Phyre2

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Description	P33924
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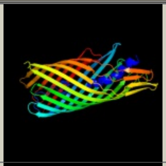
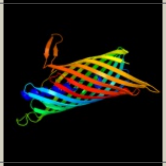
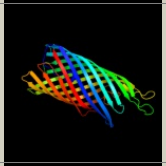
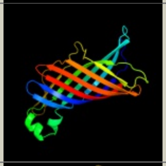
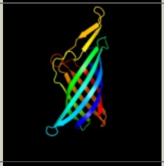
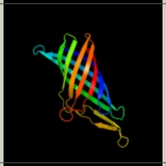
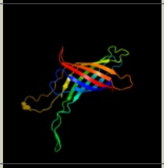
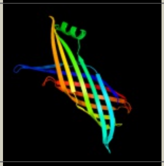
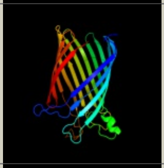
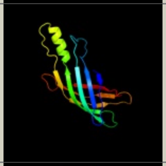
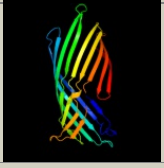
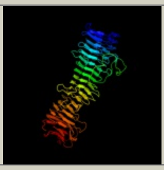
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sljA_	Alignment		100.0	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
2	c3aehB_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
3	c3qq2C_	Alignment		100.0	23	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
4	c3kvnA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
5	d1uynx_	Alignment		100.0	18	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
6	c2qomB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
7	d1p4ta_	Alignment		99.2	21	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
8	d1qjpa_	Alignment		99.1	15	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
9	d1g90a_	Alignment		99.1	18	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
10	c3nb3C_	Alignment		99.1	15	**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
11	c2x27X_	Alignment		99.1	9	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa

12	c2k0lA_	Alignment		99.1	19	**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.
13	c2f1tB_	Alignment		98.9	10	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
14	c2jmmA_	Alignment		98.9	15	**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
15	d1qj8a_	Alignment		98.8	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
16	c3qraA_	Alignment		98.8	12	**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	c2iwvD_	Alignment		98.4	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
18	c2lhfA_	Alignment		98.2	12	**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
19	c2x4mD_	Alignment		98.0	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
20	d1t16a_	Alignment		97.6	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
21	c2wjqA_	Alignment	not modelled	97.5	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
22	d1i78a_	Alignment	not modelled	97.5	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
23	c3dwoX_	Alignment	not modelled	97.1	11	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
24	c3a2rX_	Alignment	not modelled	97.1	12	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
25	d2fgqx1	Alignment	not modelled	96.6	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
26	c3brzA_	Alignment	not modelled	96.5	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
27	c3bryB_	Alignment	not modelled	96.4	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
28	d3prna_	Alignment	not modelled	96.1	26	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
						Fold: Transmembrane beta-barrels

29	d2pora_	Alignment	not modelled	94.8	11	**Superfamily:**Porins **Family:**Porin
30	d1daba_	Alignment		93.9	17	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Virulence factor P.69 pertactin
31	c2iahA_	Alignment	not modelled	93.5	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.
32	d2zfga1	Alignment	not modelled	92.1	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
33	d1osma_	Alignment	not modelled	91.5	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
34	c2hdiA_	Alignment	not modelled	87.7	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.
35	c3qlbA_	Alignment	not modelled	85.6	10	**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
36	d1phoa_	Alignment	not modelled	84.2	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
37	d1by5a_	Alignment	not modelled	82.9	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
38	c1xkwA_	Alignment	not modelled	82.7	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
39	d2vdfa1	Alignment	not modelled	81.9	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
40	d2gufa1	Alignment	not modelled	78.5	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
41	c3nsgA_	Alignment	not modelled	76.3	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
42	c3jtyB_	Alignment	not modelled	65.8	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**benf-like porin; **PDBTitle:** crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
43	c2gr7C_	Alignment	not modelled	59.9	22	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
44	d2gr7a1	Alignment	not modelled	59.9	22	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
45	c2ervA_	Alignment	not modelled	55.2	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein paer03002360; **PDBTitle:** crystal structure of the outer membrane enzyme pagl
46	d2gr8a1	Alignment	not modelled	52.4	22	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
47	c3emoA_	Alignment	not modelled	40.8	16	**PDB header:**membrane protein/cell adhesion **Chain:** A: **PDB Molecule:**hia (adhesin); **PDBTitle:** crystal structure of transmembrane hia 973-1098
48	c2o4vA_	Alignment	not modelled	39.5	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin p; **PDBTitle:** an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
49	c1po3A_	Alignment	not modelled	38.3	10	**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
50	c3h09B_	Alignment	not modelled	30.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**immunoglobulin a1 protease; **PDBTitle:** the structure of haemophilus influenzae iga1 protease
51	c3dzmB_	Alignment	not modelled	20.8	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
52	c2k4tA_	Alignment	not modelled	20.8	10	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
53	c2grxB_	Alignment	not modelled	19.4	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
54	c2gtkB	Alignment	not modelled	18.9	8	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable porin;

54	c2qtkB_	Alignment	not modelled	18.9	8	**PDBTitle:** crystal structure of the outer membrane protein opdk from2 pseudomonas aeruginosa
55	c3ml3A_	Alignment	not modelled	18.4	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**outer membrane protein icsa autotransporter; **PDBTitle:** crystal structure of the icsa autochaperone region
56	d2f0ca1	Alignment	not modelled	17.5	24	**Fold:**Virus attachment protein globular domain **Superfamily:**Virus attachment protein globular domain **Family:**Lactophage receptor-binding protein head domain
57	c3cslB_	Alignment	not modelled	15.7	16	**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
58	c3fhhA_	Alignment	not modelled	12.8	10	**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
59	c3qteA_	Alignment	not modelled	9.1	50	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**defensin-6; **PDBTitle:** crystal structure of human alpha-defensin 6 (h27w mutant)
60	c2y0hA_	Alignment	not modelled	8.7	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdl
61	c1xkhC_	Alignment	not modelled	8.5	11	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
62	c1qd6C_	Alignment	not modelled	8.4	14	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**protein (outer membrane phospholipase (ompla)); **PDBTitle:** outer membrane phospholipase a from escherichia coli
63	c3rbhC_	Alignment	not modelled	8.2	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**alginate production protein alge; **PDBTitle:** structure of alginate export protein alge from pseudomonas aeruginosa
64	d1bf2a1	Alignment	not modelled	8.0	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
65	c1al0B_	Alignment	not modelled	7.4	27	**PDB header:**virus **Chain:** B: **PDB Molecule:**scaffolding protein gpb; **PDBTitle:** procapsid of bacteriophage phix174
66	c2y0lA_	Alignment	not modelled	6.4	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cis-aconitate porin opdh; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
67	c2jxpA_	Alignment	not modelled	6.2	9	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**putative lipoprotein b; **PDBTitle:** solution nmr structure of uncharacterized lipoprotein b2 from nitrosomonas europaea. northeast structural genomics3 target ner45a
68	d1thqa_	Alignment	not modelled	5.9	15	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane enzyme PagP
69	d1a0tp_	Alignment	not modelled	5.7	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
70	d1jmxa4	Alignment	not modelled	5.6	30	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
71	d1nrja_	Alignment	not modelled	5.6	8	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**SRP alpha N-terminal domain-like