

| Isogroup | Length (bp) | Read count of AB | Read count of PB | Normalized fold change (log ₂) | P-value | SWISS-PROT annotation | E-value | TrEMBL annotation | E-value | NCBI NR annotation | E-value |
|---------------|-------------|------------------|------------------|--|-------------|---|-----------|--|-----------|--|-----------|
| isogroup06094 | 1631 | 212 | 12 | 3.86 | 0 | Sodium-dependent phosphate transporter 1 OS=Xenopus tropicalis GN=slc20a1 PE=2 | 8.00E-68 | Uncharacterized protein OS=Lottia gigantea GN=LOTGIDRAFT_239412 PE=4 SV=1 | 1.00E-159 | hypothetical protein LOTGIDRAFT_239412 [Lottia gigantea] | 1.00E-159 |
| isogroup13102 | 1454 | 240 | 19 | 3.38 | 0 | Fibroblast growth factor receptor-like 1 OS=Homo sapiens GN=FGFRL1 PE=1 SV=1 | 8.00E-09 | NDK-6 OS=Dendrocoelum lacteum PE=2 SV=1 | 1.00E-121 | Smed-NDK-3 [Schmidtea mediterranea] | 6.00E-28 |
| isogroup19006 | 874 | 256 | 32 | 2.72 | 0 | Transferrin receptor protein 1 (Fragment) OS=Rattus norvegicus GN=Tfrc PE=2 SV=1 | 0.63 | Cell wall integrity and stress response component 1 OS=Schistosoma japonicum PE=2 SV=1 | 1.00E-43 | Cell wall integrity and stress response component 1 precursor [Schistosoma japonicum] emb[CAX77492.1] Cell wall integrity and stress response component 1 precursor [Schistosoma japonicum] | 9.00E-44 |
| isogroup09800 | 2633 | 995 | 136 | 2.59 | 0 | Fibroblast growth factor receptor-like 1 OS=Homo sapiens GN=FGFRL1 PE=1 SV=1 | 2.00E-04 | Nou darake like-5 OS=Schmidtea mediterranea PE=2 SV=1 | 0 | nou darake like-5 [Schmidtea mediterranea] | 0 |
| isogroup05269 | 1804 | 844 | 125 | 2.47 | 0 | Sodium- and chloride-dependent glycine transporter 2 OS=Rattus norvegicus | 1.00E-176 | Transporter (Fragment) OS=Lottia gigantea GN=LOTGIDRAFT_104703 PE=3 SV=1 | 0 | hypothetical protein LOTGIDRAFT_104703 partial [Lottia gigantea] | 0 |
| isogroup10589 | 2094 | 228 | 34 | 2.46 | 0 | Fibroblast growth factor receptor-like 1 OS=Gallus gallus GN=FGFRL1 PE=1 SV=1 | 2.00E-19 | Smed-NDK-4 (Fragment) OS=Schmidtea mediterranea PE=2 SV=1 | 0 | Smed-NDK-4 [Schmidtea mediterranea] | 0 |
| isogroup21204 | 742 | 117 | 20 | 2.26 | 2.30E-14 | Protein lozenge OS=Drosophila melanogaster GN=lz PE=2 SV=2 | 1.00E-28 | Runt-1 OS=Schmidtea mediterranea PE=2 SV=1 | 1.00E-107 | runt-like 1 protein [Schmidtea mediterranea] gb[AFJ24721.1] runt-1 [Schmidtea mediterranea] | 1.00E-107 |
| contig14746 | 1270 | 1231 | 216 | 2.23 | 0 | Cholesterol 24-hydroxylase OS=Mus musculus GN=Cyp46a1 PE=2 SV=1 | 1.00E-42 | Predicted protein OS=Nematostella vectensis GN=v1g236002 PE=3 SV=1 | 5.00E-56 | PREDICTED: cholesterol 24-hydroxylase-like [Columba livia] | 5.00E-59 |
| isogroup14819 | 1223 | 89 | 16 | 2.19 | 6.80E-11 | Putative zinc finger protein 840 OS=Homo sapiens GN=ZNF840 PE=5 SV=5 | 1.00E-06 | Zinc finger protein 40 OS=Echinococcus granulosus GN=EgrG_000673000 PE=4 SV=1 | 9.00E-54 | zinc finger protein 40 [Echinococcus granulosus] | 6.00E-54 |
| isogroup09721 | 2698 | 150 | 27 | 2.19 | 0 | Sodium-dependent noradrenaline transporter OS=Mus musculus GN=Slc6a2 PE=2 SV=2 | 4.00E-37 | Transporter OS=Crassostrea gigas GN=CGI_10022090 PE=3 SV=1 | 3.00E-39 | Sodium- and chloride-dependent glycine transporter 2 [Crassostrea gigas] | 2.00E-39 |
| isogroup26183 | 111 | 153 | 30 | 2.07 | 1.11E-16 | Uncharacterized protein ZK112.3 OS=Caenorhabditis elegans GN=ZK112.3 PE=4 SV=1 | 0.04 | Putative proline-rich protein 21 (Fragment) OS=Hydra vulgaris GN=PRR21 PE=2 SV=1 | 9.00E-06 | hypothetical protein [Spirulina subsalsa] | 1.00E-04 |
| isogroup19349 | 845 | 55 | 11 | 2.04 | 9.64E-07 | Baculoviral IAP repeat-containing protein 7-A OS=Xenopus laevis GN=birc7-a PE=1 SV=1 | 1.00E-07 | Uncharacterized protein OS=Capitella teleta GN=CAPTEDRAFT_120337 PE=4 SV=1 | 8.00E-08 | PREDICTED: baculoviral IAP repeat-containing protein 4-like [Saccoglossus kowalevskii] | 2.00E-08 |
| isogroup21510 | 723 | 47 | 10 | 1.95 | 1.09E-05 | Protein ZBED8 OS=Bos taurus GN=ZBED8 PE=2 SV=1 | 9.00E-15 | Chromosome undetermined SCAF7481, whole genome shotgun sequence. (Fragment) OS=Tetraodon nigroviridis GN=GSTENG00004516001 PE=4 SV=1 | 9.00E-18 | unnamed protein product [Tetraodon nigroviridis] | 6.00E-18 |
| isogroup09861 | 2579 | 335 | 75 | 1.88 | 0 | Fibroblast growth factor receptor-like 1 OS=Mus musculus GN=Fgfr1 PE=1 SV=1 | 2.00E-18 | NOU-DARAKE OS=Dugesia japonica GN=nou-darake PE=2 SV=1 | 0 | NOU-DARAKE [Dugesia japonica] | 0 |
| isogroup13916 | 1323 | 56 | 13 | 1.82 | 4.41E-06 | Zinc finger protein ZIC 1 OS=Gallus gallus GN=ZIC1 PE=1 SV=1 | 1.00E-91 | Zinc finger protein Dj-ZicA OS=Dugesia japonica GN=Dj-ZicA PE=2 SV=1 | 0 | zinc finger protein Dj-ZicA [Dugesia japonica] | 0 |
| isogroup25913 | 200 | 72 | 17 | 1.80 | 2.49E-07 | Synaptic vesicle glycoprotein 2B OS=Mus musculus GN=SV2b PE=1 SV=1 | 7.2 | Predicted protein (Fragment) OS=Nematostella vectensis GN=v1g74567 PE=4 SV=1 | 4.00E-13 | predicted protein [Nematostella vectensis] gb[EDO36545.1] predicted protein [Nematostella vectensis] | 3.00E-13 |
| isogroup04716 | 9110 | 1775 | 424 | 1.78 | 0 | Translation initiation factor IF-2 OS=Persephonella marina (strain DSM 14350 / EX-H1) GN=infB PE=3 SV=1 | 0.089 | Predicted protein OS=Physcomitrella patens subsp. patens GN=PHYPADRAFT_66556 PE=4 SV=1 | 8.00E-10 | predicted protein [Physcomitrella patens subsp. patens] gb[EDQ81290.1] predicted protein [Physcomitrella patens subsp. patens] PREDICTED: uncharacterized protein LOC101886116 isoform X1 [Danio rerio] ref[XP_005172039.1] PREDICTED: uncharacterized protein LOC101886116 isoform X2 [Danio rerio] ref[XP_005172040.1] PREDICTED: uncharacterized protein LOC101886116 isoform X3 [Danio rerio] ref[XP_005172041.1] PREDICTED: uncharacterized protein LOC101886116 isoform X4 [Danio rerio] | 6.00E-10 |
| contig16471 | 943 | 50 | 12 | 1.77 | 2.05E-05 | Retrovirus-related Pol polyprotein from transposon 297 OS=Drosophila melanogaster GN=pol PE=4 SV=1 | 7.00E-24 | Retrovirus polyprotein OS=Dicentrarchus labrax GN=DLA_I03860 PE=4 SV=1 | 1.00E-24 | uncharacterized protein LOC101886116 isoform X2 [Danio rerio] ref[XP_005172040.1] PREDICTED: uncharacterized protein LOC101886116 isoform X3 [Danio rerio] ref[XP_005172041.1] PREDICTED: uncharacterized protein LOC101886116 isoform X4 [Danio rerio] | 7.00E-26 |
| isogroup24538 | 490 | 173 | 42 | 1.76 | 3.44E-15 | Apolipoporphins OS=Drosophila melanogaster GN=Rfabg PE=1 SV=2 | 5.00E-14 | Uncharacterized protein OS=Tupaia chinensis GN=TREES_T100018447 PE=4 SV=1 | 1.00E-21 | PREDICTED: vitellogenin-like, partial [Pongc abelii] | 2.00E-22 |
| isogroup05528 | 1764 | 41 | 10 | 1.75 | 0.000132148 | Probable DNA polymerase OS=Podospora anserina PE=3 SV=1 | 0.073 | Protein CBG15088 OS=Caenorhabditis briggsae GN=CBG15088 PE=4 SV=2 | 2.00E-25 | Protein CBG25579 [Caenorhabditis briggsae] | 3.00E-32 |
| isogroup03889 | 443 | 73 | 18 | 1.74 | 4.01E-07 | PR domain zinc finger protein 12 OS=Mus musculus GN=Prdm12 PE=3 SV=1 | 2.00E-06 | Predicted protein (Fragment) OS=Nematostella vectensis GN=v1g119550 PE=4 SV=1 | 1.00E-07 | predicted protein [Nematostella vectensis] gb[EDO36495.1] predicted protein [Nematostella vectensis] | 7.00E-08 |
| contig13483 | 934 | 259 | 65 | 1.71 | 0 | Zinc finger protein 737 OS=Homo sapiens GN=ZNF737 PE=2 SV=3 | 0.22 | Collagen alpha 1(VII) chain OS=Echinococcus multilocularis GN=EmuJ_000619300 PE=4 | 4.00E-10 | collagen alpha 1(VII) chain [Echinococcus granulosus] | 2.00E-09 |
| isogroup06194 | 1447 | 222 | 57 | 1.68 | 0 | Protein Wnt-2b-A OS=Xenopus laevis GN=wnt2b-a PE=2 SV=1 | 7.00E-96 | Protein Wnt (Fragment) OS=Dugesia japonica GN=DjwntB PE=2 SV=1 | 0 | WNT [Dugesia japonica] | 0 |
| isogroup05208 | 2136 | 151 | 40 | 1.63 | 2.92E-12 | Frizzled-8 OS=Xenopus laevis GN=fzd8 PE=1 SV=1 | 1.00E-109 | Frizzled receptor OS=Dugesia japonica GN=DjFzA PE=2 SV=1 | 0 | frizzled receptor [Dugesia japonica] | 0 |

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|---------------|-------|-------|-------|------|-------------|--|----------|--|-----------|--|-----------|
| isogroup17454 | 981 | 108 | 29 | 1.61 | 4.81E-09 | Secreted frizzled-related protein 2 OS=Mus musculus GN=Sfrp2 PE=2 SV=2 | 4.00E-45 | Secreted frizzled-related protein A (Fragment) OS=Dugesia japonica GN=DisFRP-A PE=2 | 0 | secreted frizzled-related protein A [Dugesia japonica] | 0 |
| isogroup09578 | 2854 | 1008 | 271 | 1.61 | 0 | Uncharacterized protein ORF91 OS=Phalaenopsis aphrodite subsp. formosana PE=4 SV=1 | 8.00E-14 | Putative uncharacterized protein OS=Clostridium carboxidivorans P7 GN=CLCAR_4307 PE=4 SV=1 | 8.00E-62 | hypothetical protein [Clostridium carboxidivorans] gb EFG86088.1 hypothetical protein CLCAR_4307 [Clostridium carboxidivorans P7] | 6.00E-62 |
| isogroup19020 | 870 | 37 | 10 | 1.60 | 0.000644894 | Ras-related protein Rap-1 OS=Caenorhabditis elegans GN=rap-1 PE=3 SV=1 | 2.00E-25 | Uncharacterized protein OS=Lottia gigantea GN=LOTGIDRAFT_229516 PE=4 SV=1 | 1.00E-31 | hypothetical protein LOTGIDRAFT_229516 [Lottia gigantea] | 9.00E-32 |
| isogroup00813 | 14144 | 60001 | 16218 | 1.60 | 0 | Replicase polyprotein OS=Cricket paralysis virus (isolate Telegoryllus commodus/Australia/CrPVVIC/1968) GN=ORF1 PE=1 SV=1 | 2.00E-45 | Non-structural polyprotein OS=Formica exsecta virus 1 GN=FEX1gp1 PE=4 SV=1 | 3.00E-49 | nonstructural polyprotein [Solenopsis invicta virus-1] gb AAU85375.1 nonstructural polyprotein [Solenopsis invicta virus-1] | 2.00E-46 |
| contig20555 | 3806 | 6709 | 1817 | 1.60 | 0 | Apolipoporphins OS=Locusta migratoria PE=1 SV=2 | 2.00E-35 | Uncharacterized protein OS=Crassostrea gigas GN=CGI_10002658 PE=4 SV=1 | 1.00E-84 | hypothetical protein CGI_10002658 [Crassostrea gigas] | 7.00E-85 |
| contig13535 | 611 | 55 | 15 | 1.59 | 3.54E-05 | Zonadhesin OS=Mus musculus GN=Zan PE=2 SV=1 | 8.00E-12 | Putative von Willebrand factor type A domain-containing protein OS=Schistosoma mansoni GN=Smp_157690 PE=4 SV=1 | 5.00E-18 | putative von Willebrand factor type A domain-containing protein [Schistosoma mansoni] | 3.00E-18 |
| isogroup13604 | 1377 | 66 | 18 | 1.59 | 5.89E-06 | Forkhead box protein J1.2 OS=Xenopus laevis GN=foxj1.2 PE=2 SV=1 | 1.00E-34 | Forkhead box J1-like protein 1 OS=Schmidtea mediterranea PE=2 SV=1 | 1.00E-169 | forkhead box J1-like protein 1 [Schmidtea mediterranea] | 1.00E-169 |
| isogroup23274 | 607 | 2439 | 666 | 1.59 | 0 | Protein E7 OS=Human papillomavirus type 55 GN=E7 PE=3 SV=1 | 0.59 | Uncharacterized protein (Fragment) OS=Schmidtea mediterranea PE=2 SV=1 | 8.00E-23 | hypothetical protein, partial [Schmidtea mediterranea] | 5.00E-23 |
| contig20552 | 1786 | 1575 | 435 | 1.57 | 0 | Protein ycf2 OS=Marchantia polymorpha GN=yfc2 PE=3 SV=1 | 2.00E-05 | Uncharacterized protein OS=Fusobacterium periodonticum ATCC 33693 GN=FUSPEROL_02206 PE=4 SV=1 | 9.00E-07 | hypothetical protein [Fusobacterium periodonticum] gb EFE85848.1 hypothetical protein FUSPEROL_02206 [Fusobacterium periodonticum ATCC 33693] | 6.00E-07 |
| isogroup07395 | 946 | 36 | 10 | 1.56 | 0.000947792 | Cellular nucleic acid-binding protein homolog OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=byr3 PE=4 SV=1 | 2.00E-11 | Singapore isolate B (sub-type 7) whole genome shotgun sequence assembly, scaffold_21 OS=Blastocystis hominis GN=GSBLH_T00002894001 PE=4 SV=1 | 1.00E-11 | PREDICTED: CCHC-type zinc finger protein CG3800-like isoform 1 [Bombus terrestris] ref XP_003397960.1 PREDICTED: CCHC-type zinc finger protein CG3800-like isoform 2 [Bombus terrestris] ref XP_003485390.1 PREDICTED: CCHC-type zinc finger protein CG3800-like | 1.00E-12 |
| contig20548 | 1479 | 6341 | 1811 | 1.52 | 0 | Apolipoporphins OS=Locusta migratoria PE=1 SV=2 | 2.00E-13 | Apolipoporphin OS=Ascaris suum GN=ASU_02895 PE=4 SV=1 | 6.00E-27 | PREDICTED: zonadhesin-like [Saccoglossus kowalevskii] | 4.00E-30 |
| isogroup16347 | 1073 | 49 | 14 | 1.52 | 0.000154728 | Unconventional myosin-Va OS=Mus musculus GN=Myo5a PE=1 SV=2 | 2.00E-07 | NAD-dependent DNA ligase OS=Pleurocapsa sp. PCC 7327 GN=Plc7327_4433 PE=4 SV=1 | 1.00E-07 | NAD-dependent DNA ligase [Pleurocapsa sp. PCC 7327] ref WP_015145834.1 NAD-dependent DNA ligase [Pleurocapsa minor] gb AFY79538.1 NAD-dependent DNA | 8.00E-08 |
| isogroup21173 | 744 | 542 | 155 | 1.52 | 0 | Elongation factor 4 OS=Leptospira borgpetersenii serovar Hardjo-bovis (strain L550) GN=lepA PE=3 SV=1 | 0.011 | SJCHGC05825 protein (Fragment) OS=Schistosoma japonicum PE=2 SV=2 | 7.00E-37 | SJCHGC05825 protein [Schistosoma japonicum] | 5.00E-37 |
| isogroup14546 | 1254 | 150 | 43 | 1.52 | 4.00E-11 | Silk gland factor 1 OS=Bombyx mori GN=SGF1 PE=2 SV=1 | 1.00E-68 | Winged helix/forkhead transcription factor DIFoxA OS=Dugesia japonica GN=DIFoxA | 0 | winged helix/forkhead transcription factor DIFoxA [Dugesia japonica] | 0 |
| isogroup10556 | 2109 | 225 | 65 | 1.51 | 8.88E-16 | Zinc finger protein ZIC 2 OS=Homo sapiens GN=ZIC2 PE=1 SV=2 | 7.00E-84 | Zinc finger protein Dj-ZicB OS=Dugesia japonica GN=Dj-ZicB PE=2 SV=1 | 0 | zinc finger protein Dj-ZicB [Dugesia japonica] | 0 |
| isogroup23806 | 564 | 38 | 11 | 1.50 | 0.000961778 | Dynein heavy chain (Fragment) OS=Oncorhynchus mykiss PE=2 SV=1 | 0.01 | Uncharacterized protein OS=Helobdella robusta GN=HELRODRAFT_176662 PE=4 SV=1 | 4.00E-10 | hypothetical protein HELRODRAFT_176662 [Helobdella robusta] | 2.00E-10 |
| contig13534 | 690 | 55 | 16 | 1.50 | 7.56E-05 | Kielin/chordin-like protein OS=Mus musculus GN=Kcp PE=1 SV=2 | 8.00E-10 | IgGFC-binding protein OS=Crassostrea gigas GN=CGI_10015609 PE=4 SV=1 | 2.00E-33 | IgGFC-binding protein [Crassostrea gigas] | 1.00E-33 |
| isogroup10908 | 1952 | 41 | 12 | 1.49 | 0.000667435 | Putative ankyrin repeat protein L66 OS=Acanthamoeba polyphaga mimivirus GN=MIMI_L66 PE=4 SV=1 | 0.01 | Location of vulva defective 1 OS=Crassostrea gigas GN=CGI_10007022 PE=4 SV=1 | 2.00E-24 | Location of vulva defective 1 [Crassostrea gigas] | 2.00E-24 |
| isogroup18798 | 885 | 41 | 12 | 1.49 | 0.000667435 | Homeobox protein SIX6 OS=Gallus gallus GN=SIX6 PE=2 SV=1 | 4.00E-86 | Six3-1 (Fragment) OS=Schmidtea mediterranea PE=2 SV=1 | 1.00E-123 | six3-1, partial [Schmidtea mediterranea] | 1.00E-124 |
| isogroup08547 | 309 | 112 | 33 | 1.48 | 2.18E-08 | Protein PF14_0175 OS=Plasmodium falciparum (isolate 3D7) GN=PF14_0175 PE=4 SV=1 | 1.1 | Putative uncharacterized protein (Fragment) OS=Camponotus floridanus GN=EAG_03031 PE=4 SV=1 | 2.00E-12 | hypothetical protein EAG_03031 [Camponotus floridanus] | 2.00E-12 |
| contig13499 | 1171 | 207 | 61 | 1.48 | 2.78E-14 | Probable DNA repair protein RAD50 OS=Plasmodium falciparum (isolate 3D7) GN=PFF0285c PE=3 SV=1 | 3.5 | Putative von Willebrand factor type A domain-containing protein OS=Schistosoma mansoni GN=Smp_157690 PE=4 SV=1 | 9.00E-06 | putative von Willebrand factor type A domain-containing protein [Schistosoma mansoni] | 6.00E-06 |
| isogroup22411 | 673 | 79 | 24 | 1.43 | 4.31E-06 | Uncharacterized protein C1751.04 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPAC1751.04 PE=4 SV=2 | 6.9 | Uncharacterized protein (Fragment) OS=Lottia gigantea GN=LOTGIDRAFT_148500 PE=4 | 2.00E-12 | hypothetical protein LOTGIDRAFT_148500 partial [Lottia gigantea] | 1.00E-12 |
| isogroup03845 | 1089 | 492 | 150 | 1.43 | 0 | Signal recognition particle receptor FtsY OS=Sulfolobus acidocaldarius (strain ATCC 33909 / DSM 639 / JCM 8929 / NBRC 15157 / NCIMB 11770) GN=ftsY PE=3 SV=1 | 7.2 | Putative uncharacterized protein OS=Daphnia pulex GN=DAPPUDRAFT_317650 PE=4 SV=1 | 6.00E-15 | hypothetical protein DAPPUDRAFT_317650 [Daphnia pulex] | 5.00E-15 |
| isogroup01942 | 433 | 308 | 94 | 1.43 | 0 | Epsin OS=Dictyostelium discoideum GN=epnA PE=3 SV=1 | 2.5 | Uncharacterized protein (Fragment) OS=Ficedula albicollis PE=4 SV=1 | 7.00E-09 | PREDICTED: BAT2 domain containing 1-like [Saccoglossus kowalevskii] | 7.00E-09 |
| isogroup14946 | 1208 | 72 | 22 | 1.43 | 1.25E-05 | SH3 domain-binding protein 4-A OS=Xenopus laevis GN=sh3bp4-a PE=2 SV=1 | 0.76 | Uncharacterized protein OS=Crassostrea gigas GN=CGI_10008774 PE=4 SV=1 | 1.00E-15 | PREDICTED: uncharacterized protein LOC101848372 isoform X1 [Aplysia californica] ref XP_005104171.1 PREDICTED: uncharacterized protein LOC101848372 isoform X2 [Aplysia californica] | 3.00E-17 |
| isogroup15224 | 1169 | 62 | 19 | 1.42 | 5.23E-05 | Uncharacterized protein C1751.04 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPAC1751.04 PE=4 SV=2 | 6.9 | Uncharacterized protein OS=Acyrthosiphon pisum PE=4 SV=1 | 1.00E-21 | conserved hypothetical protein [Trichinella spiralis] gb EFV50790.1 conserved hypothetical protein [Trichinella spiralis] | 1.00E-21 |

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|---------------|------|-------|------|------|-------------|--|-----------|--|-----------|---|-----------|
| isogroup19067 | 867 | 68 | 21 | 1.41 | 2.54E-05 | Replicase polyprotein 1ab OS=Porcine transmissible gastroenteritis coronavirus (strain Purdue) GN=rep PE=1 SV=1 | 1.7 | Putative uncharacterized protein (Fragment) OS=Acromyrmex echinator GN=G51_03377 PE=4 SV=1 | 3.00E-12 | hypothetical protein G51_03377 [Acromyrmex echinator] | 2.00E-12 |
| isogroup12727 | 1513 | 48 | 15 | 1.39 | 0.000454846 | Mariner Mos1 transposase OS=Drosophila mauritiana GN=marinerT PE=1 SV=1 | 8.00E-04 | Uncharacterized protein (Fragment) OS=Bos mutus GN=M91_17600 PE=4 SV=1 | 8.00E-14 | PREDICTED: histone-lysine N-methyltransferase SETMAR-like [Bos taurus] ref XP_005218920.1 PREDICTED: histone-lysine N-methyltransferase SETMAR- | 2.00E-15 |
| isogroup22459 | 672 | 48 | 15 | 1.39 | 0.000454846 | cAMP-dependent protein kinase type I-beta regulatory subunit OS=Homo sapiens GN=PRKAR1B PE=1 SV=4 | 3.00E-10 | Uncharacterized protein OS=Lottia gigantea GN=LOTGIDRAFT_227784 PE=4 SV=1 | 7.00E-36 | hypothetical protein LOTGIDRAFT_227784 [Lottia gigantea] | 5.00E-36 |
| isogroup12706 | 1514 | 54 | 17 | 1.38 | 0.000217931 | Zinc finger C2HC domain-containing protein 1A OS=Xenopus laevis GN=zc2hc1a PE=2 SV=1 | 3.00E-10 | Uncharacterized protein OS=Amphimedon queenslandica GN=LOC100634074 PE=4 SV=1 | 3.00E-12 | PREDICTED: hypothetical protein LOC100634074 [Amphimedon queenslandica] | 2.00E-12 |
| isogroup15935 | 1113 | 54 | 17 | 1.38 | 0.000217931 | Protein tailless OS=Drosophila virilis GN=tlf PE=3 SV=1 | 6.00E-51 | Nuclear receptor TLX-1 OS=Schmidtea mediterranea GN=tlx-1 PE=2 SV=1 | 1.00E-176 | nuclear receptor TLX-1 [Schmidtea mediterranea] | 1.00E-176 |
| contig13523 | 663 | 163 | 52 | 1.36 | 2.07E-10 | Bowman-Birk type trypsin inhibitor OS=Hordeum vulgare GN=BBBI PE=1 SV=1 | 0.54 | Collagen alpha 1VII chain OS=Echinococcus granulosus GN=EqrG_000619300 PE=4 SV=1 | 2.00E-08 | collagen alpha 1VII chain [Echinococcus granulosus] | 2.00E-08 |
| isogroup18347 | 880 | 47 | 15 | 1.36 | 0.000644795 | DNA polymerase OS=Acanthamoeba polyphaga mimivirus GN=POLB PE=3 SV=1 | 1.00E-21 | DNA polymerase (Fragment) OS=Megavirus courdo5 PE=3 SV=1 | 2.00E-23 | B-family DNA polymerase, partial [Mimivirus Bus] gb AFM52364.1 B-family DNA polymerase, partial [Megavirus courdo5] | 2.00E-23 |
| isogroup25915 | 201 | 175 | 56 | 1.36 | 5.04E-11 | Uncharacterized protein C2orf16 OS=Homo sapiens GN=C2orf16 PE=2 SV=3 | 1.00E-14 | Melatonin-related receptor OS=Pteropus alecto GN=PAL_GLEAN10000992 PE=3 SV=1 | 2.00E-15 | PREDICTED: uncharacterized protein LOC101885061 [Danio rerio] | 1.00E-20 |
| isogroup08766 | 610 | 134 | 43 | 1.36 | 9.69E-09 | Cuticle protein 16.5, isoform A OS=Locusta migratoria PE=1 SV=1 | 3.3 | Uncharacterized protein OS=Lottia gigantea GN=LOTGIDRAFT_145636 PE=4 SV=1 | 4.00E-10 | hypothetical protein LOTGIDRAFT_145636 [Lottia gigantea] | 2.00E-10 |
| isogroup10846 | 1975 | 124 | 40 | 1.35 | 3.92E-08 | Frizzled-5 OS=Xenopus laevis GN=fzd5 PE=2 SV=1 | 0 | Fzd-5/8-1 OS=Schmidtea mediterranea PE=2 SV=1 | 0 | PREDICTED: LOW QUALITY PROTEIN: frizzled-5-like [Aplysia californica] | 0 |
| isogroup25830 | 221 | 96 | 31 | 1.35 | 1.36E-06 | Delta(24(24(1)))-sterol reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ERG4 PE=1 SV=2 | 0.017 | Uncharacterized protein (Fragment) OS=Helobdella robusta GN=HELRODRAFT_90243 PE=4 SV=1 | 3.00E-09 | hypothetical protein HELRODRAFT_90243, partial [Helobdella robusta] | 2.00E-09 |
| isogroup12449 | 1559 | 609 | 200 | 1.32 | 0 | Fibroblast growth factor receptor-like 1 OS=Gallus gallus GN=FGFRL1 PE=1 SV=1 | 1.00E-11 | Smed-NDK-3 (Fragment) OS=Schmidtea mediterranea PE=2 SV=1 | 1.00E-179 | Smed-NDK-3 [Schmidtea mediterranea] | 1.00E-180 |
| isogroup13228 | 1432 | 76 | 25 | 1.32 | 2.31E-05 | Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 OS=Mus musculus GN=Plod2 PE=2 SV=2 | 1.00E-132 | Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 OS=Schistosoma japonicum GN=plod-prov PE=2 SV=1 | 1.00E-148 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 [Schistosoma japonicum] | 1.00E-149 |
| isogroup13050 | 1462 | 469 | 156 | 1.30 | 0 | Minor capsid protein L2 OS=Human papillomavirus type 45 GN=L2 PE=3 SV=1 | 2.2 | Uncharacterized protein OS=Collinsella aerofaciens ATCC 25986 GN=COLAER_01671 PE=4 SV=1 | 5.00E-36 | hypothetical protein [Collinsella aerofaciens] gb EBA38630.1 hypothetical protein COLAER_02284 [Collinsella aerofaciens ATCC 25986] gb EBA38843.1 hypothetical protein COLAER_01925 [Collinsella aerofaciens ATCC 25986] gb EBA39061.1 hypothetical protein COLAER_01671 [Collinsella aerofaciens ATCC 25986] | 4.00E-36 |
| isogroup12940 | 1473 | 105 | 35 | 1.30 | 8.67E-07 | Zinc finger protein GIS2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GIS2 PE=1 SV=1 | 4.00E-06 | Piso0_005509 protein OS=Pichia sorbitophila (strain ATCC MYA-4447 / BCRC 22081 / CBS 7064 / NBRC 10061 / NRRL Y-12695) GN=Piso0_005509 PE=4 SV=1 | 1.00E-06 | Piso0_005509 [Milleroyzma farinosa CBS 7064] emb CCE85873.1 Piso0_005509 [Milleroyzma farinosa CBS 7064] | 9.00E-07 |
| isogroup16323 | 1070 | 48 | 16 | 1.30 | 0.000880055 | Neuronal acetylcholine receptor subunit alpha-10 OS=Gallus gallus GN=CHRNA10 PE=3 | 1.00E-91 | Uncharacterized protein (Fragment) OS=Lottia gigantea GN=LOTGIDRAFT_102597 PE=3 | 1.00E-152 | hypothetical protein LOTGIDRAFT_102597, partial [Lottia gigantea] | 1.00E-152 |
| isogroup00275 | 6071 | 12952 | 4336 | 1.29 | 0 | SCO-spondin OS=Gallus gallus GN=SSPO PE=2 SV=1 | 7.00E-18 | Uncharacterized protein (Fragment) OS=Latimeria chalumnae PE=4 SV=1 | 4.00E-17 | PREDICTED: SCO-spondin-like [Latimeria chalumnae] | 3.00E-17 |
| isogroup22285 | 682 | 3349 | 1132 | 1.28 | 0 | Soma ferritin OS=Lymnaea stagnalis PE=2 SV=2 | 4.00E-71 | Ferritin (Fragment) OS=Branchiostoma lanceolatum PE=2 SV=2 | 8.00E-76 | ferritin heavy chain polypeptide 1 [Branchiostoma lanceolatum] | 6.00E-76 |
| contig12785 | 1400 | 65 | 22 | 1.28 | 0.000133376 | Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1 | 2.00E-11 | Histone-lysine N-methyltransferase SETMAR (Fragment) OS=Bos mutus GN=M91_04391 PE=4 SV=1 | 3.00E-12 | PREDICTED: histone-lysine N-methyltransferase SETMAR-like [Pantholops hodgsonii] | 3.00E-13 |
| isogroup14901 | 1212 | 96 | 33 | 1.26 | 4.66E-06 | WD repeat-containing protein 86 OS=Homo sapiens GN=WDR86 PE=2 SV=3 | 1.00E-83 | Uncharacterized protein OS=Capitella teleta GN=CAPTEDRAFT_115707 PE=4 SV=1 | 1.00E-123 | hypothetical protein CAPTEDRAFT_115707 [Capitella teleta] | 1.00E-124 |
| isogroup04007 | 3129 | 654 | 225 | 1.26 | 0 | Protein ycf2 OS=Physcomitrella patens subsp. patens GN=yfc2 PE=3 SV=1 | 2.00E-06 | Putative phenylalanyl-tRNA synthetase, beta subunit OS=Zinderia insecticola (strain CARI) GN=pheT PE=3 SV=1 | 1.00E-08 | putative phenylalanyl-tRNA synthetase subunit beta [Candidatus Zinderia insecticola CARI] ref WP_013315231.1 putative phenylalanyl-tRNA synthetase subunit beta [Candidatus Zinderia insecticola] gb ADM89654.1 putative phenylalanyl-tRNA synthetase, beta subunit [Schistosoma japonicum] SJCHGC08483 protein | 8.00E-09 |
| isogroup08369 | 420 | 58 | 20 | 1.25 | 0.00038578 | Kyphocoliosis peptidase OS=Homo sapiens GN=KY PE=1 SV=2 | 5.00E-16 | SJCHGC08483 protein (Fragment) OS=Schistosoma japonicum PE=2 SV=2 | 1.00E-55 | SJCHGC08483 protein [Schistosoma japonicum] | 1.00E-55 |
| isogroup18026 | 934 | 55 | 19 | 1.25 | 0.000558565 | Chromosomal replication initiator protein DnaA OS=Bifidobacterium longum subsp. infantis (strain ATCC 15697 / DSM 20088 / JCM 1222 / NCTC 11817 / S12) GN=dnaA PE=3 SV=1 | 8.4 | Putative uncharacterized protein OS=Tribolium castaneum GN=TcasGA2_TC009398 PE=4 SV=1 | 2.00E-33 | hypothetical protein TcasGA2_TC009398 [Tribolium castaneum] | 1.00E-33 |
| isogroup07545 | 870 | 891 | 310 | 1.24 | 0 | PLAC8-like protein 1 OS=Homo sapiens GN=PLAC8L1 PE=2 SV=1 | 6.00E-16 | Placenta-specific gene 8 protein OS=Schistosoma japonicum PE=4 SV=1 | 4.00E-26 | Placenta-specific gene 8 protein [Schistosoma japonicum] | 3.00E-26 |
| contig15998 | 1432 | 60 | 21 | 1.23 | 0.000368143 | Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1 | 3.00E-32 | Histone-lysine N-methyltransferase OS=Homo sapiens GN=SETMAR PE=2 SV=1 | 2.00E-30 | mariner transposase [Homo sapiens] | 1.00E-31 |
| isogroup01861 | 1233 | 593 | 208 | 1.23 | 0 | Solute carrier family 43 member 3 OS=Homo sapiens GN=SLC43A3 PE=1 SV=2 | 7.00E-11 | Solute carrier family 43 OS=Hymenolepis microstoma GN=HmN_000456700 PE=4 SV=1 | 3.00E-14 | solute carrier family 43 [Hymenolepis microstoma] | 2.00E-14 |

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|---------------|------|-----|-----|------|-------------|---|-----------|--|-----------|--|-----------|
| isogroup09937 | 2510 | 88 | 31 | 1.22 | 1.80E-05 | Muscle M-line assembly protein unc-89 OS=Caenorhabditis elegans GN=unc-89 PE=1 SV=3 | 9.00E-24 | Titin OS=Echinococcus multilocularis GN=EmuJ_000610500 PE=4 SV=1 | 2.00E-29 | titin [Clonorchis sinensis] | 7.00E-28 |
| isogroup13092 | 1450 | 56 | 20 | 1.20 | 0.000732596 | FMRFamide-activated amiloride-sensitive sodium channel OS=Helix aspersa PE=2 SV=1 | 5.00E-09 | FMRFamide activated amiloride sensitive sodium OS=Echinococcus multilocularis GN=EmuJ_000738300 PE=3 SV=1 | 5.00E-79 | FMRFamide activated amiloride sensitive sodium [Echinococcus granulosus] | 2.00E-78 |
| isogroup09448 | 3033 | 308 | 111 | 1.19 | 4.11E-15 | Rho GTPase-activating protein 100F OS=Drosophila melanogaster GN=RhoGAP100F PE=1 SV=2 | 9.00E-76 | Rho GTPase activating protein OS=Echinococcus multilocularis GN=EmuJ_000441500 PE=4 SV=1 | 1.00E-103 | rho GTPase activating protein [Echinococcus granulosus] | 1.00E-102 |
| contig00128 | 1203 | 86 | 31 | 1.19 | 3.35E-05 | Hepatocyte nuclear factor 6 OS=Rattus norvegicus GN=Oncut1 PE=1 SV=1 | 4.00E-44 | Uncharacterized protein (Fragment) OS=Loxodonta africana GN=LOC100676371 PE=3 SV=1 | 8.00E-47 | PREDICTED: LOW QUALITY PROTEIN: hepatocyte nuclear factor 6-like [Loxodonta africana] | 6.00E-46 |
| isogroup10011 | 2462 | 465 | 170 | 1.17 | 0 | Fibroblast growth factor receptor-like 1 OS=Gallus gallus GN=FGFRL1 PE=1 SV=1 | 2.00E-14 | NDL-4 OS=Dendrocoelum lacteum PE=2 SV=1 | 9.00E-79 | Smed-NDK-4 [Schmidtea mediterranea] | 5.00E-77 |
| isogroup14430 | 1265 | 93 | 34 | 1.17 | 2.09E-05 | Uncharacterized MFS-type transporter YhjX OS=Escherichia coli (strain K12) GN=yhjX PE=1 SV=1 | 2.00E-27 | Putative uncharacterized protein OS=Branchiostoma floridae GN=BRFLDRAFT_120194 PE=4 SV=1 | 1.00E-103 | hypothetical protein BRAFLDRAFT_120194 [Branchiostoma floridae] hypothetical protein BRAFLDRAFT_120194 [Branchiostoma floridae] | 1.00E-103 |
| isogroup06039 | 1411 | 82 | 30 | 1.17 | 6.53E-05 | Becclin-1 OS=Xenopus tropicalis GN=becn1 PE=2 SV=1 | 2.00E-05 | Predicted protein OS=Naegleria gruber GN=NAEGRDRAFT_79948 PE=4 SV=1 | 5.00E-06 | PREDICTED: trichohyalin [Ochotona princeps] | 2.00E-06 |
| isogroup09762 | 2669 | 171 | 63 | 1.16 | 1.03E-08 | Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1 | 3.00E-09 | Transposase OS=Forficula auricularia PE=4 SV=1 | 3.00E-28 | PREDICTED: histone-lysine N- methyltransferase SETMAR-like [Apis florea] | 7.00E-31 |
| contig13515 | 1122 | 473 | 175 | 1.15 | 0 | Ribosomal operon-associated A protein OS=Euglena gracilis GN=roaA PE=3 SV=1 | 2.00E-04 | Collagen alpha-1(VII) chain (Fragment) OS=Clonorchis sinensis GN=CLF_109355 PE=4 SV=1 | 3.00E-08 | collagen alpha-1(VII) chain, partial [Clonorchis sinensis] | 2.00E-08 |
| isogroup11570 | 1752 | 86 | 32 | 1.14 | 5.80E-05 | Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1 | 8.00E-63 | cDNA FLJ54643, highly similar to Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), mRNA OS=Homo | 4.00E-63 | transposase [synthetic construct] | 2.00E-68 |
| isogroup07377 | 754 | 142 | 53 | 1.14 | 2.59E-07 | Pentatricopeptide repeat-containing protein 2 mitochondrial OS=Xenopus laevis GN=ptcd2 PE=2 SV=1 | 1.8 | Uncharacterized protein (Fragment) OS=Nasonia vitripennis PE=4 SV=1 | 5.00E-10 | hypothetical protein G5I_03377 [Acromyrmex echinator] | 1.00E-04 |
| contig17607 | 1866 | 563 | 212 | 1.13 | 0 | Plasminogen OS=Rattus norvegicus GN=Plg PE=2 SV=2 | 3.00E-04 | Uncharacterized protein OS=Helobdella robusta GN=HELRODRAFT_166364 PE=4 SV=1 | 1.00E-06 | hypothetical protein HELRODRAFT_166364 [Helobdella robusta] | 1.00E-06 |
| isogroup17647 | 966 | 111 | 42 | 1.12 | 7.10E-06 | Gag polyprotein OS=Jembrana disease virus GN=gag PE=3 SV=1 | 4.00E-07 | Similar to Cellular nucleic acid-binding protein homolog acc. no. P36627 OS=Pyronema omphalodes (strain CBS 100304) GN=PCON_07655 PE=4 SV=1 | 3.00E-07 | Similar to Cellular nucleic acid-binding protein homolog; acc. no. P36627 [Pyronema omphalodes CBS 100304] | 2.00E-07 |
| isogroup02063 | 1160 | 155 | 59 | 1.11 | 1.34E-07 | Importin subunit alpha-3 OS=Caenorhabditis elegans GN=ima-3 PE=1 SV=2 | 6.00E-09 | Karyopherin alpha 4 (Fragment) OS=Ichthyophis bannanicus PE=2 SV=1 | 5.00E-09 | karyopherin alpha 4 [Ichthyophis bannanicus] | 3.00E-09 |
| isogroup16938 | 1019 | 76 | 29 | 1.11 | 0.000230042 | Aminomethyltransferase OS=Bacillus licheniformis (strain DSM 13 / ATCC 14580) GN=qcvT PE=3 SV=1 | 0.51 | Uncharacterized protein OS=Lottia gigantea GN=LOTGIDRAFT_155939 PE=4 SV=1 | 2.00E-12 | hypothetical protein LOTGIDRAFT_155939 [Lottia gigantea] | 1.00E-12 |
| isogroup17540 | 976 | 76 | 29 | 1.11 | 0.000230042 | ADP,ATP carrier protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=AAC3 PE=1 SV=1 | 1.00E-122 | Uncharacterized protein OS=Capitella teleta GN=CAPTEDRAFT_163594 PE=3 SV=1 | 1.00E-162 | hypothetical protein CAPTEDRAFT_163594 [Capitella teleta] | 1.00E-162 |
| isogroup10042 | 2445 | 466 | 178 | 1.10 | 0 | Frizzled-5 OS=Xenopus laevis GN=fzd5 PE=2 SV=1 | 0 | Fzd-5/8-4 OS=Schmidtea mediterranea PE=2 SV=1 | 0 | hypothetical protein LOTGIDRAFT_200873 partial [Lottia gigantea] | 0 |
| isogroup25838 | 218 | 94 | 36 | 1.10 | 4.49E-05 | Putative uncharacterized protein DDB_G0291608 OS=Dictyostelium discoideum GN=DDB_G0291608 PE=4 SV=1 | 0.005 | Mucin OS=Schistosoma mansoni PE=2 SV=1 | 3.00E-07 | mucin [Schistosoma mansoni] | 2.00E-07 |
| isogroup16007 | 1104 | 104 | 40 | 1.09 | 1.93E-05 | Cellular nucleic acid-binding protein homolog OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=byr3 PE=4 SV=1 | 2.00E-11 | Uncharacterized protein (Fragment) OS=Bos taurus GN=ZCCHC13 PE=4 SV=1 | 1.00E-11 | PREDICTED: CCHC-type zinc finger protein CG3800-like isoform 1 [Bombus terrestris] ref XP_003397960.1 PREDICTED: CCHC-type zinc finger protein CG3800-like isoform 2 [Bombus terrestris] ref XP_003485390.1 PREDICTED: CCHC-type zinc finger protein CG3800-like | 2.00E-12 |
| isogroup06833 | 1435 | 96 | 37 | 1.09 | 4.20E-05 | Putative ankyrin repeat protein L25 OS=Acanthamoeba polyphaga mimivirus GN=MIML_L25 PE=4 SV=1 | 5.00E-17 | AAEL014742-PA (Fragment) OS=Aedes aegypti GN=AAEL014742 PE=4 SV=1 | 1.00E-36 | ankyrin 2.3/unc44 [Aedes aegypti] gbl EAT33004.1 AAEL014742-PA, partial [Aedes aegypti] | 1.00E-36 |
| isogroup01785 | 2385 | 88 | 34 | 1.09 | 9.16E-05 | Pre-mRNA-splicing factor CWC22 OS=Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / JCM 1990 / NBRC 0083 / IGC 2968) GN=CWC22 PE=3 SV=2 | 0.16 | Transposase (Fragment) OS=Stylochus zebra PE=4 SV=1 | 2.00E-11 | PREDICTED: uncharacterized protein LOC100899128 [Metaseiulus occidentalis] | 1.00E-15 |
| isogroup25306 | 331 | 88 | 34 | 1.09 | 9.16E-05 | Soluble scavenger receptor cysteine-rich domain-containing protein SSC5D OS=Homo sapiens GN=SSC5D PE=2 SV=3 | 8.00E-09 | WGS project CAEQ00000000 data, annotated contig 2455 OS=Trypanosoma congolense (strain IL3000) GN=TCIL3000_0_61090 PE=4 | 6.00E-35 | unnamed protein product [Trypanosoma congolense IL3000] | 4.00E-35 |
| contig13471 | 1840 | 581 | 227 | 1.07 | 0 | Ribosomal operon-associated A protein OS=Euglena gracilis GN=roaA PE=3 SV=1 | 0.012 | Collagen alpha-1(VII) chain (Fragment) OS=Clonorchis sinensis GN=CLF_109355 PE=4 SV=1 | 2.00E-12 | collagen alpha-1(VII) chain, partial [Clonorchis sinensis] | 1.00E-12 |
| isogroup09295 | 3279 | 110 | 43 | 1.07 | 1.57E-05 | ATP-binding cassette sub-family A member 1 OS=Mus musculus GN=Abca1 PE=1 SV=4 | 1.00E-178 | Uncharacterized protein OS=Lottia gigantea GN=LOTGIDRAFT_212836 PE=4 SV=1 | 0 | PREDICTED: ATP-binding cassette sub-family A member 1-like [Aplysia californica] | 0 |
| isogroup01857 | 984 | 69 | 27 | 1.07 | 0.000634201 | Zinc finger protein GIS2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GIS2 PE=1 SV=1 | 3.00E-09 | Probable Zinc finger protein GIS2 OS=Zygosaccharomyces bailii ISA1307 GN=ZbGIS2 PE=4 SV=1 | 4.00E-08 | hypothetical protein FPSE_03593 [Fusarium pseudograminearum CS3096] | 6.00E-07 |

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|---------------|------|------|-----|------|-------------|--|----------|---|-----------|---|-----------|
| isogroup06033 | 1422 | 99 | 39 | 1.06 | 4.86E-05 | tRNA (guanine(37)-N1)-methyltransferase OS=Plasmodium falciparum (isolate 3D7) GN=PFI0700c PE=3 SV=1 | 1.8 | Transposable element Tc3 transposase (Fragment) OS=Camponotus floridanus GN=EAG_14192 PE=4 SV=1 | 9.00E-21 | Transposable element Tc3 transposase [Camponotus floridanus] | 6.00E-21 |
| isogroup05272 | 2235 | 241 | 95 | 1.06 | 2.39E-10 | E3 ubiquitin-protein ligase XIAP OS=Xenopus tropicalis GN=xiap PE=2 SV=1 | 5.00E-22 | E3 ubiquitin-protein ligase XIAP OS=Xenopus tropicalis GN=xiap PE=4 SV=1 | 1.00E-20 | PREDICTED: E3 ubiquitin-protein ligase XIAP [Alligator sinensis] | 2.00E-23 |
| contig13518 | 1536 | 224 | 89 | 1.05 | 1.42E-09 | Spore coat protein SP60 OS=Dictyostelium discoideum GN=cotC PE=1 SV=2 | 0.18 | Collagen alpha-1(VII) chain (Fragment) OS=Clonorchis sinensis GN=CLF_109355 PE=4 SV=1 | 9.00E-12 | collagen alpha-1(VII) chain, partial [Clonorchis sinensis] | 6.00E-12 |
| contig13459 | 4751 | 1054 | 421 | 1.04 | 0 | Ribosomal operon-associated A protein OS=Euglena gracilis GN=roaA PE=3 SV=1 | 0.065 | Putative von Willebrand factor type A domain- containing protein OS=Schistosoma mansoni GN=Smp_157690 PE=4 SV=1 | 2.00E-29 | putative von Willebrand factor type A domain- containing protein [Schistosoma mansoni] | 1.00E-29 |
| contig16712 | 1378 | 75 | 30 | 1.04 | 0.000509013 | Retrovirus-related Pol polyprotein from transposon 412 OS=Drosophila melanogaster GN=POL PE=4 SV=1 | 6.00E-09 | Putative uncharacterized protein (Fragment) OS=Caenorhabditis brenneri GN=CAEBREN_20879 PE=4 SV=1 | 4.00E-12 | hypothetical protein CAEBREN_20879 [Caenorhabditis brenneri] | 3.00E-12 |
| isogroup10940 | 1924 | 75 | 30 | 1.04 | 0.000509013 | DNA polymerase OS=Zea mays PE=3 SV=1 | 5.00E-08 | Putative uncharacterized protein OS=Tribolium castaneum GN=TcasGA2_TC006914 PE=4 SV=1 | 1.00E-116 | hypothetical protein TcasGA2_TC006914 [Tribolium castaneum] | 1.00E-116 |
| isogroup01463 | 1426 | 756 | 303 | 1.04 | 0 | Uncharacterized protein C2orf16 OS=Homo sapiens GN=C2orf16 PE=2 SV=3 | 0.002 | Putative uncharacterized protein (Fragment) OS=Camponotus floridanus GN=EAG_11248 PE=4 SV=1 | 6.00E-15 | hypothetical protein EAG_11248 [Camponotus floridanus] | 4.00E-15 |
| isogroup23048 | 629 | 147 | 59 | 1.03 | 1.25E-06 | Retrovirus-related Pol polyprotein from transposon 412 OS=Drosophila melanogaster GN=POL PE=4 SV=1 | 0.005 | Uncharacterized protein (Fragment) OS=Nasonia vitripennis PE=4 SV=1 | 2.00E-06 | PREDICTED: uncharacterized protein LOC101159144 [Oryzias latipes] | 5.00E-05 |
| contig13547 | 1882 | 1444 | 580 | 1.03 | 0 | Protease inhibitors OS=Locusta migratoria PE=1 SV=2 | 0.22 | Collagen alpha 1VII chain OS=Echinococcus granulosus GN=EgrG_000619300 PE=4 SV=1 | 8.00E-09 | collagen alpha 1VII chain [Echinococcus granulosus] | 6.00E-09 |
| isogroup21891 | 687 | 102 | 41 | 1.03 | 5.55E-05 | Retrovirus-related Pol polyprotein from transposon 412 OS=Drosophila melanogaster GN=POL PE=4 SV=1 | 0.044 | Uncharacterized protein OS=Strongylocentrotus purpuratus GN=Sp-Pppl_177 PE=4 SV=1 | 1.00E-07 | Gap-Pol polyprotein [Schistosoma japonicum] | 2.00E-06 |
| isogroup10208 | 2318 | 77 | 31 | 1.03 | 0.000472058 | Zinc finger CCHC domain-containing protein 13 OS=Homo sapiens GN=ZCCHC13 PE=2 SV=1 | 5.00E-05 | Putative transposase OS=Anopheles gambiae PE=4 SV=1 | 2.00E-55 | putative transposase [Anopheles gambiae] | 2.00E-55 |
| isogroup14127 | 1291 | 77 | 31 | 1.03 | 0.000472058 | Protein phosphatase Slingshot homolog 3 OS=Mus musculus GN=Ssh3 PE=1 SV=1 | 2 | Paired box protein and Transposase domain containing protein OS=Haemonchus contortus GN=HCOI_00676400 PE=3 SV=1 | 2.00E-07 | PREDICTED: uncharacterized protein LOC101237877 [Hydra magnipapillata] | 2.00E-07 |
| isogroup00839 | 1167 | 896 | 361 | 1.03 | 0 | Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens GN=ZC3H13 PE=1 SV=1 | 3.00E-09 | LWamide neuropeptides (Fragment) OS=Harpegnathos saltator GN=EAL_16679 PE=4 SV=1 | 8.00E-12 | hypothetical protein A306_08913, partial [Columba livia] | 1.00E-15 |
| isogroup09329 | 3225 | 544 | 222 | 1.01 | 0 | Protein FAM115 OS=Xenopus laevis GN=fam115 PE=2 SV=1 | 1.00E-32 | Uncharacterized protein OS=Lottia gigantea GN=LOTGIDRAFT_236481 PE=4 SV=1 | 2.00E-60 | hypothetical protein LOTGIDRAFT_236481 [Lottia gigantea] | 2.00E-60 |
| isogroup04582 | 1654 | 242 | 99 | 1.01 | 1.17E-09 | Transcription factor 7 OS=Homo sapiens GN=TCF7 PE=1 SV=3 | 7.00E-35 | HMG protein TCF/LEF (Fragment) OS=Dugesia japonica GN=03133HH PE=2 SV=1 | 1.00E-126 | HMG protein TCF/LEF [Dugesia japonica] | 1.00E-126 |
| isogroup16797 | 1030 | 78 | 32 | 1.00 | 0.000576628 | Retrovirus-related Pol polyprotein from transposon 412 OS=Drosophila melanogaster GN=POL PE=4 SV=1 | 2.00E-17 | Putative uncharacterized protein OS=Tribolium castaneum GN=TcasGA2_TC001491 PE=4 SV=1 | 8.00E-24 | hypothetical protein TcasGA2_TC001491 [Tribolium castaneum] | 6.00E-24 |