Phyre^2

Email	l.a.kelley@imperial.ac.uk
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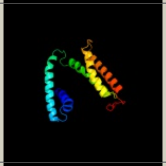
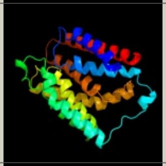
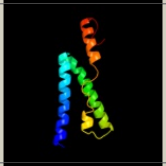
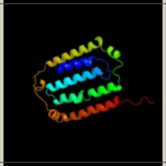
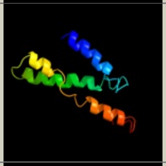
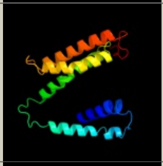
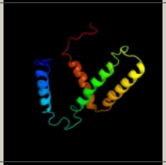
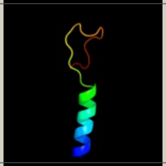
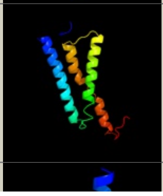
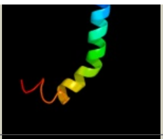
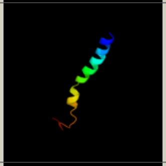
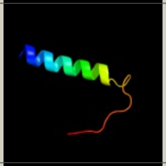
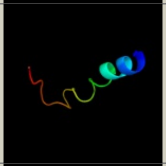
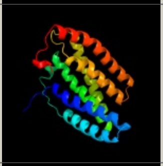
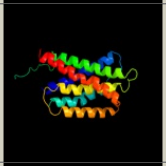
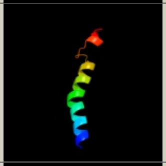
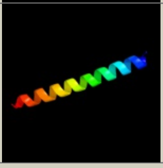
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s7ba_	Alignment		97.7	27	**Fold:**Multidrug resistance efflux transporter EmrE **Superfamily:**Multidrug resistance efflux transporter EmrE **Family:**Multidrug resistance efflux transporter EmrE
2	c2i68B_	Alignment		84.2	22	**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		75.8	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
4	c3b9yA_	Alignment		46.7	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
5	c3aqpB_	Alignment		42.8	21	**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
6	c3rkoF_	Alignment		36.8	12	**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
7	d1iwga8	Alignment		35.3	14	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
8	c3dh4A_	Alignment		26.2	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
9	c3lrcC_	Alignment		25.6	10	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**arginine/agmatine antiporter; **PDBTitle:** structure of e. coli adic (p1)
10	c2jo1A_	Alignment		25.4	9	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
11	d1iwga7	Alignment		23.2	11	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
						

12	c2jp3A_	Alignment		22.8	16	**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
13	c2kncA_	Alignment		15.6	26	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
14	d3dtub2	Alignment		15.0	9	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
15	d1fftb2	Alignment		12.9	7	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
16	c3m7bA_	Alignment		12.1	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein teha homolog; **PDBTitle:** crystal structure of plant slac1 homolog teha
17	d1pw4a_	Alignment		11.7	10	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
18	d1wpga4	Alignment		10.4	11	**Fold:**Calcium ATPase, transmembrane domain M **Superfamily:**Calcium ATPase, transmembrane domain M **Family:**Calcium ATPase, transmembrane domain M
19	d2oara1	Alignment		9.7	6	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
20	c2hg5D_	Alignment		9.5	3	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**kcsa channel; **PDBTitle:** cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
21	c2akhZ_	Alignment	not modelled	8.7	16	**PDB header:**protein transport **Chain:** Z: **PDB Molecule:**preprotein translocase sece subunit; **PDBTitle:** normal mode-based flexible fitted coordinates of a non-2 translocating secyeg protein-conducting channel into the3 cryo-em map of a secyeg-nascent chain-70s ribosome complex4 from e. coli
22	d3ehbb2	Alignment	not modelled	8.5	9	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
23	c1wazA_	Alignment	not modelled	8.2	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
24	c2w8aC_	Alignment	not modelled	8.0	12	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
25	c2jwaA_	Alignment	not modelled	7.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
26	c2oarA_	Alignment	not modelled	6.9	6	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
27	c2k21A_	Alignment	not modelled	6.4	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
28	c2rddB_	Alignment	not modelled	6.3	6	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc;

28	c2rddB_	Alignment	not modelled	6.[illegible]	6	**PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
29	c2b2hA_	 Alignment	not modelled	5.4	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)