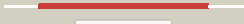
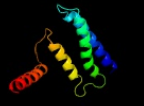


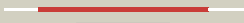
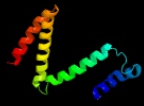









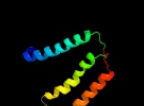

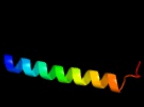



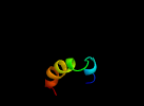


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3065_(mmr)_3430384_3430707
 Date Thu Aug 8 16:20:24 BST 2019
 Unique Job ID 720ad05c4f1d4e41

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s7ba_	 Alignment		100.0	43	Fold: Multidrug resistance efflux transporter EmrE Superfamily: Multidrug resistance efflux transporter EmrE Family: Multidrug resistance efflux transporter EmrE
2	c2i68B_	 Alignment		99.8	45	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
3	c6oh2A_	 Alignment		98.1	10	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
4	c5i20E_	 Alignment		98.0	20	PDB header: membrane protein Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein
5	c6i1rA_	 Alignment		97.9	5	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
6	c5y79A_	 Alignment		97.8	16	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
7	c5oqeE_	 Alignment		97.6	12	PDB header: membrane protein Chain: E: PDB Molecule: gdp-mannose transporter 1; PDBTitle: crystal structure of a nucleotide sugar transporter
8	c5i20C_	 Alignment		97.5	15	PDB header: membrane protein Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein
9	c4oo9A_	 Alignment		18.9	19	PDB header: membrane protein 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
10	c3mp7B_	 Alignment		16.2	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
11	c2lp1A_	 Alignment		9.0	33	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)

12	c5xnmj_	Alignment		8.7	36	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
13	c5azcA_	Alignment		7.9	19	PDB header: transferase Chain: A; PDB Molecule: prolipoprotein diacylglyceryl transferase; PDBTitle: crystal structure of escherichia coli lgt in complex with2 phosphatidylglycerol
14	c3jcu_	Alignment		7.7	43	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
15	c6e8wC_	Alignment		6.8	25	PDB header: viral protein Chain: C; PDB Molecule: envelope glycoprotein gp160; PDBTitle: mper-tm domain of hiv-1 envelope glycoprotein (env)
16	c5dirB_	Alignment		6.7	15	PDB header: hydrolase Chain: B; PDB Molecule: lipoprotein signal peptidase; PDBTitle: membrane protein at 2.8 angstroms
17	c5doqC_	Alignment		6.5	17	PDB header: oxidoreductase Chain: C; PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
18	c5ir6C_	Alignment		6.5	17	PDB header: oxidoreductase Chain: C; PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
19	c6m97A_	Alignment		6.3	17	PDB header: transport protein Chain: A; PDB Molecule: chimera protein of high affinity copper uptake protein 1 PDBTitle: crystal structure of the high-affinity copper transporter ctr1
20	c3a0hj_	Alignment		5.5	43	PDB header: electron transport Chain: J; PDB Molecule: photosystem ii reaction center protein j; PDBTitle: crystal structure of i-substituted photosystem ii complex
21	d2axtj1	Alignment	not modelled	5.5	43	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, PsbJ Family: PsbJ-like