**Top 10 NCBI Blast results for PF3D7\_02020700\*,\*\***

|  |  |  |  |
| --- | --- | --- | --- |
| **Description** | **Species** | **% Ident** | **Accession** |
| Geranylgeranyl pyrophosphate synthase | Haematococcus lacustris | 30.17% | KFY27494.1 |
| Decaprenyl-diphosphate synthase subunit 1 | Fistulifera solaris | 29.52% | APX64486.1 |
| Decaprenyl-diphosphate synthase subunit 1 | Strongylocentrotus purpuratus | 29.38% | XP\_030829069.1 |
| Trans-prenyltransferase 4 | Haslea ostrearia | 29.94% | AYV97144.1 |
| Solanesyl diphosphate synthase 3 isoform X2 | Brassica napus | 30.54% | XP\_006410610.1 |
| Solanesyl diphosphate synthase 1 isoform X1 | Asparagus officinalis | 28.51% | XP\_020277177.1 |
| Solanesyl diphosphate synthase 3 isoform X2 | Arabidopsis lyrata | 30.24% | XP\_02883166.1 |
| Geranyl diphosphate synthase 1 | Arabidopsis thaliana | 29.94% | NP\_850234.1 |
| Solanesyl diphosphate synthase 3 | Capsella rubella | 30.65% | XP\_023639436.1 |
| Solanesyl diphosphate synthase 1 | Physcomitrella patens | 28.10% | XP\_024 |

\*excluding Apicomplexan (taxid:5794)

\*\*excluding predicted and hypothetical proteins

**Top 10 HHPred results for PF3D7\_02020700\***

|  |  |  |  |
| --- | --- | --- | --- |
| **Description** | **Species** | **E-value** | **HH-Hit** |
| Geranylgeranyl pyrophosphate synthase | Arabidopsis thaliana | 5.8e-38 | 3APZ\_A |
| Geranylgeranyl pyrophosphate synthase | Corynebacterium glutamicum | 2.2e-37 | 3LMD\_A |
| Trans-hexaprenyltransferase | Pseudoalteromonas atlantica | 2.8e-37 | 4JXY\_A |
| Hexaprenyl diphosphate transferase | Micrococcus luteus | 3.7e-37 | 3AQB\_D |
| Decaprenyl diphosphate synthase | Rhodobacter capsulatus | 3.7e-37 | 3MZV\_A |
| Octaprenyl diphosphate synthase | Escherichia coli | 4.4e-37 | 3WJK\_B |
| Polyprenyl synthase | Acinetobacter baumannii | 4.4e-37 | 4LOB\_A |
| Trans-isoprenyl diphosphate synthase | Caulobacter crescentus | 7.6e-37 | 3OYR\_A |
| Geranylgeranyl pyrophosphate synthase | Lactobacillus brevis | 1.1e-36 | 3PKO\_A |
| Farnesyl pyrophosphate synthase | Staphylococcus aureus | 1.7e-36 | 5H9D\_A |

\*excluding hypothetical proteins