Phyre2

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Description	P21420
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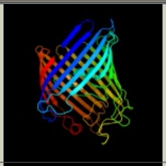
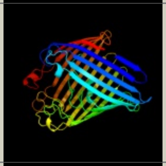
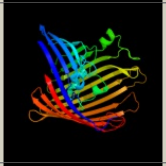
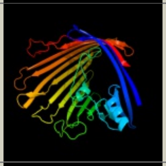
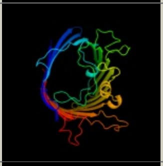
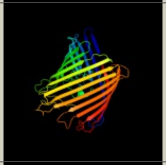
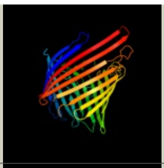
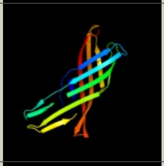
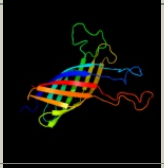
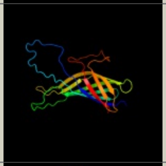
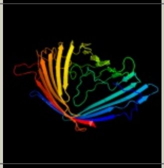
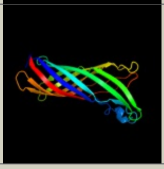
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1osma_	Alignment		100.0	68	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
2	d1phoa_	Alignment		100.0	65	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
3	c3nsgA_	Alignment		100.0	55	**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	64	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
5	d2fgqx1	Alignment		100.0	17	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
6	c3a2rX_	Alignment		100.0	22	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
7	d2pora_	Alignment		100.0	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
8	d3prna_	Alignment		100.0	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
9	c2o4vA_	Alignment		99.8	17	**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	c3qraA_	Alignment		98.8	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
11	d1p4ta_	Alignment		98.5	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein

12	c2y0kA_	Alignment		98.5	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**pyroglutatmate porin opdo; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
13	d1qj8a_	Alignment		98.5	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
14	d1g90a_	Alignment		98.1	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
15	c2k0lA_	Alignment		98.1	12	**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.
16	c2y0hA_	Alignment		97.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdl
17	c2odjA_	Alignment		97.9	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin d; **PDBTitle:** crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa
18	d1qjpa_	Alignment		97.8	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
19	c2lhfA_	Alignment		97.7	13	**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
20	c2f1tB_	Alignment		97.6	17	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
21	c2x27X_	Alignment	not modelled	97.5	14	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
22	d1t16a_	Alignment	not modelled	97.5	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
23	c3jtyB_	Alignment	not modelled	97.5	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**benf-like porin; **PDBTitle:** crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
24	c2y0lA_	Alignment	not modelled	97.5	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cis-aconitate porin opdh; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
25	c3brzA_	Alignment	not modelled	97.4	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
26	c3nb3C_	Alignment	not modelled	97.4	14	**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
27	c2qtkB_	Alignment	not modelled	97.1	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of the outer membrane protein opdk from2 pseudomonas aeruginosa
28	c3dwoX_	Alignment	not modelled	96.8	13	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue

29	d1a0tp_	Alignment	not modelled	96.3	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
30	c3qq2C_	Alignment	not modelled	95.1	11	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
31	c3bryB_	Alignment	not modelled	94.4	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
32	d1af6a_	Alignment	not modelled	94.4	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
33	d2mpra_	Alignment	not modelled	94.2	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
34	d1uynx_	Alignment	not modelled	93.8	8	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
35	c3aehB_	Alignment	not modelled	93.8	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
36	c2x4mD_	Alignment	not modelled	93.2	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
37	c2jmmA_	Alignment	not modelled	92.9	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr solution structure of a minimal transmembrane beta-2 barrel platform protein
38	c2wjqA_	Alignment	not modelled	91.4	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
39	d2gufa1	Alignment	not modelled	90.4	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
40	c3sljA_	Alignment	not modelled	89.5	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
41	d1i78a_	Alignment	not modelled	86.8	22	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
42	c2iwvD_	Alignment	not modelled	83.2	12	**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
43	c2hdiA_	Alignment	not modelled	83.0	20	**PDB header:**protein transport,antimicrobial protein **Chain:** A: **PDB Molecule:**colicin i receptor; **PDBTitle:** crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.
44	c2qomB_	Alignment	not modelled	75.6	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
45	c2grxB_	Alignment	not modelled	66.1	12	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**ferrichrome-iron receptor; **PDBTitle:** crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
46	c3fhhA_	Alignment	not modelled	58.3	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane heme receptor shua; **PDBTitle:** crystal structure of the heme/hemoglobin outer membrane2 transporter shua from shigella dysenteriae
47	c3qlbA_	Alignment	not modelled	57.6	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**enantio-pyochelin receptor; **PDBTitle:** enantiopyochelin outer membrane tonb-dependent transporter from2 pseudomonas fluorescens bound to the ferri-enantiopyochelin
48	d2jnaa1	Alignment	not modelled	49.9	19	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
49	d1by5a_	Alignment	not modelled	42.7	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
50	c3kvnA_	Alignment	not modelled	34.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
51	c3rbhC_	Alignment	not modelled	25.9	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**alginate production protein alge; **PDBTitle:** structure of alginate export protein alge from pseudomonas aeruginosa
52	c2vdaB_	Alignment	not modelled	20.0	23	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**maltoporin; **PDBTitle:** solution structure of the seca-signal peptide complex
53	d1fepa_	Alignment	not modelled	17.2	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
54	c1xkwA_	Alignment	not modelled	12.2	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
						PDB header:chaperone/oxidoreductase

55	c2pq4B_	Alignment	not modelled	8.8	39	**Chain:** B: **PDB Molecule:**periplasmic nitrate reductase precursor; **PDBTitle:** nmr solution structure of napd in complex with napa1-352 signal peptide