Phyre^2

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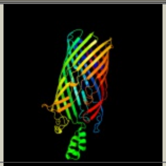
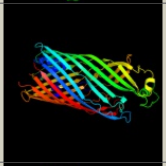
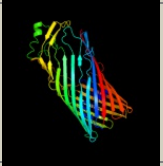
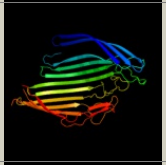
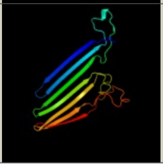
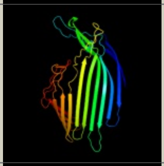
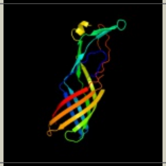
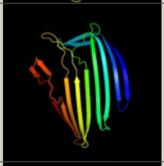
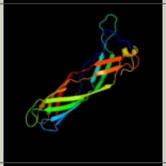
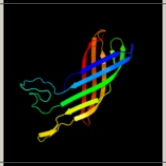
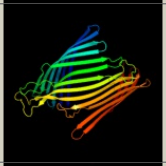
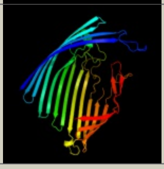
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t16a_	Alignment		100.0	100	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
2	c3dwoX_	Alignment		100.0	25	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
3	c3brzA_	Alignment		100.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
4	c3bryB_	Alignment		100.0	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
5	c2iahA_	Alignment		99.6	13	**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.
6	c1xkhC_	Alignment		99.5	14	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
7	c1xkwA_	Alignment		99.5	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
8	c2grxB_	Alignment		99.5	9	**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
9	d1by5a_	Alignment		99.5	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
10	c3qlbA_	Alignment		99.4	14	**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
11	c2hdiA_	Alignment		99.2	10	**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.

12	c3cslB_	Alignment		99.0	10	**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
13	c3fhhA_	Alignment		99.0	11	**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
14	c2f1tB_	Alignment		99.0	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
15	d1fepa_	Alignment		99.0	8	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
16	d2gufa1	Alignment		98.9	8	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
17	c2x27X_	Alignment		98.9	12	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
18	c3qraA_	Alignment		98.9	15	**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
19	c3efmA_	Alignment		98.8	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ferric alcaligin siderophore receptor; **PDBTitle:** structure of the alcaligin outer membrane recepteur faua from2 bordetella pertussis
20	d1kmoa_	Alignment		98.7	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
21	d1g90a_	Alignment	not modelled	98.7	10	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
22	d1qj8a_	Alignment	not modelled	98.6	15	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
23	c3nb3C_	Alignment	not modelled	98.6	12	**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
24	d1qjpa_	Alignment	not modelled	98.5	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
25	c2k0lA_	Alignment	not modelled	98.5	14	**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.
26	c1po3A_	Alignment	not modelled	98.5	12	**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
27	d1p4ta_	Alignment	not modelled	98.5	10	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
28	d2fgqx1	Alignment	not modelled	98.5	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin

29	d1phoa_	Alignment	not modelled	98.2	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
30	d1osma_	Alignment	not modelled	98.1	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
31	c2wjqA_	Alignment	not modelled	98.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
32	c3nsgA_	Alignment	not modelled	97.9	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
33	c2jmmA_	Alignment	not modelled	97.8	12	**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
34	c2iwvD_	Alignment	not modelled	97.6	15	**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
35	d2zfga1	Alignment	not modelled	97.5	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
36	c3kvnA_	Alignment	not modelled	97.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
37	c3a2rX_	Alignment	not modelled	97.4	13	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
38	c2x4mD_	Alignment	not modelled	97.4	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
39	d1uynx_	Alignment	not modelled	97.0	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
40	c2qomB_	Alignment	not modelled	96.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
41	d1i78a_	Alignment	not modelled	96.3	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
42	d3prna_	Alignment	not modelled	96.2	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
43	c2lhfA_	Alignment	not modelled	96.2	8	**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
44	d2pora_	Alignment	not modelled	95.4	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
45	c3sljA_	Alignment	not modelled	94.5	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
46	c2k4tA_	Alignment	not modelled	93.3	14	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
47	c2y0hA_	Alignment	not modelled	92.9	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdl
48	c3qq2C_	Alignment	not modelled	92.9	9	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
49	c2y0kA_	Alignment	not modelled	90.6	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**pyroglutatmate porin opdo; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
50	c3aehB_	Alignment	not modelled	83.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
51	c2gr7C_	Alignment	not modelled	75.8	23	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
52	d2gr7a1	Alignment	not modelled	75.8	23	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
53	d2gr8a1	Alignment	not modelled	71.0	23	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
54	c2o4vA_	Alignment	not modelled	59.4	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin p; **PDBTitle:** an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
55	c3emoA_	Alignment	not modelled	57.8	23	**PDB header:**membrane protein/cell adhesion **Chain:** A: **PDB Molecule:**hia (adhesin); **PDBTitle:** crystal structure of transmembrane hia 973-1098

56	c2y0lA_	Alignment	not modelled	56.7	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cis-aconitate porin opdh; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
57	c2vqiA_	Alignment	not modelled	28.3	12	**PDB header:**transport **Chain:** A: **PDB Molecule:**outer membrane usher protein papc; **PDBTitle:** structure of the p pilus usher (papc) translocation pore
58	c3rfzB_	Alignment	not modelled	21.8	10	**PDB header:**cell adhesion/transport/chaperone **Chain:** B: **PDB Molecule:**outer membrane usher protein, type 1 fimbrial synthesis; **PDBTitle:** crystal structure of the fimd usher bound to its cognate fimc:fimh2 substrate
59	c3ohnA_	Alignment	not modelled	21.5	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane usher protein fimd; **PDBTitle:** crystal structure of the fimd translocation domain
60	c2odjA_	Alignment	not modelled	15.4	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin d; **PDBTitle:** crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa