Phyre2

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Description	P60844
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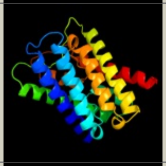
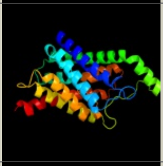
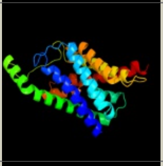
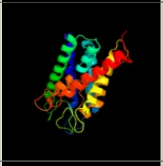
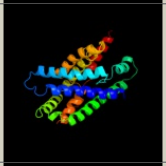
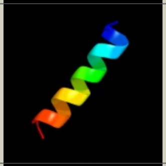
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rc2a_	Alignment		100.0	100	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
2	c3llqB_	Alignment		100.0	74	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin z 2; **PDBTitle:** aquaporin structure from plant pathogen agrobacterium tumerfaciens
3	c2w2eA_	Alignment		100.0	32	**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
4	c1ldaA_	Alignment		100.0	29	**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
5	c2f2bA_	Alignment		100.0	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin aqpm; **PDBTitle:** crystal structure of integral membrane protein aquaporin aqpm at 1.68a2 resolution
6	d1fx8a_	Alignment		100.0	29	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
7	d1j4na_	Alignment		100.0	34	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
8	c3c02A_	Alignment		100.0	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaglyceroporin; **PDBTitle:** x-ray structure of the aquaglyceroporin from plasmodium falciparum
9	d1h6ia_	Alignment		100.0	37	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
10	d1ymga1	Alignment		100.0	35	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
11	c1ymgA_	Alignment		100.0	35	**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

12	c3d9sB_	Alignment		100.0	36	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin-5; **PDBTitle:** human aquaporin 5 (aqp5) - high resolution x-ray structure
13	c2d57A_	Alignment		100.0	31	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** double layered 2d crystal structure of aquaporin-4 (aqp4m23) at 3.2 a2 resolution by electron crystallography
14	c3iyzA_	Alignment		100.0	31	**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
15	c2b5fD_	Alignment		100.0	28	**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
16	c3gd8A_	Alignment		100.0	31	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** crystal structure of human aquaporin 4 at 1.8 and its mechanism of2 conductance
17	c3kcvG_	Alignment		90.1	12	**PDB header:**transport protein **Chain:** G: **PDB Molecule:**probable formate transporter 1; **PDBTitle:** structure of formate channel
18	c3klzE_	Alignment		35.9	12	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**putative formate transporter 1; **PDBTitle:** pentameric formate channel with formate bound
19	d1f0ka_	Alignment		22.6	22	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
20	d1pn3a_	Alignment		13.4	22	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
21	d1rrva_	Alignment	not modelled	12.3	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
22	d1iira_	Alignment	not modelled	11.5	22	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
23	c1s4iC_	Alignment	not modelled	8.9	71	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**superoxide dismutase-like protein yojm; **PDBTitle:** crystal structure of a sod-like protein from bacillus subtilis
24	d1esoa_	Alignment	not modelled	8.0	67	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
25	d1eqwa_	Alignment	not modelled	7.5	57	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
26	d1oala_	Alignment	not modelled	6.9	67	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
27	c3d0qB_	Alignment	not modelled	6.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein calg3; **PDBTitle:** crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
28	c2aqmA_	Alignment	not modelled	6.4	67	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**superoxide dismutase [cu-zn]; **PDBTitle:** cu/zn superoxide dismutase from brucella abortus
29	d2apsa_	Alignment	not modelled	6.1	67	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like

						Family: Cu,Zn superoxide dismutase-like
30	d2rh3a1	Alignment	not modelled	5.9	14	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**VirC2-like
31	c1qupA_	Alignment	not modelled	5.7	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone; **PDBTitle:** crystal structure of the copper chaperone for superoxide2 dismutase
32	c1jk9D_	Alignment	not modelled	5.7	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** heterodimer between h48f-ysod1 and yccs
33	d1ej8a_	Alignment	not modelled	5.3	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like