Phyre2

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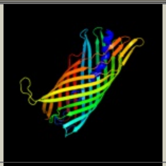
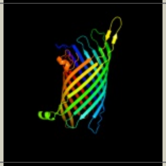
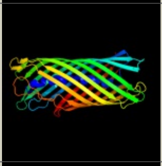
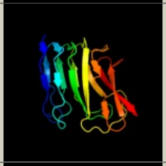
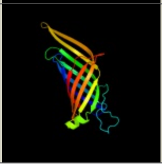
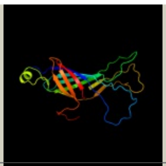
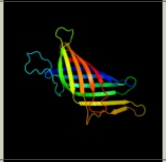
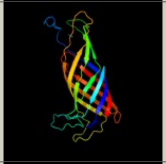
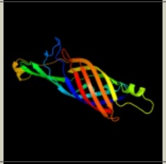
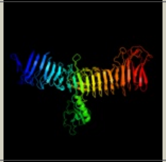
Description	Q9JMS3
Date	Wed Jan 25 15:21:16 GMT 2012
Unique Job ID	87afecb42b303d3e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sljA_	Alignment		100.0	20	**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	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
3	c3qq2C_	Alignment		100.0	24	**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	17	**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	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
7	c3ml3A_	Alignment		99.6	36	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**outer membrane protein icsa autotransporter; **PDBTitle:** crystal structure of the icsa autochaperone region
8	d1daba_	Alignment		99.6	14	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Virulence factor P.69 pertactin
9	d1g90a_	Alignment		99.1	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
10	d1p4ta_	Alignment		99.1	21	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
11	c3nb3C_	Alignment		98.9	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

12	c2k0lA_	Alignment		98.9	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.
13	d1qjpa_	Alignment		98.9	20	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
14	c2x27X_	Alignment		98.8	15	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
15	c2jmmA_	Alignment		98.8	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
16	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
17	c2f1tB_	Alignment		98.7	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
18	c3h09B_	Alignment		98.7	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**immunoglobulin a1 protease; **PDBTitle:** the structure of haemophilus influenzae iga1 protease
19	d1qj8a_	Alignment		98.4	9	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
20	c3a2rX_	Alignment		97.8	16	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
21	c2x4mD_	Alignment	not modelled	97.7	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
22	d1i78a_	Alignment	not modelled	97.6	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
23	c2lhfA_	Alignment	not modelled	97.6	18	**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
24	d2zfga1	Alignment	not modelled	97.5	19	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
25	d2pora_	Alignment	not modelled	97.5	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
26	c2iwvD_	Alignment	not modelled	97.4	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
27	d2fgqx1	Alignment	not modelled	97.3	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
28	c3syjA_	Alignment	not modelled	97.2	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**adhesion and penetration protein autotransporter; **PDBTitle:** crystal structure of the haemophilus influenzae hap adhesin

29	d1osma_	Alignment	not modelled	96.7	19	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
30	d3prna_	Alignment	not modelled	96.4	21	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
31	d2vdfa1	Alignment	not modelled	96.4	19	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
32	d1phoa_	Alignment	not modelled	96.2	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
33	c2wjqA_	Alignment	not modelled	95.8	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
34	c3nsgA_	Alignment	not modelled	93.5	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
35	c1xkhC_	Alignment	not modelled	88.9	13	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
36	c3bryB_	Alignment	not modelled	74.9	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
37	c3brzA_	Alignment	not modelled	67.3	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
38	c2ervA_	Alignment	not modelled	63.1	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein paer03002360; **PDBTitle:** crystal structure of the outer membrane enzyme pagl
39	c2iahA_	Alignment	not modelled	61.5	12	**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.
40	c2hdiA_	Alignment	not modelled	59.0	15	**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.
41	d1t16a_	Alignment	not modelled	36.6	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
42	d2gufa1	Alignment	not modelled	35.9	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
43	c3dwoX_	Alignment	not modelled	34.5	13	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
44	c1yo8A_	Alignment	not modelled	28.9	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**thrombospondin-2; **PDBTitle:** structure of the c-terminal domain of human thrombospondin-2
45	c1xkwA_	Alignment	not modelled	16.2	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
46	c1qd6C_	Alignment	not modelled	15.5	19	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**protein (outer membrane phospholipase (ompla)); **PDBTitle:** outer membrane phospholipase a from escherichia coli
47	d2f0ca1	Alignment	not modelled	14.2	16	**Fold:**Virus attachment protein globular domain **Superfamily:**Virus attachment protein globular domain **Family:**Lactophage receptor-binding protein head domain
48	c3fbyC_	Alignment	not modelled	13.6	17	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**cartilage oligomeric matrix protein; **PDBTitle:** the crystal structure of the signature domain of cartilage oligomeric2 matrix protein.
49	c1fw3A_	Alignment	not modelled	12.5	19	**PDB header:**hydrolase, membrane protein **Chain:** A: **PDB Molecule:**outer membrane phospholipase a; **PDBTitle:** outer membrane phospholipase a from escherichia coli
50	d1nrja_	Alignment	not modelled	12.3	25	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**SRP alpha N-terminal domain-like
51	c3fhhA_	Alignment	not modelled	11.5	9	**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
52	d2gr7a1	Alignment	not modelled	11.4	19	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
53	c2gr7C_	Alignment	not modelled	11.4	19	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
54	d1kmoa_	Alignment	not modelled	7.8	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
55	c2y0hA_	Alignment	not modelled	7.2	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable porin;

						PDBTitle: crystal structure of pseudomonas aeruginosa opdl
56	c3emoA_	Alignment	not modelled	7.2	18	**PDB header:**membrane protein/cell adhesion **Chain:** A: **PDB Molecule:**hia (adhesin); **PDBTitle:** crystal structure of transmembrane hia 973-1098
57	d1y02a2	Alignment	not modelled	6.7	30	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
58	d1fepa_	Alignment	not modelled	6.7	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
59	d2gr8a1	Alignment	not modelled	6.6	19	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
60	c3fidA_	Alignment	not modelled	6.4	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative outer membrane protein (lpxr); **PDBTitle:** lpxr from salmonella typhimurium
61	d1vhka1	Alignment	not modelled	5.7	80	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
62	c1al0B_	Alignment	not modelled	5.6	31	**PDB header:**virus **Chain:** B: **PDB Molecule:**scaffolding protein gpb; **PDBTitle:** procapsid of bacteriophage phix174