Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AAF1
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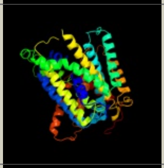
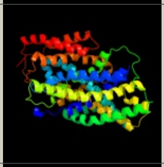
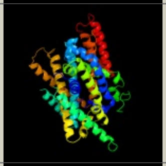
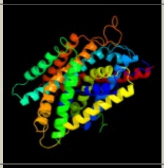
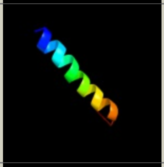
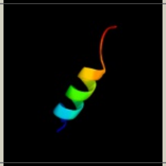
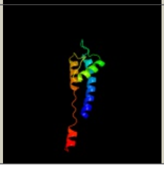
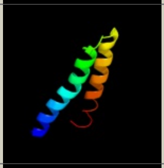
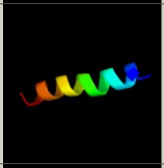
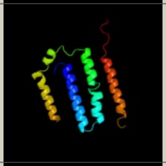
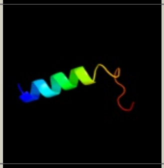
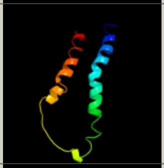
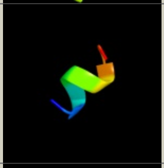
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3giaA_	Alignment		100.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized protein mj0609; **PDBTitle:** crystal structure of apct transporter
2	c3lrcC_	Alignment		100.0	33	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**arginine/agmatine antiporter; **PDBTitle:** structure of e. coli adic (p1)
3	c2jlnA_	Alignment		100.0	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
4	c2xq2A_	Alignment		99.4	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
5	c3dh4A_	Alignment		99.4	10	**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	d2a65a1	Alignment		98.5	13	**Fold:**SNF-like **Superfamily:**SNF-like **Family:**SNF-like
7	c2w8aC_	Alignment		97.6	13	**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
8	c3hfxA_	Alignment		83.2	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter; **PDBTitle:** crystal structure of carnitine transporter
9	c2l2tA_	Alignment		8.6	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
10	d1lfba_	Alignment		8.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
11	d1r3jc_	Alignment		8.4	19	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels

12	d2glia5	Alignment		8.2	45	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
13	d2iuba2	Alignment		7.8	2	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
14	c2rddB_	Alignment		6.6	14	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
15	c3rkoF_	Alignment		6.5	9	**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
16	c2kluA_	Alignment		6.0	17	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
17	d1fftb2	Alignment		5.9	9	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
18	c3og02_	Alignment		5.9	22	**PDB header:**ribosome **Chain:** 2: **PDB Molecule:**50s ribosomal protein l34; **PDBTitle:** crystal structure of the e. coli ribosome bound to clindamycin. this2 file contains the 50s subunit of the second 70s ribosome.
19	c1vt22_	Alignment		5.9	22	**PDB header:**ribosome **Chain:** 2: **PDB Molecule:**50s ribosomal protein l34; **PDBTitle:** crystal structure of the e. coli ribosome bound to cem-101. this file2 contains the 50s subunit of the second 70s ribosome.
20	c3ofd2_	Alignment		5.9	22	**PDB header:**ribosome **Chain:** 2: **PDB Molecule:**50s ribosomal protein l34; **PDBTitle:** crystal structure of the e. coli ribosome bound to chloramphenicol.2 this file contains the 50s subunit of the second 70s ribosome.
21	c2ftcQ_	Alignment	not modelled	5.5	71	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**39s ribosomal protein l34, mitochondrial; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
22	c1m57H_	Alignment	not modelled	5.2	10	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
23	c1ar1B_	Alignment	not modelled	5.0	12	**PDB header:**complex (oxidoreductase/antibody) **Chain:** B: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment