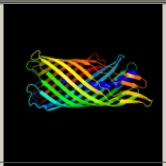
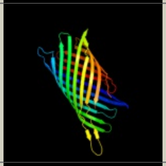
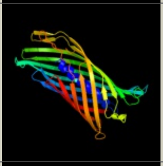
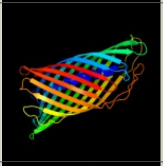
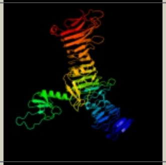
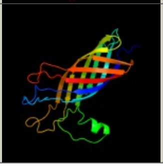
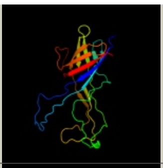
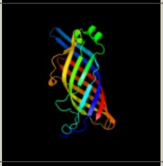
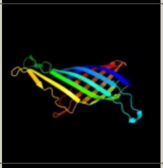
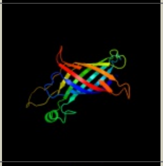
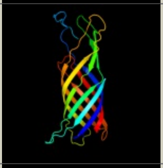
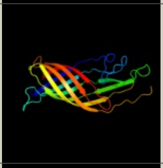
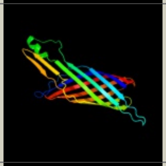
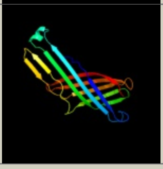
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P45508
Date	Thu Jan 5 12:02:51 GMT 2012
Unique Job ID	7163b76eaacc65ec

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sljA_	Alignment		100.0	17	**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	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
3	c3qq2C_	Alignment		100.0	22	**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	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
5	c3kvnA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
6	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.
7	d1daba_	Alignment		99.8	13	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Virulence factor P.69 pertactin
8	c3ml3A_	Alignment		99.7	27	**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	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**immunoglobulin a1 protease; **PDBTitle:** the structure of haemophilus influenzae iga1 protease
10	c3syjA_	Alignment		99.4	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**adhesion and penetration protein autotransporter; **PDBTitle:** crystal structure of the haemophilus influenzae hap adhesin
11	d1g90a_	Alignment		99.2	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein

12	c2k0lA_	Alignment		99.0	11	**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	d1p4ta_	Alignment		99.0	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
14	c3nb3C_	Alignment		98.9	13	**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	d1qjpa_	Alignment		98.9	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
16	c2jmmA_	Alignment		98.8	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
17	c2x27X_	Alignment		98.8	10	**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	c2f1tB_	Alignment		98.7	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
19	c3qraA_	Alignment		98.7	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
20	d1qj8a_	Alignment		98.3	7	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
21	c2iwvD_	Alignment	not modelled	98.0	11	**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
22	d2pora_	Alignment	not modelled	97.3	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
23	c2wjqA_	Alignment	not modelled	97.3	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
24	c3a2rX_	Alignment	not modelled	96.9	14	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
25	d1i78a_	Alignment	not modelled	96.7	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
26	d2zfga1	Alignment	not modelled	96.7	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
27	c2lhfA_	Alignment	not modelled	96.6	16	**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
28	d3prna_	Alignment	not modelled	96.5	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
						PDB header:hydrolase

29	c2x4mD_	Alignment	not modelled	96.5	10	**Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
30	d1osma_	Alignment	not modelled	95.9	18	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
31	c3dwoX_	Alignment	not modelled	94.9	14	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
32	d2fgqx1	Alignment	not modelled	94.5	20	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
33	d1phoa_	Alignment	not modelled	94.2	21	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
34	d2vdfa1	Alignment	not modelled	90.5	11	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
35	c3nsgA_	Alignment	not modelled	89.6	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
36	c3brzA_	Alignment	not modelled	87.8	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
37	c3ak5B_	Alignment	not modelled	86.5	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp; **PDBTitle:** hemoglobin protease (hbp) passenger missing domain-2
38	d1t16a_	Alignment	not modelled	78.9	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
39	c3bryB_	Alignment	not modelled	51.1	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
40	d1pm6a_	Alignment	not modelled	24.9	18	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
41	c1xkwA_	Alignment	not modelled	21.3	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
42	c2iahA_	Alignment	not modelled	21.2	9	**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.
43	c1qd6C_	Alignment	not modelled	20.9	14	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**protein (outer membrane phospholipase (ompla)); **PDBTitle:** outer membrane phospholipase a from escherichia coli
44	d1nrja_	Alignment	not modelled	18.6	58	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**SRP alpha N-terminal domain-like
45	c2grxB_	Alignment	not modelled	16.0	8	**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
46	c1fw3A_	Alignment	not modelled	15.7	14	**PDB header:**hydrolase, membrane protein **Chain:** A: **PDB Molecule:**outer membrane phospholipase a; **PDBTitle:** outer membrane phospholipase a from escherichia coli
47	d1kmoa_	Alignment	not modelled	14.0	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
48	d1by5a_	Alignment	not modelled	13.4	8	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
49	d2gr7a1	Alignment	not modelled	13.4	19	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
50	c2gr7C_	Alignment	not modelled	13.4	19	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
51	d1qqga2	Alignment	not modelled	12.3	21	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Phosphotyrosine-binding domain (PTB)
52	d1rh6a_	Alignment	not modelled	12.1	18	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
53	d1g5aa1	Alignment	not modelled	11.7	18	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
54	d2gr8a1	Alignment	not modelled	10.5	19	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
55	c1qqgA_	Alignment	not modelled	10.4	21	**PDB header:**signal transduction **Chain:** A: **PDB Molecule:**insulin receptor substrate 1; **PDBTitle:** crystal structure of the ph-ptb targeting region of irs-1
						PDB header:membrane protein

56	c2ervA_	Alignment	not modelled	8.4	17	**Chain:** A: **PDB Molecule:**hypothetical protein paer03002360; **PDBTitle:** crystal structure of the outer membrane enzyme pagl
57	d1af6a_	Alignment	not modelled	7.6	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
58	d1j0wa_	Alignment	not modelled	7.5	30	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Phosphotyrosine-binding domain (PTB)
59	c3emoA_	Alignment	not modelled	6.8	19	**PDB header:**membrane protein/cell adhesion **Chain:** A: **PDB Molecule:**hia (adhesin); **PDBTitle:** crystal structure of transmembrane hia 973-1098
60	c2j8pA_	Alignment	not modelled	6.4	27	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**cleavage stimulation factor 64 kda subunit; **PDBTitle:** nmr structure of c-terminal domain of human cstf-64
61	c2k4tA_	Alignment	not modelled	6.2	12	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
62	d1jmxa4	Alignment	not modelled	5.6	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
63	c1xkhC_	Alignment	not modelled	5.6	8	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
64	c2npbA_	Alignment	not modelled	5.4	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**selenoprotein w; **PDBTitle:** nmr solution structure of mouse selw