

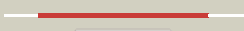
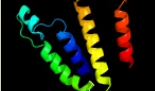

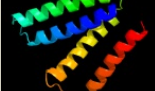





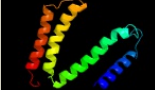

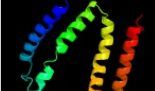








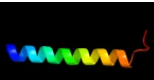
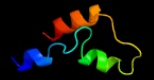
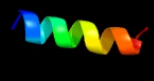
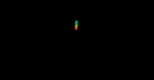

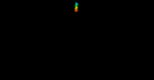





Phyre2

| | |
|---------------|--|
| Email | dlpeters@ualberta.ca |
| Description | SB2_-_putative_quaternary_ammonium_compound-resistance_protein_translation_Acinetobacter_phage_SB2_complete_genome |
| Date | Fri Jan 6 04:30:02 GMT 2023 |
| Unique Job ID | 2752e32602c05862 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | d1s7ba_ |  Alignment |  | 100.0 | 31 | Fold: Multidrug resistance efflux transporter EmrE Superfamily: Multidrug resistance efflux transporter EmrE Family: Multidrug resistance efflux transporter EmrE PDB entry: PDBe RCSB PDBj |
| 2 | c2i68B_ |  Alignment |  | 99.9 | 32 | PDB header: transport protein Chain: B: PDB Molecule: protein emre; PDBTitle: cryo-em based theoretical model structure of transmembrane2 domain of the multidrug-resistance antiporter from e. coli3 emre PDB Entry: PDBe RCSB PDBj |
| 3 | c6wk9B_ |  Alignment |  | 100.0 | 22 | PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein, smr family; PDBTitle: crystal structure of gdx-clo from small multidrug resistance family of2 transporters in complex with octylguanidium PDB Entry: PDBe RCSB PDBj |
| 4 | c7pafA_ |  Alignment |  | 97.7 | 18 | PDB header: transport protein Chain: A: PDB Molecule: licb protein; PDBTitle: streptococcus pneumoniae choline importer licb in lipid nanodiscs PDB Entry: PDBe RCSB PDBj |
| 5 | c5y79A_ |  Alignment |  | 97.9 | 14 | PDB header: transport protein Chain: A: PDB Molecule: putative hexose phosphate translocator; PDBTitle: crystal structure of the triose-phosphate/phosphate translocator in2 complex with 3-phosphoglycerate PDB Entry: PDBe RCSB PDBj |
| 6 | c5ogeE_ |  Alignment |  | 97.7 | 13 | PDB header: membrane protein Chain: E: PDB Molecule: gdp-mannose transporter 1; PDBTitle: crystal structure of a nucleotide sugar transporter PDB Entry: PDBe RCSB PDBj |
| 7 | c5i20E_ |  Alignment |  | 98.1 | 13 | PDB header: membrane protein Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein PDB Entry: PDBe RCSB PDBj |
| 8 | c6ukjA_ |  Alignment |  | 97.7 | 13 | PDB header: membrane protein Chain: A: PDB Molecule: chloroquine resistance transporter; PDBTitle: single-particle cryo-em structure of plasmodium falciparum chloroquine2 resistance transporter (pfcr1) 7g8 isoform PDB Entry: PDBe RCSB PDBj |
| 9 | c5i20C_ |  Alignment |  | 97.7 | 10 | PDB header: membrane protein Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein PDB Entry: PDBe RCSB PDBj |
| 10 | c6oh2A_ |  Alignment |  | 98.1 | 8 | PDB header: transport protein Chain: A: PDB Molecule: cmp-sialic acid transporter; PDBTitle: x-ray crystal structure of the mouse cmp-sialic acid transporter in2 complex with cmp, by lipidic cubic phase PDB Entry: PDBe RCSB PDBj |
| 11 | c6i1rA_ |  Alignment |  | 97.9 | 9 | PDB header: membrane protein Chain: A: PDB Molecule: cmp-sialic acid transporter 1; PDBTitle: crystal structure of cmp bound cst in an outward facing conformation PDB Entry: PDBe RCSB PDBj |
| | | | | | | PDB header: membrane protein |

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|----|-------------------------|-----------|---|------|----|--|
| 12 | c4oo9A_ | Alignment |  | 20.6 | 26 | Chain: A: PDB Molecule: metabotropic glutamate receptor 5, lysozyme, metabotropic PDBTitle: structure of the human class c gpcr metabotropic glutamate receptor 52 transmembrane domain in complex with the negative allosteric3 modulator mavoglurant PDB Entry: PDBe RCSB PDBj |
| 13 | c6rfsX_ | Alignment |  | 16.2 | 21 | PDB header: oxidoreductase Chain: X: PDB Molecule: subunit nuxm of nadh:ubiquinone oxidoreductase (complex i); PDBTitle: cryo-em structure of a respiratory complex i mutant lacking ndufs4 PDB Entry: PDBe RCSB PDBj |
| 14 | c3mp7B_ | Alignment |  | 12.1 | 29 | PDB header: protein transport Chain: B: PDB Molecule: preprotein translocase subunit sece; PDBTitle: lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes PDB Entry: PDBe RCSB PDBj |
| 15 | c6yp7J_ | Alignment |  | 10.9 | 7 | PDB header: photosynthesis Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: psii-lhcii c2s2 supercomplex from pisum sativum grown in high light2 conditions PDB Entry: PDBe RCSB PDBj |
| 16 | c6yp7J_ | Alignment |  | 10.9 | 7 | PDB header: photosynthesis Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: psii-lhcii c2s2 supercomplex from pisum sativum grown in high light2 conditions PDB Entry: PDBe RCSB PDBj |
| 17 | c5xnmj_ | Alignment |  | 10.7 | 7 | PDB header: membrane protein Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: structure of unstacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum PDB Entry: PDBe RCSB PDBj |
| 18 | c7shfB_ | Alignment |  | 10.5 | 3 | PDB header: signaling protein Chain: B: PDB Molecule: g-protein coupled receptor 158; PDBTitle: cryo-em structure of gpr158 coupled to the rgs7-gbeta5 complex PDB Entry: PDBe RCSB PDBj |
| 19 | c6l85A_ | Alignment |  | 9.6 | 6 | PDB header: membrane protein Chain: A: PDB Molecule: phosphate transporter; PDBTitle: the sodium-dependent phosphate transporter PDB Entry: PDBe RCSB PDBj |
| 20 | c3jcuJ_ | Alignment |  | 8.9 | 7 | PDB header: membrane protein Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution PDB Entry: PDBe RCSB PDBj |
| 21 | c7dtvA_ | Alignment | not modelled | 8.7 | 20 | PDB header: membrane protein Chain: A: PDB Molecule: extracellular calcium-sensing receptor; PDBTitle: human calcium-sensing receptor bound with l-trp and calcium ions PDB Entry: PDBe RCSB PDBj |
| 22 | c7vcfK_ | Alignment | not modelled | 8.6 | 18 | PDB header: translocase Chain: K: PDB Molecule: toc10; PDBTitle: cryo-em structure of chlamydomonas toc-tic supercomplex PDB Entry: PDBe RCSB PDBj |
| 23 | c6kacJ_ | Alignment | not modelled | 7.9 | 24 | PDB header: photosynthesis Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: cryo-em structure of the c2s2-type psii-lhcii supercomplex from2 chlamydomonas reihardtii PDB Entry: PDBe RCSB PDBj |
| 24 | c7pi0J_ | Alignment | not modelled | 6.8 | 24 | PDB header: photosynthesis Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: unstacked compact dunaliella psii PDB Entry: PDBe RCSB PDBj |
| 25 | c7pi0J_ | Alignment | not modelled | 6.8 | 24 | PDB header: photosynthesis Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: unstacked compact dunaliella psii PDB Entry: PDBe RCSB PDBj |
| 26 | c5doqC_ | Alignment | not modelled | 6.6 | 17 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans PDB Entry: PDBe RCSB PDBj |
| 27 | c5ir6C_ | Alignment | not modelled | 6.6 | 17 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans PDB Entry: PDBe RCSB PDBj PDB header: dna binding protein |

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|----|-------------------------|-----------|--------------|-----|----|--|
| 28 | c2vqcA_ | Alignment | not modelled | 6.5 | 24 | Chain: A: PDB Molecule: hypothetical 13.2 kda protein; PDBTitle: structure of a dna binding winged-helix protein, f-112, from2 sulfobolus spindle-shaped virus 1. PDB Entry: PDBe RCSB PDBj |
| 29 | d2vqca1 | Alignment | not modelled | 6.5 | 24 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: F112-like PDB entry: PDBe RCSB PDBj |
| 30 | c7rcvj_ | Alignment | not modelled | 6.3 | 21 | PDB header: photosynthesis Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: high-resolution structure of photosystem ii from the mesophilic2 cyanobacterium, synechocystis sp. pcc 6803 PDB Entry: PDBe RCSB PDBj |
| 31 | c5dirB_ | Alignment | not modelled | 6.0 | 6 | PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein signal peptidase; PDBTitle: membrane protein at 2.8 angstroms PDB Entry: PDBe RCSB PDBj |
| 32 | c2lp1A_ | Alignment | not modelled | 5.8 | 8 | PDB header: membrane protein Chain: A: PDB Molecule: c99; PDBTitle: the solution nmr structure of the transmembrane c-terminal domain of2 the amyloid precursor protein (c99) PDB Entry: PDBe RCSB PDBj |
| 33 | c6thkA_ | Alignment | not modelled | 5.8 | 15 | PDB header: antimicrobial protein Chain: A: PDB Molecule: pyocin s5; PDBTitle: structural mechanism of pyocin s5 import into pseudomonas aeruginosa PDB Entry: PDBe RCSB PDBj |
| 34 | d2axtj1 | Alignment | not modelled | 5.7 | 7 | Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, PsbJ Family: PsbJ-like PDB entry: PDBe RCSB PDBj |