Phyre^2

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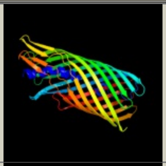
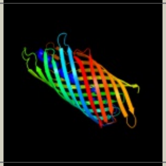
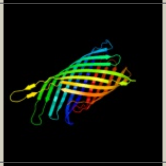
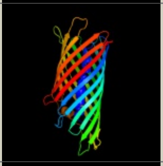
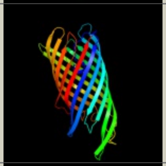
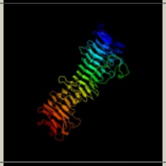
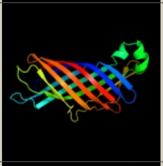
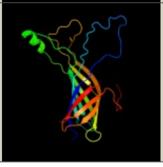
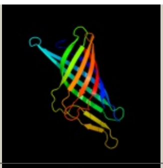
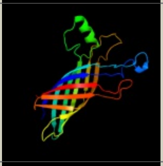
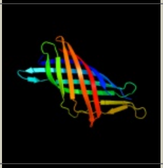
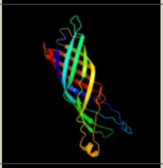
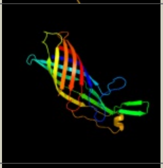
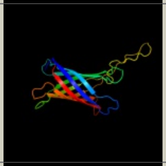
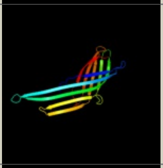
Description	P52143
Date	Wed Jan 25 15:20:58 GMT 2012
Unique Job ID	294182ceab3e8127

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sljA_	Alignment		100.0	16	**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	25	**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	d1uynx_	Alignment		100.0	17	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
5	c2qomB_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
6	c3kvnA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
7	d1daba_	Alignment		99.9	16	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Virulence factor P.69 pertactin
8	c3ml3A_	Alignment		99.6	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**outer membrane protein icsa autotransporter; **PDBTitle:** crystal structure of the icsa autochaperone region
9	c3h09B_	Alignment		99.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**immunoglobulin a1 protease; **PDBTitle:** the structure of haemophilus influenzae iga1 protease
10	d1p4ta_	Alignment		99.3	23	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
11	c2k0lA_	Alignment		99.3	13	**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.

12	d1qjpa_	Alignment		99.2	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
13	d1g90a_	Alignment		99.2	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
14	c3nb3C_	Alignment		99.2	14	**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
15	c3syjA_	Alignment		99.1	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**adhesion and penetration protein autotransporter; **PDBTitle:** crystal structure of the haemophilus influenzae hap adhesin
16	c2x27X_	Alignment		99.1	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
17	c3qraA_	Alignment		99.0	14	**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	c2f1tB_	Alignment		98.9	14	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
19	c2jmmA_	Alignment		98.9	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
20	d1qj8a_	Alignment		98.8	18	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
21	c2zj6A_	Alignment		98.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
22	c2iwvD_	Alignment	not modelled	98.4	13	**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
23	c2qubG_	Alignment		98.3	11	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**extracellular lipase; **PDBTitle:** crystal structure of extracellular lipase lipa from serratia2 marcescens
24	c2lhfA_	Alignment	not modelled	98.3	21	**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
25	c2wjqA_	Alignment	not modelled	98.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
26	c2x4mD_	Alignment	not modelled	97.8	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
						PDB header:hydrolase (serine protease)

27	c1satA_	Alignment	not modelled	97.6	13	**Chain:** A: **PDB Molecule:**serratia protease; **PDBTitle:** crystal structure of the 50 kda metallo protease from s.2 marcescens
28	c3a2rX_	Alignment	not modelled	97.6	10	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
29	c1om8A_	Alignment	not modelled	97.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serralysin; **PDBTitle:** crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallyzed with 10 mm edta
30	d2fgqx1	Alignment	not modelled	97.2	18	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
31	c1k7qA_	Alignment	not modelled	97.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**secreted protease c; **PDBTitle:** prtc from erwinia chrysanthemi: e189a mutant
32	d1g9ka1	Alignment	not modelled	96.9	10	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**beta-Roll **Family:**Serralysin-like metalloprotease, C-terminal domain
33	d2vdfa1	Alignment	not modelled	96.9	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
34	c3dwoX_	Alignment	not modelled	96.8	14	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
35	d1kapp1	Alignment	not modelled	96.7	16	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**beta-Roll **Family:**Serralysin-like metalloprotease, C-terminal domain
36	d1i78a_	Alignment	not modelled	96.6	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
37	d1k7ia1	Alignment	not modelled	96.5	15	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**beta-Roll **Family:**Serralysin-like metalloprotease, C-terminal domain
38	d1t16a_	Alignment	not modelled	96.3	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
39	c1jiwP_	Alignment	not modelled	96.3	14	**PDB header:**hydrolase/hyrolase inhibitor **Chain:** P: **PDB Molecule:**alkaline metalloproteinase; **PDBTitle:** crystal structure of the apr-aprin complex
40	d3prna_	Alignment	not modelled	96.2	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
41	d2pora_	Alignment	not modelled	96.2	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
42	d1sata1	Alignment	not modelled	95.8	13	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**beta-Roll **Family:**Serralysin-like metalloprotease, C-terminal domain
43	c2agmA_	Alignment	not modelled	95.7	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**poly(beta-d-mannuronate) c5 epimerase 4; **PDBTitle:** solution structure of the r-module from alge4
44	d2zfga1	Alignment	not modelled	95.7	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
45	d1osma_	Alignment	not modelled	95.5	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
46	c3nsgA_	Alignment	not modelled	95.3	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
47	d1phoa_	Alignment	not modelled	94.9	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
48	c3brzA_	Alignment	not modelled	93.1	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
49	c3bryB_	Alignment	not modelled	90.7	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
50	c2ervA_	Alignment	not modelled	90.6	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein paer03002360; **PDBTitle:** crystal structure of the outer membrane enzyme pagl
51	c1xkwA_	Alignment	not modelled	86.6	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
52	c3p4gD_	Alignment	not modelled	83.9	12	**PDB header:**antifreeze protein **Chain:** D: **PDB Molecule:**antifreeze protein; **PDBTitle:** x-ray crystal structure of a hyperactive, ca2+-dependent, beta-helical2 antifreeze protein from an antarctic bacterium
53	c2grxB_	Alignment	not modelled	83.8	14	**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
						PDB header:metal transport

54	c3qlbA_	Alignment	not modelled	72.6	14	**Chain:** A: **PDB Molecule:**enantio-pyochelin receptor; **PDBTitle:** enantiopyochelin outer membrane tonb-dependent transporter from2 pseudomonas fluorescens bound to the ferri-enantiopyochelin
55	c2iahA_	Alignment	not modelled	68.4	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.
56	c1xkhC_	Alignment	not modelled	61.9	13	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
57	c2hdiA_	Alignment	not modelled	54.1	11	**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.
58	c2o4vA_	Alignment	not modelled	48.5	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
59	c3jtyB_	Alignment	not modelled	37.7	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**benf-like porin; **PDBTitle:** crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
60	d1by5a_	Alignment	not modelled	27.6	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
61	d2gufa1	Alignment	not modelled	25.4	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
62	d2gr7a1	Alignment	not modelled	21.1	16	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
63	c2gr7C_	Alignment	not modelled	21.1	16	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
64	c3fy3A_	Alignment	not modelled	15.4	10	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin; **PDBTitle:** crystal structure of truncated hemolysin a from p. mirabilis
65	d2gr8a1	Alignment	not modelled	13.0	19	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
66	d1k18a_	Alignment	not modelled	11.6	27	**Fold:**Zinc finger domain of DNA polymerase-alpha **Superfamily:**Zinc finger domain of DNA polymerase-alpha **Family:**Zinc finger domain of DNA polymerase-alpha
67	c2y0hA_	Alignment	not modelled	9.6	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdl
68	c1al0B_	Alignment	not modelled	9.6	36	**PDB header:**virus **Chain:** B: **PDB Molecule:**scaffolding protein gpb; **PDBTitle:** procapsid of bacteriophage phix174
69	c3emoA_	Alignment	not modelled	8.8	14	**PDB header:**membrane protein/cell adhesion **Chain:** A: **PDB Molecule:**hia (adhesin); **PDBTitle:** crystal structure of transmembrane hia 973-1098
70	d3bbda1	Alignment	not modelled	7.1	32	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**EMG1/NEP1-like
71	d1zszc1	Alignment	not modelled	6.3	17	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB
72	d1jmxa4	Alignment	not modelled	6.1	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
73	c2qtkB_	Alignment	not modelled	5.9	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of the outer membrane protein opdk from2 pseudomonas aeruginosa
74	d1gmua2	Alignment	not modelled	5.6	33	**Fold:**Ferredoxin-like **Superfamily:**Urease metallochaperone UreE, C-terminal domain **Family:**Urease metallochaperone UreE, C-terminal domain
75	c3mjdA_	Alignment	not modelled	5.6	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.