Phyre2

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Description	P37327
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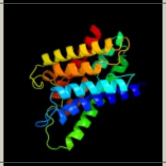
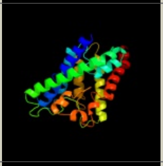
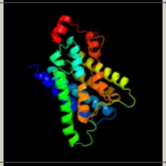
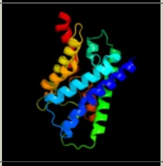
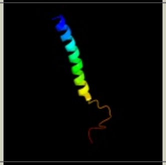
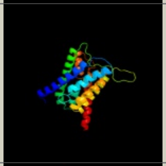
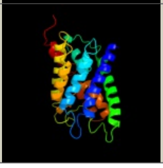
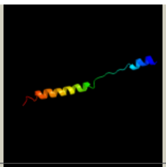
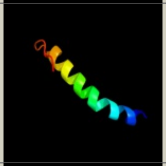
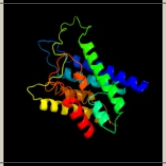
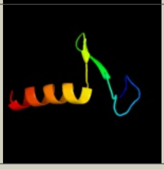
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3klzE_	Alignment		100.0	23	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**putative formate transporter 1; **PDBTitle:** pentameric formate channel with formate bound
2	c3kcvG_	Alignment		100.0	18	**PDB header:**transport protein **Chain:** G: **PDB Molecule:**probable formate transporter 1; **PDBTitle:** structure of formate channel
3	c3llqB_	Alignment		85.2	9	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin z 2; **PDBTitle:** aquaporin structure from plant pathogen agrobacterium tumerfaciens
4	c3c02A_	Alignment		83.5	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaglyceroporin; **PDBTitle:** x-ray structure of the aquaglyceroporin from plasmodium falciparum
5	c1ymgA_	Alignment		74.1	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lens fiber major intrinsic protein; **PDBTitle:** the channel architecture of aquaporin o at 2.2 angstrom resolution
6	d1ymga1	Alignment		74.1	10	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
7	c1ldaA_	Alignment		74.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycerol uptake facilitator protein; **PDBTitle:** crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol
8	d1fx8a_	Alignment		74.0	11	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
9	c2kncA_	Alignment		58.8	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
10	c2w2eA_	Alignment		58.8	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin; **PDBTitle:** 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqy1, in a closed conformation at ph 3.5
11	d1rc2a_	Alignment		45.2	7	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like

12	c2kncB_	Alignment		45.0	24	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
13	c3qnqD_	Alignment		38.7	16	**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
14	c2b5fD_	Alignment		37.4	12	**PDB header:**transport protein,membrane protein **Chain:** D: **PDB Molecule:**aquaporin; **PDBTitle:** crystal structure of the spinach aquaporin sopip2;1 in an2 open conformation to 3.9 resolution
15	d1c17m_	Alignment		24.6	39	**Fold:**F1F0 ATP synthase subunit A **Superfamily:**F1F0 ATP synthase subunit A **Family:**F1F0 ATP synthase subunit A
16	c3iyzA_	Alignment		19.1	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** structure of aquaporin-4 s180d mutant at 10.0 a resolution from2 electron micrograph
17	c3d9sB_	Alignment		12.1	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin-5; **PDBTitle:** human aquaporin 5 (aqp5) - high resolution x-ray structure
18	c3s0xB_	Alignment		11.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase a24b, flak domain protein; **PDBTitle:** the crystal structure of gxgd membrane protease flak
19	c2jy0A_	Alignment		10.5	33	**PDB header:**membrane protein, viral protein **Chain:** A: **PDB Molecule:**protease ns2-3; **PDBTitle:** solution nmr structure of hcv ns2 protein, membrane segment2 (1-27)
20	c2h3oA_	Alignment		9.6	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** structure of merft, a membrane protein with two trans-2 membrane helices
21	d2c1wa1	Alignment	not modelled	7.4	33	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Eukaryotic EndoU ribonuclease
22	c2q7cC_	Alignment	not modelled	7.2	29	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**fusion protein between yeast variant gcn4 and **PDBTitle:** crystal structure of iqn17
23	c2ywxA_	Alignment	not modelled	6.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
24	c2voyG_	Alignment	not modelled	6.2	39	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
25	d1wpna_	Alignment	not modelled	6.0	19	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
26	d2hawa1	Alignment	not modelled	6.0	19	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
27	d1k20a_	Alignment	not modelled	5.7	9	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
						Fold:RPB6/omega subunit-like

28	d1qkla_	Alignment	not modelled	5.6	19	**Superfamily:**RPB6/omega subunit-like **Family:**RPB6
29	d2foka2	Alignment	not modelled	5.5	40	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Restriction endonuclease FokI, N-terminal (recognition) domain
30	d1i74a_	Alignment	not modelled	5.4	9	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
31	c1q90L_	Alignment	not modelled	5.0	11	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**cytochrome b6f complex subunit petl; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii