Phyre^2

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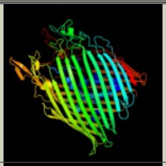
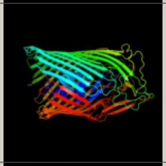
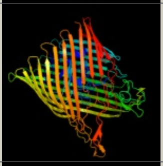
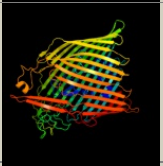
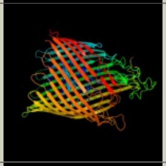
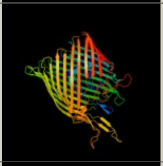
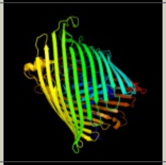
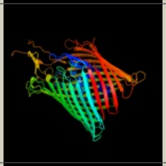
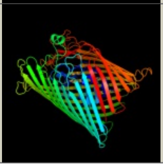
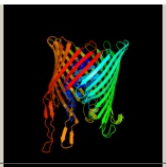
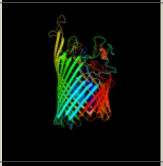
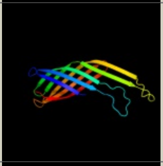
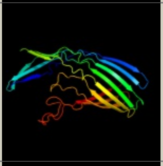
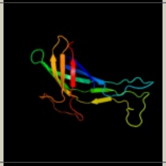
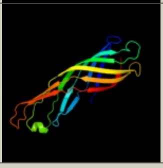
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fepa_	Alignment		100.0	97	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
2	c2iahA_	Alignment		100.0	14	**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.
3	c1xkhC_	Alignment		100.0	14	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
4	c3qlbA_	Alignment		100.0	15	**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
5	c1xkwA_	Alignment		100.0	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
6	d1by5a_	Alignment		100.0	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
7	c2grxB_	Alignment		100.0	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
8	c3fhhA_	Alignment		100.0	18	**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
9	d1kmoa_	Alignment		100.0	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
10	c2hdiA_	Alignment		100.0	30	**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.
11	c1po3A_	Alignment		100.0	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**iron(iii) dicitrate transport protein feca **PDBTitle:** crystal structure of ferric citrate transporter feca in2 complex with ferric citrate

12	d2gufa1	Alignment		100.0	24	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
13	c3efmA_	Alignment		100.0	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ferric alcaligin siderophore receptor; **PDBTitle:** structure of the alcaligin outer membrane recepteur faua from2 bordetella pertussis
14	c3cslB_	Alignment		100.0	15	**PDB header:**membrane protein/heme binding protein **Chain:** B: **PDB Molecule:**hasr protein; **PDBTitle:** structure of the serratia marcescens hemophore receptor hasr in2 complex with its hemophore hasa and heme
15	d1t16a_	Alignment		99.0	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
16	c3dwoX_	Alignment		97.6	13	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
17	c3qraA_	Alignment		96.8	7	**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
18	c3brzA_	Alignment		95.9	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
19	c2k0lA_	Alignment		95.7	16	**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.
20	c2x27X_	Alignment		95.5	7	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
21	d1qjpa_	Alignment	not modelled	94.4	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
22	c2f1tB_	Alignment	not modelled	94.1	5	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
23	d1g90a_	Alignment	not modelled	92.8	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
24	c3nb3C_	Alignment	not modelled	92.3	17	**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
25	d1qj8a_	Alignment	not modelled	88.1	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
26	c2iwvD_	Alignment	not modelled	83.6	16	**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
27	c2x4mD_	Alignment	not modelled	82.0	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
28	c2jmmA_	Alignment	not modelled	77.5	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

29	d2fgqx1	Alignment	not modelled	76.8	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
30	d1osma_	Alignment	not modelled	75.6	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
31	d1p4ta_	Alignment	not modelled	64.2	15	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
32	c3kvnA_	Alignment	not modelled	53.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
33	c2wjqA_	Alignment	not modelled	48.2	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
34	d1i78a_	Alignment	not modelled	40.2	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
35	c3bryB_	Alignment	not modelled	36.4	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
36	c3a2rX_	Alignment	not modelled	32.7	12	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
37	d1phoa_	Alignment	not modelled	28.2	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
38	c2lhfA_	Alignment	not modelled	25.1	6	**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
39	d2a1ja1	Alignment	not modelled	24.5	50	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
40	c3k07A_	Alignment	not modelled	21.8	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
41	c3lkxB_	Alignment	not modelled	12.8	47	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**nascent polypeptide-associated complex subunit alpha; **PDBTitle:** human nac dimerization domain
42	c1oy8A_	Alignment	not modelled	12.6	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
43	d2jnaa1	Alignment	not modelled	11.1	30	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
44	d1uynx_	Alignment	not modelled	10.9	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
45	c3rbhC_	Alignment	not modelled	9.8	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**alginate production protein alge; **PDBTitle:** structure of alginate export protein alge from pseudomonas aeruginosa
46	c2y0hA_	Alignment	not modelled	9.1	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdl
47	d1w0na_	Alignment	not modelled	8.2	29	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 36 carbohydrate binding module, CBM36
48	c1wx4B_	Alignment	not modelled	7.8	22	**PDB header:**oxidoreductase/metal transport **Chain:** B: **PDB Molecule:**melc; **PDBTitle:** crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a caddie protein3 prepared by the addition of dithiothreitol
49	d2i4sa1	Alignment	not modelled	7.8	11	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
50	c3sljA_	Alignment	not modelled	7.8	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
51	d3prna_	Alignment	not modelled	7.6	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
52	d2zfga1	Alignment	not modelled	6.8	8	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
53	d2aq0a1	Alignment	not modelled	6.7	31	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
54	d1pvja_	Alignment	not modelled	6.5	21	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
55	c1s5lu_	Alignment	not modelled	6.5	26	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center

56	d1dkia_	Alignment	not modelled	6.3	21	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
57	c3pgeA_	Alignment	not modelled	6.2	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**sumo-modified proliferating cell nuclear antigen; **PDBTitle:** structure of sumoylated pcna
58	d2vdfa1	Alignment	not modelled	5.8	6	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
59	c2vdaB_	Alignment	not modelled	5.7	29	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**maltoporin; **PDBTitle:** solution structure of the seca-signal peptide complex
60	c1n0wB_	Alignment	not modelled	5.6	63	**PDB header:**gene regulation/antitumor protein **Chain:** B: **PDB Molecule:**breast cancer type 2 susceptibility protein; **PDBTitle:** crystal structure of a rad51-brca2 brc repeat complex
61	d1okja1	Alignment	not modelled	5.5	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
62	c2qomB_	Alignment	not modelled	5.2	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
63	d1o7za_	Alignment	not modelled	5.2	21	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines