Phyre^2

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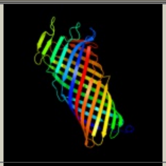
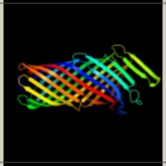
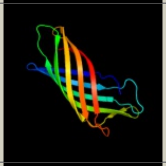
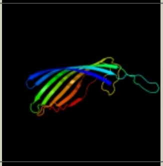
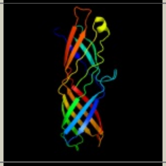
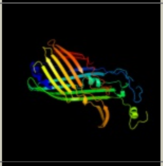
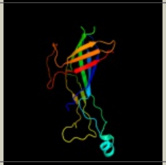
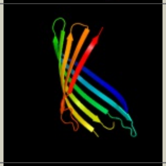
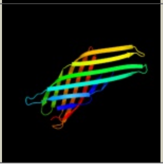
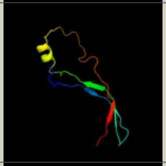
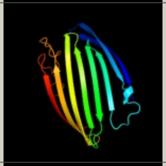
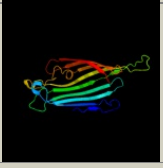
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1i78a_	Alignment		100.0	99	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
2	c2x4mD_	Alignment		100.0	52	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
3	d1p4ta_	Alignment		98.2	20	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
4	c2qomB_	Alignment		98.1	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
5	c3sljA_	Alignment		98.1	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
6	c2f1tB_	Alignment		98.0	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
7	c2x27X_	Alignment		98.0	11	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
8	c3dwoX_	Alignment		97.9	14	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
9	c2k0lA_	Alignment		97.7	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.
10	c3aehB_	Alignment		97.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
11	d1qj8a_	Alignment		97.1	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein

12	d1g90a_	Alignment		97.1	18	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
13	c3qraA_	Alignment		97.1	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
14	d1t16a_	Alignment		97.0	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
15	c2lhfA_	Alignment		96.7	10	**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
16	d1qjpa_	Alignment		96.7	23	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
17	c3nb3C_	Alignment		96.1	21	**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
18	d2fgqx1	Alignment		96.1	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
19	c3brzA_	Alignment		96.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
20	c2iwvD_	Alignment		95.9	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
21	d1uynx_	Alignment	not modelled	95.2	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
22	c3a2rX_	Alignment	not modelled	94.7	19	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
23	c3kvnA_	Alignment	not modelled	94.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
24	c3qq2C_	Alignment	not modelled	94.0	14	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
25	c2jmmA_	Alignment	not modelled	93.6	21	**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
26	c3dzmB_	Alignment	not modelled	93.3	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
27	d1phoa_	Alignment	not modelled	90.6	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
28	d2zfga1	Alignment	not modelled	87.5	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
						Fold: Transmembrane beta-barrels

29	d1osma_	Alignment	not modelled	85.6	19	**Superfamily:**Porins **Family:**Porin
30	c3bryB_	Alignment	not modelled	81.7	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
31	c3nsgA_	Alignment	not modelled	79.1	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
32	d2gufa1	Alignment	not modelled	73.8	26	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
33	d1af6a_	Alignment	not modelled	68.3	17	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
34	c2iahA_	Alignment	not modelled	53.6	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.
35	c2k4tA_	Alignment	not modelled	51.0	11	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
36	d2mpra_	Alignment	not modelled	47.9	22	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
37	c3cslB_	Alignment	not modelled	38.9	19	**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
38	d3prna_	Alignment	not modelled	33.2	27	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
39	d2pora_	Alignment	not modelled	18.4	19	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
40	c3gf6B_	Alignment	not modelled	17.5	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized bacterial lipoprotein; **PDBTitle:** crystal structure of a bacterial lipoprotein (bt_1233) from2 bacteroides thetaiotaomicron vpi-5482 at 1.69 a resolution
41	d1a0tp_	Alignment	not modelled	12.3	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
42	c3ghnA_	Alignment	not modelled	11.6	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**a disintegrin and metalloproteinase with thrombospondin **PDBTitle:** crystal structure of the exosite-containing fragment of human adamts132 (form-2)
43	d1o75a1	Alignment	not modelled	7.5	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Tp47 lipoprotein, middle and C-terminal domains **Family:**Tp47 lipoprotein, middle and C-terminal domains