Phyre2

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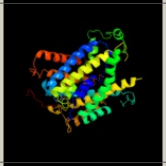
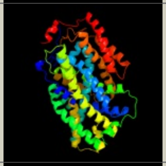
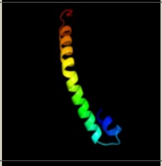
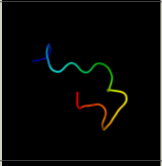
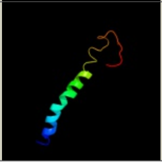
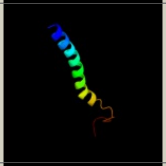
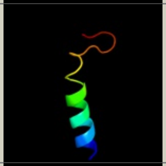
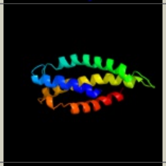
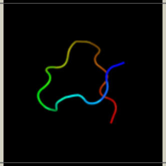
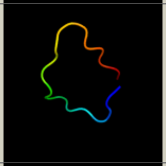
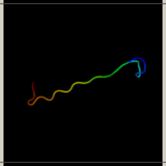
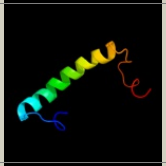
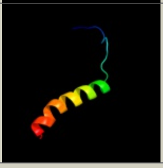
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3giaA_	Alignment		100.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized protein mj0609; **PDBTitle:** crystal structure of apct transporter
2	c3lrcC_	Alignment		100.0	17	**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		99.3	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
5	c3dh4A_	Alignment		99.2	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	c2w8aC_	Alignment		94.2	10	**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
7	c3hfxA_	Alignment		93.0	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter; **PDBTitle:** crystal structure of carnitine transporter
8	d2a65a1	Alignment		90.9	12	**Fold:**SNF-like **Superfamily:**SNF-like **Family:**SNF-like
9	c3qnqD_	Alignment		63.9	17	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
10	d1v54g_	Alignment		22.1	26	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIa **Family:**Mitochondrial cytochrome c oxidase subunit VIa
11	d1fftb2	Alignment		21.9	15	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region

12	c3mp7A_	Alignment		16.9	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
13	c2kncA_	Alignment		15.3	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
14	c2kluA_	Alignment		13.6	12	**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
15	d2yvxa3	Alignment		11.7	8	**Fold:**MgtE membrane domain-like **Superfamily:**MgtE membrane domain-like **Family:**MgtE membrane domain-like
16	d2hj1a1	Alignment		11.1	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**HI0395-like
17	c2hj1A_	Alignment		11.1	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
18	d1qhda2	Alignment		9.4	36	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Top domain of virus capsid protein
19	d1z9ha1	Alignment		8.6	18	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
20	c2y69Z_	Alignment		8.5	25	**PDB header:**electron transport **Chain:** Z: **PDB Molecule:**cytochrome c oxidase polypeptide 8h; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
21	c3rgbA_	Alignment	not modelled	7.2	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
22	c1yewI_	Alignment	not modelled	7.2	26	**PDB header:**oxidoreductase, membrane protein **Chain:** I: **PDB Molecule:**particulate methane monooxygenase, b subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
23	d1v54m_	Alignment	not modelled	6.9	25	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) **Family:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)
24	d1rh5a_	Alignment	not modelled	6.9	8	**Fold:**Preprotein translocase SecY subunit **Superfamily:**Preprotein translocase SecY subunit **Family:**Preprotein translocase SecY subunit
25	d1t98a2	Alignment	not modelled	6.4	14	**Fold:**STAT-like **Superfamily:**MukF C-terminal domain-like **Family:**MukF C-terminal domain-like
26	c2yvxD_	Alignment	not modelled	6.2	8	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
27	d2r6gf1	Alignment	not modelled	6.2	14	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
28	c3chxG_	Alignment	not modelled	6.0	21	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**pmoc; **PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
						PDB header:membrane protein/transport protein

29	c2rddB_	Alignment	not modelled	5.9	22	**Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
30	d2iuba2	Alignment	not modelled	5.8	5	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
31	c3m7bA_	Alignment	not modelled	5.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein teha homolog; **PDBTitle:** crystal structure of plant slac1 homolog teha
32	d2bpa1_	Alignment	not modelled	5.5	29	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Microviridae-like VP
33	c1yewC_	Alignment	not modelled	5.4	22	**PDB header:**oxidoreductase, membrane protein **Chain:** C: **PDB Molecule:**particulate methane monooxygenase subunit c2; **PDBTitle:** crystal structure of particulate methane monooxygenase