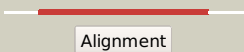

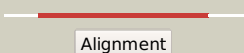
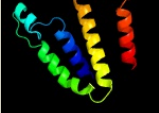
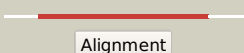
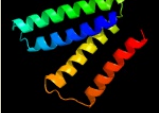


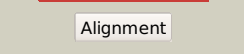





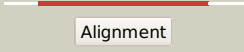

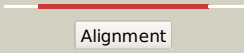



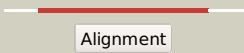


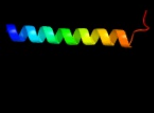

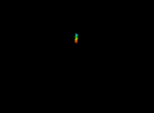
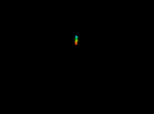
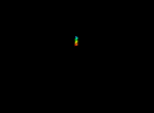
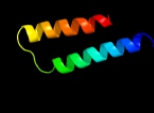
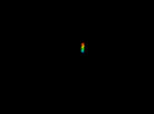



# Phyre2

Email	dlpeters@ualberta.ca
Description	SB1 - ADLP1_008_translation_Acinetobacter_phage_SB1_complete_genome
Date	Fri Jan 6 04:30:02 GMT 2023
Unique Job ID	8f19ade380738c76

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1s7ba_</a>	 Alignment		100.0	32	<b>Fold:</b> Multidrug resistance efflux transporter EmrE <b>Superfamily:</b> Multidrug resistance efflux transporter EmrE <b>Family:</b> Multidrug resistance efflux transporter EmrE <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
2	<a href="#">c2i68B_</a>	 Alignment		99.9	32	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein emre; <b>PDBTitle:</b> cryo-em based theoretical model structure of transmembrane2 domain of the multidrug-resistance antiporter from e. coli3 emre <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
3	<a href="#">c6wk9B_</a>	 Alignment		100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> multidrug resistance protein, smr family; <b>PDBTitle:</b> crystal structure of gdx-clo from small multidrug resistance family of2 transporters in complex with octylguanidium <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
4	<a href="#">c7pafA_</a>	 Alignment		97.8	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> licb protein; <b>PDBTitle:</b> streptococcus pneumoniae choline importer licb in lipid nanodiscs <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
5	<a href="#">c6ukjA_</a>	 Alignment		97.7	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> chloroquine resistance transporter; <b>PDBTitle:</b> single-particle cryo-em structure of plasmodium falciparum chloroquine2 resistance transporter (pfcr1) 7g8 isoform <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
6	<a href="#">c5i20E_</a>	 Alignment		98.2	14	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
7	<a href="#">c5y79A_</a>	 Alignment		97.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative hexose phosphate translocator; <b>PDBTitle:</b> crystal structure of the triose-phosphate/phosphate translocator in2 complex with 3-phosphoglycerate <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
8	<a href="#">c5ogeE_</a>	 Alignment		97.8	12	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> gdp-mannose transporter 1; <b>PDBTitle:</b> crystal structure of a nucleotide sugar transporter <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
9	<a href="#">c5i20C_</a>	 Alignment		97.8	11	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
10	<a href="#">c6i1rA_</a>	 Alignment		98.1	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cmp-sialic acid transporter 1; <b>PDBTitle:</b> crystal structure of cmp bound cst in an outward facing conformation <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
11	<a href="#">c6oh2A_</a>	 Alignment		98.2	7	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cmp-sialic acid transporter; <b>PDBTitle:</b> x-ray crystal structure of the mouse cmp-sialic acid transporter in2 complex with cmp, by lipidic cubic phase <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>

12	<a href="#">c6l85A_</a>	Alignment		18.5	7	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> phosphate transporter; <b>PDBTitle:</b> the sodium-dependent phosphate transporter <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
13	<a href="#">c4oo9A_</a>	Alignment		16.1	26	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> metabotropic glutamate receptor 5, lysozyme, metabotropic <b>PDBTitle:</b> structure of the human class c gpcr metabotropic glutamate receptor 52 transmembrane domain in complex with the negative allosteric3 modulator mavoglurant <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
14	<a href="#">c6rfsX_</a>	Alignment		15.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X; <b>PDB Molecule:</b> subunit nuxm of nadh:ubiquinone oxidoreductase (complex i); <b>PDBTitle:</b> cryo-em structure of a respiratory complex i mutant lacking ndufs4 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
15	<a href="#">c6yp7j_</a>	Alignment		9.4	7	<b>PDB header:</b> photosynthesis <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> psii-lhcii c2s2 supercomplex from pismus sativum grown in high light2 conditions <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
16	<a href="#">c6yp7j_</a>	Alignment		9.4	7	<b>PDB header:</b> photosynthesis <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> psii-lhcii c2s2 supercomplex from pismus sativum grown in high light2 conditions <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
17	<a href="#">c5xnmj_</a>	Alignment		9.3	7	<b>PDB header:</b> membrane protein <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> structure of unstacked c2s2m2-type psii-lhcii supercomplex from pismus2 sativum <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
18	<a href="#">c7dtvA_</a>	Alignment		9.2	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> extracellular calcium-sensing receptor; <b>PDBTitle:</b> human calcium-sensing receptor bound with l-trp and calcium ions <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
19	<a href="#">c3jcu_</a>	Alignment		8.6	7	<b>PDB header:</b> membrane protein <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
20	<a href="#">c7shfB_</a>	Alignment		8.0	3	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> g-protein coupled receptor 158; <b>PDBTitle:</b> cryo-em structure of gpr158 coupled to the rgs7-gbeta5 complex <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
21	<a href="#">c2lp1A_</a>	Alignment	not modelled	7.1	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> c99; <b>PDBTitle:</b> the solution nmr structure of the transmembrane c-terminal domain of2 the amyloid precursor protein (c99) <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
22	<a href="#">c7vcfK_</a>	Alignment	not modelled	6.6	18	<b>PDB header:</b> translocase <b>Chain:</b> K; <b>PDB Molecule:</b> toc10; <b>PDBTitle:</b> cryo-em structure of chlamydomonas toc-tic supercomplex <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
23	<a href="#">c5ir6C_</a>	Alignment	not modelled	6.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> the structure of bd oxidase from geobacillus thermodenitrificans <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
24	<a href="#">c5dogC_</a>	Alignment	not modelled	6.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> the structure of bd oxidase from geobacillus thermodenitrificans <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
25	<a href="#">c3mp7B_</a>	Alignment	not modelled	6.6	29	<b>PDB header:</b> protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> preprotein translocase subunit sece; <b>PDBTitle:</b> lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
26	<a href="#">c6thkA_</a>	Alignment	not modelled	5.8	15	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> pyocin s5; <b>PDBTitle:</b> structural mechanism of pyocin s5 import into pseudomonas aeruginosa <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
						<b>PDB header:</b> photosynthesis <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j;

27	<a href="#">c7rcvj_</a>	Alignment	not modelled	5.7	21	<b>PDBTitle:</b> high-resolution structure of photosystem ii from the mesophilic2 cyanobacterium, synechocystis sp. pcc 6803 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
28	<a href="#">d2axtj1</a>	Alignment	not modelled	5.6	7	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein J, Psbj <b>Family:</b> Psbj-like <b>PDB entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
29	<a href="#">c3a0hj_</a>	Alignment	not modelled	5.6	7	<b>PDB header:</b> electron transport <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>