Phyre2

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Description	Q1PI90
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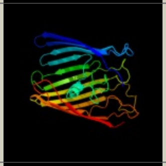
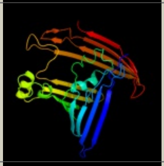
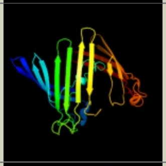
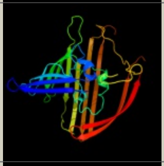
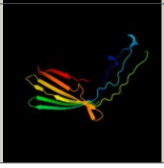
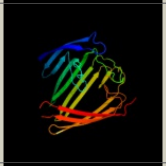
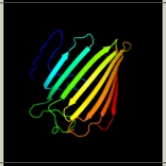
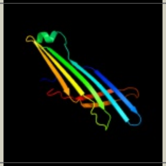
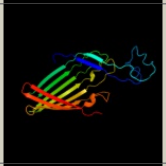
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1osma_	Alignment		100.0	75	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
2	d2fgqx1	Alignment		100.0	19	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
3	c3nsgA_	Alignment		100.0	56	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
4	d2zfga1	Alignment		100.0	63	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
5	c3a2rX_	Alignment		100.0	15	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
6	d1phoa_	Alignment		100.0	58	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
7	d3prna_	Alignment		100.0	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
8	d2pora_	Alignment		100.0	8	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
9	c2o4vA_	Alignment		99.2	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin p; **PDBTitle:** an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
10	d1t16a_	Alignment		96.9	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
11	c3brzA_	Alignment		96.8	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx

12	c2wjqA_	Alignment		95.5	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
13	c2y0lA_	Alignment		95.2	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cis-aconitate porin opdh; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
14	c2y0hA_	Alignment		94.8	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdl
15	d1qj8a_	Alignment		94.6	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
16	c3qraA_	Alignment		92.9	16	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**attachment invasion locus protein; **PDBTitle:** the crystal structure of ail, the attachment invasion locus protein of2 yersinia pestis
17	c3jtyB_	Alignment		92.2	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**benf-like porin; **PDBTitle:** crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
18	c3bryB_	Alignment		89.3	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
19	c2qtkB_	Alignment		89.1	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of the outer membrane protein opdk from2 pseudomonas aeruginosa
20	d1p4ta_	Alignment		86.7	7	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
21	c3dwoX_	Alignment	not modelled	84.8	16	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
22	c2f1tB_	Alignment	not modelled	84.0	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
23	c2y0kA_	Alignment	not modelled	81.6	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**pyroglutatmate porin opdo; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
24	d1g90a_	Alignment	not modelled	65.4	15	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
25	c3nb3C_	Alignment	not modelled	62.1	18	**PDB header:**virus **Chain:** C: **PDB Molecule:**outer membrane protein a; **PDBTitle:** the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components
26	c2x4mD_	Alignment	not modelled	55.1	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
27	c2k0lA_	Alignment	not modelled	50.1	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr structure of the transmembrane domain of the outer2 membrane protein a from klebsiella pneumoniae in dhpc3 micelles.
28	d1qjpa_	Alignment	not modelled	48.3	18	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
						PDB header:membrane protein

29	c2jmmA_	Alignment	not modelled	41.4	14	**Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr solution structure of a minimal transmembrane beta-2 barrel platform protein
30	c3rbhC_	Alignment	not modelled	34.8	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**alginate production protein alge; **PDBTitle:** structure of alginate export protein alge from pseudomonas aeruginosa
31	c2x27X_	Alignment	not modelled	32.4	13	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
32	c2iwvD_	Alignment	not modelled	25.1	10	**PDB header:**ion channel **Chain:** D: **PDB Molecule:**outer membrane protein g; **PDBTitle:** structure of the monomeric outer membrane porin ompg in the2 open and closed conformation
33	c3kvnA_	Alignment	not modelled	24.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
34	c2odjA_	Alignment	not modelled	19.5	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin d; **PDBTitle:** crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa
35	d1i78a_	Alignment	not modelled	15.7	11	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
36	c2lhfA_	Alignment	not modelled	10.0	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein h1; **PDBTitle:** solution structure of outer membrane protein h (oprh) from p.2 aeruginosa in dhpc micelles
37	c2iahA_	Alignment	not modelled	9.7	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** crystal structure of the ferripyoverdine receptor of the outer2 membrane of pseudomonas aeruginosa bound to ferripyoverdine.
38	d2gufa1	Alignment	not modelled	8.8	8	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
39	d1uynx_	Alignment	not modelled	5.9	18	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter