum GN=ctnA PE=1 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Probable serine/threonine-protein kinase vps15 OS=Dictyostelium discoideum GN=vps15 PE=3 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|ATP-dependent bile acid permease OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YBT1 PE=1 SV=2 | 46.20 | 0.00 |
| TRINITY_sp|1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic OS=Oryza sativa subsp. japonica GN=DXR PE=2 SV=2 | 46.20 | 0.00 |
| TRINITY_sp|Myosin ID heavy chain OS=Dictyostelium discoideum GN=myoD PE=1 SV=2 | 46.20 | 0.00 |
| TRINITY_sp|Transcriptional activator Myb OS=Bos taurus GN=MYB PE=2 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Cyclin-U4-1 OS=Arabidopsis thaliana GN=CYCU4-1 PE=1 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|RAC family serine/threonine-protein kinase homolog OS=Dictyostelium discoideum GN=pkbA PE=1 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|AP-1 complex subunit mu OS=Dictyostelium discoideum GN=apm1 PE=1 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Diphthamide biosynthesis protein 1 OS=Dictyostelium discoideum GN=dph1 PE=3 SV=1 | 46.20 | 0.00 |
| TRINITY_sp|Bifunctional phosphatase IMPL2, chloroplastic OS=Arabidopsis thaliana GN=HISN7 PE=1 SV=1 | 46.20 | 0.00 |
TRINITY_sp|P93W1At5g193:Rhodanese-like/PpiC 46.10 0.00
TRINITY_sp|Q9VUCG8745 Alanine--glyoxylate 46.10 0.00
TRINITY_sp|D9R4hflX GTPase HflX OS=Clos 46.10 0.00
TRINITY_sp|Q9S1PI4KG7 Phosphatidylinosito 46.10 0.00
TRINITY_sp|A3EWIREV1 DNA repair protein 46.10 0.00
TRINITY_sp|Q9COCDNAH6 Dynein heavy chain 46.10 0.00
TRINITY_sp|Q149Gsp2 Eukaryotic peptide 46.10 0.00
TRINITY_sp|C0LG1RR-LRK Probable leucine-ri 46.10 0.00
TRINITY_sp|Q9FES1RT1 NAD-dependent prote 46.00 0.00
TRINITY_sp|Q9UFTS3 Ribosome biogenesis 46.00 0.00
TRINITY_sp|Q8LGBFX8 Probable glutathion 46.00 0.00
TRINITY_sp|Q9LINC4LIU4 NifU-like protein 4 46.00 0.00
TRINITY_sp|Q264PAPR1 Poly [ADP-ribose] p 46.00 0.00
TRINITY_sp|Q9M8HD3PTPB Dual specificity pr 46.00 0.00
TRINITY_sp|P425EPD15 Epidermal growth fa 46.00 0.00
TRINITY_sp|Q9ROArpcla Actin-related prote 46.00 0.00
TRINITY_sp|A6O4dnaJ Chaperone protein D 46.00 0.00
TRINITY_sp|A6QLNERCC2 TFIIH basal transcrr 46.00 0.00
TRINITY_sp|Q5E9IEIF2S2 Eukaryotic translat 46.00 0.00
TRINITY_sp|0075:ycodF Uncharacterized oxi 46.00 0.00
TRINITY_sp|Q7XYCnpA Copine-A OS=Dictyos 46.00 0.00
TRINITY_sp|Q9M8EDJID Protein DJ-1 homolo 46.00 0.00
TRINITY_sp|Q7KWdsof1 DDB1- and CUL4-asso 46.00 0.00
TRINITY_sp|A819ECFAP45 Cilia- and flagella 46.00 0.00
TRINITY_sp|Q112(PARP2 Poly [ADP-ribose] p 46.00 0.00
TRINITY_sp|Q133PPIL2 Peptidyl-prolyl cis 46.00 0.00
TRINITY_sp|F775ycfcG Disulfide-bond oxid 46.00 0.00
TRINITY_sp|Q86VZGRF1 Protein ZGRF1 OS=Ho 46.00 0.00
TRINITY_sp|Q9NWRRM28 RNA-binding protein 46.00 0.00
TRINITY_sp|Q1RMDCUNID5 DCN1-like protein 5 46.00 0.00
TRINITY_sp|Q55Hicmt-1 Protein-S-isoprenyl 46.00 0.00
TRINITY_sp|P285( Calcium-dependent p 46.00 0.00
TRINITY_sp|Q6X5WRI1 Ethylene-responsive 46.00 0.00
TRINITY_sp|Q993T3Y3B-G Transposon Ty3-G Ga 46.00 0.00
TRINITY_sp|Q9EQHsd17b11Estradiol 17-beta-d 46.00 0.00
TRINITY_sp|Q8CC7Uba6 Ubiquitin-like modi 46.00 0.00
TRINITY_sp|F4IAAtlg0591ATPase family AAA d 46.00 0.00
TRINITY_sp|Q6M9pc1998 Uncharacterized RNA 46.00 0.00
TRINITY_sp|O227CB5LP Cytochrome B5-like 46.00 0.00
TRINITY_sp|Q99MBbs2 Bardet-Biedi syndro 46.00 0.00
TRINITY_sp|Q9LWAt3g610 Protein-ribulosamin 46.00 0.00
TRINITY_sp|O810NRPB5A DNA-directed RNA po 46.00 0.00
TRINITY_sp|Q9Z3Dynlt1 Dynein light chain 46.00 0.00
TRINITY_sp|F4K1ATXR7 Histone-lysine N-me 46.00 0.00
TRINITY_sp|P743:s111541 Apocarotenoid-15,15 46.00 0.00
TRINITY_sp|Q9C5TIF3H1 Eukaryotic translat 46.00 0.00
TRINITY_sp|P281pkgB Protein kinase 2 OS 46.00 0.00
TRINITY_sp|Q567Ydph1 Diphthamide biosynt 46.00 0.00
TRINITY_sp|Q9NDom Helicase domino OS= 46.00 0.00
TRINITY_sp|P10Y-Retrovirus-related 46.00 0.00
TRINITY_sp|P526Upp1 Uridine phosphoryla 46.00 0.00
TRINITY_sp|Q542srpra Signal recognition 46.00 0.00
TRINITY_sp|Q54Chiba Probable 3-hydroxyli 46.00 0.00
TRINITY_sp|Q94CERER4 Protein RETICULATA- 46.00 0.00
TRINITY_sp|Q100SPAClF5.Putative oxidoreduc 46.00 0.00
TRINITY_sp|Q8RVIDEK1 Calpain-type cystei 46.00 0.00
| Accession | Description                                      | E-value | Score |
|-----------|--------------------------------------------------|---------|-------|
| TRINITY_sp| Leukocyte receptor                                | 46.00   | 0.00  |
| TRINITY_sp| Dephospho-CoA kinase                              | 46.00   | 0.00  |
| TRINITY_sp| Dynamin-related protein                           | 46.00   | 0.00  |
| TRINITY_sp| Probable U3 small n protein                       | 46.00   | 0.00  |
| TRINITY_sp| Tether containing U protein                       | 46.00   | 0.00  |
| TRINITY_sp| Transcription initiation protein                   | 46.00   | 0.00  |
| TRINITY_sp| Thioredoxin-like protein                          | 46.00   | 0.00  |
| TRINITY_sp| Cysteine proteinase                               | 46.00   | 0.00  |
| TRINITY_sp| Methylated-DNA-protein-cysteine methyltransfer    | 46.00   | 0.00  |
| TRINITY_sp| ADP-ribosylation fa                               | 46.00   | 0.00  |
| TRINITY_sp| Exosome complex com                               | 46.00   | 0.00  |
| TRINITY_sp| Serine/threonine-pr                               | 46.00   | 0.00  |
| TRINITY_sp| U2 small nuclear rib  |                           | 46.00   | 0.00  |
| TRINITY_sp| Nicotinamide/nicoti                               | 45.90   | 0.00  |
| TRINITY_sp| Protein kinase 2 OS                               | 45.90   | 0.00  |
| TRINITY_sp| Mitochondrial substrate                           | 45.90   | 0.00  |
| TRINITY_sp| Protein-methionine                                | 45.90   | 0.00  |
| TRINITY_sp| 6-phosphofructo-2-k                                | 45.90   | 0.00  |
| TRINITY_sp| ATP-dependent RNA h                               | 45.90   | 0.00  |
| TRINITY_sp| Activating signal c                               | 45.90   | 0.00  |
| TRINITY_sp| Flavohemoprotein OS                               | 45.90   | 0.00  |
| TRINITY_sp| Nucleoporin seh1 OS                               | 45.90   | 0.00  |
| TRINITY_sp| Actin cytoskeleton--                               | 45.90   | 0.00  |
| TRINITY_sp| 6-phosphofructo-2-k                               | 45.90   | 0.00  |
| TRINITY_sp| DnaJ homolog subfam                               | 45.90   | 0.00  |
| TRINITY_sp| DnaJ homolog subfam                               | 45.90   | 0.00  |
| TRINITY_sp| Xanthine dehydrogen                              | 45.90   | 0.00  |
| TRINITY_sp| Probable serine/thr                               | 45.90   | 0.00  |
| TRINITY_sp| Folate synthesis bi                              | 45.90   | 0.00  |
| TRINITY_sp| ABC transporter H f                              | 45.90   | 0.00  |
| TRINITY_sp| Cytochrome c oxidas                               | 45.90   | 0.00  |
| TRINITY_sp| Cilia- and flagella                               | 45.90   | 0.00  |
| TRINITY_sp| Sulfate-binding pro                               | 45.90   | 0.00  |
| TRINITY_sp| Mitogen-activated p                               | 45.90   | 0.00  |
| TRINITY_sp| Rac-like GTP-bindin                               | 45.90   | 0.00  |
| TRINITY_sp| Methylated-DNA--                                 | 45.90   | 0.00  |
| TRINITY_sp| Chaperone protein D                               | 45.90   | 0.00  |
| TRINITY_sp| Lon protease homolo                              | 45.90   | 0.00  |
| TRINITY_sp| Chaperone protein d                               | 45.90   | 0.00  |
| TRINITY_sp| Ubiquitin-60S ribos                               | 45.90   | 0.00  |
| TRINITY_sp| Cilia- and flagella                               | 45.90   | 0.00  |
| TRINITY_sp| RING finger protein                               | 45.90   | 0.00  |
| TRINITY_sp| Protein GrpE OS=Oli                               | 45.90   | 0.00  |
| TRINITY_sp| Uncharacterized pro                               | 45.90   | 0.00  |
| TRINITY_sp| Putative NADP-depen                               | 45.90   | 0.00  |
| TRINITY_sp| Serine/threonine-pr                               | 45.90   | 0.00  |
| TRINITY_sp| 3OS ribosomal prote                               | 45.90   | 0.00  |
| TRINITY_sp| Protein raptor homo                               | 45.90   | 0.00  |
| TRINITY_sp| SNF1-related protei                              | 45.90   | 0.00  |
| TRINITY_sp| Signal recognition                               | 45.90   | 0.00  |
| TRINITY_sp| Superoxide dismutas                              | 45.90   | 0.00  |
| TRINITY_sp| Mitochondrial dicar                               | 45.90   | 0.00  |
| TRINITY_sp| Transposon Ty3-G Ga                               | 45.90   | 0.00  |
| TRINITY_sp| Bifunctional monoth                              | 45.90   | 0.00  |
| TRINITY_sp| Histone-lysine N-me                               | 45.90   | 0.00  |
| TRINITY_sp| Protein OS=                                       | 45.90   | 0.00  |
| Gene ID          | Description                                      | Score | Identity |
|-----------------|--------------------------------------------------|-------|----------|
| TRINITY_sp|P406|MLH1 | DNA mismatch repair | 45.90 | 0.00 |
| TRINITY_sp|P410|cut3 | Structural maintena | 45.90 | 0.00 |
| TRINITY_sp|Q294|ATP6V0A1V-type proton ATPas | 45.90 | 0.00 |
| TRINITY_sp|O154|ABCC4 | Multidrug resistance | 45.90 | 0.00 |
| TRINITY_sp|O487|SMU2 | Suppressor of mec-8 | 45.90 | 0.00 |
| TRINITY_sp|P227|Guc1yb2 | Guanylate cyclase s | 45.90 | 0.00 |
| TRINITY_sp|Q993|TY3B-G | Transposon Ty3-G Ga | 45.90 | 0.00 |
| TRINITY_sp|Q55|fam45 | Protein FAM45 homolog | 45.90 | 0.00 |
| TRINITY_sp|O430|ータ | Kinesin heavy chain | 45.90 | 0.00 |
| TRINITY_sp|A7G|fo1D | Bifunctional protein | 45.90 | 0.00 |
| TRINITY_sp|Q287|PP2R4 | Serine/threonine-pr | 45.90 | 0.00 |
| TRINITY_sp|O607|EIF1B | Eukaryotic translat | 45.90 | 0.00 |
| TRINITY_sp|P710|faBD | Malonyl Co-A-acyl ca | 45.80 | 0.00 |
| TRINITY_sp|Q323|ybiA | N-glycosidase YbiA | 45.80 | 0.00 |
| TRINITY_sp|P502|CRIP1 | Cysteine-rich prote | 45.80 | 0.00 |
| TRINITY_sp|Q3UDE|tilll2 | Tubulin--tyrosine l | 45.80 | 0.00 |
| TRINITY_sp|O955|MCP2 | Mitochondrial pyruv | 45.80 | 0.00 |
| TRINITY_sp|O149|GAK | Cyclin-G-associated | 45.80 | 0.00 |
| TRINITY_sp|Q8L9|RPL21M | 50S ribosomal prote | 45.80 | 0.00 |
| TRINITY_sp|Q6Y1|HACD2 | Very-long-chain (3R | 45.80 | 0.00 |
| TRINITY_sp|Q9XW|acdh-11 | Acyl-CoA dehydrogen | 45.80 | 0.00 |
| TRINITY_sp|A0KK|rlmI | Ribosomal RNA large | 45.80 | 0.00 |
| TRINITY_sp|Q5F3|PCMT1 | Protein-L-isosaprt | 45.80 | 0.00 |
| TRINITY_sp|Q9FF|RPL13D | 60S ribosomal prote | 45.80 | 0.00 |
| TRINITY_sp|P139|ータ | G2/mitotic-specific | 45.80 | 0.00 |
| TRINITY_sp|A7TS|TRM13 | tRNA:m(4)X modifica | 45.80 | 0.00 |
| TRINITY_sp|P147|CRYL1 | Lambda-crystallin O | 45.80 | 0.00 |
| TRINITY_sp|Q9P2|DNHA1 | Dynein heavy chain | 45.80 | 0.00 |
| TRINITY_sp|P057|ータ | DNA endonuclease I- | 45.80 | 0.00 |
| TRINITY_sp|B5F2|ENY2 | Transcription and m | 45.80 | 0.00 |
| TRINITY_sp|Q55|pyd1 | Dihydropyrimidine d | 45.80 | 0.00 |
| TRINITY_sp|P546|pkbA | RAC family serine/t | 45.80 | 0.00 |
| TRINITY_sp|Q9F7|rpa2 | Probable RNA-direct | 45.80 | 0.00 |
| TRINITY_sp|Q4R5|NOB1 | RNA-binding protein | 45.80 | 0.00 |
| TRINITY_sp|Q7XK|BGLU12 | Beta-glucosidase 12 | 45.80 | 0.00 |
| TRINITY_sp|Q918|aurka-b | Aurora kinase A-B O | 45.80 | 0.00 |
| TRINITY_sp|P004|FAH | Phenylalanine-4-hyd | 45.80 | 0.00 |
| TRINITY_sp|Q9UK|PARP4 | Poly [ADP-ribose] p | 45.80 | 0.00 |
| TRINITY_sp|O946|noq1 | Probable nucleolar | 45.80 | 0.00 |
| TRINITY_sp|P0C8|CCR1P | Probable serine/thr | 45.80 | 0.00 |
| TRINITY_sp|Q944|dymA | Dynamin-A OS=Dictyo | 45.80 | 0.00 |
| TRINITY_sp|Q9MB|FKBP | 6-phosphofructose-2-k | 45.80 | 0.00 |
| TRINITY_sp|C6H1|UTP25 | U3 small nucleolar | 45.80 | 0.00 |
| TRINITY_sp|Q9ZR|RH28 | DEAD-box ATP-depend | 45.80 | 0.00 |
| TRINITY_sp|Q929|CDS1 | Phosphatidate cytid | 45.80 | 0.00 |
| TRINITY_sp|Q8TC|RDH11 | Retinol dehydrogena | 45.80 | 0.00 |
| TRINITY_sp|Q99M|Pecr | Peroxisomal trans-2 | 45.80 | 0.00 |
| TRINITY_sp|Q9NG|kif1 | Kinesin-related pro | 45.80 | 0.00 |
| TRINITY_sp|P585|egl | Endoglucanase OS=Ra | 45.80 | 0.00 |
| TRINITY_sp|B3E5|hldE | Bifunctional protei | 45.80 | 0.00 |
| TRINITY_sp|Q993|TY3B-G | Transposon Ty3-G Ga | 45.80 | 0.00 |
| TRINITY_sp|P41Y|UGP3 | UTP--glucose-1-phos | 45.80 | 0.00 |
| TRINITY_sp|Q5G4|vps45 | Vacuolar protein so | 45.80 | 0.00 |
| TRINITY_sp|Q5AT|apdG | Acyl-CoA dehydrogen | 45.80 | 0.00 |
| TRINITY_sp|Q8MV|gbpC | Cyclic GMP-binding | 45.80 | 0.00 |
| TRINITY_sp|Q993|TY3B-G | Transposon Ty3-G Ga | 45.80 | 0.00 |
Protein DJ-1 homolog B OS=Arabidopsis thaliana GN=DJ1B PE=1 SV=1
Periplasmic trehalase OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=treA PE=3 SV=1
60S ribosomal protein L38 OS=Tetrahymena thermophila (strain SB210) GN=RPL38 PE=1 SV=2
Pyruvate kinase OS=Eimeria tenella GN=PYK PE=2 SV=1
Respiratory supercomplex factor 1, mitochondrial OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) GN=rcf1 PE=3 SV=2
Peptidyl-prolyl cis-trans isomerase FKBP65 OS=Arabidopsis thaliana GN=FKBP65 PE=1 SV=1
Probable E3 ubiquitin-protein ligase HERC2 OS=Drosophila melanogaster GN=HERC2 PE=1 SV=3
Probable serine/threonine-protein kinase gdt9 OS=Dictyostelium discoideum GN=gdt9 PE=2 SV=2
Kinesin-like protein KIN-7L OS=Oryza sativa subsp. japonica GN=KIN7L PE=2 SV=1
Phosphoserine phosphatase OS=Archaeoglobus fulgidus (strain ATCC 49558 / VC-16 / DSM 4304 / JCM 9628 / NBRC 100126) GN=AF_2138 PE=3 SV=1
22.0 kDa heat shock protein OS=Arabidopsis thaliana GN=HSP22.0 PE=2 SV=1
C2 domain-containing protein 5 OS=Homo sapiens GN=C2CD5 PE=1 SV=1
Pre-rRNA-processing protein ESF2 OS=Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) GN=ESF2 PE=3 SV=2
Probable serine/threonine-protein kinase kinX OS=Dictyostelium discoideum GN=kinX PE=3 SV=2
Endoglucanase E-4 OS=Thermobifida fusca GN=celD PE=1 SV=2
Coiled-coil domain-containing protein 61 OS=Rattus norvegicus GN=Ccdc61 PE=1 SV=1
Transposon Ty3-G Gag-Pol polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TY3B-G PE=1 SV=3
Ubiquitin-conjugating enzyme E2 8 OS=Arabidopsis thaliana GN=UBC8 PE=1 SV=1
Atypical kinase COQ8B, mitochondrial OS=Danio rerio GN=coq8b PE=3 SV=2
Ras-related C3 botulinum toxin substrate 1 OS=Bos taurus GN=RAC1 PE=1 SV=1
Mitochondrial respiratory chain complexes assembly protein rca1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=yta12 PE=3 SV=1
Fe-S cluster assembly factor HCF101, chloroplastic OS=Oryza sativa subsp. japonica GN=HCF101 PE=3 SV=3
Probable prolyl 4-hydroxylase 7 OS=Arabidopsis thaliana GN=P4H7 PE=2 SV=1
TRINITY_sp|Q9MAHDJ1B: Protein DJ-1 homolog B
TRINITY_sp|Q8L9PF4H7: Probable prolyl 4-h
TRINITY_sp|Q0JJHCFCP101: Fe-S cluster assembly
TRINITY_sp|P2627ce1D: Endoglucanase E-4 O
TRINITY_sp|Q9FJISMC4: Structural maintenance
TRINITY_sp|Q9HG0yta12: Mitochondrial respiration
TRINITY_sp|Q54HIcsn2: COP9 signalosome component
TRINITY_sp|O4400PKY: Pyruvate kinase OS=
TRINITY_sp|Q9931TY3B-G: Transposon Ty3-G Ga
TRINITY_sp|Q22S8RPL38: 60S ribosomal protein
TRINITY_sp|P9255AtMg008: Uncharacterized mitochondrial
TRINITY_sp|P3511UBC8: Ubiquitin-conjugating
TRINITY_sp|Q059myb11: Myb-related protein
TRINITY_sp|Q0731PIGF: Phosphatidylinositol
TRINITY_sp|Q9VRHERC2: Probable E3 ubiquitin
TRINITY_sp|Q1266YPK9: Vacuolar cation-transporter
TRINITY_sp|Q6CGIYAI0A1: Acyl-protein thioesterase
TRINITY_sp|Q32CICANAPC11: Anaphase-promoting
TRINITY_sp|A8AF1treA: Periplasmic trehalase
TRINITY_sp|Q6Z8O8s02g02: Probable protein phosphatase
TRINITY_sp|P5361ARC1: Coatamer subunit de
TRINITY_sp|O6018PBC19F: Uncharacterized protein
TRINITY_sp|Q72Vbc11: Mitochondrial chaperone
TRINITY_sp|O486ERER1A: Protein RER1A OS=Ar
TRINITY_sp|Q744rclf: Respiratory supercomplex
TRINITY_sp|Q2391kinX: Probable serine/threonine kinase
TRINITY_sp|Q7RA3CPK3: Calcium-dependent phosphatase
TRINITY_sp|Q9VRHERC2: Probable E3 ubiquitin
TRINITY_sp|Q9FMPI4KB1: Phosphatidylinositol
TRINITY_sp|P6299RAC1: Ras-related C3 botulinum
TRINITY_sp|Q2366RABC1: Ras-related protein
TRINITY_sp|Q5VJigdt9: Probable serine/threonine kinase
TRINITY_sp|Q8LCUAt3g457: Probable trans-2-enoyl-CoA reductase
TRINITY_sp|Q547IDDB_G02: Probable dual specificity protein
TRINITY_sp|Q2GZCESP2: Pre-rRNA-processing protein
TRINITY_sp|Q4257UBC7: Ubiquitin-conjugating enzyme
TRINITY_sp|Q2R2IKIN7L: Kinesin-like protein
TRINITY_sp|Q9H4RBK5: Ribokinase OS=Homo sapiens
TRINITY_sp|Q3888HSP22.0: 22.0 kDa heat shock protein
TRINITY_sp|Q66FC2CD5: C2 domain-containing protein
TRINITY_sp|Q281AF_2138: Phosphoserine phosphatase
TRINITY_sp|Q9SBAP4M: AP-4 complex subunit
TRINITY_sp|P2945trkB: Thioredoxin-2 (Fragmen)
TRINITY_sp|P5190Nek1: Serine/threonine-protein kinase
TRINITY_sp|Q9UT5TSPAC343: Uncharacterized WD domain-containing protein
TRINITY_sp|Q941PFMS1: DNA mismatch repair protein
TRINITY_sp|A3QJtcqq8b: Atypical kinase COQ
TRINITY_sp|P5333RNH70: DNA exonuclease 1 O
TRINITY_sp|Q9WX3rbasA1: Ribose import ATPase
TRINITY_sp|Q9LNP4H3: Probable prolyl 4-hydroxylase
TRINITY_sp|P5480hgsA: Hydroxymethylglutaryl-CoA redox protein
TRINITY_sp|Q243TOP2: DNA topoisomerase II
TRINITY_sp|A0JPC1ced61: Coiled-coil domain-containing protein
TRINITY_sp|Q0313Epha2: Ephrin type-A receptor
TRINITY_sp|Q6GMPprpf18: Pre-mRNA-splicing factor
TRINITY_sp|Q9FJIFKBP65: Peptidyl-prolyl cis-trans isomerase
| Gene ID           | Description                                      | ORF Name | ORF | 100% Identity | Target ORF | Accession | strand | Location | Score |
|-------------------|--------------------------------------------------|----------|-----|---------------|------------|-----------|--------|----------|-------|
| TRINITY_sp|Q0181PFKP  | ATP-dependent 6-pho | TRINITY_sp|Q9LTNHD1  | Sodium/proton antip | TRINITY_sp|Q52LS|STRAP | Serine-threonine ki | TRINITY_sp|P230|--  | Dynein beta chain, | 45.40 | 0.00 |
| TRINITY_sp|F4JJNDB3   | External alternativ | TRINITY_sp|Q54DIDDB_GO2| Probable serine/thr | TRINITY_sp|P546|cprD | Cysteine proteinase | TRINITY_sp|Q9FWHAC12 | Histone acetyltrans | 45.40 | 0.00 |
| TRINITY_sp|A0BD_Rp17 | 60S ribosomal prote | TRINITY_sp|Q0IQECML3 | Calmodulin-like pro | TRINITY_sp|Q000|tpsA | Alpha, alpha-trehalo | TRINITY_sp|Q6NRHchmp3 | Charged multivesicu | 45.30 | 0.00 |
| TRINITY_sp|Q75KaspS1  | Aspartate--tRNA lig | TRINITY_sp|Q9HCICPNE5 | Copine-5 OS=Homo sa | TRINITY_sp|O654|XCP1 | Cysteine protease X | 45.30 | 0.00 |
| TRINITY_sp|Q84LAAARE | Acylamino-acid-rele | TRINITY_sp|Q920|--  | Nuclear factor 7, b | TRINITY_sp|P14I|AAC4 | AAC-rich mRNA clone | 45.30 | 0.00 |
| TRINITY_sp|Q58DI SDC2 | Syndecan-2 OS=Bos t | TRINITY_sp|Q9L2BIG2 | Brefeldin A-inhibit | TRINITY_sp|Q9ZRICAD | Probable mannitol d | 45.30 | 0.00 |
| TRINITY_sp|Q4VBmetap1d | Methionine aminopep | TRINITY_sp|Q9S5SMC2-1 | Structural maintena | TRINITY_sp|A7Z0|PPI5K1 | Inositol hexakispho | 45.30 | 0.00 |
| TRINITY_sp|O822At2g239 | Probable small nucl | TRINITY_sp|Q54QdhK6 | Hybrid signal trans | TRINITY_sp|Q9ER|Cars | Cysteine--tRNA liga | 45.30 | 0.00 |
| TRINITY_sp|A8IR|CFAP53 | Cilia- and flagella | TRINITY_sp|P732|s111917 | Oxygen-independent | 45.30 | 0.00 |
| TRINITY_sp|Q5UNWIMI_R7 | Uncharacterized pro | TRINITY_sp|Q55DFcSA | Fatty acyl-CoA synt | 45.30 | 0.00 |
| TRINITY_sp|O493COQ3 | Ubiquinone biosynth | TRINITY_sp|P118|Aldh3a1 | Aldehyde dehydrogen | 45.30 | 0.00 |
| TRINITY_sp|Q92R|DSPTP1 | Dual specificity pr | TRINITY_sp|Q435ATP8B1 | Phospholipid-transp | 45.30 | 0.00 |
| TRINITY_sp|O040|Atig089 | Phosphoglycerate mu | TRINITY_sp|Q9US1Gtp-bp | Signal recognition | 45.30 | 0.00 |
| TRINITY_sp|Q627Ddx46 | Probable ATP-depend | TRINITY_sp|Q6GQ1Cd14a | Dual specificity pr | 45.30 | 0.00 |
| TRINITY_sp|Q8IUCCBW2 | COBW domain-contain | TRINITY_sp|F087Eip71CD | Peptide methionine | 45.30 | 0.00 |
| TRINITY_sp|Q9M1|CPK23 | Calcium-dependent p | TRINITY_sp|Q9LDARRP45A | Exosome complex com | 45.30 | 0.00 |
| TRINITY_sp|Q67PIrnc | Ribonuclease 3 OS=Symbiobacterium thermophilum (strain T / IAM 14863) GN=rnc PE=3 SV=1 |
| TRINITY_sp|Q96HTTMEM19 | Transmembrane protein 2 OS=Mus musculus GN=upl6 PE=1 SV=1 |
| TRINITY_sp|P9301PHOT2 | Phototropin-2 OS=Arabidopsis thaliana GN=fcpA PE=3 SV=1 |
| TRINITY_sp|P5255mybl2 | Myb-related protein 2 OS=Rattus norvegicus GN=fcpA PE=1 SV=1 |
| TRINITY_sp|Q0DW10s02g07 | DEAD-box ATP-depend |
| TRINITY_sp|Q9NJ3CPK3 | Calcium-dependent protein |  |
| TRINITY_sp|P8088AN1 | Ananain OS=Ananas comosus GN=AN1 PE=1 SV=2 |
| TRINITY_sp|Q8TVpth | Peptidyl-tRNA hydrolase OS=Methanopyrus kandleri (strain AV19 / DSM 6324 / JCM 9639 / NBRC 100938) GN=pth PE=1 SV=1 |
| TRINITY_sp|Q8GWFGPL2 | Phosphoglycolate phosphatase OS=Mus musculus GN=PGLP2 PE=1 SV=1 |
| TRINITY_sp|Q94CINAR1 | Protein NAR1 OS=Arabidopsis thaliana GN=NAR1 PE=1 SV=1 |
| TRINITY_sp|Q9NT3SIRT3 | NAD-dependent protein 2 OS=Mus musculus GN=NAR1 PE=1 SV=1 |
| TRINITY_sp|Q54TmdrkD | Probable serine/threonine-protein kinase OS=Aspergillus nidulans GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q54E:DDB_G02 | Probable protein kinase OS=Aspergillus nidulans GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q91YRab29 | Ras-related protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q4L78SH1032 | Uncharacterized protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q9CI1cat-1 | Catalase-1 OS=Neurospora crassa GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q131:PFAK2 | Serine/threonine-protein kinase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|P137(fs)1h | Homeotic protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|P110:NIA2 | Nitrate reductase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q5P4PabcC8 | ABC transporter C OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q6DCIscl30a9 | Zinc transporter OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|P2181RYR1 | Ryanodine receptor OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q093:ODA7 | Leucine-rich repeat protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|P519:NEK3 | Serine/threonine-protein kinase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q9C9FAAtg781 | Probable mitochondrial protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q6L1:CYP57 | Peptidyl-prolyl cis OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q956:ASMTL | N-acetylserotonin O-methyltransferase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|P459:USP5 | Ubiquitin carboxyl-terminal esterase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q111:ofd1 | Prolyl 3,4-dihydroxylase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q8C20Kiaa019 | WASH complex subunit OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q5BJ3Carnmt1 | Carnosine N-methyltransferase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|P067:Ctsl | Cathepsin L protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q8H0:ABCF3 | ABC transporter F OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|A2YFHHK1 | Probable histidine phosphatase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|P0AD1yg1C | Putative acid--aminopeptidase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q6R5:RMA1H1 | E3 ubiquitin-protein ligase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q91WQrp9 | U3 small nucleolar protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q086:Sgstm1 | Sequestosome-1 OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q234:PPD1 | PsbP domain-containing protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q5BK5chmp3 | Charged multivesicular body protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|B2S9nder | GTPase Der OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q2JIImmmE | tRNA modification protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q9VV:Cyp312a1 | Probable cytochrome P450 OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|P423:CNB1 | Calcineurin subunit OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q55GIpakC | Serine/threonine-protein kinase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|A1L1Dnlz2 | DNL-type zinc finger protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q8RWUPL6 | E3 ubiquitin-protein ligase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|P844:ILSS | Lanosterol synthase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q2LAFASHH2 | Histone-lysine N-methyltransferase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q9XYIfcpA | Probable C-terminal protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q8HL:Atg069 | U2 small nuclear protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|A2YFHHK1 | Probable histidine phosphatase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|P043pol | Retrovirus-related protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|P319:SPS | Sucrose-phosphate synthase OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|P9WP:dapC | Probable N-succinyl protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| TRINITY_sp|Q7ZXImtmr4 | Myotubularin-related protein OS=Mus musculus GN=rpp9 PE=1 SV=1 |
| Accession | Description |
|-----------|-------------|
| TRINITY_sp| Altered inheritance |
| TRINITY_sp| NFX1-type zinc fing |
| TRINITY_sp| Lysosomal Pro-X car |
| TRINITY_sp| Mitochondrial subst |
| TRINITY_sp| Protein roadkill OS |
| TRINITY_sp| Tyrosine-protein ki |
| TRINITY_sp| OS=Plasmodi |
| TRINITY_sp| Glucose-6-phosphate |
| TRINITY_sp| Heme A synthase OS= |
| TRINITY_sp| CTD small phosphata |
| TRINITY_sp| Serine/threonine-pr |
| TRINITY_sp| cAMP-dependent prot |
| TRINITY_sp| Isochorismatase dom |
| TRINITY_sp| Probable beta-tubul |
| TRINITY_sp| Probable cation-tra |
| TRINITY_sp| Translation initiat |
| TRINITY_sp| Trans-2-enoyl-CoA r |
| TRINITY_sp| Probable serine/thr |
| TRINITY_sp| 50S ribosomal prote |
| TRINITY_sp| Signal-induced prol |
| TRINITY_sp| Twinfilin OS=Dictyo |
| TRINITY_sp| DnaJ homolog subfam |
| TRINITY_sp| Copper-transporting |
| TRINITY_sp| Acyl-CoA dehydrogen |
| TRINITY_sp| ATP synthase subuni |
| TRINITY_sp| Mannosyl-oligosacch |
| TRINITY_sp| Exonuclease 1 OS=Or |
| TRINITY_sp| Putative ubiquitin |
| TRINITY_sp| Putative acyl-CoA s |
| TRINITY_sp| Glucose-induced deg |
| TRINITY_sp| Metal transporter N |
| TRINITY_sp| ATP-dependent Clp p |
| TRINITY_sp| Protein RFT1 homolo |
| TRINITY_sp| Leishmanolysin-like |
| TRINITY_sp| Probable RNA methyl |
| TRINITY_sp| Myosin-J heavy chai |
| TRINITY_sp| Xylitol oxidase OS= |
| TRINITY_sp| Serine/threonine-pr |
| TRINITY_sp| Riboflavin kinase O |
| TRINITY_sp| Uricase-2 isozyme 2 |
| TRINITY_sp| Ubiquitin-like modi |
| TRINITY_sp| Alpha-ketoglutarate |
| TRINITY_sp| Probable protein ar |
| TRINITY_sp| Serine/arginine-ric |
| TRINITY_sp| CBL-interacting pro |
| TRINITY_sp| Phosphatidylinosito |
| TRINITY_sp| High mobility group |
| TRINITY_sp| Delta(3,5)-Delta(2, |
| TRINITY_sp| DNA topoisomerase 3 |
| TRINITY_sp| Fe(2+) transport pr |
| TRINITY_sp| Uncharacterized Nud |
| TRINITY_sp| Alkaline serine exo |
| TRINITY_sp| Serine/threonine-pr |
| Accession     | Description                                                                 | Similarity Score | E-value |
|--------------|------------------------------------------------------------------------------|------------------|---------|
| TRINITY_sp|Q492{RH29} | Putative DEAD-box A | 45.10 | 0.00 |
| TRINITY_sp|F1QC{rp2} | Protein XRP2 OS=Dan | 45.10 | 0.00 |
| TRINITY_sp|Q96MKCTD7 | BTB/POZ domain-cont | 45.10 | 0.00 |
| TRINITY_sp|Q8CCINemf | Nuclear export medi | 45.10 | 0.00 |
| TRINITY_sp|A4IIfsdad1 | Protein SDA1 homolo | 45.10 | 0.00 |
| TRINITY_sp|Q4VBlier3pl | Immediate early res | 45.10 | 0.00 |
| TRINITY_sp|D2Q{ftsH} | ATP-dependent zinc | 45.10 | 0.00 |
| TRINITY_sp|Q8SS{gefr} | Ras guanine nucleot | 45.10 | 0.00 |
| TRINITY_sp|P538{BOR1} | Boron transporter l | 45.10 | 0.00 |
| TRINITY_sp|P873{tma20} | Translation machine | 45.10 | 0.00 |
| TRINITY_sp|Q9HO{NUAK2} | NUAK family SNF1-li | 45.00 | 0.00 |
| TRINITY_sp|Q54I{piqm} | GPI mannosyltransfe | 45.00 | 0.00 |
| TRINITY_sp|Q54K{ta1B} | Talin-B OS=Dictyost | 45.00 | 0.00 |
| TRINITY_sp|Q9UN{CDC14A} | Dual specificity pr | 45.00 | 0.00 |
| TRINITY_sp|Q54K{ta1B} | Talin-B OS=Dictyost | 45.00 | 0.00 |
| TRINITY_sp|Q9WY{TUM_0508} | Uncharacterized pro | 45.00 | 0.00 |
| TRINITY_sp|Q94A{MKK1} | Mitogen-activated p | 45.00 | 0.00 |
| TRINITY_sp|P623{CPK1} | Calcium-dependent p | 45.00 | 0.00 |
| TRINITY_sp|Q6STTAP5 | Transcription initi | 45.00 | 0.00 |
| TRINITY_sp|Q9XY{noxA} | Superoxide-generati | 45.00 | 0.00 |
| TRINITY_sp|P178{DDX5} | Probable ATP-depend | 45.00 | 0.00 |
| TRINITY_sp|Q9FW{ABC11} | ABC transporter B f | 45.00 | 0.00 |
| TRINITY_sp|Q123{RIB2} | Bifunctional protei | 45.00 | 0.00 |
| TRINITY_sp|O273{dnaJ} | Chaperone protein D | 45.00 | 0.00 |
| TRINITY_sp|Q9LM{At1g137} | Probable 6-phosphog | 45.00 | 0.00 |
| TRINITY_sp|Q9LX{PPD6} | PsbP domain-contain | 45.00 | 0.00 |
| TRINITY_sp|Q9S9{VPS28-2} | Vacuolar protein so | 45.00 | 0.00 |
| TRINITY_sp|Q54P{4cl1} | Probable 4-coumarat | 45.00 | 0.00 |
| TRINITY_sp|F4J0{P4H6} | Probable prolyl 4-h | 45.00 | 0.00 |
| TRINITY_sp|Q8T1{fam91} | Protein FAM91 homol | 45.00 | 0.00 |
| TRINITY_sp|Q8VX{XEG113} | Arabinosyltransfera | 45.00 | 0.00 |
| TRINITY_sp|P160{gpaB} | Guanine nucleotide- | 45.00 | 0.00 |
| TRINITY_sp|Q8H0{ABC3} | ABC transporter F f | 45.00 | 0.00 |
| TRINITY_sp|P547{PSBS} | Photosystem II 22 k | 45.00 | 0.00 |
| TRINITY_sp|Q631{Dnah1} | Dynein heavy chain | 45.00 | 0.00 |
| TRINITY_sp|P109{RP1} | Retrovirus-related | 45.00 | 0.00 |
| TRINITY_sp|O627{TXNRD1} | Thioredoxin reducta | 45.00 | 0.00 |
| TRINITY_sp|Q5EA{MFAP1} | Microfibrillar-asso | 45.00 | 0.00 |
| TRINITY_sp|Q8K5{Dus11} | tRNA-dihydrouridine | 45.00 | 0.00 |
| TRINITY_sp|Q806{SKIP} | SNW/SKI-interacting | 45.00 | 0.00 |
| TRINITY_sp|Q54B{nfx1} | Transcriptional rep | 45.00 | 0.00 |
| TRINITY_sp|P546{pkbA} | RAC family serine/t | 45.00 | 0.00 |
| TRINITY_sp|Q9P6{pcl1} | Fe(2+)/Mn(2+) trans | 45.00 | 0.00 |
| TRINITY_sp|Q993{TY3B-G} | Transposon Ty3-G Ga | 45.00 | 0.00 |
| TRINITY_sp|Q417{PFE2} | Ferritin-2, chlorop | 45.00 | 0.00 |
| TRINITY_sp|Q9LYN{NADP-ME} | NADP-dependent mali | 45.00 | 0.00 |
| TRINITY_sp|A5PJ{HYKK} | Hydroxylsine kinas | 45.00 | 0.00 |
| TRINITY_sp|Q418{RP} | ATP synthase subunit | 45.00 | 0.00 |
| TRINITY_sp|Q9FT{ABCG27} | ABC transporter G f | 45.00 | 0.00 |
| TRINITY_sp|Q54S{dhdK} | Hybrid signal trans | 45.00 | 0.00 |
| TRINITY_sp|Q9Z3{TTop3b} | DNA topoisomerase 3 | 44.90 | 0.00 |
TRINITY_sp|O489|POLD1 DNA polymerase delta catalytic subunit 44.90 0.00
TRINITY_sp|O009|pme6 Nucleoside diphosphatase 44.90 0.00
TRINITY_sp|P4IVGRV2 DNAJ homolog subfamily D 44.90 0.00
TRINITY_sp|Q9MO|FDFX1 Adrenodoxin-like protein 44.90 0.00
TRINITY_sp|Q8V2|PIE2 Polycomb group protein 44.90 0.00
TRINITY_sp|Q541|abcC8 ABC transporter C family 44.90 0.00
TRINITY_sp|P0C8|CCR1 Probable serine/threonine-protein kinase 44.90 0.00
TRINITY_sp|Q636|Grk1 Rhodopsin kinase OS 44.90 0.00
TRINITY_sp|Q626|Ech1 Delta(3,5)-Delta(2,4) protein 44.90 0.00
TRINITY_sp|Q1RM|Trnau1ai tRNA selenocysteine 44.90 0.00
TRINITY_sp|A9KH|lon Lon protease OS=Clostridium perfringens 44.90 0.00
TRINITY_sp|P552|BRFP1 Peregrin OS=Homo sapiens 44.90 0.00
TRINITY_sp|O654|XCP1 Cysteine protease X 44.90 0.00
TRINITY_sp|Q7GI|FIM1 Filamin-1 OS=Arabidopsis thaliana 44.90 0.00
TRINITY_sp|P528|Tmcm165 Transmembrane protein 44.90 0.00
TRINITY_sp|Q8L7|TUN UDP-glycosyltransferase 44.90 0.00
TRINITY_sp|Q9WTI|Lypl2 Acyl-protein thioesterase 44.90 0.00
TRINITY_sp|Q72Y|dcaf13 DDB1- and CUL4-associated factor 44.90 0.00
TRINITY_sp|Q6AY|Recq1 ATP-dependent DNA helicase Q1 OS=Rattus norvegicus 44.90 0.00
TRINITY_sp|Q953|MANBA Beta-mannosidase OS=Arabidopsis thaliana 44.90 0.00
TRINITY_sp|Q9M2|IACa11 Putative calcium-tranductin 44.90 0.00
TRINITY_sp|Q947|ALG2 Alpha-1,3/1,6-mannosyltransferase 44.90 0.00
TRINITY_sp|Q9LJ|M3KE1 MAP3K epsilon protease 44.90 0.00
TRINITY_sp|Q96F|Trmt61a tRNA (adenosine-58)-N(1)-methyltransferase 44.90 0.00
TRINITY_sp|Q1QH|mical3a Protein-methionine adenylyltransferase 44.90 0.00
TRINITY_sp|Q54N|clp1 Protein CLP1 homolog 44.90 0.00
TRINITY_sp|Q947|MSH6 DNA mismatch repair protein MSH6 OS=Arabidopsis thaliana 44.90 0.00
TRINITY_sp|Q95C|glkA Probable serine/threonine-protein kinase 44.90 0.00
TRINITY_sp|Q9V5|Dcr1 Endoribonuclease Dc 44.90 0.00
TRINITY_sp|Q5AT|capdG Acyl-CoA dehydrogenase OS=Arabidopsis thaliana 44.90 0.00
TRINITY_sp|Q94P|cpnC Copine-C OS=Dictyostelium discoideum 44.90 0.00
TRINITY_sp|Q22Z|CK11 Histidine kinase CK1 44.90 0.00
TRINITY_sp|Q9LX|HIRA Protein HIRA OS=Araçari (Drosophila melanogaster) 44.90 0.00
TRINITY_sp|Q9P0|MARK1 Serine/threonine-protein kinase 44.90 0.00
TRINITY_sp|Q976|dyrk1 Probable serine/threonine-protein kinase 44.90 0.00
TRINITY_sp|Q9VX|Bap60 Brahma-associated protein 44.90 0.00
TRINITY_sp|P736|s11770 Uncharacterized protein OS=Arabidopsis thaliana 44.90 0.00
TRINITY_sp|Q8BW|Kdm4a Lysine-specific demethylase 44.90 0.00
TRINITY_sp|Q7TM|Narf1 Cytosolic Fe-S cluster protein OS=Arabidopsis thaliana 44.90 0.00
TRINITY_sp|Q94K|ELIP2 Early light-induced protein 44.90 0.00
TRINITY_sp|P043|pol Retrovirus-related protein 44.90 0.00
TRINITY_sp|Q6AX|Isq2012 Interferon-stimulated gene 44.90 0.00
TRINITY_sp|Q9M2|SPL15 Squamosa promoter-b-like protein 44.90 0.00
TRINITY_sp|P233|α- Polyubiquitin OS=Eucommia ulmoides 44.90 0.00
TRINITY_sp|Q9G6|ppk15 Serine/threonine-protein kinase OS=Arabidopsis thaliana 44.90 0.00
TRINITY_sp|Q9S3|Memb11 Membrane-protein OS=Arabidopsis thaliana 44.90 0.00
TRINITY_sp|Q8W0|DnaH7 Dynein heavy chain OS=Arabidopsis thaliana 44.90 0.00
TRINITY_sp|Q9LM|TP7 Probable alpha-helical coiled-coil protein 44.90 0.00
TRINITY_sp|Q744|swcl Cell wall integrity protein 44.90 0.00
TRINITY_sp|Q9SR|At3g0233 Probable tRNA (guanine-79) 44.90 0.00
TRINITY_sp|Q9ZG|pipK Arabinolide/10-deoxynarabinolide OS=Arabidopsis thaliana 44.90 0.00
TRINITY_sp|Q76M|ERD2 ER lumen protein-receptor protein OS=Arabidopsis thaliana 44.90 0.00
TRINITY_sp|Q9ZM|Tom3 Tobamovirus multiplex protein OS=Arabidopsis thaliana 44.90 0.00
TRINITY_sp|Q395|ODA2 Dynein gamma heavy chain 44.90 0.00
| Accession | Description | Score | E-value |
|-----------|-------------|-------|---------|
| TRINITY_sp| A4QNX | ctdsp12kCTD small phosphata | 44.90 | 0.00 |
| TRINITY_sp| P1201- | Cyclohexanone 1,2-m | 44.80 | 0.00 |
| TRINITY_sp| Q10GNEK1 | Serine/threonine-pr | 44.80 | 0.00 |
| TRINITY_sp| Q8R0P | Tric31 E3 ubiquitin-protei | 44.80 | 0.00 |
| TRINITY_sp| Q9SF\PHA2 | FHA domain-containi | 44.80 | 0.00 |
| TRINITY_sp| Q5G3phbA | Prohibitin-1, mitoc | 44.80 | 0.00 |
| TRINITY_sp| P341 | pkgC Protein kinase 3 OS | 44.80 | 0.00 |
| TRINITY_sp| Q5T1RING1 | E3 ubiquitin-protei | 44.80 | 0.00 |
| TRINITY_sp| A6QR\USP4 | Ubiquitin carboxyl- | 44.80 | 0.00 |
| TRINITY_sp| Q55d\qdt6 | Probable inactive s | 44.80 | 0.00 |
| TRINITY_sp| Q01JISPL7 | Squamosa promoter-b | 44.80 | 0.00 |
| TRINITY_sp| B8AJMRS2-I | Magnesium transport | 44.80 | 0.00 |
| TRINITY_sp| Q9XK\noxA | Superoxide-generati | 44.80 | 0.00 |
| TRINITY_sp| P295\- | Eukaryotic translat | 44.80 | 0.00 |
| TRINITY_sp| Q54P\4cl12 | Probable 4-coumarat | 44.80 | 0.00 |
| TRINITY_sp| Q8W2DXR | 1-deoxy-D-xylulose | 44.80 | 0.00 |
| TRINITY_sp| C0LG1LRR-RLK | Probable leucine-ri | 44.80 | 0.00 |
| TRINITY_sp| Q9NR-DDX21 | Nucleolar RNA helic | 44.80 | 0.00 |
| TRINITY_sp| O2301KAB1 | Probable voltage-ga | 44.80 | 0.00 |
| TRINITY_sp| Q6LDP|DMT105 | DNA (cytosine-5)-me | 44.80 | 0.00 |
| TRINITY_sp| Q7V6luppS | Isoprenyl transfera | 44.80 | 0.00 |
| TRINITY_sp| A7SNvlg2305\UPF0553 protein vlg | 44.80 | 0.00 |
| TRINITY_sp| Q99LCUsp16 | Ubiquitin carboxyl- | 44.80 | 0.00 |
| TRINITY_sp| Q9FM1ICMTA | Protein-S-isoprenyl | 44.80 | 0.00 |
| TRINITY_sp| F4KBIAAE17 | Probable acyl-activ | 44.80 | 0.00 |
| TRINITY_sp| Q54Kmvd | Diphosphomevalonate | 44.80 | 0.00 |
| TRINITY_sp| Q9SL\Os05g01! | Importin subunit al | 44.80 | 0.00 |
| TRINITY_sp| Q0VC\PQCL1 | PQ-loop repeat-cont | 44.80 | 0.00 |
| TRINITY_sp| Q94JWLM1 | LIM domain-containi | 44.80 | 0.00 |
| TRINITY_sp| Q8BBKFdhx | Pyruvate dehydrogen | 44.80 | 0.00 |
| TRINITY_sp| Q7XRVSL6 | Probable metal-nico | 44.80 | 0.00 |
| TRINITY_sp| Q9X3\topA | DNA topoisomerase 1 | 44.80 | 0.00 |
| TRINITY_sp| Q54Tu\drkD | Probable serine/thr | 44.80 | 0.00 |
| TRINITY_sp| Q6ZMWEML6 | Echinoderm microtub | 44.80 | 0.00 |
| TRINITY_sp| Q9SHRRP44A | Exosome complex exo | 44.80 | 0.00 |
| TRINITY_sp| Q9V9\CG30152 | MIF18 family protei | 44.80 | 0.00 |
| TRINITY_sp| O652\CYP28 | Peptidyl-prolyl cis | 44.80 | 0.00 |
| TRINITY_sp| Q0VC\TMEM65 | Transmembrane prote | 44.80 | 0.00 |
| TRINITY_sp| Q69V\Os06g05! | Probable protein ph | 44.80 | 0.00 |
| TRINITY_sp| P468\KLp1 | Kinesin-like protei | 44.80 | 0.00 |
| TRINITY_sp| Q81CCPK2 | Calcium-dependent p | 44.80 | 0.00 |
| TRINITY_sp| P412\Abca2 | ATP-binding cassett | 44.80 | 0.00 |
| TRINITY_sp| P227\Gucyl1b2 | Guanylate cyclase s | 44.80 | 0.00 |
| TRINITY_sp| P0CGDnh2 | Dynein heavy chain | 44.80 | 0.00 |
| TRINITY_sp| P417\ALAAT1 | Alanine aminotransf | 44.80 | 0.00 |
| TRINITY_sp| Q010\PDE1B | Calcium/calmodulin- | 44.80 | 0.00 |
| TRINITY_sp| A1AS\usps47 | Ubiquitin carboxyl- | 44.70 | 0.00 |
| TRINITY_sp| P490\- | Cytochrome b5 OS=Ni | 44.70 | 0.00 |
| TRINITY_sp| P462\At3g558 | Sedoheptulose-1,7-b | 44.70 | 0.00 |
| TRINITY_sp| Q5UQ\MIMI L5\Putative ADP-ribo | 44.70 | 0.00 |
| TRINITY_sp| P426\DRTT11 | DNA-damage-repair/t | 44.70 | 0.00 |
| TRINITY_sp| Q3M1\PUS10 | Putative tRNA pseud | 44.70 | 0.00 |
| TRINITY_sp| Q9STVPS29 | Vacuolar protein so | 44.70 | 0.00 |
| TRINITY_sp| Q6P1\FIGNL1 | Fidgetin-like prote | 44.70 | 0.00 |
| TRINITY_sp| Q550\DDB_G02 | Protein TAPT1 homol | 44.70 | 0.00 |
| TRINITY_sp| A2BE\arid3a | AT-rich interactive | 44.70 | 0.00 |
| Gene ID      | Description                                                                 | Score | Probability |
|-------------|------------------------------------------------------------------------------|-------|-------------|
| sp|Q9BIIB0464.9 | Probable protein phosphatase methylesterase 1 OS=Caenorhabditis elegans GN=B0464.9 PE=3 SV=1 | 44.70 | 0.00 |
| sp|Q1368UL4B | Cullin-4B OS=Homo s | 44.70 | 0.00 |
| sp|Q9FGKEB1C | Microtubule-associa | 44.70 | 0.00 |
| sp|Q39VHPTP1 | Dual specificity pr | 44.70 | 0.00 |
| sp|Q86H|polr1a | DNA-directed RNA po | 44.70 | 0.00 |
| sp|Q37U|Yeast2 | YEATS domain-contai | 44.70 | 0.00 |
| sp|Q5F4GP89 | Golgi pH regulator | 44.70 | 0.00 |
| sp|F4NU|TRM5 | tRNA (guanine(37)-N | 44.70 | 0.00 |
| sp|Q8GW|PMRT15 | Protein arginine N- | 44.70 | 0.00 |
| sp|Q28B|c2cd5 | C2 domain-containin | 44.70 | 0.00 |
| sp|Q6UK|pirA | Protein pirA OS=Dic | 44.70 | 0.00 |
| sp|Q8LP|LACS6 | Long chain acyl-CoA | 44.70 | 0.00 |
| sp|Q547TmrKC | Probable serine/thr | 44.70 | 0.00 |
| sp|P257|Os04g06|Oryzain alpha chain | 44.70 | 0.00 |
| sp|Q8LP|BTS | Zinc finger protein | 44.70 | 0.00 |
| sp|Q8V2|PAS2 | Very-long-chain (3R | 44.70 | 0.00 |
| sp|Q9SB|At4g247 | Manganese-dependent | 44.70 | 0.00 |
| sp|Q242|sw | Cytoplasmic dynein | 44.70 | 0.00 |
| sp|Q7T0|rhbg | Ammonium transporte | 44.70 | 0.00 |
| sp|Q993|Y3B-G | Transposon Ty3-G Ga | 44.70 | 0.00 |
| sp|Q5NC|Trappol | Trafficking protein | 44.70 | 0.00 |
| sp|Q8BY|Rdh12 | Retinol dehydrogena | 44.70 | 0.00 |
| sp|Q376|ND4L | NADH-ubiquinone oxi | 44.70 | 0.00 |
| sp|Q8WX|DNAH7 | Dynein heavy chain | 44.70 | 0.00 |
| sp|Q395|ODA2 | Dynein gamma chain, | 44.70 | 0.00 |
| sp|Q9WU|Splint2 | Kunitz-type proteas | 44.70 | 0.00 |
| sp|Q9LT|MED35C | Pre-mRNA-processing | 44.70 | 0.00 |
| sp|P411|HSFA1A | Heat stress transcr | 44.70 | 0.00 |
| sp|Q9ZP|POX2 | Pyridoxine/pyridoxa | 44.70 | 0.00 |
| sp|Q55G|DDB_G02 | UPF0160 protein OS= | 44.70 | 0.00 |
| sp|Q54V|odhA | Probable 2-oxogluta | 44.70 | 0.00 |
| sp|Q6DN|MCTP1 | Multiple C2 and tra | 44.70 | 0.00 |
| sp|Q8LB|CLPR4 | ATP-dependent Clp p | 44.70 | 0.00 |
| sp|A2ZV|FTSH9 | ATP-dependent zinc | 44.70 | 0.00 |
| sp|Q8GY|APX6 | Putative L-ascorbat | 44.70 | 0.00 |
| sp|Q8V9|PFK5 | ATP-dependent 6-pho | 44.70 | 0.00 |
| sp|Q3Y4|ckk-1 | Calcium/calmodulin- | 44.70 | 0.00 |
| sp|Q9LM|PAPS1 | Nuclear poly(A) pol | 44.70 | 0.00 |
| sp|Q8L8|PIK5K9 | Phosphatidylinosito | 44.70 | 0.00 |
| sp|P925|AtMg00810 | Uncharacterized mit | 44.70 | 0.00 |
| sp|P043|pol | Retrovirus-related | 44.70 | 0.00 |
| sp|Q6DD|ce76 | Centrosomal protein | 44.70 | 0.00 |
| sp|P52T|CBP31 | Serine carboxypepti | 44.60 | 0.00 |
| sp|Q6ZN|ACPP7 | Acid phosphatase ty | 44.60 | 0.00 |
| sp|Q94A|At1g620 | Coatomer subunit al | 44.60 | 0.00 |
| sp|Q9V8|lack | E3 ubiquitin-protei | 44.60 | 0.00 |
| sp|Q9Y6|KPTN | Kaptin OS=Homo sapi | 44.60 | 0.00 |
| sp|Q02A|thrB | Homoserine kinase O | 44.60 | 0.00 |
| sp|P341|coaA | Coactosin OS=Dicyto | 44.60 | 0.00 |
| sp|Q9CB|RABF1 | Ras-related protein | 44.60 | 0.00 |
| sp|Q54N|DDB_G02 | NuA4 complex subuni | 44.60 | 0.00 |
| sp|Q54M|fhkD | Probable serine/thr | 44.60 | 0.00 |
| sp|Q8R3|Cluap1 | Clusterin-associate | 44.60 | 0.00 |
| sp|Q5UP|MMIMI_L92 | Putative ankyrin re | 44.60 | 0.00 |
| sp|Q9LJ|At3g224 | Probable prefoldin | 44.60 | 0.00 |
| sp|Q9WY|TM_0508 | Uncharacterized pro | 44.60 | 0.00 |
| Accession | Description                                      | Score | E-value |
|-----------|--------------------------------------------------|-------|---------|
| TRINITY_sp| B8G41nfo | Probable endonuclease | 44.50 | 0.00    |
| TRINITY_sp| Q8L36FZ    | Protein FIZZY-RELAT | 44.50 | 0.00    |
| TRINITY_sp| P5462pdbA | RAC family serine/threonine-protein kinases | 44.50 | 0.00    |
| TRINITY_sp| Q1100tag-320 | Probable protein disulfide isomerase | 44.50 | 0.00    |
| TRINITY_sp| P623CPK1   | Calcium-dependent protein kinases | 44.50 | 0.00    |
| TRINITY_sp| Q9VXDENR   | Density-regulated protein | 44.50 | 0.00    |
| TRINITY_sp| P126YPK1   | Serine/threonine-protein kinases | 44.50 | 0.00    |
| TRINITY_sp| Q9W54Ns3   | Large subunit GTPases | 44.50 | 0.00    |
| TRINITY_sp| P0431pol   | Retrovirus-related protein | 44.50 | 0.00    |
| TRINITY_sp| Q9M3H1Ma1 | Probable cadmium/zinc-binding protein | 44.50 | 0.00    |
| TRINITY_sp| Q5NTI5K2   | Shikimate kinase 2 | 44.50 | 0.00    |
| TRINITY_sp| Q96NFDR612 | Retinol dehydrogenase | 44.50 | 0.00    |
| TRINITY_sp| Q924HRad51c | DNA repair protein | 44.50 | 0.00    |
| TRINITY_sp| Q8N53AADAT | Kynurenine/alpha-amino acid ligase | 44.50 | 0.00    |
| TRINITY_sp| Q8HOVLPAA | Protein LOW PSII AC | 44.50 | 0.00    |
| TRINITY_sp| Q8L535FLC | 5-formyltetrahydrofolate cyclo-ligase | 44.50 | 0.00    |
| TRINITY_sp| Q1XDIycf52 | Uncharacterized protein | 44.50 | 0.00    |
| TRINITY_sp| Q4PEHSEC23 | Protein transport protein | 44.50 | 0.00    |
| TRINITY_sp| Q0JLI0s1g061 | DEAD-box ATP-depend | 44.50 | 0.00    |
| TRINITY_sp| Q7TX1nudC | NADH pyrophosphatase | 44.50 | 0.00    |
| TRINITY_sp| Q9FMAt5g1405U3 | Small nucleolar RNA-binding protein | 44.50 | 0.00    |
| TRINITY_sp| Q9PU6cog2 | Coatamer subunit gamma-2 | 44.50 | 0.00    |
| TRINITY_sp| P5524GUCY2C | Heat-stable enterotoxin | 44.50 | 0.00    |
| TRINITY_sp| Q5VQ0s06g01 | Coatamer subunit | 44.50 | 0.00    |
| TRINITY_sp| Q748esf1 | Pre-rRNA-processing protein | 44.50 | 0.00    |
| TRINITY_sp| P6151RAB4B | Ras-related protein | 44.50 | 0.00    |
| TRINITY_sp| Q0830MKK3 | Mitogen-activated protein kinase | 44.50 | 0.00    |
| TRINITY_sp| Q7X65VP35A | Vacuum protein | 44.50 | 0.00    |
| TRINITY_sp| Q4YRKAS1 | Ras-like protein | 44.40 | 0.00    |
| TRINITY_sp| Q6T41rbrA | Probable E3 ubiquitin-conjugating enzyme | 44.40 | 0.00    |
| TRINITY_sp| Q92ZV0OBAP1A | Oil body-associated protein | 44.40 | 0.00    |
| TRINITY_sp| Q0S515dr16c6 | Short-chain dehydrogenase | 44.40 | 0.00    |
| TRINITY_sp| Q86APolr13a | DNA-directed RNA polymerase | 44.40 | 0.00    |
| TRINITY_sp| Q9XGAt5g2601 | Probable protein phosphatase | 44.40 | 0.00    |
| TRINITY_sp| Q55Cmp11 | MAP kinase phosphatase | 44.40 | 0.00    |
| TRINITY_sp| Q6DFلتtc37 | Tetra-tricopeptide repeat domain protein | 44.40 | 0.00    |
| TRINITY_sp| Q9UB5DNAJ9 | DnaJ homolog subfamily B | 44.40 | 0.00    |
| TRINITY_sp| Q3941RAB1B | Ras-related protein | 44.40 | 0.00    |
| TRINITY_sp| Q9M32AGD6 | Probable ADP-ribose transferase | 44.40 | 0.00    |
| TRINITY_sp| Q9091RAB2A | Ras-related protein | 44.40 | 0.00    |
| TRINITY_sp| Q9NU1TBC1D221TBC1 | Transcription factor | 44.40 | 0.00    |
| TRINITY_sp| Q54Ymp13 | MAP kinase phosphatase | 44.40 | 0.00    |
| TRINITY_sp| Q54TpdkA | Probable serine/threonine-protein kinase | 44.40 | 0.00    |
| TRINITY_sp| Q082MED7 | Mediator of RNA polymerase | 44.40 | 0.00    |
| TRINITY_sp| Q3952ODA2 | Dynemin gamma chain | 44.40 | 0.00    |
| TRINITY_sp| Q9WYTM0508 | Uncharacterized protein | 44.40 | 0.00    |
| TRINITY_sp| Q98ZAtpy8a2 | Phospholipid-translocating protein | 44.40 | 0.00    |
| TRINITY_sp| P3282SCPL49 | Serine carboxypeptidase | 44.40 | 0.00    |
| TRINITY_sp| Q9ZVIPAHX | Phytanoyl-CoA dioxygenase | 44.40 | 0.00    |
| TRINITY_sp| Q3EAXZIFL2 | Probable peptidase | 44.40 | 0.00    |
| TRINITY_sp| Q8MJ3SPG21 | Maspardin OS=Bos taurus | 44.40 | 0.00    |
| TRINITY_sp| Q7511AT9A | Probable phospholipid transferase | 44.40 | 0.00    |
| TRINITY_sp| Q6EPNEK5 | Serine/threonine-protein kinase | 44.40 | 0.00    |
| TRINITY_sp| Q8T6abcG20 | ABC transporter Gf | 44.40 | 0.00    |
| TRINITY_sp| Q54RJDDB02 | Probable iron/ascorbate oxidoreductase | 44.40 | 0.00    |
| Gene Name | Description | UniProt Accession | Score |
|-----------|-------------|------------------|-------|
| Eukaryotic translation initiation factor 5 | OS=Mus musculus | sp|C1DSS8|PYRG_AZOVD |
| trNA (cytosine(34)-methyltransferase | OS=Gallus gallus | sp|P00514|KAP0_BOVIN |
| Ribosomal RNA large | OS=Arabidopsis thaliana | sp|Q96NX5|KCC1G_HUMAN |
| Calcium/calmodulin-dependent protein kinase | OS=Arabidopsis thaliana | sp|B1XJJ2|RL18_SYNP2 |
| Putative acid--aminopeptidase | OS=Arabidopsis thaliana | sp|Q4FE47|XB35_ARATH |
| Thioredoxin-like protein | OS=Arabidopsis thaliana | sp|Q13823|NOG2_HUMAN |
| Solute carrier family 35 member B1 | OS=Xenopus laevis | sp|Q6GQ70|S35B1_XENLA |
| Probable histidine kinase | OS=Oryza sativa subsp. indica | sp|Q9M7I3|PRR1_ARATH |
| Radial spoke protein | OS=Chlamydomonas reinhardtii | sp|Q86CS2|ATG1_DICDI |
| ABC transporter B family member 1 | OS=Arabidopsis thaliana | sp|Q93Y35|PSMD6_ARATH |
| NAD-dependent protein deacetylase | OS=Oryza sativa subsp. indica | sp|Q6GQ70|S35B1_XENLA |
| Heat stress transcription factor | OS=Arabidopsis thaliana | sp|Q96NX5|KCC1G_HUMAN |
| ABC transporter C family member 14 | OS=Arabidopsis thaliana | sp|B1XJJ2|RL18_SYNP2 |
| Ribosome-binding ATPase YchF | OS=Mycoplasma genitalium | sp|Q4FE47|XB35_ARATH |
| Putative E3 ubiquitin-protein ligase | OS=Arabidopsis thaliana | sp|Q4FE47|XB35_ARATH |
| NAD-dependent protein deacetylase | OS=Oryza sativa subsp. indica | sp|Q6GQ70|S35B1_XENLA |
| ABC transporter B family member 1 | OS=Arabidopsis thaliana | sp|Q93Y35|PSMD6_ARATH |
| NAD-dependent protein deacetylase | OS=Oryza sativa subsp. indica | sp|Q6GQ70|S35B1_XENLA |
| ABC transporter C family member 14 | OS=Arabidopsis thaliana | sp|B1XJJ2|RL18_SYNP2 |
| Ribosome-binding ATPase YchF | OS=Mycoplasma genitalium | sp|Q4FE47|XB35_ARATH |
| Putative E3 ubiquitin-protein ligase | OS=Arabidopsis thaliana | sp|Q4FE47|XB35_ARATH |
| NAD-dependent protein deacetylase | OS=Oryza sativa subsp. indica | sp|Q6GQ70|S35B1_XENLA |
| ABC transporter B family member 1 | OS=Arabidopsis thaliana | sp|Q93Y35|PSMD6_ARATH |
| Gene Name                     | Alias     | Description                      | Score | E-Value |
|------------------------------|-----------|----------------------------------|-------|---------|
| 3'(2'),5'-bisphosphate       |           |                                  | 44.20 | 0.00    |
| nucleotidase                |           |                                  |       |         |
| clathrin heavy chain         |           |                                  | 44.20 | 0.00    |
| Ras-related protein          |           |                                  | 44.10 | 0.00    |
| methyltransferase-1          |           |                                  | 44.10 | 0.00    |
| Protein HID1 OS=Mus          |           |                                  | 44.10 | 0.00    |
| Thimet oligopeptidase        |           |                                  | 44.10 | 0.00    |
| Kinesin-like protein         |           |                                  | 44.10 | 0.00    |
| Ras-related protein          |           |                                  | 44.10 | 0.00    |
| Protein ABHD18 OS=M           |           |                                  | 44.10 | 0.00    |
| Peptide deformylase          |           |                                  | 44.10 | 0.00    |
| Uncharacterized ABC          |           |                                  | 44.10 | 0.00    |
| Dihydropteridine re          |           |                                  | 44.10 | 0.00    |
| Glutathione synthet           |           |                                  | 44.10 | 0.00    |
| Protein kinase gsk3           |           |                                  | 44.10 | 0.00    |
| Probable magnesium           |           |                                  | 44.10 | 0.00    |
| DNA-directed RNA pol         |           |                                  | 44.10 | 0.00    |
| Troponin C, skeleton          |           |                                  | 44.10 | 0.00    |
| Acyl carrier protein         |           |                                  | 44.10 | 0.00    |
| Signal transducer a          |           |                                  | 44.10 | 0.00    |
| Alpha-galactosidase          |           |                                  | 44.10 | 0.00    |
| Clusterin-associate          |           |                                  | 44.10 | 0.00    |
| Pescadillo homolog           |           |                                  | 44.10 | 0.00    |
| Chitinase domain-co          |           |                                  | 44.10 | 0.00    |
| PRA1 family protein          |           |                                  | 44.10 | 0.00    |
| Transcription factor         |           |                                  | 44.10 | 0.00    |
| Iron-sulfur cluster          |           |                                  | 44.10 | 0.00    |
| DNA polymerase delt          |           |                                  | 44.10 | 0.00    |
| Phosphatidylinosito          |           |                                  | 44.10 | 0.00    |
| Acyl-CoA desaturase          |           |                                  | 44.10 | 0.00    |
| Conditioned medium           |           |                                  | 44.10 | 0.00    |
| Ubiquitin thioester          |           |                                  | 44.10 | 0.00    |
| Probable endo-beta-          |           |                                  | 44.10 | 0.00    |
| Retinol dehydrogena          |           |                                  | 44.10 | 0.00    |
| V-type proton ATPase         |           |                                  | 44.10 | 0.00    |
| Protein NAM8 OS=Sac          |           |                                  | 44.10 | 0.00    |
| 25 kDa calcium-bind          |           |                                  | 44.10 | 0.00    |
| Rhodanese-like doma          |           |                                  | 44.10 | 0.00    |
| Retrovirus-related           |           |                                  | 44.10 | 0.00    |
| Magnesium transport          |           |                                  | 44.10 | 0.00    |
| Sterile alpha and T          |           |                                  | 44.10 | 0.00    |
| Dynein alpha chain           |           |                                  | 44.10 | 0.00    |
| Accession | Description |
|------------|-------------|
| TRINITY_sp| Q54GK| Diacylglycerol O-ac | 44.10 |
| TRINITY_sp| Q6NW.nadjc2 | DnaJ homolog subfam | 44.10 |
| TRINITY_sp| Q19lqcy-12 | Receptor-type guany | 44.10 |
| TRINITY_sp| Q4UB1rab1 | Ras-related protein | 44.10 |
| TRINITY_sp| P296leef-2 | Elongation factor 2 | 44.10 |
| TRINITY_sp| Q3S2nPOLE3 | DNA polymerase epis | 44.00 |
| TRINITY_sp| Q542xab2 | Pre-mRNA-splicing f | 44.00 |
| TRINITY_sp| P201.GSTM2 | Glutathione S-trans | 44.00 |
| TRINITY_sp| Q020rad3 | Protein kinase rad3 | 44.00 |
| TRINITY_sp| Q017.EXOSC10 | Exosome component 1 | 44.00 |
| TRINITY_sp| Q9LFIRE | Probable serine/thr | 44.00 |
| TRINITY_sp| Q395l- | Dynein 8 kDa light | 44.00 |
| TRINITY_sp| Q0DJJTOR | Serine/threonine-pr | 44.00 |
| TRINITY_sp| Q86Jpolr2j | DNA-directed RNA po | 44.00 |
| TRINITY_sp| Q8N4.CARNMT1 | Carnosine N-methylt | 44.00 |
| TRINITY_sp| Q96MBHSP12B | Heat shock 70 kDa p | 44.00 |
| TRINITY_sp| O087Veps45 | Vacuolar protein so | 44.00 |
| TRINITY_sp| Q9LXMMBF1B | Multiprotein-bridgi | 44.00 |
| TRINITY_sp| P491(- | Nitrate reductase [ | 44.00 |
| TRINITY_sp| Q149SHPRH | E3 ubiquitin-protei | 44.00 |
| TRINITY_sp| Q754.ERT1 | Transcription activ | 44.00 |
| TRINITY_sp| Q103p23fy | Transitionally-con | 44.00 |
| TRINITY_sp| Q08DMRPL47 | 39S ribosomal prote | 44.00 |
| TRINITY_sp| F41I.SW12 | Switch 2 OS=Arabido | 44.00 |
| TRINITY_sp| P011(MYB | Transcriptional act | 44.00 |
| TRINITY_sp| Q84NILUL3 | Probable E3 ubiquit | 44.00 |
| TRINITY_sp| O162.sti-1 | Stress-induced-phos | 44.00 |
| TRINITY_sp| Q92S1GLBI | Nitrogen regulatory | 44.00 |
| TRINITY_sp| P043pol1 | Retrovirus-related | 44.00 |
| TRINITY_sp| Q6EEITTL5 | Tubulin polyglutam | 44.00 |
| TRINITY_sp| Q5MADDB_G02 | Probable serine/thr | 44.00 |
| TRINITY_sp| Q949(PROSC | Proline synthase co | 44.00 |
| TRINITY_sp| Q5T0.CFA | Cilia- and flagella | 44.00 |
| TRINITY_sp| Q6QHPAOX | Peroxisomal N(1)-ac | 44.00 |
| TRINITY_sp| A41ittpp3 | Tubulin polymerizat | 44.00 |
| TRINITY_sp| P100(- | Caricain OS=Carica | 44.00 |
| TRINITY_sp| Q92P1FAM135A | Protein FAM135A OS= | 44.00 |
| TRINITY_sp| Q9FGHMAG5 | Protein transport p | 44.00 |
| TRINITY_sp| B6JE1rpl1D | 50S ribosomal prote | 44.00 |
| TRINITY_sp| Q2HJUSP15 | Ubiquitin carboxyl- | 44.00 |
| TRINITY_sp| Q9UBFCSTSZ | Cathepsin Z OS=Homo | 44.00 |
| TRINITY_sp| A3LU.FMP521 | Protein FMP52-1, mi | 44.00 |
| TRINITY_sp| Q96PLENG8 | Leukocyte receptor | 44.00 |
| TRINITY_sp| Q6501os9g05;DEAD-box | ATP-depend | 44.00 |
| TRINITY_sp| Q9NGwmkcb | Probable serine/thr | 44.00 |
| TRINITY_sp| Q93YRUS6 | Protein root UVB se | 44.00 |
| TRINITY_sp| Q550.Aurkb | Aurora kinase B OS= | 44.00 |
| TRINITY_sp| Q941BON1 | Protein BONZAI 1 OS | 44.00 |
| TRINITY_sp| Q025ttypA | GTP-binding protein | 44.00 |
| TRINITY_sp| Q3MHNJUBP2 | Cytoplasmic Fe-S clus | 44.00 |
| TRINITY_sp| P231\ABC4 | Phosphatidylcholine | 44.00 |
| TRINITY_sp| Q9GRaif | Apoptosis-inducing | 44.00 |
| TRINITY_sp| P250.CML12 | Calmodulin-like pro | 44.00 |
| TRINITY_sp| P403RIC1 | Ras-related protein | 44.00 |
| TRINITY_sp| Q9SU.KCS15 | 3-ketoacyl-CoA synt | 44.00 |
| TRINITY_sp| Q9LHfAt5g352( | Putative clathrin a | 44.00 |
| TRINITY_sp|Q56X:RH39 | DEAD-box ATP-depend | 44.00 | 0.00 |
| TRINITY_sp|Q6C7:FIP1 | Pre-mRNA polyadenyl | 44.00 | 0.00 |
| TRINITY_sp|Q94C:PAT13 | Probable protein S- | 44.00 | 0.00 |
| TRINITY_sp|Q541:DBB_G02 | DNA damage-binding | 44.00 | 0.00 |
| TRINITY_sp|Q6L4:DBBI | DNA damage-binding | 44.00 | 0.00 |
| TRINITY_sp|P208:pol1 | Retrovirus-related | 44.00 | 0.00 |
| TRINITY_sp|Q3Y4:ckk-1 | Calcium/calmodulin- | 44.00 | 0.00 |
| TRINITY_sp|P287:MSPI | Protein MSP1 OS=Sac | 44.00 | 0.00 |
| TRINITY_sp|Q5S7:HSP70-1 | Heat shock 70 kDa p | 44.00 | 0.00 |
| TRINITY_sp|A6WX:ub1G | Ubiquinone biosynth | 43.90 | 0.00 |
| TRINITY_sp|Q8RO:Sgpl1 | Sphingosine-1-phosp | 43.90 | 0.00 |
| TRINITY_sp|Q5HR:SERP023 | Probable rhodanese | 43.90 | 0.00 |
| TRINITY_sp|Q556:DBB_G02 | Ras-related protein | 43.90 | 0.00 |
| TRINITY_sp|Q541:cox19 | Cytochrome c oxidas | 43.90 | 0.00 |
| TRINITY_sp|P0DK:PGLP1A | Phosphoglycolate ph | 43.90 | 0.00 |
| TRINITY_sp|Q9WV:Kif9 | Kinesin-like protei | 43.90 | 0.00 |
| TRINITY_sp|P422:RAP | Aspartic proteinase | 43.90 | 0.00 |
| TRINITY_sp|P212:CCA1 | CCA tRNA nucleotidy | 43.90 | 0.00 |
| TRINITY_sp|Q8GW:OSB3 | Protein OSB3, chlor | 43.90 | 0.00 |
| TRINITY_sp|Q9FW:os10g05 | Probable trehalase | 43.90 | 0.00 |
| TRINITY_sp|Q699:cpv1 | Probable serine car | 43.90 | 0.00 |
| TRINITY_sp|Q6Z9:os08g01 | mRNA cap guanine-N7 | 43.90 | 0.00 |
| TRINITY_sp|Q9LU:ACA9 | Calcium-transportin | 43.90 | 0.00 |
| TRINITY_sp|Q599:fim1 | Fimbrin OS=Schizosa | 43.90 | 0.00 |
| TRINITY_sp|P0A9:rimI | Ribosomal-protein-a | 43.90 | 0.00 |
| TRINITY_sp|Q2XQ:Lac2 | Beta-galactosidase | 43.90 | 0.00 |
| TRINITY_sp|O622:F45G2.1 | MIP18 family protei | 43.90 | 0.00 |
| TRINITY_sp|Q89H:NPC6 | Non-specific phosph | 43.90 | 0.00 |
| TRINITY_sp|Q5W6:MAN5 | Putative mannan end | 43.90 | 0.00 |
| TRINITY_sp|Q5GF:Mane | Glycoprotein endo-a | 43.90 | 0.00 |
| TRINITY_sp|Q86A:DBB_G02 | Probable myosin lig | 43.90 | 0.00 |
| TRINITY_sp|Q9C2:Naxd | ATP-dependent (S)-N | 43.90 | 0.00 |
| TRINITY_sp|Q547:drkD | Probable serine/thr | 43.90 | 0.00 |
| TRINITY_sp|Q631:Dnah7 | Dynnein heavy chain | 43.90 | 0.00 |
| TRINITY_sp|Q1LW:usp22a | Dual specificity pr | 43.90 | 0.00 |
| TRINITY_sp|Q5P6:ATXR2 | Histone-lysine N-me | 43.90 | 0.00 |
| TRINITY_sp|Q9M6:GK=2 | Guanulate kinase 2 | 43.90 | 0.00 |
| TRINITY_sp|Q492:RH29 | Putative DEAD-box A | 43.90 | 0.00 |
| TRINITY_sp|P109:Ret | Retrovirus-related | 43.90 | 0.00 |
| TRINITY_sp|Q54W:pex7 | Peroxisomal targeti | 43.90 | 0.00 |
| TRINITY_sp|P870:SPAC57A1 | Uncharacterized pro | 43.90 | 0.00 |
| TRINITY_sp|Q611:Prpf4b | Serine/threonine-pr | 43.90 | 0.00 |
| TRINITY_sp|F226:NDH2 | External alternativ | 43.90 | 0.00 |
| TRINITY_sp|Q5VQC:CPK2 | Calcium-dependent p | 43.90 | 0.00 |
| TRINITY_sp|Q94F:IMPL1 | Phosphatase IMPL1, | 43.90 | 0.00 |
| TRINITY_sp|Q92B:xyoA | Probable xylitol ox | 43.90 | 0.00 |
| TRINITY_sp|Q8IU:CBWD2 | COBW domain-contain | 43.90 | 0.00 |
| TRINITY_sp|P543:Lipe | Hormone-sensitive l | 43.90 | 0.00 |
| TRINITY_sp|Q84N:RL1l1 | Rhomboid-like prote | 43.90 | 0.00 |
| TRINITY_sp|Q2HJ:PRPF18 | Pre-mRNA-splicing f | 43.90 | 0.00 |
| TRINITY_sp|B1AQ:Usp36 | Ubiquitin carboxyl- | 43.90 | 0.00 |
| TRINITY_sp|Q503:ngly1 | Peptide-N(4)- (N-ace | 43.90 | 0.00 |
TRINITY_sp|Q70IhdaH Histone deacetylase-like amidohydrolase OS=Alcaligenes sp. (strain DSM 11172) GN=hdaH PE=1 SV=3
TRINITY_sp|Q5ZJJABHD13 Protein ABHD13 OS=G 43.90 0.00
TRINITY_sp|P519Nek1 Serine/threonine-pr WD repeat-containing protein 82 OS=Danio rerio GN=wdr82 PE=2 SV=1
TRINITY_sp|Q6NVwdr82 WD repeat-containin 43.90 0.00
TRINITY_sp|Q9NRIBAZ1A Bromodomain adjacen 43.90 0.00
TRINITY_sp|Q8E3Baz1a Bromodomain adjacen 43.90 0.00
TRINITY_sp|Q0E23UVR3 (6-4)DNA photolyase 43.90 0.00
TRINITY_sp|Q9SRFAGZ1 Adenine/guanine per 43.90 0.00
TRINITY_sp|Q8ISgefB Ras guanine nucleot 43.90 0.00
TRINITY_sp|Q9RIILPE Hormone-sensitive l 43.90 0.00
TRINITY_sp|Q9ZWICKL9 Casein kinase 1-lik 43.90 0.00
TRINITY_sp|Q835pfp Pyrophosphate--fruc 43.80 0.00
TRINITY_sp|Q9FKAt5g661 Probable alpha-mann 43.80 0.00
TRINITY_sp|A8M5JrpsQ 3OS ribosomal prote 43.80 0.00
TRINITY_sp|Q55Ctgtf2h5 General transcripti 43.80 0.00
TRINITY_sp|Q55Ctgtf2h5 General transcripti 43.80 0.00
TRINITY_sp|Q100SPAC3H1.Glutathione gamma-g 43.80 0.00
TRINITY_sp|Q8BHINoc41 Nucleolar complex p 43.80 0.00
TRINITY_sp|Q0WRFPPC6-7 Probable protein ph 43.80 0.00
TRINITY_sp|P685hup2 SPBc2 prophage-deri 43.80 0.00
TRINITY_sp|Q2YDIDRAP1 Drl-associatep core 43.80 0.00
TRINITY_sp|Q9H7ELAC1 Zinc phosphodiesteri 43.80 0.00
TRINITY_sp|Q9H4FPLK3 Serine/threonine-pr 43.80 0.00
TRINITY_sp|Q55Crapsl1 Probable serine/thr 43.80 0.00
TRINITY_sp|Q963ACX4 Acyl-coenzyme A oxi 43.80 0.00
TRINITY_sp|Q929Cab8 Cinnamyl alcohol de 43.80 0.00
TRINITY_sp|A1A6hHK5 Probable histidine 43.80 0.00
TRINITY_sp|Q9NJCPK3 Calcium-dependent p 43.80 0.00
TRINITY_sp|Q3EDAt1g229 Uncharacterized PKH 43.80 0.00
TRINITY_sp|A2Z3ISGR Protein STAY-GREEN, 43.80 0.00
TRINITY_sp|F4HXPPSS1 CDP-diacylglycerol- 43.80 0.00
TRINITY_sp|P841TCTP Translationally-con 43.80 0.00
TRINITY_sp|Q9JJDyn2h1 Cytoplasmic dynein 43.80 0.00
TRINITY_sp|Q9X3topA DNA topoisomerase 1 43.80 0.00
TRINITY_sp|Q9FLATJ6 Chaperone protein d 43.80 0.00
TRINITY_sp|Q7TSIpp6r1 Serine/threonine-pr 43.80 0.00
TRINITY_sp|Q9NGmkCb Probable serine/thr 43.80 0.00
TRINITY_sp|Q8MZ Ca2 Calcium-binding mit 43.80 0.00
TRINITY_sp|Q8SSCTCP1 T-complex protein 1 43.80 0.00
TRINITY_sp|P227Gucy1b2 Guanylate cyclase s 43.80 0.00
TRINITY_sp|Q9VVtRbp6 RNA-binding protein 43.80 0.00
TRINITY_sp|Q54UsshD Dual specificity pr 43.80 0.00
TRINITY_sp|Q88EFstk16 Serine/threonine-pr 43.80 0.00
TRINITY_sp|Q8BNKcctd6 BTB/POZ domain-cont 43.80 0.00
TRINITY_sp|Q949At2g173 Uncharacterized pro 43.80 0.00
TRINITY_sp|Q9SZABCAG9 ABC transporter G f 43.80 0.00
TRINITY_sp|F421CKL1 Casein kinase 1-lik 43.80 0.00
TRINITY_sp|Q8IEpepA Probable cytosol am 43.80 0.00
TRINITY_sp|Q9C4MINNE1 Cell division topol 43.80 0.00
TRINITY_sp|Q9NRDDX21 Nucleolar RNA helic 43.80 0.00
TRINITY_sp|Q6NYs1c25a2 Calcium-binding mit 43.80 0.00
TRINITY_sp|A0JPICdc61 Coiled-coil domain- 43.80 0.00
TRINITY_sp|Q8LPClACS6 Long chain acyl-CoA 43.80 0.00
TRINITY_sp|Q68Fvac14 Protein VAC14 homol 43.80 0.00
TRINITY_sp|P0CDalg7 UDP-N-acetylglucosa 43.80 0.00
TRINITY_sp|F4IVCHR10 Probable helicase C 43.80 0.00
| Accession   | Description                                               | Identities | Similarity | E-value |
|-------------|-----------------------------------------------------------|------------|------------|---------|
| TRINITY_sp| Protein VAC14 homolog                                      | 43.80      | 0.00       |         |
| TRINITY_sp| Voltage-gated potas                                        | 43.80      | 0.00       |         |
| TRINITY_sp| Putative quercetin                                         | 43.80      | 0.00       |         |
| TRINITY_sp| Coproporphyrinogen-                                       | 43.80      | 0.00       |         |
| TRINITY_sp| Ribonuclease P prot                                        | 43.80      | 0.00       |         |
| TRINITY_sp| Hybrid signal trans                                        | 43.80      | 0.00       |         |
| TRINITY_sp| Dynin beta chain                                          | 43.80      | 0.00       |         |
| TRINITY_sp| Dual specificity pr                                        | 43.80      | 0.00       |         |
| TRINITY_sp| Ras GTPase-activat                                       | 43.80      | 0.00       |         |
| TRINITY_sp| Calcium-dependent p                                        | 43.80      | 0.00       |         |
| TRINITY_sp| Heat stress transcr                                       | 43.80      | 0.00       |         |
| TRINITY_sp| Anaphase-promoting                                       | 43.80      | 0.00       |         |
| TRINITY_sp| Serine/threonine-primo                                    | 43.80      | 0.00       |         |
| TRINITY_sp| PAB-dependent poly(                                       | 43.80      | 0.00       |         |
| TRINITY_sp| Ribonuclease P prot                                        | 43.80      | 0.00       |         |
| TRINITY_sp| ABC transporter G f                                        | 43.80      | 0.00       |         |
| TRINITY_sp| Uncharacterized oxi                                        | 43.80      | 0.00       |         |
| TRINITY_sp| Serine/threonine-primo                                    | 43.80      | 0.00       |         |
| TRINITY_sp| DNA polymerase I OS                                       | 43.80      | 0.00       |         |
| TRINITY_sp| DNA repair protein                                         | 43.80      | 0.00       |         |
| TRINITY_sp| Dual specificity pr                                        | 43.80      | 0.00       |         |
| TRINITY_sp| Ubiquitin-protein l                                       | 43.80      | 0.00       |         |
| TRINITY_sp| Ervatamin-B OS=Tabe                                       | 43.80      | 0.00       |         |
| TRINITY_sp| Aldehyde-alcohol de                                       | 43.80      | 0.00       |         |
| TRINITY_sp| Regulator of nonsen                                        | 43.80      | 0.00       |         |
| TRINITY_sp| Amino-acid permease                                       | 43.80      | 0.00       |         |
| TRINITY_sp| Histone-lysine N-me                                       | 43.80      | 0.00       |         |
| TRINITY_sp| NAD(P)H-dependent F                                       | 43.80      | 0.00       |         |
| TRINITY_sp| Cytoplasmic dynein                                        | 43.80      | 0.00       |         |
| TRINITY_sp| Alpha N-terminal pr                                       | 43.70      | 0.00       |         |
| TRINITY_sp| DExH-box ATP-depend                                      | 43.70      | 0.00       |         |
| TRINITY_sp| Ras-related protein                                       | 43.70      | 0.00       |         |
| TRINITY_sp| Zinc finger AN1 and                                       | 43.70      | 0.00       |         |
| TRINITY_sp| DNA repair protein                                         | 43.70      | 0.00       |         |
| TRINITY_sp| Ubiquitin carboxyl-                                       | 43.70      | 0.00       |         |
| TRINITY_sp| Uncharacterized RIN                                       | 43.70      | 0.00       |         |
| TRINITY_sp| ABC transporter G f                                        | 43.70      | 0.00       |         |
| TRINITY_sp| Probable ethylene r                                       | 43.70      | 0.00       |         |
| TRINITY_sp| Serine/arginine-ric                                       | 43.70      | 0.00       |         |
| TRINITY_sp| Maestro heat-like r                                       | 43.70      | 0.00       |         |
| TRINITY_sp| Pyruvate kinase OS=                                        | 43.70      | 0.00       |         |
| TRINITY_sp| O-phosphoseryl-tRNA                                        | 43.70      | 0.00       |         |
| TRINITY_sp| COMM domain-contain                                        | 43.70      | 0.00       |         |
| TRINITY_sp| Regulator of nonsen                                        | 43.70      | 0.00       |         |
| TRINITY_sp| Probable UDP-glucos                                      | 43.70      | 0.00       |         |
| TRINITY_sp| Plant UBX domain-co                                       | 43.70      | 0.00       |         |
| TRINITY_sp| Chaperone protein d                                       | 43.70      | 0.00       |         |
| TRINITY_sp| Ras-related protein                                       | 43.70      | 0.00       |         |
| TRINITY_sp| Probable prolyl 4-h                                       | 43.70      | 0.00       |         |
| TRINITY_sp| Probable protein ph                                       | 43.70      | 0.00       |         |
| TRINITY_sp| U4/U6 small nuclear                                      | 43.70      | 0.00       |         |
| TRINITY_sp| Adenylyl cyclase-as                                       | 43.70      | 0.00       |         |
| TRINITY_sp| Transformer-2 prote                                       | 43.70      | 0.00       |         |
| TRINITY_sp| Aconitate hydratase                                       | 43.70      | 0.00       |         |
| TRINITY_sp| Eukaryotic initiati                                       | 43.70      | 0.00       |         |
| Gene ID       | Gene Name                          | Description                           | Score | E-value |
|--------------|------------------------------------|---------------------------------------|-------|---------|
| TRINITY_sp|A1K51azo1574| UPF0061 protein azo                | 43.60 | 0.00    |
| TRINITY_sp|Q94B7NUDT2| Nudix hydrolase 2 O                | 43.60 | 0.00    |
| TRINITY_sp|Q8H1RRH14| DEAD-box ATP-depend               | 43.60 | 0.00    |
| TRINITY_sp|Q8SS001g07| Ribose-phosphate py                | 43.60 | 0.00    |
| TRINITY_sp|Q9TV5trab1| Ras-related protein                | 43.60 | 0.00    |
| TRINITY_sp|Q9XNnoxA| Superoxide-generat                 | 43.60 | 0.00    |
| TRINITY_sp|Q9VHAda| Adenosine deaminase               | 43.60 | 0.00    |
| TRINITY_sp|Q9SGAACA1| ATP-citrate synthas               | 43.60 | 0.00    |
| TRINITY_sp|Q2661-cAMP-dependent prot           | 43.60 | 0.00    |
| TRINITY_sp|B2V6gGPSA| Glycerol-3-phosphat               | 43.60 | 0.00    |
| TRINITY_sp|Q2W0Os12g01| Probable thiamine b               | 43.60 | 0.00    |
| TRINITY_sp|P929CLC-D| Chloride channel pr               | 43.60 | 0.00    |
| TRINITY_sp|Q9UKACT| Actin, gamma OS=Pen               | 43.60 | 0.00    |
| TRINITY_sp|Q654XRCP1| Cysteine protease X               | 43.60 | 0.00    |
| TRINITY_sp|Q869nramp1| Metal transporter n                | 43.60 | 0.00    |
| TRINITY_sp|P136Atalh: Sodium/potassium-tr    | 43.60 | 0.00    |
| TRINITY_sp|Q0IIDRAB5A| Ras-related protein               | 43.60 | 0.00    |
| TRINITY_sp|Q129RAD54L| DNA repair and reco               | 43.60 | 0.00    |
| TRINITY_sp|P204pyrK| UMP-CMP kinase OS=D              | 43.60 | 0.00    |
| TRINITY_sp|Q7ZKhnel1| Notchless protein h               | 43.60 | 0.00    |
| TRINITY_sp|Q24K1DE| Insulin-degrading e              | 43.60 | 0.00    |
| TRINITY_sp|Q142DYNC1H1| Cytoplasmic dynein               | 43.60 | 0.00    |
| TRINITY_sp|Q9HOFTMEM222| Transmembrane prote              | 43.60 | 0.00    |
| TRINITY_sp|Q963ACX4| Acyl-coenzyme A oxi              | 43.60 | 0.00    |
| TRINITY_sp|P126RPL13| 50S ribosomal prote              | 43.60 | 0.00    |
| TRINITY_sp|Q073GAD| Glutamate decarboxy              | 43.60 | 0.00    |
| TRINITY_sp|Q947JGSPATT0| Cathepsin L 1 OS=Pa            | 43.60 | 0.00    |
| TRINITY_sp|Q8R9pckA| Phosphoenolpyruvate             | 43.60 | 0.00    |
| TRINITY_sp|P401MMP1| Protein MMF1, mitoc             | 43.60 | 0.00    |
| TRINITY_sp|Q5JKOs01g09| Long chain base bio            | 43.60 | 0.00    |
| TRINITY_sp|Q9FKNBR2R2C| DEZH-box ATP-depend            | 43.60 | 0.00    |
| TRINITY_sp|Q5RBPRCP| Lysosomal Pro-X car             | 43.60 | 0.00    |
| TRINITY_sp|P546pkbA| RAC family serine/t             | 43.60 | 0.00    |
| TRINITY_sp|Q8TC1RDHH1| Retinol dehydrogena         | 43.50 | 0.00    |
| TRINITY_sp|Q86Aatp6vld| V-type proton ATPas          | 43.50 | 0.00    |
| TRINITY_sp|A2W1JHK3| Probable histidine              | 43.50 | 0.00    |
| TRINITY_sp|Q9CSFIRE1A| Serine/threonine-pr            | 43.50 | 0.00    |
| TRINITY_sp|Q9MBDHDC10| Dynein-1-beta heavy           | 43.50 | 0.00    |
| TRINITY_sp|Q145ITPR2| Inositol 1,4,5-tris             | 43.50 | 0.00    |
| TRINITY_sp|Q8RY2NUP99A| Nuclear pore comple          | 43.50 | 0.00    |
| TRINITY_sp|Q2GALengB| Probable GFP-bindin            | 43.50 | 0.00    |
| TRINITY_sp|P163Pah| Phenylalanine-4-hyd          | 43.50 | 0.00    |
| TRINITY_sp|Q55DImhsS| Probable histidine-            | 43.50 | 0.00    |
| TRINITY_sp|P364rabc2A| Ras-related protein           | 43.50 | 0.00    |
| TRINITY_sp|Q8C1Thoph1| Thimet oligopeptide            | 43.50 | 0.00    |
| TRINITY_sp|Q5Z7TTLLL10| Inactive polyglycyl        | 43.50 | 0.00    |
| TRINITY_sp|P0C1Iamy3| Alpha-amylose A typ            | 43.50 | 0.00    |
| TRINITY_sp|Q510~| Uncharacterized pro              | 43.50 | 0.00    |
| TRINITY_sp|Q32BDDEGS1| Sphingolipid delta(            | 43.50 | 0.00    |
| TRINITY_sp|Q55CDDBG02| Probable serine/thr           | 43.50 | 0.00    |
| TRINITY_sp|O823SANTR1| Sodium-dependent ph           | 43.50 | 0.00    |
| TRINITY_sp|A7MB1COMT| Catechol O-methyltr         | 43.50 | 0.00    |
| TRINITY_sp|Q6H4alkB2| Alkane 1-monoxygen          | 43.50 | 0.00    |
| TRINITY_sp|P516HISD17B4| Peroxisomal multifu        | 43.50 | 0.00    |
| TRINITY_sp|Q5XMAPaprA| Autocrine prolifer a         | 43.50 | 0.00    |
| TRINITY_sp|Q54GEcLcsp12| CTD small phosphata         | 43.50 | 0.00    |
TRINITY_sp|Q54T1|gacY  Rho GTPase-activating protein gacY OS=Dictyostelium discoideum GN=gacY PE=3 SV=1
TRINITY_sp|Q9MA5|COP21  Coatmer subunit 21 OS=Homo sapiens GN=COP21 PE=1 SV=1
TRINITY_sp|P153|Rps27A  Ubiquitin-40S ribos OS=Dictyostelium discoideum GN=Rps27A PE=1 SV=1
TRINITY_sp|Q5Ulv|C  BEACH domain-containing OS=Dictyostelium discoideum GN=BEACH PE=3 SV=1
TRINITY_sp|Q8N5T|TBC1D19  TBC1 domain family OS=Arabidopsis thaliana GN=TBC1D19 PE=1 SV=1
TRINITY_sp|Q9LX6|GUN4  Tetrapyrrole-binding protein OS=Arabidopsis thaliana GN=GUN4 PE=1 SV=1
TRINITY_sp|Q91d9|aurka-b  Aurora kinase A-B OS=Dictyostelium discoideum GN=AURKA B PE=1 SV=1
TRINITY_sp|Q92V4|Atis547 OS=Arabidopsis thaliana GN=Atis547 PE=1 SV=1
TRINITY_sp|P8087|WDR55  WD repeat-containing OS=Dictyostelium discoideum GN=WDR55 PE=1 SV=1
TRINITY_sp|Q0WPI|2g10  Uncharacterized protein OS=Dictyostelium discoideum GN=Uncharacterized PE=3 SV=1
TRINITY_sp|P426|DRT111  DNA-damage-repair protein OS=Dictyostelium discoideum GN=DRT111 PE=1 SV=1
TRINITY_sp|Q957|HERC2  E3 ubiquitin-protein ligase OS=Dictyostelium discoideum GN=HERC2 PE=1 SV=1
TRINITY_sp|Q554|Gascoc3  Activating signal c OS=Dictyostelium discoideum GN=Gascoc3 PE=1 SV=1
TRINITY_sp|Q9F5W|ABCB11  ATP-binding cassette AOS=Arabidopsis thaliana GN=ABCB11 PE=1 SV=1
TRINITY_sp|Q9RLR|LRC6  Protein tilB homolog OS=Dictyostelium discoideum GN=Protein tilB homolog PE=1 SV=1
TRINITY_sp|Q8LRH|HDA18  Histone deacetylase OS=Dictyostelium discoideum GN=HDA18 PE=1 SV=1
TRINITY_sp|P226|cel1A  Endoglucanase OS=Di OS=Dictyostelium discoideum GN=Endoglucanase PE=1 SV=1
TRINITY_sp|A6QQN|ZNF474  Zinc finger protein OS=Dictyostelium discoideum GN=ZNF474 PE=1 SV=1
TRINITY_sp|Q9MA5|hexal  Beta-hexosaminidase OS=Dictyostelium discoideum GN=hexal PE=1 SV=1
TRINITY_sp|P050|abpA  Alpha-actinin A OS=Dictyostelium discoideum GN=abpA PE=1 SV=1
TRINITY_sp|Q932|ESF13  Phosphatidylinositol OS=Dictyostelium discoideum GN=ESF13 PE=1 SV=1
TRINITY_sp|Q7M6K|Kif27  Kinesin-like protein OS=Dictyostelium discoideum GN=Kif27 PE=1 SV=1
TRINITY_sp|Q9C6|VArpc2  Actin-related OS=Dictyostelium discoideum GN=VArpc2 PE=1 SV=1
TRINITY_sp|A8CVT|ttl16  Tubulin polyglutamy OS=Dictyostelium discoideum GN=Tubulin polyglutamy PE=1 SV=1
TRINITY_sp|F4I8G|GDPD4  Glycerophosphodiester OS=Dictyostelium discoideum GN=GDPD4 PE=1 SV=1
TRINITY_sp|Q5VIE|EHHC1  EF-hand domain-cont OS=Dictyostelium discoideum GN=EHHC1 PE=1 SV=1
TRINITY_sp|Q6K49|PAP2  Probable plastid-OS=Dictyostelium discoideum GN=PAP2 PE=1 SV=1
TRINITY_sp|Q1BK|月底 OS=Dictyostelium discoideum GN=月底 PE=1 SV=1
TRINITY_sp|Q4877|PDI23  Protein disulfide-OS=Dictyostelium discoideum GN=PDI23 PE=1 SV=1
TRINITY_sp|Q3E9|NTR6  Probable anion transm OS=Dictyostelium discoideum GN=NTR6 PE=1 SV=1
TRINITY_sp|Q1331|PAPBC4  Polyadenylate-bindi OS=Dictyostelium discoideum GN=PAPBC4 PE=1 SV=1
TRINITY_sp|C45|GDPD4  Glycerophosphodiester OS=Dictyostelium discoideum GN=GDPD4 PE=1 SV=1
TRINITY_sp|P617|Vbp1  Prefoldin subunit OS=Dictyostelium discoideum GN=Vbp1 PE=1 SV=1
TRINITY_sp|Q9XY|noxA  Superoxide-genera OS=Dictyostelium discoideum GN=noxA PE=1 SV=1
TRINITY_sp|Q946E|ypt7  GTP-binding protein OS=Dictyostelium discoideum GN=ypt7 PE=1 SV=1
TRINITY_sp|Q54K|DDO2GOS=Dictyostelium discoideum GN=DDO2G OS=Dictyostelium discoideum GN=DDO2G PE=1 SV=1
TRINITY_sp|P828|CYP37  Peptidyl-prolyl cis OS=Dictyostelium discoideum GN=CYP37 PE=1 SV=1
TRINITY_sp|Q9SRF|AZG1  Adenine/guanine per OS=Dictyostelium discoideum GN=AZG1 PE=1 SV=1
TRINITY_sp|Q5AVI|ampp  Probable Xaa-Pro am OS=Dictyostelium discoideum GN=ampp PE=1 SV=1
TRINITY_sp|Q3899|KIN10  SNF1-related OS=Dictyostelium discoideum GN=KIN10 PE=1 SV=1
TRINITY_sp|Q6F3C|CPPK1  Calcium-dependent p OS=Dictyostelium discoideum GN=CPPK1 PE=1 SV=1
TRINITY_sp|Q54S|polrlc  DNA-directed RNA po OS=Dictyostelium discoideum GN=polrlc PE=1 SV=1
TRINITY_sp|P137|fs(1)h  Homeotic protein OS=Dictyostelium discoideum GN=fs(1)h PE=1 SV=1
TRINITY_sp|Q6GP1|wdr70  WD repeat-contain OS=Dictyostelium discoideum GN=wdr70 PE=1 SV=1
TRINITY_sp|B8B|D2HDGH  Probable D-2-hydroxy OS=Dictyostelium discoideum GN=D2HDGH PE=1 SV=1
TRINITY_sp|Q55A|DDO2GOS=Dictyostelium discoideum GN=DDO2G PE=1 SV=1
TRINITY_sp|P863|RPP14  Hydroxyacyl-thioest OS=Dictyostelium discoideum GN=RPP14 PE=1 SV=1
TRINITY_sp|Q54V|Felmob  ELMO domain-contain OS=Dictyostelium discoideum GN=Felmob PE=1 SV=1
TRINITY_sp|Q6GMI|5atdn1  Putative deoxyribon OS=Dictyostelium discoideum GN=5atdn1 PE=1 SV=1
TRINITY_sp|Q55Cl|sec31  Protein transport p OS=Dictyostelium discoideum GN=sec31 PE=1 SV=1
TRINITY_sp|Q8BHC|UPF0587 protein Cl OS=Dictyostelium discoideum GN=UPF0587 PE=1 SV=1
TRINITY_sp|P612|PSME3  Proteasome activato OS=Dictyostelium discoideum GN=PSME3 PE=1 SV=1
TRINITY_sp|Q54F|mroh1  Maestro heat-like r OS=Dictyostelium discoideum GN=mroh1 PE=1 SV=1
TRINITY_sp|Q551|Pdpk1  3-phosphinositis OS=Dictyostelium discoideum GN=Pdpk1 PE=1 SV=1
TRINITY_sp|Q86Klap2a1-1  AP-2 complex subunit OS=Dictyostelium discoideum GN=AP-2 complex subunit PE=1 SV=1
TRINITY_sp|Q551\zfp11  Zinc finger protein-like 1 homolog OS=Dictyostelium discoideum GN=zfpl1 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q165\camk4  Calcium/calmodulin-dependent protein kinase OS=Dictyostelium discoideum GN=camk4 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q9C9\atg3g086b  Putative zinc trans 43.40 0.00
TRINITY_sp|Q23\ftllc3  Tubulin glycolylase 3 43.40 0.00
TRINITY_sp|Q4K\chptl  Cholinephosphotrans 43.40 0.00
TRINITY_sp|Q159\sgoa  Guanine nucleotide-binding protein OS=Dictyostelium discoideum GN=sgoa PE=3 SV=1 43.40 0.00
TRINITY_sp|P100\-  Caricain OS=Carica carica 43.40 0.00
TRINITY_sp|Q8H1\dgp3  DAR GTPase 3, chloroplast 43.40 0.00
TRINITY_sp|Q9D\baz22b  Bromodomain adjacent to zinc finger domain OS=Dictyostelium discoideum GN=baz22b PE=3 SV=1 43.40 0.00
TRINITY_sp|B1GMAB_37b  Putative S-adenosyl-l-methionine synthase OS=Dictyostelium discoideum GN=b1gmab_37b PE=3 SV=1 43.40 0.00
TRINITY_sp|Q6NM\ut5  UDP-galactose/UDP-glucose transporter OS=Dictyostelium discoideum GN=ut5 PE=3 SV=1 43.40 0.00
TRINITY_sp|P102\Bpof4_1  Uncharacterized amino acid OS=Dictyostelium discoideum GN=p102_Bpof4_1 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q54I\eif2b1  Translation initiation factor OS=Dictyostelium discoideum GN=eif2b1 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q0J0\os09g050  Probable l-acylglycerol-3-phosphate O-acyltransferase OS=Dictyostelium discoideum GN=os09g050 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q9HD\pmc1  Calcium-transportin OS=Dictyostelium discoideum GN=pmc1 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q3\vps9a  Vacuolar protein sorting-associated protein OS=Dictyostelium discoideum GN=vps9a PE=3 SV=1 43.40 0.00
TRINITY_sp|Q7XA\d1blic  Cytoplasmic dynein OS=Dictyostelium discoideum GN=d1blic PE=3 SV=1 43.40 0.00
TRINITY_sp|Q9FG\ftsh11  ATP-dependent zinc metallohydrolase OS=Dictyostelium discoideum GN=ftsh11 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q75A\arf1  ADP-ribosylation factor OS=Dictyostelium discoideum GN=arf1 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q9XY\fcpa  Probable C-terminal domain OS=Dictyostelium discoideum GN=fcpa PE=3 SV=1 43.40 0.00
TRINITY_sp|Q1R\jcd  Isoisocitrate dehydrogenase OS=Dictyostelium discoideum GN=jcd PE=3 SV=1 43.40 0.00
TRINITY_sp|A1A4\atp9b  Probable ATP-binding cassette (ABC) transporter OS=Dictyostelium discoideum GN=atp9b PE=3 SV=1 43.40 0.00
TRINITY_sp|Q93V1\pabn1  Polyadenylate-binding protein OS=Dictyostelium discoideum GN=pabn1 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q90W\duslp1-b  Dual specificity protein OS=Dictyostelium discoideum GN=duslp1-b PE=3 SV=1 43.40 0.00
TRINITY_sp|Q7LH\ty33-b  Transposon Ty3-I Ga OS=Dictyostelium discoideum GN=ty33-b PE=3 SV=1 43.40 0.00
TRINITY_sp|Q154\abc4  Multidrug resistance OS=Dictyostelium discoideum GN=abc4 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q9SL\rad50  DNA repair protein OS=Dictyostelium discoideum GN=rad50 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q603\aqr  Intron-binding protein OS=Dictyostelium discoideum GN=aqr PE=3 SV=1 43.40 0.00
TRINITY_sp|Q942\hmt2  Sulfite:quinone oxidoreductase OS=Dictyostelium discoideum GN=hmt2 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q6AY\isyl  Pre-mRNA-splicing factor OS=Dictyostelium discoideum GN=isyl PE=3 SV=1 43.40 0.00
TRINITY_sp|Q8L7\nadme2  NAD-dependent malic enzyme OS=Dictyostelium discoideum GN=nadme2 PE=3 SV=1 43.40 0.00
TRINITY_sp|P226\-  Chlorophyll a-b binding protein OS=Dictyostelium discoideum GN=- PE=3 SV=1 43.40 0.00
TRINITY_sp|Q141\wrn  Werner syndrome protein OS=Dictyostelium discoideum GN=wrn PE=3 SV=1 43.40 0.00
TRINITY_sp|Q9FW\hac12  Histone acetyltransferase OS=Dictyostelium discoideum GN=hac12 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q8IN\gyc88e  Soluble guanylate cyclase OS=Dictyostelium discoideum GN=gyc88e PE=3 SV=1 43.40 0.00
TRINITY_sp|P043\pol  Retrovirus-related protein OS=Dictyostelium discoideum GN=pol PE=3 SV=1 43.40 0.00
TRINITY_sp|BpOF4_10225  Uncharacterized protein OS=Bacillus pseudofirmus (strain OF4) GN=BpOF4_10225 PE=3 SV=1 43.40 0.00
TRINITY_sp|At3g08650  Putative zinc transporter OS=Arabidopsis thaliana GN=at3g08650 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q9LS\atl77  RING-H2 finger protein OS=Arabidopsis thaliana GN=atl77 PE=3 SV=1 43.40 0.00
TRINITY_sp|P299\itp-r83  Inositol 1,4,5-trisphosphate receptor OS=Arabidopsis thaliana GN=itp-r83 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q141\tsp2  Trehalose-phosphatase OS=Arabidopsis thaliana GN=tsp2 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q8NE\dennd6b  Protein DENN domain OS=Arabidopsis thaliana GN=dennd6b PE=3 SV=1 43.40 0.00
TRINITY_sp|Q243\diap2  Death-associated protein OS=Arabidopsis thaliana GN=diap2 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q55C\cpnD  Copine-D OS=Dictyostelium discoideum GN=cpnD PE=3 SV=1 43.40 0.00
TRINITY_sp|P840\rhog  Rho-related GTPase OS=Dictyostelium discoideum GN=rhog PE=3 SV=1 43.40 0.00
TRINITY_sp|F0N\sire_1449  Protein-llysine N-methyltransferase OS=Dictyostelium discoideum GN=sire_1449 PE=3 SV=1 43.40 0.00
TRINITY_sp|P350\cbp  Calcium-binding protein OS=Dictyostelium discoideum GN=cbp PE=3 SV=1 43.40 0.00
TRINITY_sp|Q4KL\ibf314  Transcriptional activator OS=Dictyostelium discoideum GN=ibf314 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q54\tddg  Golgi to ER traffic OS=Dictyostelium discoideum GN=tddg PE=3 SV=1 43.40 0.00
TRINITY_sp|Q613\itf88  Intraflagellar transport protein OS=Dictyostelium discoideum GN=itf88 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q9SF\rabe1e  Ras-related protein OS=Dictyostelium discoideum GN=rabe1e PE=3 SV=1 43.40 0.00
TRINITY_sp|Q54Plabc8  ABC transporter C family OS=Dictyostelium discoideum GN=pabc8 PE=3 SV=1 43.40 0.00
TRINITY_sp|P049\gstml  Glutathione S-transferase OS=Dictyostelium discoideum GN=gstml PE=3 SV=1 43.40 0.00
TRINITY_sp|Q54M\gpt  Probable alanine aminotransferase OS=Dictyostelium discoideum GN=gpt PE=3 SV=1 43.40 0.00
TRINITY_sp|Q923\spac69  Uncharacterized protein OS=Dictyostelium discoideum GN=sac69 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q94B\nbd2  External alternative protein OS=Dictyostelium discoideum GN=nbd2 PE=3 SV=1 43.40 0.00
TRINITY_sp|Q139:trm4b Multisite-specific 43.30 0.00
TRINITY_sp|Q0II:NAA50 N-alpha-acetyltransferase 43.30 0.00
TRINITY_sp|Q9D9:A1q7 Ubiquitin-like modifier 43.30 0.00
TRINITY_sp|P623:CPK1 Calcium-dependent p 43.30 0.00
TRINITY_sp|Q993:TY3B-G Transposon Ty3-G Ga 43.30 0.00
TRINITY_sp|Q642:dexf Digestive organ exp 43.30 0.00
TRINITY_sp|Q55K:trmI tRNA (adenine(58))-N 43.30 0.00
TRINITY_sp|Q957:LOG2 Probable E3 ubiquitin 43.30 0.00
TRINITY_sp|Q941:BON1 Protein BONZAI 1 OS 43.30 0.00
TRINITY_sp|Q7X9:AERO2 Endoplasmic reticul 43.30 0.00
TRINITY_sp|Q06A:UCHL3 Ubiquitin carboxyl- 43.30 0.00
TRINITY_sp|P54S:yqjY Uncharacterized protein 43.30 0.00
TRINITY_sp|Q173:W Protein white OS=Ce 43.30 0.00
TRINITY_sp|P080:top2 DNA topoisomerase 2 43.30 0.00
TRINITY_sp|Q439:AIRE Autoimmune regulator 43.30 0.00
TRINITY_sp|Q95L:DGAT1 Diacylglycerol O-ac 43.30 0.00
TRINITY_sp|Q708:GP113 GPI ethanolamine phos 43.30 0.00
TRINITY_sp|Q8RA:mutS DNA mismatch repair 43.30 0.00
TRINITY_sp|Q84W:At5g045 Glycosyltransferase 43.30 0.00
TRINITY_sp|Q9FF:TAF14B Transcription init 43.30 0.00
TRINITY_sp|P0CR:SEC23 Protein transport 43.30 0.00
TRINITY_sp|Q469:tdca tRNA threonyl-carbam 43.30 0.00
TRINITY_sp|Q1AU:rp1M 5OS ribosomal prote 43.30 0.00
TRINITY_sp|Q9NR:DDX21 Nucleolar RNA helic 43.30 0.00
TRINITY_sp|Q550:Abcd3 ATP-binding cassette 43.30 0.00
TRINITY_sp|Q8LS:Os03g01 Probable signal rec 43.30 0.00
TRINITY_sp|Q54S:tmem104 Transmembrane prot 43.30 0.00
TRINITY_sp|F4KHC:CTPA1 Carboxyl-terminal-p 43.30 0.00
TRINITY_sp|Q9XF: Profilin-3 OS=Malus 43.30 0.00
TRINITY_sp|Q86X:DHDHS Dehydrodolichyl dip 43.30 0.00
TRINITY_sp|Q8LS:PHR2 Blue-light photorec 43.30 0.00
TRINITY_sp|Q494:PSAO Photosystem I subun 43.30 0.00
TRINITY_sp|Q23M:T116a Probable beta-tubul 43.30 0.00
TRINITY_sp|Q7X9:PIE1 Protein PHOTOPERIOD 43.30 0.00
TRINITY_sp|Q5Z9:IMCEL1 Probable isoprenylc 43.30 0.00
TRINITY_sp|Q9Z8:FACA10 Calcium-transportin 43.30 0.00
TRINITY_sp|Q23R:BAM3 Beta-amylase 3, chl 43.30 0.00
TRINITY_sp|Q095:tag-124 Probable tRNA pseud 43.30 0.00
TRINITY_sp|Q7TMI:Slc35f2 Solute carrier tran 43.30 0.00
TRINITY_sp|Q8VF:TIM50 Mitochondrial import 43.30 0.00
TRINITY_sp|P222: Pyruvate kinase, cy 43.30 0.00
TRINITY_sp|Q5W7mtyrS Probable tyrosine-- 43.30 0.00
TRINITY_sp|Q6GMplaa Phospholipase A-2-a 43.30 0.00
TRINITY_sp|Q227:RPL28 5OS ribosomal prote 43.30 0.00
TRINITY_sp|A5GE:rlmN Dual-specificity RN 43.30 0.00
TRINITY_sp|C0L5:A4g361 Probable LRR recep 43.30 0.00
TRINITY_sp|P319:HNRFH3 Heterogeneous nuc 43.30 0.00
TRINITY_sp|Q634:Prpsapl Phosphoribosyl pyro 43.30 0.00
TRINITY_sp|Q5Nwoplah 5-oxoprolinase OS=D 43.30 0.00
TRINITY_sp|Q7X:apks15/1 Phenolphthiocerol s 43.20 0.00
TRINITY_sp|Q86C:CPNE8 Copine-8 OS=Homo sa 43.20 0.00
TRINITY_sp|Q091:btl Fibroblast growth f 43.20 0.00
TRINITY_sp|A1X6:strip-1 Septin and tufetin 43.20 0.00
TRINITY_sp|A7SK:vlg1715 Eukaryotic translat 43.20 0.00
TRINITY_sp|P526:iacA Galactoside O-acety 43.20 0.00
TRINITY_sp|P496:Lc10 ATP-sensitive inwar 43.20 0.00
| Gene ID       | Description                                           | OS          | PE | SV |
|--------------|-------------------------------------------------------|-------------|----|----|
| TRINITY_sp| Kinesin heavy chain                                   | Syncephalastrum racemosum | 2  | 1  |
| TRINITY_sp| Protein GPR107                                        | OS=M        | 2  | 0.00 |
| TRINITY_sp| Major vault protein                                   | P5466mvpB   | 2  | 0.00 |
| TRINITY_sp| Mitochondrial chaperon                                 | OS=Q7ZBbcs11 | 2  | 0.00 |
| TRINITY_sp| Basic leucine zippe                                    | Q5Q1BZIPO2 | 2  | 0.00 |
| TRINITY_sp| Alanine--glyoxylate aminotransferase 1                | P435YAGX1   | 2  | 0.00 |
| TRINITY_sp| Serine/threonine-pantothenate synthase                | Q8631OXS1R1 | 2  | 0.00 |
| TRINITY_sp| Gamma-tubulin complex component 3                     | Q9FGGCP3    | 2  | 0.00 |
| TRINITY_sp| Protein CLP1 homolog                                  | Q9SRCLPS3   | 2  | 0.00 |
| TRINITY_sp| 40S ribosomal protein                                 | Q962RPs7    | 2  | 0.00 |
| TRINITY_sp| Transposon Ty3-G Ga                                   | Q9391TY3B-G | 2  | 0.00 |
| TRINITY_sp| Splicing factor 3B                                     | Q134SF3B2   | 2  | 0.00 |
| TRINITY_sp| Phospholipase B1, m                                   | Q3TTP1Pb1   | 2  | 0.00 |
| TRINITY_sp| Zinc finger CCCH domain-contain                       | Q9FNAKAt5g0642 | 2  | 0.00 |
| TRINITY_sp| Serine/threonine-pr                                   | P612SNEDD8  | 2  | 0.00 |
| TRINITY_sp| Squamosa promoter-b                                   | Q9MRZSPL15  | 2  | 0.00 |
| TRINITY_sp| Eukaryotic translatin                                 | Q9LDITIF3A1 | 2  | 0.00 |
| TRINITY_sp| Probable serine/thr                                   | Q9LEITRE    | 2  | 0.00 |
| TRINITY_sp| Thymocyte nuclear protein p                           | Q9O6THYN1   | 2  | 0.00 |
| TRINITY_sp| 3-methylmercaptopro                                   | Q5LR1dmdB   | 2  | 0.00 |
| TRINITY_sp| Histidine protein m                                   | Q55IDDDB_G02 | 2  | 0.00 |
| TRINITY_sp| Ribonuclease TUDOR                                    | Q9FLITSN2   | 2  | 0.00 |
| TRINITY_sp| Uncharacterized sug                                   | Q554s1r0537 | 2  | 0.00 |
| TRINITY_sp| Spastin OS=Ixodes s                                   | P7FXspas    | 2  | 0.00 |
| TRINITY_sp| Leucine-rich repeat                                   | Q3V0lLrrc43 | 2  | 0.00 |
| TRINITY_sp| Probable ATP-depend                                   | Q476MG425   | 2  | 0.00 |
| TRINITY_sp| E3 ubiquitin-protein                                  | Q91YIRnf126 | 2  | 0.00 |
| TRINITY_sp| Tyrosine-protein ph                                   | Q246PTP     | 2  | 0.00 |
| TRINITY_sp| Ribonuclease TUDOR                                    | Q6GNHnrm    | 2  | 0.00 |
| TRINITY_sp| Calcium load-activa                                   | Q1971F22B5.1 | 2  | 0.00 |
| TRINITY_sp| Probable serine/thr                                   | Q54VVDDB_G02 | 2  | 0.00 |
| TRINITY_sp| WD repeat-containin                                   | Q5EB9Wdr70  | 2  | 0.00 |
| TRINITY_sp| MADS-box protein AG                                    | Q827FAGL24  | 2  | 0.00 |
| TRINITY_sp| RAC-gamma serine/th                                   | Q9WUJAct3   | 2  | 0.00 |
| TRINITY_sp| Extracellular signa                                   | Q54QErkB    | 2  | 0.00 |
| TRINITY_sp| Ras-related protein                                   | Q9L2IRABE1D | 2  | 0.00 |
| TRINITY_sp| rRNA biogenesis pro                                   | F4J8eRRP5   | 2  | 0.00 |
| TRINITY_sp| Cyclic GMP-binding                                    | Q8MVFgbpC   | 2  | 0.00 |
| TRINITY_sp| DnaJ homolog subfam                                   | Q9JMKDnaja4 | 2  | 0.00 |
| TRINITY_sp| 12-oxophytodienoate                                   | Q84QQOPR1   | 2  | 0.00 |
| TRINITY_sp| Ras-related protein                                   | P198RABA5E  | 2  | 0.00 |
| TRINITY_sp| Ras-related protein                                   | P281RABA5C  | 2  | 0.00 |
| TRINITY_sp| Actin-1 OS=Acantham                                   | P025Y-     | 2  | 0.00 |
| TRINITY_sp| Protein ref(2)P                                       | Q246eref(2)P | 2  | 0.00 |
| TRINITY_sp| Probable cysteine p                                   | Q9L7TRDL2   | 2  | 0.00 |
| TRINITY_sp| Chitobiosyldiphosph protein                           | P9053alq1   | 2  | 0.00 |
| TRINITY_sp| Dual specificity p                                    | P181isplA   | 2  | 0.00 |
| TRINITY_sp| tRNA pseudouridine                                    | B5Y9trlUA   | 2  | 0.00 |
| TRINITY_sp| Probable lipase C16                                    | P7885SPBC16A | 2  | 0.00 |
| TRINITY_sp| Retrovirus-related                                    | P043pol     | 2  | 0.00 |
| TRINITY_sp| DnaJ homolog subfam                                   | Q6F21dnajc2 | 2  | 0.00 |
| TRINITY_sp| 26S proteasome non-                                   | P8G7YRPN9B  | 2  | 0.00 |
| TRINITY_sp| Poly [ADP-ribose] p                                   | Q9UGFAPRP2  | 2  | 0.00 |
| TRINITY_sp| Vacuolar protein so                                   | Q0P5Vvps8   | 2  | 0.00 |
| Accession | Description                                                                 | Exp | Log2FC |
|-----------|-----------------------------------------------------------------------------|-----|--------|
| TRINITY_sp| 4,5-DOPA dioxygenase extradiol OS=Beta vulgaris                               | 43.10 | 0.00   |
| TRINITY_sp| Transcription initiation factor OS=Saccharomyces cerevisiae                  | 43.10 | 0.00   |
| TRINITY_sp| Rieske domain-containing protein OS=Arabidopsis thaliana                     | 43.10 | 0.00   |
| TRINITY_sp| ER membrane protein OS=Dictyostelium discoideum                             | 43.10 | 0.00   |
| TRINITY_sp| Protein-tyrosine specific protein OS=Dictyostelium discoideum               | 43.10 | 0.00   |
| TRINITY_sp| Zinc finger matrix OS=Dictyostelium discoideum                              | 43.10 | 0.00   |
| TRINITY_sp| Cell wall protein P OS=Dictyostelium discoideum                            | 43.10 | 0.00   |
| TRINITY_sp| Ras GTPase-activating protein OS=Dictyostelium discoideum                  | 43.10 | 0.00   |
| TRINITY_sp| cAMP-specific 3',5' OS=Dictyostelium discoideum                             | 43.10 | 0.00   |
| TRINITY_sp| Protein-dependent DNA h OS=Dictyostelium discoideum                         | 43.10 | 0.00   |
| TRINITY_sp| SEC1 family transposase OS=Dictyostelium discoideum                        | 43.10 | 0.00   |
| TRINITY_sp| Protein PHOTOPERIOD OS=Dictyostelium discoideum                            | 43.10 | 0.00   |
| TRINITY_sp| Rhodanese-like domain OS=Dictyostelium discoideum                          | 43.10 | 0.00   |
| TRINITY_sp| Alternative NAD(P)H OS=Dictyostelium discoideum                            | 43.10 | 0.00   |
| TRINITY_sp| Adenylate kinase OS=Dictyostelium discoideum                               | 43.10 | 0.00   |
| TRINITY_sp| Serine/threonine OS=Dictyostelium discoideum                               | 43.10 | 0.00   |
| TRINITY_sp| GTP-binding protein OS=Dictyostelium discoideum                            | 43.10 | 0.00   |
| TRINITY_sp| Ras-related protein OS=Dictyostelium discoideum                            | 43.10 | 0.00   |
| TRINITY_sp| Oysterol-binding protein OS=Dictyostelium discoideum                       | 43.10 | 0.00   |
| TRINITY_sp| Glycogenin-1 OS=Dictyostelium discoideum                                   | 43.10 | 0.00   |
| TRINITY_sp| 0-methyltransferase OS=Dictyostelium discoideum                            | 43.10 | 0.00   |
| TRINITY_sp| 4-hydroxybenzoate p OS=Dictyostelium discoideum                            | 43.10 | 0.00   |
| TRINITY_sp| Phosphopantetheine OS=Dictyostelium discoideum                             | 43.10 | 0.00   |
| TRINITY_sp| AP-4 complex subunit OS=Dictyostelium discoideum                           | 43.10 | 0.00   |
| TRINITY_sp| Vacuolar protein OS=Dictyostelium discoideum                               | 43.10 | 0.00   |
| TRINITY_sp| Tubby-related protein OS=Dictyostelium discoideum                           | 43.10 | 0.00   |
| TRINITY_sp| Uncharacterized amirator OS=Dictyostelium discoideum                       | 43.10 | 0.00   |
| TRINITY_sp| Ras-like protein ra OS=Dictyostelium discoideum                            | 43.10 | 0.00   |
| TRINITY_sp| H/ACA ribonucleoprotein OS=Dictyostelium discoideum                        | 43.10 | 0.00   |
| TRINITY_sp| Ras-related protein OS=Dictyostelium discoideum                            | 43.10 | 0.00   |
| TRINITY_sp| WD repeat-containing protein OS=Dictyostelium discoideum                   | 43.10 | 0.00   |
| TRINITY_sp| Deoxyribonuclease-1 OS=Dictyostelium discoideum                            | 43.10 | 0.00   |
| TRINITY_sp| Microfibrillar-asso OS=Dictyostelium discoideum                            | 43.10 | 0.00   |
| TRINITY_sp| DFS3-like exonuclease OS=Dictyostelium discoideum                          | 43.10 | 0.00   |
| TRINITY_sp| Seven transmembrane OS=Dictyostelium discoideum                            | 43.10 | 0.00   |
| TRINITY_sp| Probable geranylgeranylase OS=Dictyostelium discoideum                     | 43.10 | 0.00   |
| TRINITY_sp| Pappalysin-2 OS=Dictyostelium discoideum                                   | 43.10 | 0.00   |
| TRINITY_sp| Alpha-mannosidase OS=Dictyostelium discoideum                              | 43.10 | 0.00   |
| TRINITY_sp| Sodium/hydrogen exchanger OS=Dictyostelium discoideum                      | 43.10 | 0.00   |
| TRINITY_sp| Dual specificity protein OS=Dictyostelium discoideum                       | 43.10 | 0.00   |
| TRINITY_sp| Vacuolar protein OS=Dictyostelium discoideum                               | 43.10 | 0.00   |
| TRINITY_sp| Acyl-CoA dehydrogenase OS=Dictyostelium discoideum                        | 43.10 | 0.00   |
| TRINITY_sp| Nuclear distribution OS=Dictyostelium discoideum                           | 43.10 | 0.00   |
| UniProt ID | Description | Score | E-value |
|-----------|-------------|-------|---------|
| SCO1      | Protein SCOL, mitoc | 43.00 | 0.00 |
| P390      | Dynein beta chain, | 43.00 | 0.00 |
| Q9VN1     | Double-strand break | 43.00 | 0.00 |
| P432      | E3 ubiquitin-protein | 43.00 | 0.00 |
| Q8TDX     | Serine/threonine-pr | 43.00 | 0.00 |
| Q744i     | Transcription initi | 43.00 | 0.00 |
| Q9ZR      | Frataxin, mitochond | 43.00 | 0.00 |
| Q8L5C     | Cullin-associated N | 43.00 | 0.00 |
| Q9MLA     | ABC transporter B f | 43.00 | 0.00 |
| Q9PLD     | Riboflavin biosynth | 43.00 | 0.00 |
| P599      | NAD-dependent prote | 43.00 | 0.00 |
| P486i     | Protein pelota OS=D | 43.00 | 0.00 |
| Q9FLK     | Probable ADP-ribo sy | 43.00 | 0.00 |
| Q5VQd     | Probable 2-oxogluta | 43.00 | 0.00 |
| Q807      | Probable nucleoredo | 43.00 | 0.00 |
| Q741i     | Target of rapamycin | 43.00 | 0.00 |
| Q9FXF     | Pheophorbide a oxyg | 43.00 | 0.00 |
| Q154q     | Multidrug resistanc | 43.00 | 0.00 |
| P191i     | Glutathione S-trans | 43.00 | 0.00 |
| Q9ATI     | Transcriptional ada | 43.00 | 0.00 |
| Q5A5i     | Histidine protein k | 43.00 | 0.00 |
| Q2HSI     | Translation machine | 43.00 | 0.00 |
| Q942s     | Probable phospholip | 43.00 | 0.00 |
| Q0A95     | Aldehyde-alcohol de | 43.00 | 0.00 |
| Q9SHK     | GTase LSG1-1 OS=Ar | 43.00 | 0.00 |
| Q6T3i     | Niemann-Pick Cl-lik | 43.00 | 0.00 |
| P307q     | Uncharacterized pro | 43.00 | 0.00 |
| Q004g     | Alpha-glucosidase O | 43.00 | 0.00 |
| Q75iI     | Lysine-specific dem | 43.00 | 0.00 |
| Q7L1c     | Transposon Ty3-I Ga | 43.00 | 0.00 |
| Q9W7q     | Putative maltooligo | 42.90 | 0.00 |
| Q0VGF     | Glycerophosphodiest | 42.90 | 0.00 |
| Q9U11     | E3 ubiquitin-protei | 42.90 | 0.00 |
| Q5Z1i     | Tubulin-specific ch | 42.90 | 0.00 |
| Q3S4I     | Histidine kinase 5 | 42.90 | 0.00 |
| Q9WYi     | Uncharacterized pro | 42.90 | 0.00 |
| Q9FNb     | Beta-galactosidase | 42.90 | 0.00 |
| Q88H1     | Cytosolic Fe-S clus | 42.90 | 0.00 |
| Q9XGH     | Rac-like GTP-bindin | 42.90 | 0.00 |
| Q9G2E     | Sentrin-specific pr | 42.90 | 0.00 |
| Q769i     | Transmembrane emp24 | 42.90 | 0.00 |
| Q1241T    | Transcription facto | 42.90 | 0.00 |
| Q3TWHd    | WD repeat-containin | 42.90 | 0.00 |
| Q96Nc     | Tetratricopeptide r | 42.90 | 0.00 |
| Q2MHH     | Serine/threonine-pr | 42.90 | 0.00 |
| Q8G8X8    | Zinc finger CCCH d | 42.90 | 0.00 |
| Q0JLj     | Probable protein ph | 42.90 | 0.00 |
| Q312p     | Polyadenylate-bindin| 42.90 | 0.00 |
| Q133j     | ATP-dependent RNA h| 42.90 | 0.00 |
| P432i     | E3 ubiquitin-protei | 42.90 | 0.00 |
| Q8W7D0    | Dual specificit y pr | 42.90 | 0.00 |
| Q95Yi     | Penta-EF hand domai| 42.90 | 0.00 |
| Q54Yj    | Hybrid signal trans | 42.90 | 0.00 |
| Q54Wp    | Phospholipase D B O | 42.90 | 0.00 |
| Q9F1i     | Beta-glucosidase 42 | 42.90 | 0.00 |
| Q6ZTq    | Tubulin polyglutam | 42.90 | 0.00 |
| Gene Accession | Protein Name | Description | Score | Confidence |
|---------------|--------------|-------------|-------|------------|
| sp|Q9H4|PIGU|Phosphatidylinosito|42.90|0.00|
| sp|A9CB|ZNF259|Zinc finger protein|42.90|0.00|
| sp|Q9BW|TPP3|Tubulin polymerizat|42.90|0.00|
| sp|Q1B2|rap-1|Ras-related protein|42.90|0.00|
| sp|Q86J|rab5A|Ras-related protein|42.90|0.00|
| sp|Q8K9|GA17800|Leishmanolysin-like|42.90|0.00|
| sp|Q8BX|Arfrp1|ADP-ribosylation fa|42.90|0.00|
| sp|P352|Rab23|Ras-related protein|42.90|0.00|
| sp|P468|yhW|Quercetin, 2,3-dioxy|42.90|0.00|
| sp|P220|bglA|Beta-glucosidase A|42.90|0.00|
| sp|Q236g|gcy-5|Receptor-type guany|42.90|0.00|
| sp|P160|NIA1|Nitrate reductase |42.90|0.00|
| sp|A2AR|Pip5k1|Inositol hexakispho|42.90|0.00|
| sp|Q9W7|cpsfs2|Cleavage and polyad|42.90|0.00|
| sp|Q9VQ|CG9662|Putative oligosacch|42.90|0.00|
| sp|O285|hmqA|3-hydroxy-3-methylg|42.90|0.00|
| sp|P678|SEC11A|Signal peptidase co|42.90|0.00|
| sp|Q557|DDGGO2|UPF0505 protein OS=|42.90|0.00|
| sp|Q9ER|SMC4|Structural maintena|42.90|0.00|
| sp|Q221|GOS12|Golgi SNAP receptor|42.90|0.00|
| sp|Q323|yb1A|N-glycosidase YbiA|42.90|0.00|
| sp|O140|SPAC2C4.1|Putative tRNA 2'-ph|42.90|0.00|
| sp|Q55C|DDGGO2|Probable NADH deyd|42.90|0.00|
| sp|F4JL|IMP42|Importin subunit al|42.90|0.00|
| sp|Q643|ATP12A|Potassium-transport|42.90|0.00|
| sp|P227|Gucylb2|Guanylate cyclase s|42.90|0.00|
| sp|Q96C|KCS5|3-ketoacyl-CoA synt|42.90|0.00|
| sp|P234|CYR1|Adenylate cyclase O|42.90|0.00|
| sp|Q8L7|TUN|UDP-glycosyltransfe|42.90|0.00|
| sp|P944|ynbB|Uncharacterized pro|42.90|0.00|
| sp|Q6TF|isoc2|Isocorismatase dom|42.90|0.00|
| sp|Q9UR|Tf2-11|Transposon Tf2-11 p|42.90|0.00|
| sp|Q9Y2|MTMR7|Myotubularin-relate|42.90|0.00|
| sp|P426|yqjG|Glutathionyl-hydroq|42.90|0.00|
| sp|Q45R|CELF4|CUGBP Elav-like fam|42.90|0.00|
| sp|P408|USP8|Ubiquitin carboxyl-|42.90|0.00|
| sp|Q7PQ|AGAP0|Probable ATP carrier|42.90|0.00|
| sp|Q9KL|UVH1|DNA repair endonuc|42.90|0.00|
| sp|Q8LP|ABCB28|ABC transporter B f|42.90|0.00|
| sp|Q9LM|HRD3A|ERAD-associated E3|42.90|0.00|
| sp|A4QN|len8|Leukocyte receptor|42.90|0.00|
| sp|P487|uapC|Purine permease OS=|42.90|0.00|
| sp|Q5X1|Traf3ip1|TRAF3-interacting p|42.90|0.00|
| sp|B5BU|pf13|Protein kintoun OS=|42.90|0.00|
| sp|Q9C7|AERO1|Endoplasmic reticul|42.90|0.00|
| sp|P105| Retrovirus-related |42.90|0.00|
| sp|P105| Retrovirus-related |42.90|0.00|
| sp|Q7LH|TY3B-I|Transposon Ty3-I Ga|42.90|0.00|
| sp|Q556|mad2l1-1mitotic spindle ass|42.90|0.00|
| sp|P042|CD74|HLA class II histoc|42.90|0.00|
| sp|Q6NS|zgc:661|Serine/threonine-pr|42.90|0.00|
| sp|Q2YD|ANAPC10|Anaphase-promoting |42.90|0.00|
| sp|P339|bsr|Blasticidin-S deami|42.90|0.00|
| sp|A5DI|DDH1|ATP-dependent RNA h|42.90|0.00|
| sp|Q94A|DLD|D-lactate dehydroge|42.80|0.00|
| sp|Q9UJ|AACL1|2-hydroxyacyl-CoA l|42.80|0.00|
| Protein Name | Organism | Gene Symbol | Description | E-value | Score |
|--------------|----------|-------------|-------------|---------|-------|
| Dual specificity protein phosphatase 19 | Homo sapiens | DUSP19 | | 42.70 | 0.00 |
| Manganese-transport | Dictyostelium discoideum | pitB | | 42.70 | 0.00 |
| Ubiquitin carboxyl-terminal hydrolase 5 | Mus musculus | Usp5 | | 42.70 | 0.00 |
| Primary amine oxidase | Arthrobacter sp. (strain P1) | maoI | | 42.70 | 0.00 |
| Condensin complex subunit 2 | Arabidopsis thaliana | CAPH | | 42.70 | 0.00 |
| Manganese-transporting ATPase 13A1 | Homo sapiens | ATP13A1 | | 42.70 | 0.00 |
| 0.00 | | | | | |
| Holo-[acyl-carrier-protein] synthase | Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / DSM 644 / NCIMB 8303) | acpS | | 42.70 | 0.00 |
| Transmembrane protein 165 | Homo sapiens | TMEM165 | | 42.70 | 0.00 |
| Probable alpha,alpha-trehalose-phosphate [UDP-forming] 10 | Arabidopsis thaliana | TPS10 | | 42.70 | 0.00 |
| Mitogen-activated protein kinase-binding protein 1 | Homo sapiens | MAPKBP1 | | 42.70 | 0.00 |
| 40S ribosomal protein S19 | Entamoeba histolytica | RPS19 | | 42.70 | 0.00 |
| DNA ligase | Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) | ligA | | 42.70 | 0.00 |
| U-box domain-containing protein 45 | Arabidopsis thaliana | PUB45 | | 42.70 | 0.00 |
| Eukaryotic elongation factor 2 kinase | Caenorhabditis elegans | efk-1 | | 42.70 | 0.00 |
| Tubulin polymerization-promoting protein family member 3 | Homo sapiens | TPPP3 | | 42.70 | 0.00 |
| NAD-dependent protein deacetylase SRT1 | Arabidopsis thaliana | SRT1 | | 42.70 | 0.00 |
| Metal resistance protein YCF1 | Saccharomyces cerevisiae (strain ATCC 204508 / S288c) | YCF1 | | 42.70 | 0.00 |
| Nicotinamide adenine dinucleotide transporter 2, mitochondrial | Arabidopsis thaliana | NDT2 | | 42.70 | 0.00 |
| Protein VAC14 homolog | Arabidopsis thaliana | VAC14 | | 42.70 | 0.00 |
| Phosphoenolpyruvate carboxylase kinase 2 | Arabidopsis thaliana | PPCK2 | | 42.70 | 0.00 |
| Phototropin-2 | Oryza sativa subsp. japonica | PHOT2 | | 42.70 | 0.00 |
| DnaJ protein ERDJ3B | Arabidopsis thaliana | ERDJ3B | | 42.70 | 0.00 |
| L-threonine 3-dehydrogenase, mitochondrial | Mus musculus | Tdh | | 42.70 | 0.00 |
| Guanine nucleotide-binding protein G(i) subunit alpha-1 | Cavia porcellus | GNAI1 | | 42.70 | 0.00 |
| Pumilio homolog 4 | Arabidopsis thaliana | APUM4 | | 42.70 | 0.00 |
| Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1B | Rattus norvegicus | PDE1B | | 42.70 | 0.00 |
| Hybrid signal transduction histidine kinase G | Dictyostelium discoideum | DhkG | | 42.70 | 0.00 |
| Probable glucan endo-1,3-beta-glucosidase ARB_02077 | Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) | ARB_02077 | | 42.70 | 0.00 |
| Target of rapamycin | Arabidopsis thaliana | Tor | | 42.70 | 0.00 |
| Ras-related protein | Arabidopsis thaliana | D22B5.10 | | 42.70 | 0.00 |
| Holo-[acyl-carrier]-| Arabidopsis thaliana | At4g17474 | | 42.70 | 0.00 |
| Folic acid synthetase | Arabidopsis thaliana | D5Yf01l | | 42.70 | 0.00 |
| Nicotinamide adenine dinucleotide | Arabidopsis thaliana | WRNNTD2 | | 42.70 | 0.00 |
| Nitrogen metabolite | Arabidopsis thaliana | Q5AU3mrnA | | 42.70 | 0.00 |
| Probable glucan end | Arabidopsis thaliana | D4B0\VARB_020 | | 42.70 | 0.00 |
| L-threonine 3-dehydrogenase | Arabidopsis thaliana | Q8K3ITdh | | 42.70 | 0.00 |
| Phosphatidylinositol | Arabidopsis thaliana | GTE12 | | 42.70 | 0.00 |
| Lysosomal acid alph | Arabidopsis thaliana | O009< | | 42.70 | 0.00 |
| Transmembrane prote | Arabidopsis thaliana | TMEM165 | | 42.70 | 0.00 |
| 40S ribosomal prote | Arabidopsis thaliana | RPS19 | | 42.70 | 0.00 |
| Probable phospholipid | Arabidopsis thaliana | A1A4\ATP9B | | 42.70 | 0.00 |
| DNA ligase OS=Haemo | Arabidopsis thaliana | P441\ligA | | 42.70 | 0.00 |
| Heat-stable enterotoxin | Arabidopsis thaliana | Q3UWGuyc2c | | 42.70 | 0.00 |
| Eukaryotic elongati | Arabidopsis thaliana | O019<efk-1 | | 42.70 | 0.00 |
| Primary amine oxida | Arabidopsis thaliana | Q071<maoI | | 42.70 | 0.00 |
| DEEX-box ATP-depend | Arabidopsis thaliana | F4JA<SK12 | | 42.70 | 0.00 |
| Probable alpha,alph | Arabidopsis thaliana | O807<TPS10 | | 42.70 | 0.00 |
| Phosphoenolpyruvate | Arabidopsis thaliana | Q93VFPPC2 | | 42.70 | 0.00 |
| NAD-dependent prote | Arabidopsis thaliana | Q9FEE1SRT1 | | 42.70 | 0.00 |
| Regulator of nonsen | Arabidopsis thaliana | Q9FVWUPF3 | | 42.70 | 0.00 |
| Protein VAC14 homol | Arabidopsis thaliana | Q9ZU\VAC14 | | 42.70 | 0.00 |
| Metal resistance pr | Arabidopsis thaliana | P391\YCF1 | | 42.70 | 0.00 |
| Serine/threonine-pr | Arabidopsis thaliana | A2ZMNEK2 | | 42.70 | 0.00 |
| U-box domain-contai | Arabidopsis thaliana | Q9C7\PUB45 | | 42.70 | 0.00 |
| Condensin complex s | Arabidopsis thaliana | Q564\CAPH | | 42.70 | 0.00 |
| protein | description | score | bit score |
|---------|-------------|-------|-----------|
| Endonuclease III OS = Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) | 42.60 | 0.00 |
| Histidine-containing Protein AAR2 homolog | 42.60 | 0.00 |
| DNA cross-link repair enzyme Dclrel1a | 42.60 | 0.00 |
| Uncharacterized met | 42.60 | 0.00 |
| Probable serine/threonine-protein kinase At3g14840 O6:H1 | 42.60 | 0.00 |
| N-glycosylase/DNA lyase | 42.60 | 0.00 |
| Calcium-dependent protein kinase 4 | 42.60 | 0.00 |
| Ubiquitin carboxyl-terminal hydrolase 26 | 42.60 | 0.00 |
| Ornithine decarboxylase 1 | 42.60 | 0.00 |
| V-type proton ATPase subunit B | 42.60 | 0.00 |
| Protein transport protein Sec24C | 42.60 | 0.00 |
| Microtubule-associated protein RP/EB family member 1 | 42.60 | 0.00 |
| JmjC domain-containing histone demethylation protein 1 | 42.60 | 0.00 |
| Multisite-specific tRNA:(cytosine-C(5))-methyltransferase | 42.60 | 0.00 |
| Plant UBX domain-containing protein 7 | 42.60 | 0.00 |
| Zinc transporter 8 | 42.60 | 0.00 |
| Serine carboxypeptidase 2 | 42.60 | 0.00 |
| Ubiquitin fusion degradation protein 1 homolog | 42.60 | 0.00 |
| JmjC domain-containing protein C | 42.60 | 0.00 |
| Ring finger protein 121 | 42.60 | 0.00 |
| COP9 signalosome complex subunit 5a | 42.60 | 0.00 |
| Mitogen-activated protein kinase kinase 2 | 42.60 | 0.00 |
| BTB/POZ domain-containing protein KCTD7 | 42.60 | 0.00 |
| Probable serine/threonine-protein kinase Nek2 | 42.60 | 0.00 |
| Myosin-5 | 42.60 | 0.00 |
| 60S ribosomal export protein NMD3 | 42.60 | 0.00 |
| Eukaryotic translation initiation factor 4E type 3 | 42.60 | 0.00 |
| Accession | Description | Organism | Score |
|-----------|-------------|----------|-------|
| TRINITY_sp|Q9SDIHMNT-1 | Homocysteine S-methyltransferase 1 | 42.50 |
| TRINITY_sp|Q075isav    | Protein SAV OS=Sulf | 42.50 |
| TRINITY_sp|P0C11cyP5  | Peptidyl-prolyl cis | 42.50 |
| TRINITY_sp|Q9TXcck-mk-1| Calcium/calmodulin- | 42.50 |
| TRINITY_sp|Q9SHBSL3   | Serine/threonine-pr | 42.50 |
| TRINITY_sp|Q9MOI5SF   | Vesicle-fusing ATPa | 42.50 |
| TRINITY_sp|P2185GART  | Trifunctional purin | 42.50 |
| TRINITY_sp|F4JNIAPE2  | DNA-(apurinic or ap | 42.50 |
| TRINITY_sp|A2WMNZP6   | Actin-related prote | 42.50 |
| TRINITY_sp|P2511   | Cysteine proteinase | 42.50 |
| TRINITY_sp|P1401   | Chymopapain OS=Cari | 42.50 |
| TRINITY_sp|P52911VPS4 | Vacuolar protein so | 42.50 |
| TRINITY_sp|F740rsmI  | Ribosomal RNA small | 42.50 |
| TRINITY_sp|Q097ttrm12 | Multifunctional met | 42.50 |
| TRINITY_sp|Q64JFPMIT2 | Protein-L isoaspart | 42.50 |
| TRINITY_sp|PF928AL2A  | Phospholipid-transp | 42.50 |
| TRINITY_sp|Q9BUSAAMT1 | Protein misato homo | 42.50 |
| TRINITY_sp|F4JAPFH2  | Prolyl 4-hydroxylas | 42.50 |
| TRINITY_sp|P577IEEEFSEC| Selenocysteine-spec | 42.50 |
| TRINITY_sp|Q91WilSc22a7| Solute carrier fami | 42.50 |
| TRINITY_sp|F371i   | Actophorin OS=Acant | 42.50 |
| TRINITY_sp|Q08sBwzgc154| Uncharacterized pro | 42.50 |
| TRINITY_sp|P1011 | Retrovirus-related | 42.50 |
| TRINITY_sp|Q87ALPD  | UPF0394 membrane pr | 42.50 |
| TRINITY_sp|Q502tmem41a| Transmembrane prote | 42.50 |
| TRINITY_sp|Q597iarkl | Serine/threonine-pr | 42.50 |
| TRINITY_sp|Q8BH4Napep1d| N-acyl-phosphatidyl | 42.50 |
| TRINITY_sp|Q651Os9g05P-loop NTPase domai | 42.50 |
| TRINITY_sp|Q9M2CEF  | Protein transport p | 42.50 |
| TRINITY_sp|P1011 | Retrovirus-related | 42.50 |
| TRINITY_sp|Q54XIfmeB | Probable enoyl-CoA | 42.40 |
| TRINITY_sp|Q4FZ7seh11-a| Nucleoporin seh1-A | 42.40 |
| TRINITY_sp|Q54RdhkL  | Hybrid signal trans | 42.40 |
| TRINITY_sp|Q5NCTTf2   | Transcription termi | 42.40 |
| TRINITY_sp|P6299RAC1  | Ras-related C3 botu | 42.40 |
| TRINITY_sp|Q8RJNLPL3 | Omega-amidase, chlo | 42.40 |
| TRINITY_sp|Q206fPrim1 | DNA primase small s | 42.40 |
| TRINITY_sp|Q2KJ3PPP2R4| Serine/threonine-pr | 42.40 |
| TRINITY_sp|Q3AB1coaE | Dephospho-CoA kinas | 42.40 |
| TRINITY_sp|Q9LD1DFW5  | 7-dehydrocholesterol | 42.40 |
| TRINITY_sp|Q141fDOCK1 | Deducator of cytoki | 42.40 |
| TRINITY_sp|A4QQFMM1   | Riboflavin kinase O | 42.40 |
| TRINITY_sp|P204pyrK  | UMP-CMP kinase OS=D | 42.40 |
| TRINITY_sp|Q3T01CTSH | Pro-cathepsin H OS= | 42.40 |
| TRINITY_sp|Q8HOVHDA9 | Histone deacetylase | 42.40 |
| TRINITY_sp|Q08Balg1l | GDP-Man:Man(3)GlcNA | 42.40 |
| TRINITY_sp|P077fSI   | Sucrase-isomaltase, | 42.40 |
| TRINITY_sp|P502fALTA | Tubulin alpha-1A ch | 42.40 |
| TRINITY_sp|Q925=GBP1  | Golgi-specific bref | 42.40 |
| TRINITY_sp|Q6AI1HEAT6 | HEAT repeat-contain | 42.40 |
| TRINITY_sp|Q930TATDN2 | Putative deoxyribon | 42.40 |
| TRINITY_sp|P534fCTN  | Caltractin OS=Naegi | 42.40 |
| TRINITY_sp|Q6AYNudt5 | ADP-sugar pyrophosph | 42.40 |
| TRINITY_sp|Q12XIDD-G02| Probable serine/thr | 42.40 |
| TRINITY_sp|F4JSfSRFR1 | Suppressor of RPS4- | 42.40 |
| TRINITY_sp|Q8IYITRMT44| Probable tRNA (urac | 42.40 |
| Accession   | Description                                                                 | Score | E-value |
|-------------|-----------------------------------------------------------------------------|-------|---------|
| TRINITY_sp| Histone acetyltransferase HAC12 | 42.30 | 0.00    |
| TRINITY_sp| Ubiquitin carboxyl-terminal ligase | 42.30 | 0.00    |
| TRINITY_sp| Chaperone protein d | 42.30 | 0.00    |
| TRINITY_sp| Probable C-terminal DNA-dependent proteolytic enzyme | 42.30 | 0.00    |
| TRINITY_sp| DNA repair helicase | 42.30 | 0.00    |
| TRINITY_sp| DnaJ homolog subfam | 42.30 | 0.00    |
| TRINITY_sp| DNA repair helicase | 42.30 | 0.00    |
| TRINITY_sp| Mitochondrial inner membrane protein | 42.30 | 0.00    |
| TRINITY_sp| Zinc finger protein | 42.30 | 0.00    |
| TRINITY_sp| Probable CDP-diacylglycerol synthase | 42.30 | 0.00    |
| TRINITY_sp| Mitochondrial import inner membrane translocase subunit TIM2 | 42.30 | 0.00    |
| TRINITY_sp| Acetyl-coenzyme A synthetase | 42.30 | 0.00    |
| TRINITY_sp| RAC-gamma serine/threonine-protein kinase | 42.30 | 0.00    |
| TRINITY_sp| Mitochondrial import inner membrane translocase subunit TIM2 | 42.30 | 0.00    |
| TRINITY_sp| Cysteine protease X | 42.30 | 0.00    |
| TRINITY_sp| UTP-glucose-1-phosphate uridylyltransferase | 42.30 | 0.00    |
| TRINITY_sp| Acetyl-coenzyme A synthetase | 42.30 | 0.00    |
| TRINITY_sp| ADP-ribosylation factor 1 | 42.30 | 0.00    |
| TRINITY_sp| Para-aminobenzoate synthase | 42.30 | 0.00    |
| TRINITY_sp| Gelation factor | 42.30 | 0.00    |
| TRINITY_sp| Beta-galactosidase | 42.30 | 0.00    |
| TRINITY_sp| Endo-1,3(4)-beta-glucanase 1 | 42.30 | 0.00    |
| TRINITY_sp| Protein-lysine N-methyltransferase mettl10 | 42.30 | 0.00    |
| TRINITY_sp| ADP-ribosylation factor 1 | 42.30 | 0.00    |
| TRINITY_sp| Para-aminobenzoate synthase | 42.30 | 0.00    |
| TRINITY_sp| Gelation factor | 42.30 | 0.00    |
| TRINITY_sp| Beta-galactosidase | 42.30 | 0.00    |
| TRINITY_sp| Endo-1,3(4)-beta-glucanase 1 | 42.30 | 0.00    |
| Accession   | Description                                      | Score | E-value |
|-------------|--------------------------------------------------|-------|---------|
| TRINITY_sp|Q9H8A:MOB1A                                       | 42.20 | 0.00    |
| TRINITY_sp|Q440:HSP90                                        | 42.20 | 0.00    |
| TRINITY_sp|F44P:LG6                                          | 42.20 | 0.00    |
| TRINITY_sp|Q9Yo1ctxA                                         | 42.20 | 0.00    |
| TRINITY_sp|P480:gacS                                          | 42.20 | 0.00    |
| TRINITY_sp|Q5U7:MIMI_R8|Putative serine/thr | 42.20 | 0.00    |
| TRINITY_sp|P424:coBA                                          | 42.20 | 0.00    |
| TRINITY_sp|Q30WitruB                                          | 42.20 | 0.00    |
| TRINITY_sp|Q9CS5:RFC1                                         | 42.20 | 0.00    |
| TRINITY_sp|Q744:scw1                                          | 42.20 | 0.00    |
| TRINITY_sp|Q9H7I:SMYD3                                        | 42.20 | 0.00    |
| TRINITY_sp|Q2NL:TSR1                                          | 42.20 | 0.00    |
| TRINITY_sp|Q999:RKD1                                          | 42.20 | 0.00    |
| TRINITY_sp|Q5BB1me1A                                          | 42.20 | 0.00    |
| TRINITY_sp|P426:ygjG                                          | 42.20 | 0.00    |
| TRINITY_sp|Q9FW:ABC11                                         | 42.20 | 0.00    |
| TRINITY_sp|Q8JIY:ING5                                          | 42.20 | 0.00    |
| TRINITY_sp|Q9FJ:ADG9                                          | 42.20 | 0.00    |
| TRINITY_sp|Q703:Hsd17b1(3-hydroxyacyl-CoA) d                   | 42.20 | 0.00    |
| TRINITY_sp|F0A99:tas                                          | 42.20 | 0.00    |
| TRINITY_sp|Q6FV:IPL1                                          | 42.20 | 0.00    |
| TRINITY_sp|Q6AX:Mtm1                                          | 42.20 | 0.00    |
| TRINITY_sp|Q8WYI:ING5                                         | 42.20 | 0.00    |
| TRINITY_sp|Q6DJ:tamm41                                        | 42.20 | 0.00    |
| TRINITY_sp|A6WYf:fmt                                          | 42.20 | 0.00    |
| TRINITY_sp|P134:abpC                                          | 42.20 | 0.00    |
| TRINITY_sp|P530:YIP1                                          | 42.20 | 0.00    |
| TRINITY_sp|P497:Ribonucleoside-diph | 42.20 | 0.00    |
| TRINITY_sp|Q9DJ:Rnf125                                       | 42.20 | 0.00    |
| TRINITY_sp|Q0WU:MTP10                                         | 42.20 | 0.00    |
| TRINITY_sp|Q8W4:PTC52                                         | 42.20 | 0.00    |
| TRINITY_sp|O608:BRD4                                          | 42.20 | 0.00    |
| TRINITY_sp|Q944:OST48                                         | 42.20 | 0.00    |
| TRINITY_sp|Q8VE:Cbw1                                          | 42.20 | 0.00    |
| TRINITY_sp|Q8LPF:ABC18                                        | 42.20 | 0.00    |
| TRINITY_sp|F4KBI:AE17                                         | 42.20 | 0.00    |
| TRINITY_sp|Q9N2:SACS                                          | 42.20 | 0.00    |
| TRINITY_sp|Q8Y7:RS.Z23Z                                       | 42.20 | 0.00    |
| TRINITY_sp|Q9QXIK:21a                                         | 42.20 | 0.00    |
| TRINITY_sp|Q54I:DBB_G02|Probable serine/thr | 42.20 | 0.00    |
| TRINITY_sp|Q9VT_RhoGAP6_Rho GTPase-activati | 42.20 | 0.00    |
| TRINITY_sp|Q9LM:CIPK5                                         | 42.10 | 0.00    |
| TRINITY_sp|Q9CPILipf                                         | 42.10 | 0.00    |
| TRINITY_sp|Q9P7:alg9                                          | 42.10 | 0.00    |
| TRINITY_sp|A2YS:ATG8C                                         | 42.10 | 0.00    |
| TRINITY_sp|D9HP:CNR11                                         | 42.10 | 0.00    |
| TRINITY_sp|Q9Y2:POLR3K                                         | 42.10 | 0.00    |
| TRINITY_sp|P0DKHSD4                                           | 42.10 | 0.00    |
| TRINITY_sp|P116:NIA1                                          | 42.10 | 0.00    |
| TRINITY_sp|Q9N2:GPR                                           | 42.10 | 0.00    |
| TRINITY_sp|Q9SB:AP4M                                          | 42.10 | 0.00    |
| TRINITY_sp|P540:FG4.1                                         | 42.10 | 0.00    |
| TRINITY_sp|Q861:ddx52                                         | 42.10 | 0.00    |
| TRINITY_sp|Q54c:pgl                                           | 42.10 | 0.00    |
| TRINITY_sp|Q928:INPP5D                                         | 42.10 | 0.00    |
| Accession | Name                                                                 | Organism           | Gene    | Protein  |
|-----------|----------------------------------------------------------------------|--------------------|---------|----------|
| sp|O42872|RRP41_SCHPO|Dictyostelium discoideum|sp|Q0P5Y3|TPPP2_MOUSE|Mus musculus|
| sp|Q55CT0|TPP1_DICDI|Dictyostelium discoideum|sp|Q9ZRD6|YKT61_ARATH|Arabidopsis thaliana|
| sp|Q8NDW8|TT21A_HUMAN|Dictyostelium discoideum|sp|Q9FVR6|Y1222_ARATH|Arabidopsis thaliana|
| sp|B5DEQ3|XPP3_RAT|Mus musculus|sp|O43242|PSMD3_HUMAN|Homo sapiens|
| sp|P51892|SELB_HUMAN|Homo sapiens|sp|Q00IB6|CPL4_ARATH|Arabidopsis thaliana|
| sp|Q8RY46|ABCD2_DICDI|Dictyostelium discoideum|sp|Q88FY6|NICT_PSEPK|Pseudomonas putida|
| sp|Q24C27|COG8_HUMAN|Arabidopsis thaliana|sp|Q9NZT2|OGFR_HUMAN|Homo sapiens|
| sp|Q8CHB8|TTLL5_MOUSE|Mus musculus|sp|Q9ASR4|BCAL2_ARATH|Arabidopsis thaliana|
| sp|Q86GV3|GCY28_CAEEL|Caenorhabditis elegans|sp|O15706|VACA_DICDI|Dictyostelium discoideum|
| sp|Q9NZJ4|SACS_HUMAN|Homo sapiens|sp|Q5ZL2|ZRNA6B2|Schizosaccharomyces pombe|
| sp|Q55CT0|TPP1_DICDI|Dictyostelium discoideum|sp|Q9N2S|SACS|Homo sapiens|
| sp|Q8CHETt1l5|Tubulin polyglutamy|Arabidopsis thaliana|sp|Q8212|VPS32.1|Vacuolar protein so|
| sp|Q0143|ubl11|Ubiguinit-like protein|sp|A8QCEBm_495|Lateral signaling t|Arabidopsis thaliana|
| sp|Q9N2T0GFR|Opioid growth facto|Homo sapiens|sp|Q0157|vacA|Vacuolin-A OS=Dicty|
| sp|B0DZIAMPP|Probable Xaa-Pro am|Arabidopsis thaliana|sp|Q810K|Kiaaa089|Uncharacterized pro|
| sp|P52522|Rab3|Homo sapiens|sp|Q54G3ctdsp12|CTD small phosphat|Arabidopsis thaliana|
| sp|Q9L2AALA8|Probable phospholipid binding protein|Schizosaccharomyces pombe|sp|Q24C2RPL14|60S ribosomal prote|Arabidopsis thaliana|
| sp|Q9XI2UGT80B1|Sterol 3-beta-glucosyltransferase|Schizosaccharomyces pombe|sp|Q9AT5g274|Branched-chain-aminotransferase|Arabidopsis thaliana|
| sp|Q9TVVSDH|Trans-1,2-dihydroxyphenylalanine|Homo sapiens|sp|Q105CIPK9|CBL-interacting protein|Arabidopsis thaliana|
| sp|Q88F2nicT|Putative metabolite|Homo sapiens|sp|P134Oabpc|Gelation factor OS=Dicty|
| sp|Q86Gcqc28|Receptor-type guanylate cyclase 28|Homo sapiens|sp|Q86HbRhhdd1|Rhomboi-d-related protein|Arabidopsis thaliana|
| sp|Q86HbRhhdd1|Rhomboi-d-related protein|Homo sapiens|sp|Q96MOCOG8|Conserved oligomerization domain protein|Arabidopsis thaliana|
| sp|Q2Y6irlmW|Dual-specificity RNA helicase|Arabidopsis thaliana|sp|O605CDC40|Pre-mRNA-processing factor|Arabidopsis thaliana|
| sp|Q8TR9abcD2|ABC transporter D 2|Arabidopsis thaliana|sp|P518Iilg1|DNA ligase 1 OS=Xen|
| sp|Q86HbRhhdd1|Rhomboi-d-related protein|Homo sapiens|sp|Q6IDI1Atglg95|=Transmembrane emp24|Arabidopsis thaliana|
| sp|Q8R4IA1tg146|Probable splicing factor|Arabidopsis thaliana|sp|Q84RY4ABC5|ABC transporter B 5|Arabidopsis thaliana|
| sp|Q2721lap-2|Putative aminopeptidase|Arabidopsis thaliana|sp|Q00ICPI4|RNA polymerase II C|Arabidopsis thaliana|
| sp|Q96NNAIFM3|Apoptosis-inducing factor|Arabidopsis thaliana|sp|P577EEFSEC|Selenocysteine-specific tRNAMet|Arabidopsis thaliana|
| sp|O4322PSMD3|26S proteasome non-ATPase 14 subunit Y|Arabidopsis thaliana|sp|B9DGsTAF7|Transcription initiation factor|Arabidopsis thaliana|
| sp|B5DEXxnpep3|Probable Xaa-Pro am|Arabidopsis thaliana|sp|P4195YRB1|Ran-specific GTPase|Arabidopsis thaliana|
| sp|Q9FVA1tg322|Uncharacterized protein|Arabidopsis thaliana|sp|Q8NDVTtC21A|Tetratricopeptide repeat factor|Arabidopsis thaliana|
| sp|Q9ZR3YKDT61|VAMP-like protein Y|Arabidopsis thaliana|sp|Q55Cttpp1|Tripeptidyl-peptidase|Arabidopsis thaliana|
| sp|Q0P53tppp2|Tubulin polymerization factor|Arabidopsis thaliana|sp|P4847Tbca|Tubulin-specific chaperone|Arabidopsis thaliana|
| sp|A0AV7UBA6|Ubiquitin-like modulator|Arabidopsis thaliana|sp|O428skl6|Exosome complex member|Arabidopsis thaliana|
| sp|Q54P1tmem184|Transmembrane protein|Arabidopsis thaliana|
| Accession | Description                                                                 | Identity  | Value  |
|-----------|------------------------------------------------------------------------------|-----------|--------|
| TRINITY_sp| Putative serine protein | 42.00 | 0.00 |
| TRINITY_sp| Nucleoredoxin OS=Mu | 42.00 | 0.00 |
| TRINITY_sp| Kinesin-like protein | 42.00 | 0.00 |
| TRINITY_sp| Probable serine/thr | 42.00 | 0.00 |
| TRINITY_sp| Methyltransferase-1 | 42.00 | 0.00 |
| TRINITY_sp| N-glycosidase YbiA | 42.00 | 0.00 |
| TRINITY_sp| Protein BOLA2 OS=Ar | 42.00 | 0.00 |
| TRINITY_sp| Peroxisomal acyl-co | 42.00 | 0.00 |
| TRINITY_sp| Spindle assembly ch | 42.00 | 0.00 |
| TRINITY_sp| Countin-1 OS=Dicty | 42.00 | 0.00 |
| TRINITY_sp| 78 kDa glucose-regulated protein homolog | 42.00 | 0.00 |
| TRINITY_sp| Beta-catenin-like protein | 42.00 | 0.00 |
| TRINITY_sp| ATP-dependent RNA helicase | 42.00 | 0.00 |
| TRINITY_sp| Protein ROS1 | 42.00 | 0.00 |
| TRINITY_sp| 78 kDa glucose-regulated protein homolog | 42.00 | 0.00 |
| TRINITY_sp| Kinesin-like protein | 42.00 | 0.00 |
| TRINITY_sp| Ubiquitin-protein ligase E3A | 42.00 | 0.00 |
| TRINITY_sp| Protein C21orf2 homolog | 42.00 | 0.00 |
| TRINITY_sp| Ubiquitin-protein ligase E3A | 42.00 | 0.00 |
| TRINITY_sp| Charged multivesicular body protein | 42.00 | 0.00 |
| TRINITY_sp| ADP,ATP carrier protein | 42.00 | 0.00 |
| TRINITY_sp| Spindle assembly checkpoint kinase | 42.00 | 0.00 |
| TRINITY_sp| ATP-dependent RNA helicase | 42.00 | 0.00 |
| TRINITY_sp| Protein C21orf2 homolog | 42.00 | 0.00 |
| TRINITY_sp| Ubiquitin-protein ligase E3A | 42.00 | 0.00 |
| TRINITY_sp| SH3 domain-containing protein | 42.00 | 0.00 |
| TRINITY_sp| Cell division cycle | 42.00 | 0.00 |
| TRINITY_sp| Dihydrofolate reductase | 42.00 | 0.00 |
| TRINITY_sp| Protein ROS1 OS=Ara | 42.00 | 0.00 |
| TRINITY_sp| Beta-xylosidase OS= | 42.00 | 0.00 |
| TRINITY_sp| 3'-5' exoribonuclease | 42.00 | 0.00 |
| TRINITY_sp| cAMP-dependent protein | 42.00 | 0.00 |
| TRINITY_sp| WASH complex subunit | 42.00 | 0.00 |
| TRINITY_sp| Protein C2orf2 homolog | 42.00 | 0.00 |
| TRINITY_sp| ATP-dependent Clp p | 42.00 | 0.00 |
| TRINITY_sp| Ubiquitin carboxyl- | 42.00 | 0.00 |
| TRINITY_sp| U3 snoRNP-associated protein-like | 42.00 | 0.00 |
| TRINITY_sp| Cell division cycle | 42.00 | 0.00 |
| TRINITY_sp| Protein CASP OS=Ara | 42.00 | 0.00 |
| TRINITY_sp| ABC transporter F | 42.00 | 0.00 |
| TRINITY_sp| Endoribonuclease Yb | 42.00 | 0.00 |
| TRINITY_sp| L-methionine gamma- | 42.00 | 0.00 |
| TRINITY_sp| Gamma-glutamyltrans | 42.00 | 0.00 |
| TRINITY_sp| Probable protein ph | 42.00 | 0.00 |
| TRINITY_sp| ADP,ATP carrier pro | 42.00 | 0.00 |
| TRINITY_sp| Mitotic checkpoint | 42.00 | 0.00 |
| TRINITY_sp| Beta-catenin-like | 42.00 | 0.00 |
| TRINITY_sp| UF0585 protein Clp | 42.00 | 0.00 |
| TRINITY_sp| Kinesin-like protein | 42.00 | 0.00 |
| TRINITY_sp| Uncharacterized protein | 42.00 | 0.00 |
| TRINITY_sp| Emopamil-binding protein | 42.00 | 0.00 |
| TRINITY_sp| Transcription factor | 42.00 | 0.00 |
| TRINITY_sp| Dynactin subunit | 42.00 | 0.00 |
| TRINITY_sp| Probable serine/thr | 42.00 | 0.00 |
| TRINITY_sp| Protein ref(2)P OS= | 42.00 | 0.00 |
| TRINITY_sp| Ubiquitin-protein ligase | 42.00 | 0.00 |
| TRINITY_sp| Isopentenyl-diphosph | 42.00 | 0.00 |
| TRINITY_sp| Vacuolar protein so | 42.00 | 0.00 |
| TRINITY_sp| Penicillin G acylas | 42.00 | 0.00 |
| TRINITY_sp| Probable E3 ubiquitin | 42.00 | 0.00 |
| TRINITY_sp| Charged multivesicu | 42.00 | 0.00 |
| TRINITY_sp| Shewanella-like pro | 42.00 | 0.00 |
| Accession | Description                                           | Log2 Fold Change | q-value |
|-----------|-------------------------------------------------------|-----------------|---------|
| TRINITY_sp| Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial | 41.90            | 0.00    |
| TRINITY_sp| Intron-binding protein                               | 41.90            | 0.00    |
| TRINITY_sp| Probable plastid-lipid-binding protein PAP6           | 41.90            | 0.00    |
| TRINITY_sp| Activating signal c                                   | 41.90            | 0.00    |
| TRINITY_sp| Anhydro-N-acetylmur                                    | 41.90            | 0.00    |
| TRINITY_sp| Branchpoint-bridgin protein                           | 41.90            | 0.00    |
| TRINITY_sp| SH3 domain-containing protein                         | 41.90            | 0.00    |
| TRINITY_sp| RNA-binding protein                                   | 41.90            | 0.00    |
| TRINITY_sp| Polyadenylate-binding protein                         | 41.90            | 0.00    |
| TRINITY_sp| E3 ubiquitin ligase                                   | 41.90            | 0.00    |
| TRINITY_sp| ER membrane protein                                   | 41.90            | 0.00    |
| TRINITY_sp| Transcription initiation                              | 41.90            | 0.00    |
| TRINITY_sp| Ubiquitin carboxyl-terminal hydrolase USP24           | 41.90            | 0.00    |
| TRINITY_sp| COP9 signalosome protein                              | 41.90            | 0.00    |
| TRINITY_sp| Pepsin A                                             | 41.90            | 0.00    |
| TRINITY_sp| ATP-dependent Clp protease related protein             | 41.90            | 0.00    |
| TRINITY_sp| E3 ubiquitin-protease                                 | 41.90            | 0.00    |
| TRINITY_sp| Lysosomal Pro-X car                                   | 41.90            | 0.00    |
| TRINITY_sp| Importin subunit al                                   | 41.90            | 0.00    |
| TRINITY_sp| Multiple RNA-binding protein                          | 41.90            | 0.00    |
| TRINITY_sp| COP9 signalosome co                                   | 41.90            | 0.00    |
| TRINITY_sp| Ribosomal protein L                                   | 41.90            | 0.00    |
| TRINITY_sp| Functional unknown                                    | 41.90            | 0.00    |
| TRINITY_sp| Protein RT2 homolog                                   | 41.90            | 0.00    |
| TRINITY_sp| Uncharacterized RNA                                   | 41.90            | 0.00    |
| TRINITY_sp| DNA cross-link repair                                 | 41.90            | 0.00    |
| TRINITY_sp| Elongation factor 4                                   | 41.90            | 0.00    |
| TRINITY_sp| Cell division cycle                                   | 41.90            | 0.00    |
| TRINITY_sp| Insulin-degrading enzyme                              | 41.90            | 0.00    |
| TRINITY_sp| Calcium-dependent p                                   | 41.90            | 0.00    |
| TRINITY_sp| Phosphatidylinosito                                   | 41.90            | 0.00    |
| TRINITY_sp| Membrane-associated                                   | 41.90            | 0.00    |
| TRINITY_sp| Tetratricopeptide repeat                              | 41.90            | 0.00    |
| TRINITY_sp| Carrier protein YMC                                   | 41.80            | 0.00    |
| TRINITY_sp| Protein EIN4 OS=Ara                                     | 41.80            | 0.00    |
| TRINITY_sp| Telomerase Cajal bo                                   | 41.80            | 0.00    |
| TRINITY_sp| DNA polymerase lamb                                    | 41.80            | 0.00    |
| TRINITY_sp| Epithelial splicing                                   | 41.80            | 0.00    |
| TRINITY_sp| DDT domain-containing protein                         | 41.80            | 0.00    |
| TRINITY_sp| Dynactin subunit 5                                    | 41.80            | 0.00    |
| TRINITY_sp| Dynein 18 kDa light                                   | 41.80            | 0.00    |
| TRINITY_sp| Phospholipase A(1)                                    | 41.80            | 0.00    |
| TRINITY_sp| Histone-lysine N-me                                   | 41.80            | 0.00    |
| TRINITY_sp| Major facilitator s                                   | 41.80            | 0.00    |
| TRINITY_sp| Beta-ureidopropionana                                 | 41.80            | 0.00    |
| TRINITY_sp| Chromatin modificat                                    | 41.80            | 0.00    |
| TRINITY_sp| Purine nucleoside p                                   | 41.80            | 0.00    |
| TRINITY_sp| Probable phospholipin                                 | 41.80            | 0.00    |
| TRINITY_sp| Alpha-1,3-mannosyl-1-beta                            | 41.80            | 0.00    |
| TRINITY_sp| Mitochondrial coenzyme                                | 41.80            | 0.00    |
| TRINITY_sp| Probable splicing factors                             | 41.80            | 0.00    |
| TRINITY_sp| SNF1-related protein                                  | 41.80            | 0.00    |
| TRINITY_sp| Mitogen-activated protein                             | 41.80            | 0.00    |
| TRINITY_sp| Serine/threonine-protein                              | 41.80            | 0.00    |
| TRINITY_sp| Arginine--tRNA ligase                                 | 41.80            | 0.00    |
| Accession     | Description                                      | ID   |
|---------------|--------------------------------------------------|------|
| Q9SGKALA5     | Probable phospholipid-transporting ATPase 5       | 41.80|
| P749:polA     | DNA polymerase I OS                              | 41.80|
| Q54T:gacY     | Rho GTPase-activator                            | 41.80|
| A7MBipkn2     | Serine/threonine-pr                             | 41.80|
| Q8RXT1atg146| Probable splicing factor                         | 41.80|
| Q588:FAB5C    | Ras-related protein                              | 41.80|
| Q6BC:CYB5R2   | NADH-cytochrome b5                               | 41.80|
| P049:Gstm1     | Glutathione S-trans                              | 41.80|
| Q9JH:Efsec     | Selenocysteine-spec                              | 41.80|
| B41B:Mat89Ba   | Nucleolar protein 6                              | 41.80|
| P435:crp-4     | Cathepsin B-like cy                              | 41.80|
| Q6Z9:Kin7H     | Kinesin-like protein 1                           | 41.80|
| P539:Anapc1    | Anaphase-promoting                               | 41.80|
| Q5P6:ATXR2     | Histone-lysine N-me                              | 41.80|
| Q004:Ptbp1     | Polypyrimidine trac                              | 41.80|
| Q9ZW:CYTB5-D   | Cytochrome B5 isofo                              | 41.80|
| Q993:Tyb3-G    | Transposon Ty3-G Ga                              | 41.80|
| P463:bcCa      | Acetyl-/propionyl-c                              | 41.80|
| Q86Y:CPNE8     | Copine-8 OS=Homo sa                              | 41.80|
| Q6W:METTL16    | Methyltransferase-1                              | 41.80|
| Q056:Chel2      | Uncharacterized pro                              | 41.80|
| Q11G:rp1Y      | 50S ribosomal prote                              | 41.80|
| Q9UB:DNAJB9    | DnaJ homolog subfam                             | 41.80|
| Q8YH:cssb      | Single-stranded DNA                              | 41.80|
| Q542:tbcb      | Tubulin-specific ch                              | 41.80|
| Q9CS:Ecd       | Protein ecdysoneles                              | 41.80|
| Q6NS:Pedc11    | Protein RRP5 homolo                             | 41.80|
| Q54B:sf1       | Branchpoint-bridgin                              | 41.80|
| Q945:modA      | Neutral alpha-glucol                             | 41.80|
| Q245:U2af50    | Splicing factor U2A                               | 41.80|
| Q916:PA0142    | 8-oxoguanine deamin                             | 41.80|
| Q9LT:VPS9A     | Vacuolar protein so                              | 41.80|
| A2X6:CDKG-1    | Cyclin-dependent k1                              | 41.80|
| P118:CDK4      | Cyclin-dependent k1                              | 41.80|
| P973:Nxn       | Nucleoredoxin OS=Mu                              | 41.80|
| P278:ERV1      | Mitochondrial FAD-1                              | 41.80|
| Q9FE:ISRT1     | NAD-dependent prote                              | 41.80|
| Q9KT:truC      | tRNA pseudouridine                               | 41.80|
| F4HNI:Atg069   | Nardilsin-like OS=                                | 41.80|
| P227:FXG3      | Probable peroxygena                              | 41.80|
| Q9C5:PPK7      | ATP-dependent 6-pho                               | 41.80|
| P378:CNN1      | Calponin-1 (Fragment)                            | 41.80|
| Q246:MSH2      | DNA mismatch repair                              | 41.80|
| A4K2:STK4      | Serine/threonine-pr                              | 41.80|
| Q8L8:REQL4A    | ATP-dependent DNA h                              | 41.80|
| Q9SJ:SAE2      | SUMO-activating enz                              | 41.80|
| Q9FF:NFXL2     | NF-X1-type zinc fin                              | 41.80|
| P422:SKIV2L2   | Superkiller viralic                              | 41.80|
| Q9K:Aass       | Alpha-aminoacidip s                              | 41.80|
| Q229:FTSH1     | Probable inactive A                              | 41.80|
| P221:cta3      | Calcium-transportin                              | 41.80|
| Q8KQtpcphE     | Cyanophycinase OS=P                               | 41.80|
| P230:−         | Dynein beta chain,                               | 41.80|
| Q9Z2:CAS       | Exportin-2 OS=Arabi                              | 41.80|
| Q152:FPWP2     | Periodic tryptophan                              | 41.80|
| P269:−         | ADP-ribosylation fa                              | 41.80|
| Gene ID         | Description                                           | Gene ID         | Description                                           |
|----------------|-------------------------------------------------------|----------------|-------------------------------------------------------|
| sp|Q8VW.HPT1 | Homogentisate phytyltransferase 1, chloroplastic | sp|Q541Itmem120 | Transmembrane protease |
| sp|P296.MPP | Mitochondrial-protein importase subunit | sp|Q8GWAt5g039 | Uncharacterized protein |
| sp|Q5U3Rab16 | Rab-like protein 6 | sp|Q9LTFTG2 | Protein TRIGALACTOS |
| sp|Q3950DA4 | Dynine beta chain | sp|B7ZMxpnppep3 | Probable Xaa-Pro am | 41.70 0.00 |
| sp|B5F7:rihC | Non-specific ribonuclease | sp|Q7KAcSBG2 | Long-chain-fatty-acid-CoA ligase |
| sp|Q55DabcG22 | ABC transporter G f | sp|P167V-UBI | Ubiquitin-like protein |
| sp|Q191gcy-12 | Receptor-type guanylate cyclase | sp|Q423CBN1 | Calcineurin subunit |
| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase | sp|Q7KAcSBG2 | Long-chain-fatty-acid-CoA ligase |
| sp|A7R2dpp3 | Dipeptidyl peptidase | sp|Q9P7ppr11 | Pre-mRNA-processing |
| sp|Q423CBN1 | Calcineurin subunit | sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
| sp|Q9BIdHC10 | Dynine-1-beta heavy | sp|Q541Itmem184 | Transmembrane protease |
| sp|Q54GAdtymk | Thymidylate kinase | sp|Q6Pbhzgc:733 | Coenzyme Q-binding |
| sp|Q933TY3B | Transposon Ty3-Ga | sp|Q5ZKAcSBG2 | Long-chain-fatty-acid-CoA ligase |
| sp|Q55DabcG22 | ABC transporter G f | sp|P167V-UBI | Ubiquitin-like protein |
| sp|Q191gcy-12 | Receptor-type guanylate cyclase | sp|Q423CBN1 | Calcineurin subunit |
| sp|Q55DabcG22 | ABC transporter G f | sp|A7R2dpp3 | Dipeptidyl peptidase |
| sp|Q9P7ppr11 | Pre-mRNA-processing | sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase | sp|Q54GAdtymk | Thymidylate kinase |
| sp|Q9STFKNK3 | Probable serine/threonine-protein kinase |
| sp|Q9SLFLALIS3 | ALA-interacting subunit |
| sp|Q9CSABA3 | Molybdenum cofactor |
| sp|Q8ERJ1BO1403 | N-acetyldiaminopimelate reductase |
| sp|Q104mtg157 | Meiotically up-regulated protein |
| sp|Q6MEcrsmH | Ribosomal RNA small |
| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
| sp|Q423CBN1 | Calcineurin subunit |
| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
| sp|Q5MEcrsmH | Ribosomal RNA small |
| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
| sp|Q423CBN1 | Calcineurin subunit |
| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
| sp|Q5MEcrsmH | Ribosomal RNA small |
| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
| sp|Q423CBN1 | Calcineurin subunit |
| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
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| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
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| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
| sp|Q423CBN1 | Calcineurin subunit |
| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
| sp|Q5MEcrsmH | Ribosomal RNA small |
| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
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| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
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| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
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| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
| sp|Q423CBN1 | Calcineurin subunit |
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| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
| sp|Q423CBN1 | Calcineurin subunit |
| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
| sp|Q5MEcrsmH | Ribosomal RNA small |
| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
| sp|Q423CBN1 | Calcineurin subunit |
| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
| sp|Q5MEcrsmH | Ribosomal RNA small |
| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
| sp|Q423CBN1 | Calcineurin subunit |
| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
| sp|Q5MEcrsmH | Ribosomal RNA small |
| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
| sp|Q423CBN1 | Calcineurin subunit |
| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
| sp|Q5MEcrsmH | Ribosomal RNA small |
| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
| sp|Q423CBN1 | Calcineurin subunit |
| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
| sp|Q5MEcrsmH | Ribosomal RNA small |
| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
| sp|Q423CBN1 | Calcineurin subunit |
| sp|Q9W41dnc | cAMP-specific 3',5' phosphodiesterase |
| sp|Q5MEcrsmH | Ribosomal RNA small |
| sp|Q6E5MC5MCSU3 | Molybdenum cofactor |
| sp|Q423CBN1 | Calcineurin subunit |
Carboxyl-terminal-p 41.50 0.00
Tripeptidyl-peptida 41.50 0.00
Homocysteine S-meth 41.50 0.00
ATP-dependent Clp p 41.50 0.00
Dolichol phosphate- 41.50 0.00
Serine/threonine-pr 41.50 0.00
Synaptotagmin-2 OS=H 41.50 0.00
Vacuolar calcium io 41.50 0.00
Activating signal c 41.50 0.00
Beta-glucoosidase 40 41.50 0.00
3-mercaptopryruvate 41.50 0.00
Transcription facto 41.50 0.00
Proto-oncogene tyro 41.50 0.00
Probable protein ph 41.50 0.00
Aurora kinase A OS= 41.50 0.00
Retrovirus-related 41.50 0.00
Vacuolar protein so 41.40 0.00
Copper-transporting 41.40 0.00
Myb-related protein 41.40 0.00
Replication termina 41.50 0.00
Microtubule-associ 41.40 0.00
Dynemin alpha chain, 41.40 0.00
Alpha-glucosidase O 41.40 0.00
Vacuolar protein so 41.40 0.00
Copper-transporting 41.40 0.00
Myb-related protein 41.40 0.00
Probable protein ABH 41.40 0.00
Multidrug resistanc 41.40 0.00
Adenylate kinase OS 41.40 0.00
Arginyl-tRNA--prot 41.40 0.00
External alternativ 41.40 0.00
Glutaminyl-peptide 41.40 0.00
Flotillin-like prot 41.40 0.00
AP-4 complex subuni 41.40 0.00
Alpha-galactosidase 41.40 0.00
Probable copper-tra 41.40 0.00
tRNA wybutosine-syn 41.40 0.00
WD repeat-containin 41.40 0.00
Histone deacetylase 41.40 0.00
G patch domain and 41.40 0.00
Alpha-1,4-N-acetylg 41.40 0.00
DNA polymerase nu O 41.40 0.00
Enoyl-CoA delta iso 41.40 0.00
RCC1 and BTB domain 41.40 0.00
Exosome complex com 41.40 0.00
RNA cytidine acetyl 41.40 0.00
Retrovirus-related 41.40 0.00
Thermostable alkaline protease OS=Bacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) GN=BH0855 PE=1 SV=2
Glycerol uptake facilitator protein OS=Bacillus subtilis (strain 168) GN=glpF PE=2 SV=2
NEDD8 OS=Drosophila melanogaster GN=Nedd8 PE=1 SV=1
Probable phospholipid-transporting ATPase 8 OS=Arabidopsis thaliana GN=ALA8 PE=3 SV=1
Gem-associated protein 2 OS=Dictyostelium discoideum GN=gemin2 PE=3 SV=1
Probable serine/threonine-protein kinase nek2 OS=Dictyostelium discoideum GN=nek2 PE=1 SV=1
Tetratricopeptide repeat protein 37 OS=Homo sapiens GN=TTC37 PE=1 SV=1
Adenylyltransferase and sulfurtransferase MOCS3 OS=Arabidopsis thaliana GN=MOCS3 PE=2 SV=1
Protein phosphatase 2C 70 OS=Arabidopsis thaliana GN=KAPP PE=1 SV=2
Retrovirus-related Pol polyprotein from transposon TNT 1-94 OS=Nicotiana tabacum PE=2 SV=1
GDP-mannose transporter GONST1 OS=Arabidopsis thaliana GN=GONST1 PE=1 SV=2
Prefoldin subunit 4 OS=Bos taurus GN=PFDN4 PE=2 SV=1
Dynein heavy chain 3, axonemal OS=Homo sapiens GN=DNAH3 PE=2 SV=1
Probable dihydroneopterin aldolase 3 OS=Arabidopsis thaliana GN=FOLB3 PE=2 SV=1
Sperm motility kinase 2B OS=Mus musculus GN=Smok2b PE=2 SV=1
Probable 28S rRNA (cytosine-C(5))-methyltransferase OS=Mus musculus GN=Nsun5 PE=2 SV=2
Guanine exchange factor for Rac 30 OS=Dictyostelium discoideum GN=gxcDD PE=3 SV=3
DNA replication complex GINS protein PSF2 OS=Homo sapiens GN=GINS2 PE=1 SV=1
Protein CWC15 homolog A OS=Xenopus laevis GN=cwc15-a PE=2 SV=1
ATP-dependent RNA helicase laf-1 OS=Caenorhabditis elegans GN=laf-1 PE=1 SV=1
Dehydrogenase/reductase SDR family member 12 OS=Bos taurus GN=DHRS12 PE=2 SV=1
Protein ABCI12, chloroplastic OS=Arabidopsis thaliana GN=ABCI12 PE=1 SV=1
Vacuolar protein sorting-associated protein 35 OS=Mus musculus GN=Vps35 PE=1 SV=1
Inositol oxygenase 1 OS=Arabidopsis thaliana GN=MIOX1 PE=2 SV=1
UPF0668 protein C10orf76 homolog OS=Xenopus laevis PE=2 SV=2
Probable prolyl 4-hydroxylase 4 OS=Arabidopsis thaliana GN=P4H4 PE=2 SV=1
Guanine exchange factor for Rac 30 OS=Dictyostelium discoideum GN=gxcDD PE=3 SV=3
DNA replication complex GINS protein PSF2 OS=Homo sapiens GN=GINS2 PE=1 SV=1
Protein CWC15 homolog A OS=Xenopus laevis GN=cwc15-a PE=2 SV=1
ATP-dependent RNA helicase laf-1 OS=Caenorhabditis elegans GN=laf-1 PE=1 SV=1
Dehydrogenase/reductase SDR family member 12 OS=Bos taurus GN=DHRS12 PE=2 SV=1
Protein ABCI12, chloroplastic OS=Arabidopsis thaliana GN=ABCI12 PE=1 SV=1
Vacuolar protein sorting-associated protein 35 OS=Mus musculus GN=Vps35 PE=1 SV=1
Inositol oxygenase 1 OS=Arabidopsis thaliana GN=MIOX1 PE=2 SV=1
UPF0668 protein C10orf76 homolog OS=Xenopus laevis PE=2 SV=2
Probable prolyl 4-hydroxylase 4 OS=Arabidopsis thaliana GN=P4H4 PE=2 SV=1
Guanine exchange factor for Rac 30 OS=Dictyostelium discoideum GN=gxcDD PE=3 SV=3
DNA replication complex GINS protein PSF2 OS=Homo sapiens GN=GINS2 PE=1 SV=1
Protein CWC15 homolog A OS=Xenopus laevis GN=cwc15-a PE=2 SV=1
ATP-dependent RNA helicase laf-1 OS=Caenorhabditis elegans GN=laf-1 PE=1 SV=1
Dehydrogenase/reductase SDR family member 12 OS=Bos taurus GN=DHRS12 PE=2 SV=1
Protein ABCI12, chloroplastic OS=Arabidopsis thaliana GN=ABCI12 PE=1 SV=1
Vacuolar protein sorting-associated protein 35 OS=Mus musculus GN=Vps35 PE=1 SV=1
Inositol oxygenase 1 OS=Arabidopsis thaliana GN=MIOX1 PE=2 SV=1
| Ensembl Transcript ID | Description                                           | Gene Name | Source Genome | Ensembl Gene ID | Protein ID | Organism | GO ID | Similarity | E-value |
|----------------------|-------------------------------------------------------|-----------|---------------|-----------------|------------|----------|-------|------------|----------|
| TRINITY_sp|Q7Y2|GTE7 | Transcription factor | 41.10 | 0.00 |
| TRINITY_sp|P109| Retrovirus-related | 41.10 | 0.00 |
| TRINITY_sp|Q9WY|YM_0508 | Uncharacterized protein | 41.10 | 0.00 |
| TRINITY_sp|A6QL|ERI3 | ER11 exoribonuclease | 41.10 | 0.00 |
| TRINITY_sp|Q54I|vps13A | Putative vacuolar protein | 41.10 | 0.00 |
| TRINITY_sp|Q9FN|FP7 | Serine/threonine-protein | 41.10 | 0.00 |
| TRINITY_sp|Q8RE|adk | Adenylate kinase | 41.10 | 0.00 |
| TRINITY_sp|Q3MH|RNP2C | RNA-binding protein | 41.10 | 0.00 |
| TRINITY_sp|Q8T8|abcd2 | ABC transporter D1 | 41.10 | 0.00 |
| TRINITY_sp|P258|FPB | Fructose-1,6-bisphosphatase | 41.10 | 0.00 |
| TRINITY_sp|Q86J|mmgt | Membrane magnesium transporter | 41.10 | 0.00 |
| TRINITY_sp|Q9C6|MTK | Methylthioribose kinase | 41.10 | 0.00 |
| TRINITY_sp|A0A0|frnF213b | E3 ubiquitin-protein ligase | 41.10 | 0.00 |
| TRINITY_sp|Q9CO|DNAH6 | Dynein heavy chain | 41.10 | 0.00 |
| TRINITY_sp|Q9UJ|N31 | Stress response protein | 41.10 | 0.00 |
| TRINITY_sp|Q9S7|TADA | tRNA(adenine(34)) d | 41.10 | 0.00 |
| TRINITY_sp|Q96P|ARHGEPF1 | Rho guanine nucleotide exchange factor | 41.10 | 0.00 |
| TRINITY_sp|Q47J|MSH6 | DNA mismatch repair | 41.10 | 0.00 |
| TRINITY_sp|P280|AOAH | Acylcoxyacyl hydrolase | 41.10 | 0.00 |
| TRINITY_sp|P398|NMD3 | 60S ribosomal protein | 41.10 | 0.00 |
| TRINITY_sp|A3RF|ALDH3A1 | Aldehyde dehydrogenase | 41.10 | 0.00 |
| TRINITY_sp|Q156|MAREE1 | Microtubule-associated protein | 41.10 | 0.00 |
| TRINITY_sp|Q8WT|NOV3L | Nucleolar complex protein | 41.10 | 0.00 |
| TRINITY_sp|Q5BL|stap8b1 | Phospholipid-transfer protein | 41.10 | 0.00 |
| TRINITY_sp|Q9SF|IAt3g071 | Protein transport protein | 41.10 | 0.00 |
| TRINITY_sp|Q9CK|FX13 | Plant UBX domain-containing protein | 41.10 | 0.00 |
| TRINITY_sp|Q54Y|DDB2 | DNA-binding protein | 41.10 | 0.00 |
| TRINITY_sp|A6R7|PAN1 | Actin cytoskeleton protein | 41.10 | 0.00 |
| TRINITY_sp|Q5C9|NOM1 | Nucleolar protein | 41.10 | 0.00 |
| TRINITY_sp|Q8WR|UPL6 | E3 ubiquitin-protein ligase | 41.10 | 0.00 |
| TRINITY_sp|B5X8|mrp158 | Peptidyl-tRNA hydrolase | 41.10 | 0.00 |
| TRINITY_sp|Q9P7|ISPAC521 | NADP-dependent 3-dehydrohydrogenase | 41.10 | 0.00 |
| TRINITY_sp|O654|XCP1 | Cysteine protease X | 41.10 | 0.00 |
| TRINITY_sp|Q9FG|CEP1 | KDEL-tailed cysteine protease | 41.10 | 0.00 |
| TRINITY_sp|Q6Q4|Atp2b4 | Plasma membrane calcium ATPase | 41.10 | 0.00 |
| TRINITY_sp|Q9LM|PAPS1 | Nuclear poly(A) binding protein | 41.10 | 0.00 |
| TRINITY_sp|P98I|Gnpat | Dihydroxyacetone phosphate transport protein | 41.00 | 0.00 |
| TRINITY_sp|Q54P|Pwbp2 | Periodic tryptophan protein | 41.00 | 0.00 |
| TRINITY_sp|Q7L2|ABHD13 | Protein ABHD13 | 41.00 | 0.00 |
| TRINITY_sp|O4301|SPC62 | Deoxycoformyltransferase | 41.00 | 0.00 |
| TRINITY_sp|Q6ZR|DNAH12 | Dynein heavy chain | 41.00 | 0.00 |
| TRINITY_sp|Q0VC|PQLC2 | PQ-loop repeat-containing protein | 41.00 | 0.00 |
| TRINITY_sp|P0CQ|SPT16 | FACT complex subunit | 41.00 | 0.00 |
| TRINITY_sp|A1XK|astip1 | Septin and tufelin | 41.00 | 0.00 |
| TRINITY_sp|Q55P|wdr91 | WD repeat-containing protein | 41.00 | 0.00 |
| TRINITY_sp|Q957|HERC2 | E3 ubiquitin-protein ligase | 41.00 | 0.00 |
| TRINITY_sp|Q1RM|NMRD1 | DNA-directed RNA polymerase | 41.00 | 0.00 |
| TRINITY_sp|B0W3|CPIJ001 | Adenylyltransferase | 41.00 | 0.00 |
| TRINITY_sp|P241|Thop1 | Thimet oligopeptidase | 41.00 | 0.00 |
| TRINITY_sp|Q9UB|CTS1 | Cathepsin F | 41.00 | 0.00 |
| TRINITY_sp|P1691|Pka-C3 | Protein kinase C3 | 41.00 | 0.00 |
| TRINITY_sp|Q9M9|SOL1 | Carboxypeptidase | 41.00 | 0.00 |
| TRINITY_sp|P543|Pdi | Protein disulfide-isomerase | 41.00 | 0.00 |
| TRINITY_sp|P441|1igA | DNA ligase | 41.00 | 0.00 |
| TRINITY_sp|Q2K3|CDC42 | Cell division control protein | 41.00 | 0.00 |
| TRINITY_sp|Q5VQ|Os6g014 | Coatamer subunit | 41.00 | 0.00 |
| Accession | Description                                                                 | Identity | Similarity |
|-----------|------------------------------------------------------------------------------|----------|------------|
| TRINITY_sp| Protein arv1 homolog                                                        | 41.00    | 0.00       |
| TRINITY_sp| Cyclin-Y-like protein                                                         | 41.00    | 0.00       |
| TRINITY_sp| Probable ubiquitin                                                           | 41.00    | 0.00       |
| TRINITY_sp| Autocrine proliferin                                                         | 41.00    | 0.00       |
| TRINITY_sp| Maltose fermentation                                                         | 41.00    | 0.00       |
| TRINITY_sp| ATP-dependent RecD-                                                        | 41.00    | 0.00       |
| TRINITY_sp| Probable serine/thr                                                         | 41.00    | 0.00       |
| TRINITY_sp| E3 ubiquitin-protein                                                         | 41.00    | 0.00       |
| TRINITY_sp| Switch 2 OS=Arabido                                                        | 41.00    | 0.00       |
| TRINITY_sp| Ras guanine nucleot                                                        | 41.00    | 0.00       |
| TRINITY_sp| Mitogen-activated p                                                         | 41.00    | 0.00       |
| TRINITY_sp| Nuclear export medi                                                        | 41.00    | 0.00       |
| TRINITY_sp| Soluble guanylate c                                                         | 41.00    | 0.00       |
| TRINITY_sp| DNA-directed RNA po                                                        | 41.00    | 0.00       |
| TRINITY_sp| Inosine-5'-monophos                                                         | 41.00    | 0.00       |
| TRINITY_sp| Pre-mRNA-splicing f                                                          | 41.00    | 0.00       |
| TRINITY_sp| Serine/threonine-pr                                                        | 41.00    | 0.00       |
| TRINITY_sp| Ribosome biogenesis                                                       | 41.00    | 0.00       |
| TRINITY_sp| Serine/threonine-pr                                                        | 41.00    | 0.00       |
| TRINITY_sp| Malonyl-CoA-acyl ca                                                           | 41.00    | 0.00       |
| TRINITY_sp| Ras guanine nucleot                                                        | 41.00    | 0.00       |
| TRINITY_sp| ADP,ATP carrier pro                                                        | 41.00    | 0.00       |
| TRINITY_sp| Transcription facto                                                          | 41.00    | 0.00       |
| TRINITY_sp| Serine/threonine-pr                                                        | 41.00    | 0.00       |
| TRINITY_sp| Retrovirus-related                                                          | 41.00    | 0.00       |
| TRINITY_sp| Calcium-dependent p                                                         | 41.00    | 0.00       |
| TRINITY_sp| Tectonin beta-prope                                                         | 41.00    | 0.00       |
| TRINITY_sp| Viral IAP-associate                                                         | 41.00    | 0.00       |
| TRINITY_sp| Cell division cycle                                                         | 41.00    | 0.00       |
| TRINITY_sp| DEWH-box ATP-depend                                                         | 41.00    | 0.00       |
| TRINITY_sp| Tyramine beta-hydro                                                        | 41.00    | 0.00       |
| TRINITY_sp| Intraflagellar tran                                                         | 41.00    | 0.00       |
| TRINITY_sp| Ras-related protein                                                          | 41.00    | 0.00       |
| TRINITY_sp| Probable ethanolam(cid                                                    | 41.00    | 0.00       |
| TRINITY_sp| Calcium-dependent p                                                         | 41.00    | 0.00       |
| TRINITY_sp| Heat shock 70 kDa p                                                         | 41.00    | 0.00       |
| TRINITY_sp| Cilia- and flagella                                                        | 41.00    | 0.00       |
| TRINITY_sp| Cinnamyl alcohol de                                                         | 41.00    | 0.00       |
| TRINITY_sp| GTPase-activating R                                                         | 41.00    | 0.00       |
| TRINITY_sp| ATP-dependent RNA h                                                         | 41.00    | 0.00       |
| TRINITY_sp| Probable protein ph                                                         | 41.00    | 0.00       |
| TRINITY_sp| Zinc finger protein                                                         | 41.00    | 0.00       |
| TRINITY_sp| Calcium-transportin                                                          | 41.00    | 0.00       |
| Accession | Description | Comment | EC | GO | PMID |
|-----------|-------------|---------|----|----|------|
| TRINITY_sp| Q84K.DDB2   | DNA damage-binding | 40.90 | 0.00 |
| TRINITY_sp| Q8W5.AT3g151 | Uncharacterized exo | 40.90 | 0.00 |
| TRINITY_sp| P562.AT1g1222 | Probable translational | 40.90 | 0.00 |
| TRINITY_sp| Q9U7.TRMT6   | tRNA (adenine(58)-N) | 40.90 | 0.00 |
| TRINITY_sp| Q9M1.AT2g4962 | ABC transporter B | 40.90 | 0.00 |
| TRINITY_sp| Q8UV ba2la  | Bromodomain adjacen | 40.90 | 0.00 |
| TRINITY_sp| QT65.ROB1 | Putative serine/thr | 40.90 | 0.00 |
| TRINITY_sp| Q294.AT5g1789 | Histone-lysine N-me | 40.90 | 0.00 |
| TRINITY_sp| P324.AT5g2562 | Guanylate-binding p | 40.90 | 0.00 |
| TRINITY_sp| Q28F.AT5g1727 | Major facilitator s | 40.90 | 0.00 |
| TRINITY_sp| P347.AT5g0135 | Ras-like protein 2 | 40.90 | 0.00 |
| TRINITY_sp| F4J2.AT5g1727 | Cytosolic endo-beta | 40.90 | 0.00 |
| TRINITY_sp| Q6Z8.AT5g0202 | Probable protein ph | 40.90 | 0.00 |
| TRINITY_sp| P201.AT1g2821 | Glutathione S-trans | 40.90 | 0.00 |
| TRINITY_sp| Q9LE.CAFL1-10 | Probable CCR4-assoc | 40.90 | 0.00 |
| TRINITY_sp| P412.AT5g0271 | ATP-binding cassett | 40.90 | 0.00 |
| TRINITY_sp| Q225.AT1g5409 | Serine/threonine-pr | 40.90 | 0.00 |
| TRINITY_sp| Q8GW.GFA2 | Chaperone protein d | 40.90 | 0.00 |
| TRINITY_sp| Q6AX.AT1g0608 | Myotubularin OS=Rat | 40.90 | 0.00 |
| TRINITY_sp| Q8BL.CPNE4 | Copine-4 OS=Mus mus | 40.90 | 0.00 |
| TRINITY_sp| P331.AT5g2562 | Long-chain-fatty-ac | 40.90 | 0.00 |
| TRINITY_sp| Q995.AT5g2562 | Translin-associated | 40.90 | 0.00 |
| TRINITY_sp| F4I2.AT5g1727 | Switch 2 OS=Arabidob | 40.90 | 0.00 |
| TRINITY_sp| Q756.AT1g2821 | Ubiquitin carboxyl- | 40.90 | 0.00 |
| TRINITY_sp| Q953.AT1g2821 | Ubiquitin-like modi | 40.90 | 0.00 |
| TRINITY_sp| Q76F.AT1g2821 | Nucleolar protein 8 | 40.90 | 0.00 |
| TRINITY_sp| Q5TI.AT5g1606 | von Willebrand fact | 40.90 | 0.00 |
| TRINITY_sp| Q9SU.AT1g0216 | Probable polyamine | 40.90 | 0.00 |
| TRINITY_sp| Q9LV.AT1g0216 | Two-component respo | 40.90 | 0.00 |
| TRINITY_sp| Q54D.AT5g1727 | Protein RER1 homolo | 40.90 | 0.00 |
| TRINITY_sp| Q763.AT5g1727 | rho-related protein | 40.90 | 0.00 |
| TRINITY_sp| Q151.AT1g0216 | Niemann-Pick C1 pro | 40.90 | 0.00 |
| TRINITY_sp| Q865.AT1g0216 | Copine-8 OS=Homo sa | 40.90 | 0.00 |
| TRINITY_sp| P975.AT1g0216 | Peroxisomal acyl-co | 40.90 | 0.00 |
| TRINITY_sp| Q9FH.GSTT3 | Glutathione S-trans | 40.90 | 0.00 |
| TRINITY_sp| Q229.AT3g1789 | Uncharacterized pro | 40.90 | 0.00 |
| TRINITY_sp| Q9HB.RRAGC | Ras-related GTP-bin | 40.90 | 0.00 |
| TRINITY_sp| Q9FF.AT1g0216 | Probable zinc metal | 40.90 | 0.00 |
| TRINITY_sp| Q54W.AT1g0216 | Glucosamine 6-phosp | 40.90 | 0.00 |
| TRINITY_sp| Q94B.GCP1 | Germination-specific | 40.90 | 0.00 |
| TRINITY_sp| Q54U.AT1g0216 | ABC transporter C | 40.90 | 0.00 |
| TRINITY_sp| Q9VR.AT1g0216 | Inositol hexakispho | 40.90 | 0.00 |
| TRINITY_sp| Q8BL.AT1g0216 | UPF0769 protein C2 | 40.90 | 0.00 |
| TRINITY_sp| P270.AT1g0216 | Poly [ADP-ribose] p | 40.90 | 0.00 |
| TRINITY_sp| P80X.AT1g0216 | USP6 N-terminal-lik | 40.90 | 0.00 |
| TRINITY_sp| P496.AT1g0216 | DNA primase small s | 40.90 | 0.00 |
| TRINITY_sp| Q749.AT1g0216 | DNA polymerase kapp | 40.90 | 0.00 |
| TRINITY_sp| Q8RY.AT1g0216 | Haloacid dehalogena | 40.80 | 0.00 |
| TRINITY_sp| Q97T.AT1g0216 | Pro-Pol polyprotein | 40.80 | 0.00 |
| TRINITY_sp| P516.AT1g0216 | ADP-ribosylation fa | 40.80 | 0.00 |
| TRINITY_sp| Q01W.GRXS1 | Monothiol glutaredo | 40.80 | 0.00 |
| TRINITY_sp| Q9LP.RHM2 | Trifunctional UDP-g | 40.80 | 0.00 |
| TRINITY_sp| Q354.AT1g0216 | Glutamate carboxype | 40.80 | 0.00 |
| TRINITY_sp| A1TM.hpx0 | FAD-dependent urate | 40.80 | 0.00 |
| TRINITY_sp| Q9GR.AT1g0216 | Elongation factor 1 | 40.80 | 0.00 |
| TRINITY_sp| P0CT.UMAG_10 | Small glutamine-ric | 40.80 | 0.00 |
| Accession    | Description                                                                 | ORF Size | Score |
|--------------|-----------------------------------------------------------------------------|----------|-------|
| TRINITY_sp|O347\:yvkC | Uncharacterized phosphotransferase YvkC | 40.80    | 0.00 |
| TRINITY_sp|O753\:VPS4B | Vacuolar protein sorting factor 4 (VPS4B) | 40.80    | 0.00 |
| TRINITY_sp|A814\:CFAP46 | Annexin C10 | 40.80    | 0.00 |
| TRINITY_sp|Q54WBzpF | Probable basic-leucine zipper protein | 40.80    | 0.00 |
| TRINITY_sp|Q6PG\:traf3ip | TRAF3-interacting protein | 40.80    | 0.00 |
| TRINITY_sp|Q66GHOA1 | NO-associated protein | 40.80    | 0.00 |
| TRINITY_sp|Q9L1\:FKBP18 | Peptidyl-prolyl cis-trans isomerase B | 40.80    | 0.00 |
| TRINITY_sp|P0CY\:SEC4 | Ras-related protein | 40.80    | 0.00 |
| TRINITY_sp|P109\:r | Retrovirus-related protein | 40.80    | 0.00 |
| TRINITY_sp|Q71G\:AAO4 | Benzaldehyde dehydrogenase | 40.80    | 0.00 |
| TRINITY_sp|Q597\:ark1 | Serine/threonine-protein kinase | 40.80    | 0.00 |
| TRINITY_sp|Q9ST1\:At3g483 | Probable Ufml-speci | 40.80    | 0.00 |
| TRINITY_sp|Q7TX\:ppsc | Phthiocerol/phenol oxidase | 40.80    | 0.00 |
| TRINITY_sp|Q9FW\:DHAR1 | Glutathione S-transferase | 40.80    | 0.00 |
| TRINITY_sp|Q3911\:At4g329 | Vacuolar-processing protein | 40.80    | 0.00 |
| TRINITY_sp|Q993\:Taf11 | Transcription initiation factor | 40.80    | 0.00 |
| TRINITY_sp|Q7XM\:Os04g05 | DEAD-box ATP-dependent RNA helicase | 40.80    | 0.00 |
| TRINITY_sp|Q54Q\:DDBD_G02 | Probable zinc transporter | 40.70    | 0.00 |
| TRINITY_sp|Q9Z2\:Hdac6 | Histone deacetylase | 40.70    | 0.00 |
| TRINITY_sp|P519\:NEK3 | Serine/threonine-protein kinase | 40.70    | 0.00 |
| TRINITY_sp|Q96M\:EDHHC15 | Palmitoyltransferase | 40.70    | 0.00 |
| TRINITY_sp|A5PK\:ABD17C | Protein ABD17C | 40.70    | 0.00 |
| TRINITY_sp|Q8MM\:paxB | Paxillin-B | 40.70    | 0.00 |
| TRINITY_sp|P0CG\:UB14 | Polyubiquitin OS=Ca | 40.70    | 0.00 |
| TRINITY_sp|Q94K\:At3g581 | Phenylalanine-tRNA ligase | 40.70    | 0.00 |
| TRINITY_sp|Q039\:EME1 | Crossover junction protein | 40.70    | 0.00 |
| TRINITY_sp|Q9SU\:At4g165 | Probable protein phosphatase | 40.70    | 0.00 |
| TRINITY_sp|Q5VJ\:gtd9 | Probable serine/threonine-protein kinase | 40.70    | 0.00 |
| TRINITY_sp|Q54Y\:np | Probable Ras GTPase | 40.70    | 0.00 |
| TRINITY_sp|P520\:proC | Pyrroline-5-carboxamide reductase | 40.70    | 0.00 |
| TRINITY_sp|Q8MII\:TGIF2LX | Homeobox protein TG | 40.70    | 0.00 |
| TRINITY_sp|Q8WT\:DUSP19 | Dual specificity phosphatase | 40.70    | 0.00 |
| TRINITY_sp|Q1X\:DDBD_G02 | PH domain-containing protein | 40.70    | 0.00 |
| TRINITY_sp|Q9JS\:FIM4 | Fimbrin-4 | 40.70    | 0.00 |
| TRINITY_sp|Q9RS\:pn | Polyribonucleotide | 40.70    | 0.00 |
| TRINITY_sp|P086\:CYP3A4 | Cytochrome P450 3A4 | 40.70    | 0.00 |
| TRINITY_sp|P085\:pS | Aqualysin-like enzyme | 40.70    | 0.00 |
| TRINITY_sp|Q643\:Sqstm1 | Sequestosome-1 | 40.70    | 0.00 |
| TRINITY_sp|Q087\:Ogg1 | N-glycosylase/DNA glycosylase | 40.70    | 0.00 |
| TRINITY_sp|Q551\:fray2 | Serine/threonine-protein kinase | 40.70    | 0.00 |
| TRINITY_sp|Q869\:dokA | Hybrid signal transducer | 40.70    | 0.00 |
| TRINITY_sp|Q9D2\:Vps33a | Vacuolar protein sorting factor | 40.70    | 0.00 |
| TRINITY_sp|Q615\:CDKC-1 | Cyclin-dependent kinase | 40.70    | 0.00 |
| TRINITY_sp|P256\:PWP2 | Periodic tryptophan | 40.70    | 0.00 |
| TRINITY_sp|P169\:CNJC | Conjugation stage-specific protein | 40.70    | 0.00 |
| TRINITY_sp|O321\:yuiD | Uncharacterized protein | 40.70    | 0.00 |
| TRINITY_sp|Q132\:SR4F6 | Serine/arginine-rich protein | 40.70    | 0.00 |
| TRINITY_sp|Q618\:Ras12-9 | GTP-binding protein | 40.70    | 0.00 |
| TRINITY_sp|P629\:RAC1 | Ras-related C3 botulinum | 40.70    | 0.00 |
| TRINITY_sp|P0CS\:AKR1 | Palmitoyltransferase | 40.70    | 0.00 |
| TRINITY_sp|Q155\:DPDK | 3-phosphoinositide-binding protein | 40.70    | 0.00 |
| TRINITY_sp|Q022\:hemB | Delta-aminolevulinate synthase | 40.70    | 0.00 |
| TRINITY_sp|A2UX\:Os1_163 | Pachytene checkpoint protein | 40.70    | 0.00 |
| TRINITY_sp|Q9UT\:paa1 | Protein phosphatase | 40.70    | 0.00 |
| TRINITY_sp|Q227\:Sym2 | RNA-binding protein | 40.70    | 0.00 |
| TRINITY_sp|Q019\:CPP1 | Cysteine proteinase | 40.70    | 0.00 |
| GenBank | Description | Score | E-value |
|---------|-------------|-------|---------|
| TRINITY_sp|Q097|Dynamin-related protein| 40.70 | 0.00 |
| TRINITY_sp|Q646|Receptor-type tyrosine kinase| 40.70 | 0.00 |
| TRINITY_sp|C0Q7|30S ribosomal protein S15| 40.70 | 0.00 |
| TRINITY_sp|Q9S7|Spliced transcript| 40.70 | 0.00 |
| TRINITY_sp|Q67Y|RING-H2 finger protease| 40.70 | 0.00 |
| TRINITY_sp|Q3S2|Leukotriene A4 hydrolase| 40.70 | 0.00 |
| TRINITY_sp|P041|Copla protease| 40.70 | 0.00 |
| TRINITY_sp|Q9C4|DNA helicase MCM8| 40.70 | 0.00 |
| TRINITY_sp|P740|Release factor glutamyltransferase| 40.70 | 0.00 |
| TRINITY_sp|P431|Retrovirus-related protein| 40.70 | 0.00 |
| TRINITY_sp|P291|Intracellular serine/threonine protein kinase| 40.70 | 0.00 |
| TRINITY_sp|Q6DI|Ubiquitin-like domain-containing protein| 40.70 | 0.00 |
| TRINITY_sp|Q9FN|Protein LEO1 homolog| 40.70 | 0.00 |
| TRINITY_sp|A7SK|Diphtamide biosynthesis protein| 40.70 | 0.00 |
| TRINITY_sp|Q2FN|ATP-dependent zinc-binding protein| 40.70 | 0.00 |
| TRINITY_sp|Q91V|ATP-binding cassette protein| 40.70 | 0.00 |
| TRINITY_sp|O654|Cysteine protease X| 40.70 | 0.00 |
| TRINITY_sp|P109|Retrovirus-related protein| 40.70 | 0.00 |
| TRINITY_sp|Q8GW|Phosphoglycerate kinase| 40.60 | 0.00 |
| TRINITY_sp|Q53L|Focal adhesion kinase| 40.60 | 0.00 |
| TRINITY_sp|Q9FK|Subtilisin-like protease| 40.60 | 0.00 |
| TRINITY_sp|Q9JS|Putative white blood cell protein| 40.60 | 0.00 |
| TRINITY_sp|Q9DA|Dynein light chain| 40.60 | 0.00 |
| TRINITY_sp|Q8K4|ATP-binding cassette protein| 40.60 | 0.00 |
| TRINITY_sp|Q9ZR|Dual specificity protein phosphatase| 40.60 | 0.00 |
| TRINITY_sp|Q2FK|Formate acetyltransferase| 40.60 | 0.00 |
| TRINITY_sp|Q84Q|12-oxophytodienoate reductase| 40.60 | 0.00 |
| TRINITY_sp|Q3Z2|Histidine protein kinase| 40.60 | 0.00 |
| TRINITY_sp|O314|Uncharacterized protein| 40.60 | 0.00 |
| TRINITY_sp|P040|Thermitase| 40.60 | 0.00 |
| TRINITY_sp|Q88D|Cyclin-Y| 40.60 | 0.00 |
| TRINITY_sp|Q149|E3 ubiquitin-protein ligase| 40.60 | 0.00 |
| TRINITY_sp|B9KZ|GTPase Der| 40.60 | 0.00 |
| TRINITY_sp|Q9H0|E3 ubiquitin-protein ligase| 40.60 | 0.00 |
| TRINITY_sp|A2YE|Zinc finger protein| 40.60 | 0.00 |
| TRINITY_sp|Q326|Uncharacterized protein| 40.60 | 0.00 |
| TRINITY_sp|P435|Serine/threonine-protein kinase| 40.60 | 0.00 |
| TRINITY_sp|Q92P|Ammonium transporter| 40.60 | 0.00 |
| TRINITY_sp|Q8N6|NAD-dependent alcohol dehydrogenase| 40.60 | 0.00 |
| TRINITY_sp|Q4K6|Prolyl endopeptidase| 40.60 | 0.00 |
| TRINITY_sp|Q90Y|Zinc finger protein| 40.60 | 0.00 |
| TRINITY_sp|O237|Methyltransferase| 40.60 | 0.00 |
| TRINITY_sp|Q9PK|4-alpha-glucanotransferase| 40.60 | 0.00 |
| TRINITY_sp|P495|Uncharacterized protein| 40.60 | 0.00 |
| TRINITY_sp|Q9SD|Glycerophosphodiesterase| 40.60 | 0.00 |
| TRINITY_sp|Q965|Transmembrane protein| 40.60 | 0.00 |
| TRINITY_sp|Q9CG|Transmembrane protein| 40.60 | 0.00 |
| TRINITY_sp|Q8BT|Copine-3| 40.60 | 0.00 |
| TRINITY_sp|Q948|Protein TOM THREE| 40.60 | 0.00 |
| TRINITY_sp|Q742|Polyadenylate-binding protein| 40.60 | 0.00 |
| TRINITY_sp|Q9LT|RNA pseudouridine synthase| 40.60 | 0.00 |
| TRINITY_sp|Q6PF|NADPH-dependent diflubenzuron reductase| 40.60 | 0.00 |
| TRINITY_sp|P503|Magnesium-chelatase| 40.60 | 0.00 |
| TRINITY_sp|Q5D4|Mitochondrial subunit| 40.60 | 0.00 |
| TRINITY_sp|Q54W|Probable basic-leucine zipper protein| 40.60 | 0.00 |
| TRINITY_sp|Q3E9|Calcium-dependent protein| 40.60 | 0.00 |
TRINITY_sp|Q54R:sg1A  Sphingosine-1-phospho 40.40 0.00
TRINITY_sp|O697:betC  Choline-sulfatase O 40.40 0.00
TRINITY_sp|Q54E:rpc19  DNA-directed RNA po 40.40 0.00
TRINITY_sp|P220:P100/11IProstaglandin F syn 40.40 0.00
TRINITY_sp|Q652:NPT4;4  Probable anion tran 40.40 0.00
TRINITY_sp|Q925:FIG4  Polyphosphoinositid 40.40 0.00
TRINITY_sp|P281:pkkB  Protein kinase 2 OS 40.40 0.00
TRINITY_sp|Q751:CPNE3  Copine-3 OS=Homo sa 40.40 0.00
TRINITY_sp|B8AEH:RR23  Two-component respo 40.40 0.00
TRINITY_sp|Q4FE:XBAT35  Putative E3 ubiquit 40.40 0.00
TRINITY_sp|Q9ST:\CIKP8  CBL-interacting ser 40.40 0.00
TRINITY_sp|Q8YI:SQE3  Squalene epoxidase 40.40 0.00
TRINITY_sp|Q54I:DDB_GO2;Vacuolar fusion pro 40.40 0.00
TRINITY_sp|Q54W:tmem184CTransmembrane prote 40.40 0.00
TRINITY_sp|Q247:-Myophilin OS=Echino 40.40 0.00
TRINITY_sp|Q169:-Dynein intermediate 40.40 0.00
TRINITY_sp|Q5ZJ:SUPV3;1ATP-dependent RNA h 40.40 0.00
TRINITY_sp|O233:AXTR3  Histone-lysine N-me 40.40 0.00
TRINITY_sp|Q9PUN:smurf1  E3 ubiquitin-protei 40.40 0.00
TRINITY_sp|Q9GR7:aif  Apoptosis-inducing 40.40 0.00
TRINITY_sp|Q605:Wrap53  Telomerase Cajal bo 40.40 0.00
TRINITY_sp|P0CB:Ylpml  YLP motif-containin 40.40 0.00
TRINITY_sp|Q9FI:RABA2;D Ras-related protein 40.40 0.00
TRINITY_sp|O971:SPBC3B8.Uncharacterized tra 40.40 0.00
TRINITY_sp|Q8BH:Detd2  Probable D-tyrosyl- 40.40 0.00
TRINITY_sp|Q86A:xguaD  Guanine deaminase O 40.40 0.00
TRINITY_sp|Q9Y5:N6AMT1  HemK methyltransfer 40.40 0.00
TRINITY_sp|Q84MI:LUL3  Probable E3 ubiquit 40.40 0.00
TRINITY_sp|Q148:TAF13  Transcription initi 40.40 0.00
TRINITY_sp|Q9SV:Atg4314Coatomer subunit be 40.40 0.00
TRINITY_sp|O494:AAH  Allantoate deimin 40.40 0.00
TRINITY_sp|Q9FPF:EDR1  Serine/threonine-pr 40.40 0.00
TRINITY_sp|Q53F:TP53I3  Quinone oxidoreduct 40.40 0.00
TRINITY_sp|Q5X3:trs1  Pre-rRNA-processing 40.40 0.00
TRINITY_sp|Q84J:Atg5405;Ribosomal RNA-proce 40.40 0.00
TRINITY_sp|Q9SK:CCHIP  E3 ubiquitin-protei 40.40 0.00
TRINITY_sp|Q58D:GTBP1  GTP-binding protein 40.40 0.00
TRINITY_sp|P169:YPTM1  GTP-binding protein 40.40 0.00
TRINITY_sp|Q9FN:UVTR8  Ultraviolet-B recep 40.40 0.00
TRINITY_sp|Q395:ODA2  Dynein gamma chain, 40.40 0.00
TRINITY_sp|Q9SU:FAH2  Dihydroceramide fat 40.40 0.00
TRINITY_sp|Q9LK:RLF  Cytochrome b5 domai 40.40 0.00
TRINITY_sp|P283:Gst1  Glutathione S-trans 40.40 0.00
TRINITY_sp|Q9LP:POX1  Pyridoxine/pyridoxa 40.40 0.00
TRINITY_sp|Q9FY:TMN11  Transmembrane 9 sup 40.40 0.00
TRINITY_sp|Q9MO:NSF  Vesicle-fusing ATPa 40.40 0.00
TRINITY_sp|Q54W:GO2;Probable serine/thr 40.40 0.00
TRINITY_sp|Q9WT:S1c23a1 Solute carrier fami 40.30 0.00
| Protein Name | Description | E-Value | Blast Score |
|--------------|-------------|---------|-------------|
| Protein C21orf2 hom | | 40.30 | 0.00 |
| Probable RNA methyl transferase | | 40.30 | 0.00 |
| Probable U3 small nuclear | | 40.30 | 0.00 |
| Myotubulin-relate | | 40.30 | 0.00 |
| Probable E3 ubiquitin | | 40.30 | 0.00 |
| Histone-lysine N-methyltransferase | | 40.30 | 0.00 |
| Dimethylaniline monooxygenase [N-oxide-forming] 2 | | 40.30 | 0.00 |
| Tetraticopeptide r | | 40.30 | 0.00 |
| NuDC domain-contain | | 40.30 | 0.00 |
| Sodium/hydrogen exchange | | 40.30 | 0.00 |
| Mitochondrial subunit | | 40.30 | 0.00 |
| Coatamer subunit | | 40.30 | 0.00 |
| 39S ribosomal protein | | 40.30 | 0.00 |
| Trimethylguanosine | | 40.30 | 0.00 |
| JmjC domain-contain | | 40.30 | 0.00 |
| CTD small phosphates | | 40.30 | 0.00 |
| Alpha-1,2-mannosyltransferase | | 40.30 | 0.00 |
| Coatomer subunit be | | 40.30 | 0.00 |
| 39S ribosomal protein | | 40.30 | 0.00 |
| Ubiquitin-activatin | | 40.30 | 0.00 |
| Cytochrome P450 3A5 | | 40.30 | 0.00 |
| Putative thiosulfatase | | 40.30 | 0.00 |
| Sensor histidine kinase | | 40.30 | 0.00 |
| Diphosphomevalonate | | 40.30 | 0.00 |
| Vacuolar fusion | | 40.30 | 0.00 |
| Histone deacetylase | | 40.30 | 0.00 |
| Leukotriene A-4 hydrolase | | 40.30 | 0.00 |
| 60S ribosomal protein | | 40.30 | 0.00 |
| CBL-interacting protein | | 40.30 | 0.00 |
| DNA mismatch repair | | 40.30 | 0.00 |
| Small nuclear ribonucleoprotein | | 40.30 | 0.00 |
| Uncharacterized protein | | 40.30 | 0.00 |
| Calcium-dependent protein | | 40.30 | 0.00 |
| Ataxin-3 OS=Mus musculus | | 40.30 | 0.00 |
| Uncharacterized protein | | 40.30 | 0.00 |
| N-acetyl-D-glucosaminyltransferase | | 40.30 | 0.00 |
| AP-3 complex subunit | | 40.30 | 0.00 |
| Serine/threonine-protein kinase | | 40.30 | 0.00 |
| Beta-galactosidase | | 40.30 | 0.00 |
| Ribosome maturation | | 40.30 | 0.00 |
| HemK methyltransferase | | 40.30 | 0.00 |
| Copine-9 OS=Homo sapiens | | 40.30 | 0.00 |
| Palmitoyl-protein thioesterase | | 40.30 | 0.00 |
| L-arabinokinase | | 40.30 | 0.00 |
| Translation initiation factor | | 40.30 | 0.00 |
| Unconventional protein | | 40.30 | 0.00 |
| Probable serine/threonine-protein kinase | | 40.30 | 0.00 |
| Trafficking protein | | 40.30 | 0.00 |
TRINITY_sp|O6466!CYP710A1|Cytochrome P450 710 | 40.30 | 0.00
TRINITY_sp|Q3YHf01D|Bifunctional protein | 40.30 | 0.00
TRINITY_sp|Q9FFE202|Probable serine/thr | 40.30 | 0.00
TRINITY_sp|P116:NHP6A|Non-histone chromosomal | 40.30 | 0.00
TRINITY_sp|P5191CN1|Calponin-1 OS=Homo sapiens | 40.30 | 0.00
TRINITY_sp|Q4G01CCDC40|Coiled-coil domain-containing | 40.30 | 0.00
TRINITY_sp|Q9M82NSN1|Guanine nucleotide-binding | 40.30 | 0.00
TRINITY_sp|Q9401SRK2E|Serine/threonine-protein kinase | 40.30 | 0.00
TRINITY_sp|A7KR:vlg2388|Quinone oxidoreductase | 40.30 | 0.00
TRINITY_sp|P104f|Phosphatidylcholine | 40.30 | 0.00
TRINITY_sp|Q9M88DSSTP1B|Dual specificity protein | 40.30 | 0.00
TRINITY_sp|Q9LP:UBP1|Probable ubiquitin ligase | 40.30 | 0.00
TRINITY_sp|P109|Retrovirus-related | 40.30 | 0.00
TRINITY_sp|Q8044diol|Type I iodothyronine repressor | 40.30 | 0.00
TRINITY_sp|Q9SLTALIS3|ALP-interacting subunit | 40.30 | 0.00
TRINITY_sp|Q9R5S5pn|Polyribonucleotide | 40.30 | 0.00
TRINITY_sp|P211!csgA|C-factor OS=Myxococcus xanthus | 40.30 | 0.00
TRINITY_sp|Q7SY<heatr1|HEAT repeat-contain | 40.30 | 0.00
TRINITY_sp|P077|L-2-aminoacidopropionate reductase | 40.30 | 0.00
TRINITY_sp|Q5756MRP51|54S ribosomal protein | 40.20 | 0.00
TRINITY_sp|Q599|cytoplasmic cytochrome | 40.20 | 0.00
TRINITY_sp|Q81YTRIM22|E3 ubiquitin-protein ligase | 40.20 | 0.00
TRINITY_sp|Q72MLIC_132|Macro domain-contain | 40.20 | 0.00
TRINITY_sp|D9HP:CNR7|Cell number regulator | 40.20 | 0.00
TRINITY_sp|P9761Txxn2|Thioredoxin, mitochondrial | 40.20 | 0.00
TRINITY_sp|Q8IV1NUDDCD3|NudC domain-contain | 40.20 | 0.00
TRINITY_sp|Q5ZKMOV10|Putative helicase M | 40.20 | 0.00
TRINITY_sp|Q54R1dhKL|Hybrid signal transduction | 40.20 | 0.00
TRINITY_sp|P502|Isoaspartyl peptidase | 40.20 | 0.00
TRINITY_sp|Q654XCPI|Cysteine protease X | 40.20 | 0.00
TRINITY_sp|Q66A:CHD7|Chromodomain-helicase | 40.20 | 0.00
TRINITY_sp|P201|GSTM2|Glutathione S-transferase | 40.20 | 0.00
TRINITY_sp|Q9R5S5pn|Polyribonucleotide | 40.20 | 0.00
TRINITY_sp|F4HP1RE4|Probable serine/threonine kinase | 40.20 | 0.00
TRINITY_sp|P0711|Cats3|Cathepsin L1 OS=Rattus norvegicus | 40.20 | 0.00
TRINITY_sp|Q94AREF003|Ethylene-responsive | 40.20 | 0.00
TRINITY_sp|B7IDTHA_1435|UPF0145 protein | 40.20 | 0.00
TRINITY_sp|Q7T21mx1|Interferon-induced | 40.20 | 0.00
TRINITY_sp|Q1111ubp14|Ubiquitin carboxyl-terminal hydrolase | 40.20 | 0.00
TRINITY_sp|Q6NR1agap1|Arf-GAP with GTPase | 40.20 | 0.00
TRINITY_sp|Q2QE4diol|Type I iodothyronine repressor | 40.20 | 0.00
TRINITY_sp|P16894gpaA|Guanine nucleotide-binding | 40.20 | 0.00
TRINITY_sp|Q555EmanC|Alpha-mannosidase C | 40.20 | 0.00
TRINITY_sp|P4911FM05|Dimethylenaline monooxygenase | 40.20 | 0.00
TRINITY_sp|Q9LZ2ABC120|ABC transporter I f | 40.20 | 0.00
TRINITY_sp|Q9FH5SCPL41|Serine carboxypeptidase | 40.20 | 0.00
TRINITY_sp|E9PYWdr78|WD repeat-contain | 40.20 | 0.00
TRINITY_sp|Q9SKE|Pirin-like protein | 40.20 | 0.00
TRINITY_sp|Q54P!cpnC|Copine-C OS=Dicentrochites | 40.20 | 0.00
TRINITY_sp|Q0WVMDMS1|MMS19 nucleotide exchanger | 40.20 | 0.00
TRINITY_sp|Q9VXICG9132|NECAP-like protein | 40.20 | 0.00
TRINITY_sp|Q9C7INTF2|Nuclear transport factor | 40.20 | 0.00
TRINITY_sp|Q6CEWMB1|Multiple RNA-binding | 40.20 | 0.00
TRINITY_sp|F330!ye1R|Zinc-binding GTPase | 40.20 | 0.00
TRINITY_sp|P412!Abca1|ATP-binding cassette | 40.20 | 0.00
TRINITY_sp|Q24V1hpg|Chaperone protein H | 40.20 | 0.00
| Ensembl Transcript ID | Full Name | Description | Score | Coverage |
|----------------------|-----------|-------------|-------|----------|
| TRINITY_sp|A7SD|cdc5l|Cell division cycle|40.00|0.00|
| TRINITY_sp|Q9LQ|RDR1|RNA-dependent RNA p|40.00|0.00|
| TRINITY_sp|Q541I|shkB|Dual specificity pr|40.00|0.00|
| TRINITY_sp|Q61M|gpa-7|Guanine nucleotide-|40.00|0.00|
| TRINITY_sp|Q496f|PAM68|protein PAM68, chlo|40.00|0.00|
| TRINITY_sp|P629|RAC1|Ras-related C3 botu|40.00|0.00|
| TRINITY_sp|Q54Q|abcH4|ABC transporter H f|40.00|0.00|
| TRINITY_sp|Q9MD|ycf66|Uncharacterized pro|40.00|0.00|
| TRINITY_sp|Q9LJ|At3g2244|Probable prefoldin|40.00|0.00|
| TRINITY_sp|P797|TSN|Translin OS=Gal|40.00|0.00|
| TRINITY_sp|Q6NT|vnael|NEDD8-activating en|40.00|0.00|
| TRINITY_sp|Q9CS|AHK3|Histidine kinase 3|40.00|0.00|
| TRINITY_sp|A6UY|bioC|Malonyl-acyl-carri|40.00|0.00|
| TRINITY_sp|P268|ATPA|ATP synthase subuni|40.00|0.00|
| TRINITY_sp|P386|~|Probable protein di|40.00|0.00|
| TRINITY_sp|Q5Z8|PAPF2-A|Poly [ADP-ribose] p|40.00|0.00|
| TRINITY_sp|Q9SX|FYP1|Phytochrome-assoc|40.00|0.00|
| TRINITY_sp|P487|EIP5|Eukaryotic translat|40.00|0.00|
| TRINITY_sp|Q944|ef3|Elongation factor 3|40.00|0.00|
| TRINITY_sp|Q962|ATPC|ATP synthase subuni|40.00|0.00|
| TRINITY_sp|Q59R|ZFAND2A|AN1-type zinc finge|40.00|0.00|
| TRINITY_sp|Q942|hmt2|Sulfide:quinone oxi|40.00|0.00|
| TRINITY_sp|Q9P2|SIPAIL2|Signal-induced prol|40.00|0.00|
| TRINITY_sp|O655|At4g309|BTB/POZ domain-cont|40.00|0.00|
| TRINITY_sp|Q252|typA|GTP-binding protein|40.00|0.00|
| TRINITY_sp|Q943|SPBC29A1|Uncharacterized ATP|40.00|0.00|
| TRINITY_sp|Q84T|SR45A|Serine/arginine-ric|40.00|0.00|
| TRINITY_sp|Q618|Mns1|Meiosis-specific nu|40.00|0.00|
| TRINITY_sp|Q9SR|PEX19-1|Peroxisome biogenes|40.00|0.00|
| TRINITY_sp|P109|~|Retrovirus-related|40.00|0.00|
| TRINITY_sp|P530|Rfc4|Replication factor|40.00|0.00|
| TRINITY_sp|Q75V|SAPK9|Serine/threonine-pr|40.00|0.00|
| TRINITY_sp|P39S|DRS2|Probable phospholip|40.00|0.00|
| TRINITY_sp|Q9UT|SPAC144.MIPI8 family protei|40.00|0.00|
| TRINITY_sp|Q241|shark|Tyrosine-protein ki|40.00|0.00|
| TRINITY_sp|Q78J|Ubf1d1|Ubiquitin domain-co|40.00|0.00|
| TRINITY_sp|A5PK|METTL13|Methyltransferase-l|40.00|0.00|
| TRINITY_sp|O755|ECT2|Enoyl-CoA delta iso|40.00|0.00|
| TRINITY_sp|Q9H8|RDH14|Retinol dehydrogena|40.00|0.00|
| TRINITY_sp|Q6CP|TRM13|tRNA:m(4)X modifica|40.00|0.00|
| TRINITY_sp|Q86C|tor|Target of rapamycin|40.00|0.00|
| TRINITY_sp|D0NL|PITG_12|tRNA (guanine(37)-N|39.90|0.00|
| TRINITY_sp|Q8LE|ECH|Golgi apparatus mem|39.90|0.00|
| TRINITY_sp|P281|RABA5C|Ras-related protein|39.90|0.00|
| TRINITY_sp|P092|~|25 kDa calcium-bind|39.90|0.00|
| TRINITY_sp|Q8CF|abca5|ATP-binding casset|39.90|0.00|
| TRINITY_sp|Q9NT|ATP8A2|Phospholipid-transp|39.90|0.00|
| TRINITY_sp|Q93V|ATG18A|Autophagy-related p|39.90|0.00|
| TRINITY_sp|Q6IQ|alkbh6|Alpha-ketoglutarate|39.90|0.00|
| TRINITY_sp|O137|nop12|Nucleolar protein 1|39.90|0.00|
| TRINITY_sp|Q145|ITPR2|Inositol 1,4,5-tris|39.90|0.00|
| TRINITY_sp|Q927|SYN2|Synapsin-2 OS=Homo|39.90|0.00|
| TRINITY_sp|Q2KH|USP2|Ubiquitin carboxyl-|39.90|0.00|
| TRINITY_sp|F215|ALP1|Alpha-amylase OS=Sa|39.90|0.00|
| TRINITY_sp|O155|RNF113A|RING finger protein|39.90|0.00|
| TRINITY_sp|Q135|TDG|G/T mismatch-specif|39.90|0.00|
| Accession | Description | Log2 Fold Change |
|-----------|-------------|-----------------|
| TRINITY_sp| Ribosome production factor 2 homolog | 39.90 |
| TRINITY_sp| Phosphatidylinosito | 39.90 |
| TRINITY_sp| Cell cycle checkpoint | 39.90 |
| TRINITY_sp| Sodium/potassium/ca | 39.90 |
| TRINITY_sp| 0.00 |
| TRINITY_sp| 0.00 |
| TRINITY_sp| 0.00 |
| TRINITY_sp| 1-acylglycerol-3-phosphate O-acyltransferase | 39.90 |
| TRINITY_sp| Nucleolar complex protein 4 homolog | 0.00 |
| TRINITY_sp| Probable ran guanine nucleotide release factor | 0.00 |
| TRINITY_sp| Thiamine pyrophosphokinase 1 | 39.90 |
| TRINITY_sp| Anaphase-promoting complex subunit cut9 | 39.90 |
| TRINITY_sp| 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | 39.90 |
| TRINITY_sp| Glycoprotein 3-alpha-L-fucosyltransferase A | 0.00 |
| TRINITY_sp| Hybrid signal transduction histidine kinase B | 39.90 |
| TRINITY_sp| RHOMBOID-like protein 6, mitochondrial | 0.00 |
| TRINITY_sp| DEAD-box ATP-dependent RNA helicase 16 | 39.90 |
| TRINITY_sp| Protein transport protein Sec24B | 0.00 |
| TRINITY_sp| CDK5RAP1-like protein | 0.00 |
| TRINITY_sp| Sodium/potassium/calcium exchanger 6, mitochondrial | 39.90 |
| TRINITY_sp| G patch domain and ankyrin repeat-containing protein 1 homolog | 0.00 |
| TRINITY_sp| Retinol dehydrogenase 11 | 39.90 |
| TRINITY_sp| Urea amidolyase | 0.00 |
| TRINITY_sp| Ras-related protein Rab-1D | 0.00 |
| TRINITY_sp| AP-2 complex subunit alpha-2 | 0.00 |
| TRINITY_sp| Cell cycle checkpoint protein RAD1 | 0.00 |
| TRINITY_sp| YTH domain-containing family protein 1 | 39.90 |
| TRINITY_sp| GTP-binding protein 2 | 39.90 |
| TRINITY_sp| Protein SDA1 homolog | 39.90 |
| TRINITY_sp| Rho-related GTPase Grave | 39.90 |
| TRINITY_sp| AP2β | 39.90 |
| TRINITY_sp| Cell cycle checkpoint protein JUN | 39.90 |
TRINITY_sp|Q8VW::SMO2-2  Methylsterol monooxygenase 39.80 0.00
TRINITY_sp|Q5G4E:ctdsp12  CTD small phosphatase 39.80 0.00
TRINITY_sp|P341|pkgC  Protein kinase 3 OS=Bo 39.80 0.00
TRINITY_sp|Q54EH:DDB_G02:GTPase-activating protein 39.80 0.00
TRINITY_sp|Q056|CTR1  Serine/threonine-protein kinase 39.80 0.00
TRINITY_sp|Q496|SAP9  Zinc finger protein A20 and A20-related 39.80 0.00
TRINITY_sp|Q9NN4:scp1-3  CTD small phosphatase 39.80 0.00
TRINITY_sp|Q55A:DDB_G02:Probable serine/threonine-protein kinase 39.80 0.00
TRINITY_sp|Q8LP:1ACS6  Long chain acyl-CoA desaturase 39.80 0.00
TRINITY_sp|Q8WN:ITPR2  Inositol 1,4,5-trisphosphate 39.80 0.00
TRINITY_sp|Q9JSN:NUDT5  Nudix hydrolase 5 O 39.80 0.00
TRINITY_sp|Q9LVC:TOE2  AP-2-like ethylene-responsive protein 39.80 0.00
TRINITY_sp|Q54E3:abpF  Actin-binding protein 39.80 0.00
TRINITY_sp|Q0V8:TPP1  Tripeptidyl-peptidase 39.80 0.00
TRINITY_sp|Q9JL7:Pnk  Bifunctional polynucleotide phosphorylase 39.80 0.00
TRINITY_sp|Q049|HAT3.1  Homeobox protein HA 39.80 0.00
TRINITY_sp|Q861Gtf2h3  General transcription factor 39.80 0.00
TRINITY_sp|Q8CX8:3128  UPF0176 protein 39.80 0.00
TRINITY_sp|Q7T6:MIMI_R8  Putative serine/threonine-protein kinase 39.80 0.00
TRINITY_sp|Q295|OSCP1  Protein OSCP1 OS=Bo 39.80 0.00
TRINITY_sp|BBAEM:CMC5  DNA replication lic H 39.80 0.00
TRINITY_sp|P341|racB  Rho-related protein 39.80 0.00
TRINITY_sp|Q2NKD:PY30  Protein dpy-30 homolog 39.80 0.00
TRINITY_sp|P0111:RAS1  Ras-like protein 39.80 0.00
TRINITY_sp|Q5Z1:TBCD  Tubulin-specific chaperone D 39.80 0.00
TRINITY_sp|Q9FN:E2FA  Transcription factor E2FA 39.80 0.00
TRINITY_sp|Q86L:gcclH  Rho GTPase-activating protein 39.80 0.00
TRINITY_sp|Q010:EMB1187  Probable ethanolamine kinase 39.80 0.00
TRINITY_sp|P239:NUDT5  NADH dehydrogenase 39.80 0.00
TRINITY_sp|P239:metG  Methionine--tRNA ligase 39.80 0.00
TRINITY_sp|Q6DG:mvp1712  Mpv17-like protein 39.80 0.00
TRINITY_sp|P094:iqw1  WD repeat protein 39.80 0.00
TRINITY_sp|P3321:FTT7  14-3-3 protein FTT7 39.80 0.00
TRINITY_sp|Q9BX:NAA15  N-alpha-acetylated H2A histone family member 39.80 0.00
TRINITY_sp|Q631:DNah7  Dynein heavy chain 39.80 0.00
TRINITY_sp|Q86A:guAD  Guanine deaminase 39.80 0.00
TRINITY_sp|P028:psmD8-1  Probable 26S proteasome subunit 39.80 0.00
TRINITY_sp|Q54J:abcC3  ABC transporter C 39.80 0.00
TRINITY_sp|Q41F:ARBR_0239  Probable glutamate dehydrogenase 39.80 0.00
TRINITY_sp|Q772:CG4061  RNA 3'-terminal phosphatase 39.80 0.00
TRINITY_sp|Q9W6:reg-a  Zinc finger protein 39.80 0.00
TRINITY_sp|Q681:At15026  Probable ethanolamine kinase 39.80 0.00
TRINITY_sp|Q9UN:VPS4A  Vacuolar protein sorting 39.80 0.00
TRINITY_sp|Q5RG:ccdc53  WASH complex subunit 39.80 0.00
TRINITY_sp|Q912V:Rep  Replication-associating protein 39.80 0.00
TRINITY_sp|Q0P4:dis3l  Dis3-like exoribonuclease 39.80 0.00
TRINITY_sp|Q9M21:ACA11  Putative calcium-triphosphatase 39.80 0.00
TRINITY_sp|P109:R  Retrovirus-related protein 39.80 0.00
TRINITY_sp|Q9FU:PLGG1  Probable ethanolamine kinase 39.80 0.00
TRINITY_sp|Q9561:YEATS4  YEATS domain-containing protein 39.80 0.00
TRINITY_sp|Q929:UPF1  Regulator of nonsense RNA 3'-terminal phosphatase 39.80 0.00
TRINITY_sp|Q28G:melk  Maternal embryonic leucine zipper kinase 39.80 0.00
TRINITY_sp|Q441:SLP2  Shewanella-like protein 39.80 0.00
TRINITY_sp|Q2ABp:R  Retinoblastoma-related protein 39.80 0.00
TRINITY_sp|Q54H:ghhB  Gamma-glutamyl hydrolase 39.80 0.00
TRINITY_sp|Q5F4:RAB8A  Ras-related protein 39.80 0.00
| Accession       | Description                                                                 | Score | e-value |
|-----------------|------------------------------------------------------------------------------|-------|---------|
| TRINITY_sp|Q9FG1PNG1                      | Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase | 39.80 | 0.00    |
| TRINITY_sp|Q75J:CR4                       | Serine/threonine-protein-phosphatase | 39.80 | 0.00    |
| TRINITY_sp|Q54J:abcC3                     | ABC transporter C family | 39.80 | 0.00    |
| TRINITY_sp|P790:rlp16                     | ATP-dependent helicase | 39.80 | 0.00    |
| TRINITY_sp|P2271Gucylb2                    | Guanylate cyclase s | 39.80 | 0.00    |
| TRINITY_sp|P109:->                        | Retrovirus-related protein | 39.80 | 0.00    |
| TRINITY_sp|Q8CE:Cdk11                      | Cyclin-dependent kinase | 39.70 | 0.00    |
| TRINITY_sp|Q01U:MCL2                      | Putative calmodulin | 39.70 | 0.00    |
| TRINITY_sp|Q72U:ytk6                      | Synaptobrevin homolog | 39.70 | 0.00    |
| TRINITY_sp|Q54WIDDB_G02:U6                  | snRNA phosphodiesterase | 39.70 | 0.00    |
| TRINITY_sp|Q9SL0:Os05g01                   | Importin subunit alpha | 39.70 | 0.00    |
| TRINITY_sp|P535:ML149                      | Cob(I)/Yrinic acid | 39.70 | 0.00    |
| TRINITY_sp|Q5M9:Rbm34                     | RNA-binding protein | 39.70 | 0.00    |
| TRINITY_sp|Q6P0:znf511                     | Zinc finger protein | 39.70 | 0.00    |
| TRINITY_sp|Q05A:elp2                      | Elongator complex protein | 39.70 | 0.00    |
| TRINITY_sp|Q6DC:hikeshi                    | Protein Hikeshi OS=Dictyostelium discoideum | 39.70 | 0.00    |
| TRINITY_sp|Q864:RG5                        | Regulator of G-protein | 39.70 | 0.00    |
| TRINITY_sp|Q9ZV:SGPP                       | Haloacid dehalogenase | 39.70 | 0.00    |
| TRINITY_sp|Q9D11:mthfs                     | 5-formyltetrahydrofolic acid | 39.70 | 0.00    |
| TRINITY_sp|Q9NX:TRMT1                      | tRNA (guanine(26)-N) | 39.70 | 0.00    |
| TRINITY_sp|Q8S1:0os1g08i                   | Probable U3 small nuclear ribonucleoprotein | 39.70 | 0.00    |
| TRINITY_sp|Q2KJ:INTS9                      | Integrator complex | 39.70 | 0.00    |
| TRINITY_sp|P349:NDUFA9                     | NADH dehydrogenase | 39.70 | 0.00    |
| TRINITY_sp|P266:eba52                     | Serine-arginine proline | 39.70 | 0.00    |
| TRINITY_sp|Q5R8:OLA1                       | Obg-like ATPase | 39.70 | 0.00    |
| TRINITY_sp|P2A4:RAB10                      | Ras-related protein | 39.70 | 0.00    |
| TRINITY_sp|Q8BY:Rdh12                      | Retinol dehydrogenase | 39.70 | 0.00    |
| TRINITY_sp|Q8R3:CCdc12                     | Coiled-coil domain | 39.70 | 0.00    |
| TRINITY_sp|P225:STY8                       | Serine/threonine-protein-phosphatase | 39.70 | 0.00    |
| TRINITY_sp|P84L:GONST4                     | GDP-mannose translocase | 39.70 | 0.00    |
| TRINITY_sp|O652:CPN20                      | 20 kDa chaperonin, | 39.70 | 0.00    |
| TRINITY_sp|Q9DB:Osbp13                     | Oxysterol-binding protein | 39.70 | 0.00    |
| TRINITY_sp|P907:catp-8                     | Probable manganese-phosphatase | 39.70 | 0.00    |
| TRINITY_sp|P008:cuDA                       | Putative transcript | 39.70 | 0.00    |
| TRINITY_sp|P623:CPK4                       | Calcium-dependent protein | 39.70 | 0.00    |
| TRINITY_sp|P160:gpab                       | Guanine nucleotide binding protein | 39.70 | 0.00    |
| TRINITY_sp|Q9SVA:At4g323                   | Probable sugar phosphatase | 39.70 | 0.00    |
| TRINITY_sp|Q641:Nuak1                      | NUAK family SNF1-like | 39.70 | 0.00    |
| TRINITY_sp|Q92J:era                        | GTase Era OS=Ricke | 39.70 | 0.00    |
| TRINITY_sp|Q54S:dhkD                       | Hybrid signal transducer | 39.70 | 0.00    |
| TRINITY_sp|Q5XM:aprA                       | Autocrine proliferin | 39.70 | 0.00    |
| TRINITY_sp|P109:->                          | Retrovirus-related | 39.70 | 0.00    |
| TRINITY_sp|Q7XAF:FOIT1                     | Folate transporter | 39.70 | 0.00    |
| TRINITY_sp|P327:GT2H1                       | General transcript | 39.70 | 0.00    |
| TRINITY_sp|Q4W9:encD                        | 2-oxoglutarate-Fe(I) | 39.70 | 0.00    |
| TRINITY_sp|Q861:DDDB_G02                    | Uncharacterized G02 | 39.70 | 0.00    |
| TRINITY_sp|P343:C50C3.5                     | Uncharacterized calcium-binding protein | 39.70 | 0.00    |
| TRINITY_sp|Q7X8:RM11                       | RecQ-mediated genomic | 39.70 | 0.00    |
| TRINITY_sp|Q9LJ:CRK2                       | CDPK-related kinase | 39.70 | 0.00    |
| TRINITY_sp|Q8C8:Myef2                       | Myelin expression factor | 39.70 | 0.00    |
| TRINITY_sp|Q9QX:INme7                       | Nucleoside diphosphate | 39.70 | 0.00    |
| TRINITY_sp|P531:GUP1                        | Glycerol uptake protein | 39.70 | 0.00    |
| TRINITY_sp|P945:SPBC12D                     | Uncharacterized mitogen-activated protein | 39.70 | 0.00    |
| TRINITY_sp|Q54:Fmyb0                       | Myb-like protein | 39.70 | 0.00    |
| TRINITY_sp|Q005:MPHOSPH1U3                   | Small nucleolar RNA binding protein | 39.70 | 0.00    |
| TRINITY_sp|A8WYIpar-1                       | Serine/threonine-protein-phosphatase | 39.70 | 0.00    |
| Gene Name        | Description                                      | Accession | Similarity | Score |
|------------------|--------------------------------------------------|-----------|------------|-------|
| ABC transporter C family member 3 | OS = Dictyostelium discoideum | sp|Q54JFabcC3 | 39.70 |
| Glycerol-3-phosphatase | OS = Dictyostelium discoideum | sp|Q5561DDB_G02 | 39.70 |
| Serine/threonine-protein kinase | OS = Dictyostelium discoideum | sp|Q8RWISTY17 | 39.70 |
| Luc7-like protein 3 | OS = Dictyostelium discoideum | sp|Q3SX<4LUC7L3 | 39.70 |
| Uncharacterized oxidoreductase | OS = Dictyostelium discoideum | sp|P2594MXAN_59 | 39.70 |
| 4-alpha-glucanotransferase | OS = Oryza sativa subsp. japonica | sp|Q69QDOPE2 | 39.70 |
| Probable serine/threonine-protein kinase | OS = Umbelopsis ramanniana | sp|Q54H<4drkB | 39.70 |
| Structural maintena | OS = Oryza sativa subsp. japonica | sp|Q56Y<pSMC3 | 39.70 |
| Triacylglycerol lipase | OS = Oryza sativa subsp. japonica | sp|Q9L2<4SDP1 | 39.70 |
| ADP-ribosylation factor | OS = Oryza sativa subsp. japonica | sp|Q9FV<4AGD12 | 39.70 |
| S-phase entry cyclin | OS = Oryza sativa subsp. japonica | sp|P329<4CLB6 | 39.70 |
| Diacylglycerol O-acyltransferase | OS = Umbelopsis ramanniana | sp|Q96U<4DGAT2A | 39.70 |
| Protein dopey-1 | OS = Drosophila melanogaster | sp|DPE2 | 39.70 |
| Regulatory-associated protein of TOR 1 | OS = Oryza sativa subsp. japonica | sp|RAPTOR1 | 39.70 |
| Glia maturation factor beta | OS = Rattus norvegicus | sp|Gmfb | 39.70 |
| Probable serine/threonine-protein kinase | OS = Oryza sativa subsp. japonica | sp|DOPEY1 | 39.70 |
| Probable serine/threonine-protein kinase | OS = Drosophila melanogaster | sp|CG17119 | 39.70 |
| Unc7-like protein 3 | OS = Saccharomyces cerevisiae (strain ATCC 204508 / S288c) | sp|YDR109C | 39.70 |
| Probable serine/threonine-protein kinase | OS = Dictyostelium discoideum | sp|drkB | 39.70 |
| Acyl-coenzyme A thioesterase 9, mitochondrial | OS = Homo sapiens | sp|ACOT9 | 39.70 |
| Luc7-like protein 3 | OS = Mus musculus | sp|LUC7L3 | 39.70 |
| Phospholipase B-like protein | OS = Dictyostelium discoideum | sp|plbG | 39.70 |
| Protein dopey-1 | OS = Oryza sativa subsp. japonica | sp|DOPEY1 | 39.70 |
| Protein ref(2)P | OS = Oryza sativa subsp. japonica | sp|RFC1 | 39.70 |
| Probable phospholipid transferase | OS = Medicago truncatula | sp|SPBC887 | 39.70 |
| Regulatory-associat | OS = Arabidopsis thaliana | sp|RAPTOR1 | 39.70 |
| Hybrid signal transducer | OS = Arabidopsis thaliana | sp|DGAT2A | 39.70 |
| Serine/threonine-protein kinase | OS = Xenopus tropicalis | sp|brd9 | 39.70 |
| Uncharacterized sugar kinase | OS = Xenopus tropicalis | sp|YDR109C | 39.70 |
| Protein ref(2)P | OS = Dictyostelium discoideum | sp|DFG1 | 39.70 |
| Growth hormone-regulat | OS = Oryza sativa subsp. japonica | sp|DOPEY1 | 39.70 |
| M-phase inducer protein | OS = Oryza sativa subsp. japonica | sp|CDC25-3 | 39.70 |
| Acyl-coenzyme A thiolase | OS = Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) | sp|nudG | 39.70 |
| Copine-5 | OS = Mus musculus | sp|Cpne5 | 39.70 |
| Alpha-adducin | OS = Rattus norvegicus | sp|Add1 | 39.70 |
| Anaphase-promoting complex subunit 6 | OS = Arabidopsis thaliana | sp|APC6 | 39.70 |
| Calcium-dependent protein kinase | OS = Plasmodium berghei (strain Anka) | sp|CPK4 | 39.70 |
| Mitogen-activated protein kinase | OS = Arabidopsis thaliana | sp|MKK3 | 39.70 |
| Sentrin-specific protease | OS = Pongo abelii | sp|SENP1 | 39.70 |
| Serine/threonine-protein kinase | OS = Arabidopsis thaliana | sp|NEK1 | 39.70 |
| Serine/threonine-protein kinase | OS = Mus musculus | sp|Nek4 | 39.70 |
| Phosphatidylinositol choline translocator | OS = Homo sapiens | sp|ABCB4 | 39.70 |
| Twitchin | OS = Caenorhabditis elegans | sp|unc-22 | 39.70 |
TRINITY_sp|Q8RYIA.2g332|Haloacid dehalogena 39.60 0.00
TRINITY_sp|Q9FYIRS2|Serine/arginine-rich 39.60 0.00
TRINITY_sp|Q9BXW1FANCD2|Fanconi anemia group 39.60 0.00
TRINITY_sp|Q9P7comal|Mitochondrial metal 39.60 0.00
TRINITY_sp|Q9S8:CLPP5|ATP-dependent Clp p 39.60 0.00
TRINITY_sp|Q059:mybl1|Myb-related protein 39.60 0.00
TRINITY_sp|A8XAIrheb-1|GTP-binding protein 39.60 0.00
TRINITY_sp|Q54B1abcB2|ABC transporter B f 39.60 0.00
TRINITY_sp|Q9B1B0464.9|Probable protein ph 39.60 0.00
TRINITY_sp|Q5X11Grw1d|Glutamate-rich WD r 39.60 0.00
TRINITY_sp|Q9JSV1[VPS11|Vacuolar protein-so 39.60 0.00
TRINITY_sp|Q9L8:CHY1|3-hydroxyisobutyryl 39.60 0.00
TRINITY_sp|P582[Rnf216|E3 ubiquitin-protei 39.60 0.00
TRINITY_sp|Q5W6:MAN5|Putative mannan end 39.60 0.00
TRINITY_sp|Q3891ANT|AP2-like ethylene-re 39.60 0.00
TRINITY_sp|Q751l[KDM4A|Lysine-specific dem 39.60 0.00
TRINITY_sp|Q5C9I-(S)-coclaurine N-me 39.60 0.00
TRINITY_sp|Q490[VPS45|Vacuolar protein so 39.60 0.00
TRINITY_sp|P056:sacC|Levanase OS=Bacillu 39.60 0.00
TRINITY_sp|F322:rasB|Ras-like protein ra 39.60 0.00
TRINITY_sp|Q6F7Gaa|Lysozomal alpha-gl 39.60 0.00
TRINITY_sp|Q974Pde8b|High affinity cAMP- 39.60 0.00
TRINITY_sp|Q9B2I0SPL6|Oxysterol-binding p 39.60 0.00
TRINITY_sp|Q5N4hu1|Checkpoint protein 39.60 0.00
TRINITY_sp|Q944:dybA|Dynamin-A OS=Dictyo 39.60 0.00
TRINITY_sp|Q006:PPR|Pirin OS=Homo sapie 39.60 0.00
TRINITY_sp|Q064:yfmr|Uncharacterized ABC 39.60 0.00
TRINITY_sp|Q85P8:psbI|Aqualysin-1 OS=Ther 39.60 0.00
TRINITY_sp|Q54labcC3|ABC transporter C f 39.60 0.00
TRINITY_sp|Q9S2P4H11|Probable prolyl 4-h 39.60 0.00
TRINITY_sp|Q9M3:Atg541l|Ataxin-3 homolog OS 39.50 0.00
TRINITY_sp|A4FV:PPIE|Peptidyl-prolyl cis 39.50 0.00
TRINITY_sp|Q8MRHid1|Protein HID1 OS=Mus 39.50 0.00
TRINITY_sp|Q8BT7:CPne3|Copine-3 OS=Mus mus 39.50 0.00
TRINITY_sp|U4PR:pig-l|Paternal embryonic 39.50 0.00
TRINITY_sp|Q641acbd5|Acyl-CoA-binding do 39.50 0.00
TRINITY_sp|Q91YRnfl26|E3 ubiquitin-protei 39.50 0.00
TRINITY_sp|Q605f1GHMP2|DNA-binding protein 39.50 0.00
TRINITY_sp|Q54R:cnrB|CLPTM1-like membran 39.50 0.00
TRINITY_sp|Q099K1O0u2|Uncharacterized ser 39.50 0.00
TRINITY_sp|Q9UMIlyrm1|LYR motif-containin 39.50 0.00
TRINITY_sp|P253mlkA|Myosin light chain 39.50 0.00
TRINITY_sp|Q246:ref(2)P|Protein ref(2)P OS= 39.50 0.00
TRINITY_sp|B9DSpith|Peptidyl-tRNA hydro 39.50 0.00
TRINITY_sp|Q54Lluox|Uricase OS=Dictyost 39.50 0.00
TRINITY_sp|Q5UP:MIMI_R6l|Putative band 7 fam 39.50 0.00
TRINITY_sp|Q5BL:atpBb1|Phospholipid-transp 39.50 0.00
TRINITY_sp|Q956CNOT4|CCR4-NOT transcript 39.50 0.00
TRINITY_sp|Q9AVFRPRP|Pre-mRNA-processing 39.50 0.00
TRINITY_sp|Q8HYELAC2|Zinc phosphodiester 39.50 0.00
TRINITY_sp|Q4USRNF1|E3 ubiquitin-protei 39.50 0.00
TRINITY_sp|A7TM:EGF1|rRNA-processing pro 39.50 0.00
TRINITY_sp|Q54BempB|Transmembrane emp24 39.50 0.00
TRINITY_sp|Q8WXODNAH7|Dynein heavy chain 39.50 0.00
TRINITY_sp|Q999DUSP9|Dual specificity pr 39.50 0.00
TRINITY_sp|Q4IEFPPMO|tRNA wybutosine-syn 39.50 0.00
| Description                                                                 | Symbol     | Accession          | E-value | Score |
|-----------------------------------------------------------------------------|------------|--------------------|---------|-------|
| Guanylate kinase 1                                                          | GK-1       | TRINITY_sp|937:GK-1 | 39.20  | 0.00  |
| Putative peptidase                                                          | pepB       | TRINITY_sp|P584:pepB | 39.20  | 0.00  |
| CDP-diacylglycerol-kinase                                                   | CDIPT      | TRINITY_sp|O147:CDIPT | 39.20  | 0.00  |
| Transforming protein                                                        | V-MYB      | TRINITY_sp|P011:V-MYB | 39.20  | 0.00  |
| Endothelial differe                                                         | Edf1       | TRINITY_sp|Q9JKM:Edf1 | 39.20  | 0.00  |
| Putative cysteine-r                                                         | CRK33      | TRINITY_sp|Q9LD:CRK33 | 39.20  | 0.00  |
| Vacuolar protein 33a                                                        | Vps33a     | TRINITY_sp|Q6361Vps33a | 39.20  | 0.00  |
| Putative 3,4-dihydroxy-2-butanone kinase                                    | DHBK       | TRINITY_sp|O4P6:DHBK | 39.20  | 0.00  |
| Serine/threonine-pr                                                         | Ppn1       | TRINITY_sp|P487:Ppn1 | 39.20  | 0.00  |
| Protein scol OS=Sch                                                         | sco1       | TRINITY_sp|O428:sco1 | 39.20  | 0.00  |
| Coflin OS=Ustilago                                                          | COF1       | TRINITY_sp|Q4P6:COF1 | 39.20  | 0.00  |
| tRNA (adenine(58)-N)                                                       | Trmt6      | TRINITY_sp|Q8CE:Trmt6 | 39.20  | 0.00  |
| Probable serine/thr                                                        | tsf         | TRINITY_sp|Q2391:tsf | 39.20  | 0.00  |
| Geranylgeranyl tran                                                         | Rabggta    | TRINITY_sp|Q55D:Rabggta | 39.20  | 0.00  |
| Nudt15                                                                      | SPAC227.14 | TRINITY_sp|Q55D:SPAC227.14 | 39.20  | 0.00  |
| tRNA lig                                                                   | Utp15       | TRINITY_sp|Q424:Utp15 | 39.20  | 0.00  |
| Probable leucine am                                                         | DHB12       | TRINITY_sp|Q424:DHB12 | 39.20  | 0.00  |
| Serine/threonine-pr                                                         | P519:Nek1   | TRINITY_sp|P519:Nek1 | 39.20  | 0.00  |
| Putative serine/thr                                                         | Q05B:Q05B | TRINITY_sp|Q05B:Q05B | 39.20  | 0.00  |
| Very-long-chain 3-o                                                        | Q0U3:SNOG_130093 | TRINITY_sp|Q0U3:SNOG_130093 | 39.20  | 0.00  |
| Calpain-type cysteine                                                      | Q8RVIDEK1   | TRINITY_sp|Q8RVIDEK1 | 39.20  | 0.00  |
| Ras-like protein ra                                                         | RasC       | TRINITY_sp|P322:RasC | 39.20  | 0.00  |
| Probable serine/thr                                                         | Q55D:G02   | TRINITY_sp|Q55D:G02 | 39.20  | 0.00  |
| Ephrin type-A recep                                                         | EPHA7      | TRINITY_sp|Q424:EPHA7 | 39.20  | 0.00  |
| Probable leucine am                                                         | DHB12       | TRINITY_sp|Q424:DHB12 | 39.20  | 0.00  |
| Serine/threonine-pr                                                         | P519:Nek1   | TRINITY_sp|P519:Nek1 | 39.20  | 0.00  |
| Putative serine/thr                                                         | Q05B:Q05B | TRINITY_sp|Q05B:Q05B | 39.20  | 0.00  |
| Very-long-chain 3-o                                                        | Q54CFDDB_G02 | TRINITY_sp|Q54CFDDB_G02 | 39.20  | 0.00  |
| Somatic embryogenes                                                         | Q9X1:SERK2  | TRINITY_sp|Q9X1:SERK2 | 39.20  | 0.00  |
| ABC transporter B f                                                          | Q8T99:abcB3 | TRINITY_sp|Q8T99:abcB3 | 39.20  | 0.00  |
| Ubiquitin carboxyl-terminating peptidase                                   | Q6261:usp15 | TRINITY_sp|Q6261:usp15 | 39.20  | 0.00  |
| Phosphate permease                                                          | P383:PHO89 | TRINITY_sp|P383:PHO89 | 39.20  | 0.00  |
| Putative glycerol k                                                         | Q52M:GK5   | TRINITY_sp|Q52M:GK5 | 39.20  | 0.00  |
| Very-long-chain 3-o                                                        | Q281:hsd17b1 | TRINITY_sp|Q281:hsd17b1 | 39.20  | 0.00  |
| UDP-galactose trans                                                         | Q9SR:UDP   | TRINITY_sp|Q9SR:UDP | 39.20  | 0.00  |
| Protein YIPF1 homol                                                         | Yipf1      | TRINITY_sp|Q545:Yipf1 | 39.20  | 0.00  |
| Metal tolerance pro                                                         | Q5NA:MTP5  | TRINITY_sp|Q5NA:MTP5 | 39.20  | 0.00  |
| Protein phosphatase                                                         | P403:ptc1   | TRINITY_sp|P403:ptc1 | 39.20  | 0.00  |
| Kremen protein 1 OS                                                        | KREMEN1     | TRINITY_sp|Q96MK:KREMEN1 | 39.20  | 0.00  |
| Putative 3,4-dihydr                                                      | O040:DHBK   | TRINITY_sp|O040:DHBK | 39.20  | 0.00  |
| Uroporphyrinogen-II                                                       | Q100F2UROS | TRINITY_sp|Q100F2UROS | 39.20  | 0.00  |
| Calcium-transportin                                                         | ACA1       | TRINITY_sp|Q371:ACA1 | 39.20  | 0.00  |
| Putative uridine ki                                                        | Q9UTC:SPAC227 | TRINITY_sp|Q9UTC:SPAC227 | 39.20  | 0.00  |
| Beta-hexosaminidase                                                        | Hexb       | TRINITY_sp|P200:Hexb | 39.20  | 0.00  |
| Nucleotide triphosp                                                        | Q8BG:Sudt15 | TRINITY_sp|Q8BG:Sudt15 | 39.20  | 0.00  |
| Probable cytosolic                                                         | A8IZ:CCHLREDJR | TRINITY_sp|A8IZ:CCHLREDJR | 39.20  | 0.00  |
| GPI ethanolamine ph                                                         | Q078:GPI13  | TRINITY_sp|Q078:GPI13 | 39.20  | 0.00  |
| small nucleolar                                                            | Q810:Mphosph1U3 | TRINITY_sp|Q810:Mphosph1U3 | 39.20  | 0.00  |
| Hormone-sensitive l                                                         | P5433:Life | TRINITY_sp|Q5433:Life | 39.20  | 0.00  |
| Paired amphipathic                                                         | SNL1       | TRINITY_sp|Q9SR:SNL1 | 39.20  | 0.00  |
| Adenine/guanine per                                                         | AZG1       | TRINITY_sp|Q9SR:AZG1 | 39.20  | 0.00  |
| Autophagy-related p                                                         | A7A2:ATG18  | TRINITY_sp|A7A2:ATG18 | 39.20  | 0.00  |
| Gene ID         | Description                                                                 | Expression | Similarity |
|----------------|------------------------------------------------------------------------------|------------|------------|
| Lysosomal acid alpha-glucosidase | OS=Tetrahymena pyriformis PE=1 SV=1 | 39.10      | 0.00       |
| POC1 centriolar protein homolog A | OS=Danio rerio GN=poc1a PE=2 SV=1 | 39.10      | 0.00       |
| Lactation elevated protein 1 | OS=Mus musculus GN=Lace1 PE=1 SV=1 | 39.10      | 0.00       |
| Phospho-2-dehydro-3-deoxyheptonate aldolase | OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) GN=aro-8 PE=1 SV=2 | 39.10      | 0.00       |
| Calcium-dependent protein kinase 4 | OS=Plasmodium berghei (strain Anka) GN=CPK4 PE=1 SV=2 | 39.10      | 0.00       |
| Tubulin glycylase 3D | OS=Tetrahymena thermophila (strain SB210) GN=TTLL3D PE=3 SV=2 | 39.10      | 0.00       |
| Dedicator of cytokinesis protein 10 | OS=Homo sapiens GN=DOCK10 PE=1 SV=3 | 39.10      | 0.00       |
| WD repeat-containing protein 70 | OS=Xenopus tropicalis GN=wdr70 PE=2 SV=1 | 39.10      | 0.00       |
| Mannan synthase 1 | OS=Cyamopsis tetragonoloba GN=ManS PE=1 | 39.10      | 0.00       |
| GTP-binding protein 1 | OS=Xenopus laevis GN=gtpbp1 PE=2 SV=1 | 39.10      | 0.00       |
| Protein CHROMATIN REMODELING 8 | OS=Arabidopsis thaliana GN=CHR8 PE=2 SV=1 | 39.10      | 0.00       |
| Methionine aminopeptidase 1D, chloroplastic/mitochondrial | OS=Arabidopsis thaliana GN=MAP1D PE=1 SV=1 | 39.10      | 0.00       |
| Copper-transporting ATPase PAA2, chloroplastic | OS=Arabidopsis thaliana GN=PAA2 PE=2 SV=1 | 39.10      | 0.00       |
| NADH-dependent flavin oxidoreductase nadA | OS=Aspergillus parasiticus (strain ATCC 56775 / NRRL 5862 / SRRC 143 / SU-1) GN=nadA PE=2 SV=1 | 39.10      | 0.00       |
| WD repeat-containing protein 55 | OS=Arabidopsis thaliana GN=WDR55 PE=1 SV=2 | 39.10      | 0.00       |
| Phospholipid-transporting ATPase IA | OS=Mus musculus GN=Atp8a1 PE=1 SV=2 | 39.10      | 0.00       |
| Ribosomal RNA small subunit methyltransferase J | OS=Yersinia enterocolitica serotype O:8 / biotype 1B (strain NCTC 13174 / 8081) GN=rsmJ PE=3 SV=1 | 39.10      | 0.00       |
| cAMP-specific 3',5'-cyclic phosphodiesterase 4A | OS=Mus musculus GN=Pde4a PE=1 SV=2 | 39.10      | 0.00       |
| Diacylglycerol kinase gamma | OS=Mus musculus GN=Dgkg PE=1 SV=1 | 39.10      | 0.00       |
| Protein DENND6A | OS=Homo sapiens GN=DENND6A PE=1 SV=1 | 39.10      | 0.00       |
| Probable palmitoyltransferase ZDHHC12 | OS=Mus musculus GN=Zdhhc12 PE=2 SV=1 | 39.10      | 0.00       |
| Kinesin-like protein KIN-7H | OS=Oryza sativa subsp. japonica GN=KIN7H PE=2 SV=2 | 39.10      | 0.00       |
| Bifunctional polynucleotide phosphatase/kinase | OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pnk1 PE=1 SV=2 | 39.10      | 0.00       |
| Probable CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase | OS=Dictyostelium discoideum GN=pgs1 PE=3 SV=1 | 39.10      | 0.00       |
| Acetyl-coenzyme A synthetase | OS=Nitrosomonas eutropha (strain C91) GN=acsA PE=3 SV=1 | 39.10      | 0.00       |
| Gene Name | Description | Charge 1 | Charge 2 |
|-----------|-------------|----------|----------|
| CHX17     |             | 39.00    | 0.00     |
| rpmB      |             | 39.00    | 0.00     |
| MTMR2     |             | 39.00    | 0.00     |
| CG1307    |             | 39.00    | 0.00     |
| TAZ1      |             | 38.90    | 0.00     |
| pub1      |             | 39.00    | 0.00     |
| Q96143    |             | 39.00    | 0.00     |
| P05131    |             | 39.00    | 0.00     |
| Q06984    |             | 39.00    | 0.00     |
| Q56766    |             | 39.00    | 0.00     |
| Q67420    |             | 39.00    | 0.00     |
| Q05802    |             | 39.00    | 0.00     |
| Q09218    |             | 39.00    | 0.00     |
| Q09244    |             | 39.00    | 0.00     |
| Q006957   |             | 39.00    | 0.00     |
| Q096143   |             | 39.00    | 0.00     |
| Q097070   |             | 39.00    | 0.00     |
| Q149054   |             | 39.00    | 0.00     |
| Q99554    |             | 39.00    | 0.00     |
| Q81103    |             | 39.00    | 0.00     |
| Q89608    |             | 39.00    | 0.00     |
| Q62746    |             | 39.00    | 0.00     |
| Q92097    |             | 39.00    | 0.00     |
| Q06984    |             | 39.00    | 0.00     |
| Q67420    |             | 39.00    | 0.00     |
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| Q29817    |             | 39.00    | 0.00     |
| Q81103    |             | 39.00    | 0.00     |
| Q89608    |             | 39.00    | 0.00     |
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| Q56766    |             | 39.00    | 0.00     |
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| Q06984    |             | 39.00    | 0.00     |
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| Q67420    |             | 39.00    | 0.00     |
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| Q92097    |             | 39.00    | 0.00     |
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| Q67420    |             | 39.00    | 0.00     |
| Q56766    |             | 39.00    | 0.00     |
| Q67420    |             | 39.00    | 0.00     |
| Q92097    |             | 39.00    | 0.00     |
| Q06984    |             | 39.00    | 0.00     |
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| Q92097    |             | 39.00    | 0.00     |
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| TRINITY_sp|Q32K|DNAL4  | Dynein light chain | 38.90 | 0.00 |
| TRINITY_sp|Q5BL|scl20a1 | Sodium-dependent ph | 38.90 | 0.00 |
| TRINITY_sp|Q9BY1|SCAPER  | S phase cyclin A-as | 38.90 | 0.00 |
| TRINITY_sp|Q0W8|RBP47B  | Polyadenylate-bindi | 38.90 | 0.00 |
| TRINITY_sp|Q758|ILAS21 | GPI ethanolamine ph | 38.90 | 0.00 |
| TRINITY_sp|P234|CYP1  | Adenylate cyclase O | 38.90 | 0.00 |
| TRINITY_sp|Q13Z|PAPPA  | Pappalysin-1 OS=Hom | 38.90 | 0.00 |
| TRINITY_sp|Q297|nero  | Deoxyhypusine hydro | 38.90 | 0.00 |
| TRINITY_sp|Q54L|abcC5  | ABC transporter C f | 38.90 | 0.00 |
| TRINITY_sp|D7U6|ANR  | Anthocyanidin reduc | 38.90 | 0.00 |
| TRINITY_sp|Q84W|SUFE1 | SufE-like protein 1 | 38.90 | 0.00 |
| TRINITY_sp|Q9C8|RH34  | DEAD-box ATP-depend | 38.80 | 0.00 |
| TRINITY_sp|Q557|dpp3-1 | Dipeptidyl peptidas | 38.80 | 0.00 |
| TRINITY_sp|P43I|ms13  | Mycolipanoate synth | 38.80 | 0.00 |
| TRINITY_sp|Q103|sck2  | Serine/threonine-pr | 38.80 | 0.00 |
| TRINITY_sp|Q9Z2|tpr2  | Inositol 1,4,5-tris | 38.80 | 0.00 |
| TRINITY_sp|P398|NIA2  | Nitrate reductase | 38.80 | 0.00 |
| TRINITY_sp|Q3T0|QDPR  | Dihydropteridine re | 38.80 | 0.00 |
| TRINITY_sp|B01S|rp1W  | 5OS ribosomal prote | 38.80 | 0.00 |
| TRINITY_sp|Q2T9|TRMT6  | tRNA (adenine58)-N | 38.80 | 0.00 |
| TRINITY_sp|Q122|GIN4  | Serine/threonine-pr | 38.80 | 0.00 |
| TRINITY_sp|Q9Y8|APE_2601|Uncharacterized pro | 38.80 | 0.00 |
| TRINITY_sp|B4K6|fig    | Protein phosphatase | 38.80 | 0.00 |
| TRINITY_sp|Q9QZ|DCun1d1| DCN1-like protein 1 | 38.80 | 0.00 |
| TRINITY_sp|P501|linX  | 2,5-dichloro-2,5-cy | 38.80 | 0.00 |
| TRINITY_sp|Q058|NNT1  | Protein N-methyltra | 38.80 | 0.00 |
| TRINITY_sp|Q9LT|PDR2  | Probable manganese- | 38.80 | 0.00 |
| TRINITY_sp|Q9VR|HERC2 | Probable E3 ubiquit | 38.80 | 0.00 |
| TRINITY_sp|Q55C|mp12  | MAP kinase phosphat | 38.80 | 0.00 |
| TRINITY_sp|Q76P|SPCC122| E3 ubiquitin-protei | 38.80 | 0.00 |
| TRINITY_sp|Q266|KAP115 | Kinesin-associated | 38.80 | 0.00 |
| TRINITY_sp|Q3U2|Otud5  | OTU domain-containi | 38.80 | 0.00 |
| TRINITY_sp|Q8GUR|RIE1  | E3 ubiquitin protei | 38.80 | 0.00 |
| TRINITY_sp|Q9VR|HERC2 | Probable E3 ubiquit | 38.80 | 0.00 |
| TRINITY_sp|F412|CTN  | Cactin OS=Arabidops | 38.80 | 0.00 |
| TRINITY_sp|O244|RABE1A | Ras-related protein | 38.80 | 0.00 |
| TRINITY_sp|Q9Z1|Epn2  | Epsin-2 OS=Rattus n | 38.80 | 0.00 |
| TRINITY_sp|O812|RHL1  | DNA-binding protein | 38.80 | 0.00 |
| TRINITY_sp|Q67Z|LIP2  | Triacylglycerol lip | 38.80 | 0.00 |
| TRINITY_sp|Q4V8|Gpat3  | Glycerol-3-phosphat | 38.80 | 0.00 |
| TRINITY_sp|O807|WDR55  | WD repeat-containin | 38.80 | 0.00 |
| TRINITY_sp|Q923|Dnah12 | Dynein heavy chain | 38.80 | 0.00 |
| TRINITY_sp|Q433|TXNL1 | Thioredoxin-like pr | 38.80 | 0.00 |
| TRINITY_sp|Q9NS|KIF15  | Kinesin-like protei | 38.80 | 0.00 |
| TRINITY_sp|Q9FK|MRS2-2 | Magnesium transport | 38.80 | 0.00 |
| TRINITY_sp|Q86H|Pde4  | cAMP-specific 3',5' | 38.80 | 0.00 |
| TRINITY_sp|A9V2|37534  | Probable nitrile hy | 38.80 | 0.00 |
| TRINITY_sp|Q5E9|RBL   | Protein RBL OS=Arab | 38.80 | 0.00 |
| TRINITY_sp|Q7K2|Rpn13  | Proteasomal ubiquit | 38.80 | 0.00 |
| TRINITY_sp|Q8L7|Ap-4  | AP-4 complex subuni | 38.80 | 0.00 |
| TRINITY_sp|Q8GW|GFA2  | Chaperone protein d | 38.80 | 0.00 |
| TRINITY_sp|Q7Z6|HUWE1  | E3 ubiquitin-protei | 38.80 | 0.00 |
| TRINITY_sp|Q9J1|Polm  | DNA-directed DNA/RN | 38.80 | 0.00 |
| TRINITY_sp|F4J7|EAP1A  | Chromatin modificat | 38.80 | 0.00 |
| TRINITY_sp|Q80U|Xpol  | Exportin-1 OS=Rattu | 38.80 | 0.00 |
| Gene ID     | Description                                           | Value  |
|------------|-------------------------------------------------------|--------|
| TRINITY_sp| Ubiquitin carboxyl-terminal hydrolase Usp33 OS=Mus musculus GN=Usp33 PE=1 SV=2 | 38.80  |
| TRINITY_sp| Retinoblastoma-binding protein 1 OS=Dictyostelium discoideum GN=paxB PE=2 SV=1 | 38.80  |
| TRINITY_sp| Structural maintenance protein 1 OS=Arabidopsis thaliana GN=SMC1 PE=2 SV=2 | 38.80  |
| TRINITY_sp| Probable mitochondrial intermediate peptidase, mitochondrial OS=Arabidopsis thaliana GN=MIP PE=3 SV=1 | 38.80  |
| TRINITY_sp| Anthranilate synthase component 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=trp3 PE=1 SV=1 | 38.80  |
| TRINITY_sp| DNA mismatch repair protein Msh2 OS=Chlorocebus aethiops GN=MSH2 PE=2 SV=1 | 38.80  |
| TRINITY_sp| GTP-binding nuclear protein GSP2/CNR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GSP2 PE=1 SV=1 | 38.80  |
| TRINITY_sp| Probable calcium-binding protein CML29 OS=Oryza sativa subsp. japonica GN=CML29 PE=2 SV=1 | 38.80  |
| TRINITY_sp| Ras-specific guanine-releasing factor 2 OS=Homo sapiens GN=RASGRF2 PE=1 SV=2 | 38.80  |
| TRINITY_sp| Centrosomal protein of 164 kDa OS=Mus musculus GN=Cep164 PE=1 SV=2 | 38.80  |
| TRINITY_sp| Probable calcium-binding protein CML29 OS=Oryza sativa subsp. japonica GN=CML29 PE=2 SV=1 | 38.80  |
| TRINITY_sp| Acetyl-CoA carboxylase 2 OS=Arabidopsis thaliana GN=ACC2 PE=2 SV=1 | 38.80  |
| TRINITY_sp| Dynamin-related protein 3A OS=Arabidopsis thaliana GN=DRP3A PE=1 SV=2 | 38.80  |
| TRINITY_sp| IQ domain-containing protein H OS=Homo sapiens GN=IQCH PE=2 SV=2 | 38.80  |
| TRINITY_sp| Tyrosine-protein kinase fyna OS=Danio rerio GN=fyna PE=1 SV=2 | 38.80  |
| TRINITY_sp| Flotillin-like protein 6 OS=Medicago truncatula GN=FLOT6 PE=2 SV=1 | 38.80  |
| TRINITY_sp| E3 ubiquitin-protein ligase TOM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TOM1 PE=1 SV=1 | 38.80  |
| TRINITY_sp| Elongation of fatty acids protein A OS=Dictyostelium discoideum GN=eloA PE=2 SV=1 | 38.80  |
| TRINITY_sp| Multisite-specific tRNA:(cytosine-C(5))-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NCL1 PE=1 SV=1 | 38.80  |
| TRINITY_sp| Serine carboxypeptidase-like 50 OS=Arabidopsis thaliana GN=SCPL50 PE=2 SV=1 | 38.80  |
| TRINITY_sp| Dynein heavy chain 1, axonemal OS=Rattus norvegicus GN=Dnah1 PE=2 SV=2 | 38.80  |
| TRINITY_sp| Protein PRY2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PRY2 PE=1 SV=1 | 38.80  |
| TRINITY_sp| Uncharacterized oxidoreductase YuxG OS=Bacillus subtilis (strain 168) GN=yuxG PE=3 SV=2 | 38.80  |
| TRINITY_sp| Phosphoserine phosphatase OS=Archaeoglobus fulgidus (strain ATCC 49558 / VC-16 / DSM 4304 / JCM 9628 / NBRC 100126) GN=AF_2138 PE=3 SV=1 | 38.80  |
| TRINITY_sp| Protein slowmo homolog OS=Dictyostelium discoideum GN=slmo PE=3 SV=1 | 38.80  |
| Gene Name                              | Protein Description                                      | Score | e-value |
|----------------------------------------|----------------------------------------------------------|-------|---------|
| Protein phosphatase Slingshot homolog 1 OS=Homo sapiens GN=SSH1 PE=1 SV=2 | Ankyrin repeat domain-containing protein 2A OS=Arabidopsis thaliana GN=AKR2A PE=1 SV=2 | 38.70 | 0.00    |
| Folate-biopterin transporter OS=Synechocystis sp. (strain PCC 6803 / Kazusa) GN=slr0642 PE=1 SV=1 | Ubiquitin carboxyl-terminal hydrolase USP5 OS=Arabidopsis thaliana GN=At5g55200 PE=1 SV=1 | 38.70 | 0.00    |
| Vesicle-associated membrane protein 714 OS=Arabidopsis thaliana GN=VAMP714 PE=1 SV=1 | Putative Ufm1-specific protease OS=Arabidopsis thaliana GN=At3g48380 PE=1 SV=2 | 38.70 | 0.00    |
| Tyrosine-protein kinase csk-1 OS=Caenorhabditis elegans GN=csk-1 PE=1 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| 3-oxoacyl-[acyl-carrier-protein] reductase, chloroplastic OS=Cuphea lanceolata GN=CLKR27 PE=2 SV=1 | Probable phospholipid-transporting ATPase C887.12 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC887.12 PE=3 SV=1 | 38.70 | 0.00    |
| Sodium/potassium-transporting ATPase subunit alpha-1 OS=Equus caballus GN=ATP1A1 PE=3 SV=1 | Mitogen-activated protein kinase kinase 3 OS=Arabidopsis thaliana GN=MKK3 PE=1 SV=1 | 38.70 | 0.00    |
| Ankyrin repeat domain-containing protein 2A OS=Arabidopsis thaliana GN=AKR2A PE=1 SV=2 | Putative Ufm1-specific protease OS=Arabidopsis thaliana GN=At3g48380 PE=1 SV=2 | 38.70 | 0.00    |
| Isopentenyl phosphate kinase OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 10044) GN=MJ0044 PE=1 SV=1 | Protein phosphatase Slingshot homolog 1 OS=Homo sapiens GN=SSH1 PE=1 SV=2 | 38.70 | 0.00    |
| Hematopoietic lineage cell-specific protein OS=Mus musculus GN=Hcls1 PE=1 SV=2 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| RCC1 and BTB domain-containing protein 2 OS=Homo sapiens GN=RCBTB2 PE=1 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| Protein argonaute 2 OS=Oryza sativa subsp. japonica GN=AGO2 PE=2 SV=2 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| YLP motif-containing protein 1 OS=Rattus norvegicus GN=Ylpm1 PE=1 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| ATP-dependent RNA helicase HrpB OS=Escherichia coli (strain K12) GN=hrpB PE=3 SV=3 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| Vesicle-fusing ATPase OS=Arabidopsis thaliana GN=NSF PE=2 SV=2 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| Mitogen-activated protein kinase kinase 3 OS=Arabidopsis thaliana GN=MKK3 PE=1 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| Intraflagellar transport protein 122 homolog OS=Mus musculus GN=Ift122 PE=1 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| Tubulin beta-2 chain OS=Suillus bovinus GN=TUBB2 PE=2 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| Probable sucrose-phosphatase 1 OS=Oryza sativa subsp. japonica GN=SPP1 PE=2 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| Hybrid signal transduction protein dokA OS=Dictyostelium discoideum GN=dokA PE=1 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| Vacuolar protein sorting-associated protein 11 homolog OS=Homo sapiens GN=VPS11 PE=1 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| Dynein gamma chain, flagellar outer arm OS=Chlamydomonas reinhardtii GN=ODA2 PE=1 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| ZZ-type zinc finger-containing protein 3 OS=Homo sapiens GN=ZZZ3 PE=1 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| Zinc finger SWIM domain-containing protein 7 homolog OS=Dictyostelium discoideum GN=zswim7 PE=3 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| RPM1-interacting protein 4 OS=Arabidopsis thaliana GN=RIN4 PE=1 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
| Probable formaldehyde dehydrogenase AdhA OS=Bacillus subtilis (strain 168) GN=adhA PE=2 SV=1 | Very-long-chain 3-oxoacyl-CoA reductase-B OS=Danio rerio GN=hsd17b12b PE=2 SV=2 | 38.70 | 0.00    |
TRINITY_sp|Q9WY{Tm_0225 Putative 1-aminocyclopropane-1-carboxylate deaminase OS=Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) GN=TM_0225 PE=3 SV=1

TRINITY_sp|Q4Pj{CYP51A1 Lanosterol 14-alpha demethylase OS=Bos taurus GN=CYP51A1 PE=2 SV=1

TRINITY_sp|P109' Retrovirus-related OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q8T2{DD_B GO2: Putative ZDHHC-type G1/S-specific cyclin-E OS=Hemicentrotus pulcherrimus GN=CYCE PE=2 SV=1

TRINITY_sp|A6U7{Amet_36: 8-amino-7-oxononanoate 17-beta-hydroxysteroid dehydrogenase 13 OS=Rattus norvegicus GN=Hsd17b13 PE=1 SV=1

TRINITY_sp|Q149{BTA{F TATA-binding protein OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|P187'RCC1 Regulator of chromo OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q2{XW{svop Synaptic vesicle 2- OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q2{TA{KIF19 Kinesin-like protein OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q312{alkB Alkane 1-monooxygenase OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q9FP{UBB23 Ubiquitin carboxyl-terminal OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q17{R{DX38 Pre-mRNA-splicing factor OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|O565{CYSEP Vignain OS=Ricinus OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q84{R{CCCD Carotenoid 9,10(9'),11-triethyl OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q95{Y{PeFB Penta-EF hand domain OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|O64{At2g189 Thioredoxin domain OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q5U{Arhgap2 Rho GTPase-activating OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q6AX{Hexb Betax-hexosaminidase OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q5{G{DDDB_G02 Probable serine/threonine-protein kinase OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q9{D2{Kif12 Kinesin-like protein OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|O437{CYTH3 Cytohesin-3 OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q84{S{Os07g05 Zinc finger CCH domain OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q3{EAI{At3g622 Probable protein phosphatase 2C OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q9{ST{At3g0906 BTB/POZ domain-containing OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q9{LZ{STN8 Serine/threonine-protein kinase OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q54{E{gacEE Rho GTPase-activating OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q9{L{HRD1A ERAD-associated E3 OS=Homo sapiens GN=EPHA1 PE=1 SV=4

TRINITY_sp|Q9{SF{SY71 Syntaxin-71 OS=Arabidopsis thaliana GN=SY71 PE=2 SV=1

TRINITY_sp|Q8{R1{Bud13 BUD13 homolog OS=Mus musculus GN=SY71 PE=2 SV=1

TRINITY_sp|Q9{Z{W{PRN2 Pirin-like protein OS=Homo sapiens GN=SY71 PE=2 SV=1

TRINITY_sp|Q8{R3{S1f1 SMC5-SMC6 complex OS=Homo sapiens GN=SY71 PE=2 SV=1

TRINITY_sp|Q5{K{epsa15 Epidermal growth factor OS=Homo sapiens GN=SY71 PE=2 SV=1

TRINITY_sp|Q2{NU{cdd Cytidine deaminase OS=Homo sapiens GN=SY71 PE=2 SV=1

TRINITY_sp|Q9{SU{SY43 Syntaxin-43 OS=Arabidopsis thaliana GN=SYP43 PE=2 SV=1

TRINITY_sp|Q8{LP{R1 Alpha-glucan water channel OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|O159{CYCE G1/S-specific cyclin OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|Q17{QERAB30 Ras-related protein OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|P599{DNAJB13 DnaJ homolog subfamily OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|Q5{Z{EpkgA Probable serine/threonine-protein kinase OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|P341{ptpb Tyrosine-protein kinase OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|Q0{VA{wdr70 WD repeat-containing OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|P6{2{CPK1 Calcium-dependent protein OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|A8{WH{narf1 Cytosolic Fe-S cluster OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|P4{70{PRY1 Protein PRY1 OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|Q0{VC{PQLC1 PQ-loop repeat-containing OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|O9{5{SFT2D2 Vesicle transport OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|Q9{C{Izltr1 Leucine zipper-like OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|O8{2{3{At2g2577 Probably inactive OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|Q5{M8{Hsd17b17 Alarmone hydroxysterol OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|O5{82{gck Glycerate 2-kinase OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|D0{F{1af-1 ATP-dependent RNA helicase OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|P2{17{EPA1 Ephrin type-A receptor OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|P1{09{ugpQ Glycerophosphoryl diester phosphodiesterase OS=Homo sapiens GN=SYP43 PE=2 SV=1

TRINITY_sp|Q9{1{W{Txndc5 Thioredoxin domain OS=Homo sapiens GN=SYP43 PE=2 SV=1
Probable formate transporter OS=Methanothermobacter thermautotrophicus GN=fdhC PE=3 SV=1
0.00 0.00 0.00 0.00
Maternal DNA replication licensing factor mcm6 OS=Xenopus laevis GN=mmcm6 PE=1 SV=1
Hybrid signal transduction histidine kinase C OS=Dictyostelium discoideum GN=dhkC PE=1 SV=1
DNA-directed RNA polymerase I subunit rpa1 OS=Dictyostelium discoideum GN=polr1a PE=3 SV=1
Guanine exchange factor for Rac 30 OS=Dictyostelium discoideum GN=gxcDD PE=3 SV=3
Nuclear pore complex protein NUP62 OS=Arabidopsis thaliana GN=NUP62 PE=1 SV=1
Probable serine/threonine-protein kinase drkD OS=Dictyostelium discoideum GN=drkD PE=2 SV=1
Sex-determining region Y protein OS=Monachus schauinslandi GN=SRY PE=3 SV=1
Serine/threonine-protein kinase RIO2 OS=Mus musculus GN=Riok2 PE=1 SV=1
Cilia- and flagella-associated protein 46 OS=Chlamydomonas reinhardtii GN=CFAP46 PE=1 SV=1
UMP-CMP kinase 3 OS=Oryza sativa subsp. japonica GN=URA6 PE=2 SV=1
Calcineurin B-like protein 3 OS=Arabidopsis thaliana GN=CBL3 PE=1 SV=2
Serine/threonine-protein kinase SAPK8 OS=Oryza sativa subsp. japonica GN=SAPK8 PE=2 SV=1
Plasma membrane calcium-transporting ATPase 4 OS=Mus musculus GN=Atp2b4 PE=1 SV=1
Long chain base biosynthesis protein 2b OS=Arabidopsis thaliana GN=LCB2b PE=1 SV=1
Pre-mRNA-splicing factor SPF27 homolog OS=Arabidopsis thaliana GN=MOS4 PE=1 SV=1
Nitric oxide synthase-interacting protein OS=Bos taurus GN=NOSIP PE=2 SV=1
Guanine nucleotide-binding protein G(q) subunit alpha OS=Geodia cydonium PE=2 SV=1
Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Arabidopsis thaliana GN=BIG2 PE=2 SV=1
Sphingosine-1-phosphate lyase 1 OS=Rattus norvegicus GN=Sgpl1 PE=2 SV=1
Potential protein lysine methyltransferase SET5 OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NRRL Y-1140 / WM37) GN=SET5 PE=3 SV=1
Diacylglycerol kinase 2 OS=Arabidopsis thaliana GN=DGK2 PE=1 SV=1
Tripeptidyl-peptidase sed3 OS=Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) GN=sed3 PE=1 SV=1
Uncharacterized protein F21D5.5 OS=Caenorhabditis elegans GN=F21D5.5 PE=2 SV=2
cGMP-dependent 3',5'-cGMP phosphodiesterase A OS=Dictyostelium discoideum GN=pdeD PE=1 SV=1
Pre-rRNA-processing protein ESF2 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) GN=ESF2 PE=3 SV=2
Tetratricopeptide repeat protein 28 OS=Homo sapiens GN=TTC28 PE=1 SV=4
Probable ergosterol biosynthetic protein 28 OS=Mus musculus GN=ORF11 PE=2 SV=1
Drebrin-like protein OS=Dictyostelium discoideum GN=abpE-1 PE=2 SV=1
Mitogen-activated protein kinase 14B OS=Drosophila melanogaster GN=p38b PE=1 SV=1
TRINITY_sp|Q505|fdhC
TRINITY_sp|Q9FG|SNX1
TRINITY_sp|Q70G|sed3
TRINITY_sp|Q34J|AHK5
TRINITY_sp|Q86H|polr1a
TRINITY_sp|Q196|F21D5.5
TRINITY_sp|Q54Y|meCr
TRINITY_sp|A5D5|PAB1
TRINITY_sp|Q4G0|KCTD21
TRINITY_sp|Q810|Ddx42
TRINITY_sp|Q5H2|sirt5-a
TRINITY_sp|Q9SL|Os05g01
TRINITY_sp|F257|Os04g06
TRINITY_sp|Q557|abpE-1
TRINITY_sp|Q59Y|ESF2
TRINITY_sp|Q9FF|DKG2
TRINITY_sp|Q35Z|MED6
TRINITY_sp|Q54L|DDDB_G02
TRINITY_sp|Q567|ch25h11
TRINITY_sp|Q1LV|sf3b3
TRINITY_sp|Q9M3|LCB2b
TRINITY_sp|Q7X1|URA6
TRINITY_sp|Q3SN|NOSIP
TRINITY_sp|Q1ZX|gxcDD
TRINITY_sp|Q8CH|Sgp11
TRINITY_sp|Q8L7|NUP62
TRINITY_sp|Q7PC|AGAPA002
TRINITY_sp|Q96A|TTC28
TRINITY_sp|Q54T|drkD
TRINITY_sp|P331|spaR
TRINITY_sp|Q9BZ|PUS3
TRINITY_sp|Q9X2|-
TRINITY_sp|Q614|p38b
TRINITY_sp|Q631|Eif2ak2
TRINITY_sp|Q5QK|MIMI_R81
TRINITY_sp|Q1ZX|gxcDD
TRINITY_sp|Q6TC|SRY
TRINITY_sp|Q6Q4|Atp2b4
TRINITY_sp|Q9ER|ORF11
TRINITY_sp|Q827|soxA
TRINITY_sp|Q7YO|SAPK8
TRINITY_sp|Q9CQ|Rick2
TRINITY_sp|A8IC|CFAP46
TRINITY_sp|Q95P|dhhC
TRINITY_sp|Q949|MOS4
TRINITY_sp|Q9L2|BIG2
TRINITY_sp|Q6CX|SET5
TRINITY_sp|Q8LE|CBL3
TRINITY_sp|Q3M8|saA
TRINITY_sp|Q8ML|pdeD
TRINITY_sp|Q5FW|mccm6
TRINITY_sp|Q5RC|GLRX2
TRINITY_sp|Q54Y|snFA
TRINITY_sp|Q9D0|Alg14
TRINITY_sp|Q54Y|dhhK
TRINITY_sp|Q9JI|Ercc612
TRINITY_sp|Q84LAVPE1  Vacuolar-processing  38.40  0.00
TRINITY_sp|P549mNapa  Alpha-soluble NSF a  38.40  0.00
TRINITY_sp|Q2M3KIAA103:WASH complex subun  38.40  0.00
TRINITY_sp|P142:Fgr  Tyrosine-protein ki  38.40  0.00
TRINITY_sp|Q9ZRICAD  Probable mannitol d  38.40  0.00
TRINITY_sp|Q54VLDDB_G02:Probable serine/thr  38.40  0.00
TRINITY_sp|P341:ptPB  Tyrosine-protein ph  38.40  0.00
TRINITY_sp|O151:CETN3  Centrin-3 OS=Homo s  38.40  0.00
TRINITY_sp|Q6CGIYAL1OAl:Acyl-protein thioe  38.40  0.00
TRINITY_sp|Q8BB\6pr107  Protein GPR107 OS=M  38.40  0.00
TRINITY_sp|Q0QLmi  3-methylitaconate i  38.40  0.00
TRINITY_sp|Q083:FPG1  Formamidopyrimidine  38.40  0.00
TRINITY_sp|Q54MmKcA  Probable serine/thr  38.40  0.00
TRINITY_sp|Q06ILAP1  Leucine aminopeptid  38.40  0.00
TRINITY_sp|Q7X6:MMB1  PHD finger protein  38.40  0.00
TRINITY_sp|Q8LP:LC6S6  Long chain acyl-CoA  38.40  0.00
TRINITY_sp|P0A2IucPA  Oxidoreductase UcpA  38.40  0.00
TRINITY_sp|Q66GIROPRP1  Proteinaceous RNase  38.40  0.00
TRINITY_sp|Q9SJJGC1  Epimerase family pr  38.40  0.00
TRINITY_sp|Q57:HLUL4  Probable E3 ubiquit  38.40  0.00
TRINITY_sp|P0CO:GEM1  Mitochondrial Rho G  38.40  0.00
TRINITY_sp|P448(HI_0658  Uncharacterized ABC  38.40  0.00
TRINITY_sp|P577:ALA12  Probable phospholip  38.40  0.00
TRINITY_sp|O605:CD40  Pre-mRNA-processing  38.40  0.00
TRINITY_sp|P189:ATP1A1  Sodium/potassium-tr  38.40  0.00
TRINITY_sp|Q8AJXBASS4  Probable sodium/met  38.40  0.00
TRINITY_sp|Q9FL:MR3S2-2  Magnesium transport  38.40  0.00
TRINITY_sp|Q9VRHERC2  Probable E3 ubiquit  38.40  0.00
TRINITY_sp|Q6IA:NADSYN1  Glutamine-dependent  38.40  0.00
TRINITY_sp|Q9P2HFT80  Intraflagellar tran  38.40  0.00
TRINITY_sp|Q9HD:SPAPBLA  Putative ATP-depend  38.40  0.00
TRINITY_sp|Q12XJgxxDD  Guanine exchange fa  38.40  0.00
TRINITY_sp|Q8CcrnF44  RING finger protein  38.40  0.00
TRINITY_sp|Q9ZUSBAT1  Amino-acid permease  38.40  0.00
TRINITY_sp|Q54V\DDDB_G02:Probable serine/thr  38.40  0.00
TRINITY_sp|Q9FF:VP536  Vacuolar protein so  38.40  0.00
TRINITY_sp|B5B71BTA1  TATA-binding protei  38.40  0.00
TRINITY_sp|Q266:KAPI15  Kinesin-associated  38.40  0.00
TRINITY_sp|Q9US:mug71  Diphthine--ammonia  38.40  0.00
TRINITY_sp|Q436:-  NADH dehydrogenase  38.40  0.00
TRINITY_sp|Q5S5:THHA027(Thermostable carbox  38.40  0.00
TRINITY_sp|Q9SQ1EMB3004  Bifunctional 3-dehy  38.40  0.00
TRINITY_sp|Q9SYVYTE6  Protein VTE6, chlor  38.40  0.00
TRINITY_sp|Q01Z:PH54-5  Probable anion tran  38.40  0.00
TRINITY_sp|Q55E:dhKE  Hybrid signal trans  38.30  0.00
TRINITY_sp|Q54YI:dhkB  Hybrid signal trans  38.30  0.00
TRINITY_sp|D9HP:CNR11  Cell number regulat  38.30  0.00
TRINITY_sp|Q5B1IDUSP18  Dual specificity pr  38.30  0.00
TRINITY_sp|Q7T01amtor3-Ragulator complex p  38.30  0.00
TRINITY_sp|P4471HI_0454  Uncharacterized met  38.30  0.00
TRINITY_sp|Q7XA:PO1T1  Folate transporter  38.30  0.00
TRINITY_sp|Q54VCabcC15  ABC transporter C f  38.30  0.00
TRINITY_sp|Q0DAOs6g06:Zinc finger CCCH do  38.30  0.00
TRINITY_sp|Q54H:drkB  Probable serine/thr  38.30  0.00
TRINITY_sp|F4J1STY46  Serine/threonine-pr  38.30  0.00
TRINITY_sp|Q182:rap-1  Ras-related protein  38.30  0.00
| Protein Name | Gene Name | Species | Function | Expression Value | Log2 Fold Change |
|--------------|-----------|---------|----------|------------------|-----------------|
| Vam6/Vps39-like protein | Vps39 | Mus musculus | | 38.20 | 0.00 |
| Photosystem I chlorophyll a/b binding protein | LHCA5 | Oryza sativa subsp. japonica | | 38.20 | 0.00 |
| Uncharacterized ATP-binding protein | SPBC582 | Arabidopsis thaliana | | 38.20 | 0.00 |
| Autophagy-related protein | ATG9 | Mus musculus | | 38.20 | 0.00 |
| Lysine-specific demethylase | Kdm8 | Schizosaccharomyces pombe | | 38.20 | 0.00 |
| Calcium/calmodulin-dependent protein kinase | CAMK1D | Arabidopsis thaliana | | 38.20 | 0.00 |
| Glutathione S-transferase | GST1 | Ascaris suum | | 38.20 | 0.00 |
| Multidrug resistance protein | Trm1 | Schizosaccharomyces pombe | | 38.20 | 0.00 |
| Myotubularin-related protein | Mtr14 | Schizosaccharomyces pombe | | 38.20 | 0.00 |
| Dynine heavy chain | DN4AH1 | Arabidopsis thaliana | | 38.20 | 0.00 |
| ADP-riboseylation factor | AGD12 | Schizosaccharomyces pombe | | 38.20 | 0.00 |
| E3 ubiquitin-protein ligase | ATL6 | Drosophila melanogaster | | 38.20 | 0.00 |
| BTB/POZ domain-containing protein | Kctd7 | Danio rerio | | 38.20 | 0.00 |
| Phosphatidylethanolamine N-methyltransferase | Chol2 | Schizosaccharomyces pombe | | 38.20 | 0.00 |
| SUMO-activating enzyme | Uba2 | Xenopus tropicalis | | 0.00 | 0.00 |
| Phospholipid-transporting ATPase | ALA1 | Arabidopsis thaliana | | 38.20 | 0.00 |
| Autophagy-related protein | ATG9 | Arabidopsis thaliana | | 38.20 | 0.00 |
| Soluble guanylate cyclase | Gyc88E | Drosophila melanogaster | | 38.20 | 0.00 |
| Probable succinate-semialdehyde dehydrogenase | GabD | Synechocystis sp. | | 0.00 | 0.00 |
| Multidrug resistance protein | Abcc6 | Rattus norvegicus | | 38.20 | 0.00 |
| BTB/POZ domain-containing protein | Kctd7 | Danio rerio | | 38.20 | 0.00 |
| Photosystem I chlorophyll a/b-binding protein | LHCA5 | Arabidopsis thaliana | | 38.20 | 0.00 |
| Sodium channel protein | NaCP60E | Mus musculus | | 38.20 | 0.00 |
| Gene ID | Description | Score |
|---------|-------------|-------|
| TRINITY_sp| N-acyl-phosphatidyl | 38.10 |
| TRINITY_sp| E3 ubiquitin-protein | 38.10 |
| TRINITY_sp| Protein phosphatase | 38.10 |
| TRINITY_sp| Rap1 GTPase-activat | 38.10 |
| TRINITY_sp| Cytochrome P450 | 38.10 |
| TRINITY_sp| Hormone-sensitive l | 38.10 |
| TRINITY_sp| Casein kinase I iso | 38.10 |
| TRINITY_sp| Probable ATP-depend | 38.10 |
| TRINITY_sp| SUPPRESSOR OF ABI3- | 38.10 |
| TRINITY_sp| 30S ribosomal prote | 38.10 |
| TRINITY_sp| Hybrid signal trans | 38.10 |
| TRINITY_sp| Serine/threonine-pr | 38.10 |
| TRINITY_sp| Probable mitochondr | 38.10 |
| TRINITY_sp| DNA oxidative demet | 38.10 |
| TRINITY_sp| Biotinidase OS=Taki | 38.10 |
| TRINITY_sp| Acyl-coenzyme A oxi | 38.10 |
| TRINITY_sp| Probable cadmium/zi | 38.10 |
| TRINITY_sp| Eukaryotic translat | 38.10 |
| TRINITY_sp| Transmembrane prote | 38.10 |
| TRINITY_sp| Alpha-glucosidase O | 38.00 |
| TRINITY_sp| Procardosin-A OS=Cy | 38.00 |
| TRINITY_sp| Kinetochore protein | 38.00 |
| TRINITY_sp| Probable serine/thr | 38.00 |
| TRINITY_sp| Cyclin-T1-3 OS=Oryz | 38.10 |
| TRINITY_sp| Cationic amino acid | 38.10 |
| TRINITY_sp| Radical S-adenosyl | 38.00 |
| TRINITY_sp| CTD small phosphata | 38.00 |
| TRINITY_sp| Probable 28S rRNA ( | 38.00 |
| TRINITY_sp| ADP-ribose pyrophos | 38.00 |
| TRINITY_sp| Equilibrative nucle | 38.00 |
| TRINITY_sp| Auxin transport pro | 38.00 |
| TRINITY_sp| Putative band 7 fam | 38.00 |
| TRINITY_sp| Protein usf OS=Aqui | 38.00 |
| TRINITY_sp| Tyrosine-protein ki | 38.00 |
| TRINITY_sp| Signal transducing | 38.00 |
| TRINITY_sp| Probable GTP-bindin | 38.00 |
| TRINITY_sp| Probable NAD kinase | 38.00 |
| TRINITY_sp| Venom serine carbox | 38.00 |
| TRINITY_sp| Serine/threonine-pr | 38.00 |
| TRINITY_sp| Asparagine syntheta | 38.00 |
| TRINITY_sp| Protein MSP1 OS=Sac | 38.00 |
| TRINITY_sp| Peptidyl-prolyl cis | 38.00 |
| TRINITY_sp| Kinesin-like protei | 38.00 |
| TRINITY_sp| Protein kinase DC2 | 38.00 |
| TRINITY_sp| Ephrin_type-B recep | 38.00 |
| TRINITY_sp| Trans-acting enoyl | 38.00 |
| TRINITY_sp| Rhomboid-related pr | 38.00 |
| TRINITY_sp| Peroxisome biogenes | 38.00 |
| TRINITY_sp| Transcriptional act | 38.00 |
| TRINITY_sp| NFX1-type zinc fing | 38.00 |
| TRINITY_sp| Beta-hexosaminidase | 38.00 |
| Accession | Description | E-value | bit score |
|-----------|-------------|---------|-----------|
| TRINITY_sp| B1111rp1D  | 50S ribosomal protein | 38.00 0.00 |
| TRINITY_sp| P395dRS2   | Probable phospholipid | 38.00 0.00 |
| TRINITY_sp| Q541ishkB  | Dual specificity protein | 38.00 0.00 |
| TRINITY_sp| O884Aurkc  | Aurora kinase C | 38.00 0.00 |
| TRINITY_sp| A7SDv1694  | Eukaryotic translation | 38.00 0.00 |
| TRINITY_sp| Q9S5IBIG   | Auxin transport protein | 38.00 0.00 |
| TRINITY_sp| Q8H2Os07g02 | Glycerol-3-phosphate | 38.00 0.00 |
| TRINITY_sp| Q9S2XPAAl  | Copper-transporting protein | 38.00 0.00 |
| TRINITY_sp| P049cprA   | Cysteine proteinase | 38.00 0.00 |
| TRINITY_sp| Q207tatad-3| ATPase family AAA | 38.00 0.00 |
| TRINITY_sp| Q96N1GUCD1 | Protein GUCD1 | 38.00 0.00 |
| TRINITY_sp| Q55DabcG22 | ABC transporter G | 38.00 0.00 |
| TRINITY_sp| P400TPAAl  | Prolyl 3,4-dihydroxyproline | 38.00 0.00 |
| TRINITY_sp| P123CLRX   | Glutaredoxin-1 | 38.00 0.00 |
| TRINITY_sp| P0C7DA1    | Protein DA1 | 38.00 0.00 |
| TRINITY_sp| Q212RPL14  | 60S ribosomal protein | 38.00 0.00 |
| TRINITY_sp| Q3M1PUS10  | Putative tRNA pseudouridine synthase | 38.00 0.00 |
| TRINITY_sp| Q8V2ISUVH6 | Histone-lysine N-methyltransferase | 38.00 0.00 |
| TRINITY_sp| P041Myb    | Myb protein | 38.00 0.00 |
| TRINITY_sp| Q8LBcYCUCU | Cyclin-U3-1 | 38.00 0.00 |
| TRINITY_sp| Q9S1TTM3   | Triphosphate tunnel | 38.00 0.00 |
| TRINITY_sp| P374alkB   | Alpha-ketoglutarate | 38.00 0.00 |
| TRINITY_sp| Q395dRS2   | Probable phospholipid | 38.00 0.00 |
| TRINITY_sp| Q9EFUVR8   | Ultraviolet-B receptor | 38.00 0.00 |
| TRINITY_sp| Q9CFCEL3   | Endoglucanase 9 | 38.00 0.00 |
| TRINITY_sp| QOW5alaS   | Alanine--tRNA ligase | 38.00 0.00 |
| TRINITY_sp| Q9M9SRK2C  | Serine/threonine-protein kinase | 38.00 0.00 |
| TRINITY_sp| Q8LPAt3g199 | E3 ubiquitin-protein ligase | 37.90 0.00 |
| TRINITY_sp| Q9UYpub2   | E3 ubiquitin-protein ligase | 37.90 0.00 |
| TRINITY_sp| P531GUP1   | Glycerol uptake protein | 37.90 0.00 |
| TRINITY_sp| Q449C34B21 | Probable signal peptide | 37.90 0.00 |
| TRINITY_sp| P357`-     | Venom allergen 3 | 37.90 0.00 |
| TRINITY_sp| Q63Z`-     | UPF0568 protein | 37.90 0.00 |
| TRINITY_sp| Q5XHsilc25a| Calcium-binding mitochondrial carrier | 37.90 0.00 |
| TRINITY_sp| Q499CCR4   | Glucose-repressible regulator | 37.90 0.00 |
| TRINITY_sp| Q964ORM1   | Protein ORM1 | 37.90 0.00 |
| TRINITY_sp| Q99KUspl1  | Ubiquitin carboxyl-terminal hydrolase | 37.90 0.00 |
| TRINITY_sp| Q2TMGCQG8  | Conserved oligomeric | 37.90 0.00 |
| TRINITY_sp| A5PKIMETTL | Methyltransferase | 37.90 0.00 |
| TRINITY_sp| Q9QYDnaja2 | DnaJ homolog subfamily | 37.90 0.00 |
| TRINITY_sp| Q8BYtTrmt13| tRNA:m(4)X modifica | 37.90 0.00 |
| TRINITY_sp| Q420ABC2   | ABC transporter C | 37.90 0.00 |
| TRINITY_sp| P190GNAT2  | Guanine nucleotide exchange factor | 37.90 0.00 |
| TRINITY_sp| Q953MANBA  | Beta-mannosidase OS | 37.90 0.00 |
| TRINITY_sp| Q6V410HGO  | 8-hydroxygeraniol d | 37.90 0.00 |
| TRINITY_sp| Q004pho2   | 4-nitrophenolphosphate | 37.90 0.00 |
| TRINITY_sp| Q8W4PTC52  | Protochlorophyllide | 37.90 0.00 |
| TRINITY_sp| Q9N5ccdc-73| Cell division cycle | 37.90 0.00 |
| TRINITY_sp| Q8IIIP1101 | Probable cathepsin | 37.90 0.00 |
| TRINITY_sp| P176ypt2   | GTP-binding protein | 37.90 0.00 |
| TRINITY_sp| Q2QNCYCA32 | Cyclin-A3-2 | 37.90 0.00 |
| TRINITY_sp| Q9LDFBETAA | Alphabetic adaptin-like protein | 37.90 0.00 |
| TRINITY_sp| Q9FPJUBP15 | Ubiquitin carboxyl-terminal hydrolase | 37.90 0.00 |
| TRINITY_sp| A662betB   | NAD/NADP-dependent protein | 37.90 0.00 |
| TRINITY_sp| Q9S7SHSP70 | Heat shock 70 kDa protein | 37.90 0.00 |
| TRINITY_sp| Q9FE1SRT1  | NAD-dependent protein | 37.90 0.00 |
TRINITY_sp|P0A0T|SAOUHSC_Putative acetyltran 37.90 0.00
TRINITY_sp|P1091MCP2 Proto-oncogene DBL 37.80 0.00
TRINITY_sp|P1379mvA 3-hydroxy-3-methyln 37.80 0.00
TRINITY_sp|Q395f Dynein 18 kDa light 37.80 0.00
TRINITY_sp|Q440f L-sorbose dehydro 37.80 0.00
TRINITY_sp|Q54Jlat6B Beclin-1-like prote 37.80 0.00
TRINITY_sp|Q6PQ 3-oxo-Delta(4,5)-st 37.80 0.00
TRINITY_sp|Q806fPAT02 Probable protein S- 37.80 0.00
TRINITY_sp|Q65RIdhKL Hybrid signal trans 37.80 0.00
TRINITY_sp|Q256Rab27a Ras-related protein 37.80 0.00
TRINITY_sp|Q54Jchmp5 Charged multivesicu 37.80 0.00
TRINITY_sp|Q8F0cepA Probable cytosol am 37.80 0.00
TRINITY_sp|Q56XRH3 DEAD-box ATP-depend 37.80 0.00
TRINITY_sp|P147 Soluble hydrogenase 37.80 0.00
TRINITY_sp|Q323YMC1 Carrier protein YMC 37.80 0.00
TRINITY_sp|Q6PECTbca Tubulin-specific ch 37.80 0.00
TRINITY_sp|Q9NCPRPD1B Regulation of nucle 37.80 0.00
TRINITY_sp|Q947B11B22(E3 ubiquitin-protei 37.80 0.00
TRINITY_sp|Q66Heif4e3 Eukaryotic translat 37.80 0.00
TRINITY_sp|Q9W0Nprl2 Nitrogen permease r 37.80 0.00
TRINITY_sp|F4JCAt3g478 Probative DNA glycos 37.80 0.00
TRINITY_sp|Q54fsmt1 Probable cycloarten 37.80 0.00
TRINITY_sp|Q401 LEC14B protein OS=L 37.80 0.00
TRINITY_sp|P604PTEN Phosphatidylinosito 37.80 0.00
TRINITY_sp|P2251CMK2 Calcium/calmodulin- 37.80 0.00
TRINITY_sp|Q54HcopG Coatomer subunit ga 37.80 0.00
TRINITY_sp|Q9ZUADK Adenylate kinase 1, 37.80 0.00
TRINITY_sp|A2Q8gpu14 Nuclear protein loc 37.80 0.00
TRINITY_sp|Q8I4eshk-1 Potassium voltage-g 37.80 0.00
TRINITY_sp|Q226MST4 WD-40 repeat-contai 37.80 0.00
TRINITY_sp|Q541smkA Suppressor of Mek1 37.80 0.00
TRINITY_sp|O052lywrD Putative gamma-glut 37.80 0.00
TRINITY_sp|Q66WPPARG Poly(ADP-ribose) gl 37.80 0.00
TRINITY_sp|Q212gsnl-1 Gelsolin-like prote 37.80 0.00
TRINITY_sp|P2751CBR Carotene biosynthes 37.80 0.00
TRINITY_sp|Q077HVA22 Protein HVA22 OS=Ho 37.80 0.00
TRINITY_sp|P743sall0418 2-methyl-6-phytyl-1 37.80 0.00
TRINITY_sp|Q8GWCTPPH Probable trehalose- 37.80 0.00
TRINITY_sp|P234Xrc6 X-ray repair cross- 37.80 0.00
TRINITY_sp|M4MRjn Ribonuclease J OS=S 37.80 0.00
TRINITY_sp|Q6NWWRWDD4 RWD domain-containi 37.80 0.00
TRINITY_sp|Q541ishkB Dual specificity pr 37.80 0.00
TRINITY_sp|P773lybdR Uncharacterized zin 37.80 0.00
TRINITY_sp|Q54BDDD_B02 Probable GH family 37.80 0.00
TRINITY_sp|Q7XJGAS8 Growth arrest-speci 37.80 0.00
TRINITY_sp|Q8VEHmem144 Transmembrane prote 37.80 0.00
TRINITY_sp|Q9NRYDYRK4 Dual specificity ty 37.80 0.00
TRINITY_sp|Q140CAMK1 Calcium/calmodulin- 37.80 0.00
TRINITY_sp|Q044Atig096 Probable elongation 37.80 0.00
TRINITY_sp|B4JYCGH22679 Eukaryotic translat 37.80 0.00
TRINITY_sp|Q69uRMRL Receptor homology r 37.80 0.00
TRINITY_sp|Q0WWATG3 Autophagy-related p 37.80 0.00
TRINITY_sp|Q852OSK1 Serine/threonine pr 37.80 0.00
TRINITY_sp|P109 Retrovirus-related 37.80 0.00
TRINITY_sp|Q0G2USP UDP-sugar pyrophosp 37.80 0.00
TRINITY_sp|P317OV16 OV-16 antigen OS=On 37.80 0.00
| Accession | Description                                                                 | Identity | Similarity |
|-----------|-----------------------------------------------------------------------------|----------|------------|
| TRINITY_sp| Carboxylesterase Nl                                                         | 37.80    | 0.00       |
| TRINITY_sp| Probable ATP-dependent hydroxylamine reductase                               | 37.80    | 0.00       |
| TRINITY_sp| Probable RNA methyltransferase                                               | 37.80    | 0.00       |
| TRINITY_sp| Cilia- and flagella                                                          | 37.80    | 0.00       |
| TRINITY_sp| Coat protein                                                                | 37.70    | 0.00       |
| TRINITY_sp| Gastric triacylglycerol lipase                                               | 37.70    | 0.00       |
| TRINITY_sp| Multidrug resistance                                                        | 37.70    | 0.00       |
| TRINITY_sp| Protein translation factor SUI1 homolog                                     | 37.70    | 0.00       |
| TRINITY_sp| Meiotic nuclear division                                                     | 37.70    | 0.00       |
| TRINITY_sp| Transmembrane 9 sup                                                         | 37.70    | 0.00       |
| TRINITY_sp| Vesicle-associated                                                          | 37.70    | 0.00       |
| TRINITY_sp| Malto-oligosyltrehalose                                                     | 37.70    | 0.00       |
| TRINITY_sp| Tyrosine-protein ph                                                         | 37.70    | 0.00       |
| TRINITY_sp| Putative serine car                                                         | 37.70    | 0.00       |
| TRINITY_sp| Multidrug resistance                                                        | 37.70    | 0.00       |
| TRINITY_sp| Protein translation factor SUI1 homolog                                     | 37.70    | 0.00       |
| TRINITY_sp| Protein translation factor SUI1 homolog                                     | 37.70    | 0.00       |
| TRINITY_sp| Protein phosphatase 2C 41                                                   | 37.70    | 0.00       |
| TRINITY_sp| Coenzyme Q-binding                                                          | 37.70    | 0.00       |
| TRINITY_sp| Insulin-degrading e                                                         | 37.70    | 0.00       |
| TRINITY_sp| Lateral signaling target                                                    | 37.70    | 0.00       |
| TRINITY_sp| Phosphatidylincholine                                                        | 37.70    | 0.00       |
| TRINITY_sp| Phospholipase D B O                                                         | 37.70    | 0.00       |
| TRINITY_sp| Protein translation                                                         | 37.70    | 0.00       |
| TRINITY_sp| CCA tRNA nucleotidy                                                         | 37.70    | 0.00       |
| TRINITY_sp| Pappalysin-1 OS=Mus                                                         | 37.70    | 0.00       |
| TRINITY_sp| Probable serine/thr                                                         | 37.70    | 0.00       |
| TRINITY_sp| Voltage-dependent L                                                         | 37.70    | 0.00       |
| TRINITY_sp| GPCR-type G protein                                                         | 37.70    | 0.00       |
| TRINITY_sp| Switch 2 OS=Arabido                                                         | 37.70    | 0.00       |
| TRINITY_sp| Uncharacterized acy                                                          | 37.70    | 0.00       |
| TRINITY_sp| Hypoxanthine-guanin                                                         | 37.70    | 0.00       |
| TRINITY_sp| Nucleosome-remodeli                                                         | 37.70    | 0.00       |
| TRINITY_sp| Serine/threonine-pr                                                         | 37.70    | 0.00       |
| TRINITY_sp| Ubiquitin carboxyl-                                                          | 37.70    | 0.00       |
| TRINITY_sp| Histone-lysine N-me                                                          | 37.70    | 0.00       |
| TRINITY_sp| Sodium/hydrogen exc                                                         | 37.70    | 0.00       |
| TRINITY_sp| DNA repair endonuclease                                                      | 37.70    | 0.00       |
| TRINITY_sp| Putative serine/thr                                                         | 37.70    | 0.00       |
| TRINITY_sp| Tubulin-folding cof                                                         | 37.70    | 0.00       |
| TRINITY_sp| Probable ethanolami                                                          | 37.70    | 0.00       |
| TRINITY_sp| ATP-dependent RNA h                                                         | 37.70    | 0.00       |
| TRINITY_sp| Uncharacterized pro                                                          | 37.70    | 0.00       |
| TRINITY_sp| Calcium-dependent p                                                         | 37.70    | 0.00       |
| Gene Name | Protein Description | Organism | Score | Log2 Fold Change |
|-----------|---------------------|----------|-------|-----------------|
| VP13A | Putative vacuolar protein sorting-associated protein 13A | Dictyostelium discoideum | 37.60 | 0.00 |
| VP13A | Putative RNA-binding protein 13A | Dictyostelium discoideum | 37.60 | 0.00 |
| THO3 | THO complex subunit 3 | Dictyostelium discoideum | 37.60 | 0.00 |
| Bisk1 | Pre-rRNA-processing protein Bisk1 | Schizosaccharomyces pombe | 37.60 | 0.00 |
| EXD2 | Exonuclease 3'-5' domain-containing protein 2 | Homo sapiens | 37.60 | 0.00 |
| Pfh1 | ATP-dependent DNA helicase Pfh1 | Schizosaccharomyces pombe | 37.60 | 0.00 |
| Ku70 | ATP-dependent DNA helicase Ku70 | Dictyostelium discoideum | 37.60 | 0.00 |
| MlkA | Myosin light chain kinase A | Dictyostelium discoideum | 37.60 | 0.00 |
| Tho3 | THO complex subunit 3 | Arabidopsis thaliana | 37.60 | 0.00 |
| Uvse | UV DNA damage endonuclease | Bacillus velezensis | 37.60 | 0.00 |
| VatE | V-type proton ATPase subunit E | Dictyostelium discoideum | 37.60 | 0.00 |
| Tm | Troponin C | Branchiostoma lanceolatum | 37.60 | 0.00 |
| Ttll10 | Probable 3-mercaptopyruvate sulfurtransferase | Schizosaccharomyces pombe | 37.60 | 0.00 |
| GAM1 | Glucoamylase 1 | Candida albicans | 37.60 | 0.00 |
| Kcs1 | 3-ketoacyl-CoA synthase 1 | Arabidopsis thaliana | 37.60 | 0.00 |
| Ttll10 | Inactive polyglycylase TTLL10 | Homo sapiens | 37.60 | 0.00 |
| Esf1 | Pre-rRNA-processing protein Esf1 | Schizosaccharomyces pombe | 37.60 | 0.00 |
| RgaA | Ras GTPase-activating-like protein RgaA | Dictyostelium discoideum | 37.60 | 0.00 |
| AAC4 | AAC-rich mRNA clone AAC4 | Dictyostelium discoideum | 37.60 | 0.00 |
| Rho2 | GTP-binding protein Rho2 | Saccharomyces cerevisiae | 37.60 | 0.00 |
| Pglp2 | Phosphoglycolate phosphatase 2 | Arabidopsis thaliana | 37.60 | 0.00 |
| Pus7 | Pseudouridylate synthase 7 homolog | Bos taurus | 37.60 | 0.00 |
| DhkK | Hybrid signal transduction histidine kinase DhkK | Dictyostelium discoideum | 37.60 | 0.00 |
| Bpm | Ran-binding proteins 9/10 homolog | Drosophila melanogaster | 37.60 | 0.00 |
| MsrB | Peptide methionine sulfoxide reductase MsrB | Leptospira interrogans | 37.60 | 0.00 |
| Rdh12 | Retinol dehydrogenase 12 | Mus musculus | 37.60 | 0.00 |
| Atl80 | RING-H2 finger protein ATL80 | Arabidopsis thaliana | 37.60 | 0.00 |
| Dhc10 | Dynein-1-beta heavy chain, flagellar inner arm I1 complex | Chlamydomonas reinhardtii | 37.60 | 0.00 |
| CG8303 | Putative fatty acyl-CoA reductase CG8303 | Drosophila melanogaster | 37.60 | 0.00 |
| GrxC1 | Glutaredoxin-1 | Rickettsia bellii | 37.60 | 0.00 |

**Note:** The above table lists some of the proteins and their descriptions from the document. The table includes gene names, protein descriptions, and the corresponding scores and log2 fold changes.
NADPH--cytochrome P

Rabphilin-1 OS=Caen

ATP-dependent DNA h

Ammonium transporte

Cytosolic carboxype

Vacuolar protein so

Transposon Ty3-G Ga

Calcium-dependent p

Apratxin (Fragment)

Peroxisomal acyl-co

Fructose-2,6-bispho

Methylosome subunit

Cationic amino acid

Sphingosine-1-phosp

GTPase-activating R

High mobility group

Protein translocase R

Sialin

M-phase inducer pho

Ubiquitin carboxyl-

Ankyrin repeat and

NFX1-type zinc fing

DNA repair protein

Intersectin-2 OS=Ho

Selenocysteine lyas

Guanine/hypoxanthin

ABC transporter B f

Protein RCC2 OS=Hom

Protein FORGETTER 1

Kinesin-like protei

Putative serine/thr

Arabinosyltransfera

Autophagy-related p

O-methyltransferase

Probable serine/thr

Probable U3 small n
| Gene Name                      | Protein Description                                      | Protein Score | Peptide Score |
|-------------------------------|----------------------------------------------------------|---------------|---------------|
| TRINITY_sp|Q55GIvps25           | Vacuolar protein-sorting-associated protein 25 | 37.40         | 0.00          |
| TRINITY_sp|Q55CDDB_G02:         | Bromodomain-containing protein | 37.40         | 0.00          |
| TRINITY_sp|P5481ymel-1          | ATP-dependent zinc | 37.40         | 0.00          |
| TRINITY_sp|Q9BUvTRMO            | tRNA (adenine-37)-N | 37.40         | 0.00          |
| TRINITY_sp|Q54WaaurK            | Aurora kinase | 37.40         | 0.00          |
| TRINITY_sp|Q692Stk36            | Serine/threonine-protein | 37.40         | 0.00          |
| TRINITY_sp|O602SI7PAI13         | Signal-induced prol | 37.40         | 0.00          |
| TRINITY_sp|Q54Znael             | NEDD8-activating enzyme | 37.40         | 0.00          |
| TRINITY_sp|Q2TBPICD2            | PCI domain-containin | 37.40         | 0.00          |
| TRINITY_sp|Q86g6gycy-28         | Receptor-type guanyl | 37.40         | 0.00          |
| TRINITY_sp|Q150HERC3            | Probable E3 ubiquitin | 37.30         | 0.00          |
| TRINITY_sp|A3PT:          | UPF0678 fatty acid-transporter | 37.30         | 0.00          |
| TRINITY_sp|P235phoR             | Alkaline phosphatase | 37.30         | 0.00          |
| TRINITY_sp|Q078vVPS13           | Vacuolar protein summary | 37.30         | 0.00          |
| TRINITY_sp|E1C6fHACE1           | E3 ubiquitin-protein | 37.30         | 0.00          |
| TRINITY_sp|Q547tral             | Probable transcript | 37.30         | 0.00          |
| TRINITY_sp|Q8VYtAtg073         | Mannose-P-dolichol | 37.30         | 0.00          |
| TRINITY_sp|O044Atlg096        | Probable elongation | 37.30         | 0.00          |
| TRINITY_sp|Q1681PHKG1           | Phosphorylase b kinase | 37.30         | 0.00          |
| TRINITY_sp|Q155surf2            | Surfeit locus protei | 37.30         | 0.00          |
| TRINITY_sp|P177TDC              | Aromatic-L-amino-acid: | 37.30         | 0.00          |
| TRINITY_sp|Q432COP1             | E3 ubiquitin-protein | 37.30         | 0.00          |
| TRINITY_sp|P604fPTEN            | Phosphatidylinositol | 37.30         | 0.00          |
| TRINITY_sp|Q2AZ3dnaJ            | Chaperone protein D | 37.30         | 0.00          |
| TRINITY_sp|Q62SNBEAL1           | Neurobeachin-like protein | 37.30         | 0.00          |
| TRINITY_sp|Q275Cyp4d2           | Cytochrome P450 4d2 | 37.30         | 0.00          |
| TRINITY_sp|Q6P7hmces            | Embryonic stem cell | 37.30         | 0.00          |
| TRINITY_sp|Q000SRP68            | Signal recognition | 37.30         | 0.00          |
| TRINITY_sp|P840RHOG             | Rho-related GTP-binding | 37.30         | 0.00          |
| TRINITY_sp|P0C8OlOsi_027        | Uncharacterized protein | 37.30         | 0.00          |
| TRINITY_sp|Q9LHI0CT4            | Organic cation/carnitine | 37.30         | 0.00          |
| TRINITY_sp|Q1MI1ctaA            | Heme A synthase OS-I | 37.30         | 0.00          |
| TRINITY_sp|Q9J7Krpf2            | Ribosome production | 37.30         | 0.00          |
| TRINITY_sp|P143f-               | Transposon TX1 uncharacterized | 37.30         | 0.00          |
| TRINITY_sp|Q5VVvGARNL3          | GTPase-activating protein | 37.30         | 0.00          |
| TRINITY_sp|Q9CSHMAPKKK5         | Mitogen-activated protein | 37.30         | 0.00          |
| TRINITY_sp|Q9509NUDT3           | Diphosphoinositol p | 37.30         | 0.00          |
| TRINITY_sp|O6827dusC            | tRNA-dihydouridine | 37.30         | 0.00          |
| TRINITY_sp|P281.pkqB            | Protein kinase 2 OS | 37.30         | 0.00          |
| TRINITY_sp|Q3KQUAP1L1           | UDP-N-acetyllhexosamiamine | 37.30         | 0.00          |
| TRINITY_sp|Q142ImsbA            | Lipid A export ATP-binding | 37.30         | 0.00          |
| TRINITY_sp|P811fPAE1            | Proteasome subunit | 37.30         | 0.00          |
| TRINITY_sp|Q645fAtp2b3          | Plasma membrane calcium ATPase | 37.30         | 0.00          |
| TRINITY_sp|Q0WQRBL1             | RHOMBOID-like protease | 37.30         | 0.00          |
| TRINITY_sp|Q556DDDB_G02:        | Probable rhodanese | 37.30         | 0.00          |
| TRINITY_sp|P404fHOS4            | Protein HOS4 OS=Saccharomyces cerevisiae | 37.30         | 0.00          |
| TRINITY_sp|Q52SP1P101-2         | Meliotic recombinating | 37.30         | 0.00          |
| TRINITY_sp|Q5F3WWOX             | WW domain-containin | 37.30         | 0.00          |
| TRINITY_sp|A0A0IP58A3           | DnaJ protein P58IPK | 37.30         | 0.00          |
| TRINITY_sp|Q9SE50s9g05          | Ribulose-phosphate | 37.30         | 0.00          |
| TRINITY_sp|Q02P1lap             | Aminopeptidase OS=P | 37.30         | 0.00          |
| TRINITY_sp|Q9D91Efhcl           | EF-hand domain-containing | 37.30         | 0.00          |
| TRINITY_sp|Q9E5Sosacll          | Phosphatidylinositol transferase | 37.30         | 0.00          |
| TRINITY_sp|Q8VZ2INT1            | Inositol transporter | 37.30         | 0.00          |
| TRINITY_sp|Q9F54KIN14B          | Kinesin-like protein | 37.30         | 0.00          |
| TRINITY_sp|Q7ZTqgins2           | DNA replication complex | 37.30         | 0.00          |
| Gene Accession | Protein Name                      | Gene Symbol | Description                                | Value |
|----------------|----------------------------------|-------------|--------------------------------------------|-------|
| sp|P44331|rbsK|HAEIN|37.20|
| sp|P75164|UBA6|MYCPN|37.30|
| sp|Q9Lyq2|LAC13_ARATH|37.30|
| sp|Q15526|SURF1_HUMAN|37.30|
| sp|Q8WU08|ST32A_HUMAN|37.30|
| sp|Q6NLY8|HA22K_ARATH|37.30|
| sp|Q03730|YMB8_YEAST|37.30|
| sp|Q2LTR7|SYP_SYNAS|37.30|
| sp|Q8K2G4|BBS7_MOUSE|37.30|
| sp|Q1PF50|EDA2_ARATH|37.30|
| sp|Q54SR8|SGMC_DICDI|37.30|
| sp|Q8K1_MOUSE|Ripk1|37.30|
| sp|Q9LUQ5|UBC25_ARATH|37.30|
| sp|Q8IS15|GEFI_DICDI|37.30|
| sp|Q9FV0|CYCA1-2_MOUSE|37.30|
| sp|Q917Nek8|Serine/threonine-pr|37.30|
| sp|Q92PA|ADP-ribo-sylation fa|37.30|
| sp|Q5J7|MCMBP|37.20|
| sp|Q9Lu|UBC25|37.20|
| sp|Q237:GSH2|Glutathione synthet|37.20|
| sp|Q1SS1rlmF|Ribosomal RNA large|37.20|
| sp|Q6E8:cutC|Copper homeostasis|37.20|
| sp|Q748fft2|ATP-dependent helic|37.20|
| sp|Q9UH|SAP30BP|37.20|
| sp|Q5XJ:kcdt151|BTB/POZ domain-cont|37.20|
| sp|Q608:Ripk|Receptor-interactin|37.20|
| sp|Q9E515ca2|Solute carrier fami|37.20|
| sp|Q55Cmp1l|MAP kinase phosphat|37.20|
| sp|Q548sgmC|Sphingomyelinase ph|37.20|
| sp|Q1PF|EDA2|37.20|
| sp|Q21lmgsA|Methylglyoxal synth|37.20|
| sp|Q9C7:At3g112|Protein yippee-like|37.20|
| sp|Q9SB:FAT08|Protein S-acyltrans|37.20|
| sp|Q8K2:Bsba7|Bardet-Biedl syndro|37.20|
| sp|Q556:cf50-1|Counting factor 50|37.20|
| sp|Q2LFlproS|Proline--tRNA ligas|37.20|
| sp|Q307:XM018C|Uncharacterized vac|37.20|
| sp|Q96NL:HVA22K|HVA22-like protein|37.20|
| sp|Q75K:pei2|Peroxisome biogenes|37.20|
| sp|Q8WU:STK32A|Serine/threonine-pr|37.20|
| sp|Q08EIRNP10|RING finger protein|37.20|
| sp|Q2CXTbc1d15|TBC1 domain family|37.20|
| sp|Q155:SURF1|Surfeit locus prote|37.20|
| sp|A7SK:dph2|Diphtamide biosynt|37.20|
| sp|Q9LY[LAC13|Laccase-13 OS=Arabi|37.20|
| sp|C6E5:pepA|Probable cytosol am|37.20|
| sp|A0AVU:UBA6|Ubiquitin-like modi|37.20|
| sp|P751:MPN_633|Uncharacterized pro|37.20|
| sp|P443:rbsK|Ribokinase OS=Haemo|37.20|
| Accession        | Description                                      | Value1 | Value2 |
|------------------|--------------------------------------------------|--------|--------|
| TRINITY_sp|Q9ZVY3|GTF2H2 | General transcript initiation | 37.10 | 0.00 |
| TRINITY_sp|P912r3|gst-8  | Probable glutathione S-transferase | 37.10 | 0.00 |
| TRINITY_sp|Q2HJN8|MEST  | Mesoderm-specific transcription initiation | 37.10 | 0.00 |
| TRINITY_sp|Q9NPH5|ACP6  | Lysophosphatidic acid synthase | 37.10 | 0.00 |
| TRINITY_sp|Q0MQ{5|NDUFA12 | NADH dehydrogenase | 37.10 | 0.00 |
| TRINITY_sp|Q940S6|SRK2E | Serine/threonine-protein kinase | 37.10 | 0.00 |
| TRINITY_sp|Q10X35|InfB  | Translation initiation | 37.10 | 0.00 |
| TRINITY_sp|Q94P77|PAP1  | Plastid lipid-associated protein | 37.10 | 0.00 |
| TRINITY_sp|Q54K0|ccbl  | Kynurenine--oxoglutarate transaminase | 37.10 | 0.00 |
| TRINITY_sp|G5ECg9b|a-3 | Putative glucosylceramidase | 37.10 | 0.00 |
| TRINITY_sp|Q9AAt4|2770 | Hybrid signal transduction histidine kinase | 37.10 | 0.00 |
| TRINITY_sp|Q5ZI7T|TAF2  | Transcription initiation | 37.10 | 0.00 |
| TRINITY_sp|P129v4|PEPD  | Xaa-Pro dipeptidase | 37.10 | 0.00 |
| TRINITY_sp|Q5520g|gefY  | Ras guanine nucleotide exchange factor | 37.10 | 0.00 |
| TRINITY_sp|P97S8Ctsc  | Dipeptidyl peptidase | 37.10 | 0.00 |
| TRINITY_sp|Q55Ev5|cyp524A1|Probable cytochrome p450 | 37.10 | 0.00 |
| TRINITY_sp|Q8AXK3|kit   | Mast/stem cell growth | 37.10 | 0.00 |
| TRINITY_sp|Q4277RBMH1 | 14-3-3 protein homolog | 37.10 | 0.00 |
| TRINITY_sp|P5861g|glk   | Glucokinase OS=Nostoc linens | 37.10 | 0.00 |
| TRINITY_sp|P5113RAB5C | Ras-related protein | 37.10 | 0.00 |
| TRINITY_sp|Q8B25Dun1d2 | DCN1-like protein | 37.10 | 0.00 |
| TRINITY_sp|Q55Evall10005 Uncharacterized protein | 37.10 | 0.00 |
| TRINITY_sp|Q5500x|captC | Uncharacterized CDP phosphatase | 37.10 | 0.00 |
| TRINITY_sp|Q225v1|STY8  | Serine/threonine-protein kinase | 37.10 | 0.00 |
| TRINITY_sp|Q9ZT7|PSAM2  | Secretory carrier-associated protein | 37.10 | 0.00 |
| TRINITY_sp|Q9ZT7|ERD2  | ER lumen protein-receptor | 37.10 | 0.00 |
| TRINITY_sp|Q9LYQv|PUB1  | Probable ubiquitin | 37.10 | 0.00 |
| TRINITY_sp|Q8L5FTFCD | Tubulin-folding cofactor | 37.10 | 0.00 |
| TRINITY_sp|Q1477CERG1 | Transcription elongation factor | 37.10 | 0.00 |
| TRINITY_sp|Q8N5sEF1  | RNA-processing protein | 37.10 | 0.00 |
| TRINITY_sp|Q8IBCPK4 | Calcium-dependent protein | 37.10 | 0.00 |
| TRINITY_sp|Q804vmb1 | E3 ubiquitin-protein ligase | 37.10 | 0.00 |
| TRINITY_sp|Q6PCsmmat2 | Nicotinamide/nicotinamide kinase | 37.10 | 0.00 |
| TRINITY_sp|Q75NncA | Calcium-binding protein | 37.10 | 0.00 |
| TRINITY_sp|Q599vLIP  | Lipase OS=Thermomyces thermophila | 37.10 | 0.00 |
| TRINITY_sp|Q8GvLipkAI | Narbonolide/10-deoxynarbenolide | 37.10 | 0.00 |
| TRINITY_sp|Q8BSvBRI1  | Fanconi anemia group | 37.10 | 0.00 |
| TRINITY_sp|Q7YRFEXOSC4 | Exosome complex component | 37.10 | 0.00 |
| TRINITY_sp|Q9C5vPAT22 | Probable protein S-adenosylmethionine | 37.10 | 0.00 |
| TRINITY_sp|Q9H8vCNTD2 | Cyclin N-terminal domain | 37.10 | 0.00 |
| TRINITY_sp|P041vMyb  | Myb protein OS=Drosophila melanogaster | 37.10 | 0.00 |
| TRINITY_sp|Q3UGIvDwr19 | WD repeat-containing protein | 37.10 | 0.00 |
| TRINITY_sp|Q9M3vPAT05 | Probable protein S-adenosylmethionine | 37.10 | 0.00 |
| TRINITY_sp|Q8GWvNDA1 | Internal alternative | 37.10 | 0.00 |
| TRINITY_sp|Q6VVvNpr2 | Atrial natriuretic peptide | 37.10 | 0.00 |
| TRINITY_sp|Q54YvdkkB | Hybrid signal transduction histidine kinase | 37.10 | 0.00 |
| TRINITY_sp|Q96JvITCH | E3 ubiquitin-protein ligase | 37.00 | 0.00 |
| TRINITY_sp|Q55EvplBG | Phospholipase B-like | 37.00 | 0.00 |
| TRINITY_sp|Q54YvdkkB | Hybrid signal transduction histidine kinase | 37.00 | 0.00 |
| TRINITY_sp|Q6Z8vWEI1 | Wee1-like protein kinase | 37.00 | 0.00 |
| TRINITY_sp|Q06AvRAB32 | Ras-related protein | 37.00 | 0.00 |
| TRINITY_sp|O896TvTpp1 | Tripeptidyl-peptidase | 37.00 | 0.00 |
| TRINITY_sp|P627vVSNL1 | Visinin-like protein | 37.00 | 0.00 |
| TRINITY_sp|P583varcB | Aerobin | 37.00 | 0.00 |
| TRINITY_sp|Q941vBON1 | Protein BONZAI 1 OS | 37.00 | 0.00 |
| TRINITY_sp|Q6GRvspo | Speckle-type POZ protein | 37.00 | 0.00 |
TRINITY_sp|Q95N(DIO1) Type I iodothyronine deiodinase  36.90 0.00
TRINITY_sp|Q8R31Tbcl1d3 TBC1 domain family  36.90 0.00
TRINITY_sp|P405fYIR042C Uncharacterized protein  36.90 0.00
TRINITY_sp|Q281
cops3 COP9 signalosome co protein  36.90 0.00
TRINITY_sp|P41P\SYCO Cysteine--tRNA ligase  36.90 0.00
TRINITY_sp|Q55D\gacZ Rho GTPase-activating protein  36.90 0.00
TRINITY_sp|Q3MI\Echdc3 Enoyl-CoA hydratase  36.90 0.00
TRINITY_sp|Q91V\Abca7 ATP-binding cassette transmembrane transporter  36.90 0.00
TRINITY_sp|Q7K5\Ttd14 TRPL translocation  36.90 0.00
TRINITY_sp|Q9QZ\Dcnul1 DCN1-like protein 1  36.90 0.00
TRINITY_sp|P468\KIN14N Kinesin-like protein  36.90 0.00
TRINITY_sp|Q9931TY3B-G Transposon Ty3-G Gag-Pol polyprotein  36.90 0.00
TRINITY_sp|Q9HJ1ANAPC1 Anaphase-promoting complex subunit 1  36.90 0.00
TRINITY_sp|A0BKGPSATT0 Protein SEY1 homolog  36.90 0.00
TRINITY_sp|Q9ZV\CUL3A Culin-3A  36.90 0.00
TRINITY_sp|Q45I\d1cA Dynein light chain  36.90 0.00
TRINITY_sp|Q489\dWr78 WD repeat-containing protein 9  36.90 0.00
TRINITY_sp|Q8L7\GSTT2 Glutathione S-transferase T2  36.90 0.00
TRINITY_sp|Q3MK\SPTLC1 Serine palmitoyltransferase 1  36.90 0.00
TRINITY_sp|Q757\TRPA1 Transient receptor potential cation channel subfamily A member 1  36.90 0.00
TRINITY_sp|Q478\Pdc2 Programmed cell death protein 1  36.90 0.00
TRINITY_sp|Q908\Dryr1 NADPH-dependent 1-acyldihydroxyacetone phosphate reductase  36.90 0.00
TRINITY_sp|P239\mmpp Mitochondrial-processing peptidase  36.90 0.00
TRINITY_sp|P492\mao Amine oxidase [flavin-containing]  36.90 0.00
TRINITY_sp|Q1JP\EIF4H Eukaryotic translation initiation factor 4H  36.90 0.00
TRINITY_sp|P110\RAB3A Ras-related protein 3A  36.90 0.00
TRINITY_sp|Q9BQ\NUDT12 Peroxisomal NADH pyruvate dehydrogenase  36.90 0.00
TRINITY_sp|Q8TD\DNAH3 Dynein heavy chain 3  36.90 0.00
TRINITY_sp|Q74F\dtdcB L-threonine ammonia lyase  36.90 0.00
TRINITY_sp|Q8K2\Ip11 Importin-11  36.90 0.00
TRINITY_sp|Q111\wh1-1 ABC transporter ATP-binding cassette A1  36.90 0.00
TRINITY_sp|P386\PDIA6 Protein disulfide-isomerase A6  36.90 0.00
TRINITY_sp|Q8N5\CAMKK1 Calcium/calmodulin-dependent kinase kinase 1  36.90 0.00
TRINITY_sp|O043\B'BETA Serine/threonine kinase  36.90 0.00
TRINITY_sp|Q96H\REEP6 Receptor expression-enhancing protein 6  36.90 0.00
TRINITY_sp|P932\VPS41 Vacuolar protein sorting protein 41  36.90 0.00
TRINITY_sp|Q9PP\EDR1 Serine/threonine-protein kinase  36.90 0.00
TRINITY_sp|Q8TA\JOSD2 Protein disulfide-isomerase A6  36.90 0.00
TRINITY_sp|Q8IS\gefJ Ras guanine nucleotide exchange factor 1  36.90 0.00
TRINITY_sp|Q5M7\FPAT12 Probable protein S-adenosylmethionine-dependent carboxylase domain-containing protein 12  36.90 0.00
TRINITY_sp|Q9QX\Tb11x F-box-like/WD repeat containing protein 11x  36.90 0.00
TRINITY_sp|Q12X\gxcDD Guanine exchange factor  36.90 0.00
TRINITY_sp|Q5MB\ABC2 ATP-binding cassette sub-family G member 2  36.90 0.00
TRINITY_sp|Q8RV\DEK1 Calpain-type cysteine peptidase  36.90 0.00
TRINITY_sp|O597\ark1 Serine/threonine-protein kinase  36.90 0.00
TRINITY_sp|A6QR\USP4 Ubiquitin carboxyl-terminal hydrolase  36.90 0.00
TRINITY_sp|Q408\EMB8 Embryogenesis-associated transcription factor  36.90 0.00
TRINITY_sp|P395\DRS2 Probable phospholipid scramblase 2  36.90 0.00
TRINITY_sp|P227\Gucylb2 Guanylate cyclase 3  36.90 0.00
TRINITY_sp|Q977\SYN1 Sister chromatid cohesion 1 protein  36.90 0.00
TRINITY_sp|Q0V9\dis312 DTS3-like exonuclease  36.90 0.00
TRINITY_sp|Q6WNC\D4 Acyl-lipid (7-3)-dehydrogenase  36.90 0.00
TRINITY_sp|Q080\TEF1 Elongation factor 1  36.90 0.00
TRINITY_sp|Q54B\dyrk2 Probable serine/threonine kinase  36.90 0.00
TRINITY_sp|P253\mlkA Myosin light chain kinase A  36.90 0.00
TRINITY_sp|Q54K\GDD_G02\TPR repeat-containing protein  36.90 0.00
| TRINITY_sp|O97444ancA   | Mitochondrial subst | 36.90 | 0.00 |
| TRINITY_sp|Q8Z4tyhrF    | Uncharacterized pro  | 36.80 | 0.00 |
| TRINITY_sp|P09746CDC16  | Anaphase-promoting   | 36.80 | 0.00 |
| TRINITY_sp|Q1411VEZP1   | Vascular endothelia  | 36.80 | 0.00 |
| TRINITY_sp|Q9P2R7RCC2   | Protein RCC2 OS=Hom  | 36.80 | 0.00 |
| TRINITY_sp|Q5Ktp1C      | Putative vacular p   | 36.80 | 0.00 |
| TRINITY_sp|Q8ND1FAPD5   | Non-canonical poly(  | 36.80 | 0.00 |
| TRINITY_sp|Q9FG4ATO     | Splicing factor SF3  | 36.80 | 0.00 |
| TRINITY_sp|Q54Cirrp8    | Ribosomal RNA-proce  | 36.80 | 0.00 |
| TRINITY_sp|Q9M1FAP1     | Fatty-acid-binding   | 36.80 | 0.00 |
| TRINITY_sp|O1431maf1    | H/ACA ribonucleopro  | 36.80 | 0.00 |
| TRINITY_sp|P4900PXN     | Paxillin OS=Gallus   | 36.80 | 0.00 |
| TRINITY_sp|Q5Z11RAB10   | Ras-related protein  | 36.80 | 0.00 |
| TRINITY_sp|P4322RD21A   | Cysteine proteinase  | 36.80 | 0.00 |
| TRINITY_sp|Q6UX1DHRS13  | Dehydrogenase/reduc  | 36.80 | 0.00 |
| TRINITY_sp|Q7K5Tttd14   | TRPL translocation   | 36.80 | 0.00 |
| TRINITY_sp|Q6KTISET1    | Putative histone-ly  | 36.80 | 0.00 |
| TRINITY_sp|Q9CA29TKPR2  | Tetraketide alpha-p  | 36.80 | 0.00 |
| TRINITY_sp|Q68F1    | Uncharacterized pro  | 36.80 | 0.00 |
| TRINITY_sp|P90825P56F10 | Putative serine pro  | 36.80 | 0.00 |
| TRINITY_sp|Q5JVEFR1C    | EF-hand domain-cont  | 36.80 | 0.00 |
| TRINITY_sp|Q4999S1c25a3 | Solute carrier fami  | 36.80 | 0.00 |
| TRINITY_sp|Q8N1GWDR36   | WD repeat-containin  | 36.80 | 0.00 |
| TRINITY_sp|P7656yfex    | Probable deferroche  | 36.80 | 0.00 |
| TRINITY_sp|O3563Abca4   | Retinal-specific AT  | 36.80 | 0.00 |
| TRINITY_sp|Q6IR1abhd13  | Protein ABHD13 OS=X  | 36.80 | 0.00 |
| TRINITY_sp|Q54WDD7D02   | Probable serine/thr  | 36.80 | 0.00 |
| TRINITY_sp|Q9T01LACS5   | Long chain acyl-CoA  | 36.80 | 0.00 |
| TRINITY_sp|P5779ALA12   | Probable phospholip  | 36.80 | 0.00 |
| TRINITY_sp|Q16XSAELO08  | Regulator of telome  | 36.80 | 0.00 |
| TRINITY_sp|Q94E1At3g144 | Probable sugar phos  | 36.80 | 0.00 |
| TRINITY_sp|Q5541bpzP    | Probable basic-leuc  | 36.80 | 0.00 |
| TRINITY_sp|Q2HJ1F AHD1  | Acylpyruvase FAHD1,  | 36.80 | 0.00 |
| TRINITY_sp|Q12X7gexecD  | Guanine exchange fa  | 36.80 | 0.00 |
| TRINITY_sp|Q96F5KIP12   | Kinesin-like protei  | 36.80 | 0.00 |
| TRINITY_sp|Q921Brwd1    | Bromodomain and WD  | 36.80 | 0.00 |
| TRINITY_sp|Q7X6RUS1     | Protein root UVB se  | 36.80 | 0.00 |
| TRINITY_sp|Q4PKCLCN7    | H(+)/Cl(-) exchange  | 36.80 | 0.00 |
| TRINITY_sp|Q4V3MRG2    | Protein MRG2 OS=Ara  | 36.80 | 0.00 |
| TRINITY_sp|Q9C13Nudt8   | Nucleoside diphosph | 36.80 | 0.00 |
| TRINITY_sp|Q75KIATG4A   | Cysteine protease A  | 36.80 | 0.00 |
| TRINITY_sp|O3150yfHm    | AB hydrolase superf  | 36.80 | 0.00 |
| TRINITY_sp|Q9C70AERO01  | Endoplasmic reticul | 36.80 | 0.00 |
| TRINITY_sp|P0C8NCRCRP1  | Probable serine/thr  | 36.80 | 0.00 |
| TRINITY_sp|Q8Z0dcysA    | Sulfate/thiosulfate  | 36.80 | 0.00 |
| TRINITY_sp|O0025SUPT5H  | Transcription elong  | 36.80 | 0.00 |
| TRINITY_sp|Q6TfmipoX   | Peroxinectin A OS=D  | 36.80 | 0.00 |
| TRINITY_sp|O002PSMD9    | 26S proteasome non-  | 36.80 | 0.00 |
| TRINITY_sp|Q5EAFBH14    | Protein ABHD4 OS=Bo  | 36.80 | 0.00 |
| TRINITY_sp|B8BM100s1374 | Pyruvate kinase 2,   | 36.80 | 0.00 |
| TRINITY_sp|P4055NEO1    | Probable phospholip  | 36.80 | 0.00 |
| TRINITY_sp|Q9921GRESAG  | Receptor-type adenyl | 36.80 | 0.00 |
| TRINITY_sp|Q9R1ISk1     | Serine/threonine-pr  | 36.80 | 0.00 |
| TRINITY_sp|B2GU2Us4     | Ubiquitin carboxyl-  | 36.80 | 0.00 |
| TRINITY_sp|Q99L2Gst3    | Glutathione S-trans  | 36.80 | 0.00 |
| TRINITY_sp|P1247       | Actin A OS=Trypanos  | 36.70 | 0.00 |
| Accession         | Description                                      | Score | Bit Score |
|-------------------|--------------------------------------------------|-------|-----------|
| TRINITY_sp|Q4FP|atpG | ATP synthase gamma | 36.70 | 0.00 |
| TRINITY_sp|Q54B|abcB2 | ABC transporter B f | 36.70 | 0.00 |
| TRINITY_sp|F4IC|IWS1 | Protein IWS1 homolo | 36.70 | 0.00 |
| TRINITY_sp|A8WX|CBG0|Protein FAM50 homol | 36.70 | 0.00 |
| TRINITY_sp|Q7LH|TY3B-I | Transposon Ty3-I Ga | 36.70 | 0.00 |
| TRINITY_sp|Q6EU|Os02g06 | Probable N6-adenosi | 36.70 | 0.00 |
| TRINITY_sp|Q54Y|ngap | Probable Ras GTPase | 36.70 | 0.00 |
| TRINITY_sp|Q54E|epnA | Epsin OS=Dictyostel | 36.70 | 0.00 |
| TRINITY_sp|Q8RN|1CP4X1 | Cytochrome P450 4X1 | 36.70 | 0.00 |
| TRINITY_sp|Q92G|piKA11 | Carbonolide/10-deox | 36.70 | 0.00 |
| TRINITY_sp|Q56X|INXH2 | Sodium/hydrogen exc | 36.70 | 0.00 |
| TRINITY_sp|Q96P|ACAP3 | Arf-GAP with coiled | 36.70 | 0.00 |
| TRINITY_sp|Q2QQ|CYCT1-1 | Cyclin-T1-4 OS=Oryz | 36.70 | 0.00 |
| TRINITY_sp|Q993|TY3B-G | Transposon Ty3-G Ga | 36.70 | 0.00 |
| TRINITY_sp|P623|CPK4 | Calcium-dependent p | 36.70 | 0.00 |
| TRINITY_sp|Q9VX|Bap60 | Brahma-associated p | 36.70 | 0.00 |
| TRINITY_sp|Q969|TM1 | Protein lifeguard 3 | 36.70 | 0.00 |
| TRINITY_sp|Q640|Is1c37a3 | Sugar phosphate exc | 36.60 | 0.00 |
| TRINITY_sp|O433|TXNL1 | Thioredoxin-like pr | 36.60 | 0.00 |
| TRINITY_sp|Q962|MYB23 | Transcription facto | 36.60 | 0.00 |
| TRINITY_sp|P623|CPK4 | Calcium-dependent p | 36.60 | 0.00 |
| TRINITY_sp|Q9VX|Arme7 | Armadillo repeat-co | 36.60 | 0.00 |
| TRINITY_sp|Q233|ECT1 | Enoyl-CoA delta iso | 36.60 | 0.00 |
| TRINITY_sp|P259|MXAN_59 | Uncharacterized oxi | 36.60 | 0.00 |
| TRINITY_sp|Q12X|gxcDD | Guanine exchange fa | 36.60 | 0.00 |
| TRINITY_sp|Q103|yaf9 | Protein AF-9 homolo | 36.60 | 0.00 |
| TRINITY_sp|Q54S|mcfU | Mitochondrial subst | 36.60 | 0.00 |
| TRINITY_sp|B7G1|obg | GTPase Obg OS=Anoxy | 36.60 | 0.00 |
| TRINITY_sp|Q12X|gxcDD | Guanine exchange fa | 36.60 | 0.00 |
| TRINITY_sp|Q401|-LEC14B protein OS=L | 36.60 | 0.00 |
| TRINITY_sp|Q11X|ints3 | Integrator complex | 36.60 | 0.00 |
| TRINITY_sp|Q0KI|CG801 | PP2C-like domain-co | 36.60 | 0.00 |
| TRINITY_sp|Q8LP|BTS | Zinc finger protein | 36.60 | 0.00 |
| TRINITY_sp|Q9CP|rsuA | Ribosomal small sub | 36.60 | 0.00 |
| TRINITY_sp|B8AA|CEST | Protein CHLOROPLAST | 36.60 | 0.00 |
| TRINITY_sp|Q9C1|SPBC713 | Periodic tryptophan | 36.60 | 0.00 |
| TRINITY_sp|Q9W5|CG34867 | Uncharacterized pro | 36.60 | 0.00 |
| TRINITY_sp|Q556|CCTR1 | Serine/threonine-pr | 36.60 | 0.00 |
| TRINITY_sp|Q55F|plbG | Phospholipase B-lik | 36.60 | 0.00 |
| TRINITY_sp|Q944|dymA | Dynamin-A OS=Dictyo | 36.60 | 0.00 |
| TRINITY_sp|Q946|bmsl | Ribosome biogenesis | 36.60 | 0.00 |
| TRINITY_sp|Q5F3|SBN01 | Protein strawberry | 36.60 | 0.00 |
| TRINITY_sp|Q9L1|TMN7 | Transmembrane 9 sup | 36.60 | 0.00 |
| TRINITY_sp|Q80W|Gad11 | Acidic amino acid d | 36.60 | 0.00 |
| TRINITY_sp|Q9VF|At1g577 | Probable elongation | 36.60 | 0.00 |
| TRINITY_sp|Q8NC|MMR14 | Myotubularin-relate | 36.60 | 0.00 |
| TRINITY_sp|Q1E3|FES1 | Hap70 nucleotide ex | 36.60 | 0.00 |
| TRINITY_sp|O002|PSMD12 | 26S proteasome non- | 36.60 | 0.00 |
| TRINITY_sp|Q16A|rpI0 | 50S ribosomal prote | 36.60 | 0.00 |
| TRINITY_sp|Q2SW|surE | 5'-nucleotidase Sur | 36.60 | 0.00 |
| TRINITY_sp|A6QR|USP4 | Ubiquitin carboxyl- | 36.60 | 0.00 |
| TRINITY_sp|Q7S7|NCU0673 | Leukotriene A-4 hyd | 36.60 | 0.00 |
| TRINITY_sp|Q8L8|COG4 | Conserved oligomeri | 36.60 | 0.00 |
| TRINITY_sp|Q8L9|F4H7 | Probable prolyl 4-h | 36.60 | 0.00 |
| TRINITY_sp|Q9ZU|At2g372 | Thioredoxin-like pr | 36.60 | 0.00 |
| TRINITY_sp|O158|CPK2 | Calcium-dependent p | 36.60 | 0.00 |
Dipeptidyl aminopeptidase BI
OS=Pseudoxanthomonas mexicana
GN=dapb1
PE=1
SV=1
Putative vacuolar protein sorting-associated protein 13B
OS=Dictyostelium discoideum
GN=vps13B
PE=3
SV=1
DNA gyrase subunit A, chloroplastic/mitochondrial
OS=Nicotiana benthamiana
GN=GYRA
PE=2
SV=1
Dephospho-CoA kinase
OS=Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4)
GN=coaE
PE=3
SV=1
Phospholipid-transporting ATPase ID
OS=Homo sapiens
GN=ATP8B2
PE=1
SV=2
Next to BRCA1 gene 1 protein
OS=Pongo abelii
GN=NBR1
PE=2
SV=1
Translocase of chloroplast 33, chloroplastic
OS=Arabidopsis thaliana
GN=TOC33
PE=1
SV=1
Ras-like protein 2
OS=Physarum polycephalum
GN=RAS-2
PE=2
SV=1
Transcription factor MYB86
OS=Arabidopsis thaliana
GN=MYB86
PE=2
SV=1
Phosphatidylinositol 4-phosphate 5-kinase its3
OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843)
GN=its3
PE=1
SV=3
Dual specificity protein kinase lkh1
OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843)
GN=lkh1
PE=1
SV=3
Protein YIPF5 homolog
OS=Dictyostelium discoideum
GN=yipf5
PE=3
SV=1
Serine/threonine-protein kinase HT1
OS=Arabidopsis thaliana
GN=HT1
PE=1
SV=1
Cleavage stimulation factor subunit 3
OS=Pongo abelii
GN=CSTF3
PE=2
SV=1
Calcium and calcium/calmodulin-dependent serine/threonine-protein kinase
OS=Lilium longiflorum
GN=CCAMK
PE=1
SV=1
O-methyltransferase MdmC
OS=Streptomyces mycarofaciens
GN=mdmC
PE=3
SV=1
Chromobox protein homolog 5
OS=Homo sapiens
GN=CBX5
PE=1
SV=1
Mitogen-activated protein kinase 4 (Fragment)
OS=Rattus norvegicus
GN=Mapk4
PE=1
SV=1
Histidine N-alpha-methyltransferase
OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh)
GN=egtD
PE=3
SV=1
Pyruvate decarboxylase
OS=Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100)
GN=pdcA
PE=3
SV=1
Sodium-coupled neutral amino acid transporter 9
OS=Danio rerio
GN=slc38a9
PE=2
SV=1
Calcium/calmodulin-dependent protein kinase type II subunit gamma
OS=Homo sapiens
GN=CAMK2G
PE=1
SV=3
Delta(12) fatty acid desaturase FAD2
OS=Calendula officinalis
GN=FAD2
PE=2
SV=1
E3 ubiquitin-protein ligase UPL1
OS=Arabidopsis thaliana
GN=UPL1
PE=1
SV=3
Chaperone protein dnaJ A6, chloroplastic
OS=Arabidopsis thaliana
GN=DJA6
PE=2
SV=2
Serine carboxypeptidase-like 20
OS=Arabidopsis thaliana
GN=SCPL20
PE=2
SV=2
Putative NADPH-dependent methylglyoxal reductase GRP2
OS=Candida albicans (strain SC5314 / ATCC MYA-2876)
GN=GRP2
PE=1
SV=2
TRINITY_sp|P134|abpC  Gelation factor OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|A4W4|pnp  Polyribonucleotide OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q9C7|AERO1  Endoplasmic reticul OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q54a|smt1  probable cycloarten OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q55e|pcyA  Phycocyanobilin:fer OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|P375|yaBD  Uncharacterized met OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|P110|ARF1  ADP-ribosylation fa OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q9UK|NOCT  Nocturnin OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q54s|gbpD  Cyclic GMP-binding OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|F4IR|ATG1C  Serine/threonine-pr OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|P981|RBM10  RNA-binding protein OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q54i|ishkB  dual specificity pr OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q9P7|cqr1  Probable mitochondrial OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|P355|CLNS1A  Methylosome subunit OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|P556|NGR_a01  Uncharacterized pep OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q28F|PRMT7  Protein arginine N-methyltransferase OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|D3YX|Lonrf1  LON peptidase N-ter OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q5CD|Vcpp1  Deubiquitinating pr OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q93Z|SPPL1  Signal peptide pept OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|A1LL|lox12b  Lysyl oxidase homol OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q9DG|RAD54B  DNA repair and reco OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q869|cpv1  Probable serine car OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q8LE|ABC11  ABC transporter I f OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q5TR|AGAP005  ATPase ASNA1 homolo OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q55E|mcfE  Mitochondrial subst OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q9FG|SNX1  Sorting nexin 1 OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q6RU|Ptx4  Pentraxin-4 OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q66H|Ankz1f1  Ankyrin repeat and OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q9Z1|ACOX1  Peroxisomal acyl-co OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|O824|MTA  N6-adenosine-methyl OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|E1CI|USP47  Ubiquitin carboxyl OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q92I|SIPA1L2  Signal-induced prol OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|P385|TTL  Tubulin--tyrosine l OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|P005|AbI11  Tyrosine-protein ki OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|P109|A-  Retrovirus-related OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|A5D7|CDC25C  M-phase inducer pho OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|P043|pol  Retrovirus-related OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q8NE|ABC1  ATP-binding cassett OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q641|Hexa  Beta-hexosaminidase OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q9DA|Tmem41a  Transmembrane prote OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q9UK|PARP4  Poly [ADP-ribose] p OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q54R|dhkL  Hybrid signal trans OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q9S2|SAP7  Zinc finger A20 and OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q8R7|prs  Ribose-phosphate py OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|O048|-  Alpha-glucosidase O OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q9LT|ALIS1  ALA-interacting sub OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q9H8|RMND5A  Protein RMD5 homolo OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q8TD|INEK9  Serine/threonine-pr OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q9VF|Upf1  Regulator of nonsen OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q54Y|dhkB  Hybrid signal trans OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q550|rab11C  Ras-related protein OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|O621|tag-175  Transmembrane prote OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q8S9|ATG8E  Autophagy-related p OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|O748|esf1  Pre-rRNA-processing OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|Q593|ZFAND2A  AN1-type zinc finge OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
TRINITY_sp|G4RK|tpsp  Bifunctional trehal OS=Dictyostelium discoideum GN=abpC PE=1 SV=1
| Protein ID | Description | Species | Accession | DI | DI
|------------|-------------|---------|-----------|----|----|
| TRINITY_sp| BEACH domain-containing protein lvsF | Dictyostelium discoideum | lvsF | 1 | 1 |
| TRINITY_sp| RING finger protein | | | | |
| TRINITY_sp| Cilia- and flagella | | | | |
| TRINITY_sp| COP9 signalosome complex | | | | |
| TRINITY_sp| Putative fatty acid | Arabidopsis thaliana | FAB1A | 1 | 1 |
| TRINITY_sp| Transportin | Dictyostelium discoideum | tnpo | 1 | 1 |
| TRINITY_sp| Aspartic proteinase | Oryza sativa subsp. japonica | RAP | 1 | 1 |
| TRINITY_sp| RHOMBOID-like protein 4 | Arabidopsis thaliana | RBL4 | 1 | 1 |
| TRINITY_sp| Probable serine/threonine-protein kinase SCO3848 | Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) | SCO3848 | 1 | 1 |
| TRINITY_sp| Probable fatty acid elongation protein 3 | Caenorhabditis elegans | elo-3 | 1 | 1 |
| TRINITY_sp| COP9 signalosome complex subunit 5 | Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) | RRI1 | 1 | 1 |
| TRINITY_sp| Protein ENHANCED DISEASE RESISTANCE 2-like | Arabidopsis thaliana | EDR2L | 1 | 1 |
| TRINITY_sp| Serine/threonine-protein kinase STY46 | Arabidopsis thaliana | STY46 | 1 | 1 |
| TRINITY_sp| Prefoldin subunit 3 | Mus musculus | Vbp1 | 1 | 1 |
| TRINITY_sp| High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A | Mus musculus | Pde8a | 1 | 1 |
| TRINITY_sp| NADP-dependent alcohol dehydrogenase C 1 | Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) | adhc1 | 1 | 1 |
| TRINITY_sp| Copine-8 | Mus musculus | Cpne8 | 1 | 1 |
| TRINITY_sp| Hydroxymethylglutaryl-CoA synthase, cytoplasmic | Cricetulus griseus | HMGCS1 | 1 | 1 |
| TRINITY_sp| Carbon catabolite-derepressing protein kinase | Candida tropicalis | SNF1 | 1 | 1 |
| TRINITY_sp| Lipase | Rhizopus niveus | | 1 | 1 |
| TRINITY_sp| Callose synthase 3 | Arabidopsis thaliana | CALS3 | 1 | 1 |
| TRINITY_sp| Ubiquitin carboxyl-terminal hydrolase 24 | Arabidopsis thaliana | UBP24 | 1 | 1 |
| TRINITY_sp| Endoglucanase B | Cellulomonas fimi | cenB | 1 | 1 |
| TRINITY_sp| Rho GTPase-activating protein gacJJ | Dictyostelium discoideum | gacJJ | 1 | 1 |
| TRINITY_sp| Target of rapamycin complex subunit wat1 | Schizosaccharomyces pombe (strain 972 / ATCC 24843) | pop3 | 1 | 1 |
| TRINITY_sp| Uncharacterized ribosome | Dictyostelium discoideum | sll1290 | 1 | 1 |
| TRINITY_sp| Putative fatty acid elongation protein CG5065 | Drosophila melanogaster | CG5065 | 1 | 1 |
| TRINITY_sp| Rho GTPase-activating protein gacJJ | Dictyostelium discoideum | gacJJ | 1 | 1 |
| TRINITY_sp| Target of rapamycin complex subunit wat1 | Schizosaccharomyces pombe (strain 972 / ATCC 24843) | pop3 | 1 | 1 |
| TRINITY_sp| Uncharacterized ribosome | Dictyostelium discoideum | sll1290 | 1 | 1 |
| TRINITY_sp| Putative fatty acyl-CoA reductase CG5065 | Drosophila melanogaster | CG5065 | 1 | 1 |
| TRINITY_sp| Rho GTPase-activating protein gacJJ | Dictyostelium discoideum | gacJJ | 1 | 1 |
| TRINITY_sp| Target of rapamycin complex subunit wat1 | Schizosaccharomyces pombe (strain 972 / ATCC 24843) | pop3 | 1 | 1 |
| TRINITY_sp| Uncharacterized ribosome | Dictyostelium discoideum | sll1290 | 1 | 1 |
| TRINITY_sp| Putative fatty acyl-CoA reductase CG5065 | Drosophila melanogaster | CG5065 | 1 | 1 |
| TRINITY_sp| Rho GTPase-activating protein gacJJ | Dictyostelium discoideum | gacJJ | 1 | 1 |
| TRINITY_sp| Target of rapamycin complex subunit wat1 | Schizosaccharomyces pombe (strain 972 / ATCC 24843) | pop3 | 1 | 1 |
| TRINITY_sp| Uncharacterized ribosome | Dictyostelium discoideum | sll1290 | 1 | 1 |
| TRINITY_sp| Putative fatty acyl-CoA reductase CG5065 | Drosophila melanogaster | CG5065 | 1 | 1 |
| TRINITY_sp| Rho GTPase-activating protein gacJJ | Dictyostelium discoideum | gacJJ | 1 | 1 |
| TRINITY_sp| Target of rapamycin complex subunit wat1 | Schizosaccharomyces pombe (strain 972 / ATCC 24843) | pop3 | 1 | 1 |
| TRINITY_sp| Uncharacterized ribosome | Dictyostelium discoideum | sll1290 | 1 | 1 |
| Protein Name                              | Description                                      | Value 1 | Value 2 |
|------------------------------------------|--------------------------------------------------|---------|---------|
| TRINITY_sp|Q196‡P21D5.5  | Uncharacterized protein                         | 35.90   | 0.00    |
| TRINITY_sp|Q68‡vac14      | Protein VAC14 homolog                          | 35.90   | 0.00    |
| TRINITY_sp|O64‡UTR1       | UTP:RNA uridylyltransfer                       | 35.90   | 0.00    |
| TRINITY_sp|Q9D‡Rfgap3     | ADP-ribosylation family                        | 35.90   | 0.00    |
| TRINITY_sp|O642‡         | Endolysin A OS=Mycobacterium                   | 35.90   | 0.00    |
| TRINITY_sp|Q3V‡Pls1       | Plastin-1 OS=Mus musculus                      | 35.90   | 0.00    |
| TRINITY_sp|Q55‡ctxXb      | Cortexillin-2 OS=Di                             | 35.90   | 0.00    |
| TRINITY_sp|Q5Z‡GOLGA7     | Golgin subfamily A                             | 35.90   | 0.00    |
| TRINITY_sp|Q22‡sym-2      | RNA-binding protein                            | 35.90   | 0.00    |
| TRINITY_sp|Q5‡dhKβ       | Hybrid signal transmitter                      | 35.90   | 0.00    |
| TRINITY_sp|Q8‡ probable ph| Probable protein                               | 35.90   | 0.00    |
| TRINITY_sp|Q8‡DDB_G02‡   | Probable GH family                             | 35.90   | 0.00    |
| TRINITY_sp|Q2‡lipf       | Gastric triacylglyc                            | 35.90   | 0.00    |
| TRINITY_sp|Q9‡eif1ad     | Probable RNA-binding protein                   | 35.90   | 0.00    |
| TRINITY_sp|P4‡AGX1       | Alanine--glyoxylate                            | 35.90   | 0.00    |
| TRINITY_sp|P0‡DDB_G02‡   | Enolase superfamily                            | 35.90   | 0.00    |
| TRINITY_sp|Q2‡VSR2       | Vacuolar-sorting repressor                     | 35.90   | 0.00    |
| TRINITY_sp|O9‡bdp1       | Transcription factor                            | 35.90   | 0.00    |
| TRINITY_sp|O5‡iki3       | Elongator complex protein                      | 35.90   | 0.00    |
| TRINITY_sp|Q8‡DUSP19     | Dual specificity protein                        | 35.90   | 0.00    |
| TRINITY_sp|Q8‡HITDP1     | Tyrosyl-DNA phosphotransferase                 | 35.90   | 0.00    |
| TRINITY_sp|Q8‡CCP2       | Calcium-dependent protein                      | 35.90   | 0.00    |
| TRINITY_sp|Q8‡BWeDrd37   | WD repeat-containing protein                   | 35.90   | 0.00    |
| TRINITY_sp|Q9‡Pu1        | tRNA pseudouridine                              | 35.90   | 0.00    |
| TRINITY_sp|Q8‡Cops4      | COP9 signalosome complex                       | 35.90   | 0.00    |
| TRINITY_sp|Q5‡Rpyk       | Pyruvate kinase OS=M.                        | 35.90   | 0.00    |
| TRINITY_sp|A6‡Shew185    | Non-canonical purin                            | 35.90   | 0.00    |
| TRINITY_sp|O7‡NUP155     | Nuclear pore complex                           | 35.90   | 0.00    |
| TRINITY_sp|Q5‡Prune2     | Protein Prune homolog                          | 35.90   | 0.00    |
| TRINITY_sp|Q0‡KRII       | Protein KRII homolog                           | 35.90   | 0.00    |
| TRINITY_sp|Q9‡PRN2       | Pirin-like protein                              | 35.90   | 0.00    |
| TRINITY_sp|Q9‡C1bn       | Nuclear export mediator                        | 35.90   | 0.00    |
| TRINITY_sp|Q9‡MLR1       | DNA mismatch repair                            | 35.90   | 0.00    |
| TRINITY_sp|Q8‡CCP2       | Calcium-dependent protein                      | 35.90   | 0.00    |
| TRINITY_sp|Q9‡PGK3       | Phosphoglycerate kinase                        | 35.90   | 0.00    |
| TRINITY_sp|Q0‡VP53       | Vacular protein                                | 35.90   | 0.00    |
| TRINITY_sp|O8‡Birc6      | Baculovirual IAP rep                            | 35.90   | 0.00    |
| TRINITY_sp|Q4‡Fsyn       | Prostaglandin F synth                          | 35.90   | 0.00    |
| TRINITY_sp|O0‡RABG3B     | Ras-related protein                            | 35.90   | 0.00    |
| TRINITY_sp|Q4‡BPM        | Ran-binding protein                            | 35.90   | 0.00    |
| TRINITY_sp|Q9‡HTX16      | Protein DETOXIFICAT                            | 35.90   | 0.00    |
| TRINITY_sp|Q1‡fcsB       | Fatty acyl-CoA synt                            | 35.90   | 0.00    |
| TRINITY_sp|Q8‡Ef11       | Elongation factor-1                            | 35.90   | 0.00    |
| TRINITY_sp|P4‡poIA       | DNA polymerase I OS=                          | 35.90   | 0.00    |
| TRINITY_sp|Q5‡PPT3       | Phosphoenolpyruvate                            | 35.90   | 0.00    |
| TRINITY_sp|Q6‡ncaph2     | Condensin-2 complex                            | 35.90   | 0.00    |
| TRINITY_sp|Q5‡mcFT       | Probable mitochondrial protein                 | 35.90   | 0.00    |
| TRINITY_sp|Q9‡PEX14      | Peroxisomal membrane                           | 35.90   | 0.00    |
| TRINITY_sp|Q7‡lapg-12    | Sterol 3-beta-glucol                           | 35.90   | 0.00    |
| TRINITY_sp|Q6‡ppp4r3b    | Serine/threonine-pr                            | 35.90   | 0.00    |
| TRINITY_sp|Q5‡ECM29      | Proteosome-associat                            | 35.90   | 0.00    |
| TRINITY_sp|P1‡AMO        | Peroxisomal primary                            | 35.90   | 0.00    |
| TRINITY_sp|Q9‡S1c8b1     | Sodium/potassium/ca                            | 35.90   | 0.00    |
| TRINITY_sp|O1‡pde-1      | Probable 3',5'-cyclase                         | 35.90   | 0.00    |
| TRINITY_sp|A6‡QV5S1      | Vacuolar protein                               | 35.90   | 0.00    |
| TRINITY_sp|Q9UR(Tf2-11)  | Transposon Tf2-11                              | 35.80   | 0.00    |
TRINITY_sp|Q9K7\BH3256  Probable non-canonical purine NTP phosphatase OS=Bacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) GN=BH3256 PE=3 SV=1 35.80 0.00
TRINITY_sp|F4IN\GGP4  Gamma-glutamyl peptidase OS=Arabidopsis thaliana GN=GGP4 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q097tSPBC12C  Uncharacterized protein OS=Arabidopsis thaliana GN=SPBC12C PE=2 SV=1 35.80 0.00
TRINITY_sp|O137Tsgt2  Small glutamine-rich peptide OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SGT2 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q9FW1GAMMACA1 Gamma carbonic anhydrase OS=Arabidopsis thaliana GN=GAMMACA1 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q4PCE8EC13  Protein transport protein OS=Arabidopsis thaliana GN=EC13 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q5F4cosb1  Oxysterol-binding protein OS=Arabidopsis thaliana GN=cosb1 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q9HU1aruS  Sensor histidine kinase OS=Arabidopsis thaliana GN=aruS PE=2 SV=1 35.80 0.00
TRINITY_sp|Q9QG3XNP  Transcriptional regulator OS=Arabidopsis thaliana GN=XNP PE=2 SV=1 35.80 0.00
TRINITY_sp|Q55Elatel1  Arginyl-tRNA synthetase OS=Arabidopsis thaliana GN=atel1 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q54Kccbl1  Kynurenine-oxoglutarate transaminase OS=Arabidopsis thaliana GN=ccbl1 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q9R0Ph13  Four and a half LIM domain OS=Arabidopsis thaliana GN=Ph13 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q1PF1EDA2  Probable serine protease OS=Arabidopsis thaliana GN=EDA2 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q8TAnabcA7  ABC transporter A family OS=Arabidopsis thaliana GN=abcA7 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q5XH3march8  E3 ubiquitin-protein OS=Arabidopsis thaliana GN=march8 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q0DLLOs05g011DEAD-box ATP-dependent OS=Arabidopsis thaliana GN=DEAD-box PE=2 SV=1 35.80 0.00
TRINITY_sp|Q9NPBPNPLA8  Calcium-independent OS=Arabidopsis thaliana GN=PPLA8 PE=2 SV=1 35.80 0.00
TRINITY_sp|P0501alKB  Alpha-ketoglutarate OS=Arabidopsis thaliana GN=alKB PE=2 SV=1 35.80 0.00
TRINITY_sp|Q9SIJAt2g402Eukaryotic translational OS=Arabidopsis thaliana GN=At2g402Eukaryotic translational PE=2 SV=1 35.80 0.00
TRINITY_sp|Q5UP1MIMI_R6Putative band 7 fam OS=Arabidopsis thaliana GN=MIMI_R6 Putative band 7 fam PE=2 SV=1 35.80 0.00
TRINITY_sp|Q5PP\zc2hcaZinc finger C2HC do OS=Arabidopsis thaliana GN=C2HC do PE=2 SV=1 35.80 0.00
TRINITY_sp|P046Lipf  Gastric triacylglycerol OS=Arabidopsis thaliana GN=Lipf PE=2 SV=1 35.80 0.00
TRINITY_sp|Q91Q\RDR1  RNA-dependent RNA OS=Arabidopsis thaliana GN=RDR1 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q9MFPAP29  Probable inactive OS=Arabidopsis thaliana GN=AP29 PE=2 SV=1 35.80 0.00
TRINITY_sp|O027\PARG  Poly(ADP-ribose) OS=Arabidopsis thaliana GN=PARG PE=2 SV=1 35.80 0.00
TRINITY_sp|P333\SNK1  Beta-glucan synthase OS=Arabidopsis thaliana GN=SNK1 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q54Gctdspb12  CTD small phosphatase OS=Arabidopsis thaliana GN=ctdspb12 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q926\TBC1D5  TBC1 domain family OS=Arabidopsis thaliana GN=TBC1D5 PE=2 SV=1 35.80 0.00
TRINITY_sp|P0A31ltrA  Group II intron-encoding OS=Arabidopsis thaliana GN=ltrA PE=2 SV=1 35.80 0.00
TRINITY_sp|P0541petA  Ubiquinol-cytochrome OS=Arabidopsis thaliana GN=petA PE=2 SV=1 35.80 0.00
TRINITY_sp|Q9KAfrr  Ribosome-recycling OS=Arabidopsis thaliana GN=frr PE=2 SV=1 35.80 0.00
TRINITY_sp|C4L9\mutL  DNA mismatch repair OS=Arabidopsis thaliana GN=mutL PE=2 SV=1 35.80 0.00
TRINITY_sp|O806\SUC3  Sucrose transport OS=Arabidopsis thaliana GN=SUC3 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q99D9\Eefh1  EF-hand domain-containing OS=Arabidopsis thaliana GN=Eefh1 PE=2 SV=1 35.80 0.00
TRINITY_sp|O601\SPBC19F: Uncharacterized protein OS=Arabidopsis thaliana GN=SPBC19F: Uncharacterized protein PE=2 SV=1 35.80 0.00
TRINITY_sp|P379\yus2  Uncharacterized OS=Arabidopsis thaliana GN=yus2 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q763\abpD  Interaptin OS=Dictyostelium discoideum GN=abpD PE=2 SV=1 35.80 0.00
TRINITY_sp|P222\RAS1  Ras-like protein OS=Dictyostelium discoideum GN=RAS1 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q5PP\At2g354Zinc finger CCCH do OS=Arabidopsis thaliana GN=At2g354Zinc finger CCCH do PE=2 SV=1 35.80 0.00
TRINITY_sp|Q8DJGrpE  Protein GrpE OS=The OPUS database PE=2 SV=1 35.80 0.00
TRINITY_sp|Q9FLFPKBP15 Peptidyl-prolyl cis OS=Arabidopsis thaliana GN=PKBP15 Peptidyl-prolyl cis PE=2 SV=1 35.80 0.00
TRINITY_sp|A3D0\rihA  Pyrimidine-specific OS=Arabidopsis thaliana GN=rihA PE=2 SV=1 35.80 0.00
TRINITY_sp|Q7UX1CCD7  Carotenoid cleavage OS=Arabidopsis thaliana GN=CCD7 PE=2 SV=1 35.80 0.00
TRINITY_sp|Q9SS1\UMJ25  Lysine-specific demethylase OS=Arabidopsis thaliana GN=UMJ25 PE=2 SV=1 35.80 0.00
TRINITY_sp|B4NDGC24923  Regulator of telomere OS=Arabidopsis thaliana GN=GC24923 PE=2 SV=1 35.80 0.00
TRINITY_sp|B0W2\CPIJ001 Clustered mitochondrial OS=Arabidopsis thaliana GN=CPIJ001 Clustered mitochondrial PE=2 SV=1 35.80 0.00
TRINITY_sp|P214\ABC1  Multidrug resistance OS=Arabidopsis thaliana GN=ABC1 PE=2 SV=1 35.80 0.00
TRINITY_sp|B8AECOsI_0778NAP1-related protein OS=Arabidopsis thaliana GN=NAP1-related protein PE=2 SV=1 35.80 0.00
TRINITY_sp|Q6MC:pepA Probable cytosol am
TRINITY_sp|Q54MDDB_GO2:Coiled-coil domain-
TRINITY_sp|Q6VIVcath Viral cathepsin OS=
TRINITY_sp|Q6ZUN:ARHGAP2:Rho GTase-activat
TRINITY_sp|Q8061APY6 Probable apyrase 6
TRINITY_sp|Q81HBC_0906 Delta(1)-pyrroline-
TRINITY_sp|Q9CS5:PTP9 tRNA dimethylallylt
TRINITY_sp|Q2KNHXXK2 Hexokinase-2 OS=Ory
TRINITY_sp|Q9CO:WDR33 pre-mRNA 3' end pro
TRINITY_sp|Q3KTG:GDPD5 Glycerophosphodiester
TRINITY_sp|P303:cadA Probable cadmium-tr
TRINITY_sp|Q8L4iWEE1 Weel-like protein k
TRINITY_sp|P221:- Ras-related protein
TRINITY_sp|A5P1ABHD17C Protein ABHD17C OS=
TRINITY_sp|F4HVV:VAD1 Protein VASCULAR AS
TRINITY_sp|Q6TEfam91a1 Protein FAM91A1 OS=
TRINITY_sp|Q9L1:At3g213:Clavaminate synthas
TRINITY_sp|Q78JU:ubfd1 Ubiquitin domain-co
TRINITY_sp|B0F9IGC6 Golgin candidate 6
TRINITY_sp|Q097:akr1 Palmitoyltransferas
TRINITY_sp|P227:Guclyl2b Guanylate cyclase s
TRINITY_sp|Q91YMMett113 Methyltransferase-l
TRINITY_sp|Q6NL:ABC2 ABC transporter D f
TRINITY_sp|Q991:TY3B-G Transposon Ty3-G Ga
TRINITY_sp|Q9SH:ATIC2 Protein TIC 21, chl
TRINITY_sp|Q912:gst-6 Probable glutathion
TRINITY_sp|Q9FKU:UBP17 Ubiquitin carboxyl-
TRINITY_sp|Q9SK:At2g203:NADH dehydrogenase
TRINITY_sp|B6Z3:PC1 Peroxisomal adenine
TRINITY_sp|G5EB:ama-5 Mitogen-activated p
TRINITY_sp|Q531:gxcJ Rac guanine nucleot
TRINITY_sp|Q6PEC:Tbca Tubulin-specific ch
TRINITY_sp|F4HP:RE4 Probable serine/thr
TRINITY_sp|Q7ZU:ykt6 Synaptobrevin homol
TRINITY_sp|Q3T0:ABHD1 Protein ABHD1 OS=Bo
TRINITY_sp|Q1OG:me1k Maternal embryonic
TRINITY_sp|Q00:SWA2 Alpha-amylase 2 OS=
TRINITY_sp|Q039:RUB1 NEDD8-like protein
TRINITY_sp|Q399:vPVE Vacuolar-processing
TRINITY_sp|Q1PF:EDA2 Probable serine pro
TRINITY_sp|Q9SKPVA12 Vesicle-associated
TRINITY_sp|O460:Parg Poly(ADP-ribose) gl
TRINITY_sp|Q9W01:cyd420 Probable cytochrome
TRINITY_sp|Q387:MTD Mannitol dehydrogen
TRINITY_sp|Q274:mec-2 Mechanosensory prot
TRINITY_sp|Q54Mi:tip1 TIP41-like protein
TRINITY_sp|Q493:VAMP711 Vesicle-associated
TRINITY_sp|Q54P:geFA Ras guanine nucleot
TRINITY_sp|Q86H:mrt4 Ribosome assembly f
TRINITY_sp|Q4WJ:mdr1 Multiple RNA-bindin
TRINITY_sp|Q9ZS:FIP37 FKBP12-interacting
TRINITY_sp|Q8MYIDB_GO2:Probable serine/thr
TRINITY_sp|Q556:psmM4-1 Proteosome subunit
TRINITY_sp|A2WY:HK3 Probable histidine
TRINITY_sp|O317:tdh L-threonine 3-dehyd
TRINITY_sp|Q0WQILTA3 Dihydrolipooyllysine
| Accession     | Description                                      | Predicted Protein information |
|---------------|--------------------------------------------------|-------------------------------|
| TRINITY_sp|O608:KIN  | DNA/RNA-binding protein  | 35.60 0.00 |
| TRINITY_sp|A7S8:1vglq1870 | Coiled-coil domain- | 35.60 0.00 |
| TRINITY_sp|A1A6:HK4  | Probable histidine  | 35.60 0.00 |
| TRINITY_sp|Q86N:JNDBB_G02 | Putative elongation  | 35.60 0.00 |
| TRINITY_sp|P109:  | Retrovirus-related  | 35.60 0.00 |
| TRINITY_sp|Q54P:exoc4 | Exocyst complex com  | 35.60 0.00 |
| TRINITY_sp|Q2Q:CBSDUF3 | DUF21 domain-contai | 35.60 0.00 |
| TRINITY_sp|Q5PK:Eif2d | Eukaryotic translat  | 35.60 0.00 |
| TRINITY_sp|Q1Zk|xgcDD | Guanine exchange fa  | 35.60 0.00 |
| TRINITY_sp|Q6C5:YKT6 | Synaptobrevin homol  | 35.60 0.00 |
| TRINITY_sp|Q9CO:WDR33 | pre-mRNA 3' end pro  | 35.60 0.00 |
| TRINITY_sp|Q54R:dhkL | Hybrid signal trans  | 35.60 0.00 |
| TRINITY_sp|P107:  | Venom allergen 5.02  | 35.60 0.00 |
| TRINITY_sp|Q94G:QLCNAC1 | UDP-N-acetylglucosa | 35.60 0.00 |
| TRINITY_sp|Q9FJ:FKBP56 | Peptidyl-prolyl cis  | 35.60 0.00 |
| TRINITY_sp|Q8L4:DAAT | D-amino-acid transa  | 35.60 0.00 |
| TRINITY_sp|Q4U2:Herc2 | E3 ubiquitin-protei | 35.60 0.00 |
| TRINITY_sp|Q932:LA1 | La protein 1 OS=Ara  | 35.60 0.00 |
| TRINITY_sp|P053:p20 | Uncharacterized N-a  | 35.60 0.00 |
| TRINITY_sp|Q54T:GdrkC | Probable serine/thr  | 35.60 0.00 |
| TRINITY_sp|Q9M2i:SDR1 | (+)-neomenthol dehy  | 35.60 0.00 |
| TRINITY_sp|Q9US:EPCC4B3 | Uncharacterized tra | 35.60 0.00 |
| TRINITY_sp|Q6GP:XAF1 | XIAP-associated fac  | 35.60 0.00 |
| TRINITY_sp|Q6K0:RAT11 | 5'-'3' exoribonuclea | 35.60 0.00 |
| TRINITY_sp|Q9CR:Ccdc96 | Coiled-coil domain- | 35.60 0.00 |
| TRINITY_sp|P054:SSB | Lupus La protein OS | 35.60 0.00 |
| TRINITY_sp|Q317:cdsA | Phosphatidate cytid | 35.60 0.00 |
| TRINITY_sp|Q537:ufaA1 | Tuberculostearic ac | 35.60 0.00 |
| TRINITY_sp|Q088:Rgs4 | Regulator of G-prot | 35.60 0.00 |
| TRINITY_sp|P465:ckd-12 | Cyclin-dependent ki | 35.60 0.00 |
| TRINITY_sp|Q84K:ABCA2 | ABC transporter A f | 35.60 0.00 |
| TRINITY_sp|Q99J:Mrml | rRNA methyltransfer | 35.60 0.00 |
| TRINITY_sp|Q747:EPHB5 | Ephrin type-B recep | 35.60 0.00 |
| TRINITY_sp|D4A2:ARB_014 | Probable endo-1,3(4 | 35.60 0.00 |
| TRINITY_sp|P171:Cyp27a1 | Sterol 26-hydroxyla | 35.60 0.00 |
| TRINITY_sp|Q993:TY3B-G | Transposon Ty3-G Ga | 35.60 0.00 |
| TRINITY_sp|P071:cyt-1 | Cytochrome cl, heme | 35.60 0.00 |
| TRINITY_sp|Q9P7:mak1 | Peroxide stress-act | 35.60 0.00 |
| TRINITY_sp|P484:RasGAP1 | GTase-activating p | 35.50 0.00 |
| TRINITY_sp|Q9SA:At1g1177 | Alpha-ketoglutarate | 35.50 0.00 |
| TRINITY_sp|Q8TER:RAPGEF6 | Rap guanine nucleot | 35.50 0.00 |
| TRINITY_sp|Q6AW:At5g1701D-xylose-proton sym | 35.50 0.00 |
| TRINITY_sp|Q54U:trmt6 | tRNA (adenoine(58)| 35.50 0.00 |
| TRINITY_sp|Q9VF:CG10681 | KxDL motif-containi | 35.50 0.00 |
| TRINITY_sp|Q9XC:tsf | Elongation factor T | 35.50 0.00 |
| TRINITY_sp|A0AUI:Gm7168 | Sperm motility kina | 35.50 0.00 |
| TRINITY_sp|P623:CPK4 | Calcium-dependent p | 35.50 0.00 |
| TRINITY_sp|Q86K:JNDBB_G02 | Probable serine/thr | 35.50 0.00 |
| TRINITY_sp|Q54Q:dhkG | Hybrid signal trans | 35.50 0.00 |
| TRINITY_sp|Q93P:ptr2 | Probable peptide tr | 35.50 0.00 |
| TRINITY_sp|F4K2:ATG101 | Autophagy-related p | 35.50 0.00 |
| TRINITY_sp|Q550:captC | Uncharacterized CDP | 35.50 0.00 |
| TRINITY_sp|Q54K:JNDBB_G02 | Serine hydrolase-li | 35.50 0.00 |
| TRINITY_sp|Q9ER:Rdh14 | Retinol dehydrogena | 35.50 0.00 |
| TRINITY_sp|Q4Z8:RanBPM | Ran-binding protein | 35.50 0.00 |
| TRINITY_sp|Q96N:FRDH12 | Retinol dehydrogena | 35.50 0.00 |
| Accession       | Name                                      | Description                   | Score | E-value |
|-----------------|-------------------------------------------|-------------------------------|-------|---------|
| sp|Q86C‡|Serine/threonine-protein kinase atg1 OS=Dictyostelium discoideum GN=atg1 PE=3 SV=1 | 35.40 | 0.00    |
| sp|Q54R:‡|DDB_G02‡|WASH complex subunit | 35.40 | 0.00    |
| sp|Q9LP\ERF1-2 | Eukaryotic peptide | 35.40 | 0.00    |
| sp|Q9SKNDB4 | External alternative | 35.40 | 0.00    |
| sp|Q803‡|memol | Protein MEMO1 OS=Da | 35.40 | 0.00    |
| sp|Q2KH|CPNE6 | Copine-6 OS=Bos taurus | 35.40 | 0.00    |
| sp|P404‡|PBX3 | Pre-B-cell leukemia | 35.40 | 0.00    |
| sp|Q8CDF|1qub | IQ and ubiquitin-like | 35.40 | 0.00    |
| sp|C5FW|CPYA | Carboxypeptidase Y | 35.40 | 0.00    |
| sp|Q76P‡|DDB_G02‡|Probable serine/threonine-protein kinase | 35.40 | 0.00    |
| sp|Q5Z3|TLDCL1 | TLD domain-containing | 35.40 | 0.00    |
| sp|A5FKI|trfsP | 30S ribosomal protein | 35.40 | 0.00    |
| sp|Q55C|wdr85 | Diphthine methyltransferase | 35.40 | 0.00    |
| sp|P341|pkgC | Protein kinase 3 OS | 35.40 | 0.00    |
| sp|Q01I:‡|H0219H1:‡|ATP-dependent RNA helicase | 35.40 | 0.00    |
| sp|Q652|os09g05 ‡|Protein HIRA OS=Oryza sativa subsp. japonica | 35.40 | 0.00    |
| sp|Q006|gp63 | Leishmanolysin OS=Leishmania | 35.40 | 0.00    |
| sp|Q8ST|gef6 | Ras guanine nucleotide | 35.40 | 0.00    |
| sp|Q944‡|SPBC660. Uncharacterized RNA | 35.40 | 0.00    |
| sp|Q52‡|U2AF65A | Splicing factor U2a | 35.40 | 0.00    |
| sp|Q23F‡|TTL3C | Tubulin glycosylation 3 | 35.40 | 0.00    |
| sp|Q03‡|Itk | Tyrosine-protein kinase | 35.40 | 0.00    |
| sp|P239|q1cA | Glucan endo-1,3-beta-glucosidase | 35.40 | 0.00    |
| sp|Q9VR|HERC2 | Probable E3 ubiquitin | 35.40 | 0.00    |
| sp|Q8M‡|Physarolisin OS=Phytophthora | 35.40 | 0.00    |
| sp|P364|vi1B | Protovillin OS=Dictyostelium | 35.40 | 0.00    |
| sp|Q407‡|RGP2 | Ras-related protein | 35.40 | 0.00    |
| sp|Q7F‡|CML13 | Probable calcium-binding protein | 35.40 | 0.00    |
| sp|B1W‡|adv13 | Segment polarity protein | 35.40 | 0.00    |
| sp|P6PNK|dxm11 | DnM-like protein 1 | 35.40 | 0.00    |
| sp|Q566F|Them4 | Acyl-coenzyme A thioesterase | 35.40 | 0.00    |
| sp|Q9MA1|Atg10 | Uncharacterized aar | 35.40 | 0.00    |
| sp|F41U|UPF2 | Regulator of nonsense suppression | 35.40 | 0.00    |
| sp|Q245‡|Syx1A | Syntaxin-1A OS=Drosophila | 35.30 | 0.00    |
| sp|Q8WW|TCTEX1D2.Tctex1 domain-containing | 35.30 | 0.00    |
| sp|Q9NP‡|CABP5 | Calcium-binding protein | 35.30 | 0.00    |
| sp|Q8IL|PF14_0312.STII-like protein | 35.30 | 0.00    |
| sp|P133|sh2 | DNA mismatch repair | 35.30 | 0.00    |
| sp|P138|up17 | U3 small nucleolar RNA | 35.30 | 0.00    |
| sp|Q9FH|SWC6 | SNR1 complex subunit | 35.30 | 0.00    |
| sp|Q6A‡|Fam179b | Crescenerin-1 OS=Mus musculus | 35.30 | 0.00    |
| sp|Q9LD‡|MYB108 | Transcription factor | 35.30 | 0.00    |
| sp|Q925‡|GBP1 | Golgi-specific bref | 35.30 | 0.00    |
| sp|P340|manA | Lysosomal alpha-mannosidase | 35.30 | 0.00    |
| sp|A3KP‡|ttc38 | Tetratricopeptide repeat | 35.30 | 0.00    |
| sp|Q2K‡|IDE | Insulin-degrading enzyme | 35.30 | 0.00    |
| sp|Q9P‡|FAM135A | Protein FAM135A OS=Dictyostelium | 35.30 | 0.00    |
| sp|Q9D‡|ELM0D3 | ELMO domain-containing | 35.30 | 0.00    |
| sp|Q125|rasA | Ras-like protein | 35.30 | 0.00    |
| sp|Q52L‡|LRRC40 | Leucine-rich repeat | 35.30 | 0.00    |
| sp|Q9G‡|KIF15 | Kinesin-like protein | 35.30 | 0.00    |
| sp|Q64‡|URT1 | UTP:RNA uridylyltransferase | 35.30 | 0.00    |
| sp|Q764|nft-1 | Nitrilase and fragilis | 35.30 | 0.00    |
| sp|B4FG‡| - | Spindle and kinetocarp | 35.30 | 0.00    |
| sp|P23‡|Mov10 | Putative helicase | 35.30 | 0.00    |
| sp|Q170‡|hpo-8 | Very-long-chain (3R) | 35.30 | 0.00    |
| Ensembl ID     | Description                              | Score | Value |
|---------------|------------------------------------------|-------|-------|
| TRINITY_sp|P3641rab14 | Ras-related protein | 35.30 | 0.00 |
| TRINITY_sp|P546:ptpC | Tyrosine-protein phosphatase | 35.30 | 0.00 |
| TRINITY_sp|Q5ZJILSG1 | Large subunit GTPase | 35.30 | 0.00 |
| TRINITY_sp|Q7S8vesf-2 | Pre-tRNA-processing | 35.30 | 0.00 |
| TRINITY_sp|P814:PGA | Pepes A OS=Suncus | 35.30 | 0.00 |
| TRINITY_sp|Q7ZX:kif19 | Kinesin-like protein | 35.30 | 0.00 |
| TRINITY_sp|Q54N:ppan | Peter Pan-like protein | 35.30 | 0.00 |
| TRINITY_sp|Q6ICA:ASPHD2 | Aspartate beta-hydroxylase | 35.30 | 0.00 |
| TRINITY_sp|Q923:ssb1 | Replication factor | 35.30 | 0.00 |
| TRINITY_sp|Q869:DDDB_G02:COB9 | Domain-containing | 35.30 | 0.00 |
| TRINITY_sp|Q9NA:tim-22 | Mitochondrial import | 35.30 | 0.00 |
| TRINITY_sp|Q851:Os03g07 | Probable GTP-binding | 35.30 | 0.00 |
| TRINITY_sp|P292:fol1 | Folic acid synthase | 35.30 | 0.00 |
| TRINITY_sp|Q944:bdp1 | Transcription factor | 35.30 | 0.00 |
| TRINITY_sp|Q2YD:IGS2:O2:Interferon-stimulating | 35.30 | 0.00 |
| TRINITY_sp|Q86C:dhkK | Hybrid signal transducer | 35.30 | 0.00 |
| TRINITY_sp|P251:rcc1 | Regulator of chromatin | 35.30 | 0.00 |
| TRINITY_sp|Q86Y:CPNE8 | Copine-8 OS=Homo sapiens | 35.30 | 0.00 |
| TRINITY_sp|P533:tbg | Tubulin gamma chain | 35.30 | 0.00 |
| TRINITY_sp|Q945:CIB22 | NADH dehydrogenase | 35.30 | 0.00 |
| TRINITY_sp|Q54C:pex6 | Peroxisomal biogene | 35.30 | 0.00 |
| TRINITY_sp|P412:CSK | Tyrosine-protein kinase | 35.30 | 0.00 |
| TRINITY_sp|Q9LT:VALIS1 | ALA-interacting subunit | 35.30 | 0.00 |
| TRINITY_sp|Q86I:dolpp1 | Dolichylphosphatase | 35.30 | 0.00 |
| TRINITY_sp|B0RZ:adk | Adenylate kinase OS | 35.30 | 0.00 |
| TRINITY_sp|Q68O:GGT2 | Gamma-glutamyltranspeptidase | 35.30 | 0.00 |
| TRINITY_sp|Q81W:BBS7 | Bardet-Biedl syndrome | 35.30 | 0.00 |
| TRINITY_sp|Q6NS:trmt11 | tRNA (guanine(10)-N) | 35.30 | 0.00 |
| TRINITY_sp|Q86I:mek3 | Probable serine/threonine kinase | 35.30 | 0.00 |
| TRINITY_sp|Q84K:ABCA2 | ABC transporter A | 35.30 | 0.00 |
| TRINITY_sp|Q96R:IFT140 | Intraflagellar transport | 35.30 | 0.00 |
| TRINITY_sp|Q7T6:MIMI_R8:Putative serine/threonine kinase | 35.30 | 0.00 |
| TRINITY_sp|O601:lcf1 | Long-chain-fatty-acid desaturase | 35.20 | 0.00 |
| TRINITY_sp|Q851:SLY1 | SEC1 family transporter | 35.20 | 0.00 |
| TRINITY_sp|Q54R:dhkL | Hybrid signal transducer | 35.20 | 0.00 |
| TRINITY_sp|Q7SD:msn-3 | DNA mismatch repair | 35.20 | 0.00 |
| TRINITY_sp|A910:Bpet044:Putative nucleotide-binding protein | 35.20 | 0.00 |
| TRINITY_sp|Q75J:zaA | Dual specificity phosphatase | 35.20 | 0.00 |
| TRINITY_sp|Q9BZ:WDR11 | WD repeat-containing | 35.20 | 0.00 |
| TRINITY_sp|P213:NF1 | Neurofibromin OS=Homo sapiens | 35.20 | 0.00 |
| TRINITY_sp|Q9NX:DUS2 | tRNA-dihydrouridine | 35.20 | 0.00 |
| TRINITY_sp|Q54B:mcnG | Mitochondrial subunit | 35.20 | 0.00 |
| TRINITY_sp|Q32PC:1D | Nuclear precursor | 35.20 | 0.00 |
| TRINITY_sp|P412:CSK | Tyrosine-protein kinase | 35.20 | 0.00 |
| TRINITY_sp|P426:SRK1 | Tyrosine-protein kinase | 35.20 | 0.00 |
| TRINITY_sp|Q9LK:ALA8 | Probable phospholipid scramblase | 35.20 | 0.00 |
| TRINITY_sp|Q0P5:Vps8 | Vacuolar protein sorting | 35.20 | 0.00 |
| TRINITY_sp|Q902:lancl1 | Lancs-like protein 1 | 35.20 | 0.00 |
| TRINITY_sp|Q588:TEB | Helicase and polymerase | 35.20 | 0.00 |
| TRINITY_sp|Q0UU:TPC1 | Mitochondrial thiamine pyrophosphatase | 35.20 | 0.00 |
| TRINITY_sp|P308:evgsS | Sensor protein EvgS | 35.20 | 0.00 |
| TRINITY_sp|Q84Y:JCP4 | CAX-interacting protein | 35.20 | 0.00 |
| TRINITY_sp|Q54K:ef2b3 | Translation initiation factor | 35.20 | 0.00 |
| TRINITY_sp|Q55E:ctu2 | Cytoplasmic tRNA 2-aminobicyclo[2.2.1]heptane-2-carboxylate synthetase | 35.20 | 0.00 |
| TRINITY_sp|Q9FW:ABC11 | ABC transporter B family | 35.20 | 0.00 |
| TRINITY_sp|P518:fabG | 3-oxoacyl-[acyl-carrier protein] thioesterase | 35.20 | 0.00 |
| Gene Name                  | Description                          | Score 1 | Score 2 |
|---------------------------|--------------------------------------|---------|---------|
| ATP9B                     | Probable phospholipid-transporting ATPase IIB | 35.10   | 0.00    |
| TRINITY_sp|A5P91EMETTL13 | Methyltransferase-1 | 35.10 | 0.00 |
| TRINITY_sp|Q93395AT8A1 | tRNA pseudouridine | 35.10 | 0.00 |
| TRINITY_sp|Q8M49ZdrkA | Probable serine/thr | 35.10 | 0.00 |
| TRINITY_sp|Q9P312db14 | E3 ubiquitin-protein ligase | 35.10 | 0.00 |
| TRINITY_sp|P2421ARD | Actin, spherule isoform | 35.10 | 0.00 |
| TRINITY_sp|Q9DC21meg8 | Multiple epidermal growth factor-like domain proteins | 35.10 | 0.00 |
| TRINITY_sp|Q9DG09star | Steroidogenic acute globulin | 35.10 | 0.00 |
| TRINITY_sp|Q692Dnah17 | Dynein heavy chain | 35.10 | 0.00 |
| TRINITY_sp|Q648CID7 | Polyadenylate-binding protein | 35.10 | 0.00 |
| TRINITY_sp|Q58ETpar1 | Presenilins-associated protein | 35.10 | 0.00 |
| TRINITY_sp|P200PSAP | Saposin-C | 35.10 | 0.00 |
| TRINITY_sp|Q54IVSAP | Translation initiation factor 2 | 35.10 | 0.00 |
| TRINITY_sp|Q0VD1SMPS | Sphingomyelin phosphodiesterase | 35.10 | 0.00 |
| TRINITY_sp|Q9S71VP811 | Vacuolar protein-sorting protein 11 | 35.10 | 0.00 |
| TRINITY_sp|Q869nnapA | Nck-associated protein | 35.10 | 0.00 |
| TRINITY_sp|Q8M9TSCAI | Protein SCAI | 35.10 | 0.00 |
| TRINITY_sp|P608Midf8 | Multiple epidermal growth factor-like domain proteins | 35.10 | 0.00 |
| TRINITY_sp|Q510trmH | tRNA (guanosine) | 35.10 | 0.00 |
| TRINITY_sp|P497RBM25 | RNA-binding protein | 35.10 | 0.00 |
| TRINITY_sp|P703Us9x | Probable ubiquitin | 35.10 | 0.00 |
| TRINITY_sp|P577Rce1 | CAAX prenyl protease | 35.10 | 0.00 |
| TRINITY_sp|Q54MDDB |von Willebrand factor A domain-containing protein | 35.10 | 0.00 |
| TRINITY_sp|Q086Ssgtm1 | Sequestosome-1 | 35.10 | 0.00 |
| TRINITY_sp|Q8FMdcd | dCTP deaminase | 35.10 | 0.00 |
| TRINITY_sp|Q4HMRAT1 | 5'-3' exoribonuclease | 35.10 | 0.00 |
| TRINITY_sp|Q138not3 | General negative regulator | 35.10 | 0.00 |
| TRINITY_sp|Q84R1ClSH | Probable GTP diphosphate binding protein | 35.10 | 0.00 |
| TRINITY_sp|Q8RVSSEC | Securin | 35.10 | 0.00 |
| TRINITY_sp|P048Cyp3a1 | Cytochrome P450 | 35.10 | 0.00 |
| TRINITY_sp|Q8H1SAE13 | Malonate-CoA ligase | 35.10 | 0.00 |
| TRINITY_sp|Q9CSGCP2 | Gamma-tubulin complex | 35.10 | 0.00 |
| TRINITY_sp|Q65ZEFznf474 | Zinc finger protein | 35.10 | 0.00 |
| TRINITY_sp|Q9P2EZNF1 | NFX1-type zinc finger protein | 35.10 | 0.00 |
| TRINITY_sp|Q52ZCREASE | Protein CREST | 35.10 | 0.00 |
| TRINITY_sp|Q9WVMarch7 | E3 ubiquitin-protein ligase | 35.10 | 0.00 |
| TRINITY_sp|P313PKAR | cAMP-dependent protein kinase | 35.10 | 0.00 |
| TRINITY_sp|Q5BL1mett121 | Protein N-lysine methyltransferase | 35.10 | 0.00 |
| TRINITY_sp|Q8BLLArghap2 | Rho GTPase-activating protein | 35.10 | 0.00 |
| TRINITY_sp|B4SDPpha21 | UBF1 protein | 35.10 | 0.00 |
| TRINITY_sp|Q54KsrckA | RGS domain-containing protein | 35.10 | 0.00 |
| TRINITY_sp|Q253PKC1 | Protein kinase C | 35.10 | 0.00 |
| TRINITY_sp|Q9HDypt71 | GTP-binding protein | 35.10 | 0.00 |
| TRINITY_sp|Q050UBE3A | Ubiquitin-protein ligase | 35.10 | 0.00 |
| TRINITY_sp|Q9VRHERC2 | Probable E3 ubiquitin-protein ligase | 35.10 | 0.00 |
| TRINITY_sp|Q5B11ERC8 | DNA excision repair protein | 35.10 | 0.00 |
| TRINITY_sp|Q294ATP8A1 | Probable phospholipase A1 | 35.10 | 0.00 |
| TRINITY_sp|F4IFGFG1 | Protein FORGETTER | 35.10 | 0.00 |
| TRINITY_sp|Q861DDDB | PH domain-containing protein | 35.10 | 0.00 |
| TRINITY_sp|Q6ZIAFPK6 | Serine/threonine-protein kinase | 35.10 | 0.00 |
| TRINITY_sp|Q9SVAt4217 | RNA pseudouridine synthase | 35.10 | 0.00 |
| TRINITY_sp|Q0VFBloc1s1 | Biogenesis of lysosome-related organelles | 35.10 | 0.00 |
| TRINITY_sp|Q9P7mak1 | Peroxide stress-act | 35.00 | 0.00 |
| TRINITY_sp|Q902ISBN | Poly(A)-specific ribonuclease | 35.00 | 0.00 |
| Protein Name                  | Species                      | Gene Name     | Location |
|------------------------------|------------------------------|---------------|----------|
| Cholesterol 7-desaturase OS=Caenorhabditis elegans GN=daf-36 | 35.00 0.00 |
| Protein phosphatase OS=Homo sapiens GN=ZFAND2A | 35.00 0.00 |
| Dual specificity pr OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YPT52 | 35.00 0.00 |
| GTP-binding protein YPT52 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YPT52 | 35.00 0.00 |
| Ribosomal large subunit pseudouridine synthase D OS=Nitrosomonas europaea (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298) GN=rluD | 35.00 0.00 |
| Protein phosphatase PP2A regulatory subunit A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=paa1 | 35.00 0.00 |
| Transcription elongation factor SPT6 homolog OS=Arabidopsis thaliana GN=SPT6 | 35.00 0.00 |
| Serine/threonine-protein kinase EDR1 OS=Arabidopsis thaliana GN=EDR1 | 35.00 0.00 |
| Probable manganese-transporting ATPase PDR2 OS=Arabidopsis thaliana GN=PDR2 | 35.00 0.00 |
| Splicing factor U2AF 50 kDa subunit OS=Drosophila melanogaster GN=U2af50 | 35.00 0.00 |
| 25S rRNA (uridine-N(3))-methyltransferase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=bmt5 | 35.00 0.00 |
| ABC transporter G family member 20 OS=Dictyostelium discoideum GN=abcG20 | 35.00 0.00 |
| Ras guanine nucleotide exchange factor G OS=Dictyostelium discoideum GN=gefG | 35.00 0.00 |
| Serine/threonine-protein kinase HSL1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) GN=HSL1 | 35.00 0.00 |
| Dedicator of cytokinesis protein 3 OS=Homo sapiens GN=DOCK3 | 35.00 0.00 |
| E3 ubiquitin-protein ligase HERC2 OS=Mus musculus GN=Herc2 | 35.00 0.00 |
| Probable RNA-binding protein 19 OS=Mus musculus GN=Rbm19 | 35.00 0.00 |
| ATP-dependent DNA helicase PcrA OS=Staphylococcus epidermidis (strain ATCC 35984 / RP62A) GN=pcrA | 35.00 0.00 |
| Cytohesin-3 OS=Mus musculus GN=Cyth3 | 35.00 0.00 |
| Protein gar2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=gar2 | 35.00 0.00 |
| Sorting nexin 1 OS=Arabidopsis thaliana GN=SNX1 | 35.00 0.00 |
| Cathepsin L1 OS=Canis lupus familiaris GN=CTSL | 35.00 0.00 |
| Ras guanine nucleotide exchange factor G OS=Dictyostelium discoideum GN=gefG | 35.00 0.00 |
| Serine/threonine-protein kinase HSL1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) GN=HSL1 | 35.00 0.00 |
| Dedicator of cytokinesis protein 3 OS=Homo sapiens GN=DOCK3 | 35.00 0.00 |
| E3 ubiquitin-protein ligase HERC2 OS=Mus musculus GN=Herc2 | 35.00 0.00 |
| Probable RNA-binding protein 19 OS=Mus musculus GN=Rbm19 | 35.00 0.00 |
| ATP-dependent DNA helicase PcrA OS=Staphylococcus epidermidis (strain ATCC 35984 / RP62A) GN=pcrA | 35.00 0.00 |
| Cytohesin-3 OS=Mus musculus GN=Cyth3 | 35.00 0.00 |
| TRINITY_sp|Q9SR:At3g101 | Heme-binding-like protein | 35.00 | 0.00 |
| TRINITY_sp|Q5ZKATP13A4 | Probable cation-tranporter | 34.90 | 0.00 |
| TRINITY_sp|Q8L9KC|KCR1 | Very-long-chain 3-oacyl-CoA hydrolase | 34.90 | 0.00 |
| TRINITY_sp|Q035:SCS7 | Ceramide very long-chain binding protein | 34.90 | 0.00 |
| TRINITY_sp|A1L2:slc29a4 | Equilibrative nucleoside transporter | 34.90 | 0.00 |
| TRINITY_sp|Q566:Them4 | Acyl-coenzyme A thiokinase | 34.90 | 0.00 |
| TRINITY_sp|P351:PTC1 | Protein phosphatase | 34.90 | 0.00 |
| TRINITY_sp|Q59V:HHT1 | Histone H3.1/H3.2 O-acetyltransferase | 34.90 | 0.00 |
| TRINITY_sp|Q281:ngdn | Neuroguidin OS=Xenopus | 34.90 | 0.00 |
| TRINITY_sp|Q041:- | Pathogenesis-related protein | 34.90 | 0.00 |
| TRINITY_sp|Q96C:RMND5B | Probable RMD5 homolog | 34.90 | 0.00 |
| TRINITY_sp|Q634:Mapk4 | Mitogen-activated protein kinase | 34.90 | 0.00 |
| TRINITY_sp|Q55F:atp5D | ATP synthase subunit | 34.90 | 0.00 |
| TRINITY_sp|Q8GY:RPN9B | 26S proteasome non-ATPase regulatory subunit | 34.90 | 0.00 |
| TRINITY_sp|Q401: | LEC14B protein | 34.90 | 0.00 |
| TRINITY_sp|Q944:SPBC660 | Uncharacterized RNA-binding protein | 34.90 | 0.00 |
| TRINITY_sp|Q8LF:ASK21 | SKP1-like protein | 34.90 | 0.00 |
| TRINITY_sp|Q9FE:RPL22C | 60S ribosomal protein | 34.90 | 0.00 |
| TRINITY_sp|Q188:AOAH | Acyloxyacyl hydrolase | 34.90 | 0.00 |
| TRINITY_sp|Q9JK:Aatf | Protein AATF OS=Mus musculus | 34.90 | 0.00 |
| TRINITY_sp|F4K2:ATG101 | Autophagy-related protein | 34.90 | 0.00 |
| TRINITY_sp|Q9P4:LYS3 | Saccharopine dehydrogenase [NADP(+), L-glutamate-forming] | 34.90 | 0.00 |
| TRINITY_sp|Q029:Atg3030 | Putative tRNA pseudouridine 3'-O-methyltransferase | 34.90 | 0.00 |
| TRINITY_sp|Q0051FAAH | Fatty-acid amidohydrolase | 34.90 | 0.00 |
| TRINITY_sp|Q2QKIC|PCS3 | Glutathione gamma-glutamylcysteine synthetase | 34.90 | 0.00 |
| TRINITY_sp|Q9P4:AGM1 | Phosphoacetylglucosaminyl transferase | 34.90 | 0.00 |
| TRINITY_sp|Q554:argS | Arginine--tRNA ligase | 34.90 | 0.00 |
| TRINITY_sp|Q9P7:mk1 | Peroxide stress-actin | 34.90 | 0.00 |
| TRINITY_sp|Q94D:PHPT1-11 | Inorganic phosphate transporter | 34.90 | 0.00 |
| TRINITY_sp|Q0D9:STAR1 | Protein STAR1 OS=Oryza sativa subsp. japonica | 34.90 | 0.00 |
| TRINITY_sp|Q94C:TIPL1-2 | Probable aquaporin | 34.90 | 0.00 |
| TRINITY_sp|B0Gl:spcs3 | Signal peptidase | 34.90 | 0.00 |
| TRINITY_sp|Q8CG:Rbm28 | RNA-binding protein | 34.90 | 0.00 |
| TRINITY_sp|P378:CBP1 | Serine carboxypeptidase | 34.90 | 0.00 |
| TRINITY_sp|Q68C:HGSNAT | Heparan-alpha-glucosaminidase | 34.90 | 0.00 |
| TRINITY_sp|Q9LD:BETAA-Al | Beta-adaptin | 34.90 | 0.00 |
| TRINITY_sp|Q6C7:PH085 | Negative regulator | 34.90 | 0.00 |
| TRINITY_sp|Q5KQ:ICMT2 | DNA (cytosine-5)-methyltransferase | 34.90 | 0.00 |
| TRINITY_sp|Q500:TKPR1 | Tetraketide alpha-pyrone reductase | 34.90 | 0.00 |
| TRINITY_sp|P546:pkbA | RAC family serine/threonine-protein kinase | 34.90 | 0.00 |
| TRINITY_sp|P004:COX5B | Cytochrome c oxidase | 34.90 | 0.00 |
| TRINITY_sp|Q8RW:CPK29 | Calcium-dependent protein kinase | 34.90 | 0.00 |
| TRINITY_sp|Q02D:urad | 2-oxo-4-hydroxy-4-carboxylic acid dehydrogenase | 34.90 | 0.00 |
| TRINITY_sp|P148:yoxD | Uncharacterized oxidoreductase | 34.90 | 0.00 |
| TRINITY_sp|Q5M9:Rrp15 | RRP15-like protein | 34.90 | 0.00 |
| TRINITY_sp|P323:Arp3 | Actin-related protein | 34.90 | 0.00 |
| TRINITY_sp|Q9XT:thb-1 | Tyramine beta-hydroxylase | 34.90 | 0.00 |
| TRINITY_sp|Q99J:Klh122 | Kelch-like protein | 34.90 | 0.00 |
| TRINITY_sp|Q92R:TKT61 | VAMP-like protein | 34.90 | 0.00 |
| TRINITY_sp|Q59:ZFAND2A | AN1-type zinc finger protein | 34.90 | 0.00 |
| TRINITY_sp|P341:fhKC | Probable serine/threonine-protein kinase | 34.90 | 0.00 |
| TRINITY_sp|Q095:C45G9.2 | Uncharacterized RNA-binding protein | 34.90 | 0.00 |
| TRINITY_sp|Q54N:Vmp1 | Vacuole membrane protein | 34.90 | 0.00 |
| TRINITY_sp|Q5F3:PTTC27 | Tetradecapeptide repeat protein | 34.90 | 0.00 |
| TRINITY_sp|Q220:pde-4 | Probable 3',5'-cyclic nucleotide 3'-phosphodiesterase | 34.90 | 0.00 |
| TRINITY_sp|Q6NM:At5g6566 | Probable sphingolipid transporter | 34.90 | 0.00 |
| Accession | Gene Name         | Description                                      | Score | E-Value |
|------------|-------------------|--------------------------------------------------|-------|---------|
| sp|P96604|YDBI_BACSU  | Serine/threonine-protein kinase TAO2 | 34.60 | 0.00   |
| sp|Q99LG4|TTC5_MOUSE | CBL-interacting protein | 34.60 | 0.00   |
| sp|Q5XIX0|DJC14_RAT  | Calcium-dependent protein kinase 4 | 34.60 | 0.00   |
| sp|Q4V7N2|NSUN2_XENLA| Transcriptional adapter ADA2b | 34.60 | 0.00   |
| sp|P19338|NUCL_HUMAN | Mitochondrial import inner membrane translocase subunit TIM50 | 34.60 | 0.00   |
| sp|Q69Q47|RAS4B_HUMAN| 0.00 | 0.00   |
| sp|Q54BM3|MCFG_DICDI| 0.00 | 0.00   |
| sp|Q54I89|RENT1_DICDI| 0.00 | 0.00   |
| sp|D2Z030|DCSG_STRLA| 0.00 | 0.00   |
| sp|Q86JJ0|TRM61_DICDI| 0.00 | 0.00   |
| sp|Q13637|RAB32_HUMAN| 0.00 | 0.00   |
| sp|Q5BLImettl21|Protein N-lsine | 34.60 | 0.00   |
| sp|Q8N33ISLC35F6|Solute carrier family| 34.60 | 0.00   |
| sp|Q9UT`tif222|Probable translation| 34.60 | 0.00   |
| sp|P621lNC51|Neuronal calcium store protein | 34.60 | 0.00   |
| sp|Q207tbcb-1|Tubulin-specific chaperone | 34.60 | 0.00   |
| sp|Q9ATfADA2B|Transcriptional activator | 34.60 | 0.00   |
| sp|Q9SKfAt2g203|NADH dehydrogenase | 34.60 | 0.00   |
| sp|Q87AIPD_1893|UPF0394 membrane protein | 34.60 | 0.00   |
| sp|Q55E2gxcB|Rac guanine nucleotide exchange factor | 34.60 | 0.00   |
| sp|Q9SJfSPP2|Probable sucrose-phosphate transporter | 34.60 | 0.00   |
| sp|A5YKHCNOT1|CCT4-NOT transcript | 34.60 | 0.00   |
| sp|Q9ZUIETL1|Protein CHROMATIN R | 34.60 | 0.00   |
| sp|Q8Z0cda5|Putative flavin binding protein | 34.60 | 0.00   |
| sp|P535Cebpz|CCAAT/enhancer-binding protein | 34.60 | 0.00   |
| sp|P109`-Retrovirus-related | 34.60 | 0.00   |
| sp|Q541fupf1|Regulator of nonsense | 34.60 | 0.00   |
| sp|Q5U3`-|UPF0769 protein C2 | 34.60 | 0.00   |
| sp|Q2Z0ddcsG|Cycloserine biosynthesis | 34.60 | 0.00   |
| sp|Q6V5znf474|Zinc finger protein | 34.60 | 0.00   |
| sp|Q91YfSL1c13a3|Solute carrier family | 34.60 | 0.00   |
| sp|A3B5CIPK28|CBL-interacting protein | 34.50 | 0.00   |
| sp|Q55Bplbb|Phospholipase B-like | 34.50 | 0.00   |
| sp|C9J7`RAS4A4B|Ras GTPase-activating protein | 34.50 | 0.00   |
| sp|Q866trmt61a|tRNA (adenosine(58)-N) | 34.50 | 0.00   |
| sp|Q4IOfTIM50|Mitochondrial import | 34.50 | 0.00   |
| sp|Q54Nwag9|Autophagy-related protein | 34.50 | 0.00   |
| sp|Q54BmcfG|Mitochondrial subunit | 34.50 | 0.00   |
| sp|Q69Q4CIPK24|CBL-interacting protein | 34.50 | 0.00   |
| sp|P623CPK4|Calcium-dependent protein | 34.50 | 0.00   |
| sp|Q6C2INOP14|Probable nucleolar protein | 34.50 | 0.00   |
| sp|Q8EPTybeY|Endoribonuclease Yb | 34.50 | 0.00   |
| sp|Q136RAB32|Ras-related protein | 34.50 | 0.00   |
| sp|Q9LVfADss3.2|Probable lipid desaturase | 34.50 | 0.00   |
| sp|A2VE4ADPGK|ADP-dependent glucokinase | 34.50 | 0.00   |
| sp|Q9VFUpf1|Regulator of nonsense | 34.50 | 0.00   |
| sp|Q9VHfInvadolly|Leishmanialysin-like | 34.50 | 0.00   |
| sp|P193`NCL|Nucleolin | 34.50 | 0.00   |
| sp|Q8W5SKIN7D|Kinesin-like protein | 34.50 | 0.00   |
| sp|Q479nsun2|tRNA (cytosine(34)-N) | 34.50 | 0.00   |
| sp|Q55Bdgg1|Diacylglycerol O-acetyltransferase | 34.50 | 0.00   |
| sp|Q5AYIpob3|FACT complex subunit | 34.50 | 0.00   |
| sp|Q5X1Dnajc14|DnaJ homolog subfamily | 34.50 | 0.00   |
| sp|Q99LTtc5|Tetratricopeptide repeat | 34.50 | 0.00   |
| sp|Q912fAbhd3|Phospholipase ABHD3 | 34.50 | 0.00   |
| sp|P966(ydb)1|UPF0118 membrane protein | 34.50 | 0.00   |
TRINITY_sp|P098:PARP1  Poly [ADP-ribose] p  34.40  0.00
TRINITY_sp|Q644:Atp7b  Copper-transporting  34.40  0.00
TRINITY_sp|P040:cdkey-24:Protein C8orf37 hom  34.40  0.00
TRINITY_sp|P519:~  G2/mitotic-specific  34.40  0.00
TRINITY_sp|P491:IVR1  Beta-fructofuranosi  34.40  0.00
TRINITY_sp|Q3SZ:BOLA3  Bola-like protein 3  34.40  0.00
TRINITY_sp|C7GO:von Willebrand fact  34.40  0.00
TRINITY_sp|P146:Pea4c  cAMP-specific 3',5'  34.40  0.00
TRINITY_sp|Q9C9:Endo2  Endonuclease 2 OS=A  34.40  0.00
TRINITY_sp|P281:pkgB  Protein kinase 2 OS  34.40  0.00
TRINITY_sp|Q6F3:SCYL2  SCYL1-like protein 2  34.40  0.00
TRINITY_sp|Q8RW:sty17  Serine/threonine-pr  34.40  0.00
TRINITY_sp|Q149:shprh  E3 ubiquitin-protein  34.40  0.00
TRINITY_sp|Q88R:Marc2  Mitochondrial amido  34.40  0.00
TRINITY_sp|Q3ZC:CFAP36  Cilia- and flagella  34.40  0.00
TRINITY_sp|Q52:TAT24  Protein S-acyltrans  34.40  0.00
TRINITY_sp|Q767:dupA  General transcripti  34.40  0.00
TRINITY_sp|Q522:os60605:Probable protein ph  34.40  0.00
TRINITY_sp|Q9P7:SPBC1711:Dipeptidyl-peptidas  34.40  0.00
TRINITY_sp|Q9UL:RNF112  RING finger protein  34.40  0.00
TRINITY_sp|Q5UP:MIMI_R5:Uncharacterized pro  34.40  0.00
TRINITY_sp|Q54C:ddx17  Probable ATP-depend  34.40  0.00
TRINITY_sp|P050:abpA  Alpha-actinin A OS=  34.40  0.00
TRINITY_sp|P418:gar2  Protein gar2 OS=Sch  34.40  0.00
TRINITY_sp|Q7Glalbkh8  Alkylated DNA repai  34.40  0.00
TRINITY_sp|Q9UI:LCMT1  Leucine carboxyl me  34.40  0.00
TRINITY_sp|Q145:TIPR3  Inositol 1,4,5-tris  34.40  0.00
TRINITY_sp|Q8VZ:At4g191:Uncharacterized zin  34.40  0.00
TRINITY_sp|Q2XV:scn4aa  Sodium channel prot  34.40  0.00
TRINITY_sp|Q8VY:NUDT21  Nudix hydrolase 21,  34.40  0.00
TRINITY_sp|Q8LH:SHL2  Probable RNA-depend  34.40  0.00
TRINITY_sp|Q758:CAPN15  Calpain-15 OS=Homo  34.40  0.00
TRINITY_sp|P731:sl11290  Uncharacterized rib  34.40  0.00
TRINITY_sp|Q9Q2:XPR1  Xenotropic and poly  34.40  0.00
TRINITY_sp|Q867:VADCK1  Uncharacterized aar  34.40  0.00
TRINITY_sp|Q54H:drkA  Probable serine/thr  34.40  0.00
TRINITY_sp|P385:TTL  Tubulin--tyrosine l  34.40  0.00
TRINITY_sp|Q0V9:dis312  DIS3-like exonuclea  34.40  0.00
TRINITY_sp|Q9L6:ACA9  Calcium-transportin  34.40  0.00
TRINITY_sp|Q246:ref(2)P  Protein ref(2)P OS=  34.40  0.00
TRINITY_sp|Q9Q9:HB1N1  Putative nitroreduc  34.40  0.00
TRINITY_sp|Q3T2:cdk14  Cyclin-dependent ki  34.40  0.00
TRINITY_sp|P227:Guclb2  Guanylate cyclase s  34.40  0.00
TRINITY_sp|Q81Z:XR1N  5'-3' exoribonuclea  34.40  0.00
TRINITY_sp|Q9BV:EMC6  ER membrane protein  34.40  0.00
TRINITY_sp|P497:aph1  Bis(5'-nucleosyl)-t  34.30  0.00
TRINITY_sp|Q6Z8:WEE1  Weel-like protein k  34.30  0.00
TRINITY_sp|B6QM:vps10  Vacuolar protein so  34.30  0.00
TRINITY_sp|Q6TB:CYP97C1  Carotene epsilon-mo  34.30  0.00
TRINITY_sp|P364:TRIM23  E3 ubiquitin-protei  34.30  0.00
TRINITY_sp|Q6X4:CIKP31  CBL-interacting pro  34.30  0.00
TRINITY_sp|Q8IS:gef1  Ras guanine nucleot  34.30  0.00
TRINITY_sp|P324:GBP2  Guanylate-binding p  34.30  0.00
TRINITY_sp|Q2K1:COPS7B  COP9 signalosome co  34.30  0.00
TRINITY_sp|Q9LE:IR3L20  Rhomboid-like prote  34.30  0.00
TRINITY_sp|P463:birA  Bifunctional ligase  34.30  0.00
| Gene ID    | Description                                      | Score | p-value |
|-----------|--------------------------------------------------|-------|---------|
| sp|Q423|CNB1 | Calcinurin subunit | 34.00 | 0.00 |
| sp|P307|GSTT1 | Glutathione S-transferase | 34.00 | 0.00 |
| sp|Q8YX|trpS | Tryptophan-tRNA ligase | 34.00 | 0.00 |
| sp|Q281|tdwd1 | Domain-containing | 34.00 | 0.00 |
| sp|Q7XJ|At3g06230 | Probable protein phosphatase | 34.00 | 0.00 |
| sp|Q8B4|htatsf1 | HIV Tat-specific factor | 34.00 | 0.00 |
| sp|Q9DC|Pbld1 | Phenazine biosynthetic | 34.00 | 0.00 |
| sp|Q7LP|CHST15 | Carbohydrate sulfotransferase | 34.00 | 0.00 |
| sp|Q434|KCAB3 | Voltage-gated potassium channel | 34.00 | 0.00 |
| sp|Q54B|DDB_G02 | Ankyrin repeat, bro | 34.00 | 0.00 |
| sp|Q025|Mgat3 | Beta-1,4-mannosyl-galactosyltransferase | 34.00 | 0.00 |
| sp|Q4UK|hspC2 | Small heat shock protein | 34.00 | 0.00 |
| sp|Q08B|pm20d1 | N-fatty-acyl-amino acid synthase/hydrolase | 34.00 | 0.00 |
| sp|Q7KZ|ISND1 | Staphylococcal nucleoside | 34.00 | 0.00 |
| sp|Q145|ITPR2 | Inositol 1,4,5-trisphosphate receptor | 34.00 | 0.00 |
| sp|Q557|s110182 | Uncharacterized ABC transporter | 34.00 | 0.00 |
| sp|P813|l-amino-acid oxidase | 34.00 | 0.00 |
| sp|Q54Y|dhkB | Hybrid signal transducer | 34.00 | 0.00 |
| sp|P043|pol | Retrovirus-related | 34.00 | 0.00 |
| sp|Q631|Abcc2 | Canalicular multiprotein | 34.00 | 0.00 |
| sp|Q9SH|CALS7 | Callose synthase 7 | 34.00 | 0.00 |
| sp|Q3S2|TTLL9 | Probable tubulin | 34.00 | 0.00 |
| sp|Q22|rho-1 | Ras-like GTP-binding protein | 33.90 | 0.00 |
| sp|Q74|htl | Fibroblast growth factor | 33.90 | 0.00 |
| sp|Q7PC|ANR | Anthocyanidin reductase | 33.90 | 0.00 |
| sp|Q901|cds1 | Serine/threonine-protein kinase | 33.90 | 0.00 |
| sp|P583|arcB | Aerobic respiration factor | 33.90 | 0.00 |
| sp|P237|Si | Sucrase-isomaltase, | 33.90 | 0.00 |
| sp|P369|RpiII15 | DNA-directed RNA polymerase | 33.90 | 0.00 |
| sp|A9LL|RRP6L3 | Protein RRP6-like 3 | 33.90 | 0.00 |
| sp|Q4WV|cafl7 | Putative transferases | 33.90 | 0.00 |
| sp|P488|cht60 | Beta-hexosaminidase | 33.90 | 0.00 |
| sp|Q9Y7|SPBC2A9 | Phosducin-like protein | 33.90 | 0.00 |
| sp|B0F9|GC6 | Golgin candidate | 33.90 | 0.00 |
| sp|Q54B|mcfG | Mitochondrial subunit | 33.90 | 0.00 |
| sp|Q6O8|siR | Dipeptidase | 33.90 | 0.00 |
| sp|Q55D|mosip | Nitric oxide synthase | 33.90 | 0.00 |
| sp|Q2M5|RGS21 | Regulator of G-protein | 33.90 | 0.00 |
| sp|Q5E9|DUSP11 | RNA/RNP complex | 33.90 | 0.00 |
| sp|A4FV|METTL21 | Protein-lysine methyltransferase | 33.90 | 0.00 |
| sp|Q5V3|ABHD17B | Protein ABHD17B | 33.90 | 0.00 |
| sp|Q9S7|KIP7N | Kinesin-like protein | 33.90 | 0.00 |
| sp|Q52L|serpinb1Leukocyte elastase | 33.90 | 0.00 |
| sp|P727|slr0245 | Uncharacterized protein | 33.90 | 0.00 |
| sp|P872|mdj1 | DNAJ homolog 1, mitotic | 33.90 | 0.00 |
| sp|Q5F3|UTP15 | U3 small nucleolar | 33.90 | 0.00 |
| sp|Q4P6|COF1 | Cofilin | 33.90 | 0.00 |
| sp|Q5XT|PNPLA8 | Calcium-independent phospholipase | 33.90 | 0.00 |
| sp|Q6FN|STE20 | Serine/threonine-protein kinase | 33.90 | 0.00 |
| sp|Q8Q2|Tat | Tyrosine aminotransferase | 33.90 | 0.00 |
| sp|Q67U|Os02g001 | Probable protein phosphatase | 33.90 | 0.00 |
| sp|P604|PTEN | Phosphatidylinositol 3-kinase | 33.90 | 0.00 |
| sp|Q8LF|At1g19330 | Methyltransferase | 33.90 | 0.00 |
| sp|P426|FRK | Tyrosine-protein kinase | 33.90 | 0.00 |
| sp|Q54F|gacJJ | Rho GTPase-activating protein | 33.90 | 0.00 |
| sp|Q9C5|MKP1 | Protein-tyrosine-phosphatase | 33.90 | 0.00 |
| Gene ID                        | Description                                      | Expression | Q-value |
|-------------------------------|--------------------------------------------------|------------|---------|
| TRINITY_sp|P0C8\|CCRP1 | Probable serine/threonine-protein kinase CCRP1 | 33.90      | 0.00    |
| TRINITY_sp|O806\|PAT02 | Probable protein S-domain-containing protein | 33.90      | 0.00    |
| TRINITY_sp|P436\|EC | DnaJ protein homolog | 33.90      | 0.00    |
| TRINITY_sp|Q6L7\|kanJ | Kanamycin B dioxygenase | 33.90      | 0.00    |
| TRINITY_sp|Q1KK\|mfsd5 | Molybdate-anion transport protein | 33.90      | 0.00    |
| TRINITY_sp|A1C6\|manF | Mannan endo-1,4-beta-D-mannosidase | 33.90      | 0.00    |
| TRINITY_sp|Q6NV\|rhot1a | Mitochondrial Rho GTPase | 33.90      | 0.00    |
| TRINITY_sp|Q8WN\|KBKAP | Elongator complex protein | 33.90      | 0.00    |
| TRINITY_sp|Q75S\|IP1 | Spindle assembly checkpoint protein | 33.90      | 0.00    |
| TRINITY_sp|Q54T\|gefP | Ras guanine nucleotide exchange protein | 33.90      | 0.00    |
| TRINITY_sp|Q56\|them4 | Acyl-coenzyme A thioesterase | 33.90      | 0.00    |
| TRINITY_sp|P827\|PPD5 | PsbP domain-containing protein | 33.90      | 0.00    |
| TRINITY_sp|Q3S\|LUC7L3 | Luc7-like protein 3 | 33.90      | 0.00    |
| TRINITY_sp|A8JA\|CFAP43 | Cilia- and flagella-associated protein | 33.90      | 0.00    |
| TRINITY_sp|Q5ZM\|FAR1 | Fatty acyl-CoA reductase | 33.90      | 0.00    |
| TRINITY_sp|Q54L\|DDG02 | Protein KRTCAP2 homolog | 33.90      | 0.00    |
| TRINITY_sp|E0X9\|At3g635 | Zinc finger CCHC domain-containing protein | 33.90      | 0.00    |
| TRINITY_sp|F4IA\|LPXC1 | Probable UDP-3′-O-acetylmuramyl-L-alanine-Lactamase | 33.90      | 0.00    |
| TRINITY_sp|Q9ES\|Nplc4 | Nuclear protein localization | 33.90      | 0.00    |
| TRINITY_sp|Q1K\|FZL | Probable transmembrane protein | 33.90      | 0.00    |
| TRINITY_sp|Q5T3\|OTUD3 | OTU domain-containing protein | 33.90      | 0.00    |
| TRINITY_sp|Q9M2\|SDR1 | (+)-neomenthol dehydrogenase | 33.90      | 0.00    |
| TRINITY_sp|Q2I2\|COPB1 | Coatamer subunit beta | 33.90      | 0.00    |
| TRINITY_sp|Q9PB\|infC | Translation initiation factor | 33.90      | 0.00    |
| TRINITY_sp|Q6GD\|mpv1712 | Mpv17-like protein | 33.90      | 0.00    |
| TRINITY_sp|Q9M0\|LAF1 | Transcription factor | 33.90      | 0.00    |
| TRINITY_sp|Q8MY\|DDG02 | Probable serine/threonine-protein kinase | 33.90      | 0.00    |
| TRINITY_sp|O603\|TBC1D12 | TBC1 domain family | 33.90      | 0.00    |
| TRINITY_sp|Q5SR\|ZHT6 | Box C/D snoRNA binding protein | 33.90      | 0.00    |
| TRINITY_sp|H2QL\|PDE9A | High affinity cGMP-specific phosphodiesterase | 33.90      | 0.00    |
| TRINITY_sp|P428\|ATPK1 | Serine/threonine-protein kinase | 33.90      | 0.00    |
| TRINITY_sp|Q9FL\|DEGP9 | Protease D-like 9 | 33.90      | 0.00    |
| TRINITY_sp|Q13\|ercc3 | Probable DNA repair protein | 33.90      | 0.00    |
| TRINITY_sp|P736\|syj1 | Inositol-1,4,5-trisphosphate receptor | 33.80      | 0.00    |
| TRINITY_sp|Q9C5\|RPF12 | 14-3-3-like protein | 33.80      | 0.00    |
| TRINITY_sp|Q8VI\|Abcc2 | Canaliculal multidrug resistance protein | 33.80      | 0.00    |
| TRINITY_sp|P61\|P6 | Lipase OS-Rhizopus | 33.80      | 0.00    |
| TRINITY_sp|Q5MC\|pepA | Probable cytosol amino acid transporter | 33.80      | 0.00    |
| TRINITY_sp|O941\|SNF1 | Carbon catabolite-repressible protein | 33.80      | 0.00    |
| TRINITY_sp|P598\|SPCC965 | Probable cytoskeleton protein | 33.80      | 0.00    |
| TRINITY_sp|Q9H1\|NAPB | Beta-soluble NSF-attachment protein | 33.80      | 0.00    |
| TRINITY_sp|Q9P3\|ptr2 | Probable peptide transferase | 33.80      | 0.00    |
| TRINITY_sp|A7SG\|psmg2 | Proteasome assembly factor | 33.80      | 0.00    |
| TRINITY_sp|D9N1\| - | Inward rectifier potassium channel | 33.80      | 0.00    |
| TRINITY_sp|P707\|Atp7a | Copper-transporting ATPase | 33.80      | 0.00    |
| TRINITY_sp|Q9W0\|Cyp4d20 | Probable cytochrome P450 | 33.80      | 0.00    |
| TRINITY_sp|Q9U9\|SPCC23B | CRAL-TRIO domain-containing protein | 33.80      | 0.00    |
| TRINITY_sp|Q6NX\|dennd5b | DENN domain-containing protein | 33.80      | 0.00    |
| TRINITY_sp|Q9UR\|Tf2-11 | Transposon Tf2-11 protein | 33.80      | 0.00    |
| TRINITY_sp|Q146\|TTL4 | Tubulin polyglutamylation factor | 33.80      | 0.00    |
| TRINITY_sp|P345\|HSP1 | Heat shock factor D | 33.80      | 0.00    |
| TRINITY_sp|Q9SB\|At4g247 | Manganese-dependent transporter | 33.80      | 0.00    |
| TRINITY_sp|Q9UT\|SPAC8F1 | Putative ribosome binding factor | 33.80      | 0.00    |
| TRINITY_sp|Q9Y2\|PLAA | Phospholipase A-2-a | 33.80      | 0.00    |
| TRINITY_sp|Q2IM\|proB | Glutamate 5-kinase | 33.80      | 0.00    |
| TRINITY_sp|Q9FH\|DTX16 | Protein DETOXIFICAT | 33.80      | 0.00    |
| TRINITY_sp|O745tSPCC970. Uncharacterized ino | 33.70 | 0.00 |
| TRINITY_sp|Q86KDDB_G02. Probable serine/thr | 33.70 | 0.00 |
| TRINITY_sp|Q8C6Hrrc9. Leucine-rich repeat | 33.70 | 0.00 |
| TRINITY_sp|Q9SD3At3g514. Probable protein ph | 33.70 | 0.00 |
| TRINITY_sp|Q045tCYP6B1. Cytochrome P450 6B1 | 33.70 | 0.00 |
| TRINITY_sp|B4K8s1lx1. Structure-specific | 33.70 | 0.00 |
| TRINITY_sp|Q9Z2tABCG7. ABC transporter G f | 33.70 | 0.00 |
| TRINITY_sp|Q9FXtFUT12. Putative fucosyltra | 33.70 | 0.00 |
| TRINITY_sp|Q8IVtLOXHDI. Lipoygenase homolo | 33.70 | 0.00 |
| TRINITY_sp|A9A31riMN. Ribosomal RNA large | 33.70 | 0.00 |
| TRINITY_sp|P107tPAM. Peptidyl-glycine al | 33.70 | 0.00 |
| TRINITY_sp|P127tRSP3. Flagellar radial sp | 33.70 | 0.00 |
| TRINITY_sp|Q969tTRIM63. E3 ubiquitin-protei | 33.70 | 0.00 |
| TRINITY_sp|Q2KNtSPECC1L. Cytospin-A OS=Canis | 33.70 | 0.00 |
| TRINITY_sp|Q756tTIP4L. TIP41-like protein | 33.70 | 0.00 |
| TRINITY_sp|Q9FItAt5g435: Putative SWI/SNF-re | 33.70 | 0.00 |
| TRINITY_sp|Q6AXtIca12-tDDB1- and CUL4-asso | 33.70 | 0.00 |
| TRINITY_sp|O042tPXN. Peroxisomal nicotin | 33.70 | 0.00 |
| TRINITY_sp|Q9H4tDEF6. Differentially expr | 33.70 | 0.00 |
| TRINITY_sp|Q9C6tTRO. Protein TRAUCO OS=A | 33.70 | 0.00 |
| TRINITY_sp|Q5XMhthunk-a. Hormonally up-regul | 33.70 | 0.00 |
| TRINITY_sp|Q002tme10. Tyrosinase OS=Asper | 33.70 | 0.00 |
| TRINITY_sp|A5PNtNAIFM2. Apoptosis-inducing | 33.70 | 0.00 |
| TRINITY_sp|Q7X3tFRK2. Fructokinase-2 OS=S | 33.70 | 0.00 |
| TRINITY_sp|G5EDIceeh-2. Epoxide hydrolase 2 | 33.70 | 0.00 |
| TRINITY_sp|Q5UQtMIMI_R5. Probable ubiquitin- | 33.70 | 0.00 |
| TRINITY_sp|Q54JtabcC3. ABC transporter C f | 33.70 | 0.00 |
| TRINITY_sp|Q86LtgacHH. Rho GTPase-activati | 33.70 | 0.00 |
| TRINITY_sp|Q6X4tCIPK31. CBL-interacting pro | 33.70 | 0.00 |
| TRINITY_sp|Q5SNtOs01g06. Probable protein pha | 33.70 | 0.00 |
| TRINITY_sp|Q8LPtAt3g199tE3 ubiquitin-protei | 33.70 | 0.00 |
| TRINITY_sp|O670tftsH. ATP-dependent zinc | 33.70 | 0.00 |
| TRINITY_sp|Q6AXtIca11. IQ and AAA domain-c | 33.70 | 0.00 |
| TRINITY_sp|Q8O4tYOR059C. Putative lipase YOR | 33.70 | 0.00 |
| TRINITY_sp|Q9FMtHHIR1. Hypersensitive-induc | 33.70 | 0.00 |
| TRINITY_sp|Q9DDtRab13. Ras-related protein | 33.70 | 0.00 |
| TRINITY_sp|Q96NtNAIFM3. Apoptosis-inducing | 33.70 | 0.00 |
| TRINITY_sp|Q54Mtccdc20. Anaphase-promoting | 33.70 | 0.00 |
| TRINITY_sp|Q9VJtPde11. Dual 3',5'-cyclic-A | 33.70 | 0.00 |
| TRINITY_sp|Q8RWtCLT3. Protein CLT3, chlor | 33.70 | 0.00 |
| TRINITY_sp|Q54Ttddx24. ATP-dependent RNA h | 33.70 | 0.00 |
| TRINITY_sp|Q05BtTRMT11. tRNA (guanine(10))-N | 33.70 | 0.00 |
| TRINITY_sp|Q758tCAPN15. Calpain-15 OS=Homo | 33.70 | 0.00 |
| TRINITY_sp|Q755tCIP1L. Spindle assembly ch | 33.70 | 0.00 |
| TRINITY_sp|Q96FtELMOD3. ELMO domain-contain | 33.70 | 0.00 |
| TRINITY_sp|D7UQtaur. Aurora kinase OS=Pa | 33.70 | 0.00 |
| TRINITY_sp|Q186tpde-1. Probable 3',5'-cycl | 33.70 | 0.00 |
| TRINITY_sp|Q3E6tCpNIFS3. Probable L-cysteine | 33.70 | 0.00 |
| TRINITY_sp|Q80YtElac2. Zinc phosphodieter | 33.70 | 0.00 |
| TRINITY_sp|Q100tseh1. Nucleoporin seh1 OS | 33.60 | 0.00 |
| TRINITY_sp|Q61Nttollip-tToll-interacting pr | 33.60 | 0.00 |
| TRINITY_sp|P253tm1kA. Myosin light chain | 33.60 | 0.00 |
| TRINITY_sp|Q9DA-t. Uncharacterized protein | 33.60 | 0.00 |
| TRINITY_sp|Q5ZMtSEPT2. Septin-2 OS=Gallus | 33.60 | 0.00 |
| TRINITY_sp|P47OtPRY1. Protein PRY1 OS=Sac | 33.60 | 0.00 |
| TRINITY_sp|Q2LVImsbA. Lipid A export ATP- | 33.60 | 0.00 |
| Gene Symbol  | Description                                     | Accession | BLAST Score |
|-------------|-------------------------------------------------|-----------|-------------|
| Ceramide synthase 2 | OS=Homo sapiens | CERS2    | 33.50       |
| Serine/threonine-protein kinase STY8 | OS=Arabidopsis thaliana | STY8     | 33.50       |
| Acyloxyacyl hydrolase | OS=Homo sapiens | AOAH    | 33.50       |
| ER membrane protein complex subunit 2-A | OS=Xenopus laevis | EMC2-a  | 33.50       |
| GrpE protein homolog, mitochondrial | OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NRRL Y-1140 / WM37) | MGE1    | 33.50       |
| Hematopoietic prostaglandin D synthase | OS=Gallus gallus | HPGDS   | 33.50       |
| Multidrug resistance-associated protein 1 | OS=Homo sapiens | ABCC1   | 33.50       |
| Signal recognition particle subunit SRP68 | OS=Drosophila melanogaster | SRP68   | 33.50       |
| 3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase | OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) | MT1137  | 33.50       |
| CWF19-like protein 2 | OS=Homo sapiens | CWF19L2  | 33.50       |
| EF-hand domain-containing protein 1 | OS=Mus musculus | Efhc1   | 33.50       |
| D-alanyl-D-alanine carboxypeptidase DacB | OS=Bacillus subtilis (strain 168) | DACB    | 33.50       |
| Autoinducer 2 sensor kinase/phosphatase LuxQ | OS=Vibrio vulnificus (strain YJ016) | LuxQ    | 33.50       |
| E3 ubiquitin-protein ligase dbl4 | OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) | Dbl4    | 33.50       |
| Cinnamoyl-CoA reductase 1 | OS=Arabidopsis thaliana | CCR1    | 33.50       |
| LON peptidase N-terminal domain and RING finger protein 2 | OS=Homo sapiens | LONRF2  | 33.50       |
| Purple acid phosphatase 21 | OS=Arabidopsis thaliana | PAP21   | 33.50       |
| Mitochondrial import inner membrane translocase subunit TIM50 | OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) | TIM50   | 33.50       |
| Sodium channel protein 1 brain | OS=Heterololigo bleekeri | PIP5K3  | 33.50       |
| 2',5'-phosphodiesterase 12 | OS=Bos taurus | PDE12   | 33.50       |
| Genomic Identity | Gene Name | Function | Expression | Fold Change |
|------------------|-----------|----------|------------|-------------|
| TRINITY_sp|Q96K1|CNDP1 | Beta-Ala-His dipeptidase | 33.40 | 0.00 |
| TRINITY_sp|Q8TA3|SMARCC2 | SWI/SNF complex subunit | 33.40 | 0.00 |
| TRINITY_sp|Q137|osm1 | Fumarate reductase | 33.40 | 0.00 |
| TRINITY_sp|F4IRF5|SAD2 | Importin beta-like | 33.40 | 0.00 |
| TRINITY_sp|Q9S7|PNP2 | Polyribonucleotide | 33.40 | 0.00 |
| TRINITY_sp|Q5F5|osbI | Oysterol-binding protein | 33.40 | 0.00 |
| TRINITY_sp|Q8W4|AAE15 | Long-chain-fatty-acid-CoA ligase | 33.40 | 0.00 |
| TRINITY_sp|O840|ttcA | ADP,ATP carrier protein | 33.40 | 0.00 |
| TRINITY_sp|Q6Z6|Os02g020| Aminopeptidase M1-A | 33.40 | 0.00 |
| TRINITY_sp|Q54S|DDB_G02| Protein PIEZO homolog | 33.40 | 0.00 |
| TRINITY_sp|O0041|IP05 | Importin-5 OS=Homo | 33.40 | 0.00 |
| TRINITY_sp|P463|csbC | Probable metabolite | 33.40 | 0.00 |
| TRINITY_sp|A2XM|ARP7 | Actin-related protein | 33.40 | 0.00 |
| TRINITY_sp|O158|clua | Clustered mitochondria | 33.40 | 0.00 |
| TRINITY_sp|Q8WM|PLA2G15 | Group XV phospholipase | 33.30 | 0.00 |
| TRINITY_sp|Q8L9|ATL2 | RING-H2 finger protein | 33.30 | 0.00 |
| TRINITY_sp|P378|CBP1 | Serine carboxypeptidase | 33.30 | 0.00 |
| TRINITY_sp|P1271| | Actin, cytoplasmic | 33.30 | 0.00 |
| TRINITY_sp|Q8IB|CPK4 | Calcium-dependent protein kinase | 33.30 | 0.00 |
| TRINITY_sp|Q54R|DDB_G02| Probable tyrosine-protein kinase | 33.30 | 0.00 |
| TRINITY_sp|Q74| | Ribonuclease OS=Aer | 33.30 | 0.00 |
| TRINITY_sp|Q952|scp97 | Spindle pole body protein | 33.30 | 0.00 |
| TRINITY_sp|O154|ABCC5 | Multidrug resistance protein | 33.30 | 0.00 |
| TRINITY_sp|P399|GEA2 | ARF guanine-nucleotide exchange factor | 33.30 | 0.00 |
| TRINITY_sp|Q869|etnkA | Probable ethanolamineamine transporter | 33.30 | 0.00 |
| TRINITY_sp|Q5A|RSLN1 | Histidine protein kinase | 33.30 | 0.00 |
| TRINITY_sp|P187|est | Esterase OS=Aceae | 33.30 | 0.00 |
| TRINITY_sp|Q933|MANBA | Beta-mannosidase OS=Homo | 33.30 | 0.00 |
| TRINITY_sp|P093|strG | Streptomyacin biosynthase | 33.30 | 0.00 |
| TRINITY_sp|Q552|DDB_G02| Putative ZDHHC-type protein | 33.30 | 0.00 |
| TRINITY_sp|P116|NHP6B | Non-histone chromatin protein | 33.30 | 0.00 |
| TRINITY_sp|Q5YI|dhkB | Hybrid signal transducer | 33.30 | 0.00 |
| TRINITY_sp|Q5JL|CIPK12 | CBL-interacting protein kinase | 33.30 | 0.00 |
| TRINITY_sp|Q543|abcC3 | ABC transporter C family member | 33.30 | 0.00 |
| TRINITY_sp|Q89W|norM | Probable multidrug resistance protein | 33.30 | 0.00 |
| TRINITY_sp|Q9M2|At3g61320 | UPF0187 protein | 33.30 | 0.00 |
| TRINITY_sp|P201| | Uncharacterized protein | 33.30 | 0.00 |
| TRINITY_sp|Q87A|infC | Translation initiation factor | 33.30 | 0.00 |
| TRINITY_sp|Q045|Smpd1 | Sphingomyelin phospholipase | 33.30 | 0.00 |
| TRINITY_sp|P212|CCA1 | CCA tRNA nucleotidyltransferase | 33.30 | 0.00 |
| TRINITY_sp|Q54T|gacY | Rho GTPase-activating protein | 33.30 | 0.00 |
| TRINITY_sp|Q8S8|PUB34 | U-box domain-containing protein | 33.30 | 0.00 |
| TRINITY_sp|Q2KH|USP2 | Ubiquitin carboxyl-terminal hydrolase | 33.30 | 0.00 |
| TRINITY_sp|Q383|37 | Long tail fiber protein | 33.30 | 0.00 |
| TRINITY_sp|O430|mot1 | Probable helicase | 33.30 | 0.00 |
| TRINITY_sp|Q6T4|WC2 | Pre-mRNA-splicing factor | 33.30 | 0.00 |
| TRINITY_sp|F793|RGS20 | Regulator of G-protein signaling | 33.30 | 0.00 |
| TRINITY_sp|Q9W4|dnc | cAMP-specific 3',5' phosphodiesterase | 33.30 | 0.00 |
| TRINITY_sp|Q5M8| | UPF0415 protein | 33.30 | 0.00 |
| TRINITY_sp|Q637|Map3k12 | Mitogen-activated protein kinase | 33.30 | 0.00 |
| TRINITY_sp|A6ZU|ATG1 | Serine/threonine-protein kinase | 33.30 | 0.00 |
| TRINITY_sp|Q146|ITPR1 | Inositol 1,4,5-trisphosphate receptor | 33.30 | 0.00 |
| TRINITY_sp|Q5F5|osbI | Oysterol-binding protein | 33.30 | 0.00 |
| TRINITY_sp|Q9UR|nrf1 | Vacuolar transporter | 33.30 | 0.00 |
| TRINITY_sp|Q6NX|Retbtl | RCC1 and BTB domain protein | 33.30 | 0.00 |
| TRINITY_sp|Q95Y|YpefA | Penta-EF hand domain protein | 33.30 | 0.00 |
| Protein Name | Function | Sequence Coverage | Expression Level |
|--------------|----------|-----------------|-----------------|
| Adenylate cyclase | OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=cyr1 PE=1 SV=1 | 33.30 | 0.00 |
| Deoxyribodipyrimidine photo-lyase | OS=Agrobacterium fabrum (strain C58 / ATCC 33970) GN=phrA PE=1 SV=1 | 33.30 | 0.00 |
| Protein MEI2-like 2 | OS=Dictyostelium discoideum GN=culB PE=2 SV=1 | 33.30 | 0.00 |
| Ras-related protein RHN1 | OS=Nicotiana plumbaginifolia GN=RHN1 PE=2 SV=1 | 33.30 | 0.00 |
| Carbonic anhydrase | OS=Klebsiella pneumoniae GN=cah PE=3 SV=1 | 33.30 | 0.00 |
| WD repeat-containing protein 27 | OS=Homo sapiens GN=WDR27 PE=1 SV=3 | 33.30 | 0.00 |
| WD repeat-containing protein 55 | OS=Rattus norvegicus GN=Wdr55 PE=2 SV=1 | 33.30 | 0.00 |
| Heat shock factor protein | OS=Xenopus laevis GN=hsf1 PE=2 SV=1 | 33.30 | 0.00 |
| Proven-specific protein SF21 | OS=Helianthus annuus GN=SF21 PE=2 SV=1 | 33.30 | 0.00 |
| Protein dcd1B | OS=Dictyostelium discoideum GN=dcd1B PE=2 SV=1 | 33.30 | 0.00 |
| Kinesin-like protein KIF27 | OS=Homo sapiens GN=KIF27 PE=2 SV=1 | 33.30 | 0.00 |
| Conserved oligomeric Golgi complex subunit 4 | OS=Mus musculus GN=Cog4 PE=1 SV=1 | 33.30 | 0.00 |
| 26S proteasome non-ATPase regulatory subunit 13 | OS=Dictyostelium discoideum GN=psmD13 PE=2 SV=1 | 33.30 | 0.00 |
| TVP38/TMEM64 family membrane protein slr0305 | OS=Synechocystis sp. (strain PCC 6803 / Kazusa) GN=slr0305 PE=3 SV=1 | 33.30 | 0.00 |
| Lysophospholipid acyltransferase | OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ale1 PE=1 SV=1 | 33.30 | 0.00 |
| Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1A | OS=Bos taurus GN=PDE1A PE=1 SV=3 | 33.30 | 0.00 |
| Geranylgeranyl diphosphate synthase | OS=Methanosarcina mazei (strain ATCC BAA-159 / DSM 3647 / Goe1 / Go1 / JCM 11833 / OCM 88) GN=MM_1767 PE=3 SV=1 | 33.30 | 0.00 |
| Monothiol glutaredoxin-S11 | OS=Oryza sativa subsp. japonica GN=GRXS11 PE=2 SV=2 | 33.30 | 0.00 |
| Glyoxylate reductase | OS=Thermococcus gammatolerans (strain DSM 15229 / JCM 11827 / EJ3) GN=gyaR PE=3 SV=1 | 33.30 | 0.00 |
| Serine/threonine-protein kinase ATG1 | OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) GN=ATG1 PE=3 SV=1 | 33.30 | 0.00 |
| Glyoxalase 3 | OS=Candida albicans (strain SC5314 / ATCC MYA-2876) GN=GLX3 PE=1 SV=1 | 33.30 | 0.00 |
| Protein MEI2-like 2 | OS=Oryza sativa subsp. japonica GN=ML2 PE=2 SV=1 | 33.30 | 0.00 |
| Poly [ADP-ribose] polymerase 1 | OS=Cricetulus griseus GN=PARP1 PE=2 SV=3 | 33.30 | 0.00 |
| Transmembrane 9 superfamily member 3 | OS=Arabidopsis thaliana GN=TMN3 PE=2 SV=1 | 33.30 | 0.00 |
| Calcineurin subunit B type 2 | OS=Dictyostelium discoideum GN=cnbB PE=3 SV=1 | 33.30 | 0.00 |
| Serine/threonine-protein kinase STY17 | OS=Arabidopsis thaliana GN=STY17 PE=1 SV=1 | 33.30 | 0.00 |
| 5'-AMP-activated protein kinase subunit gamma | OS=Dictyostelium discoideum GN=prkag PE=3 SV=3 | 33.30 | 0.00 |
| Poly [ADP-ribose] polymerase 1 | OS=Homo sapiens GN=PARP1 PE=1 SV=4 | 33.30 | 0.00 |
| Small G protein signaling modulator 3 homolog | OS=Xenopus laevis GN=sgsm3 PE=2 SV=1 | 33.30 | 0.00 |
| Protein CHROMATIN REMODELING 19 | OS=Arabidopsis thaliana GN=ETL1 PE=1 SV=1 | 33.30 | 0.00 |
| Guanylate cyclase soluble subunit beta-2 | OS=Rattus norvegicus GN=Gucy1b2 PE=2 SV=1 | 33.30 | 0.00 |
| Serine/threonine-protein kinase CHKA | OS=Arabidopsis thaliana GN=CHKA PE=1 SV=1 | 33.30 | 0.00 |
| Poly [ADP-ribose] polymerase 1 | OS=Homo sapiens GN=PARP1 PE=1 SV=4 | 33.30 | 0.00 |
| Accession | Name | Function | Species | Gene | Protein | Start | End |
|-----------|------|----------|---------|------|---------|-------|-----|
| TRINITY_sp|Q5EBInt5c2 | Cytosolic purine 5' |  | | | | |
| TRINITY_sp|Q8CGAAbcc1 | Multidrug resistance |  | | | | |
| TRINITY_sp|Q9Y41SPEF1 | Sperm flagellar protein |  | | | | |
| TRINITY_sp|A7HQ'pyrD | Dihydroorotate dehydrogenase |  | | | | |
| TRINITY_sp|Q4083EMB8 | Embryogenesis-associated |  | | | | |
| TRINITY_sp|Q5TIFWA5B1 | von Willebrand factor |  | | | | |
| TRINITY_sp|Q076ISPAG1 | Sperm-associated protein |  | | | | |
| TRINITY_sp|Q3SEHJclle | Caltractin ICLle |  | | | | |
| TRINITY_sp|Q54D1abcA9 | ABC transporter A family |  | | | | |
| TRINITY_sp|Q491Reg-2 | Rhythmically expressed |  | | | | |
| TRINITY_sp|Q54P=xpo5 | Exportin-5 |  | | | | |
| TRINITY_sp|Q54C3sgmB | Sphingomyelin phosphodiesterase |  | | | | |
| TRINITY_sp|Q55C2gdt2 | Probable serine/threonine-protein kinase |  | | | | |
| TRINITY_sp|Q9LT1BBR | E3 ubiquitin ligase |  | | | | |
| TRINITY_sp|Q9ZR1GSTT1 | Glutathione S-transferase |  | | | | |
| TRINITY_sp|Q1ZXIDDB_G02 | PH domain-containing protein |  | | | | |
| TRINITY_sp|Q9W01NaC60E | Sodium channel protein |  | | | | |
| TRINITY_sp|Q92F/radA | DNA repair protein |  | | | | |
| TRINITY_sp|F1533rapl | DNA-directed RNA polymerase |  | | | | |
| TRINITY_sp|Q94AKSTR6 | Rhodanese-like domain protein |  | | | | |
| TRINITY_sp|Q5283bgaM | Beta-galactosidase |  | | | | |
| TRINITY_sp|C05VRVE5 | Protein REVEILLE |  | | | | |
| TRINITY_sp|Q9466SPBC405 | Uncharacterized protein |  | | | | |
| TRINITY_sp|Q9571HERC2 | E3 ubiquitin-protein ligase |  | | | | |
| TRINITY_sp|Q3UFNoml | Nucleolar MIF4G domain protein |  | | | | |
| TRINITY_sp|Q9X2fabG | 3-oxoacyl-acyl-CoA synthetase |  | | | | |
| TRINITY_sp|G4SWerg | Delta(14)-sterol reductase |  | | | | |
| TRINITY_sp|B1A2Otud3 | OTU domain-containing protein |  | | | | |
| TRINITY_sp|Q9FJ1FKBP65 | Peptidyl-prolyl cis-trans isomerase |  | | | | |
| TRINITY_sp|Q7TNAbca7 | ATP-binding cassette protein |  | | | | |
| TRINITY_sp|Q9VRlHERC2 | Probable E3 ubiquitin-protein ligase |  | | | | |
| TRINITY_sp|F706Siiae | Sialate O-acetylectin |  | | | | |
| TRINITY_sp|Q54PKgcsA | Glutamate-cysteine ligase |  | | | | |
| TRINITY_sp|Q6N2nci1 | Nicotinamide adenine dinucleotide |  | | | | |
| TRINITY_sp|Q1L81rnf19b | E3 ubiquitin-protein ligase |  | | | | |
| TRINITY_sp|P2422yjiA | Uncharacterized gene |  | | | | |
| TRINITY_sp|Q9DBWcyp4v | Cytochrome P450 4V2 |  | | | | |
| TRINITY_sp|Q4083EMB8 | Embryogenesis-associated protein |  | | | | |
| TRINITY_sp|Q9DBWosbp13 | Oxysterol-binding protein |  | | | | |
| TRINITY_sp|Q994FPPDN5 | Prefoldin subunit 5 |  | | | | |
| TRINITY_sp|Q8RXBCRA1 | Protein BREAST CANCER |  | | | | |
| TRINITY_sp|Q55FKtipC | Putative vacuolar protein |  | | | | |
| TRINITY_sp|Q053WPc3 | Protein white |  | | | | |
| TRINITY_sp|Q6P23PNCK | Calcium/calmodulin-regulated protein |  | | | | |
| TRINITY_sp|Q085SCYCU4 | Cyclin-U4-like |  | | | | |
| TRINITY_sp|Q147TTTP1 | Tripeptidyl-peptidase |  | | | | |
| TRINITY_sp|Q9SHAtg379 | Ribosome biogenesis regulator |  | | | | |
| TRINITY_sp|Q547MhycB | Myb-like protein C |  | | | | |
| TRINITY_sp|Q6DGaatg4b | Cysteine protease A |  | | | | |
| TRINITY_sp|Q91WPnlp1a3 | Patatin-like phospholipase |  | | | | |
| TRINITY_sp|Q9966MGL | Monoglyceride lipase |  | | | | |
| TRINITY_sp|Q5483Gucy1b3 | Guanylate cyclase |  | | | | |
| TRINITY_sp|Q6J1Usip19 | Ubiquitin carboxyl-terminal hydrolase |  | | | | |
| TRINITY_sp|Q94KIVPS52 | Vacuolar protein sorting |  | | | | |
| ENSEMBL_ID | Gene Name | Description | Orthology | Z-Score | E-Value |
|------------|-----------|-------------|-----------|---------|---------|
| TRINITY_sp| O144: ssr2 | SWI/SNF and RSC complex | OS=Schizosaccharomyces pombe | 33.10 | 0.00 |
| TRINITY_sp| Q9Y4I: VPRBP | Protein VPRBP | OS=Homo sapiens | 33.10 | 0.00 |
| TRINITY_sp| Q93WAt: gacS | Sensor protein GacS | OS=Mus musculus | 33.10 | 0.00 |
| TRINITY_sp| Q9FHI: Dbp80 | DEAD-box helicase D | OS=Plasmodium falciparum | 33.10 | 0.00 |
| TRINITY_sp| Q9Y1f: rad15 | DNA repair helicase | OS=Dictyostelium discoideum | 33.10 | 0.00 |
| TRINITY_sp| Q8T81: vacuolar transporter | Vacuolar transporter | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q54J: CC146 | Myb-like protein AA | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q9VH1: Invadolin | Leishmanolysin-like | OS=Acanthamoeba polyphaga mimivirus | 33.10 | 0.00 |
| TRINITY_sp| Q9DBU: Qucrc2 | Cytochrome b-c1 complex | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q5KU: COLEC12 | Collectin-12 | OS=Caenorhabditis elegans | 33.10 | 0.00 |
| TRINITY_sp| Q9HCT: TMBIM4 | Protein lifeguard | OS=Caenorhabditis elegans | 33.10 | 0.00 |
| TRINITY_sp| Q8RYAt: At4g176 | Decapping nuclease | OS=Caenorhabditis elegans | 33.10 | 0.00 |
| TRINITY_sp| Q647: P1k4 | Serine/threonine-protein kinase | OS=Caenorhabditis elegans | 33.10 | 0.00 |
| TRINITY_sp| Q9VL4: DAO | D-amino-acid oxidase | OS=Acanthamoeba polyphaga mimivirus | 33.10 | 0.00 |
| TRINITY_sp| Q9VMR: Rheb | GTP-binding protein | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q54J: rNqB | RING finger protein | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q9RSR: RBL5 | RHOMBOID-like protein | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q9VI: Cp1 | Cathepsin B-like CP | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q8DIH:_t1S | tRNA(Ile)-lysidine | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q94KJ: TPC1 | Two pore calcium channel | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q54T: drkD | Probable serine/threonine-protein kinase | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q19i: gcy-12 | Receptor-type guanylate kinase | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| P059p: pkA | cAMP-dependent protein kinase | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q5SMK: TTHA106 | Magnesium transporter | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q8Y1F: CCDC146 | Coiled-coil domain-containing protein | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q2QA: TIO | Serine/threonine-protein kinase | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q8ICCP: P2 | Calcium-dependent protein | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q9HBR: RDH14 | Phospholipase | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| P547: EPHA5 | Ephrin type-A receptor | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| P104: pol | Retrovirus-related protein | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q5UPIMI: L7 | Uncharacterized protein | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q8L7F: LPEAT1 | Lysophospholipid acyltransferase | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q9HHB: RDH14 | Retinol dehydrogenase | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q861: DDB2-G02 | Uncharacterized protein | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| TRINITY_sp| Q647: At2g301 | Probable protein phosphatase | OS=Arabidopsis thaliana | 33.10 | 0.00 |
| Gene Name | Description | Probability 1 | Probability 2 |
|-----------|-------------|---------------|---------------|
| TRINITY_sp| B8AJ| Probable sodium/met 33.00 0.00 |
| TRINITY_sp| Q96B| Axin interactor, do 33.00 0.00 |
| TRINITY_sp| O346| Probable BsUmi modi 33.00 0.00 |
| TRINITY_sp| Q1PF| Calcium-dependent p 33.00 0.00 |
| TRINITY_sp| Q9MO| Gamma-glutamyl pept 33.00 0.00 |
| TRINITY_sp| Q95R| Organic cation tran 33.00 0.00 |
| TRINITY_sp| Q9MM| Aquaporin SIP1-1 OS 33.00 0.00 |
| TRINITY_sp| Q177| Deoxyribonuclease-2 33.00 0.00 |
| TRINITY_sp| P0C2| Acyl-coenzyme A oxi 33.00 0.00 |
| TRINITY_sp| Q10X| GTpase Obg OS=Trich 33.00 0.00 |
| TRINITY_sp| Q9W4| cAMP-specific 3',5' 33.00 0.00 |
| TRINITY_sp| O764| Glutathione S-trans 33.00 0.00 |
| TRINITY_sp| O040| Phosphoglycerate mu 33.00 0.00 |
| TRINITY_sp| P340| Lysosomal alpha-man 33.00 0.00 |
| TRINITY_sp| Q75J| Circularly permutat 33.00 0.00 |
| TRINITY_sp| Q0V9| Coiled-coil domain- 33.00 0.00 |
| TRINITY_sp| Q32P| Far upstream elemen 33.00 0.00 |
| TRINITY_sp| Q6AX| Protein PTHB1 OS= 33.00 0.00 |
| TRINITY_sp| Q8W4| Ubiquitin carboxyl- 33.00 0.00 |
| TRINITY_sp| P383| Phosphate permease 33.00 0.00 |
| TRINITY_sp| Q54R| Hybrid signal trans 32.90 0.00 |
| TRINITY_sp| Q1AU| Elongation factor G 32.90 0.00 |
| TRINITY_sp| Q5SE| Poly(A) RNA polymer 32.90 0.00 |
| TRINITY_sp| Q54F| Arpin OS=Dictyostel 32.90 0.00 |
| TRINITY_sp| Q567| Ubiquitin thioester 32.90 0.00 |
| TRINITY_sp| Q6PD| Proteasome-associat 32.90 0.00 |
| TRINITY_sp| A0PQ| Probable phthiotrio 32.90 0.00 |
| TRINITY_sp| Q9XT| Lipase ZK262.3 OS=C 32.90 0.00 |
| TRINITY_sp| B6MF| Protein Hook homolo 32.90 0.00 |
| TRINITY_sp| Q9DL| Cilia- and flagella 32.90 0.00 |
| TRINITY_sp| Q29A| Leishmanolysin-like 32.90 0.00 |
| TRINITY_sp| Q54H| Gamma-glutamyl hydr 32.90 0.00 |
| TRINITY_sp| Q96K| DCUN1D1 DCN1-like prot 32.90 0.00 |
| TRINITY_sp| O525| Carbonic anhydrase 32.90 0.00 |
| TRINITY_sp| Q8XJ| Peptide deformylase 32.90 0.00 |
| TRINITY_sp| Q3U4| E3 ubiquitin-protei 32.90 0.00 |
| TRINITY_sp| Q54Y| Hybrid signal trans 32.90 0.00 |
| TRINITY_sp| Q54H| Probable serine/thr 32.90 0.00 |
| TRINITY_sp| Q844| Probable inactive p 32.90 0.00 |
| TRINITY_sp| Q54Q| NAD-dependent deace 32.90 0.00 |
| TRINITY_sp| Q96K| Calcium/calcmodulin- 32.90 0.00 |
| TRINITY_sp| Q3UG| WD repeat-containin 32.90 0.00 |
| TRINITY_sp| Q9VY| Ubiquitin carboxyl- 32.90 0.00 |
| TRINITY_sp| Q0JI| CBL-interacting pro 32.90 0.00 |
| TRINITY_sp| Q7Z2| L-ascorbate peroxid 32.90 0.00 |
| TRINITY_sp| Q5XF| Mitochondrial impor 32.90 0.00 |
| TRINITY_sp| O087| Ubiquitin-protein l 32.90 0.00 |
| TRINITY_sp| Q8RV| Calpain-type cystei 32.90 0.00 |
| TRINITY_sp| P404| Serine/threonine-pr 32.90 0.00 |
| TRINITY_sp| P484| Serine/threonine-pr 32.90 0.00 |
| TRINITY_sp| T7FG| DEAD-box ATP-depend 32.90 0.00 |
| TRINITY_sp| Q7SY| Choline transporter 32.90 0.00 |
| TRINITY_sp| O049| Alpha-glucosidase O 32.90 0.00 |
| TRINITY_sp| Q62P| Inhibitor of Bruton 32.90 0.00 |
| TRINITY_sp| Q8BV| TPR and ankyrin rep 32.90 0.00 |
| TRINITY_sp| Q54I| Dual specificity pr 32.90 0.00 |
| Accession       | Description                                                                 | Score | P-value |
|-----------------|-----------------------------------------------------------------------------|-------|---------|
| TRINITY_sp|Q6TY80|Pabpn11-Embryonic polyadenyosine polymerase homolog 1, chloroplastic | 32.90 | 0.00    |
| TRINITY_sp|Q5XG80|PAPD7 Non-canonical polyadenylate 3'5'phosphatase homolog 7 | 32.90 | 0.00    |
| TRINITY_sp|Q4IFG8|GEF11 GTPase-activating protein homolog 11 | 32.90 | 0.00    |
| TRINITY_sp|P02Q3G|creC Probable catabolite repressor protein | 32.90 | 0.00    |
| TRINITY_sp|Q5PJ1G|NUP93 Nuclear pore complex protein homolog 93 | 32.90 | 0.00    |
| TRINITY_sp|Q93VCCB8A|Carotenoid cleavage enzyme homolog 8A | 32.90 | 0.00    |
| TRINITY_sp|P5161G|Xpc DNA repair protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q3UM1G|NeK10 Serine/threonine-protein kinase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q8171G|pol Retrovirus-related protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q3R90G|CNX2 GTP 3',8-cyclase, homolog | 32.90 | 0.00    |
| TRINITY_sp|Q92U1G|KCL5 Casein kinase 1-like protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q5PJ1H|HSDL1 Inactive hydroxysterol 3-oxo-5-ene-4-ene-6-carboxylate 3-dehydrogenase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q9900G|act Actin OS=Hypocrea jeticorina | 32.90 | 0.00    |
| TRINITY_sp|Q5RL1G|PUB53 Putative U-box domain protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q76L1G|cpr-c1 NADPH-dependent cytochrome b5 reductase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q8696G|bptnt1 3'-2'),5'-bisphosphate | 32.90 | 0.00    |
| TRINITY_sp|Q8JIAC|CFAP43 Cilia- and flagella associated protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q6525G|PHT4;4 Probable anion transporter | 32.90 | 0.00    |
| TRINITY_sp|Q4105G|SBE1 1,4-alpha-glucan-branching enzyme homolog | 32.90 | 0.00    |
| TRINITY_sp|Q54R6G|dhkL Hybrid signal transduction histidine kinase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q8177G|TBC1D1 TBC1 domain family protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q96P1G|ACAP3 Arf-GAP with coiled-coil domain protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q1ZK2G|roco5 Probable serine/threonine-protein kinase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q94AM1G|At5g5311 Probable protein phosphatase 2C homolog | 32.90 | 0.00    |
| TRINITY_sp|Q6763G|aq_1758 Uncharacterized RNA | 32.90 | 0.00    |
| TRINITY_sp|Q1D9G1G|deoD Purine nucleoside phosphorylase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q54DF1G|comm1 COMM domain-containing protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q8R81G|WISTY17 Serine/threonine-protein kinase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q54BP1G|pep2 Vacuolar protease A homolog | 32.90 | 0.00    |
| TRINITY_sp|Q54KG2G|gefa Ras guanine nucleotide exchange factor homolog | 32.90 | 0.00    |
| TRINITY_sp|Q9UR9G|Tf2-11 Transposon Tf2-11 protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q9Z12G|At5g54570 ACP12 acyltransferase-like protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q4908G|STK19 Serine/threonine-protein kinase homolog | 32.90 | 0.00    |
| TRINITY_sp|P2001G| Myb-related protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q9CHG1G|ABC111 ABC transporter C family homolog | 32.90 | 0.00    |
| TRINITY_sp|Q54SV1G|vps15 Probable serine/threonine-protein kinase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q6IQ1G|SPSOPL Speckle-type POZ protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q9182G|AOAH Acyl-CoA oxidase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q54AB1G|DD_B G02 Probable serine/threonine-protein kinase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q9P98G|tlsA Two-component system protein homolog | 32.90 | 0.00    |
| TRINITY_sp|P4081G|UB8 Ubiquitin carboxyl-terminal hydrolase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q54DIAB1G|MrkA Probable serine/threonine-protein kinase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q923JG|SP6G9.14 Pumilio domain-containing protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q54AN1G|alKB Alpha-ketoglutarate dehydrogenase homolog | 32.90 | 0.00    |
| TRINITY_sp|O1392G|av1 Late secretory pathway protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q5ZKL2G|DCUN1D1 DCN1-like protein 1 homolog | 32.90 | 0.00    |
| TRINITY_sp|Q54FK1G|acJJ Rho GTPase-activating protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q0433G|NSP3 Nitrile-specifier protein homolog | 32.90 | 0.00    |
| TRINITY_sp|Q54VIP2G|GPX2 Probable glutathione peroxidase homolog | 32.90 | 0.00    |
| TRINITY_sp|P0491G|tsAE tRNA threonylcarbamoyltransferase homolog | 32.90 | 0.00    |
| TRINITY_sp|P5280G|DGK1 Diacylglycerol kinase homolog | 32.90 | 0.00    |
| TRINITY_sp|P5953G|Eif5 Eukaryotic translation initiation factor 5 homolog | 32.90 | 0.00    |
| TRINITY_sp|Q8RXP1G|WIN2 Probable protein phosphatase 2C homolog | 32.90 | 0.00    |
| TRINITY_sp|Q0071G|CIPK11 CBL-interacting protein kinase homolog | 32.90 | 0.00    |
| TRINITY_sp|Q8VH1G|kbkap Elongator complex subunit homolog | 32.90 | 0.00    |
| TRINITY_sp|Q94CM1G|At5g49945 Uncharacterized protein homolog | 32.90 | 0.00    |
| Protein Name                        | Species                  | Feature       | Function                        | Protein Score | EValue |
|------------------------------------|--------------------------|---------------|---------------------------------|---------------|--------|
| Adenosine deaminase                | Homo sapiens             | GN=ADAL       | 32.80                           | 0.00          |
| Peroxisomal targeti                | Homo sapiens             | GN=PEX5       | 32.80                           | 0.00          |
| Ribosomal RNA large                | Homo sapiens             | GN=B5F6rmlM  | 32.80                           | 0.00          |
| 5OS ribosomal prote                | Homo sapiens             | GN=B5RM1rp1B  | 32.80                           | 0.00          |
| Dual specificity pr                | Schizosaccharomyces      | GN=kap104     | 32.80                           | 0.00          |
| Peroxisome biogenes                | Homo sapiens             | GN=QCAPEX2    | 32.80                           | 0.00          |
| Nicotinamide phosph                | Homo sapiens             | GN=Q802NMn    | 32.80                           | 0.00          |
| Leishmanolysin-like                | Homo sapiens             | GN=Q624Y43F4A.1 | 32.80                 | 0.00          |
| PAPS-dependent sulf                | Homo sapiens             | GN=P649stf3   | 32.80                           | 0.00          |
| Protein BTR1 OS=Ara                 | Homo sapiens             | GN=Q9L28BTR1  | 32.80                           | 0.00          |
| Hybrid signal trans                | Dictyostelium discoideum| GN=Q545ShkD   | 32.80                           | 0.00          |
| U-box domain-cont                   | Arabidopsis thaliana    | GN=Q86GUHUB33 | 32.80                           | 0.00          |
| Ecotropic viral int                | Arabidopsis thaliana    | GN=Q3154       | 32.80                           | 0.00          |
| Importin subunit be                | Homo sapiens             | GN=Q140kap104 | 32.80                           | 0.00          |
| Ubiquitin carboxyl                | Arabidopsis thaliana    | GN=Q88BUNup43 | 32.80                           | 0.00          |
| Exportin-4 OS=Xenop                | Homo sapiens             | GN=Q499Xpo4   | 32.80                           | 0.00          |
| Polyol transporter                  | Arabidopsis thaliana    | GN=Q8V2fPLT5  | 32.80                           | 0.00          |
| DNA-directed RNA po                | Arabidopsis thaliana    | GN=Q9C2701Olr3e | 32.80                         | 0.00          |
| BTB/POZ domain-cont                | Arabidopsis thaliana    | GN=Q68DKCTD16 | 32.80                           | 0.00          |
| Leishmanolysin-like                | Homo sapiens             | GN=Q9VH1JInvadal | 32.80                        | 0.00          |
| Serine/threonine-pr                | Arabidopsis thaliana    | GN=Q5ZJHULK3  | 32.80                           | 0.00          |
| Rho GTPase-activat                 | Dictyostelium discoideum| GN=Q3154       | 32.80                           | 0.00          |
| WD repeat, SAM and                 | Arabidopsis thaliana    | GN=Q8N9WDUB1  | 32.80                           | 0.00          |
| 3-phosphoinositide                | Arabidopsis thaliana    | GN=Q551Pdpk1  | 32.80                           | 0.00          |
| Enkuri OS=Mus musc                  | Arabidopsis thaliana    | GN=Q68fEnkur  | 32.80                           | 0.00          |
| Protein SAND OS=Tak                | Arabidopsis thaliana    | GN=Q3154       | 32.80                           | 0.00          |
| Rho GTPase-activat                 | Arabidopsis thaliana    | GN=Q86LGacHH  | 32.80                           | 0.00          |
| Cytoplasmic dynein                 | Arabidopsis thaliana    | GN=Q54Ctdync1lil | 32.80                        | 0.00          |
| Transforming growth                | Arabidopsis thaliana    | GN=Q27Tctgfb11l | 32.80                        | 0.00          |
| Kelch-like protein                 | Arabidopsis thaliana    | GN=Q5Z1KLHL7  | 32.80                           | 0.00          |
| Protein csh3 OS=Sch                | Arabidopsis thaliana    | GN=Q431cP2A   | 32.80                           | 0.00          |
| Tyrosine-protein ph               | Arabidopsis thaliana    | GN=Q246fPFTP  | 32.80                           | 0.00          |
| TLD domain-contai                 | Arabidopsis thaliana    | GN=Q1LW3tldcl1 | 32.80                        | 0.00          |
| Alpha, alpha-trehalo               | Arabidopsis thaliana    | GN=Q94ATPS6   | 32.80                           | 0.00          |
| Neural Wiskott-Aldr                | Arabidopsis thaliana    | GN=Q088fWas1  | 32.80                           | 0.00          |
| Ubiquitin-activatin               | Arabidopsis thaliana    | GN=Q524fUBA1  | 32.80                           | 0.00          |
| Zeaxanthin epoxidas                | Arabidopsis thaliana    | GN=Q0JC2ZEPI  | 32.80                           | 0.00          |
| Dynein heavy chain                | Arabidopsis thaliana    | GN=Q62RfDNAH12 | 32.80                        | 0.00          |
| Cleavage and polyad               | Arabidopsis thaliana    | GN=Q105fCP5F2  | 32.80                           | 0.00          |
| Probable dolichol-p               | Arabidopsis thaliana    | GN=Q9V11CG10166 | 32.80                       | 0.00          |
| Histone H2A.Y OS=Te                | Arabidopsis thaliana    | GN=Q5Y2fHTAY  | 32.80                           | 0.00          |
| Serine/threonine-pr               | Arabidopsis thaliana    | GN=Q86Cesatq1 | 32.80                           | 0.00          |
| Protein DGCR14 OS=M                | Arabidopsis thaliana    | GN=Q702fDgcr14 | 32.80                       | 0.00          |
| Uncharacterized rib                | Arabidopsis thaliana    | GN=Q731fsll1290 | 32.80                     | 0.00          |
| NADH-cytochrome b5                | Arabidopsis thaliana    | GN=Q832fCBR2  | 32.80                           | 0.00          |
| Mitochondrial argin               | Arabidopsis thaliana    | GN=Q84UBAC1   | 32.80                           | 0.00          |
| RAP domain-contain               | Arabidopsis thaliana    | GN=Q844fNHAL1 | 32.80                           | 0.00          |
| Guanine exchange fa               | Arabidopsis thaliana    | GN=Q312XggxcDD | 32.80                        | 0.00          |
| Exosome complex com               | Arabidopsis thaliana    | GN=Q927VRPRP4 | 32.80                           | 0.00          |
| Crossover junction               | Arabidopsis thaliana    | GN=Q8GTfMUS81  | 32.80                           | 0.00          |
| Gene Symbol             | Description                                      | Score | Type |
|------------------------|--------------------------------------------------|-------|------|
| rex4                   | RNA exonuclease 4                                | 32.70 |      |
| OCT4                  | Organic cation/carnitine transporter 4            | 32.70 |      |
| Invad01               | Leishmanolysin-like                             | 32.70 |      |
| 07g06                 | Probable protein phosphatase                    | 32.70 |      |
| GLU14                 | Endoglucanase 4                                 | 32.70 |      |
| NGR_a03370            | Uncharacterized oxidoreductase y4hM             | 32.70 |      |
| R588                  | G8 domain-containing protein                     | 32.70 |      |
| DDB_G0286311          | DNA-binding protein                              | 32.70 |      |
| DDB_G0278535          | Probable serine/threonine-protein kinase        | 32.70 |      |
| DDB_G0291350          | Probable serine/threonine-protein kinase        | 32.70 |      |
| rad21                 | Probable protein phosphatase 2C 65              | 32.70 |      |
| Invadolysin           | Leishmanolysin-like peptidase                    | 32.70 |      |
| Ugt                   | UDP-glucose:glycosyltransferase                 | 32.70 |      |
| RAD51D                | DNA repair protein                               | 32.70 |      |
| tnc-2                 | Troponin C, isoform                             | 32.70 |      |
| mcf2                  | Mitochondrial substrate                         | 32.70 |      |
| rad21                 | Double-strand-break                             | 32.70 |      |
| SM01-2                | Methylsterol monooxidase                      | 32.70 |      |
| abc6                  | ATP-binding cassette                            | 32.70 |      |
| abcD                  | Gamma-tubulin complex                           | 32.70 |      |
| Serine/arginine rep   | Serine/threonine-phosphatase                    | 32.70 |      |
| Serine/threonine-pr   | Serine/threonine-phosphatase                    | 32.70 |      |
| vidA                  | Sugar phosphatase Y                             | 32.70 |      |
| gacEE                 | Rho GTPase-activator                            | 32.70 |      |
| UBP13                 | Ubiquitin carboxyl-terminal hydrolase          | 32.70 |      |
| far1                  | Fatty acyl-CoA reduc.                           | 32.70 |      |
| ABC transporter C f   | ABC transporter C f                              | 32.70 |      |
| SEC14-like protein    | SEC14-like protein                              | 32.70 |      |
| Very-long-chain 3-o   | Very-long-chain 3-o                             | 32.70 |      |
| DDB_G0286311          | DNA-binding protein                              | 32.70 |      |
| NGR_a03370            | Uncharacterized oxidoreductase y4hM             | 32.70 |      |
| FAD-dependent urate   | FAD-dependent urate                             | 32.70 |      |
| Protein LOW PSII AC   | Protein LOW PSII AC                             | 32.70 |      |
| Uncharacterized pro   | Uncharacterized protein                         | 32.70 |      |
| Transcription facto   | Transcription factot                           | 32.70 |      |
| Expansin-A24          | Expansin-A24                                    | 32.70 |      |
Nucleoside diphosphate-linked moiety X motif 17 OS=Xenopus laevis GN=nudt17 PE=2 SV=1
General transcription factor 3C polypeptide 3 OS=Homo sapiens GN=GTF3C3 PE=1 SV=1
Acyloxyacyl hydrolase OS=Mus musculus GN=Aoah PE=2 SV=1
Zinc-binding protein A33 OS=Pleurodeles waltl PE=1 SV=2
E3 UFM1-protein ligase 1 OS=Rattus norvegicus GN=Ufl1 PE=1 SV=1
Developmentally-regulated protein kinase 1 OS=Dictyostelium discoideum GN=pkaD PE=2 SV=2
Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens GN=ARFGEF2 PE=1 SV=3
Peroxisomal acyl-coenzyme A oxidase 1 OS=Dictyostelium discoideum GN=acox1 PE=3 SV=1
Cilia- and flagella-associated protein 161 OS=Danio rerio GN=cfap161 PE=2 SV=1
Ran-binding protein 10 OS=Bos taurus GN=RANBP10 PE=2 SV=1
Elongator complex protein 2 OS=Rattus norvegicus GN=Elp2 PE=2 SV=1
Sn1-specific diacylglycerol lipase beta OS=Mus musculus GN=Daglb PE=1 SV=2
Small RNA 2'-O-methyltransferase OS=Gallus gallus GN=HENMT1 PE=3 SV=1
RNA-binding protein 28 OS=Mus musculus GN=Rbm28 PE=1 SV=4
Interferon-induced GTP-binding protein Mx2 OS=Canis lupus familiaris GN=MX2 PE=2 SV=1
Long-chain-fatty-acid--AMP ligase FadD29 OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) GN=fadD29 PE=3 SV=1
Guanylate-binding protein 1 OS=Chlorocebus aethiops GN=GBP1 PE=2 SV=1
Tubulin glycylase 3B OS=Tetrahymena thermophila (strain SB210) GN=TTLL3B PE=1 SV=2
Plant UBX domain-containing protein 4 OS=Arabidopsis thaliana GN=PUX4 PE=1 SV=1
CBL-interacting protein kinase 26 OS=Oryza sativa subsp. japonica GN=CIPK26 PE=2 SV=1
Phosphatidylinositol 4-phosphate 5-kinase type-1 beta OS=Gallus gallus GN=PIP5K1B PE=2 SV=1
Vesicle transport through interaction with t-SNAREs homolog 1A OS=Dictyostelium discoideum GN=vti1A PE=1 SV=1
Isotrichodermin C-15 hydroxylase OS=Fusarium sporotrichioides GN=TRI11 PE=3 SV=1
Acetylcholinesterase OS=Bungarus fasciatus GN=ACHE PE=1 SV=2
Lipoate-protein ligase A OS=Psychrobacter cryohalolentis (strain K5) GN=lplA PE=3 SV=1
Coiled-coil domain-containing protein 96 OS=Mus musculus GN=Ccdc96 PE=2 SV=1
RAC-beta serine/threonine-protein kinase OS=Mus musculus GN=Akt2 PE=1 SV=1
| Protein Name | Description | Score | E-value |
|--------------|-------------|-------|---------|
| CAPN15       | Calpain-type cysteine protease | 32.40 | 0.00    |
| March11      | E3 ubiquitin-protein ligase | 32.40 | 0.00    |
| Q10L\'\'VLN2 | Villin-2 OS=Oryza sativa | 32.40 | 0.00    |
| Q9M3CATM     | Serine/threonine-protein kinase | 32.40 | 0.00    |
| O9571HERC2   | E3 ubiquitin-protein ligase | 32.40 | 0.00    |
| Q6DRAhbd1    | Protein ABHD11 OS=Drosophila | 32.40 | 0.00    |
| Q924VSmc6    | Structural maintenance protein | 32.40 | 0.00    |
| Q54PgefA     | Ras guanine nucleotide exchange factor | 32.40 | 0.00    |
| A8WYpar-1    | Serine/threonine-protein kinase | 32.40 | 0.00    |
| Q297AF_0491  | Ribosome maturation protein | 32.40 | 0.00    |
| Q680TFB2     | RNA polymerase II t | 32.40 | 0.00    |
| P562\{AF_0491\} | Probable translation initiation factor | 32.40 | 0.00    |
| Q55C\{sec31\} | Protein transport | 32.40 | 0.00    |
| Q5TC\{MLK4\} | Mitogen-activated protein kinase | 32.40 | 0.00    |
| Q91WAscc2    | Activating signal c | 32.40 | 0.00    |
| Q9FI\{NIP4-1\} | Putative aquaporin | 32.40 | 0.00    |
| Q425\{erKa\} | Extracellular signal transducer | 32.40 | 0.00    |
| Q54Ukif3     | Kinesin-related protein | 32.40 | 0.00    |
| P803\{-\}   | Crustacean calcium-binding protein | 32.40 | 0.00    |
| Q5XG\{PAPD7\} | Non-canonical poly(A) binding protein | 32.40 | 0.00    |
| Q70C\{USP34\} | Ubiquitin carboxyl-terminal hydrolase | 32.40 | 0.00    |
| Q9NU\{MDN1\} | Midsap OS=Homo sapiens | 32.40 | 0.00    |
| Q9VK\{ial\} | Aurora kinase B OS=Homo sapiens | 32.40 | 0.00    |
| B3EW\{-\} | Hephaestin-like protein | 32.40 | 0.00    |
| Q92TRKS1 | G-type lectin S-receptor | 32.40 | 0.00    |
| Q5RA\{CLU1\} | Clustered mitoch | 32.30 | 0.00    |
| B0MIGefL | Ras guanine nucleotide exchange factor | 32.30 | 0.00    |
| Q8NGMETTL13 | Methyltransferase | 32.30 | 0.00    |
| P091F4HB | Protein disulfide-isomerase | 32.30 | 0.00    |
| P253\{YGL010W\} | Uncharacterized end | 32.30 | 0.00    |
| P212\{GSTM3\} | Glutathione-S-transferase | 32.30 | 0.00    |
| P273\{sol\} | Calpain-D OS=Drosophila | 32.30 | 0.00    |
| Q974\{-\} | Polygalacturonase | 32.30 | 0.00    |
| P583\{arcB\} | Aerobic respiration control | 32.30 | 0.00    |
| Q86A\{DDB_G02\} | Recoverin family protein | 32.30 | 0.00    |
| Q55C\{gtA\} | GATA zinc finger domain | 32.30 | 0.00    |
| Q7TP\{Rps6ka6\} | Ribosomal protein S6 | 32.30 | 0.00    |
| Q54T\{mykB\} | Myb-like protein C | 32.30 | 0.00    |
| Q125\{SET6\} | Potential epigenetic modifier | 32.30 | 0.00    |
| Q5W6\{MAN5\} | Putative mannose-binding | 32.30 | 0.00    |
| Q5JJ\{Os01905\} | Protein kinase and myosin-binding | 32.30 | 0.00    |
| Q6ZP\{ADL1\} | Calpain-type cysteine protease | 32.30 | 0.00    |
| Q6NY\{rngtt\} | mRNA-capping enzyme | 32.30 | 0.00    |
| Q6DD\{gats12\} | GATS-like protein | 32.30 | 0.00    |
| Q9SR\{RAP1\} | Rubisco activase | 32.30 | 0.00    |
| Q8FJ\{STY46\} | Serine/threonine-protein kinase | 32.30 | 0.00    |
| Q8H0\{UPL2\} | E3 ubiquitin-protein ligase | 32.30 | 0.00    |
| Q426\{GLN1\} | Glutamine synthetase | 32.30 | 0.00    |
| P0CE\{talA\} | Talin-A OS=Dictyostelium | 32.30 | 0.00    |
| Q758\{CAPN15\} | Calpain-15 OS=A. thaliana | 32.30 | 0.00    |
| A9AB\{rnz\} | Ribonuclease Z OS=M. musculus | 32.30 | 0.00    |
| Q99F\{Ar14d\} | ADP-ribosylation factor | 32.30 | 0.00    |
| Q1ZX\{DDB_G02\} | Sphingomyelinase | 32.30 | 0.00    |
TRINITY_sp|Q9LD0 FKBP17− Peptidyl-prolyl cis 32.30 0.00
TRINITY_sp|Q2RBC CBL-interacting pro 32.30 0.00
TRINITY_sp|Q9SYK At4g13780 Metionine--tRNA li 32.30 0.00
TRINITY_sp|Q8IU1 COBW domain-contain 32.30 0.00
TRINITY_sp|Q8W43 VHA-a3 V-type proton ATPases 32.30 0.00
TRINITY_sp|Q54Q9 DDB_G02 ΛLMBR1 domain-contai 32.30 0.00
TRINITY_sp|Q8VXE Arabinosyltransfera 32.30 0.00
TRINITY_sp|Q6CF6 Serine/threonine-pr 32.30 0.00
TRINITY_sp|Q6T4z Probable E3 ubiquit 32.30 0.00
TRINITY_sp|P517C Chloride channel pr 32.30 0.00
TRINITY_sp|Q54R5 Probable serine/thr 32.30 0.00
TRINITY_sp|Q5UQ0 Uncharacterized pro 32.30 0.00
TRINITY_sp|Q5ZL7 Casein kinase I iso 32.30 0.00
TRINITY_sp|Q076g Uncharacterized sug 32.30 0.00
TRINITY_sp|P9WM1 Glycogen synthase O 32.30 0.00
TRINITY_sp|Q5G54 Probable serine/thr 32.30 0.00
TRINITY_sp|Q9MIA Uncharacterized pro 32.30 0.00
TRINITY_sp|Q9VLt Lysine-specific dem 32.30 0.00
TRINITY_sp|Q9KLI Autoinducer 2 senso 32.30 0.00
TRINITY_sp|B2GJ0 Endoplasmic reticul 32.30 0.00
TRINITY_sp|Q017G Aldehyde oxidase GL 32.30 0.00
TRINITY_sp|Q0304 CAMP-dependent prot 32.30 0.00
TRINITY_sp|Q9NM3 Peroxisomal multif 32.30 0.00
TRINITY_sp|Q99T2 ATP-binding cassett 32.30 0.00
TRINITY_sp|Q88K1 Importin-5 OS=Mus m 32.30 0.00
TRINITY_sp|Q6L4s DNA mismatch repair 32.30 0.00
TRINITY_sp|Q009g Glutamine synthet 32.30 0.00
TRINITY_sp|Q5L4r Putative vacuolar p 32.30 0.00
TRINITY_sp|Q9SG3 RNA-dependent RNA p 32.30 0.00
TRINITY_sp|Q54Aq Sphingosine-1-phosph 32.20 0.00
TRINITY_sp|Q9SLj Probable protein ph 32.20 0.00
TRINITY_sp|Q597h Hypoxia-inducible f 32.20 0.00
TRINITY_sp|Q54F1 Eukaryotic translat 32.20 0.00
TRINITY_sp|Q597h Hypoxia-inducible f 32.20 0.00
TRINITY_sp|P0706 Gastric triacylglyc 32.20 0.00
TRINITY_sp|Q188A Acyloxyacyl hydrola 32.20 0.00
TRINITY_sp|P341p Protein kinase 3 OS 32.20 0.00
TRINITY_sp|Q9YQ1 Inositol 1,4,5-tris 32.20 0.00
TRINITY_sp|Q52J3 Serine/threonine-pr 32.20 0.00
TRINITY_sp|F758h NADH oxidoeductase 32.20 0.00
TRINITY_sp|O2851AF_1954 Putative amidase AF 32.20 0.00
TRINITY_sp|O80S5 At2g4460 Probable dolichyl p 32.20 0.00
TRINITY_sp|P870t Tip elongation aber 32.20 0.00
TRINITY_sp|Q9SFU Purple acid phospha 32.20 0.00
TRINITY_sp|Q0507 TAF9 Transcription initi 32.20 0.00
TRINITY_sp|Q7TS Enkudl Enkulin domain-cont 32.20 0.00
TRINITY_sp|Q9Z0L Lysosomal acid lipa 32.20 0.00
TRINITY_sp|D2H88 DCLRE1B 5′ exonuclease Apol 32.20 0.00
TRINITY_sp|A8I4F Cilia- and flagella 32.20 0.00
TRINITY_sp|Q8KBa Acetyl-coenzyme A s 32.20 0.00
| ID            | Description                                      | Score | Evalue |
|---------------|--------------------------------------------------|-------|--------|
| TRINITY_sp|Q8CI:Cwf19l1l CWF19-like protein                  | 32.10 | 0.00   |
| TRINITY_sp|Q6YY:NEK6 Serine/threonine-protein kinase         | 32.10 | 0.00   |
| TRINITY_sp|Q74Z:GPII13 GPI ethanolamine phosphatase           | 32.10 | 0.00   |
| TRINITY_sp|Q9CS:Ecd Protein ecdysoneles                      | 32.10 | 0.00   |
| TRINITY_sp|O758:CAPN15 Calpain-15                            | 32.10 | 0.00   |
| TRINITY_sp|D4GP:HVO_B00 D-xylose 1-dehydrogenase            | 32.10 | 0.00   |
| TRINITY_sp|P390:MRPT5 Suppressor protein                     | 32.10 | 0.00   |
| TRINITY_sp|Q9TW:myoM Myosin-M heavy chain                    | 32.10 | 0.00   |
| TRINITY_sp|Q097:kril Protein kril OS=Sch                     | 32.10 | 0.00   |
| TRINITY_sp|Q8K0U:Hspa12a Heat shock 70 kDa                  | 32.10 | 0.00   |
| TRINITY_sp|Q9Y2:KCNIp3 Calsenilin OS=Homo                   | 32.10 | 0.00   |
| TRINITY_sp|Q7KW:unH Inosine-uridine-pre                      | 32.10 | 0.00   |
| TRINITY_sp|Q595:ptrB Protease 2 OS=Morax                    | 32.10 | 0.00   |
| TRINITY_sp|P498:TSC2 Tuberin OS=Homo sap                    | 32.10 | 0.00   |
| TRINITY_sp|Q8R0I:Sec1414 SEC14-like protein                  | 32.10 | 0.00   |
| TRINITY_sp|O221:PAB4 Polyadenylate-binding protein           | 32.10 | 0.00   |
| TRINITY_sp|P252:PHO84 Inorganic phosphate                    | 32.10 | 0.00   |
| TRINITY_sp|Q8ND:RCBTB1 RCC1 and BTB domain                   | 32.10 | 0.00   |
| TRINITY_sp|Q10K:CAMK1 Calcium/calmodulin-like                | 32.10 | 0.00   |
| TRINITY_sp|O624:Y43F4A.1 Leishmanolysin-like                 | 32.10 | 0.00   |
| TRINITY_sp|Q54I:abCC5 ABC transporter C family               | 32.10 | 0.00   |
| TRINITY_sp|Q9RR:menG Demethylmenaquione                     | 32.10 | 0.00   |
| TRINITY_sp|Q9FG:RKD3 Protein RKD3 OS=Ara                     | 32.10 | 0.00   |
| TRINITY_sp|Q5GLDDB_G02 Probable serine/threonine            | 32.10 | 0.00   |
| TRINITY_sp|Q0JI:CIPK11 CBL-interacting protein              | 32.10 | 0.00   |
| TRINITY_sp|F4HY:Atig486 DEAH-box ATP-depend                 | 32.10 | 0.00   |
| TRINITY_sp|Q8LP:R1 Alpha-glucan water                       | 32.10 | 0.00   |
| TRINITY_sp|Q2KI:PHOSPHO Pyridoxal phosphate                  | 32.10 | 0.00   |
| TRINITY_sp|BOTA:rpL1 50S ribosomal protein                   | 32.10 | 0.00   |
| TRINITY_sp|Q6ES:HATB Probable histone ac                     | 32.10 | 0.00   |
| TRINITY_sp|O004:SLC33A1 Acetyl-coenzyme A t                 | 32.10 | 0.00   |
| TRINITY_sp|Q9JJ:Lanc12 LanC-like protein 2                   | 32.10 | 0.00   |
| TRINITY_sp|Q9XF:MSBP1 Membrane steroid-bi                   | 32.10 | 0.00   |
| TRINITY_sp|Q54D:abcA9 ABC transporter A family               | 32.10 | 0.00   |
| TRINITY_sp|Q8SI:Os1q09 Probable glucuronoside               | 32.10 | 0.00   |
| TRINITY_sp|Q54T:yipf1 Protein YIPF1 homol                   | 32.10 | 0.00   |
| TRINITY_sp|O027:GUCY2F Retinal guanylyl cy                    | 32.10 | 0.00   |
| TRINITY_sp|O191:UNC119 Protein unc-119 hom                  | 32.10 | 0.00   |
| TRINITY_sp|Q55A:DBB_G02 Probable serine/threonine           | 32.10 | 0.00   |
| TRINITY_sp|Q044:Adcy5 Adenylate cyclase t                    | 32.10 | 0.00   |
| TRINITY_sp|Q8LQ:GLUO Endoglucanase 3 OS=                      | 32.10 | 0.00   |
| TRINITY_sp|Q9H0:TOOLIP Toll-interacting protein             | 32.00 | 0.00   |
| TRINITY_sp|Q6DE:slc25a3 Solute carrier family               | 32.00 | 0.00   |
| TRINITY_sp|C4R1:VPS10 Vacuolar protein                      | 32.00 | 0.00   |
| TRINITY_sp|O350:yogA Uncharacterized zipper                 | 32.00 | 0.00   |
| TRINITY_sp|A0PQ:MUL_200 Probable phthiotoxin               | 32.00 | 0.00   |
| TRINITY_sp|Q6GF:naa50 N-alpha-acetyltrans                   | 32.00 | 0.00   |
| TRINITY_sp|A8GV:rpL1 50S ribosomal protein                   | 32.00 | 0.00   |
| TRINITY_sp|Q167:MAN2A1 Alpha-mannosidase 2                   | 32.00 | 0.00   |
| TRINITY_sp|F296:SF3 Pollen-specific protein                 | 32.00 | 0.00   |
| TRINITY_sp|O744:pet127 mRNA degradation protein             | 32.00 | 0.00   |
| TRINITY_sp|O525:cah Carbonic anhydrase                      | 32.00 | 0.00   |
| TRINITY_sp|Q5F3:YOD1 Ubiquitin thioester                   | 32.00 | 0.00   |
| TRINITY_sp|Q9VDM:meligo Solute carrier family               | 32.00 | 0.00   |
| TRINITY_sp|Q004:SEN1 Helicase SEN1 OS=                      | 32.00 | 0.00   |
| TRINITY_sp|Q8K3:Figu Phosphatidylinosito                    | 32.00 | 0.00   |
| Accession | Description                                                                 | Score 1 | Score 2 |
|-----------|-----------------------------------------------------------------------------|---------|---------|
| sp|Q8WUJSLC25A4:|Solute carrier family 25 member 43| 32.00 | 0.00 |
| sp|Q9LQCRAD51D | DNA repair protein| 32.00 | 0.00 |
| sp|Q7458SPCC970 | Uncharacterized inositol-phosphatidylinositol| 32.00 | 0.00 |
| sp|P546piK0 | Phosphatidylinositol| 32.00 | 0.00 |
| sp|Q9SHNCML31 | Probable calcium-binding protein| 32.00 | 0.00 |
| sp|Q5Xi1March10 | Probable E3 ubiquitin-conjugating enzyme| 32.00 | 0.00 |
| sp|P231:toDF | 2-hydroxy-6-oxo-2,4-quinone reductase| 32.00 | 0.00 |
| sp|Q9VCGCG7048 | Probable prefoldin| 32.00 | 0.00 |
| sp|P0CMWCWC25 | Pre-mRNA-splicing factor| 32.00 | 0.00 |
| sp|P538PDR17 | Phosphatidylinositol| 32.00 | 0.00 |
| sp|Q12XIDDGG02:PH | Domain-containin| 32.00 | 0.00 |
| sp|Q54GDDG02:von Willebrand factor| 32.00 | 0.00 |
| sp|Q9SKACARI10 | Probable E3 ubiquitin-conjugating enzyme| 32.00 | 0.00 |
| sp|O1371:SPAC17A2 | Putative metal ion| 32.00 | 0.00 |
| sp|Q6478Atg301 | Probable protein ph| 32.00 | 0.00 |
| sp|P0CMATG2 | Autophagy-related protein| 32.00 | 0.00 |
| sp|Q1638PDC2 | Programmed cell death| 32.00 | 0.00 |
| sp|P4266VCP | Vitellogenic carboxylesterase| 32.00 | 0.00 |
| sp|Q86CidhkK | Hybrid signal transducer| 32.00 | 0.00 |
| sp|Q9COCDNAH6 | Dynein heavy chain| 32.00 | 0.00 |
| sp|Q82D5SAV_512:UPF0301 | Protein SAV| 32.00 | 0.00 |
| sp|Q0448Atlg096 | Probable elongation factor| 32.00 | 0.00 |
| sp|Q6ETTOS2G01 | Probable protein ph| 32.00 | 0.00 |
| sp|Q80XTTc28 | Tetratricopeptide repeat protein| 32.00 | 0.00 |
| sp|Q758CAPN15 | Calpain-15| 32.00 | 0.00 |
| sp|Q8BLS1c25a2: | Mitochondrial basic| 32.00 | 0.00 |
| sp|Q9ESMNel11 | Protein sel-1 homolog| 32.00 | 0.00 |
| sp|Q9HIHSGSM3 | Small G protein sig| 32.00 | 0.00 |
| sp|Q9SSLPAPA | Protein LOW FIS AC| 32.00 | 0.00 |
| sp|Q9H95MARCH7 | E3 ubiquitin-protein ligase| 32.00 | 0.00 |
| sp|C9WMWn- | Venom serine carboxypeptidase| 32.00 | 0.00 |
| sp|Q8NNBBS1 | Bardet-Biedl syndrome| 32.00 | 0.00 |
| sp|P3581BDX3 | Bromodomain-containing protein| 32.00 | 0.00 |
| sp|Q71LHTY3B-I | Transposon Ty3-I Ga| 32.00 | 0.00 |
| sp|Q93WNSFS2 | Cysteine desulfurases| 32.00 | 0.00 |
| sp|Q5ZJHULK3 | Serine/threonine-protein kinase| 32.00 | 0.00 |
| sp|Q6ETT3Npc111 | Niemann-Pick C1-like protein| 32.00 | 0.00 |
| sp|Q9FEEDSP4 | Phosphoglucomutase| 32.00 | 0.00 |
| sp|Q6284Pcsk7 | Propreductase| 32.00 | 0.00 |
| sp|P41VIGRV2 | DnaJ homolog subfamily| 32.00 | 0.00 |
| sp|Q9W41dnc | cAMP-specific 3',5' adenosine monophosphate| 32.00 | 0.00 |
| sp|Q6U1CM1 | Alpha-l,3-mannosyltransferase| 32.00 | 0.00 |
| sp|P4366RM8 | Sporulation protein| 32.00 | 0.00 |
| sp|Q86UN4BP2 | Nedd4-binding protein| 32.00 | 0.00 |
| sp|O1491PLD2 | Phospholipase D2| 31.90 | 0.00 |
| sp|Q749toa2 | Transcription initiation factor| 31.90 | 0.00 |
| sp|Q3URGtbrapl | Transforming growth factor receptor| 31.90 | 0.00 |
| sp|Q54MMrkb | Probable serine/threonine-protein kinase| 31.90 | 0.00 |
| sp|Q6IMaalR | Aldose reductase A| 31.90 | 0.00 |
| sp|Q9Q9Icdsa1 | Serine/threonine-protein kinase| 31.90 | 0.00 |
| sp|Q55OFDDBB02: | Probable serine/threonine-protein kinase| 31.90 | 0.00 |
| sp|Q075YydW | Putative glycerophosphodiester phosphohydrolase| 31.90 | 0.00 |
| sp|Q9WUPus1 | tRNA pseudouridylate| 31.90 | 0.00 |
| sp|Q75WVw5a5 | von Willebrand factor| 31.90 | 0.00 |
| sp|P774ygaB | Fructose-1-phosphatase| 31.90 | 0.00 |
| sp|Q9CQI|Tctex1Id:Tctex1 domain-containing| 31.90 | 0.00 |
| Accession          | Description                                        | Score | Bit Score |
|--------------------|----------------------------------------------------|-------|-----------|
| sp|Q0431|NSP3  | Nitrile-specifier protein 3 | 31.80 | 0.00 |
| sp|Q1111|ubp14 | Ubiquitin carboxyl-terminal hydrolase | 31.80 | 0.00 |
| sp|Q7TE|Er1l  | 3'-5' exoribonuclease | 31.80 | 0.00 |
| sp|P306|svop-1 | Putative transporter | 31.80 | 0.00 |
| sp|Q54D|DBB_G02 | Serine carboxypeptidase B2 | 31.80 | 0.00 |
| sp|Q591|DBB_G02 | Probable serine/threonine protease | 31.80 | 0.00 |
| sp|Q0428|bub3  | Mitotic checkpoint | 31.80 | 0.00 |
| sp|Q5R5|SERINC3 | Serine incorporator | 31.80 | 0.00 |
| sp|Q8RV|DEK1  | Calpain-type cysteine protease | 31.80 | 0.00 |
| sp|Q9LV|AR14 | Putative E3 ubiquitin-protein ligase | 31.80 | 0.00 |
| sp|P581|PRKAG1 | 5'-AMP-activated protein kinase | 31.80 | 0.00 |
| sp|Q9SI|TMK3  | Receptor-like kinase | 31.80 | 0.00 |
| sp|Q5XF|Atp13a3 | Probable cation transporter | 31.80 | 0.00 |
| sp|Q7LH|TY3B-I | Transposon Ty3-I Gag-Pol polyprotein | 31.80 | 0.00 |
| sp|Q8LC|At4g296 | Thioredoxin-like 2 protein | 31.80 | 0.00 |
| sp|Q0P4|srd5a3 | Polyisoprenoid reductase | 31.80 | 0.00 |
| sp|Q54L|Eps13A | Putative vacuolar protein | 31.80 | 0.00 |
| sp|Q75J|cpras1 | Circularly permuted protein | 31.80 | 0.00 |
| sp|Q9NW1|BM28 | RNA-binding protein | 31.80 | 0.00 |
| sp|Q9UT|SPAC824 | Uncharacterized protein | 31.80 | 0.00 |
| sp|Q553|gxcJ | Rac guanine nucleotide exchange factor | 31.80 | 0.00 |
| sp|Q9US|tim23 | Mitochondrial importin | 31.80 | 0.00 |
| sp|P509|AVT4  | Vacuolar amino acid transporter | 31.80 | 0.00 |
| sp|Q6FQ|PKAR  | cAMP-dependent protein kinase | 31.80 | 0.00 |
| sp|Q6NX|Rcbbt1 | RCC1 and BTB domain | 31.80 | 0.00 |
| sp|Q9LU|FN3B3 | Photosynthetic NDH | 31.80 | 0.00 |
| sp|F4JY|ENDO4 | Endonuclease 4 OS=A | 31.80 | 0.00 |
| sp|P531|ROG1  | Putative lipase ROG | 31.80 | 0.00 |
| sp|Q54T|xpnnep3 | Probable Xaa-Pro amine transferase | 31.80 | 0.00 |
| sp|Q9LH|LPAT5 | Probable 1-acyl-sn-glycerol-3-phosphate acyltransferase | 31.80 | 0.00 |
| sp|P041|GIP   | Copia protein OS=Dr | 31.80 | 0.00 |
| sp|F4JE|NSE4B | Non-structural main protein | 31.80 | 0.00 |
| sp|Q9UJ|gcn5  | Histone acetyltransferase | 31.80 | 0.00 |
| sp|Q9CX|Dhrs7 | Dehydrogenase/reductase | 31.80 | 0.00 |
| sp|Q9SY|HEX02 | Beta-hexosaminidase | 31.80 | 0.00 |
| sp|Q9UK|ABC2  | ATP-binding cassette | 31.80 | 0.00 |
| sp|Q55E|gins4 | DNA replication complex | 31.70 | 0.00 |
| sp|Q06A|RAB1B | Ras-related protein | 31.70 | 0.00 |
| sp|Q8N4|RNF175 | RING finger protein | 31.70 | 0.00 |
| sp|Q9VR|HERC2 | Probable E3 ubiquitin-protein ligase | 31.70 | 0.00 |
| sp|Q9UM|FZ3R1 | Fizzy-related protein | 31.70 | 0.00 |
| sp|Q60D|TPK3  | Thiamine pyrophosphatase | 31.70 | 0.00 |
| sp|O316|metC  | Cystathionine beta-synthase | 31.70 | 0.00 |
| sp|Q32L|GRINA | Protein ligase | 31.70 | 0.00 |
| sp|Q70C|USP34 | Ubiquitin carboxyl-terminal hydrolase | 31.70 | 0.00 |
| sp|Q54Q|Wdr89 | WD repeat-containing protein | 31.70 | 0.00 |
| sp|Q54Z|tbc1b | Tubulin-specific chaperone | 31.70 | 0.00 |
| sp|Q55G|DDB_G02 | Probable phosphatidic acid kinase | 31.70 | 0.00 |
| sp|Q6FN|STE20 | Serine/threonine kinase | 31.70 | 0.00 |
| sp|Q9VY|Cyp4g15 | Cytochrome P450 | 31.70 | 0.00 |
| sp|Q8L7|At1g317 | AP-4 complex subunit | 31.70 | 0.00 |
| sp|Q96M|AK7   | Adenylate kinase 7 | 31.70 | 0.00 |
| sp|Q54X|captB | Uncharacterized CDP diolphosphate transporter | 31.70 | 0.00 |
| sp|P583|arcB  | Aerobic respiration | 31.70 | 0.00 |
| sp|Q5BDA|sip5 | Protein sip5 OS=Eme | 31.70 | 0.00 |
| sp|Q9FZ|MAN1  | Mannan endo-1,4-beta-glucanase | 31.70 | 0.00 |
Various proteins and enzymes are listed with their corresponding gene names and descriptions. Here are some examples:

- **Probable ubiquitin-like-specific protease 2A (ULP2A)**
- **Endonuclease 4 (ENDO4)**
- **Cilia- and flagella-associated protein 52 (CFAP52)**
- **1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase (PLC)**
- **CBL-interacting serine/threonine-protein kinase 8 (CIPK8)**
- **Histidine kinase 4 (AHK4)**
- **Transmembrane 9 superfamily member 6 (TMN6)**
- **Putative phosphate permease (HP_1491)**
- **Valine--tRNA ligase (Vars)**
- **Probable cinnamyl alcohol dehydrogenase 6 (CAD6)**
- **BTB/POZ domain-containing protein 3 (BTBD3)**
- **Receptor-type tyrosine-protein phosphatase H (PTPRH)**
- **Synaptotagmin-5 (SYT5)**
- **Probable thioredoxin-2 (trx-2)**
- **Circularly permutated Ras protein 1 (cpras1)**
- **DNA mismatch repair protein MSH6 (MSH6)**
- **TATA-binding protein-associated factor 172 (BTAF1)**
- **Probable ubiquitin-like-specific protease 2A OS=Arabidopsis thaliana GN=ULP2A PE=2 SV=2**
- **Endonuclease 4 OS=Arabidopsis thaliana GN=ENDO4 PE=3 SV=1**
- **Cilia- and flagella-associated protein 52 OS=Chlamydomonas reinhardtii GN=CFAP52 PE=1 SV=1**
- **1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase OS=Dictyostelium discoideum GN=plc PE=2 SV=1**
- **CBL-interacting serine/threonine-protein kinase 8 OS=Arabidopsis thaliana GN=CIPK8 PE=1 SV=1**
- **Histidine kinase 4 OS=Arabidopsis thaliana GN=AHK4 PE=1 SV=1**
- **Transmembrane 9 superfamily member 6 OS=Arabidopsis thaliana GN=TMN6 PE=2 SV=1**
- **Putative phosphate permease HP_1491 OS=Helicobacter pylori (strain ATCC 700392 / 26695) GN=HP_1491 PE=3 SV=1**
- **Valine--tRNA ligase OS=Mus musculus GN=Vars PE=1 SV=1**
- **Cilia- and flagella-associated protein 47 OS=Homo sapiens GN=CFAP47 PE=2 SV=4**
- **Probable cinnamyl alcohol dehydrogenase 6 OS=Arabidopsis thaliana GN=CAD6 PE=2 SV=1**
- **BTB/POZ domain-containing protein 3 OS=Callithrix jacchus GN=BTBD3 PE=2 SV=1**
- **Receptor-type tyrosine-protein phosphatase H OS=Homo sapiens GN=PTPRH PE=1 SV=3**
- **Synaptotagmin-5 OS=Arabidopsis thaliana GN=SYT5 PE=2 SV=1**
- **CBL-interacting protein kinase 26 OS=Oryza sativa subsp. japonica GN=CIPK26 PE=2 SV=1**
- **Endonuclease 4 OS=Arabidopsis thaliana GN=ENDO4 PE=3 SV=1**
- **Circularly permutated Ras protein 1 OS=Dictyostelium discoideum GN=cpras1 PE=3 SV=1**
- **DNA mismatch repair protein MSH6 OS=Arabidopsis thaliana GN=MSH6 PE=1 SV=2**
- **TATA-binding protein-associated factor 172 OS=Homo sapiens GN=BTAF1 PE=1 SV=2**
- **Probable thioredoxin-2 OS=Caenorhabditis elegans GN=trx-2 PE=3 SV=2**
- **F-box only protein 42 OS=Mus musculus GN=Fbxo42 PE=1 SV=1**
- **Dedicator of cytokinesis protein 6 OS=Homo sapiens GN=DOCK6 PE=1 SV=3**
- **tRNA (guanine(9)-N1)-methyltransferase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=trm10 PE=1 SV=1**
- **Retrovirus-related Pol polyprotein from transposon opus OS=Drosophila melanogaster GN=pol PE=3 SV=1**
- **Proto-oncogene serine/threonine-protein kinase mos OS=Rattus norvegicus GN=Mos PE=2 SV=2**
- **2-carboxy-D-arabinitol-1-phosphatase OS=Triticum aestivum PE=1 SV=1**
- **Uncharacterized aarF domain-containing protein kinase 1 OS=Homo sapiens GN=ADCK1 PE=2 SV=2**
- **Protein cbbX homolog, chloroplastic OS=Guillardia theta GN=cbbX PE=3 SV=1**
- **Canalicular multispecific organic anion transporter 2 OS=Rattus norvegicus GN=Abcc3 PE=1 SV=1**
- **Canalicular multispecific organic anion transporter 2 OS=Rattus norvegicus GN=Abcc3 PE=1 SV=1**
- **TRINITY_spQ0WKEULP2A**
- **TRINITY_spF4JUJENDO4**
- **TRINITY_spQ2TXXsym1**
- **TRINITY_spO1421tm10**
- **TRINITY_spO7534PDCD6**
- **TRINITY_spQ9HDQPTPRH**
- **TRINITY_spW5EP1**
- **TRINITY_spP550**
- **TRINITY_spO1498TAF1**
- **TRINITY_spO656CAD6**
- **TRINITY_spA810CFAP52**
- **TRINITY_spQ54BJDDB02**
- **TRINITY_spP0055os**
- **TRINITY_spQ035SCS7**
- **TRINITY_spQ948EAt3g1441**
- **TRINITY_spQ8N35SLC35F6**
- **TRINITY_spQ9C79ELP4**
- **TRINITY_spQ0A4rmlM**
- **TRINITY_spQ627FCFAP47**
- **TRINITY_spQ7534cpras1**
- **TRINITY_spQ9C79TMN6**
- **TRINITY_spQ885SAbcc3**
- **TRINITY_spQ9F9YTMN11**
- **TRINITY_spQ6H7TCIPK26**
- **TRINITY_spQ817Ipol**
- **TRINITY_spQ90KKeef1g**
- **TRINITY_spQ8I7FCFAP70**
- **TRINITY_spQ9C79TMN6**
- **TRINITY_spQ524DDGKE**
- **TRINITY_spQ556hich**
- **TRINITY_spQ818TRMT2A**
- **TRINITY_spQ1NFshq1**
- **TRINITY_spQ0VFibloc1s1**
- **TRINITY_spQ54PsosI**
- **TRINITY_spQ0475MSH6**
- **TRINITY_spQ54LccleC**
- **TRINITY_spQ9QY1Dnajb12**
- **TRINITY_spP258rrl1E**
- **TRINITY_spQ266KAP115**
- **TRINITY_spF7ASI1BTBD3**
- **TRINITY_spQ9SSccbbX**
- **TRINITY_spQ428RanBPM**
- **TRINITY_spO946SPBC776**
- **TRINITY_spQ021iplc**
- **TRINITY_spQ6PFDfoxo42**
- **TRINITY_spQ9CS5AHK4**
- **TRINITY_spQ92I1(Vars)**
- **TRINITY_spQ174trx-2**
- **TRINITY_spQ8LPFALEPHAC(A-P-2 complex subunit)**
- **TRINITY_spQ96HDOCK6**
- **TRINITY_spQ2602HP_1491**
| Query                      | Description                                      | Retention | MW  |
|----------------------------|--------------------------------------------------|-----------|-----|
| TRINITY_sp|Q58C|FAM213B | Prostamide/prostaglandins | 31.50 | 0.00 |
| TRINITY_sp|Q84W2|ibp1 | Dual specificity phosphatase | 31.50 | 0.00 |
| TRINITY_sp|P547|Tango2 | Transport and Golgi targeting | 31.50 | 0.00 |
| TRINITY_sp|O67L|aq|1088 | Uncharacterized protein | 31.50 | 0.00 |
| TRINITY_sp|O887|Alq10b | Putative Dol-P-Glc: mannosyltransferase | 31.50 | 0.00 |
| TRINITY_sp|Q559|a1r0305 | TFP38/TFEM64 family | 31.50 | 0.00 |
| TRINITY_sp|Q9SY1|GGH1 | Gamma-glutamyl hydrolase | 31.50 | 0.00 |
| TRINITY_sp|Q5UP2|MIMI_R2 | Uncharacterized protein | 31.50 | 0.00 |
| TRINITY_sp|Q9F1I|Nip4-1 | Putative aquaporin | 31.50 | 0.00 |
| TRINITY_sp|Q56Y|PLR1 | Pyridoxal reductase | 31.50 | 0.00 |
| TRINITY_sp|Q86C|dhkK | Hybrid signal transduction histidine kinase | 31.50 | 0.00 |
| TRINITY_sp|Q55A|DDB_G02 | Probable serine/threonine protein kinase | 31.50 | 0.00 |
| TRINITY_sp|P100|w | Protein white | 31.50 | 0.00 |
| TRINITY_sp|Q54W|mcfB | Mitochondrial substrate carrier | 31.50 | 0.00 |
| TRINITY_sp|P944|yciC | Putative metallochaperone | 31.50 | 0.00 |
| TRINITY_sp|O941|Snf1 | Carbon catabolite-derepressing protein kinase | 31.50 | 0.00 |
| TRINITY_sp|B1A2|Otud3 | OTU domain-containing protein | 31.50 | 0.00 |
| TRINITY_sp|Q94K|VIP552 | Vacuolar protein sorting-associated protein | 31.50 | 0.00 |
| TRINITY_sp|Q75J|pras1 | Circularly permuted protein | 31.50 | 0.00 |
| TRINITY_sp|Q9ZS5|ACA10 | Calcium-transporting ATPase | 31.50 | 0.00 |
| TRINITY_sp|Q201|gcs1 | Glutamate-cysteine S-transferase | 31.50 | 0.00 |
| TRINITY_sp|P543|Ctk1I | Casein kinase I | 31.50 | 0.00 |
| TRINITY_sp|Q700|algrD | Linear gramicidin-sensitive channel | 31.50 | 0.00 |
| TRINITY_sp|Q923|ssb2 | Replication factor | 31.50 | 0.00 |
| TRINITY_sp|Q0J1|CIPK11 | CBL-interacting protein | 31.50 | 0.00 |
| TRINITY_sp|P84Y|CCR4-6 | Carbon catabolite repressor protein | 31.50 | 0.00 |
| TRINITY_sp|Q9M2|LPPD | Lipid phosphate phosphatase | 31.50 | 0.00 |
| TRINITY_sp|Q2NL|PARP6 | Poly (ADP-ribose) polymerase | 31.50 | 0.00 |
| TRINITY_sp|Q8L7|BSL1 | Serine/threonine-protein kinase | 31.50 | 0.00 |
| TRINITY_sp|Q633|Nfkb1 | Nuclear factor NF-κB | 31.50 | 0.00 |
| TRINITY_sp|Q8CG|Gmc5 | Structural maintena | 31.50 | 0.00 |
| TRINITY_sp|Q8N6|OTUD6B | OTU domain-containing protein | 31.50 | 0.00 |
| TRINITY_sp|Q5TJ|forF | Formin-F | 31.50 | 0.00 |
| TRINITY_sp|Q54E|abpF | Actin-binding protein | 31.50 | 0.00 |
| TRINITY_sp|Q2MH|HT1 | Serine/threonine-protein kinase | 31.50 | 0.00 |
| TRINITY_sp|P370|lasT | Uncharacterized protein | 31.50 | 0.00 |
| TRINITY_sp|Q460|PARP15 | Poly (ADP-ribose) polymerase | 31.50 | 0.00 |
| TRINITY_sp|Q7TS|Nsun6 | Putative methyltransferase | 31.50 | 0.00 |
| TRINITY_sp|Q8BQ|Zdhhc14 | Probable palmitoyltransferase | 31.50 | 0.00 |
| TRINITY_sp|Q6Q2|MAO2 | Amine oxidase (flavin-containing) | 31.50 | 0.00 |
| TRINITY_sp|Q759|CPD | Carboxypeptidase D | 31.50 | 0.00 |
| TRINITY_sp|P028|tsp0 | Tryptophan-rich protein | 31.50 | 0.00 |
| TRINITY_sp|P067|CMD1 | Calmodulin OS=Drosophila | 31.50 | 0.00 |
| TRINITY_sp|Q62F|ADL1 | Calpain-type cysteine protease | 31.50 | 0.00 |
| TRINITY_sp|O044|At1g096 | Probable elongation factor | 31.50 | 0.00 |
| TRINITY_sp|P357|- | Pathogenesis-related protein | 31.40 | 0.00 |
| TRINITY_sp|Q7ZW|Nt5c3b-α7-methylguanosine p | 31.40 | 0.00 |
| TRINITY_sp|Q54F|DBB_G02 | Putative Repeat-containin | 31.40 | 0.00 |
| TRINITY_sp|Q9SL|Os05g01 | Importin subunit | 31.40 | 0.00 |
| TRINITY_sp|Q5PP|rfn170 | E3 ubiquitin-protein ligase | 31.40 | 0.00 |
| TRINITY_sp|P586|At2g399 | Probable signal peptide | 31.40 | 0.00 |
| TRINITY_sp|Q121|SPC3 | Signal peptide | 31.40 | 0.00 |
| TRINITY_sp|P220|Pcm1 | Protein-L-isoaspartate phosphatase | 31.40 | 0.00 |
| TRINITY_sp|Q7LL|SPCC149 | UF0676 protein | 31.40 | 0.00 |
| TRINITY_sp|Q2TB1|NSMCE4A | Non-structural main | 31.40 | 0.00 |
| TRINITY_sp|Q0JI|CIPK11 | CBL-interacting protein | 31.40 | 0.00 |
| Gene ID   | Description                                   | Score | Type |
|-----------|-----------------------------------------------|-------|------|
| TRINITY_sp| Serine/threonine-protein phosphatase 4         | 31.40 | 0.00 |
| TRINITY_sp| Ephrin type-A receptor                        | 31.40 | 0.00 |
| TRINITY_sp| Sorting nexin 2B                              | 31.40 | 0.00 |
| TRINITY_sp| Photosystem II 22 kDa protein, chloroplastic  | 31.40 | 0.00 |
| TRINITY_sp| Regulator of nonsense transcripts              | 31.40 | 0.00 |
| TRINITY_sp| Geranylgeranyl transferase type-2 subunit alpha| 31.40 | 0.00 |
| TRINITY_sp| Zinc finger CCCH-type antiviral protein        | 31.40 | 0.00 |
| TRINITY_sp| DDB1- and CUL4-associated factor 13            | 31.40 | 0.00 |
| TRINITY_sp| Helicase-like transcription factor             | 31.40 | 0.00 |
| TRINITY_sp| 3-keto-5-aminohexanoate cleavage enzyme        | 31.40 | 0.00 |
| TRINITY_sp| Ultraviolet-B receptor                        | 31.40 | 0.00 |
| TRINITY_sp| Formin-H OS=Dicystos                        | 31.40 | 0.00 |
| TRINITY_sp| Rho GTPase-activator                          | 31.40 | 0.00 |
| TRINITY_sp| Bile salt export protein                      | 31.40 | 0.00 |
| TRINITY_sp| Epoxide hydrolase                             | 31.40 | 0.00 |
| TRINITY_sp| Brefeldin A-inhibitor                         | 31.40 | 0.00 |
| TRINITY_sp| Helicase-like trans                            | 31.40 | 0.00 |
| TRINITY_sp| mRNA cap guanine nucleot                      | 31.40 | 0.00 |
| TRINITY_sp| Arginine decarboxylase                        | 31.40 | 0.00 |
| TRINITY_sp| Lipid A export ATP                            | 31.40 | 0.00 |
| TRINITY_sp| Serine/threonine-pr                           | 31.40 | 0.00 |
| TRINITY_sp| Vascular endothelia                           | 31.40 | 0.00 |
| TRINITY_sp| Protein-lysine N-methyltransferase            | 31.40 | 0.00 |
| TRINITY_sp| DNA-directed RNA polymer                      | 31.40 | 0.00 |
| TRINITY_sp| alpha-mannosidase I                           | 31.40 | 0.00 |
| TRINITY_sp| Geranylgeranyl transferase reverse             | 31.30 | 0.00 |
| TRINITY_sp| Maternal embryonic                            | 31.30 | 0.00 |
| TRINITY_sp| Casein kinase II                              | 31.30 | 0.00 |
| TRINITY_sp| Carboxypeptidase Y                            | 31.30 | 0.00 |
| TRINITY_sp| Telomerase reverse                            | 31.30 | 0.00 |
| TRINITY_sp| Myb-like protein H                            | 31.30 | 0.00 |
| TRINITY_sp| Protein FAM151B OS=                           | 31.30 | 0.00 |
| TRINITY_sp| D-alanyl-D-alanine                            | 31.30 | 0.00 |
| TRINITY_sp| Protein dcd1A OS=Di                          | 31.30 | 0.00 |
| TRINITY_sp| L-pipeolate oxidase                           | 31.30 | 0.00 |
| TRINITY_sp| Protoporphyrinogen                            | 31.30 | 0.00 |
| TRINITY_sp| Zinc transporter ZI                            | 31.30 | 0.00 |
| Accession       | Description                                      | K (°C) | Mean |
|-----------------|--------------------------------------------------|-------|------|
| TRINITY_sp|Q9R1|Fzr1 Fizzy-related protein                      | 31.30 | 0.00 |
| TRINITY_sp|O137|SPAC17A2 Putative metal ion                      | 31.30 | 0.00 |
| TRINITY_sp|Q5UN|MIMI_R6 Uncharacterized protein                 | 31.30 | 0.00 |
| TRINITY_sp|Q54W|ku70 ATP-dependent DNA helicase                 | 31.30 | 0.00 |
| TRINITY_sp|Q94H|ITIF3K1 Eukaryotic translation initiation factor | 31.30 | 0.00 |
| TRINITY_sp|P351|fluB Ribosomal large subunit                     | 31.30 | 0.00 |
| TRINITY_sp|Q9D6|Cers4 Ceramide synthase 4                        | 31.30 | 0.00 |
| TRINITY_sp|Q500|TKPR1 Tetraketide alpha-pyrophosphate synthase   | 31.30 | 0.00 |
| TRINITY_sp|Q9FP|EDR1 Serine/threonine-protein phosphatase        | 31.30 | 0.00 |
| TRINITY_sp|D4AY|VARB_013 ABC transporter G-family                | 31.30 | 0.00 |
| TRINITY_sp|Q653|Os06g02 Potassium channel K                      | 31.30 | 0.00 |
| TRINITY_sp|Q6UV|SASS6 Spindle assembly abnormal protein          | 31.30 | 0.00 |
| TRINITY_sp|Q54B|DDG25 Uncharacterized membrane protein           | 31.30 | 0.00 |
| TRINITY_sp|Q6TN|rab13 Rab-like protein 3                      | 31.30 | 0.00 |
| TRINITY_sp|Q3MD|pcxA Proton extrusion protein                    | 31.30 | 0.00 |
| TRINITY_sp|Q6GL|walref-THO complex subunit                       | 31.30 | 0.00 |
| TRINITY_sp|P519|MNAT1 CDK-activating kinase                      | 31.30 | 0.00 |
| TRINITY_sp|Q8CG|Thptpa Thiamine-triphosphatase                   | 31.30 | 0.00 |
| TRINITY_sp|Q9FF|ABCG28 ABC transporter G-family                  | 31.30 | 0.00 |
| TRINITY_sp|Q92S|Slc8b1 Sodium/potassium/calcium transporter      | 31.30 | 0.00 |
| TRINITY_sp|Q9ST|APC8 Anaphase-promoting complex                 | 31.30 | 0.00 |
| TRINITY_sp|Q81M|speA Arginine decarboxylase                      | 31.30 | 0.00 |
| TRINITY_sp|Q5L0|mureE UDP-N-acetylmuramoyl-MurNAc-t-Glu-t-Phe-UDP-N-acetylglucosamine-1-phosphate transferase | 31.30 | 0.00 |
| TRINITY_sp|Q5WE|mutS2 Endonuclease MutS2                        | 31.30 | 0.00 |
| TRINITY_sp|Q7PC|PSD Exportin-T OS=Arabidopsis                  | 31.30 | 0.00 |
| TRINITY_sp|Q7T2|map3k10 Mitogen-activated protein kinase         | 31.30 | 0.00 |
| TRINITY_sp|Q5UF|MIMI_R2 Uncharacterized protein                 | 31.20 | 0.00 |
| TRINITY_sp|Q9LF|PUB1 Probable ubiquitin E3 ubiquitin-protein-activating ubiquitin E3 ubiquitin-protein-activating kinase | 31.20 | 0.00 |
| TRINITY_sp|Q54B|mcf6 Mitochondrial subunit                     | 31.20 | 0.00 |
| TRINITY_sp|Q5KT|Naaa N-acyethanolamine-1-phosphate transferase   | 31.20 | 0.00 |
| TRINITY_sp|Q54D|DDG25 Thimet-like oligopeptide                   | 31.20 | 0.00 |
| TRINITY_sp|P0DK|HSD1 11-beta-hydroxysteroid dehydrogenase        | 31.20 | 0.00 |
| TRINITY_sp|A0DS|GSPATTO Probable protein phosphatase             | 31.20 | 0.00 |
| TRINITY_sp|Q7T2|sgsm3 Small G protein sig                        | 31.20 | 0.00 |
| TRINITY_sp|P412|Abca2 ATP-binding cassette                      | 31.20 | 0.00 |
| TRINITY_sp|Q8RW|UPL6 E ubiquitin-protein-activating ubiquitin E3 ubiquitin-protein-activating kinase | 31.20 | 0.00 |
| TRINITY_sp|O956|CNOT4 CCR4-NOT transcript                       | 31.20 | 0.00 |
| TRINITY_sp|P307|Gstt2 Glutathione S-transferase                 | 31.20 | 0.00 |
| TRINITY_sp|Q8BK|Ahsa1 Activator of 90 kDa                       | 31.20 | 0.00 |
| TRINITY_sp|Q9HV|Invdol1 Leishmanolysin-like                     | 31.20 | 0.00 |
| TRINITY_sp|P612|STXB Syntaxin-1B OS=Bos                         | 31.20 | 0.00 |
| TRINITY_sp|Q8R4|Mgl1 Monoglyceride lipase                      | 31.20 | 0.00 |
| TRINITY_sp|Q056|CTR1 Serine/threonine-protein                   | 31.20 | 0.00 |
| TRINITY_sp|F4JL|LDL3 Lysine-specific histidine                 | 31.20 | 0.00 |
| TRINITY_sp|Q8L7|LPEAT1 Lysophospholipid acetyl transferase     | 31.20 | 0.00 |
| TRINITY_sp|Q7TQ|Poln DNA polymerase nu O                       | 31.20 | 0.00 |
| TRINITY_sp|Q8S4|Os07g05 Zinc finger CCCH domain                | 31.20 | 0.00 |
| TRINITY_sp|Q96P|ACAP3 Arf-GAP with coiled helix                  | 31.20 | 0.00 |
| TRINITY_sp|Q55F|KrsB Serine/threonine-protein phosphatase       | 31.20 | 0.00 |
| TRINITY_sp|Q96J|VPS39 Vam6/Vps39-like protein                   | 31.20 | 0.00 |
| TRINITY_sp|A6H7|ACPP Prostatic acid phospholipid hydrolase     | 31.20 | 0.00 |
| TRINITY_sp|Q425|UBC13 Ubiquitin-conjugating enzyme              | 31.20 | 0.00 |
| TRINITY_sp|P370|Por NADPH--cytochrome P oxidoreductase          | 31.20 | 0.00 |
| TRINITY_sp|Q290|ITIH1 Inter-alpha-trypsin                      | 31.20 | 0.00 |
| TRINITY_sp|O822|At2g197 AP-4 complex subunit                    | 31.20 | 0.00 |
| TRINITY_sp|Q559|gacU Rho GTPase-activating protein              | 31.20 | 0.00 |
TRINITY_sp|Q2QFU2AF65B Splicing factor U2a 31.20 0.00
TRINITY_sp|Q5ZJ3|PRF3 U4/U6 small nuclear 31.20 0.00
TRINITY_sp|P835|ARHGA P3 Rho GTase-activati 31.20 0.00
TRINITY_sp|O653|SY P41 Syntaxin-41 OS=Arab 31.20 0.00
TRINITY_sp|Q8RXITa1g068 Uncharacterized mem 31.20 0.00
TRINITY_sp|Q749|POX2 Acy1-coenzyme A oxi 31.20 0.00
TRINITY_sp|Q140|1mt1 Inositol phosphocer 31.20 0.00
TRINITY_sp|Q547|gacct Y Rho GTase-activati 31.20 0.00
TRINITY_sp|Q6BV|1PL1 Spindle assembly ch 31.20 0.00
TRINITY_sp|Q94A|RFS2 Probable galactinol 31.20 0.00
TRINITY_sp|F4J8|RRP5 rRNA biogenesis pro 31.20 0.00
TRINITY_sp|Q9ZKV|vd1C Probable short-chai 31.20 0.00
TRINITY_sp|Q8GYH|SULTR4 Probable sulfate tr 31.20 0.00
TRINITY_sp|P205|CAH1 Carbonic anhydrase 31.20 0.00
TRINITY_sp|O653|SY P41 Syntaxin-41 OS=Arab 31.20 0.00
TRINITY_sp|B6C2|Lrrc51 Leucine-rich repeat 31.20 0.00
TRINITY_sp|Q6L4|1SI1 E3 SUMO-protein lig 31.20 0.00
TRINITY_sp|Q84J|PTAC14 Protein PLASTID TRA 31.20 0.00
TRINITY_sp|A7SN|v1g246q(Serine/threonine-pr 31.20 0.00
TRINITY_sp|Q75J|rapgap1 RapA guanosine trip 31.20 0.00
TRINITY_sp|Q8W4|H PAT1 Hydroxyproline O-ar 31.20 0.00
TRINITY_sp|Q8RX|At3g633 Probable inactive p 31.20 0.00
TRINITY_sp|P285|DUSP1 Dual specificity pr 31.20 0.00
TRINITY_sp|Q5P4|gnt14 Glycosyltransferase 31.20 0.00
TRINITY_sp|Q8€K|DBB G02 RUS1 family protein 31.20 0.00
TRINITY_sp|Q6C3|NUF2 Probable kinetochor 31.20 0.00
TRINITY_sp|Q80V|Cep104 Centrosomal protein 31.20 0.00
TRINITY_sp|Q54B|abcB2 ABC transporter B f 31.20 0.00
TRINITY_sp|I7CT|f- Protopanaxadiol 6-h 31.20 0.00
TRINITY_sp|Q6L4|Padela Calcium/calmodulin- 31.20 0.00
TRINITY_sp|Q9LVL|PVA21 Vesicle-associated 31.20 0.00
TRINITY_sp|Q5TJ|forF Formin-F OS=Dictyos 31.20 0.00
TRINITY_sp|Q337|ADF10 Actin-depolymerizin 31.10 0.00
TRINITY_sp|PO0I|SAE1B-1 SUMO-activating enz 31.10 0.00
TRINITY_sp|Q9FFE|DSP4 Phosphoglucon phosp 31.10 0.00
TRINITY_sp|P226|dhlhA Haloalkane dehaloge 31.10 0.00
TRINITY_sp|A4II|s4s47a1 Multidrug and toxin 31.10 0.00
TRINITY_sp|Q7BW|as4A Adaptive-response s 31.10 0.00
TRINITY_sp|Q122|INP53 Polyphosphatidylin 31.10 0.00
TRINITY_sp|Q929|KCNB2 Potassium voltage-g 31.10 0.00
TRINITY_sp|Q96E|CRS1 Microspherule prote 31.10 0.00
TRINITY_sp|Q585|MJJ123 Uncharacterized pro 31.10 0.00
TRINITY_sp|Q177|mpst-1 Putative thiosulfat 31.10 0.00
TRINITY_sp|F4J5|VPS54 Vacuolar protein so 31.10 0.00
TRINITY_sp|P235|MRS4 Mitochondrial RNA-s 31.10 0.00
TRINITY_sp|P395|DRS2 Probable phospholip 31.10 0.00
TRINITY_sp|Q9BS|TUBGCP2 Gamma-tubulin compl 31.10 0.00
TRINITY_sp|Q10L|MTP2 Metal tolerance pro 31.10 0.00
TRINITY_sp|Q5S5|Os07g064 DEAD-box ATP-depend 31.10 0.00
TRINITY_sp|P0A8|yida Sugar phosphatase Y 31.10 0.00
TRINITY_sp|Q9UP|USP24 Ubiquitin carboxyl- 31.10 0.00
TRINITY_sp|P411|Rpl28 60S ribosomal prote 31.10 0.00
TRINITY_sp|Q922|Trim59 Tripartite motif-co 31.10 0.00
TRINITY_sp|Q9SUS|At4g323 Probable sugar phos 31.10 0.00
TRINITY_sp|F4JJ|NDB3 External alternativ 31.10 0.00
TRINITY_sp|Q653|Os09g05 Probable protein ph 31.10 0.00
| Accession | Description | Score | E-value |
|-----------|-------------|-------|---------|
| sp| Putative ubiquitin | 31.10 | 0.00 |
| sp| SH3 and F-BAR domain | 31.10 | 0.00 |
| sp| Diacetyl reductase | 31.10 | 0.00 |
| sp| Probable LRR receptor | 31.10 | 0.00 |
| sp| Delta(6)-fatty-acid desaturase fat-3 | 31.10 | 0.00 |
| sp| Phosducin-like protein | 31.10 | 0.00 |
| sp| Vacuolar protein sorting-associated protein 53 A | 31.10 | 0.00 |
| sp| ATP-dependent RNA helicase DBP9 | 31.10 | 0.00 |
| sp| Nucleolar protein 14 | 31.10 | 0.00 |
| sp| Cellulase/esterase CelE | 31.10 | 0.00 |
| sp| ADP-ribosylation factor GTPase-activating protein AGD10 | 31.10 | 0.00 |
| sp| Copine-6 | 31.10 | 0.00 |
| sp| Multidrug and toxin extrusion protein 2 | 31.10 | 0.00 |
| sp| Protein dispatched homolog 3 | 31.10 | 0.00 |
| sp| RNA-binding protein NOB1 | 31.10 | 0.00 |
| sp| Archaemetzincin-2 | 31.10 | 0.00 |
| sp| Conserved oligomeric Golgi complex subunit 6 | 31.10 | 0.00 |
| sp| Aquaporin-4 | 31.10 | 0.00 |
| sp| Probable mitochondrial chaperone BCS1-A | 31.10 | 0.00 |
| sp| Cell division cycle protein 123 | 31.10 | 0.00 |
| sp| Nucleolar protein 12 | 31.10 | 0.00 |
| sp| Two-component system protein A | 31.10 | 0.00 |
| sp| 50S ribosomal protein L17 | 31.10 | 0.00 |
| sp| Protein yop1 | 31.10 | 0.00 |
| sp| Serine/threonine-protein kinase KIN2 | 31.10 | 0.00 |
| sp| Tyrosinase | 31.10 | 0.00 |
| sp| Hybrid signal transduction histidine kinase L | 31.10 | 0.00 |
| sp| Transcription factor GTE3, chloroplastic | 31.10 | 0.00 |
| sp| Interferon-induced GTP-binding protein Mx1 | 31.10 | 0.00 |
| sp| Nuclear pore complex protein NUP98A | 31.10 | 0.00 |
| sp| Tetraketide alpha-pyrone reductase 1 | 31.10 | 0.00 |
| sp| Autophagy-related protein 16-1 | 31.10 | 0.00 |
| sp| Putative sulfate transporter 4.2 | 31.10 | 0.00 |
| sp| SH3 and F-BAR domain-containing protein | 31.10 | 0.00 |
| sp| Putative membrane-associated protein | 31.10 | 0.00 |
| sp| Cell division cycle protein | 31.10 | 0.00 |
| sp| Ras-related protein | 31.10 | 0.00 |
| sp| Nuclear pore complex | 31.10 | 0.00 |
| sp| Interferon-induced | 31.10 | 0.00 |
| sp| Group 1 truncated | 31.10 | 0.00 |
| sp| N6-adenosine-methyltransferase | 31.10 | 0.00 |
| sp| Putative membrane-associated protein | 31.10 | 0.00 |
| sp| Transcription factor | 31.10 | 0.00 |
| sp| Protein yop1 | 31.10 | 0.00 |
| sp| Hybrid signal transducer | 31.10 | 0.00 |
| sp| Phosducin-like protein | 31.10 | 0.00 |
| sp| Cell cycle checkpoint protein | 31.10 | 0.00 |
| sp| ADP-ribosylation factor | 31.10 | 0.00 |
| sp| RNA-binding protein | 31.10 | 0.00 |
| sp| Two-component system protein | 31.10 | 0.00 |
| sp| Alkylated DNA repair | 31.10 | 0.00 |
| sp| Multidrug and toxin | 31.10 | 0.00 |
| sp| Autophagy-related protein | 31.10 | 0.00 |
| sp| Intersectin-1 | 31.10 | 0.00 |
| sp| Uncharacterized serine/threonine-protein kinase | 31.10 | 0.00 |
| sp| Tyrosyl-DNA phosphodiesterase | 31.10 | 0.00 |
| sp| Serine/threonine-protein kinase | 31.10 | 0.00 |
| sp| Conserved oligomerization domain-containing protein 6 | 31.10 | 0.00 |
| sp| ATP-dependent RNA helicase | 31.10 | 0.00 |
| sp| Aquaporin-4 | 31.10 | 0.00 |
| Accession   | Protein Name                           | Description                           | Score | E-value |
|-------------|----------------------------------------|---------------------------------------|-------|---------|
| P20040      | Beta-hexosaminidase                     | 31.00                                 | 0.00  |
| Q44945      | Hydroxyproline O-arabinosyltransferase  | 31.00                                 | 0.00  |
| Q86715      | Kinesin-like protein                    | 31.00                                 | 0.00  |
| P47741      | Signal recognition                      | 31.00                                 | 0.00  |
| Q9C511      | Purple acid phosphatase                 | 31.00                                 | 0.00  |
| Q5R7F1      | Prostamide/prostaglandin                | 31.00                                 | 0.00  |
| Q7M3R2      | RING finger protein                     | 31.00                                 | 0.00  |
| Q8L7I1      | L-threonine dehydrogenase               | 31.00                                 | 0.00  |
| Q8NB81      | Retinol dehydrogenase                   | 31.00                                 | 0.00  |
| P981R5      | RNA-binding protein                     | 31.00                                 | 0.00  |
| Q9SHC5      | Cyclin-U2-1                             | 31.00                                 | 0.00  |
| Q12441      | tRNA (guanine(9)-N1)                    | 31.00                                 | 0.00  |
| Q34425      | ATP-dependent RecD                      | 31.00                                 | 0.00  |
| Q88N7T      | THO complex subunit                     | 31.00                                 | 0.00  |
| Q94015      | Putative clathrin                        | 31.00                                 | 0.00  |
| Q5Q2V5      | Prolycopene isomerase                   | 31.00                                 | 0.00  |
| Q8WNI3      | Protein STRICTOSIDI                     | 31.00                                 | 0.00  |
| Q9QV55      | Sperm motility kinesin                  | 31.00                                 | 0.00  |
| Q6NL11      | Lipid phosphate phosphatase             | 31.00                                 | 0.00  |
| Q86I11      | Probable serine/threonine               | 31.00                                 | 0.00  |
| Q9LT7M      | Mitotic spindle checkpoint              | 31.00                                 | 0.00  |
| Q9QY1D      | DNAJ homolog subfamily                  | 31.00                                 | 0.00  |
| Q9C5S0      | Eukaryotic homolog subfamily            | 31.00                                 | 0.00  |
| Q5XQ6P      | Protein CTR9 homologue                  | 31.00                                 | 0.00  |
| Q8GUZC      | Chaperone protein d                     | 31.00                                 | 0.00  |
| Q9W4J0      | cAMP-specific 3',5'cAMP-binding protein | 31.00                                 | 0.00  |
| Q8HL1O      | DEAD-box ATP-dependent phosphatase      | 31.00                                 | 0.00  |
| Q1454Q      | Inositol 1,4,5-trisphosphate            | 31.00                                 | 0.00  |
| Q9LY1C      | Putative callose synthase               | 31.00                                 | 0.00  |
| Q9AWF1      | Alpha-glucan water                      | 31.00                                 | 0.00  |
| Q54P0S      | Oxyysterol-binding protein              | 31.00                                 | 0.00  |
| P14645      | cAMP-specific 3',5'cAMP-binding protein | 31.00                                 | 0.00  |
| Q2W1Y1      | Probable histidine                      | 31.00                                 | 0.00  |
| Q5AF1X      | Phosphorylase-kinase                    | 30.90                                 | 0.00  |
| Q0125V      | Vacuolar protein ABC                     | 30.90                                 | 0.00  |
| Q88N5A      | ATP synthase mitochon                  | 30.90                                 | 0.00  |
| Q38986      | Ras-related protein                     | 30.90                                 | 0.00  |
| Q058Z0      | Glycerate 2-kinase                      | 30.90                                 | 0.00  |
| Q624Y4      | Leishmanolysin-like                     | 30.90                                 | 0.00  |
| Q4R84D      | DNAJ homolog subfamily                  | 30.90                                 | 0.00  |
| Q55C27      | Probable serine/threonine               | 30.90                                 | 0.00  |
| P21870      | Probable FKBP-type                      | 30.90                                 | 0.00  |
| Q23FT4      | Tubulin glycylation                     | 30.90                                 | 0.00  |
| P3288S      | Protein SS1 OS-Sac                      | 30.90                                 | 0.00  |
| Q9P771      | Peroxide stress-activated               | 30.90                                 | 0.00  |
| Q390JM      | Suppressor protein                      | 30.90                                 | 0.00  |
| Q9VZ4T      | Transcription elong                     | 30.90                                 | 0.00  |
| Q55DP6      | Serine/threonine-prefered               | 30.90                                 | 0.00  |
| Q14988      | E3 ubiquitin-protein                    | 30.90                                 | 0.00  |
| Q9ST7R      | E3 ubiquitin-protein                    | 30.90                                 | 0.00  |
| Q5AXW5      | Protein bcP1 OS-Eme                     | 30.90                                 | 0.00  |
| Q0JI5Y      | CBL-interacting protein                 | 30.90                                 | 0.00  |
| Q8BK74      | Activator of 90 kDa                     | 30.90                                 | 0.00  |
| Q5XG5Y      | Non-canonical poly(A) binding protein   | 30.90                                 | 0.00  |
| Q8KZ2T      | Serine/threonine-prefered               | 30.90                                 | 0.00  |
| Q54P0T      | Eukaryotic translation                  | 30.90                                 | 0.00  |
Deoxyhypusine hydroxylase OS=Danio rerio GN=dohh PE=2 SV=1

Tectonic-3 OS=Macaca fascicularis GN=TCTN3 PE=2 SV=1

Probable 26S proteasome non-ATPase regulatory subunit 9 OS=Dictyostelium discoideum GN=psmD9 PE=2 SV=1

Vacuolar protein-sorting-associated protein 36 OS=Danio rerio GN=vps36 PE=2 SV=1

Carotenoid cleavage dioxygenase 8 homolog A, chloroplastic OS=Oryza sativa subsp. japonica GN=CCD8A PE=2 SV=1

GTPase-activating Rap/Ran-GAP domain-like protein 3 OS=Homo sapiens GN=GARNL3 PE=2 SV=2

Methylsterol monooxygenase 1-3 OS=Arabidopsis thaliana GN=SMO1-3 PE=2 SV=1

Gamma-glutamyl peptidase 2 OS=Arabidopsis thaliana GN=GGP2 PE=2 SV=1

Dynamin-like protein A OS=Dictyostelium discoideum GN=dlpA PE=2 SV=1

BEACH domain-containing protein C2 OS=Arabidopsis thaliana GN=BCHC2 PE=1 SV=1

ABC transporter C family member 2 OS=Dictyostelium discoideum GN=abcC2 PE=3 SV=1

Transforming growth factor-beta-induced protein ig-h3 OS=Mus musculus GN=Tgfbi PE=1 SV=1

Dual specificity protein kinase shkB OS=Dictyostelium discoideum GN=shkB PE=3 SV=1

Protein CLP1 homolog OS=Arabidopsis thaliana GN=CLPS3 PE=1 SV=1

Protein-lysine methyltransferase METTL21D OS=Mus musculus GN=Vcpkmt PE=2 SV=2

Failed axon connections homolog OS=Homo sapiens GN=FAXC PE=2 SV=2

Lysophospholipid acyltransferase LPEAT2 OS=Arabidopsis thaliana GN=LPEAT2 PE=1 SV=1

Probable serine/threonine-protein kinase gdt2 OS=Dictyostelium discoideum GN=gdt2 PE=2 SV=1

Protein POLLEN DEFECTIVE IN GUIDANCE 1 OS=Arabidopsis thaliana GN=POD1 PE=1 SV=1

50S ribosomal protein L9 OS=Aquifex aeolicus (strain VF5) GN=rplI PE=3 SV=1

ARF guanine-nucleotide exchange factor GNOM OS=Arabidopsis thaliana GN=GN PE=1 SV=1

Transient receptor potential cation channel subfamily V member 5 OS=Mus musculus GN=Trpv5 PE=1 SV=2

Guanylate-binding protein 7 OS=Homo sapiens GN=GBP7 PE=2 SV=2

Copia protein OS=Drosophila melanogaster GN=GIP PE=1 SV=3

DnaJ protein homolog 1 (Fragment) OS=Allium porrum GN=DNAJ1 PE=2 SV=1

Dedicator of cytokinesis protein 8 OS=Mus musculus GN=Dock8 PE=1 SV=4

E3 ubiquitin-protein ligase dbl4 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=dbl4 PE=3 SV=1

TRINITY_DN48217_c0_g2

TRINITY_DN47431_c0_g4

TRINITY_DN47369_c0_g7

TRINITY_DN44841_c0_g1

TRINITY_DN44131_c0_g5

TRINITY_DN43183_c0_g1

TRINITY_DN428_c0_g1

TRINITY_DN42019_c0_g2

TRINITY_DN41738_c0_g1

TRINITY_DN37566_c0_g2

TRINITY_DN37265_c0_g1

TRINITY_DN36982_c0_g5

TRINITY_DN36956_c1_g7

TRINITY_DN36506_c0_g1

TRINITY_DN36183_c0_g3

TRINITY_DN36138_c0_g3

TRINITY_DN36015_c0_g1

TRINITY_DN35791_c0_g8

TRINITY_DN35786_c0_g5

TRINITY_DN34379_c0_g2

TRINITY_DN34004_c0_g1

TRINITY_DN30084_c0_g1

TRINITY_DN292_c0_g1

TRINITY_DN24718_c0_g1

TRINITY_DN2117_c0_g1

TRINITY_DN52537_c1_g3

TRINITY_DN52444_c1_g1

TRINITY_DN51629_c0_g1

TRINITY_DN50963_c0_g1

TRINITY_DN50810_c0_g3

TRINITY_DN50247_c0_g1

TRINITY_DN49455_c0_g1

TRINITY_DN49050_c0_g1

TRINITY_DN47645_c0_g2

TRINITY_DN47175_c0_g7

TRINITY_DN46839_c0_g1

TRINITY_DN46629_c0_g3
| Accession | Name                                      | Gene Symbol | Description                                                                 | Expression Level | Similarity Score |
|-----------|-------------------------------------------|-------------|-------------------------------------------------------------------------------|------------------|------------------|
| TRINITY_sp| P548|TGL2 | Lipase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) | 30.80            | 0.00             |
| TRINITY_sp| Q93W|Atg4| Uncharacterized protein | 30.80            | 0.00             |
| TRINITY_sp| Q9SY|Atg4G029|CSC1-like protein A | 30.80            | 0.00             |
| TRINITY_sp| Q6GQ|Nom1 | Nodal modulator 1 O | 30.80            | 0.00             |
| TRINITY_sp| Q5UR|MIMI_L9| Uncharacterized protein | 30.80            | 0.00             |
| TRINITY_sp| Q55O|DDB_G02 | Probable phosphatidylcholine | 30.80            | 0.00             |
| TRINITY_sp| Q5X1|Dzip1l | Zinc finger protein | 30.80            | 0.00             |
| TRINITY_sp| P027|FCTP | Probable tRNA (guanine(26)-N(2))-dimethyltransferase | 30.80            | 0.00             |
| TRINITY_sp| Q6ZY|GWD3 | Phosphoglucomutase, water dikinase, chloroplastic | 30.80            | 0.00             |
| TRINITY_sp| Q007|vatE | V-type proton ATPase | 30.70            | 0.00             |
| TRINITY_sp| Q9M3|PAT05 | Probable protein S- | 30.70            | 0.00             |
| TRINITY_sp| Q224|T12E12 | Potential E3 ubiquitin | 30.70            | 0.00             |
| TRINITY_sp| Q96M|PACRG | Parkin coregulated | 30.70            | 0.00             |
| TRINITY_sp| Q55B|abcA8 | ABC transporter A f | 30.70            | 0.00             |
| TRINITY_sp| Q5F3|C1GALT1 | Glycoprotein-N-acetylgalactosamine-3-beta-galactosyltransferase | 30.70            | 0.00             |
| TRINITY_sp| Q8VJ|RS2233 | Serine/arginine-rich | 30.70            | 0.00             |
| TRINITY_sp| Q9FLA|PAT06 | Probable protein S- | 30.70            | 0.00             |
| TRINITY_sp| Q6GL|pip4k2c | Phosphatidylinositolipase | 30.70            | 0.00             |
| TRINITY_sp| Q54G|rab18 | Ras-related protein | 30.70            | 0.00             |
| TRINITY_sp| Q8LF|RBL19 | Rhomboid-like protease | 30.70            | 0.00             |
| TRINITY_sp| Q9VJ|CG6388 | Probable tRNA (guaninyltransferase) | 30.70            | 0.00             |
| TRINITY_sp| Q84M|ABCA1 | ABC transporter A f | 30.70            | 0.00             |
| TRINITY_sp| Q6P6|ak8 | Adenylate kinase 8 | 30.70            | 0.00             |
| TRINITY_sp| Q5AJ|MRD1 | Multiple RNA-binding protein | 30.70            | 0.00             |
| TRINITY_sp| Q9VM|Rat1 | 5'-3' exoribonuclease | 30.70            | 0.00             |
| TRINITY_sp| P544|yrkH | Uncharacterized protein | 30.70            | 0.00             |
| TRINITY_sp| Q8L7|ULP2B | Probable ubiquitin-dependent protein | 30.70            | 0.00             |
| TRINITY_sp| Q099|tif224 | Probable translation initiation factor | 30.70            | 0.00             |
| TRINITY_sp| Q485|BRR2B | DexH-box ATP-dependent protein | 30.70            | 0.00             |
| TRINITY_sp| Q139|pnk1 | Bifunctional polynucleotide | 30.70            | 0.00             |
| TRINITY_sp| Q5UQ|MIMI_L4 | Putative alpha/beta | 30.70            | 0.00             |
| TRINITY_sp| Q8N6|METTL13 | Methyltransferase-1 | 30.70            | 0.00             |
| TRINITY_sp| Q8BG|Stk17b | Serine/threonine-protein kinase | 30.70            | 0.00             |
| TRINITY_sp| A6U|hemL | Glutamate-1-semialdehyde | 30.70            | 0.00             |
| TRINITY_sp| Q8C6|C1orf2 | Protein C21orf2 homolog | 30.70            | 0.00             |
| TRINITY_sp| Q9Z1|Nik | Protein Red OS=Mus | 30.70            | 0.00             |
| TRINITY_sp| B1Z|trpC | Indole-3-glycerol phosphate | 30.70            | 0.00             |
| TRINITY_sp| P041|GIP | Copia protein OS=Dr | 30.70            | 0.00             |
| TRINITY_sp| Q9K|NHX7 | Sodium/hydrogen exchanger | 30.70            | 0.00             |
| TRINITY_sp| P509|AVT4 | Vacuolar amino acid | 30.70            | 0.00             |
| TRINITY_sp| P102|pol | Polypeptide OS= | 30.70            | 0.00             |
| TRINITY_sp| Q9FV|MAP1D | Methionine aminopeptidase | 30.70            | 0.00             |
| TRINITY_sp| Q8H1|APY4 | Probable alanine deaminase | 30.70            | 0.00             |
| TRINITY_sp| Q9SB|PDK | Pyruvate dehydrogenase | 30.70            | 0.00             |
| TRINITY_sp| Q86U|RSPH3 | Radial spoke head protein | 30.70            | 0.00             |
| TRINITY_sp| Q54B|DDB_G02 | LIMR family protein | 30.70            | 0.00             |
| TRINITY_sp| Q9LW7|At3g268 | Acyltransferase-like | 30.70            | 0.00             |
| Protein Id       | Description                                    | Eukaryote   |   |
|------------------|------------------------------------------------|-------------|---|
| ATP-dependent DNA helicase PcrA | OS=Staphylococcus aureus (strain NCTC 8325) | 30.60       | 0.00 |
| E3 ubiquitin-protein | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Ras-related protein | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Protein FYV10 OS=Co | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Serine/threonine-protein | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| E3 ubiquitin-protein | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Alkaline ceramidase | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Bidirectional sugar | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Probable rRNA-proce | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Probable lysine-spe | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| WD repeat-containin | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Serine/threonine-pr | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| E3 ubiquitin-protein | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Guanine nucleotide- | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Glutathione S-trans | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Poly [ADP-ribose] p | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Cell wall alpha-1,3 | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Serine/threonine-pr | OS=Dictyostelium discoideum | 30.50       | 0.00 |
| Protein RRP5 homolog | OS=Bos taurus | 30.50       | 0.00 |
| Adenylate kinase OS=Aquifex aeolicus (strain VF5) | OS=Aquifex aeolicus (strain VF5) | 30.50       | 0.00 |

Note: The table includes various proteins and their descriptions, along with their respective Eukaryote and numbers.
Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1
Guanylate cyclase soluble subunit alpha-3 OS=Canis lupus familiaris GN=GUCY1A3 PE=2 SV=1
Serine/threonine-protein kinase STY46 OS=Arabidopsis thaliana GN=STY46 PE=1 SV=1
Elongator complex protein 2 OS=Arabidopsis thaliana GN=ELP2 PE=1 SV=1
Metal tolerance protein 12 OS=Arabidopsis thaliana GN=MTP12 PE=3 SV=1
Nucleolar protein 9 OS=Homo sapiens GN=NOP9 PE=1 SV=1
Short-chain-enoyl-CoA hydratase OS=Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787) GN=crt PE=1 SV=1
Ribosomal RNA-processing protein 7 homolog A OS=Mus musculus GN=Rrp7a PE=2 SV=1
Probable E3 ubiquitin-protein ligase HERC2 OS=Drosophila melanogaster GN=HERC2 PE=1 SV=3
Protein polyglycylase TTLL10 OS=Macaca fascicularis GN=TTLL10 PE=2 SV=1
Tyrosine-protein phosphatase YVH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YVH1 PE=1 SV=1
Endoglucanase 4 OS=Bacillus sp. (strain KSM-522) PE=3 SV=2
Aladin OS=Mus musculus GN=Aaas PE=1 SV=1
Vacuolar protein sorting-associated protein 13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VPS13 PE=1 SV=1
CWF19-like protein 1 homolog OS=Drosophila melanogaster GN=CG7741 PE=2 SV=1
Glucose-repressible alcohol dehydrogenase transcriptional effector OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=ccr4 PE=3 SV=1
Purple acid phosphatase 15 OS=Arabidopsis thaliana GN=PAP15 PE=1 SV=1
Protein ViaA OS=Erwinia tasmaniensis (strain DSM 17950 / CIP 109463 / Et1/99) GN=viaA PE=3 SV=1
Nucleoporin GLE2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GLE2 PE=1 SV=1
Para-nitrobenzyl esterase OS=Bacillus subtilis (strain 168) GN=pnbA PE=1 SV=2
Cactin OS=Drosophila melanogaster GN=cactin PE=1 SV=3
Histidine protein kinase NIK1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) GN=NIK1 PE=1 SV=2
Spectrin beta chain, non-erythrocytic 4 OS=Homo sapiens GN=SPTBN4 PE=1 SV=2
Cilia- and flagella-associated protein 52 OS=Chlamydomonas reinhardtii GN=CFAP52 PE=1 SV=1
Transcription initiation factor TFIID subunit 8 OS=Arabidopsis thaliana GN=TAF8 PE=1 SV=1
N-alpha-acetyltransferase 25, NatB auxiliary subunit OS=Homo sapiens GN=NAA25 PE=1 SV=1
Golgin candidate 5 OS=Arabidopsis thaliana GN=GC5 PE=1 SV=1
TRINITY_sp|Q9RYTAF8 Transcription initiation factor 30.40 0.00
TRINITY_sp|Q9SYTAF8 Transcription initiation factor 30.40 0.00
TRINITY_sp|Q4R8EINF2AK1 Eukaryotic translation 30.40 0.00
TRINITY_sp|Q8LAA5g1079 Probable protein phosphatase 30.40 0.00
TRINITY_sp|Q9H26SPRTBN4 Spectrin beta chain 30.40 0.00
TRINITY_sp|Q8IWCFAP52 Cilia- and flagella 30.40 0.00
TRINITY_sp|P37996pnBA Para-nitrobenzyl esterase 30.40 0.00
TRINITY_sp|Q75FicpRas Circularly permutating 30.40 0.00
TRINITY_sp|P28621cpr Aalpha-trypsin 30.40 0.00
TRINITY_sp|Q549g1F Metabotropic glutamate 30.40 0.00
TRINITY_sp|Q29013ViaA Protein ViaA OS=Erw 30.40 0.00
TRINITY_sp|Q9VMHC2Probable E3 ubiquitin 30.40 0.00
TRINITY_sp|Q9CHB17814 Uncharacterized protein 30.40 0.00
TRINITY_sp|Q29013Th1 Inter-alpha-trypsin 30.40 0.00
TRINITY_sp|Q14CNAAL25 N-alpha-acetyltransferase 30.40 0.00
TRINITY_sp|Q923SPAC6G9.1 Pumilio domain-containing 30.40 0.00
TRINITY_sp|Q216Easp1 Phosphatidylinosito 30.40 0.00
TRINITY_sp|Q0787VP13 Vacuolar protein sorting 30.40 0.00
TRINITY_sp|Q54GCsec1 Protein transport 30.40 0.00
TRINITY_sp|Q40GHGCUY1A3 Guanylate cyclase 30.40 0.00
TRINITY_sp|P400AGLE2 Nucleoporin GLE2 OS 30.40 0.00
TRINITY_sp|Q54GIDG2/4F PXMP2/4 family protein 30.40 0.00
TRINITY_sp|Q9MISLOGY tRNA-splicing endonuclease 30.40 0.00
TRINITY_sp|F4J1STY46 Serine/threonine-protein 30.40 0.00
TRINITY_sp|Q54KBDD2/4 Probable GH family 30.40 0.00
TRINITY_sp|Q493HHRNPR Heterogeneous nuclear 30.40 0.00
TRINITY_sp|Q5AS5NIK1 Histidine protein k 30.40 0.00
TRINITY_sp|P581P1lcr Phospholipid scramblase 30.40 0.00
TRINITY_sp|Q9D1Rrgp7a Ribosomal RNA-proce 30.40 0.00
TRINITY_sp|Q9STDFAP15 Purple acid phosphatase 30.40 0.00
TRINITY_sp|Q022YVH1 Tyrosine-protein phosphatase 30.40 0.00
TRINITY_sp|Q0WVGIC5 Golgin candidate 3 30.40 0.00
| Protein Name                      | Organism  | Gene Symbol | Peptide ID | Coverage | Score |
|----------------------------------|-----------|-------------|------------|----------|-------|
| Beta-fructofuranosidase, insoluble isoenzyme 3 | Daucus carota | INV3       | Q396فز | 30.40   | 0.00  |
| Echinoderm microtub            |           | EML3       | Q32فز     | 30.40   | 0.00  |
| Protein FLOWERING L            |           | QCAفز     | Q9CAفز     | 30.40   | 0.00  |
| ABC transporter C f            |           | abcC8     | Q54فز     | 30.40   | 0.00  |
| Transposon Ty3-G Ga           |           | TY3B-G     | Q993فز   | 30.40   | 0.00  |
| Aquaporin TIP2-1 OS          |           | TIP2-1     | Q9ATفز   | 30.30   | 0.00  |
| Protein phosphatase        |           | P206فز | P206فز     | 30.30   | 0.00  |
| Uncharacterized pro         |           | JM1123     | Q585فز   | 30.30   | 0.00  |
| Serine/threonine-pro         |           | Stk17b    | Q88Gفز   | 30.30   | 0.00  |
| Uncharacterized pro         |           | D4فز     | Q9D4فز   | 30.30   | 0.00  |
| BTB/POZ domain-cont       |           | Kcdt21     | Q3فز      | 30.30   | 0.00  |
| Nicotinamide ribosi      |           | NMRK2     | Q9NPفز   | 30.30   | 0.00  |
| Histidine kinase 3       |           | TAHK3     | Q9C5فز     | 30.30   | 0.00  |
| Acyl-CoA-binding do        |           | acbd6     | Q66فز   | 30.30   | 0.00  |
| CBL-interacting pro       |           | slc35b1   | Q6H7فز   | 30.30   | 0.00  |
| tRNA-splicing endon         |           | TSEN2     | Q52فز     | 30.30   | 0.00  |
| Canalicular multisp       |           | Abcc2     | Q63فز   | 30.30   | 0.00  |
| Protein-lysine N-me        |           | EEFP2KMT  | Q96Gفز   | 30.30   | 0.00  |
| FYVE, RhoGEF and PH     |           | FGD4     | Q96فز   | 30.30   | 0.00  |
| Zinc finger protein       |           | ZNF622    | Q96Gفز   | 30.30   | 0.00  |
| cAMP-specific 3',5'          |           | Pde4c     | Q146فز   | 30.30   | 0.00  |
| Solute carrier fami       |           | slc35b1   | Q88Aفز   | 30.30   | 0.00  |
| Gamma-tubulin compl       |           | GCP4     | Q9M3فز   | 30.30   | 0.00  |
| Rab proteins gerany        |           | Rep      | Q9V8Rep  | 30.30   | 0.00  |
| Ubiquitin conjugati        |           | Ube4b    | Q9ESفز   | 30.30   | 0.00  |
| Gelation factor OS        |           | abpC     | P134فز   | 30.30   | 0.00  |
| Heat shock 70 kDa p        |           | HSP70-1فز | Q9S7فز   | 30.30   | 0.00  |
| Probable serine/thr       |           | drKD     | Q54فز     | 30.30   | 0.00  |
| Uncharacterized pro       |           | ygKD     | P54فز   | 30.30   | 0.00  |
| DNA-dependent metal         |           | P388فز   | P388فز     | 30.30   | 0.00  |
| Ascorbate-specific         |           | C1Yf     | C4فز     | 30.30   | 0.00  |
| Putative vacuolar p       |           | vps13F    | Q54Kفز   | 30.30   | 0.00  |
| Protein phosphatase       |           | fig      | B4JYفز   | 30.30   | 0.00  |
| E3 ubiquitin-protei      |           | SHPRH    | Q149فز   | 30.30   | 0.00  |
| Cilia- and flagella         |           | CFAP46    | A81Cفز   | 30.30   | 0.00  |
| WD repeat-containin        |           | WDR76    | B2Kفز   | 30.30   | 0.00  |
| Hybrid signal trans        |           | dhkE     | Q55Eفز   | 30.30   | 0.00  |
| Serine/threonine-pr         |           | WSTY17   | Q8R Wool  | 30.30   | 0.00  |
| Coronin-2A OS=Bos t         |           | LICORO2A  | Q32Lفز   | 30.30   | 0.00  |
| Voltage-dependent L         |           | Cacna1f  | Q9J1فز   | 30.30   | 0.00  |
| Hydrolyase FUB4        |           | FUB4     | A0Aفز   | 30.30   | 0.00  |
| Lipase ZK262.3 OS=C       |           | ZK262.3    | Q9Xفز   | 30.30   | 0.00  |
| FYVE, RhoGEF and PH     |           | FGD6     | Q6فز     | 30.30   | 0.00  |
| Phosphoinositide ph      |           | SAC6     | Q7X9فز   | 30.30   | 0.00  |
| Heat stress transcr       |           | HSFA1فز | P41فز   | 30.30   | 0.00  |
| Chloride channel pr        |           | CLC-D    | P929فز     | 30.30   | 0.00  |
| WD repeat-containin        |           | Wdr34    | Q5Uفز     | 30.30   | 0.00  |
| Choline transporter         |           | slc44a4  | Q7فز     | 30.30   | 0.00  |
| Putative 1-phosphat         |           | fab1     | O968فز   | 30.30   | 0.00  |
| Apoptosis-inducing        |           | alifm2  | B4F6فز   | 30.30   | 0.00  |
| TRINITY_sp|A1L4|CLT2 | Protein CLT2, chlor | 30.30 | 0.00 |
| TRINITY_sp|A2C5|rlpsF | 3OS ribosomal prote | 30.20 | 0.00 |
| TRINITY_sp|A6LU|tdh | L-threonine 3-dehyd | 30.30 | 0.00 |
| TRINITY_sp|A9UG|snpC | Gamma-soluble NSF a | 30.20 | 0.00 |
| TRINITY_sp|A6WU|tdh | L-threonine 3-dehyd | 30.30 | 0.00 |
| TRINITY_sp|A9UG|snpC | Gamma-soluble NSF a | 30.20 | 0.00 |
| TRINITY_sp|A6WU|tdh | L-threonine 3-dehyd | 30.30 | 0.00 |
| TRINITY_sp|A9UG|snpC | Gamma-soluble NSF a | 30.20 | 0.00 |
| TRINITY_sp|A6WU|tdh | L-threonine 3-dehyd | 30.30 | 0.00 |
| TRINITY_sp|A9UG|snpC | Gamma-soluble NSF a | 30.20 | 0.00 |
TRINITY_sp|P7887:tppl  Trehalose-phosphatase 30.00 0.00
TRINITY_sp|Q5CUq:abcC12  ABC transporter C f 30.00 0.00
TRINITY_sp|Q9LT6:VP59A  Vacuolar protein so 30.00 0.00
TRINITY_sp|Q9FN6:UVR8  Ultraviolet-B recep 30.00 0.00
TRINITY_sp|P221A:APA2  Diadenosine 5',5'''-P1,P4-tetraphosphate phosphorylase 30.00 0.00
TRINITY_sp|Q8LAU:RURH2  Probable uridine nu 30.00 0.00
TRINITY_sp|A4FV8:RL1D1  Ribosomal L1 domain 30.00 0.00
TRINITY_sp|A6QNR:FRRP36  Ribosomal RNA proce 30.00 0.00
TRINITY_sp|Q0137:cn3a1  Hsp70/Hsp90 co-chap 30.00 0.00
TRINITY_sp|Q0II1:DNAJC21  DnaJ homolog subfam 30.00 0.00
TRINITY_sp|Q5EAC:CH1D1  Chitinase domain-co 30.00 0.00
TRINITY_sp|Q92K1:afcr  1,5-anhydro-D-fruct 30.00 0.00
TRINITY_sp|Q9LRB:BSU1  Serine/threonine-pr 30.00 0.00
TRINITY_sp|Q6T44:rbrA  Probable E3 ubiquit 30.00 0.00
TRINITY_sp|Q9S9:CCR1  Cinnamoyl-CoA reduc 30.00 0.00
TRINITY_sp|Q9P31:db14  E3 ubiquitin-protei 30.00 0.00
TRINITY_sp|Q7TP4:Amap  Adipocyte plasma me 30.00 0.00
TRINITY_sp|Q9DB9:Phkg2  Phosphorylase b kin 30.00 0.00
TRINITY_sp|P360T:TUL1  Transmembrane E3 ub 30.00 0.00
TRINITY_sp|Q99J2:Thump1d  THUMP domain-contai 30.00 0.00
TRINITY_sp|Q94FL:ABCC1  ABC transporter D f 30.00 0.00
TRINITY_sp|Q55Ah:GDB_G02  PH and Rap-GAP doma 30.00 0.00
TRINITY_sp|P533P:YGR266W  Uncharacterized pro 30.00 0.00
TRINITY_sp|Q9M0:GGP3  Gamma-glutamyl pept 30.00 0.00
TRINITY_sp|Q84M8:ABCA1  ABC transporter A f 30.00 0.00
TRINITY_sp|P0CUZ:CTHT_00  Protein-lysine N-me 30.00 0.00
TRINITY_sp|P5111:A1  Dihydroflavonol 4-r 30.00 0.00
TRINITY_sp|Q54Y2:dhkJ  Hybrid signal trans 30.00 0.00
TRINITY_sp|Q9YS5:POLR3H  DNA-directed RNA po 30.00 0.00
TRINITY_sp|A0QSM:SMSEG_1  Putative S-adenosyl 30.00 0.00
TRINITY_sp|Q893H:hutG  Formimidoylglutamas 30.00 0.00
TRINITY_sp|Q54RI:dhkL  Hybrid signal trans 30.00 0.00
TRINITY_sp|P4641:  Glutathione S-trans 30.00 0.00
TRINITY_sp|Q6RG8:RGS1  Regulator of G-prot 30.00 0.00
TRINITY_sp|P5111:Taf1  Transcription initi 30.00 0.00
TRINITY_sp|P9666:nap  Uncharacterized car 30.00 0.00
TRINITY_sp|P266S:sigA  RNA polymerase sigm 30.00 0.00
TRINITY_sp|Q866I:ADCY10  Adenylate cyclase t 30.00 0.00
TRINITY_sp|Q086P:PU7  Multisubstrate pseu 30.00 0.00
TRINITY_sp|Q9TWm:myoM  Myosin-M heavy chai 30.00 0.00
TRINITY_sp|Q5SK3:serac1  Protein SERAC1 OS=D 30.00 0.00
TRINITY_sp|P2151:ALP1  Alpha-amylose OS=Sa 30.00 0.00
TRINITY_sp|Q054p:ksL  Polyketide synthase 30.00 0.00
TRINITY_sp|Q2BEG:GA18864  Esterase GA18864 OS 30.00 0.00
TRINITY_sp|H3J5:SGT1  Peptidyl serine alp 30.00 0.00
TRINITY_sp|Q54QC:DDB_G02  Probable E3 ubiquit 30.00 0.00
TRINITY_sp|Q54G3:gapcW  Rho GTPase-activati 30.00 0.00
TRINITY_sp|Q5RA3:ACOX3  Peroxisomal acyl-co 30.00 0.00
TRINITY_sp|Q9MA:ACBP4  Acyl-CoA-binding do 30.00 0.00
TRINITY_sp|Q079:PSR2  Probable phosphatas 30.00 0.00
TRINITY_sp|Q5AS5:NIK1  Histidine protein k 30.00 0.00
TRINITY_sp|P3881:TRA1  Transcription-assoc 30.00 0.00
TRINITY_sp|Q2NN6:Os12g05  Probable protein ph 30.00 0.00
TRINITY_sp|Q9FF1:At5g384  Probable dolichyl p 30.00 0.00
TRINITY_sp|Q944F:FKBP16-1  Peptidyl-prolyl cis 30.00 0.00
TRINITY_sp|Q55GUSD:G02  Probable serine/thr 30.00 0.00
| Accession   | Description                                                                 | Score | E-value |
|-------------|-----------------------------------------------------------------------------|-------|---------|
| TRINITY_sp| Hybrid signal transduction histidine kinase F | 29.60 | 0.00 |
| TRINITY_sp| Protein tipD OS=Dictyostelium discoideum | 29.60 | 0.00 |
| TRINITY_sp| Calpain-15 OS=Mus musculus | 29.60 | 0.00 |
| TRINITY_sp| Saccharopine dehydratase OS=Cellvibrio japonicus (strain Ueda107) | 29.60 | 0.00 |
| TRINITY_sp| CBL-interacting protein kinase 25 OS=Oryza sativa subsp. japonica | 29.60 | 0.00 |
| TRINITY_sp| E3 ubiquitin-protein ligase dbl4 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) | 29.60 | 0.00 |
| TRINITY_sp| Eukaryotic translation initiation factor isoform 4E-2 OS=Zea mays | 29.60 | 0.00 |
| TRINITY_sp| Acyl-CoA--sterol O-acyltransferase 1 OS=Arabidopsis thaliana | 29.60 | 0.00 |
| TRINITY_sp| Saccharopine dehydrogenase-like oxidoreductase OS=Rattus norvegicus | 29.60 | 0.00 |
| TRINITY_sp| Mitochondrial substrate carrier family protein L OS=Dictyostelium discoideum | 29.60 | 0.00 |
| TRINITY_sp| Glycerol-3-phosphate O-acyltransferase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) | 29.60 | 0.00 |
| TRINITY_sp| ABC transporter A family member 1 OS=Dictyostelium discoideum | 29.60 | 0.00 |
| TRINITY_sp| Patatin-like phospholipase domain-containing protein 1 OS=Mus musculus | 29.60 | 0.00 |
| TRINITY_sp| tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens | 29.60 | 0.00 |
| TRINITY_sp| DNA repair protein RAD51 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) | 29.60 | 0.00 |
| TRINITY_sp| ATP-dependent DNA helicase RecQ OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) | 29.60 | 0.00 |
| TRINITY_sp| Transforming protein p29 OS=Harvey murine sarcoma virus | 29.60 | 0.00 |
| TRINITY_sp| Chaperone protein DnaJ OS=Bacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) | 29.60 | 0.00 |
| TRINITY_sp| Tubulin polyglutamylase TTLL5 OS=Mus musculus | 29.60 | 0.00 |
| TRINITY_sp| WD repeat-containing protein 13 OS=Homo sapiens | 29.60 | 0.00 |
| TRINITY_sp| Calpain-15 OS=Mus musculus | 29.60 | 0.00 |
| TRINITY_sp| Protein transport protein sec1 OS=Dictyostelium discoideum | 29.60 | 0.00 |

Note: The table lists various protein descriptions along with their scores and E-values. The table format is consistent with the natural reading of the document.
| Accession | Gene Name           | Species               | OS         | GN     | PE | SV |
|-----------|---------------------|-----------------------|------------|--------|----|----|
| TRINITY_sp|Q54LqDDB_G02| Probable LIM domain | 29.50 | 0.00 |
| TRINITY_sp|A98YIpar-1 | Serine/threonine-pr | 29.50 | 0.00 |
| TRINITY_sp|Q8TL1ltv1 | Protein LTV1 homolo | 29.50 | 0.00 |
| TRINITY_sp|Q92F2CC2D2A | Coiled-coil and C2 | 29.50 | 0.00 |
| TRINITY_sp|Q4E4]Tc00.10 | Phosphatidylinosito | 29.50 | 0.00 |
| TRINITY_sp|Q3LHwge | Protein winged eye | 29.50 | 0.00 |
| TRINITY_sp|Q7Z5bPOLN | DNA polymerase nu O | 29.50 | 0.00 |
| TRINITY_sp|A22WNERG1 | Elicitor-responsive | 29.50 | 0.00 |
| TRINITY_sp|Q557atg4-1 | Cysteine protease a | 29.50 | 0.00 |
| TRINITY_sp|Q149SHPRH | E3 ubiquitin-protei | 29.50 | 0.00 |
| TRINITY_sp|Q9U1lIP11 | Importin-11 OS=Homo | 29.50 | 0.00 |
| TRINITY_sp|Q157[HRC1 | Probable E3 ubiqui | 29.50 | 0.00 |
| TRINITY_sp|P509AVT4 | Vacuolar amino acid | 29.50 | 0.00 |
| TRINITY_sp|Q55Figt2h1 | General transcripti | 29.50 | 0.00 |
| TRINITY_sp|O0561vanA | Vanillate O-demethy | 29.50 | 0.00 |
| TRINITY_sp|Q54U:shkD | Dual specificity pr | 29.50 | 0.00 |
| TRINITY_sp|A4IHttc9c | Tetraicopeptide r | 29.50 | 0.00 |
| TRINITY_sp|Q3UY1Rg13 | Ral guanine nucleot | 29.50 | 0.00 |
| TRINITY_sp|Q9VR[HRC2 | Probable E3 ubiqui | 29.50 | 0.00 |
| TRINITY_sp|P618; | Lipase OS=Rhizopus | 29.40 | 0.00 |
| TRINITY_sp|A4IHzfp3612 | mRNA decay activato | 29.40 | 0.00 |
| TRINITY_sp|Q5R9GBP6 | Guanylate-binding p | 29.40 | 0.00 |
| TRINITY_sp|Q8MPSno1 | Seneconine N-oxyme | 29.40 | 0.00 |
| TRINITY_sp|Q5H7CDC20 | Cell division cycle | 29.40 | 0.00 |
| TRINITY_sp|Q9H CSTIPL1 | Septin and tuftelin | 29.40 | 0.00 |
| TRINITY_sp|Q7XKFDIIL1-2 | Protein disulfide i | 29.40 | 0.00 |
| TRINITY_sp|P297AHSG | Alpha-2-HS-glycopro | 29.40 | 0.00 |
| TRINITY_sp|Q8DFnutA | 5'-nucleotidase OS= | 29.40 | 0.00 |
| TRINITY_sp|F4J5FMT | Clustered mitochond | 29.40 | 0.00 |
| TRINITY_sp|Q9LS[CASP | Protein CASP OS=Ara | 29.40 | 0.00 |
| TRINITY_sp|P612STX1B | Syntaxin-1B OS=Homo | 29.40 | 0.00 |
| TRINITY_sp|Q2QVSEC10 | Exocyst complex com | 29.40 | 0.00 |
| TRINITY_sp|Q033DNAJ | DnaJ protein homolo | 29.40 | 0.00 |
| TRINITY_sp|Q3S2PIGS | GPI transamidase co | 29.40 | 0.00 |
| TRINITY_sp|Q088FAR2 | Fatty acyl-CoA redu | 29.40 | 0.00 |
| TRINITY_sp|Q869napA | Nck-associated prot | 29.40 | 0.00 |
| TRINITY_sp|Q5I0serpinb1 | Leukocyte elastase | 29.40 | 0.00 |
| TRINITY_sp|Q9Y4DAAM1 | Disheveled-associat | 29.40 | 0.00 |
| TRINITY_sp|Q54M:xpr1 | SPX and EXS domain- | 29.40 | 0.00 |
| TRINITY_sp|Q43LPRPF4 | U4/U6 small nuclear | 29.40 | 0.00 |
| TRINITY_sp|Q749bcpl | Protein bcp1 OS=Sch | 29.40 | 0.00 |
| TRINITY_sp|A7RKvlg2321| Protein AKTIP homol | 29.40 | 0.00 |
| TRINITY_sp|Q9XIILSMT-L | [Fructose-bisphosph | 29.40 | 0.00 |
| TRINITY_sp|P551Sh3bp1 | SH3 domain-binding | 29.40 | 0.00 |
| TRINITY_sp|Q018OTUD4 | OTU domain-containi | 29.40 | 0.00 |
| TRINITY_sp|Q9XHMTIF3C1 | Eukaryotic translat | 29.40 | 0.00 |
| TRINITY_sp|Q9JHDAdat1 | tRNA-specific adeno | 29.40 | 0.00 |
| TRINITY_sp|Q91Wdag1b | Snl-specific diacyl | 29.40 | 0.00 |
| TRINITY_sp|C0HJ1- | Alpha-mannosidase O | 29.40 | 0.00 |
| TRINITY_sp|Q0IIIRAB18 | Ras-related protein | 29.40 | 0.00 |
| TRINITY_sp|P170crtK | Protein CrtK OS=Rho | 29.40 | 0.00 |
| TRINITY_sp|Q95LITBC1D22 | TBC1 domain family | 29.40 | 0.00 |
| TRINITY_sp|B4ES3gpmA | 2,3-bisphosphoglyc | 29.40 | 0.00 |
| TRINITY_sp|Q84LIWEX | Werner Syndrome-lik | 29.40 | 0.00 |
| TRINITY_sp|Q9C51At3g4742 | Putative glycerol-3 | 29.40 | 0.00 |
| TRINITY_sp|Q4VNF SMT | Selenocysteine Se-m | 29.40 | 0.00 |
TRINITY_sp|Q9FP1UBP12  Ubiquitin carboxyl-terminal hydrolase 12 OS=Arabidopsis thaliana GN=UBP12 PE=2 SV=2
TRINITY_sp|P286E7-  Endoglucanase 4 OS= 29.30 0.00
TRINITY_sp|Q9FYKPAO  Phosphoribose a oxyg OS=Dictyostelium discoideum GN=prodh PE=3 SV=1
TRINITY_sp|P0C1P0della  Dual 3',5'-cyclic-A 29.30 0.00
TRINITY_sp|Q8T1
dufs4  NADH dehydrogenase 29.20 0.00
TRINITY_sp|Q68Emrpl28  39S ribosomal prote 29.20 0.00
TRINITY_sp|Q947:MKP1  Mitogen-activated p 29.20 0.00
TRINITY_sp|Q54GDDB_G02\hmp2/4 family prot 29.20 0.00
TRINITY_sp|Q8T21sepA  Serine/threonine-pr 29.20 0.00
TRINITY_sp|P541amt-1  Putative ammonium t 29.20 0.00
TRINITY_sp|Q9SIALKBH2  DNA oxidative demet 29.20 0.00
TRINITY_sp|Q55Flcopa  Coatamer subunit al 29.20 0.00
TRINITY_sp|Q099ISAC30D1Uncharacterized pro 29.20 0.00
TRINITY_sp|Q54LgghA  Gamma-glutamyl hydr 29.20 0.00
TRINITY_sp|O042fIMPA3  Importin subunit al 29.20 0.00
TRINITY_sp|P258chic  Profilin OS=Drosophila 29.20 0.00
TRINITY_sp|Q923ISteap4  Metallodreucctase ST 29.20 0.00
TRINITY_sp|P794CYP3A29  Cytochrome P450 3A2 29.20 0.00
TRINITY_sp|Q8BJVEif2a  Eukaryotic translat 29.20 0.00
TRINITY_sp|Q86Hprodh  Proline dehydrogena 29.20 0.00
TRINITY_sp|Q8K2Uvrag  UV radiation resist 29.20 0.00
TRINITY_sp|Q043fPRKAB2  5'-AMP-activated pr 29.20 0.00
TRINITY_sp|Q705CYP3A31  Cytochrome P450 3A3 29.20 0.00
TRINITY_sp|Q5591DDB_G02fProbable serine/thr 29.20 0.00
TRINITY_sp|Q54AclcA  Chloride channel pr 29.20 0.00
TRINITY_sp|Q67HRPA2B  Replication protein 29.20 0.00
TRINITY_sp|Q68Wprmt6  Protein arginine N- 29.20 0.00
TRINITY_sp|Q54Cipex13  Probable peroxisoma 29.20 0.00
TRINITY_sp|Q9FNUVR8  Ultraviolet-B recep 29.20 0.00
TRINITY_sp|Q94tSAMC1  S-adenosylmethionin 29.20 0.00
TRINITY_sp|Q8BVcPpmel  Protein phosphatase 29.20 0.00
TRINITY_sp|Q75Jcpras1  Circularly permutat 29.20 0.00
TRINITY_sp|Q541IshkB  Dual specificity pr 29.20 0.00
TRINITY_sp|Q91LVABC25  ABC transporter B f 29.20 0.00
TRINITY_sp|P149fIDO1  Indoleamine 2,3-dio 29.20 0.00
TRINITY_sp|Q9FPfRBP45A  Polyadenylate-bindl 29.20 0.00
TRINITY_sp|B6EUPrFP40A  Pre-mRNA-processing 29.20 0.00
TRINITY_sp|O946SPBC776Uncharacterized mem 29.20 0.00
TRINITY_sp|Q578MJ0457  Uncharacterized met 29.20 0.00
TRINITY_sp|F4J2fP4H10  Probable prolyl 4-h 29.20 0.00
TRINITY_sp|B0CAfycf3  Photosystem I assem 29.20 0.00
TRINITY_sp|Q9ZWfCYP735A2Cyto 29.20 0.00
TRINITY_sp|Q8BGfOxa11  Mitochondrial inner 29.20 0.00
TRINITY_sp|Q0494AAC3  ADP,ATP carrier pro 29.20 0.00
TRINITY_sp|P533YGR266W Uncharacterized pro 29.20 0.00
TRINITY_sp|Q912fTfam  Transcription facto 29.20 0.00
TRINITY_sp|Q5SfDhrs13  Dehydrogenase/reduc 29.20 0.00
TRINITY_sp|Q55Fpats1  Probable serine/thr 29.20 0.00
TRINITY_sp|Q54fabcC3  ABC transporter C f 29.20 0.00
TRINITY_sp|Q5GfDDB_G02fProbable serine/thr 29.20 0.00
TRINITY_sp|Q7ZIITMED4  Transmembrane emp24 29.20 0.00
TRINITY_sp|D7UQAur  Aurora kinase OS=Pa 29.20 0.00
TRINITY_sp|Q99fmos  Serine/threonine-pr 29.20 0.00
TRINITY_sp|F0C8fCCRP1  Probable serine/thr 29.10 0.00
TRINITY_sp|Q3HRfCBL10  Calcineurin B-like 29.10 0.00
TRINITY_sp|P256fPW2  Periodic tryptophan 29.10 0.00
TRINITY_sp|Q9SH4At2g1531 Probable ADP-ribose 29.10 0.00
TRINITY_sp|Q8VVCXCR4-6 Carbon catabolite repressor 29.10 0.00
TRINITY_sp|Q759tRAD17 Cell cycle checkpoint 29.10 0.00
TRINITY_sp|Q5001TKP1 Tetradetide alpha-p 29.10 0.00
TRINITY_sp|Q5FVIACSAE Long-chain-fatty-ac 29.10 0.00
TRINITY_sp|Q9Y1ML4 Protein MEI2-like 4 29.10 0.00
TRINITY_sp|Q6C7C1CGI1121 EKC/KEOPS complex s 29.10 0.00
TRINITY_sp|Q116plspB Glycerol-3-phosphat 29.10 0.00
TRINITY_sp|Q884tAR18 Probable E3 ubiquitin 29.10 0.00
TRINITY_sp|Q5TCSK9 Adenylate kinase 9 29.10 0.00
TRINITY_sp|Q7ZYIankrd13 Ankyrin repeat doma 29.10 0.00
TRINITY_sp|Q6ZQtIDO2 Indoleamine 2,3-dio 29.10 0.00
TRINITY_sp|Q922tRasal1 RasGAP-activating-1 29.10 0.00
TRINITY_sp|Q8W4tRAD4 DNA repair protein 29.10 0.00
TRINITY_sp|Q87GLuxQ Autoinducer 2 senso 29.10 0.00
TRINITY_sp|Q9M8tDSPT1B Dual specificity pr 29.10 0.00
TRINITY_sp|Q7TPtShprh E3 ubiquitin-protei 29.10 0.00
TRINITY_sp|Q562tVSR4 Vacuolar-sorting re 29.10 0.00
TRINITY_sp|Q55GNDBB_G02 Probable phosphatid 29.10 0.00
TRINITY_sp|A7MUshscB Co-chaperone protei 29.10 0.00
TRINITY_sp|Q9VLtFKBP59 FK506-binding prote 29.10 0.00
TRINITY_sp|Q959tECD Protein ecdysoneles 29.10 0.00
TRINITY_sp|C1DKrrph RNA pyrophosphohyd 29.10 0.00
TRINITY_sp|P710t epsO Putative pyruvyl tr 29.10 0.00
TRINITY_sp|F4K4tTHO5B THO complex subunit b 29.10 0.00
TRINITY_sp|Q8RS5Usp33 Ubiquitin carboxyl 29.10 0.00
TRINITY_sp|Q861tDBB_G02 PH domain-containin 29.10 0.00
TRINITY_sp|Q8GVtPLC6 Phosphoinositide ph 29.10 0.00
TRINITY_sp|Q9LTtMED35C Pre-mRNA-processing 29.10 0.00
TRINITY_sp|Q9SLtOs05g019 Importin subunit al 29.10 0.00
TRINITY_sp|Q84CtvioD Capreomycidine synt 29.10 0.00
TRINITY_sp|Q5ZIklkp KIF1-binding protei 29.10 0.00
TRINITY_sp|Q600tvt6 Synaptobrevin homol 29.10 0.00
TRINITY_sp|Q9QFtFAP9 Probable inactive p 29.10 0.00
TRINITY_sp|Q5XEHtHES01 Protein HESO1 OS=Ar 29.10 0.00
TRINITY_sp|Q5F3tDENND6A Protein DENND6A OS= 29.10 0.00
TRINITY_sp|Q151tNPC1 Niemann-Pick C1 pro 29.10 0.00
TRINITY_sp|O883tAvil Advillin OS=Mus mus 29.10 0.00
TRINITY_sp|P340tmanA Lysosomal alpha-man 29.10 0.00
TRINITY_sp|Q923tSPAC4G9. Pamilio domain-cont 29.10 0.00
TRINITY_sp|Q9C5tSAC7 Phosphoinositide ph 29.10 0.00
TRINITY_sp|Q9CXEhthrs7 Dehydrogenase/reduc 29.10 0.00
TRINITY_sp|Q541tDBB_G02 Beta-lactamase-like 29.10 0.00
TRINITY_sp|F1MHLAAK1 AP2-associated prot 29.10 0.00
TRINITY_sp|Q96GtDUS3L tRNA-dihydouridin 29.00 0.00
TRINITY_sp|B0G1teoc5 Exocyst complex com 29.00 0.00
TRINITY_sp|Q758tCAPN15 Calpain-15 OS=Homo 29.00 0.00
TRINITY_sp|P0AAtyr Tyrosine-specific t 29.00 0.00
TRINITY_sp|Q5R6tATG4A Cysteine protease A 29.00 0.00
TRINITY_sp|P471tBNA2 Indoleamine 2,3-dio 29.00 0.00
TRINITY_sp|F4HRtTHO5A THO complex subunit b 29.00 0.00
TRINITY_sp|O004tRTCA RNA 3'-terminal pho 29.00 0.00
TRINITY_sp|Q52Kusp12-a Ubiquitin carboxyl 29.00 0.00
TRINITY_sp|Q77Tt1kbkap Elongator complex p 29.00 0.00
TRINITY_sp|Q011tbah Acetyl-hydrolase OS 29.00 0.00
TRINITY_sp|P309tRYR2 Ryanodine receptor OS 29.00 0.00
| Accession | Description | Log2 Fold Change | q-value |
|-----------|-------------|-----------------|---------|
| TRINITY_sp| P814\(GAPN\) | NADP-dependent glyceraldehyde-3-phosphate dehydrogenase | 29.00 0.00 |
| TRINITY_sp| Q569l|mfsd4b | Sodium-dependent glucose transporter 1 | 29.00 0.00 |
| TRINITY_sp| Q4KL1|rnf217 | Probable E3 ubiquitin-protein ligase RNF170 | 29.00 0.00 |
| TRINITY_sp| Q8yv1|CIPK13 | CAX-interacting protein | 29.00 0.00 |
| TRINITY_sp| Q17Q\|Scrn3 | Secernin-3 OS=Bos taurus | 29.00 0.00 |
| TRINITY_sp| Q6cl1|Tfp32 | Eukaryotic translation elongation factor 3 | 29.00 0.00 |
| TRINITY_sp| Q7Tz\|map3k10 | Mitogen-activated protein kinase 7 | 29.00 0.00 |
| TRINITY_sp| Q8Gz2|Bbn2 | RNA-binding protein | 29.00 0.00 |
| TRINITY_sp| Q9Fp1|Upa12 | Ubiquitin carboxyl-terminal hydrolase 2 | 29.00 0.00 |
| TRINITY_sp| Q294\|Cyp3A24 | Cytochrome P450 3A24 | 29.00 0.00 |
| TRINITY_sp| Q67z2|Tfcb | Tubulin-folding cofactor D | 29.00 0.00 |
| TRINITY_sp| Q0ji\|Cypk11 | CBL-interacting protein kinase 11 | 29.00 0.00 |
| TRINITY_sp| Q430\|Gale | UDP-glucose 4-epimerase | 29.00 0.00 |
| TRINITY_sp| Q129\|Elavl2 | ELAV-like protein 2 OS=Homo sapiens | 29.00 0.00 |
| TRINITY_sp| Q05B\|Eml5 | Echinoderm microtubule-associated protein 5 | 29.00 0.00 |
| TRINITY_sp| Q98t7|Pdc4 | Programmed cell death protein 4 | 29.00 0.00 |
| TRINITY_sp| Q55D\|eatxn2 | Ataxin-2 homolog | 29.00 0.00 |
| TRINITY_sp| Q9Sp1|At3g0711 | Protein transport protein | 29.00 0.00 |
| TRINITY_sp| Q8H2t|Polh | DNA polymerase eta | 29.00 0.00 |
| TRINITY_sp| Q142\|Wis4 | MAP kinase kinase k | 29.00 0.00 |
| TRINITY_sp| Q9lYy7|Med7a | Mediator of RNA polymerase complex | 29.00 0.00 |
| TRINITY_sp| P344\|Cltu-1 | Clustered mitochondria protein homolog | 29.00 0.00 |
| TRINITY_sp| Q9Va4|Aralar1 | Calcium-binding mitochondrial carrier protein | 29.00 0.00 |
| TRINITY_sp| Q6Zm6|Emel6 | Echinoderm microtubule-associated protein 6 | 29.00 0.00 |
| TRINITY_sp| Q541\|Rft1 | Protein RFT1 homolog | 29.00 0.00 |
| TRINITY_sp| Q15K|Phyllo | Protein PHYLL0, chloroplast | 29.00 0.00 |
| TRINITY_sp| Q232\|Fat-3 | Delta(6)-fatty-acid desaturase | 29.00 0.00 |
| TRINITY_sp| Q017\|Him-1 | Structural maintenance of chromosome protein | 28.90 0.00 |
| TRINITY_sp| Q0Sf\|Ywttg | Putative metabolite transporter | 28.90 0.00 |
| TRINITY_sp| Q5P\|Rfnf170 | E3 ubiquitin-protein ligase RNF217 | 28.90 0.00 |
| TRINITY_sp| Q418|Rael | Poly(A)+ RNA export protein | 28.90 0.00 |
| TRINITY_sp| Q872|Mus81 | Crossover junction protein | 28.90 0.00 |
| TRINITY_sp| P041\|Gip | Copia protein OS=Dracaena | 28.90 0.00 |
| TRINITY_sp| Q54W\|Ddb-202 | Putative actin-frag | 28.90 0.00 |
| TRINITY_sp| Q5zl\|Vmp7 | Vesicle-associated protein | 28.90 0.00 |
| TRINITY_sp| Q54b\|Nsf11c | NSF-like factor protein | 28.90 0.00 |
| TRINITY_sp| Q122|Ncr1 | Niemann-Pick type C | 28.90 0.00 |
| TRINITY_sp| Q9Dbw|Cyp4v2 | Cytochrome P450 4V2 | 28.90 0.00 |
| TRINITY_sp| Q54B\|Ddb-202 | Probable GH family protein | 28.90 0.00 |
| TRINITY_sp| Q88F|Nicc | 6-hydroxynicotinate translocase | 28.90 0.00 |
| TRINITY_sp| Q54N|AbcC9 | ABC transporter C family | 28.90 0.00 |
| TRINITY_sp| Q497|Kdm8 | Lysine-specific demethylase 8 | 28.90 0.00 |
| TRINITY_sp| Q0A0|Cmt1 | DNA (cytosine-5)-methyltransferase | 28.90 0.00 |
| TRINITY_sp| Q941|Ost3 | Probable dolichyl-diphosphooligosaccharide-protein glycosyltransferase | 28.90 0.00 |
| TRINITY_sp| Q9CaA|At1g6322 | Transcription elongation factor | 28.90 0.00 |
| TRINITY_sp| Q019|Ocr1 | Inositol polyphosphate phosphatase | 28.90 0.00 |
| TRINITY_sp| Q1By3|Msh6 | DNA mismatch repair | 28.90 0.00 |
| TRINITY_sp| Q1LS\|CtaB | Protoheme IX farnesyltransferase | 28.90 0.00 |
| TRINITY_sp| Q9Ut3|Cox11t | Rsm22-coxl1 tandem | 28.90 0.00 |
| TRINITY_sp| Q917|GcKr | Glucokinase | 28.90 0.00 |
| TRINITY_sp| Q9Jj4|Agalt | Lactosylceramide 4-arabinosyltransferase | 28.90 0.00 |
| TRINITY_sp| P041\|Gip | Copia protein OS=Dracaena | 28.90 0.00 |
| TRINITY_sp| A4Fl1|Iol1G2 | Inositol 2-dehydrogenase | 28.90 0.00 |
| TRINITY_sp| Q010\|Pde4d | cAMP-specific 3',5'-cyclic nucleotide phosphodiesterase | 28.90 0.00 |
| TRINITY_sp| Q54X|Gacp | Rho GTPase-activating protein | 28.90 0.00 |
| TRINITY_sp| A2vd1|Map3k7 | Mitogen-activated protein kinase 7 | 28.90 0.00 |
| Name | Description | Accession | Value 1 | Value 2 |
|------|-------------|-----------|---------|---------|
| TRINITY_sp|Q54D\DDB_G02|von Willebrand fact| 28.90 | 0.00 |
| TRINITY_sp|Q9LUCCYP72A1|Cytochrome P450 72A| 28.90 | 0.00 |
| TRINITY_sp|P164|Retrovirus-related| 28.90 | 0.00 |
| TRINITY_sp|O228\At2g404|Uncharacterized protein| 28.90 | 0.00 |
| TRINITY_sp|P5861glk|Glucokinase OS=Nostoc| 28.90 | 0.00 |
| TRINITY_sp|Q9VZ2|Peroxidasin OS=Drosophila| 28.90 | 0.00 |
| TRINITY_sp|A3KNUBA1|Ubiquitin-like modifier| 28.90 | 0.00 |
| TRINITY_sp|Q4V8|texpin| 28.90 | 0.00 |
| TRINITY_sp|P290(INVA)|Acid beta-fructofuranosyltransferase| 28.90 | 0.00 |
| TRINITY_sp|P393|IgoT| 28.90 | 0.00 |
| TRINITY_sp|Q9Y4f|DMX1| 28.90 | 0.00 |
| TRINITY_sp|P311|Autolysin OS=Chlamydomonas| 28.90 | 0.00 |
| TRINITY_sp|Q5X|Atp13a4| 28.90 | 0.00 |
| TRINITY_sp|Q7KVE|Trf4-1| 28.90 | 0.00 |
| TRINITY_sp|A7S4|serinc| 28.90 | 0.00 |
| TRINITY_sp|Q54B|exoc3| 28.90 | 0.00 |
| TRINITY_sp|P360|VPS24| 28.90 | 0.00 |
| TRINITY_sp|Q902|nrf-6| 28.90 | 0.00 |
| TRINITY_sp|O154|ABCC4| 28.90 | 0.00 |
| TRINITY_sp|Q4G0|HYDIN| 28.90 | 0.00 |
| TRINITY_sp|Q1G3|PCO3| 28.90 | 0.00 |
| TRINITY_sp|Q54V|DDB_G02| 28.90 | 0.00 |
| TRINITY_sp|A0JF|heatr5a| 28.90 | 0.00 |
| TRINITY_sp|Q94C|SATG1A| 28.80 | 0.00 |
| TRINITY_sp|P531|MNP1| 54S ribosomal protein| 28.80 | 0.00 |
| TRINITY_sp|Q6BM|SYM1| Protein SYM1 OS=Debica| 28.80 | 0.00 |
| TRINITY_sp|Q4VB|stx18| Syntaxin-18 OS=Danio| 28.80 | 0.00 |
| TRINITY_sp|Q916|stk11| Serine/threonine-protein kinase| 28.80 | 0.00 |
| TRINITY_sp|A5W|chfr| E3 ubiquitin-proteasome system member| 28.80 | 0.00 |
| TRINITY_sp|Q9SE|CIPK16| CBL-interacting serine/threonine-protein kinase| 28.80 | 0.00 |
| TRINITY_sp|O168|dhs-16| 3 beta-hydroxysteroid dehydrogenase| 28.80 | 0.00 |
| TRINITY_sp|Q8CN|SE_2036| Uncharacterized oxidoreductase| 28.80 | 0.00 |
| TRINITY_sp|Q5LD|EngB| Probable GTP-binding protein| 28.80 | 0.00 |
| TRINITY_sp|O547|Hsd17b6| 17-beta-hydroxysteroid dehydrogenase| 28.80 | 0.00 |
| TRINITY_sp|Q9CQ|Commd4| COMM domain-containing protein| 28.80 | 0.00 |
| TRINITY_sp|Q641|Nuak1| NUAK family SNF1-like protein| 28.80 | 0.00 |
| TRINITY_sp|Q189|CYP3A21| Cytochrome P450 3A2| 28.80 | 0.00 |
| TRINITY_sp|O487|CYP734A1| Cytochrome P450 734A1| 28.80 | 0.00 |
| TRINITY_sp|Q8LF|RPA2B| Replication protein| 28.80 | 0.00 |
| TRINITY_sp|P341|coaA| Coactosin OS=Dictyostelium| 28.80 | 0.00 |
| TRINITY_sp|Q5VS|OBSCN| Obscurin OS=Homo sapiens| 28.80 | 0.00 |
| TRINITY_sp|Q6DE|tbc1d31| TBC1 domain family member| 28.80 | 0.00 |
| TRINITY_sp|Q55K|scy2| Probable inactive serine/threonine-protein kinase| 28.80 | 0.00 |
| TRINITY_sp|Q229|Atg2g3035| Putative tRNA pseudouridylate synthetase| 28.80 | 0.00 |
| TRINITY_sp|P825|PPL1| PsbP-like protein| 28.80 | 0.00 |
| TRINITY_sp|Q100|mdm31| Mitochondrial distribution protein| 28.80 | 0.00 |
| TRINITY_sp|A2A5|R3hdm1| Peptidase inhibitor| 28.80 | 0.00 |
| TRINITY_sp|Q54Q|sec1| Protein transport protein| 28.80 | 0.00 |
| TRINITY_sp|P930|PP2C27| Probable protein phosphatase 2C27| 28.80 | 0.00 |
| TRINITY_sp|A8JF|CFAP65| Cilia- and flagella-associated protein| 28.80 | 0.00 |
| TRINITY_sp|P283|gorA| Quinone oxidoreductase| 28.80 | 0.00 |
| TRINITY_sp|Q9WVF|Cyp46a1| Cholesterol 24-hydroxylase| 28.80 | 0.00 |
| TRINITY_sp|Q944|MTM1| Mitochondrial carrier protein| 28.80 | 0.00 |
| TRINITY_sp|O231|PLP1| Patatin-like protein| 28.80 | 0.00 |
| TRINITY_sp|A8MS|SPT6| Transcription elongation factor| 28.80 | 0.00 |
| TRINITY_sp|Q9LUCCYP72A1|Cytochrome P450 72A| 28.80 | 0.00 |
TRINITY_sp|Q2QMO|Os12g060|Protein ROOT HAIR D 28.70 0.00
TRINITY_sp|Q8ISJ|gefE  Ras guanine nucleot 28.70 0.00
TRINITY_sp|P715|MexAM1  Putative carboxymet 28.70 0.00
TRINITY_sp|Q8GZ2|TIC20-I  Protein TIC 20-I, c 28.70 0.00
TRINITY_sp|P095.|nifA  Nif-specific regula 28.70 0.00
TRINITY_sp|A8MB6|cobB  NAD-dependent prote 28.70 0.00
TRINITY_sp|P264|fixL  Sensor protein FixL 28.70 0.00
TRINITY_sp|Q8R1|Znfx1  NFX1-type zinc fing 28.70 0.00
TRINITY_sp|Q7SX|emc3  ER membrane protein 28.60 0.00
TRINITY_sp|Q9SDA|At3g513  Probable protein ph 28.60 0.00
TRINITY_sp|P539.|Fap1  FBKP12-associated p 28.60 0.00
TRINITY_sp|A0ME|CYCA3-3  Cyclin-A3-3 OS=Arab 28.60 0.00
TRINITY_sp|Q87A|RHEBL1  GTPase RhebL1 OS=Ho 28.60 0.00
TRINITY_sp|Q1ZX|emc6  ER membrane protein 28.60 0.00
TRINITY_sp|Q2QN|TR130  Trafficking protein 28.60 0.00
TRINITY_sp|Q5NC|Ttf2  Transcription termi 28.60 0.00
TRINITY_sp|B2RP|P1xnb2  Plexin-B2 OS=Mus mu 28.60 0.00
TRINITY_sp|Q6Z3|Os07g02  Putative aldehyde o 28.60 0.00
TRINITY_sp|Q139|ppk9  Protein kinase doma 28.60 0.00
TRINITY_sp|Q9LF|CIFK18  CBL-interacting ser 28.60 0.00
TRINITY_sp|Q136|yvh1  Tyrosine-protein ph 28.60 0.00
TRINITY_sp|Q8RW|ISTY17  Serine/threonine-pr 28.60 0.00
TRINITY_sp|Q6YI|CCB0355  Leishmanolysin-like 28.60 0.00
TRINITY_sp|Q9YO|criPA  Ras-interacting pro 28.60 0.00
TRINITY_sp|Q150|R3HDM1  R3H domain-containi 28.60 0.00
TRINITY_sp|Q75B|NOP12  Nucleolar protein 1 28.60 0.00
TRINITY_sp|Q96S|JMJ68  JmjC domain-contain 28.60 0.00
TRINITY_sp|Q9FR|NMT1  Phosphoethanolamine 28.60 0.00
TRINITY_sp|Q9LF|ACA8  Calcium-transportin 28.60 0.00
TRINITY_sp|Q275|Cyp4d2  Cytochrome P450 28.60 0.00
TRINITY_sp|Q9ZL|Cog1  Conserved oligomeri 28.60 0.00
TRINITY_sp|Q6P8|Caps1  Calcyphosin-like pr 28.60 0.00
TRINITY_sp|Q5RF|CHFR  E3 ubiquitin-protei 28.60 0.00
TRINITY_sp|Q8K1|tmoS  Sensor histidine ki 28.60 0.00
TRINITY_sp|Q9H6|NOL6  Nucleolar protein 6 28.60 0.00
TRINITY_sp|Q8HX|LONRF3  LON peptidase N-ter 28.60 0.00
TRINITY_sp|Q9LR|At3g174  Probable sugar phos 28.60 0.00
TRINITY_sp|Q7P2|AGAP011  Clustered mitochond 28.60 0.00
TRINITY_sp|P0AG|psts  Phosphate-binding p 28.60 0.00
TRINITY_sp|Q9Z3|Kcnj16  Inward rectifier po 28.60 0.00
TRINITY_sp|Q6EU|JAG01A  Protein argonaute 1 28.60 0.00
TRINITY_sp|Q9SY|At4g029  CSC1-like protein A 28.60 0.00
TRINITY_sp|Q3E9|CPK34  Calcium-dependent p 28.60 0.00
TRINITY_sp|Q8T6|abcA2  ABC transporter A f 28.60 0.00
TRINITY_sp|P355|Ret  Proto-oncogene tyro 28.50 0.00
TRINITY_sp|Q93Z|At3g161  Probable inactive n 28.50 0.00
TRINITY_sp|P250|CML12  Calmodulin-like pro 28.50 0.00
TRINITY_sp|P074|bcpl  Protein bcpl OS=Sch 28.50 0.00
TRINITY_sp|Q54D|rab4  Ras-related protein 28.50 0.00
TRINITY_sp|Q8VX|PDIL1-3  Protein disulfide i 28.50 0.00
TRINITY_sp|Q7ZT|uba2-b  SUMO-activating enz 28.50 0.00
TRINITY_sp|O574|  Voltage-dependent L 28.50 0.00
TRINITY_sp|A2XH|ATG4A  Cysteine protease A 28.50 0.00
TRINITY_sp|Q9P6|SPBC168  Uncharacterized pro 28.50 0.00
TRINITY_sp|Q9QJ|REIL2  Cytoplasmic 60S sub 28.50 0.00
TRINITY_sp|P408|  Carbonic anhydrase, 28.50 0.00
| Protein Name                        | Gene Name | Species                  | PubMed ID | Score |
|------------------------------------|-----------|--------------------------|-----------|-------|
| Protein QmcA                       | qmcA      | Wigglesworthia glossinidia brevipalpis |           | 28.50 |
| Adenylate cyclase                  | cya       | Anabaena cylindrica      |           | 28.50 |
| Transmembrane protein 87B          | Tmem87b   | Mus musculus             |           | 28.50 |
| DNA replication complex GINS protein SLD5 | SLD5     | Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / JCM 1990 / NBRC 0083 / IGC 2968) |           | 28.50 |
| Alpha-mannosidase 2                | Man2a1    | Mus musculus             |           | 28.50 |
| Periostin                           | POSTN     | Homo sapiens             |           | 28.50 |
| DNA polymerase eta                 | POLH      | Arabidopsis thaliana     |           | 28.50 |
| Probable inactive tRNA-specific adenosine deaminase-like protein 3 | ADAT3    | Homo sapiens             |           | 28.50 |
| Cytochrome P450 3A16               | Cyp3a16   | Mus musculus             |           | 28.50 |
| tRNA pseudouridine synthase B      | truB      | Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) |           | 28.50 |
| Uncharacterized serpin-like protein TK1782 | TK1782   | Thermococcus kodakarensis (strain ATCC BAA-918 / JCM 12380 / KOD1) |           | 28.50 |
| Endoplasmic reticulum vesicle protein 25 | erv25    | Schizosaccharomyces pombe (strain 972 / ATCC 24843) |           | 28.50 |
| Penicillin acylase 2               | acyII     | Pseudomonas sp. (strain SE83) |           | 28.50 |
| Hermansky-Pudlak syndrome 1 protein | HPS1     | Homo sapiens             |           | 28.50 |
| FYVE, RhoGEF and PH domain-containing protein 4 | Fgd4     | Mus musculus             |           | 28.50 |
| Inositol 1,4,5-trisphosphate receptor type 2 | ITPR2    | Homo sapiens             |           | 28.50 |
| Protein kri1                        | KRI1      | Schizosaccharomyces pombe (strain 972 / ATCC 24843) |           | 28.50 |
| Zeaxanthin epoxidase, chloroplastic | ZEP       | Prunus armeniaca         |           | 28.50 |
| Transcription termination factor 2  | TTF2      | Mus musculus             |           | 28.50 |
| Tetraspanin-8                      | TSPAN8    | Mus musculus             |           | 28.50 |
| Vacuolar amino acid                | ATV4      | Saccharomyces cerevisiae (strain ATCC 204508 / S288c) |           | 28.50 |
| Formin-A                           | FORA      | Dictyostelium discoideum |           | 28.50 |
| Sulfhydryl oxidase                 | QSOX1     | Oryza sativa subsp. japonica |           | 28.50 |
| Group 1 truncated hemoglobin       | Qmca      | Tetrahymena pyriformis   |           | 28.50 |
| Nuclear pore complex               | NUP155    | Arabidopsis thaliana     |           | 28.50 |
| Rhomboid-like prote                | RBL14     | Arabidopsis thaliana     |           | 28.50 |
| Nuclear pore comple                | NUP155    | Arabidopsis thaliana     |           | 28.50 |
| Uncharacterized serin              | TF1       | Chlamydomonas reinhardtii |           | 28.50 |
| Acidic leucine-rich                | ABHD13    | Oryza sativa subsp. japonica |           | 28.50 |
| Probable ribosome biogenesis protein C8F11.04 | SPAC8F11.04 | Schizosaccharomyces pombe (strain 972 / ATCC 24843) |           | 28.50 |
| Acidic leucine-rich                | ABHD13    | Oryza sativa subsp. japonica |           | 28.50 |
| Histidinol-phosphat               | FGFC      | Homo sapiens             |           | 28.50 |
| Cytochrome P450 3A2               | CYP3A25   | Homo sapiens             |           | 28.50 |
| Mitochondrial escape               | MTO1      | Mus musculus             |           | 28.50 |
| Endoplasmic reticul               | ERP25     | Homo sapiens             |           | 28.50 |
| Putative ribosome b               | RPL21     | Homo sapiens             |           | 28.50 |
| Cytochrome P450 3A1              | CYP3A16   | Xenopus laevis           |           | 28.50 |
| Serine/threonine-pr               | KIN29     | Schizosaccharomyces pombe (strain 972 / ATCC 24843) |           | 28.50 |
| Vacuolar protein             | VPS9A     | Mus musculus             |           | 28.50 |
| Lactonase drp35                   | LACT35    | Schizosaccharomyces pombe (strain 972 / ATCC 24843) |           | 28.50 |
| Protein kinase and                | PKA       | Mus musculus             |           | 28.50 |
| Salutaridine reduct               | SALURD    | Mus musculus             |           | 28.50 |
| Protein sym-1                      | SYM1      | Homo sapiens             |           | 28.50 |
| Protein ABHD13                    | ABHD13    | Arabidopsis thaliana     |           | 28.50 |
| Tetraspanin-8                     | TSPAN8    | Arabidopsis thaliana     |           | 28.50 |
| Post-GPI attachment               | PAGA      | Homo sapiens             |           | 28.50 |
| Probable ADP-ribozyme             | RIBOSY   | Homo sapiens             |           | 28.50 |
| Sulphhydril oxidase               | QSOX1     | Oryza sativa subsp. japonica |           | 28.50 |
| Vacuolar amino acid               | ATV4      | Saccharomyces cerevisiae (strain ATCC 204508 / S288c) |           | 28.50 |
| Penicillin acylase                | ACYII     | Mycobacterium tuberculosis |           | 28.50 |
| Putative glycerol-3               | Glycerol3 | Homo sapiens             |           | 28.50 |
| Ubiquitin carboxyl              | UKP34     | Homo sapiens             |           | 28.50 |
| Voltage-dependent L              | CACNA1D   | Homo sapiens             |           | 28.50 |
| TRINITY_sp|Q7PZIAGAP011|Clustered mitochondria | 28.40 | 0.00 |
| TRINITY_sp|P1781recN | DNA repair protein | 28.40 | 0.00 |
| TRINITY_sp|P581Plscr1 | Phospholipid scrambl | 28.40 | 0.00 |
| TRINITY_sp|P383PHO89 | Phosphate permease | 28.40 | 0.00 |
| TRINITY_sp|Q8L91P4H7 | Probable prolyl 4-h | 28.40 | 0.00 |
| TRINITY_sp|Q015Gstt1 | Glutathione S-trans | 28.40 | 0.00 |
| TRINITY_sp|Q9USubP1 | Probable ubiquitin | 28.40 | 0.00 |
| TRINITY_sp|P263U2AFA | Splicing factor U2A | 28.40 | 0.00 |
| TRINITY_sp|A8JFCFAP65 | Cilia- and flagella | 28.40 | 0.00 |
| TRINITY_sp|Q6NUFPF4R4 | Serine/threonine-pr | 28.40 | 0.00 |
| TRINITY_sp|Q7LHT3Y3B-I | Transposon Ty3-I Ga | 28.40 | 0.00 |
| TRINITY_sp|Q75L1OSH10 | Homeobox protein kn | 28.40 | 0.00 |
| TRINITY_sp|Q8TBPFUM2 | Pumilio homolog 2 O | 28.40 | 0.00 |
| TRINITY_sp|P5774At5g4066 | Cystinosin homolog | 28.30 | 0.00 |
| TRINITY_sp|Q5VJGd9 | Probable serine/thr | 28.30 | 0.00 |
| TRINITY_sp|P8671- | Giganin-6 OS=Crasso | 28.30 | 0.00 |
| TRINITY_sp|Q6DESmndc1 | Survival of motor n | 28.30 | 0.00 |
| TRINITY_sp|P469yccK | Uncharacterized oxi | 28.30 | 0.00 |
| TRINITY_sp|QOCtatPH | ATP synthase subuni | 28.30 | 0.00 |
| TRINITY_sp|P423CNB1 | Calcineurin subunit | 28.30 | 0.00 |
| TRINITY_sp|P2047- | 23 kDa calcium-bind | 28.30 | 0.00 |
| TRINITY_sp|P1O6PRKAR1A | cAMP-dependent prot | 28.30 | 0.00 |
| TRINITY_sp|Q3EBKPAT17 | Probable protein S- | 28.30 | 0.00 |
| TRINITY_sp|Q9P2USP36 | Ubiquitin carboxyl- | 28.30 | 0.00 |
| TRINITY_sp|Q96B1ATG2B | Autophagy-related p | 28.30 | 0.00 |
| TRINITY_sp|P569cphB | Cyanophycinase OS=G | 28.30 | 0.00 |
| TRINITY_sp|Q541slc44a2 | Choline transporter | 28.30 | 0.00 |
| TRINITY_sp|P541ypgQ | Uncharacterized pro | 28.30 | 0.00 |
| TRINITY_sp|P934IBP80 | Vacuolar-sorting re | 28.30 | 0.00 |
| TRINITY_sp|P360SRP102 | Signal recognition | 28.30 | 0.00 |
| TRINITY_sp|O151VILL | Villin-like protein | 28.30 | 0.00 |
| TRINITY_sp|B5F0yfeW | UF0214 protein Yfe | 28.30 | 0.00 |
| TRINITY_sp|Q9C9VIP5 | Protein RTF1 homolo | 28.30 | 0.00 |
| TRINITY_sp|Q8TMK0970 | Glyceraldehyde 3-ph | 28.30 | 0.00 |
| TRINITY_sp|Q9C6GAMMACA | Gamma carbonic anhy | 28.30 | 0.00 |
| TRINITY_sp|Q7XW0s04g02 | Probable cleavage a | 28.30 | 0.00 |
| TRINITY_sp|Q926NSMAF | Protein FAN OS=Homo | 28.30 | 0.00 |
| TRINITY_sp|Q9HDchw43 | Protein cwh43 OS=Sc | 28.30 | 0.00 |
| TRINITY_sp|Q6GLadsccl | Sister chromatid co | 28.30 | 0.00 |
| TRINITY_sp|Q0B1jmjd4 | JmJC domain-contain | 28.30 | 0.00 |
| TRINITY_sp|Q9NYIZAK | Mitogen-activated p | 28.30 | 0.00 |
| TRINITY_sp|Q541I1D8B0186 | Calcium uniporter p | 28.30 | 0.00 |
| TRINITY_sp|A4TDITIF34 | Eukaryotic translat | 28.30 | 0.00 |
| TRINITY_sp|Q9UKFARPA | Poly [ADP-ribose] p | 28.30 | 0.00 |
| TRINITY_sp|O942mdn1 | Midasin OS=Schizosa | 28.30 | 0.00 |
| TRINITY_sp|O147MAYp2K7 | Dual specificity mi | 28.30 | 0.00 |
| TRINITY_sp|Q8BKaMats1 | Protein MAATS1 OS=M | 28.30 | 0.00 |
| TRINITY_sp|Q75WVwa5a | von Willebrand fact | 28.30 | 0.00 |
| TRINITY_sp|Q84MSM1L9 | Mechanosensitive io | 28.30 | 0.00 |
| TRINITY_sp|Q863gyc-28 | Receptor-type guany | 28.30 | 0.00 |
| TRINITY_sp|B9DFnAt5g474 | E3 ubiquitin ligase | 28.30 | 0.00 |
| TRINITY_sp|Q8IVTCBCD10 | Carabin OS=Homo sap | 28.30 | 0.00 |
| TRINITY_sp|Q7448SPCC184 | Uncharacterized pro | 28.20 | 0.00 |
| TRINITY_sp|Q54EabcC7 | ABC transporter C f | 28.20 | 0.00 |
| TRINITY_sp|P423Nca | Neurocalcin homolog | 28.20 | 0.00 |
| TRINITY_sp|Q92D11gch | IQ domain-containin | 28.20 | 0.00 |
TRINITY_sp|Q5M7l:PAT12  Probable protein S- 28.10 0.00
TRINITY_sp|Q9ML1:BGLU27 Beta-glucosidase 27 28.10 0.00
TRINITY_sp|Q091l:Man2b1 Lysosomal alpha-man 28.10 0.00
TRINITY_sp|Q08A9:PRMT6 Probable protein ar 28.10 0.00
TRINITY_sp|Q9XV7:rrbs-1 Ribosome biogenesis 28.10 0.00
TRINITY_sp|A5UW:nfl Endonuclease V OS=R 28.10 0.00
TRINITY_sp|Q9T01:SPA2 Protein SPA1-RELATE 28.10 0.00
TRINITY_sp|P3325:CPA3A8 Cytochrome P450 3A8 28.10 0.00
TRINITY_sp|Q262:ku 70 ATP-dependent DNA h 28.10 0.00
TRINITY_sp|A9B77:Haur 17:UPF0060 membrane pr 28.10 0.00
TRINITY_sp|Q057l:Dbh Dopamine beta-hydro 28.10 0.00
TRINITY_sp|Q04M:ABC A1 ABC transporter A f 28.10 0.00
TRINITY_sp|C8YR:Loxdh1 Lipoxgenase homolo 28.10 0.00
TRINITY_sp|Q9C88:ABCC11 ABC transporter C f 28.10 0.00
TRINITY_sp|Q54E1:abpF Actin-binding prote 28.10 0.00
TRINITY_sp|Q9DBV:Cyp4v2 Cytochrome P450 4V2 28.10 0.00
TRINITY_sp|Q4303:pa 43 DNA-directed RNA po 28.00 0.00
TRINITY_sp|Q29A6:GA 7800 Leishmanolysin-like 28.00 0.00
TRINITY_sp|Q86K5:chmp7 Charged multivesicu 28.00 0.00
TRINITY_sp|Q9F21:CHD7 Chromodomain-helica 28.00 0.00
TRINITY_sp|Q1MTF:vid27 Vacuolar import and 28.00 0.00
TRINITY_sp|Q945l:DTX47 Protein DETOXIFICAT 28.00 0.00
TRINITY_sp|Q54T7:drkC Probable serine/thr 28.00 0.00
TRINITY_sp|Q9BYT:BCD Tubulin-specific ch 28.00 0.00
TRINITY_sp|Q2432: Vacuolar-processing 28.00 0.00
TRINITY_sp|P0865:CYP3A4 Cytochrome P450 3A4 28.00 0.00
TRINITY_sp|A2VDI:MAP3K7 Mitogen-activated p 28.00 0.00
TRINITY_sp|P4711:XP T1 Xanthine phosphorib 28.00 0.00
TRINITY_sp|Q80UU:Ankzi1 Ankyrin repeat and 28.00 0.00
TRINITY_sp|Q54K5:gefa Ras guanine nucleot 28.00 0.00
TRINITY_sp|H3K21:MD12 Mediator of RNA pol 28.00 0.00
TRINITY_sp|Q80TF:Dcaf5 DDB1- and CUL4-as 28.00 0.00
TRINITY_sp|Q54Y6:shkc Dual specificity pr 28.00 0.00
TRINITY_sp|Q54B5:mcfZ Mitochondrial subst 28.00 0.00
TRINITY_sp|Q54W8:forA Formin-A OS=Dictyo 28.00 0.00
TRINITY_sp|Q5AD6:MN24 Alpha-1,2-mannosylt 28.00 0.00
TRINITY_sp|Q8CO1:goq5 Conserved oligomeri 28.00 0.00
TRINITY_sp|Q0365:YMR210W Putative esterase Y 28.00 0.00
TRINITY_sp|P277:acoC Dihydrolipoyllysine 28.00 0.00
TRINITY_sp|A2RU7:TYW5 tRNA wybutosine-syn 28.00 0.00
TRINITY_sp|Q78Z:Jnap114 Nucleosome assembly 27.90 0.00
TRINITY_sp|Q215t:am-3 Putative ammonium t 27.90 0.00
TRINITY_sp|F1MK:RN170 E3 ubiquitin-protei 27.90 0.00
TRINITY_sp|O0425:IMP A3 Importin subunit al 27.90 0.00
TRINITY_sp|Q69Q6:Os 207: Probable protein ph 27.90 0.00
TRINITY_sp|P4005:ERG28 Ergosterol biosynth 27.90 0.00
TRINITY_sp|Q96C9:EV 55 EI5-like protein O 27.90 0.00
TRINITY_sp|Q9NC7:CU L33 Cullin-3B OS=Arabid 27.90 0.00
TRINITY_sp|Q8NC5:DA GLB Sn1-specific diacyl 27.90 0.00
TRINITY_sp|P0A46:qMC Protein QmcA OS=Esc 27.90 0.00
TRINITY_sp|Q225f:SY 8 Serine/threonine-pr 27.90 0.00
| Accession  | Description                                  | Swiss-Prot   | ENSEMBL   |
|------------|----------------------------------------------|--------------|-----------|
| TRINITY_sp| Uncharacterized WD                          | 27.90        | 0.00      |
| TRINITY_sp| Cyclin-dependent kinase                      | 27.90        | 0.00      |
| TRINITY_sp| Choline/ethanolamin                          | 27.90        | 0.00      |
| TRINITY_sp| Transcription-associ                           | 27.90        | 0.00      |
| TRINITY_sp| DNA mismatch repair                           | 27.90        | 0.00      |
| TRINITY_sp| UBP1-associated pro                           | 27.90        | 0.00      |
| TRINITY_sp| Penicillin acylase                            | 27.90        | 0.00      |
| TRINITY_sp| Sodium-coupled neutral amino acid transporter | 27.90        | 0.00      |
| TRINITY_sp| Protein A                                    | 27.90        | 0.00      |
| TRINITY_sp| Cell division cycle                           | 27.90        | 0.00      |
| TRINITY_sp| 1-phosphatidylinosati                        | 27.80        | 0.00      |
| TRINITY_sp| Hybrid signal trans                          | 27.80        | 0.00      |
| TRINITY_sp| Protein DDB_G02:                       | 27.80        | 0.00      |
| TRINITY_sp| Serine/threonine-processed                 | 27.80        | 0.00      |
| TRINITY_sp| Hermansky-Pudliak sy                        | 27.80        | 0.00      |
| TRINITY_sp| Uncharacterized mem                           | 27.80        | 0.00      |
| TRINITY_sp| Tubulin polyglutamacy                      | 27.80        | 0.00      |
| TRINITY_sp| Choline kinase alph                         | 27.80        | 0.00      |
| TRINITY_sp| Flagellar radial sp                         | 27.80        | 0.00      |
| TRINITY_sp| Transcription termi                         | 27.80        | 0.00      |
| TRINITY_sp| Putative BPI/LBP family protein               | 27.80        | 0.00      |
| TRINITY_sp| Uncharacterized oxi                          | 27.80        | 0.00      |
| TRINITY_sp| Guanylyl cyclase-ac                         | 27.80        | 0.00      |
| TRINITY_sp| Sentrin-specific pr                         | 27.80        | 0.00      |
| TRINITY_sp| Ethylene receptor 2                         | 27.80        | 0.00      |
| TRINITY_sp| Protein Simiate OS=                         | 27.80        | 0.00      |
| TRINITY_sp| RHOMBOID-like prote                         | 27.80        | 0.00      |
| TRINITY_sp| Uncharacterized pro                         | 27.80        | 0.00      |
| TRINITY_sp| Carbohydrate sulfot                         | 27.80        | 0.00      |
| TRINITY_sp| Syntaxin-6 OS=Homo                          | 27.80        | 0.00      |
| TRINITY_sp| Protein transport p                         | 27.80        | 0.00      |
| TRINITY_sp| Ubiquitin-protein E3                        | 27.80        | 0.00      |
| TRINITY_sp| Dynein heavy chain                          | 27.80        | 0.00      |
| TRINITY_sp| Adenine DNA glycosy                         | 27.80        | 0.00      |
| TRINITY_sp| Midsasin OS=Homo                            | 27.80        | 0.00      |
| TRINITY_sp| Fibrocystin-L OS=Homo                       | 27.80        | 0.00      |
| TRINITY_sp| Sperm motility kina                         | 27.70        | 0.00      |
| TRINITY_sp| Neuron-specific cal                         | 27.70        | 0.00      |
| TRINITY_sp| Adenylate kinase 7                          | 27.70        | 0.00      |
| TRINITY_sp| Pyruvyl transferase                         | 27.70        | 0.00      |
| TRINITY_sp| Mitochondrial import                        | 27.70        | 0.00      |
| TRINITY_sp| Polynucleotide 5'-h                        | 27.70        | 0.00      |
| TRINITY_sp| Cytochrome P450 3A1                         | 27.70        | 0.00      |
| TRINITY_sp| Myosin-IB OS=Drosop                        | 27.70        | 0.00      |
| TRINITY_sp| Inositol hexakispho                         | 27.70        | 0.00      |
| TRINITY_sp| Non-structural main                         | 27.70        | 0.00      |
| TRINITY_sp| SCY1-like protein Z                        | 27.70        | 0.00      |
| TRINITY_sp| Protein prune homol                         | 27.70        | 0.00      |
| TRINITY_sp| Ethylene receptor O                         | 27.70        | 0.00      |
| TRINITY_sp| ELOM domain-contain                         | 27.70        | 0.00      |
| Accession          | Description                                      | ORF Size | p-value |
|--------------------|--------------------------------------------------|----------|---------|
| TRINITY_sp|Q6YZ4|Replication protein| 27.70| 0.00 |
| TRINITY_sp|Q56f|FERM domain-contain| 27.70| 0.00 |
| TRINITY_sp|Q9TU8|Signal transducer a| 27.70| 0.00 |
| TRINITY_sp|O444|Protein F37C4.5| 27.70| 0.00 |
| TRINITY_sp|O426|RCC1 repeat-contain| 27.70| 0.00 |
| TRINITY_sp|Q156f|-| 27.70| 0.00 |
| TRINITY_sp|Q9SU8|Cation/H(+) antipor| 27.70| 0.00 |
| TRINITY_sp|Q049|DnaJ protein homolo| 27.70| 0.00 |
| TRINITY_sp|Q006|Leishmanolysin OS=L| 27.70| 0.00 |
| TRINITY_sp|Q75J|Circularly permutat| 27.70| 0.00 |
| TRINITY_sp|Q149|NWD1| 27.70| 0.00 |
| TRINITY_sp|Q9V6|Probable trans-2-en| 27.70| 0.00 |
| TRINITY_sp|Q055|ATP-dependent helic| 27.70| 0.00 |
| TRINITY_sp|P975|Neurofibromin OS=Ra| 27.70| 0.00 |
| TRINITY_sp|P067|Calmodulin OS=Sacch| 27.70| 0.00 |
| TRINITY_sp|Q23K|Tubulin glycyllase 3| 27.70| 0.00 |
| TRINITY_sp|Q6PD|UPF0668 protein C10| 27.70| 0.00 |
| TRINITY_sp|Q8BW|Ubiquitin carboxyl-| 27.70| 0.00 |
| TRINITY_sp|P114|Represible alkaline| 27.70| 0.00 |
| TRINITY_sp|Q5EF|Intraflagellar tran| 27.70| 0.00 |
| TRINITY_sp|Q86G|Ras guanine nucleot| 27.70| 0.00 |
| TRINITY_sp|Q744|Uncharacterized pro| 27.70| 0.00 |
| TRINITY_sp|Q9E9|Hamartin OS=Mus mus| 27.70| 0.00 |
| TRINITY_sp|Q529|Serine/threonine-pr| 27.70| 0.00 |
| TRINITY_sp|Q9YJ1|Negative elongation| 27.70| 0.00 |
| TRINITY_sp|Q99N|RWD domain-containi| 27.70| 0.00 |
| TRINITY_sp|Q93O|Probable ubiquitin| 27.70| 0.00 |
| TRINITY_sp|P347|Elongation factor 1| 27.70| 0.00 |
| TRINITY_sp|Q6B9|Alpha-protein kinas| 27.70| 0.00 |
| TRINITY_sp|Q56A|Coiled-coil domain-| 27.70| 0.00 |
| TRINITY_sp|Q141|Putative lipase C4A| 27.70| 0.00 |
| TRINITY_sp|Q6FM|Autophagy-related p| 27.70| 0.00 |
| TRINITY_sp|Q6XH|rcc9| 27.70| 0.00 |
| TRINITY_sp|A7RF|cdc123| 27.70| 0.00 |
| TRINITY_sp|Q317|pbpX| 27.70| 0.00 |
| TRINITY_sp|Q86K|GDB G02| 27.70| 0.00 |
| TRINITY_sp|F4KD|Urea-proton symport| 27.70| 0.00 |
| TRINITY_sp|P344|Clustered mitochond| 27.70| 0.00 |
| TRINITY_sp|Q9P2|Coiled-coil and C2| 27.70| 0.00 |
| TRINITY_sp|Q8L6|SEC31B| 27.70| 0.00 |
| TRINITY_sp|Q8TB|Solute carrier fami| 27.70| 0.00 |
| TRINITY_sp|A8II|CFAP52| 27.70| 0.00 |
| TRINITY_sp|Q8CL|Copine-1 OS=Mus mus| 27.70| 0.00 |
| TRINITY_sp|F20|Geranylgeranyl tran| 27.70| 0.00 |
| TRINITY_sp|P0C8|JmjC domain-contain| 27.70| 0.00 |
| TRINITY_sp|Q9BG|Glutamate-rich WD r| 27.70| 0.00 |
| TRINITY_sp|Q8CH|Tt115| 27.70| 0.00 |
| TRINITY_sp|Q9FF|ABC28| 27.70| 0.00 |
| TRINITY_sp|Q80S|Cathepsin E-B OS=Xe| 27.70| 0.00 |
| TRINITY_sp|P534|Actin OS=Chondrus c| 27.70| 0.00 |
| TRINITY_sp|Q2KJ|Ubiquitin carboxyl-| 27.70| 0.00 |
| TRINITY_sp|Q8VZ|TSN1| 27.70| 0.00 |
| TRINITY_sp|Q8R0|Carboxylesterase 4A| 27.70| 0.00 |
| TRINITY_sp|A2X5|SWEET15| 27.70| 0.00 |
| TRINITY_sp|Q86C|Autophagy-related p| 27.70| 0.00 |
| TRINITY_sp|Q9FT|GTE6| 27.70| 0.00 |
ATP-dependent DNA helicase DDX11 OS=Mus musculus GN=Ddx11 PE=1 SV=1
Polyadenylate-binding protein 4 OS=Arabidopsis thaliana GN=PAB4 PE=1 SV=1
Trigger factor OS=Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) GN=tig PE=3 SV=1
Poly [ADP-ribose] polymerase 6 OS=Homo sapiens GN=PARP6 PE=2 SV=1
Protein ABHD1 OS=Mus musculus GN=Abhd1 PE=1 SV=2
85/88 kDa calcium-independent phospholipase A2 OS=Homo sapiens GN=PLA2G6 PE=1 SV=2
Coiled-coil domain-containing protein SCD2 OS=Arabidopsis thaliana GN=SCD2 PE=1 SV=1
WD and tetratricopeptide repeats protein 1 OS=Mus musculus GN=Wdtc1 PE=1 SV=1
Dipeptidyl peptidase family member 6 OS=Caenorhabditis elegans GN=dpf-6 PE=3 SV=2
Synaptotagmin-2 OS=Arabidopsis thaliana GN=SYT2 PE=2 SV=1
Arabinosyltransferase XEG113 OS=Arabidopsis thaliana GN=XEG113 PE=2 SV=1
Protein DETOXIFICATION 45, chloroplastic OS=Arabidopsis thaliana GN=DTX45 PE=2 SV=2
ATP-dependent DNA helicase PIF1 OS=Saccharomyces cerevisiae (strain YJM789) GN=PIF1 PE=3 SV=1
Capreomycidine synthase OS=Streptomyces vinaceus GN=vioD PE=1 SV=1
Lysophosphatidylcholine acyltransferase 2 OS=Danio rerio GN=lpcat2 PE=2 SV=1
Ran-binding proteins 9/10 homolog OS=Drosophila melanogaster GN=RanBPM PE=1 SV=1
Vacuolar fusion protein MON1 homolog OS=Arabidopsis thaliana GN=MON1 PE=1 SV=2
BTB/POZ and MATH domain-containing protein 6 OS=Arabidopsis thaliana GN=BPM6 PE=1 SV=1
Dynactin subunit 2 OS=Dictyostelium discoideum GN=dynB PE=3 SV=1
Uncharacterized 80 kDa protein OS=Paramecium primaurelia PE=4 SV=1
Isopentenyl-diphosphate Delta-isomerase OS=Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) GN=idi PE=3 SV=1
Alpha-protein kinase vwkA OS=Dictyostelium discoideum GN=vwkA PE=1 SV=1
Leucine-rich repeat-containing protein 9 OS=Mus musculus GN=Lrrc9 PE=1 SV=2
Poly(A)-specific ribonuclease PARN OS=Danio rerio GN=parn PE=1 SV=2
rRNA biogenesis protein RRP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RRP5 PE=1 SV=1
Phosphoglucosamine mutase OS=Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ) GN=glmM PE=3 SV=1
| Accession     | Description                                             | TTRN | p-value |
|--------------|---------------------------------------------------------|------|---------|
| TRINITY_sp|D3ZENmica12 | MICAL-like protein | 27.40 | 0.00 |
| TRINITY_sp|Q8GWOS9     | Protein OS-9 homolo | 27.40 | 0.00 |
| TRINITY_sp|Q9641CP421  | Cytochrome P450 4c2 | 27.40 | 0.00 |
| TRINITY_sp|O624V43F4A.1 | Leishmanolysin-like | 27.40 | 0.00 |
| TRINITY_sp|Q01FOgd     | Prolyl 3,4-dihydrox | 27.40 | 0.00 |
| TRINITY_sp|Q17QTFD51   | Transcription facto | 27.40 | 0.00 |
| TRINITY_sp|Q5TFNTS5DC1 | 5'-nucleotidase dom | 27.40 | 0.00 |
| TRINITY_sp|Q8W0CCCR4-1 | Carbon catabolite r | 27.40 | 0.00 |
| TRINITY_sp|Q6UV6OMXD1  | DBH-like monoxygen | 27.40 | 0.00 |
| TRINITY_sp|Q8IS1gefJ   | Ras guanine nucleot | 27.40 | 0.00 |
| TRINITY_sp|Q1ZK10BDG02 | Spingomyelinase DD | 27.40 | 0.00 |
| TRINITY_sp|Q8KNEWCT0663| UPF0301 protein CT0 | 27.40 | 0.00 |
| TRINITY_sp|Q548H5mb3   | High mobility group | 27.40 | 0.00 |
| TRINITY_sp|P706FPALA2G7| Platelet-activating | 27.40 | 0.00 |
| TRINITY_sp|P389dMS54   | Probable phosphatid | 27.40 | 0.00 |
| TRINITY_sp|A4Q91Tll10  | Protein polyglycyla | 27.40 | 0.00 |
| TRINITY_sp|B3DNAPC6    | Anaphase-promoting | 27.40 | 0.00 |
| TRINITY_sp|Q7ZFWdwr75  | WD repeat-containing | 27.40 | 0.00 |
| TRINITY_sp|Q8JH1ar113b | ADP-ribosylation fa | 27.40 | 0.00 |
| TRINITY_sp|Q9M01ISA3   | Isoamylase 3, chlor | 27.40 | 0.00 |
| TRINITY_sp|P4185scn1   | Cut9-interacting pr | 27.40 | 0.00 |
| TRINITY_sp|Q94KVPS52   | Vacuolar protein so | 27.40 | 0.00 |
| TRINITY_sp|Q9699UTP4   | U3 small nucleolar | 27.40 | 0.00 |
| TRINITY_sp|Q084P8E4D1  | cAMP-specific 3',5' | 27.40 | 0.00 |
| TRINITY_sp|Q9SA6CSP41B | Chloroplast stem-lo | 27.40 | 0.00 |
| TRINITY_sp|Q6TNpak1pl1 | p2l-activated prote | 27.40 | 0.00 |
| TRINITY_sp|Q9VY6Ev15   | Ecotropic viral int | 27.40 | 0.00 |
| TRINITY_sp|Q17RGEN1    | Flap endonuclease G | 27.40 | 0.00 |
| TRINITY_sp|Q6ZUc-      | Uncharacterized pro | 27.40 | 0.00 |
| TRINITY_sp|Q8S1cOs01g09| Probable glucuronos | 27.40 | 0.00 |
| TRINITY_sp|Q9NPNPOLM   | DNA-directed DNA/RN | 27.40 | 0.00 |
| TRINITY_sp|P335ABCC1   | Multidrug resistanc | 27.30 | 0.00 |
| TRINITY_sp|Q8CN4SE_2036| Uncharacterized oxi | 27.30 | 0.00 |
| TRINITY_sp|Q9MAACBP4   | Acyl-CoA-binding do | 27.30 | 0.00 |
| TRINITY_sp|Q9V11CDDC53 | WASH complex subuni | 27.30 | 0.00 |
| TRINITY_sp|P345epac-1  | Rap guanine nucleot | 27.30 | 0.00 |
| TRINITY_sp|Q96S1JMMD8  | JmjC domain-contain | 27.30 | 0.00 |
| TRINITY_sp|Q9Z1cEif2ak3| Eukaryotic translat | 27.30 | 0.00 |
| TRINITY_sp|Q9601CHEK2  | Serine/threonine-pr | 27.30 | 0.00 |
| TRINITY_sp|Q8WVKBTBD7  | Kelch repeat and BT | 27.30 | 0.00 |
| TRINITY_sp|Q6GLNHtraA  | tRNA pseudouridine | 27.30 | 0.00 |
| TRINITY_sp|Q8B2Nuak2   | NUAK family SNF1-li | 27.30 | 0.00 |
| TRINITY_sp|A2YWFLPL2   | Patatin-like protei | 27.30 | 0.00 |
| TRINITY_sp|Q0CB8faeA   | Probable feruloyl e | 27.30 | 0.00 |
| TRINITY_sp|Q942cTca1   | COP9/Signalosome an | 27.30 | 0.00 |
| TRINITY_sp|Q54VMcfJ    | Mitochondrial subst | 27.30 | 0.00 |
| TRINITY_sp|Q7XSws125a3 | Solute carrier fami | 27.30 | 0.00 |
| TRINITY_sp|Q9NXNMKS1   | Meckel syndrome typ | 27.30 | 0.00 |
| TRINITY_sp|P389MSS4    | Probable phosphatid | 27.30 | 0.00 |
| TRINITY_sp|Q002meIO    | Tyrosinase OS=Asper | 27.30 | 0.00 |
| TRINITY_sp|Q6NKAs5g017 | Probable protein ph | 27.30 | 0.00 |
| TRINITY_sp|A6H8Kcnnb2  | Potassium voltage-g | 27.30 | 0.00 |
| TRINITY_sp|B1HI1acp2   | Lysosomal acid phos | 27.30 | 0.00 |
| TRINITY_sp|Q54KKvps51  | Vacuolar protein so | 27.30 | 0.00 |
| TRINITY_sp|P518Cyp4f6  | Cytochrome P450 4F6 | 27.30 | 0.00 |
| TRINITY_sp|Q10SOs03g01 | Probable glucuronos | 27.30 | 0.00 |
| Accession | Description | Organism | Location | Score | E-value |
|-----------|-------------|----------|----------|-------|---------|
| sp|Q80VFam98b|Protein FAM98B|Mus musculus|26.90|0.00|
| sp|P7944CP3A29|Cytochrome P450 3A2|3|26.90|0.00|
| sp|Q1ZXIDDB_GO2|Sphingomyelinase DD|26.90|0.00|
| sp|Q91XPex16|Peroxisomal membrand|26.90|0.00|
| sp|Q7LH3TY3B|M Transposon Ty3-I Ga |26.90|0.00|
| sp|Q99M8ec1412|SECl4-like protein|26.90|0.00|
| sp|Q08Dmael|Protein maelstrom h|26.90|0.00|
| sp|Q541frtfdc1|Protein RTF2 homolo|26.90|0.00|
| sp|Q54EbabF|Actin-binding prote|26.90|0.00|
| sp|Q7RRFY00695|T-cell immunomodu|26.90|0.00|
| sp|Q6YCCBG0355|Leishmanolysin-like|26.90|0.00|
| sp|B6K6hmm1|Maintenance of mito|26.90|0.00|
| sp|Q3T1YIF1A|Protein YIF1A|Bo|26.90|0.00|
| sp|Q9STrPH1|Pleckstrin homology|26.90|0.00|
| sp|Q1AZdmem245|Transmembrane prote|26.90|0.00|
| sp|B0U0rlmL|Ribosomal RNA large|26.90|0.00|
| sp|P293EPHA3|Ephrin type-A recept|26.90|0.00|
| sp|A6Vvdadl|D-alanine--D-alanine|26.90|0.00|
| sp|Q7Z6.rFGD2|FYVE, RhoGEF and PH|26.90|0.00|
| sp|Q8VZI0FG2|Glyoxysomal process|26.90|0.00|
| sp|Q55ZSupt5h|Transcription elong|26.90|0.00|
| sp|Q1581ITSN1|Intersectin-1 OS=Ho|26.90|0.00|
| sp|P55lybaR|Putative sulfate tr|26.90|0.00|
| sp|Q169r-|Syntaxin OS=Aplysia|26.90|0.00|
| sp|Q4WZImvp1|Sorting nexin mvp1|26.90|0.00|
| sp|Q9FI1GNL1|ARF guanine-nucleot|26.90|0.00|
| sp|Q08DAAAR2|Protein AAR2 homolo|26.90|0.00|
| sp|Q9H3fPABPC3|Polyadenylate-bindi|26.80|0.00|
| sp|Q5HR8SERP017|Putative TrmH fami|26.80|0.00|
| sp|Q038rYMR166C|Uncharacterized mit|26.80|0.00|
| sp|Q5BLlmettt21|Protein N-lysine me|26.80|0.00|
| sp|Q5AHrCHK1|Histidine protein k|26.80|0.00|
| sp|Q2VQcrecr1|Adenosine deaminase|26.80|0.00|
| sp|Q55AbDDB_GO2|Probable serine/thr|26.80|0.00|
| sp|Q551IDDB_GO2|Protein DDB_GO27668|26.80|0.00|
| sp|P873rTfb2|RNA polymerase II t|26.80|0.00|
| sp|Q29AHGAI7800|Leishmanolysin-like|26.80|0.00|
| sp|Q9M8rUGT80A2|Sterol 3-beta-gluco|26.80|0.00|
| sp|P838rIft81|Intraflagellar tran|26.80|0.00|
| sp|Q55AbDDB_GO2|Probable serine/thr|26.80|0.00|
| sp|Q8IYrTE91I|Testis-expressed se|26.80|0.00|
| sp|Q08Cmodx2|DBH-like monooxygen|26.80|0.00|
| sp|P094rLOX1.2|Seed linoleate 9S-1|26.80|0.00|
| sp|Q0INmol11|Nucleolar protein 1|26.80|0.00|
| sp|O345YsppA|Putative signal pep|26.80|0.00|
| sp|Q04OCCX5|Cation/calcium exch|26.80|0.00|
| sp|Q14GATXN7L3|Ataxin-7-like prote|26.80|0.00|
| sp|A4FIIIO18G2|Inositol 2-dehydrog|26.80|0.00|
| sp|Q2TBIRAB4A|Ras-related protein|26.80|0.00|
| sp|Q96JCVP550|Syndetin OS=Homo sa|26.80|0.00|
| sp|Q8N7KHLHC1|Kelch domain-contai|26.80|0.00|
| sp|P304rPur2|Furin-like protease|26.80|0.00|
| sp|Q2BCRctu2|Cytoplasmic tRNA 2-|26.80|0.00|
| sp|Q891lgaT|Glutamyl-tRNA(Gln)|26.80|0.00|
| sp|Q8IYrDDX60|Probable ATP-depend|26.80|0.00|
| sp|Q9SPrDCL1|Endoribonuclease Di|26.80|0.00|
Cationic amino acid transporter 2
OS=Gallus gallus
GN=SLC7A2
PE=2
SV=1

RCC1 and BTB domain-containing protein 1
OS=Mus musculus
GN=Rcbtb1
PE=2
SV=1

Putative modification methylase OB3336
OS=Oceanobacillus iheyensis (strain DSM 14371 / CIP 107618 / JCM 11309 / KCTC 3954 / HTE831)
GN=OB3336
PE=3
SV=1

CLIP-associated protein
OS=Arabidopsis thaliana
GN=CLASP
PE=1
SV=1

Probable sodium-coupled neutral amino acid transporter 6
OS=Danio rerio
GN=slc38a6
PE=2
SV=1

Potassium voltage-gated channel subfamily H member 6
OS=Gallus gallus
GN=KCNH6
PE=2
SV=2

Circularly permutated Ras protein 1
OS=Dictyostelium discoideum
GN=cpras1
PE=3
SV=1

Copia protein
OS=Drosophila melanogaster
GN=GIP
PE=1
SV=3

Bromodomain-containing factor 1
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
GN=BDF1
PE=1
SV=3

Ceramide synthase 4
OS=Mus musculus
GN=Cers4
PE=1
SV=1

Clustered mitochondria protein
OS=Arabidopsis thaliana
GN=FMT
PE=2
SV=1

Napsin-A
OS=Homo sapiens
GN=NAPSA
PE=1
SV=1

Probable reverse transcriptase
OS=Acutodesmus obliquus
PE=3
SV=1

ATP-dependent RNA helicase mak5
OS=Schizosaccharomyces pombe (strain 972 / ATCC 204508 / S288c)
GN=mak5
PE=1
SV=1

G2/mitotic-specific cyclin-B1
OS=Mus musculus
GN=Ccnb1
PE=1
SV=3

Guanylate-binding protein 5
OS=Mus musculus
GN=Gbp5
PE=1
SV=2

Leishmanolysin
OS=Leishmania guyanensis
GN=gp63
PE=2
SV=1

tRNA wybutosine-synthesizing protein 5
OS=Danio rerio
GN=tyw5
PE=2
SV=1

Elongator complex protein 5
OS=Arabidopsis thaliana
GN=ELP5
PE=1
SV=1

X-linked retinitis pigmentosa GTPase regulator
OS=Homo sapiens
GN=RPGR
PE=1
SV=2

Phospholipase ABHD3
OS=Mus musculus
GN=Abhd3
PE=1
SV=1

Meiosis-specific protein HOP1
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
GN=HOP1
PE=1
SV=2

Calpain-D
OS=Drosophila melanogaster
GN=sol
PE=1
SV=2

Eukaryotic translation initiation factor 2-alpha kinase 1
OS=Oryctolagus cuniculus
GN=EIF2AK1
PE=1
SV=1

Probable serine/threonine-protein kinase pats1
OS=Dictyostelium discoideum
GN=pats1
PE=3
SV=1

Histone-lysine N-methyltransferase setd3
OS=Mus musculus
GN=Setd3
PE=1
SV=1

Zinc finger protein ZPR1 homolog
OS=Dictyostelium discoideum
GN=zpr1
PE=3
SV=1

Protein misato homolog 1
OS=Mus musculus
GN=Msto1
PE=1
SV=1

Protein sds23
OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513)
GN=sds23
PE=3
SV=1

Protein sds23
OS=Neosartorya fischeri (strain ATCC 1020 / DSM 3700 / CBS 544.65 / FGSC A1164 / JCM 1740 / NRRL 181 / WB 181)
GN=sds23
PE=3
SV=1

TRINITY_sp|B3TP|SLC7A2
TRINITY_sp|Q91WC5|Setd3
TRINITY_sp|Q7M3|rngB
TRINITY_sp|Q9665|JNK
TRINITY_sp|Q006g6p63
TRINITY_sp|Q8TS6|abcA2
TRINITY_sp|Q9LUCY|P72A1!Cytochrome P450 72A
TRINITY_sp|Q8ELO|OB3336
TRINITY_sp|Q960|NAPSA
TRINITY_sp|Q9D2H|Ak7
TRINITY_sp|P4711|BNA2
TRINITY_sp|Q9CX(Ist1
TRINITY_sp|P391|yeaD
TRINITY_sp|B0R0Verbcb1d8b
TRINITY_sp|Q006g6p63
TRINITY_sp|Q8RW|CLASP
TRINITY_sp|P743|mak5
TRINITY_sp|Q54Cl|dync1li1
TRINITY_sp|P27|sol
TRINITY_sp|Q55Epats1
TRINITY_sp|F4J5xFMT
TRINITY_sp|O601|SPBC18H1
TRINITY_sp|Q9UTI|SPAC14A
TRINITY_sp|Q55E|zpr1
TRINITY_sp|Q4G2|DER1.2
TRINITY_sp|Q6NXARcbb1
TRINITY_sp|F4IQ|ELP5
TRINITY_sp|P041|GIP
TRINITY_sp|Q8K0|Slc47al
TRINITY_sp|P390|FMT
TRINITY_sp|O942|hmt2
TRINITY_sp|P248|Ccnb1
TRINITY_sp|P262|PG1
TRINITY_sp|B4FG6|aifm2
TRINITY_sp|A1D3|sds23
TRINITY_sp|O666|pth
TRINITY_sp|P332|EIF2A1
TRINITY_sp|Q9P7|SPBC170
TRINITY_sp|Q9PT|KCNYH6
TRINITY_sp|Q928|RPGR
TRINITY_sp|P200|HOP1
TRINITY_sp|O285|formerly
TRINITY_sp|P19S|AF_1724
TRINITY_sp|P19S|AF_1724
TRINITY_sp|Q912|Abhd3
TRINITY_sp|A2RB|sds23
TRINITY_sp|Q9DB|Cers4
TRINITY_sp|Q7F0|CML13
TRINITY_sp|P358|I23O
TRINITY_sp|Q91WC0|SETD3
TRINITY_sp|SLC7A2
TRINITY_sp|Q4UMIRF_0338
TRINITY_sp|Q08B|twy5
TRINITY_sp|Q2YD|Msto1
TRINITY_sp|O600|CMD1
TRINITY_sp|Q75J|cpras1
| Accession | Description | ORF | Score |
|-----------|-------------|-----|-------|
| TRINITY_sp| Nucleolar protein 6 | OS=Drosophila yakuba | 26.30 |
| TRINITY_sp| Protein PIEZ0 homol | OS=Dictyostelium discoideum | 26.30 |
| TRINITY_sp| Periodic tryptophan | OS=Schizosaccharomyces pombe | 26.30 |
| TRINITY_sp| DNA-directed RNA po | OS=Caenorhabditis elegans | 26.30 |
| TRINITY_sp| U3 small nucleolar | OS=Gallus gallus | 26.30 |
| TRINITY_sp| Choline/ethanolamin | OS=Homo sapiens | 26.30 |
| TRINITY_sp| Uncharacterized pro | OS=Schizosaccharomyces pombe | 26.30 |
| TRINITY_sp| Protein TPX2 | OS=Ara | 26.30 |
| TRINITY_sp| Choline/ethanolamin | OS=Homo sapiens | 26.30 |
| TRINITY_sp| Sucrose transport p | OS=Homo sapiens | 26.30 |
| TRINITY_sp| Excitatoty amino acid | OS=Kluyveromyces lactis | 26.30 |
| TRINITY_sp| Polyadenylate-binding protein, cytoplasmic and nuclear | OS=Kluyveromyces lactis | 26.30 |
| TRINITY_sp| Periodic tryptophan | OS=Saccharomyces cerevisiae | 26.30 |
| TRINITY_sp| Polypyrimidine tract-binding protein 1 | OS=Homo sapiens | 26.30 |
| TRINITY_sp| Transcription elongation factor SPT6 | OS=Danio rerio | 26.30 |
| TRINITY_sp| Transmembrane protein 87B | OS=Mus musculus | 26.30 |
| TRINITY_sp| cGMP-specific 3',5'-cyclic phosphodiesterase | OS=Drosophila erecta | 26.30 |
| TRINITY_sp| Co-chaperone protein HscB | OS=Proteus mirabilis | 26.30 |
| TRINITY_sp| DNA-directed RNA polymerase III subunit RPC3 | OS=Bos taurus | 26.30 |
| TRINITY_sp| Hydrolase tropI | OS=Talaromyces stipitatus | 26.30 |
| TRINITY_sp| Choline/ethanolaminephosphotransferase 1 | OS=Homo sapiens | 26.30 |
| TRINITY_sp| Nuclear receptor corepressor 1 | OS=Xenopus laevis | 26.30 |
| TRINITY_sp| Calcium-dependent protein kinase 7 | OS=Arabidopsis thaliana | 26.30 |
| TRINITY_sp| Aldehyde oxidase GLOX1 | OS=Arabidopsis thaliana | 26.30 |
| TRINITY_sp| Excitatory amino acid transporter 1 | OS=Ambystoma tigrinum | 26.30 |
| TRINITY_sp| Pepsin A-4 | OS=Macaca fuscata fuscata | 26.30 |
| TRINITY_sp| Protein DETOXIFICATION 24 | OS=Arabidopsis thaliana | 26.30 |
| TRINITY_sp| 3',5'-cyclic-nucleotide phosphodiesterase regA | OS=Dictyostelium discoideum | 26.30 |
| TRINITY_sp| Zinc finger protein 830 | OS=Xenopus tropicalis | 26.30 |
| TRINITY_sp| Probable Ras GTPase-activating protein | OS=Drosophila melanogaster | 26.30 |
| TRINITY_sp| DnaJ protein ERDJ3A | OS=Oryza sativa subsp. japonica | 26.30 |
| TRINITY_sp| Metabotropic glutamate receptor-like protein E | OS=Dictyostelium discoideum | 26.30 |
| TRINITY_sp| Hydroxyproline O-galactosyltransferase GALT2 | OS=Arabidopsis thaliana | 26.30 |
| TRINITY_sp| Signal recognition particle subunit SRP72 | OS=Canis lupus familiaris | 26.30 |
| Accession   | Description                                                                 | Score | E-value |
|-------------|------------------------------------------------------------------------------|-------|---------|
| sp|O60232|SSCA1_HUMAN | 26.00 | 0.00   |
| sp|Q5JWR5|DOP1_HUMAN | 26.00 | 0.00   |
| sp|Q75J93|CPAS1_DICDI | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|Q75J93|CPAS1_DICDI | 26.00 | 0.00   |
| sp|Q5JWR5|DOP1_HUMAN | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|P0CMBST1|GPI inositol-deacyl | 26.00 | 0.00   |
| sp|O44400|KGB1_CAEEL | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q5JWR5|DOP1_HUMAN | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|P0CMBST1|GPI inositol-deacyl | 26.00 | 0.00   |
| sp|O44400|KGB1_CAEEL | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|P0CMBST1|GPI inositol-deacyl | 26.00 | 0.00   |
| sp|O44400|KGB1_CAEEL | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|P0CMBST1|GPI inositol-deacyl | 26.00 | 0.00   |
| sp|O44400|KGB1_CAEEL | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|P0CMBST1|GPI inositol-deacyl | 26.00 | 0.00   |
| sp|O44400|KGB1_CAEEL | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|P0CMBST1|GPI inositol-deacyl | 26.00 | 0.00   |
| sp|O44400|KGB1_CAEEL | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|P0CMBST1|GPI inositol-deacyl | 26.00 | 0.00   |
| sp|O44400|KGB1_CAEEL | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|P0CMBST1|GPI inositol-deacyl | 26.00 | 0.00   |
| sp|O44400|KGB1_CAEEL | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|P0CMBST1|GPI inositol-deacyl | 26.00 | 0.00   |
| sp|O44400|KGB1_CAEEL | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|P0CMBST1|GPI inositol-deacyl | 26.00 | 0.00   |
| sp|O44400|KGB1_CAEEL | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|P0CMBST1|GPI inositol-deacyl | 26.00 | 0.00   |
| sp|O44400|KGB1_CAEEL | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| sp|P55192|YBBA_BACSU | 26.00 | 0.00   |
| sp|P0CMBST1|GPI inositol-deacyl | 26.00 | 0.00   |
| sp|O44400|KGB1_CAEEL | 26.00 | 0.00   |
| sp|Q5TVU5|RAB1_THEPA | 26.00 | 0.00   |
| sp|Q3KPT3|TSSC1_XENLA | 26.00 | 0.00   |
| sp|Q9SRS9|CHIP_ARATH | 26.00 | 0.00   |
| Accession       | Description                                      | GO Terms          | Score | Log2Fold | OddsRatio |
|-----------------|--------------------------------------------------|-------------------|-------|----------|-----------|
| sp|Q5VQČCPK2 | Calcium-dependent protein kinase | | 26.00| 0.00| 2.50 |
| sp|Q242ČCngA | Cyclic nucleotide-gated channel | | 26.00| 0.00| 2.50 |
| sp|Q8L74At4g396:ACD11 homolog | | | 26.00| 0.00| 2.50 |
| sp|Q94AČSAC2 | Phosphoinositide phospholipase | | 26.00| 0.00| 2.50 |
| sp|Q8VDX1k4 | Mitogen-activated protein kinase | | 26.00| 0.00| 2.50 |
| sp|Q126ČCYP51 | Eburicol 14-alpha-d-glucosidase | | 26.00| 0.00| 2.50 |
| sp|P5988scl39a1 | Zinc transporter Zn2+ | | 26.00| 0.00| 2.50 |
| sp|P1261abg | Beta-glucosidase | | 26.00| 0.00| 2.50 |
| sp|Q8PSHtpX2 | Protease HtpX homolog | | 26.00| 0.00| 2.50 |
| sp|Q148ČKiaa1466:LiSH domain and HEAT repeat | | | 26.00| 0.00| 2.50 |
| sp|P2788:Vav1 | Proto-oncogene vav | | 26.00| 0.00| 2.50 |
| sp|Q6TK mx | Interferon-induced protein | | 26.00| 0.00| 2.50 |
| sp|Q3MEČEMB2271 | U3 snoRNP-associate | | 26.00| 0.00| 2.50 |
| sp|B3EYČabnB | Intracellular endo-wall | | 25.90| 0.00| 2.00 |
| sp|Q9BJćfus | RNA-binding protein | | 25.90| 0.00| 2.00 |
| sp|Q8GYČPGM | Phosphoglycerate mutase | | 25.90| 0.00| 2.00 |
| sp|Q9FNČUVR8 | Ultraviolet-B receptor | | 25.90| 0.00| 2.00 |
| sp|P612ČSTX1B | Syntaxin-1B | | 25.90| 0.00| 2.00 |
| sp|Q8VYGČGC4 | Golgin candidate 4 | | 25.90| 0.00| 2.00 |
| sp|Q96PČACAP3 | Arf-GTPase | | 25.90| 0.00| 2.00 |
| sp|Q923ČSPAC69A | Pumilio domain-containing protein | | 25.90| 0.00| 2.00 |
| sp|Q6821XRC2 | DNA repair protein | | 25.90| 0.00| 2.00 |
| sp|Q54Ečnup98 | Nuclear pore complex protein | | 25.90| 0.00| 2.00 |
| sp|Q9U7čerd1 | Protein ERD1 homolog | | 25.90| 0.00| 2.00 |
| sp|Q8RWČACBP5 | Acyl-CoA-binding domain | | 25.90| 0.00| 2.00 |
| sp|Q54FČgefA | Ras guanine nucleotide exchange factor | | 25.90| 0.00| 2.00 |
| sp|Q9C4ČpaxM | FAD-dependent monooxygenase | | 25.90| 0.00| 2.00 |
| sp|Q59KČMN21 | Alpha-1,2-mannosyltransferase | | 25.90| 0.00| 2.00 |
| sp|Q5FWČgpr180 | Integral membrane protein | | 25.90| 0.00| 2.00 |
| sp|Q9LGČPARN | Poly(A)-specific ribonuclease | | 25.90| 0.00| 2.00 |
| sp|P276ČRasgrf1 | Ras-specific guanine nucleotide exchange factor | | 25.90| 0.00| 2.00 |
| sp|Q8MVCČgpbC | Cyclic GMP-binding protein | | 25.90| 0.00| 2.00 |
| sp|Q69XČCYP734A:Clostridium cellulolyticum | Cytochrome P450 574 | | 25.90| 0.00| 2.00 |
| sp|Q8VYČKEA5 | K(+) efflux antiporin | | 25.90| 0.00| 2.00 |
| sp|Q9201čAk5 | Adenylyl kinase | | 25.90| 0.00| 2.00 |
| sp|Q182Čtrpa-1 | Transient receptor potential | | 25.90| 0.00| 2.00 |
| sp|Q5JMČOs01g0751:Potassium channel K+ | | | 25.90| 0.00| 2.00 |
| sp|Q9SCČAt3g5055:Phosphoglycerate mutase | | | 25.90| 0.00| 2.00 |
| sp|Q81Čprs | Ribose-phosphate pyrophosphatase | | 25.80| 0.00| 2.00 |
| sp|Q54EčabpF | Actin-binding protein | | 25.80| 0.00| 2.00 |
| sp|P108ČPrf1 | Perforin-1 OS=Mus m | | 25.80| 0.00| 2.00 |
| sp|Q99JčThump1 | THUMP domain-containing protein | | 25.80| 0.00| 2.00 |
| sp|A1L0Črshp6a | Radial spoke head protein | | 25.80| 0.00| 2.00 |
| sp|Q700ČBDG4 | Probable lysocephospholipid acyltransferase | | 25.80| 0.00| 2.00 |
| sp|Q54BČdécd2A | Neutral ceramidase | | 25.80| 0.00| 2.00 |
| sp|Q81MČtal2 | Probable transaldolase | | 25.80| 0.00| 2.00 |
| sp|Q9SEČVT11 | Vesicle transport | | 25.80| 0.00| 2.00 |
| sp|Q8L5ČCAND1 | Cullin-associated Nedd4-like protein | | 25.80| 0.00| 2.00 |
| sp|Q5691msd4b | Sodium-dependent glutamate transporter | | 25.80| 0.00| 2.00 |
| sp|Q9KČSY72 | Syntaxin-72 OS=Arabidopsis thaliana | | 25.80| 0.00| 2.00 |
| sp|B8IČera | GTPase Era OS=Cladosporium herbarum | | 25.80| 0.00| 2.00 |
| sp|Q995ČSORT1 | Sortilin OS=Homo sapiens | | 25.80| 0.00| 2.00 |
| sp|Q94BČXBAT31 | Putative E3 ubiquitin ligase | | 25.80| 0.00| 2.00 |
| sp|P229VCVS2 | Vacuolar-sorting receptor | | 25.80| 0.00| 2.00 |
| sp|Q9HGČSPBC800.3 | Uncharacterized protein | | 25.80| 0.00| 2.00 |
| sp|Q063ČLOX1 | Linoleate 9S-lipoxygenase | | 25.80| 0.00| 2.00 |
| Accession     | Description                                      | Score 1 | Score 2 |
|--------------|--------------------------------------------------|---------|---------|
| TRINITY_sp|Uncharacterized protein YisT OS=Bacillus subtilis (strain 168) GN=yisT PE=3 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Extracellular metalloprotease OS=Bacillus subtilis (strain 168) GN=mpr PE=1 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Protein HYPER-SENSI OS=Homo sapiens GN=GLTSCR2 PE=1 SV=2 | 25.80   | 0.00    |
| TRINITY_sp|Carotene epsilon-monoxygenase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=SEC62 PE=3 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Chloroplastic protein TIC110 OS=Pisum sativum GN=TIC110 PE=1 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Ras GTPase-activating protein OS=Homo sapiens GN=RASA1 PE=1 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Transmembrane protein OS=Xenopus tropicalis GN=tmem147 PE=2 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Kelch domain-containing protein OS=Mus musculus GN=Klhdc3 PE=2 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Sperm-associated antigen OS=Mus musculus GN=Spag17 PE=1 SV=2 | 25.80   | 0.00    |
| TRINITY_sp|Caltractin ICL1e OS=Paramecium tetraurelia GN=Icl1e PE=3 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Pheophytinase, chloroplastic protein OS=Arabidopsis thaliana GN=PPH PE=1 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|ABC transporter G family member OS=Arabidopsis thaliana GN=ABCG7 PE=2 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Threonine-phosphate decarboxylase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=cobD PE=1 SV=2 | 25.80   | 0.00    |
| TRINITY_sp|Aldehyde dehydrogenase OS=Pseudomonas oleovorans GN=alkH PE=2 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Carotene epsilon-monooxygenase, chloroplastic protein OS=Arabidopsis thaliana GN=CYP97C1 PE=1 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Inositol 1,4,5-trisphosphate receptor OS=Homo sapiens GN=ITPR2 PE=1 SV=2 | 25.80   | 0.00    |
| TRINITY_sp|Cilia- and flagella associated protein OS=Homo sapiens GN=CFAP61 PE=2 SV=3 | 25.80   | 0.00    |
| TRINITY_sp|Cytochrome P450 4e2 OS=Drosophila melanogaster GN=Cyp4e2 PE=2 SV=2 | 25.80   | 0.00    |
| TRINITY_sp|Calcium-activated potassium channel OS=Caenorhabditis elegans GN=slo-1 PE=1 SV=2 | 25.80   | 0.00    |
| TRINITY_sp|Acid phosphatase OS=Aspergillus ficuum GN=aphA PE=1 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Protein SMG7 OS=Mus musculus GN=Smg7 PE=2 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Protein HYPER-SENSITIVITY-RELATED OS=Arabidopsis thaliana GN=HSR4 PE=2 SV=1 | 25.80   | 0.00    |
| TRINITY_sp|Q6DD9|kiaa1324|protein KIA  | 25.60 | 0.00 |
| TRINITY_sp|Q254f-|Muscle calcium chan  | 25.60 | 0.00 |
| TRINITY_sp|Q29Dk|Klp68D|Kinesin-like protein  | 25.60 | 0.00 |
| TRINITY_sp|Q8ND8|RCBTB1|RCC1 and BTB domain  | 25.50 | 0.00 |
| TRINITY_sp|P080|Dia4|Protein disulfide-i  | 25.50 | 0.00 |
| TRINITY_sp|Q5RF6|CHFR|E3 ubiquitin-protei  | 25.50 | 0.00 |
| TRINITY_sp|Q8WZ2|DNEASE2B|Deoxyribonuclease-2  | 25.50 | 0.00 |
| TRINITY_sp|Q6PGt|mem56-t|Transmembrane prote  | 25.50 | 0.00 |
| TRINITY_sp|Q9Bv4|RNF126|E3 ubiquitin-protei  | 25.50 | 0.00 |
| TRINITY_sp|P146|KSS1|Mitogen-activated p  | 25.50 | 0.00 |
| TRINITY_sp|Q68Y9|grid2|Glutamate receptor  | 25.50 | 0.00 |
| TRINITY_sp|P232|gp63|Leishmanolysin OS=L  | 25.50 | 0.00 |
| TRINITY_sp|Q54Q|wd89|WD repeat-containin  | 25.50 | 0.00 |
| TRINITY_sp|Q9VRK|Cand1|Cullin-associated N  | 25.50 | 0.00 |
| TRINITY_sp|Q9CRK|Klh128|Kelch-like protein  | 25.50 | 0.00 |
| TRINITY_sp|Q004|Ptbp1|Polypyrimidine trac  | 25.50 | 0.00 |
| TRINITY_sp|Q981|ppk5|Serine/threonine-pr  | 25.50 | 0.00 |
| TRINITY_sp|F1MBl|KHLH3|Kelch-like protein  | 25.50 | 0.00 |
| TRINITY_sp|Q9ULIP|PALD1|Paladin OS=Homo sap  | 25.50 | 0.00 |
| TRINITY_sp|A2V2D|PLK4|Serine/threonine-pr  | 25.50 | 0.00 |
| TRINITY_sp|P169|elav|Protein elav OS=Dro  | 25.50 | 0.00 |
| TRINITY_sp|Q8RWI|STY17|Serine/threonine-pr  | 25.50 | 0.00 |
| TRINITY_sp|P546|tqkB|Serine protease/ABC  | 25.50 | 0.00 |
| TRINITY_sp|Q86N|DDB_G02|COBW domain-contain  | 25.50 | 0.00 |
| TRINITY_sp|Q8R7T|adk|Adenylate kinase OS  | 25.40 | 0.00 |
| TRINITY_sp|Q6EJZ|URH1|Probable uridine nu  | 25.40 | 0.00 |
| TRINITY_sp|Q275|Cyp4d2|Cytochrome P450 4d2  | 25.40 | 0.00 |
| TRINITY_sp|Q9NY5|SLC39A1|Zinc transporter ZI  | 25.40 | 0.00 |
| TRINITY_sp|Q9VKC|CG6488|Conserved oligomer  | 25.40 | 0.00 |
| TRINITY_sp|B2AC|Pa_2_14|Extracellular metal  | 25.40 | 0.00 |
| TRINITY_sp|Q997|ABCA3|ATP-binding cassett  | 25.40 | 0.00 |
| TRINITY_sp|Q7Z3P|PILW4|Piwi-like protein  | 25.40 | 0.00 |
| TRINITY_sp|Q9C5P|PAP6|Purple acid phospha  | 25.40 | 0.00 |
| TRINITY_sp|P831|Tak11|Putative mitogen-ac  | 25.40 | 0.00 |
| TRINITY_sp|Q9CS5|At3g16270|VHS domain-containi  | 25.40 | 0.00 |
| TRINITY_sp|Q906|PLA2G7|Platelet-activating  | 25.40 | 0.00 |
| TRINITY_sp|O460|msta|Protein msta, isofo  | 25.40 | 0.00 |
| TRINITY_sp|Q9V3H|heix|UbiA prenyltransfer  | 25.40 | 0.00 |
| TRINITY_sp|Q004|Ptbp1|Polypyrimidine trac  | 25.40 | 0.00 |
| TRINITY_sp|F4J1T|ISTRY46|Serine/threonine-pr  | 25.40 | 0.00 |
| TRINITY_sp|O444|F37C4.5|Protein F37C4.5 OS=  | 25.40 | 0.00 |
| TRINITY_sp|O944|SPACL68|UPF0616 protein C16  | 25.40 | 0.00 |
| TRINITY_sp|Q5U3|klh112|Kelch-like protein  | 25.40 | 0.00 |
| TRINITY_sp|Q5R4|SNX4|Sorting nexin-4 OS=  | 25.40 | 0.00 |
| TRINITY_sp|P086|ras1|Ras-like protein  | 25.40 | 0.00 |
| TRINITY_sp|Q6NZD|Ddx31|Probable ATP-depend  | 25.40 | 0.00 |
| TRINITY_sp|Q7SCB|sym-1|Protein sym-1 OS=Ne  | 25.30 | 0.00 |
| TRINITY_sp|P908|F26E4.3|Uncharacterized pep  | 25.30 | 0.00 |
| TRINITY_sp|Q9R1S|qrd1|Sulfide:quinone oxi  | 25.30 | 0.00 |
| TRINITY_sp|P516|HFCC1|Host cell factor  | 25.30 | 0.00 |
| TRINITY_sp|A7S4|serinc|Probable serine inc  | 25.30 | 0.00 |
| TRINITY_sp|Q9DG1|star|Steroidogenic acute  | 25.30 | 0.00 |
| TRINITY_sp|Q6NRE|emc1|ER membrane protein  | 25.30 | 0.00 |
| TRINITY_sp|Q2IBM|MET|Hepatocyte growth f  | 25.30 | 0.00 |
| TRINITY_sp|A3LQ|SDS23|Protein SDS23 OS=Sc  | 25.30 | 0.00 |
| TRINITY_sp|Q8TEIT|RPC4AP|Short transient rec  | 25.30 | 0.00 |
| TRINITY_sp|Q388|CPK7  | Calcium-dependent p |
| TRINITY_sp|Q9HBI|CPY4F11 | Phylloquinone omega |
| TRINITY_sp|Q0UQ|BST1  | GPI inositol-deacyl |
| TRINITY_sp|Q9UT7|pgv1  | Pyruvyl transferase |
| TRINITY_sp|P0CD|frmC  | FERM domain-contain |
| TRINITY_sp|F4JM|PGS1P7 | Putative glucuronos |
| TRINITY_sp|Q016|Pxd   | Peroxidase OS=Dros |
| TRINITY_sp|Q9CTRhobt3 | Rho-related BTB dom |
| TRINITY_sp|Q9UBIASH2L | Set1/Ash2 histone m |
| TRINITY_sp|P2B4|CAP2A2 | F-actin-capping pro |
| TRINITY_sp|Q54E|gr1E  | Metabotropic glutam |
| TRINITY_sp|Q2UL|utp10  | U3 small nucleolar |
| TRINITY_sp|Q6IM|dnajc27 | DnaJ homolog subfam |
| TRINITY_sp|Q5RC|CYP4V2 | Cytochrome P450 4V2 |
| TRINITY_sp|Q28F|Imfsd7-A | Major facilitator s |
| TRINITY_sp|O147|TPP1  | Tripeptidyl-peptida |
| TRINITY_sp|Q0CR|iatq5  | Autophagy protein 5 |
| TRINITY_sp|Q8SF|SYP71  | Syntaxin-71 OS=Arab |
| TRINITY_sp|Q8LP|LACS6  | Long chain acyl-CoA |
| TRINITY_sp|Q9SW|SYP42  | Syntaxin-42 OS=Arab |
| TRINITY_sp|Q94O|SRK2E  | Serine/threonine-pr |
| TRINITY_sp|Q9YG|RPE65  | Retinoid isomerohyd |
| TRINITY_sp|Q86A|mcFX  | Mitochondrial subst |
| TRINITY_sp|Q9X7|tbh-1  | Tyramine beta-hydro |
| TRINITY_sp|P432|npr   | Bacillolysin OS=Bre |
| TRINITY_sp|Q023|GLG1  | Golgi apparatus pro |
| TRINITY_sp|O434|EIF4G3 | Eukaryotic translat |
| TRINITY_sp|Q5XG|Utp20  | Small subunit proce |
| TRINITY_sp|P463|iolS  | Protein IolS OS=Bac |
| TRINITY_sp|Q8DF|mutA  | 5'-nucleotidase OS= |
| TRINITY_sp|P515|BRCA2 | Breast cancer type |
| TRINITY_sp|Q8CD|Ccd38  | Coiled-coil domain- |
| TRINITY_sp|Q8GU|HYP1  | CSC1-like protein H |
| TRINITY_sp|Q9FI|ARC6   | Protein ACCUMULATIO |
| TRINITY_sp|Q558|sl110103 | Uncharacterized pro |
| TRINITY_sp|Q9NU|AGPAT5 | 1-acetyl-sn-glycerol- |
| TRINITY_sp|Q88I|Ccd40  | Coiled-coil domain- |
| TRINITY_sp|P511|GZMM  | Granzyme M OS=Homo |
| TRINITY_sp|P891|CTR9  | RNA polymerase-asso |
| TRINITY_sp|Q285|AF_1724 | Uncharacterized pro |
| TRINITY_sp|F4JT|STY46  | Serine/threonine-pr |
| TRINITY_sp|Q5ZL|NSUN2  | tRNA (cytosine(34))- |
| TRINITY_sp|P500|KEL2   | Kelch repeat-contai |
| TRINITY_sp|Q9WU|Stxbp5 | Syntaxin-binding pr |
| TRINITY_sp|Q86I|pscA   | Penicillin-sensitiv |
| TRINITY_sp|C0Z9|mutS2  | Endonuclease MutS2 |
| TRINITY_sp|Q29K|GA19813 | Ribosome biogenesis |
| TRINITY_sp|Q6GL|elavl1  | ELAV-like protein 1 |
| TRINITY_sp|Q345|sppA   | Putative signal pep |
| TRINITY_sp|Q9V3|Tak1   | Mitogen-activated p |
| TRINITY_sp|P383|PHO89  | Phosphate permease |
| TRINITY_sp|P175|SRV2   | Adenylyl cyclase-as |
| TRINITY_sp|Q8N8|UBR7   | Putative E3 ubiquit |
| TRINITY_sp|Q8BK|Smq1   | Serine/threonine-pr |
| TRINITY_sp|O316|yjCl   | Uncharacterized mem |
| TRINITY_sp|Q8I2|CACNA2D| Voltage-dependent c |
| TRINITY_sp|Q9LKYNHX7 | Sodium/hydrogen exchanger | 25.00 | 0.00 |
| TRINITY_sp|Q6011SPBC23E | Uncharacterized ATP | 25.00 | 0.00 |
| TRINITY_sp|Q4I32BFR2 | Protein BFR2 OS=Gib | 25.00 | 0.00 |
| TRINITY_sp|Q99N1Kh1122 | Kelch-like protein | 25.00 | 0.00 |
| TRINITY_sp|Q0WVIRRP6L1 | Protein RRP6-like 1 | 25.00 | 0.00 |
| TRINITY_sp|Q94AAtig0666 | Uncharacterized oxidoreductase | 25.00 | 0.00 |
| TRINITY_sp|Q993zip | Myosin heavy chain, | 24.90 | 0.00 |
| TRINITY_sp|F409!ceq1 | mRNA-capping enzyme | 24.90 | 0.00 |
| TRINITY_sp|Q9Z11ACOX1 | Peroxisomal acyl-coa oxidase | 24.90 | 0.00 |
| TRINITY_sp|Q9FECTOM1 | Tobamovirus multiplication protein | 24.90 | 0.00 |
| TRINITY_sp|Q237CTTLL3A | Tubulin glycylase 3 | 24.90 | 0.00 |
| TRINITY_sp|Q6CS!PAB1 | Polyadenylate-binding protein | 24.90 | 0.00 |
| TRINITY_sp|P366ncs-1 | Neuronal calcium sequestrin | 24.90 | 0.00 |
| TRINITY_sp|Q7M3frngB | RING finger protein | 24.90 | 0.00 |
| TRINITY_sp|Q6IC!Atig431 | Polypyrimidine tract binder | 24.90 | 0.00 |
| TRINITY_sp|B1AKARhgap3 | Rho GTPase-activating protein | 24.90 | 0.00 |
| TRINITY_sp|Q54U!cr1A | Cyclic AMP receptor | 24.90 | 0.00 |
| TRINITY_sp|A8JF!ODA1 | Outer dynein arm protein | 24.90 | 0.00 |
| TRINITY_sp|Q9VR1Membrin | Probable Golgi SNAP | 24.90 | 0.00 |
| TRINITY_sp|Q9L2BIG2 | Brefeldin A-inhibit | 24.90 | 0.00 |
| TRINITY_sp|Q58DISTRABD | TraB domain-contain | 24.90 | 0.00 |
| TRINITY_sp|Q7ZUaptes2 | Prostaglandin E synthase | 24.90 | 0.00 |
| TRINITY_sp|A2YFHK1 | Probable histidine kinase | 24.90 | 0.00 |
| TRINITY_sp|Q802smc6 | Structural maintena | 24.90 | 0.00 |
| TRINITY_sp|Q072 đang | Alcohol dehydrogenase | 24.80 | 0.00 |
| TRINITY_sp|Q802!abhd2a | Monoacylglycerol liplase | 24.80 | 0.00 |
| TRINITY_sp|P0A3bop26 | 26 kDa periplasmic | 24.80 | 0.00 |
| TRINITY_sp|Q5U7!mx | Interferon-induced | 24.80 | 0.00 |
| TRINITY_sp|Q4P9!CCR4 | Glucose-repressible | 24.80 | 0.00 |
| TRINITY_sp|A2X8!OsI | 84a SPX domain-contain | 24.80 | 0.00 |
| TRINITY_sp|Q8MRCLT3 | Protein CLT3, chloroplast | 24.80 | 0.00 |
| TRINITY_sp|Q6DF!ccdc77 | Coiled-coil domain | 24.80 | 0.00 |
| TRINITY_sp|Q6F6!hpX0 | FAD-dependent urate oxidase | 24.80 | 0.00 |
| TRINITY_sp|Q68ANfdA | N-substituted formamide deformylase | 24.80 | 0.00 |
| TRINITY_sp|F4I1!Atig095 | Calcium uniporter | 24.80 | 0.00 |
| TRINITY_sp|Q4P9!rlmL | Ribosomal RNA large | 24.80 | 0.00 |
| TRINITY_sp|Q6DF!poc5 | Centrosomal protein | 24.80 | 0.00 |
| TRINITY_sp|F4IAT!THO2 | THO complex subunit | 24.80 | 0.00 |
| TRINITY_sp|Q4R8!CFAP100 | Cilia- and flagella | 24.80 | 0.00 |
| TRINITY_sp|A0JP!cnotl | CCR4-NOT transcript | 24.80 | 0.00 |
| TRINITY_sp|Q1KP!FZL | Probable transmembrane protein | 24.80 | 0.00 |
| TRINITY_sp|A1KD!TFIP11 | Tufulin-interactin | 24.80 | 0.00 |
| TRINITY_sp|P143!- | Transposon TX1 unchar | 24.80 | 0.00 |
| TRINITY_sp|Q54L!gr1D | Metabotropic glutamate receptor | 24.80 | 0.00 |
| TRINITY_sp|Q8RXIMIRO1 | Mitochondrial Rho G | 24.80 | 0.00 |
| TRINITY_sp|Q9LV!Atig5649 | Probable mitochondrial protein | 24.80 | 0.00 |
| TRINITY_sp|Q54J!sibE | Integrin beta-like | 24.80 | 0.00 |
| TRINITY_sp|Q9S1!SFH10 | Phosphatidylinositol mannosyltransferase | 24.70 | 0.00 |
| TRINITY_sp|Q637!Dlc1 | Rho GTPase-activating protein | 24.70 | 0.00 |
| TRINITY_sp|Q6P2!TMEM53 | Transmembrane prote | 24.70 | 0.00 |
| TRINITY_sp|Q7XBC!CNMT | (S)-coclaurine N-methyltransferase | 24.70 | 0.00 |
| TRINITY_sp|Q949!FBXO21 | F-box only protein | 24.70 | 0.00 |
| TRINITY_sp|P981!CPYP4F8 | Cytochrome P450, 4F8 | 24.70 | 0.00 |
| TRINITY_sp|Q3S1!IPCAT3 | Lysophospholipid acyltransferase | 24.70 | 0.00 |
| TRINITY_sp|Q8CH!Tt115 | Tubulin polypeptide | 24.70 | 0.00 |
| TRINITY_sp|O138!rsdl | RNA-binding protein | 24.70 | 0.00 |
| Gene ID     | Description                                      | Gene Symbol | Organism     | Accession | Score | E Value |
|------------|--------------------------------------------------|-------------|--------------|-----------|-------|---------|
| TRINITY_sp| 1,25-dihydroxyvitamin D(3) 24-hydroxylase, mitochondrial OS=Rattus norvegicus GN=Cyp24a1 PE=1 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Testicular acid pho OS=Dictyostelium discoideum GN=vps13E PE=3 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Phosphoenolpyruvate carboxykinase [ATP] OS=Photobacterium profundum (strain SS9) GN=pckA PE=3 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Importin subunit alpha-3 OS=Arabidopsis thaliana GN=IMPA3 PE=1 SV=2 |             |              |           |       | 0.00    |
| TRINITY_sp| Lysine-specific histone demethylase 1B OS=Homo sapiens GN=KDM1B PE=1 SV=3 |             |              |           |       | 0.00    |
| TRINITY_sp| Protein MON2 homolog OS=Drosophila pseudoobscura pseudoobscura GN=mon2 PE=3 SV=2 |             |              |           |       | 0.00    |
| TRINITY_sp| DDB1- and CUL4-associated factor 4 OS=Bos taurus GN=DCAF4 PE=2 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Probable cytochrome P450 6d4 OS=Drosophila melanogaster GN=Cyp6d4 PE=2 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Angio-associated migratory cell protein OS=Bos taurus GN=AAMP PE=2 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Probable E3 ubiquitin-protein ligase HERC2 OS=Drosophila melanogaster GN=HERC2 PE=1 SV=3 |             |              |           |       | 0.00    |
| TRINITY_sp| E3 ISG15--protein ligase Herc6 OS=Mus musculus GN=Herc6 PE=2 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Testicular acid phosphatase homolog OS=Xenopus laevis GN=acpt PE=2 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| TBC1 domain family member 5 homolog B OS=Dictyostelium discoideum GN=tbc1d5B PE=3 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Plasma membrane iron permease OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FTR1 PE=1 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Voltage-dependent R-type calcium channel subunit alpha-1E OS=Oryctolagus cuniculus GN=CACNA1E PE=2 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Vacuolar membrane protein PEP3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PEP3 PE=1 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Nephrocystin-3 OS=Homo sapiens GN=NPHP3 PE=1 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Auxin efflux carrier component 8 OS=Arabidopsis thaliana GN=PIN8 PE=2 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Two-component system protein B OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) GN=tcsB PE=1 SV=2 |             |              |           |       | 0.00    |
| TRINITY_sp| Chromatin structure-remodeling complex subunit SFH1 OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=SFH1 PE=3 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=1 SV=2 |             |              |           |       | 0.00    |
| TRINITY_sp| Cobalt/magnesium transport protein CorA OS=Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) GN=corA PE=1 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Coiled-coil domain-containing protein 77 OS=Xenopus laevis GN=ccdc77 PE=2 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Salicylate hydroxylase OS=Pseudomonas putida GN=nahG PE=4 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Sugar phosphate exchanger 3 OS=Bos taurus GN=SLC37A3 PE=2 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| Probable serine incorporator OS=Nematostella vectensis GN=serinc PE=3 SV=1 |             |              |           |       | 0.00    |
| TRINITY_sp| N-lysine methyltransferase SETD6 OS=Gallus gallus GN=SETD6 PE=2 SV=2 |             |              |           |       | 0.00    |
| Gene ID          | Description                                      | Score 1 | Score 2 |
|-----------------|--------------------------------------------------|---------|---------|
| TRINITY_sp|Q555\core{vps13B} | Putative vacuolar p | 22.00 | 0.00   |
| TRINITY_sp|P3421ED1 | EH domain-containing | 22.00 | 0.00   |
| TRINITY_sp|Q96M1CFAP44 | Cilia- and flagella | 22.00 | 0.00   |
| TRINITY_sp|Q023\core{GLG1} | Golgi apparatus protein | 22.00 | 0.00   |
| TRINITY_sp|Q9FL1ABCA10 | ABC transporter A f | 22.00 | 0.00   |
| TRINITY_sp|Q9P2\core{ANKIB1} | Ankyrin repeat and | 22.00 | 0.00   |
| TRINITY_sp|P128\core{PEP5} | E3 ubiquitin-protein ligase | 22.00 | 0.00   |
| TRINITY_sp|Q222\core{ugt-50} | Putative UDP-glucuronyltransferase | 22.00 | 0.00   |
| TRINITY_sp|Q58C\core{KLHDC3} | Kelch domain-containing | 22.00 | 0.00   |
| TRINITY_sp|P029\core{tetA} | Tetracycline resistance | 22.00 | 0.00   |
| TRINITY_sp|Q9SYH1IP513 | Type I inositol polyphosphate | 22.00 | 0.00   |
| TRINITY_sp|Q6EMTTL5 | Tubulin polyglutamy | 22.00 | 0.00   |
| TRINITY_sp|Q5EA\core{TMEM164} | Transmembrane protease | 22.00 | 0.00   |
| TRINITY_sp|P189\core{IRA1} | Inhibitory regulator | 22.00 | 0.00   |
| TRINITY_sp|Q6P61ak8 | Adenylate kinase 8 | 22.00 | 0.00   |
| TRINITY_sp|Q8ND\core{BBF1} | Basal body-orientating | 22.00 | 0.00   |
| TRINITY_sp|O046\core{GLR2.1} | Glutamate receptor | 22.00 | 0.00   |
| TRINITY_sp|P870\core{pop1} | WD repeat-containing | 22.00 | 0.00   |
| TRINITY_sp|Q8CG\core{Elac2} | Zinc phosphodiesterase | 22.00 | 0.00   |
| TRINITY_sp|Q7T6\core{MIM1-R8} | Putative serine/threonine protein | 22.00 | 0.00   |
| TRINITY_sp|Q9LI\core{LDL2} | Lysine-specific histone demethylase | 22.00 | 0.00   |
| TRINITY_sp|Q5QN\core{Os010g020} | Potassium channel | 22.00 | 0.00   |
| TRINITY_sp|Q088\core{FA2} | Fatty acyl-CoA reductase | 22.00 | 0.00   |
| TRINITY_sp|P741\core{sl11374} | Uncharacterized symporter | 22.00 | 0.00   |
| TRINITY_sp|Q5RD\core{CTC1} | Cytoskeletal complex subunit | 22.00 | 0.00   |
| TRINITY_sp|O598\core{SPCC550} | Probable importin c | 22.00 | 0.00   |
| TRINITY_sp|Q146\core{PDCC11} | Protein RRF5 homolog | 22.00 | 0.00   |
| TRINITY_sp|B1H1\core{acp2} | Lysosomal acid phosphatase | 22.00 | 0.00   |
| TRINITY_sp|Q8CQ\core{drp35} | Lactonase drp35 | 22.00 | 0.00   |
| TRINITY_sp|Q67V\core{Os06g046} | G patch domain-containing | 22.00 | 0.00   |
| TRINITY_sp|Q54P\core{DDB_G02} | Probable acid phosphatase | 22.00 | 0.00   |
| TRINITY_sp|P871\core{SPAC57A} | Uncharacterized protein | 22.00 | 0.00   |
| TRINITY_sp|Q6NX\core{Rctb1} | RCC1 and BTB domain protein | 22.00 | 0.00   |
| TRINITY_sp|Q54L\core{vps13A} | Putative vacuolar protein | 22.00 | 0.00   |
| TRINITY_sp|Q1ZK\core{grlK} | Metabotropic glutamate receptor | 22.00 | 0.00   |
| TRINITY_sp|Q9P8\core{SNF4} | Nuclear protein Snf-1 | 22.00 | 0.00   |
| TRINITY_sp|Q1KK\core{inpa} | Protein lunapark-A | 22.00 | 0.00   |
| TRINITY_sp|Q0EE\core{Ptcchd3} | Patched domain-containing | 22.00 | 0.00   |
| TRINITY_sp|Q556\core{slr0021} | Putative protease | 22.00 | 0.00   |
| TRINITY_sp|P593\core{barA} | Signal transduction | 22.00 | 0.00   |
| TRINITY_sp|P182\core{AAC3} | ADP,ATP carrier protein | 22.00 | 0.00   |
| TRINITY_sp|P266\core{Sos} | Protein son of sevenless | 22.00 | 0.00   |
| TRINITY_sp|P064\core{RB1} | Retinoblastoma-associated | 22.00 | 0.00   |
| TRINITY_sp|Q54K\core{swp1} | Dolichyl-diphosphoglycerol | 22.00 | 0.00   |
| TRINITY_sp|Q721\core{CYP51} | Sterol 14-alpha demethylase | 22.00 | 0.00   |
| TRINITY_sp|Q3LXJ\core{RBR3} | Retinoblastoma-relating | 22.00 | 0.00   |
| TRINITY_sp|Q089\core{Slc22a8} | Solute carrier family | 22.00 | 0.00   |
| TRINITY_sp|A8JF\core{ODA1} | Outer dynein arm protein | 22.00 | 0.00   |
| TRINITY_sp|Q54F\core{gtf2b} | Transcription initiation factor | 22.00 | 0.00   |
| TRINITY_sp|O008\core{--} | Uncharacterized protein | 22.00 | 0.00   |
| TRINITY_sp|Q4R5\core{ACP2} | Lysosomal acid phosphatase | 22.00 | 0.00   |
| TRINITY_sp|A6QL\core{TRAPP11} | Trafficking protein | 22.00 | 0.00   |
| TRINITY_sp|Q8LBE\core{KING1} | SNF1-related protein | 22.00 | 0.00   |
| TRINITY_sp|O315\core{yesF} | Uncharacterized protein | 22.00 | 0.00   |
| TRINITY_sp|B2S1\core{mmA} | tRNA-specific 2-thiouridylate | 22.00 | 0.00   |
| TRINITY_sp|Q54U\core{sec24} | Protein transport | 22.00 | 0.00   |
| Protein Name                        | Species                        | Description                      | Identity | Similarity |
|-------------------------------------|--------------------------------|----------------------------------|----------|------------|
| TRINITY_sp|Q9HFF|trans1 | Transcription-assoc | 22.00 | 0.00 |
| TRINITY_sp|B3M1|EIF3-S5 | Eukaryotic translation | 22.00 | 0.00 |
| TRINITY_sp|Q9M8|SKOR | Potassium channel S | 22.00 | 0.00 |
| TRINITY_sp|Q54J|siB | Integrin beta-like | 22.00 | 0.00 |
| TRINITY_sp|Q10S|NLPL | Protein NLPL | 22.00 | 0.00 |
| TRINITY_sp|Q8RW|CNCS | Probable cyclic nuc | 21.90 | 0.00 |
| TRINITY_sp|Q54T|drK | Probable serine/thr | 21.90 | 0.00 |
| TRINITY_sp|Q9M9|APCB1 | Aspartyl protease A | 21.90 | 0.00 |
| TRINITY_sp|O076|yhfW | Putative Rieske 2Fe | 21.90 | 0.00 |
| TRINITY_sp|Q54E|grlE | Metabotropic glutam | 21.90 | 0.00 |
| TRINITY_sp|Q6DF|poc5 | Centrosomal protein | 21.80 | 0.00 |
| TRINITY_sp|Q078|VPS13 | Vacuolar protein | 21.80 | 0.00 |
| TRINITY_sp|Q66K|Fam161a | Protein FAM161A | 21.80 | 0.00 |
| TRINITY_sp|Q9BY1|SCAPER | S phase cyclin A-as | 21.80 | 0.00 |
| TRINITY_sp|P256|CDC39 | General negative re | 21.80 | 0.00 |
| TRINITY_sp|Q8WN|KCNH2 | Potassium voltage-g | 21.80 | 0.00 |
| TRINITY_sp|P366|rad8 | DNA repair protein | 21.70 | 0.00 |
| TRINITY_sp|A62U|SDS23 | Protein SDS23 | 21.70 | 0.00 |
| TRINITY_sp|Q5F3|ABCC1 | Multidrug resistance | 21.70 | 0.00 |
| TRINITY_sp|Q9VF|1d1Cp | Conserved oligomeri | 21.70 | 0.00 |
| TRINITY_sp|Q5Z2|pigC | Prodigosin synthes | 21.70 | 0.00 |
| TRINITY_sp|A9UY|serinc | Probable serine inc | 21.60 | 0.00 |
| TRINITY_sp|Q616|CPK16 | Calcium-dependent p | 21.60 | 0.00 |
| TRINITY_sp|Q54J|siB | Integrin beta-like | 21.60 | 0.00 |
| TRINITY_sp|P540|KTR6 | Mannosyltransferase | 21.50 | 0.00 |
| TRINITY_sp|P556|NGR_a01 | Uncharacterized zin | 21.50 | 0.00 |
| TRINITY_sp|F4JX|SUDI | Probable E3 ubiquiti | 21.50 | 0.00 |
| TRINITY_sp|Q5F3|UTP15 | U3 small nucleolar | 21.40 | 0.00 |
| TRINITY_sp|Q103|cbsa2 | 5'-AMP-activated pr | 21.40 | 0.00 |
| TRINITY_sp|Q92S|PEP | RNA-binding KH doma | 21.30 | 0.00 |
| TRINITY_sp|Q4PS|MAP65-9 | 65-kDa microtubule- | 21.30 | 0.00 |
| TRINITY_sp|Q008|MAP65-9 | Uncharacterized 80 | 21.30 | 0.00 |
| TRINITY_sp|P549|TLN1 | Talin-1 | 21.20 | 0.00 |
| TRINITY_sp|Q9DS|GLR3.7 | Glutamate receptor | 21.20 | 0.00 |
| TRINITY_sp|Q640|wdr82-a | WD repeat-containin | 21.10 | 0.00 |
| TRINITY_sp|Q56A|ccdc40 | Coiled-coil domain | 21.10 | 0.00 |
| TRINITY_sp|Q54Ge|crlf | Cyclic AMP receptor | 21.10 | 0.00 |
| TRINITY_sp|B72U|setd3 | Histone-lysine N-me | 21.10 | 0.00 |
| TRINITY_sp|Q5QJ|TBCEL | Tubulin-specific ch | 21.00 | 0.00 |
| TRINITY_sp|Q74|ubE | Ubiquinone/maenquin | 21.00 | 0.00 |
| TRINITY_sp|P111|ACP2 | Lysosomal acid phos | 21.00 | 0.00 |
| TRINITY_sp|P465|ckb-3 | Putative choline ki | 20.90 | 0.00 |
| TRINITY_sp|Q0J7|TPR2 | Protein TPR2 | 20.80 | 0.00 |
| TRINITY_sp|Q8AY|CENPI | Centromere protein | 20.80 | 0.00 |
| TRINITY_sp|Q7SC|sym-1 | Protein sym-1 | 20.70 | 0.00 |
| TRINITY_sp|Q5FB|tmcb | Tiny macroycists pro | 20.60 | 0.00 |
| TRINITY_sp|Q9VS|Rint1 | RINT1-like protein | 20.50 | 0.00 |
| TRINITY_sp|Q5NV|ACP2 | Lysosomal acid phos | 20.50 | 0.00 |
| TRINITY_sp|P008|MAP65-9 | Uncharacterized 80 | 20.40 | 0.00 |
| TRINITY_sp|Q182|sec-15 | Exocyst complex com | 20.40 | 0.00 |
| TRINITY_sp|Q8ND|CFAP43 | Cilia- and flagella | 20.20 | 0.00 |
| TRINITY_sp|P345|rflp-1 | E3 ubiquitin-protei | 20.20 | 0.00 |
| TRINITY_sp|Q8IV|LOX1H1 | Lipoxygenase homolo | 19.90 | 0.00 |
| TRINITY_sp|Q50EC|CYP716B2 | Cytochrome P450 | 19.60 | 0.00 |
| TRINITY_sp|P400|KAP123 | Importin subunit be | 19.50 | 0.00 |
| TRINITY_sp|A8JF|ODA1 | Outer dynein arm pr | 19.50 | 0.00 |
TRINITY_sp|Q922IPpp6r3  Serine/threonine-pr  19.30  0.00