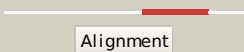
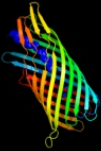
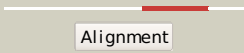
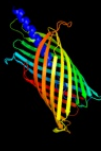



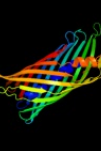
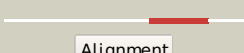
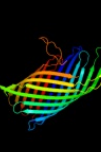



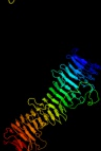





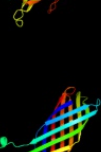


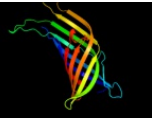










Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P76017
Date	Thu Jan 5 12:17:29 GMT 2012
Unique Job ID	10122e2f87dec11c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sljA_	 Alignment		100.0	24	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	25	PDB header: hydrolase Chain: B: PDB Molecule: hemoglobin-binding protease hbp autotransporter; PDBTitle: integral membrane domain of autotransporter hbp
3	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
4	d1uynx_	 Alignment		100.0	13	Fold: Transmembrane beta-barrels Superfamily: Autotransporter Family: Autotransporter
5	c3qq2C_	 Alignment		100.0	26	PDB header: membrane protein/protein transport Chain: C: PDB Molecule: brka autotransporter; PDBTitle: crystal structure of the beta domain of the bordetella autotransporter2 brka
6	c2qomB_	 Alignment		100.0	26	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		99.4	17	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Virulence factor P.69 pertactin
8	d1g90a_	 Alignment		99.4	21	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
9	c2k0lA_	 Alignment		99.3	18	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	c3qraA_	 Alignment		99.2	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
11	d1qjpa_	 Alignment		99.2	17	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein

12	c3nb3C_	Alignment		99.2	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
13	c2f1tB_	Alignment		99.1	17	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
14	c2x27X_	Alignment		99.1	14	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	d1p4ta_	Alignment		99.1	19	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
16	c2iwwD_	Alignment		99.0	14	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
17	c2jmmA_	Alignment		99.0	19	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
18	d1qj8a_	Alignment		98.9	11	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
19	c2x4mD_	Alignment		98.6	11	PDB header: hydrolase Chain: D: PDB Molecule: coagulase/fibrinolysin; PDBTitle: yersinia pestis plasminogen activator pla
20	d1i78a_	Alignment		98.2	12	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane protease OMPT
21	c2lhfa_	Alignment	not modelled	98.2	8	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
22	c2wjqa_	Alignment	not modelled	98.0	20	PDB header: transport protein Chain: A: PDB Molecule: probable n-acetylneuraminic acid outer membrane channel PDBTitle: nanc porin structure in hexagonal crystal form.
23	c3ml3A_	Alignment	not modelled	98.0	22	PDB header: protein transport Chain: A: PDB Molecule: outer membrane protein icsa autotransporter; PDBTitle: crystal structure of the icsa autochaperone region
24	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
25	c3brzA_	Alignment	not modelled	97.4	13	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx
26	c3dwoX_	Alignment	not modelled	97.4	16	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadl homologue
27	d1t16a_	Alignment	not modelled	97.4	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
28	d3prna_	Alignment	not modelled	97.0	16	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
29	d2fgqx1	Alignment	not modelled	96.8	16	Fold: Transmembrane beta-barrels Superfamily: Porins

					Family: Porin
30	d2pora_	Alignment	not modelled	96.8	15 Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
31	d1osma_	Alignment	not modelled	96.8	13 Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
32	d2vdfa1	Alignment	not modelled	95.8	11 Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane adhesin/invasin OpcA
33	d2zfga1	Alignment	not modelled	95.7	14 Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
34	c3nsgA_	Alignment	not modelled	95.7	15 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	d1phoa_	Alignment	not modelled	95.3	12 Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
36	c3bryB_	Alignment	not modelled	95.2	15 PDB header: transport protein Chain: B: PDB Molecule: tbux; PDBTitle: crystal structure of the ralstonia pickettii toluene2 transporter tbux
37	c3h09B_	Alignment	not modelled	94.8	14 PDB header: hydrolase Chain: B: PDB Molecule: immunoglobulin a1 protease; PDBTitle: the structure of haemophilus influenzae iga1 protease
38	c1xkwA_	Alignment	not modelled	94.1	14 PDB header: membrane protein Chain: A: PDB Molecule: fe(iii)-pyochelin receptor; PDBTitle: pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
39	c2iahA_	Alignment	not modelled	93.3	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	c3syjA_	Alignment	not modelled	93.2	13 PDB header: cell adhesion Chain: A: PDB Molecule: adhesion and penetration protein autotransporter; PDBTitle: crystal structure of the haemophilus influenzae hap adhesin
41	c1xkhC_	Alignment	not modelled	90.9	13 PDB header: membrane protein Chain: C: PDB Molecule: ferripyoverdine receptor; PDBTitle: pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
42	c2ervA_	Alignment	not modelled	90.9	8 PDB header: membrane protein Chain: A: PDB Molecule: hypothetical protein paer03002360; PDBTitle: crystal structure of the outer membrane enzyme pagl
43	c2hdiA_	Alignment	not modelled	87.9	13 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.
44	d2gufa1	Alignment	not modelled	69.8	9 Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
45	c2grxB_	Alignment	not modelled	62.4	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
46	d1laf6a_	Alignment	not modelled	57.9	10 Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
47	c3qlbA_	Alignment	not modelled	56.3	13 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
48	c2o4vA_	Alignment	not modelled	47.6	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
49	d1by5a_	Alignment	not modelled	43.0	12 Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
50	d1thqa_	Alignment	not modelled	32.1	13 Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane enzyme PagP
51	c3fidA_	Alignment	not modelled	28.4	12 PDB header: membrane protein Chain: A: PDB Molecule: putative outer membrane protein (lpxr); PDBTitle: lpxr from salmonella typhimurium
52	c3rbhC_	Alignment	not modelled	18.8	12 PDB header: transport protein Chain: C: PDB Molecule: alginate production protein alge; PDBTitle: structure of alginate export protein alge from pseudomonas aeruginosa
53	d2gr7a1	Alignment	not modelled	16.0	19 Fold: Pili subunits Superfamily: Pili subunits Family: YadA C-terminal domain-like
54	c2gr7C_	Alignment	not modelled	16.0	19 PDB header: membrane protein Chain: C: PDB Molecule: adhesin; PDBTitle: hia 992-1098
55	d1fepa_	Alignment	not modelled	14.3	8 Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel

56	c3dzmb_	Alignment	not modelled	14.1	11	PDB header: unknown function Chain: B: PDB Molecule: hypothetical conserved protein; PDBTitle: crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
57	c1ux6A_	Alignment	not modelled	13.5	22	PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin-1; PDBTitle: structure of a thrombospondin c-terminal fragment reveals a2 novel calcium core in the type 3 repeats
58	d1a0tp_	Alignment	not modelled	12.9	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
59	c1yuaA_	Alignment	not modelled	12.1	17	PDB header: viral protein Chain: A: PDB Molecule: head vertex protein gp24; PDBTitle: bacteriophage t4 capsid vertex protein gp24
60	c3fbyC_	Alignment	not modelled	11.9	13	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.
61	d1nrja_	Alignment	not modelled	11.0	33	Fold: Profilin-like Superfamily: SNARE-like Family: SRP alpha N-terminal domain-like
62	d2gr8a1	Alignment	not modelled	10.9	19	Fold: Pili subunits Superfamily: Pili subunits Family: YadA C-terminal domain-like
63	c2odjA_	Alignment	not modelled	10.8	10	PDB header: membrane protein Chain: A: PDB Molecule: porin d; PDBTitle: crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa
64	d1jmx4	Alignment	not modelled	10.3	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
65	c2ns2A_	Alignment	not modelled	9.5	15	PDB header: cell cycle Chain: A: PDB Molecule: spindlin-1; PDBTitle: crystal structure of spindlin1
66	c3fhhA_	Alignment	not modelled	9.2	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
67	d2f0ca1	Alignment	not modelled	7.7	21	Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Lactophage receptor-binding protein head domain
68	d1ux6a1	Alignment	not modelled	7.4	22	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Thrombospondin C-terminal domain
69	c3emoA_	Alignment	not modelled	6.7	19	PDB header: membrane protein/cell adhesion Chain: A: PDB Molecule: hia (adhesin); PDBTitle: crystal structure of transmembrane hia 973-1098
70	c3efmA_	Alignment	not modelled	6.3	11	PDB header: membrane protein Chain: A: PDB Molecule: ferric alcaligin siderophore receptor; PDBTitle: structure of the alcaligin outer membrane recepteur faua from2 bordetella pertussis
71	c1fw3A_	Alignment	not modelled	6.3	15	PDB header: hydrolase, membrane protein Chain: A: PDB Molecule: outer membrane phospholipase a; PDBTitle: outer membrane phospholipase a from escherichia coli
72	c2y0hA_	Alignment	not modelled	5.7	11	PDB header: transport protein Chain: A: PDB Molecule: probable porin; PDBTitle: crystal structure of pseudomonas aeruginosa opd1
73	c3cs1B_	Alignment	not modelled	5.5	15	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