Phyre2

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Description	P0AA70
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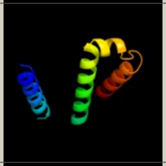
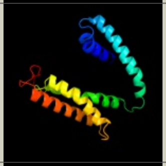
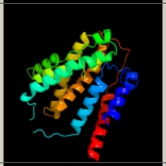
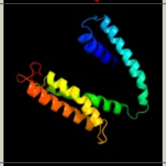
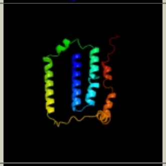
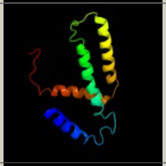
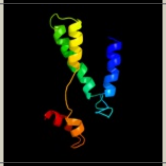
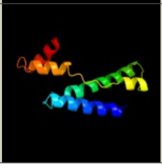
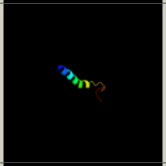
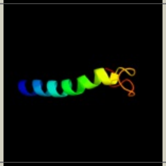
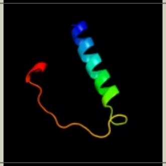
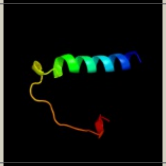
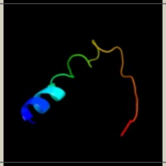
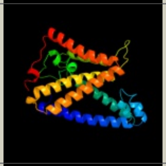
Unique Job ID	233c2c776ceaaaf2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s7ba_	Alignment		97.4	16	**Fold:**Multidrug resistance efflux transporter EmrE **Superfamily:**Multidrug resistance efflux transporter EmrE **Family:**Multidrug resistance efflux transporter EmrE
2	c2i68B_	Alignment		91.1	24	**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	c2xq2A_	Alignment		74.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
4	d1u7ga_	Alignment		68.1	15	**Fold:**Ammonium transporter **Superfamily:**Ammonium transporter **Family:**Ammonium transporter
5	c3dh4A_	Alignment		60.4	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
6	c2jp3A_	Alignment		57.3	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
7	c3rkoF_	Alignment		38.9	10	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nadh-quinone oxidoreductase subunit j; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
8	c3lrcC_	Alignment		36.4	12	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**arginine/agmatine antiporter; **PDBTitle:** structure of e. coli adic (p1)
9	d1iwga8	Alignment		32.1	13	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
10	c2jlnA_	Alignment		17.6	5	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
11	d1iwga7	Alignment		17.0	10	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain

12	c1oy8A_	Alignment		16.9	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
13	c2kncA_	Alignment		16.2	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
14	c3aqpB_	Alignment		16.2	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
15	c2jo1A_	Alignment		13.7	8	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
16	d3dtub2	Alignment		11.5	16	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
17	d3ehbb2	Alignment		10.5	22	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
18	d1fftb2	Alignment		9.0	13	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
19	c3giaA_	Alignment		6.3	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized protein mj0609; **PDBTitle:** crystal structure of apct transporter
20	c2b2hA_	Alignment		6.0	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)
21	c2mltB_	Alignment	not modelled	5.2	12	**PDB header:**toxin (hemolytic polypeptide) **Chain:** B: **PDB Molecule:**melittin; **PDBTitle:** melittin
22	c2mltA_	Alignment	not modelled	5.2	12	**PDB header:**toxin (hemolytic polypeptide) **Chain:** A: **PDB Molecule:**melittin; **PDBTitle:** melittin