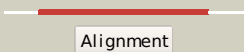
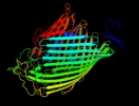
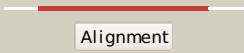
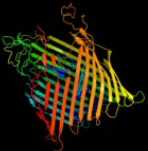
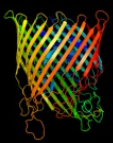
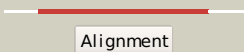
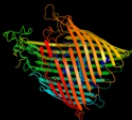
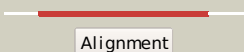
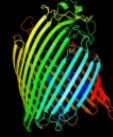
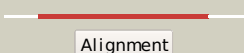
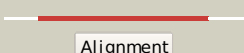
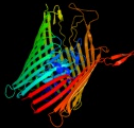
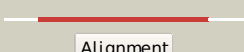
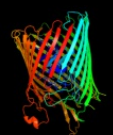
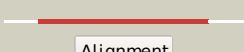
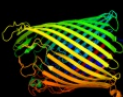
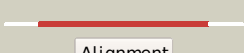
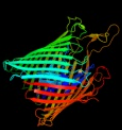
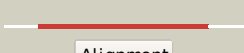
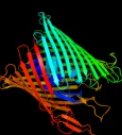
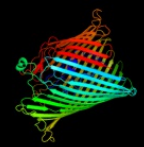
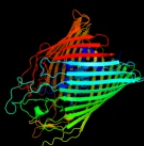
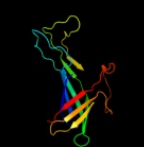


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P16869
Date	Thu Jan 5 11:35:50 GMT 2012
Unique Job ID	7d663c12e5e415d6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2iahA_	 Alignment		100.0	31	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.
2	c1xkhC_	 Alignment		100.0	31	PDB header: membrane protein Chain: C: PDB Molecule: ferripyoverdine receptor; PDBTitle: pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
3	c3qlbA_	 Alignment		100.0	19	PDB header: metal transport Chain: A: PDB Molecule: enantiopyochelin receptor; PDBTitle: enantiopyochelin outer membrane tonb-dependent transporter from2 pseudomonas fluorescens bound to the ferri-enantiopyochelin
4	c2grxB_	 Alignment		100.0	18	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
5	d1by5a_	 Alignment		100.0	19	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
6	c1xkwA_	 Alignment		100.0	27	PDB header: membrane protein Chain: A: PDB Molecule: fe(iii)-pyochelin receptor; PDBTitle: pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
7	c3efmA_	 Alignment		100.0	38	PDB header: membrane protein Chain: A: PDB Molecule: ferric alcaligin siderophore receptor; PDBTitle: structure of the alcaligin outer membrane recepteur faua from2 bordetella pertussis
8	c3fhhA_	 Alignment		100.0	17	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
9	d1kmoa_	 Alignment		100.0	16	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
10	c2hdiA_	 Alignment		100.0	18	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.
11	d2gufa1	 Alignment		100.0	15	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel

12	c1po3A_	Alignment		100.0	15	PDB header: membrane protein Chain: A: PDB Molecule: iron(iii) dicitrate transport protein feca PDBTitle: crystal structure of ferric citrate transporter feca in2 complex with ferric citrate
13	c3cslB_	Alignment		100.0	17	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
14	d1fepa_	Alignment		100.0	15	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
15	d1t16a_	Alignment		99.4	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
16	c3dwoX_	Alignment		99.2	16	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadl homologue
17	c2k0lA_	Alignment		97.6	12	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.
18	c3brzA_	Alignment		97.4	11	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx
19	c3qraA_	Alignment		97.3	11	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	d1g90a_	Alignment		97.1	12	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
21	c2f1tB_	Alignment	not modelled	96.8	12	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
22	c3nb3C_	Alignment	not modelled	96.2	12	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
23	d1qjpa_	Alignment	not modelled	95.9	14	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
24	c3bryB_	Alignment	not modelled	95.3	14	PDB header: transport protein Chain: B: PDB Molecule: tbux; PDBTitle: crystal structure of the ralstonia pickettii toluene2 transporter tbux
25	c2x27X_	Alignment	not modelled	92.9	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
26	d1qi8a_	Alignment	not modelled	92.5	10	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
27	d1p4ta_	Alignment	not modelled	92.3	12	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
28	c2jmmA_	Alignment	not modelled	90.1	11	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

29	c2iwwD_	Alignment	not modelled	89.1	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
30	c3kvnA_	Alignment	not modelled	88.7	12	PDB header: hydrolase Chain: A: PDB Molecule: esterase esta; PDBTitle: crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
31	d2fgqx1	Alignment	not modelled	82.1	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
32	c3sljA_	Alignment	not modelled	78.0	14	PDB header: protein transport Chain: A: PDB Molecule: serine protease espp; PDBTitle: pre-cleavage structure of the autotransporter espp - n1023a mutant
33	d1phoa_	Alignment	not modelled	74.6	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
34	c3aehB_	Alignment	not modelled	69.3	15	PDB header: hydrolase Chain: B: PDB Molecule: hemoglobin-binding protease hbp autotransporter; PDBTitle: integral membrane domain of autotransporter hbp
35	d1osma_	Alignment	not modelled	65.8	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
36	c2wjgA_	Alignment	not modelled	54.0	7	PDB header: transport protein Chain: A: PDB Molecule: probable n-acetylneuraminic acid outer membrane channel PDBTitle: nanc porin structure in hexagonal crystal form.
37	d1uynx_	Alignment	not modelled	50.5	8	Fold: Transmembrane beta-barrels Superfamily: Autotransporter Family: Autotransporter
38	c2qomB_	Alignment	not modelled	48.2	13	PDB header: hydrolase Chain: B: PDB Molecule: serine protease espp; PDBTitle: the crystal structure of the e.coli espp autotransporter beta-domain.
39	c2y0kA_	Alignment	not modelled	44.0	13	PDB header: transport protein Chain: A: PDB Molecule: pyroglutamate porin opdo; PDBTitle: crystal structure of pseudomonas aeruginosa opdo
40	d2zfga1	Alignment	not modelled	33.9	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
41	c2lhfa_	Alignment	not modelled	32.7	11	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
42	c2x4mD_	Alignment	not modelled	27.8	14	PDB header: hydrolase Chain: D: PDB Molecule: coagulase/fibrinolysin; PDBTitle: yersinia pestis plasminogen activator pla
43	c3qq2C_	Alignment	not modelled	25.2	11	PDB header: membrane protein/protein transport Chain: C: PDB Molecule: brka autotransporter; PDBTitle: crystal structure of the beta domain of the bordetella autotransporter2 brka
44	d1i78a_	Alignment	not modelled	22.3	15	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane protease OMPT
45	d2a1ja1	Alignment	not modelled	20.3	10	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
46	c2o4vA_	Alignment	not modelled	14.8	11	PDB header: membrane protein Chain: A: PDB Molecule: porin p; PDBTitle: an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
47	c3a2rX_	Alignment	not modelled	11.5	15	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein ii; PDBTitle: crystal structure of outer membrane protein porb from neisseria2 meningitidis
48	c1wx4B_	Alignment	not modelled	6.9	24	PDB header: oxidoreductase/metal transport Chain: B: PDB Molecule: melc; PDBTitle: crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a caddie protein3 prepared by the addition of dithiothreitol
49	c3nsgA_	Alignment	not modelled	6.6	8	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein f; PDBTitle: crystal structure of ompf, an outer membrane protein from salmonella2 typhi
50	c3rbhC_	Alignment	not modelled	6.0	11	PDB header: transport protein Chain: C: PDB Molecule: alginate production protein alge; PDBTitle: structure of alginate export protein alge from pseudomonas aeruginosa
51	c2vdaB_	Alignment	not modelled	5.9	29	PDB header: protein transport Chain: B: PDB Molecule: maltoporin; PDBTitle: solution structure of the seca-signal peptide complex
52	c2w3pB_	Alignment	not modelled	5.4	11	PDB header: lyase Chain: B: PDB Molecule: benzoyl-coa-dihydrodiol lyase; PDBTitle: boxc crystal structure
53	c3jtyB_	Alignment	not modelled	5.3	10	PDB header: transport protein Chain: B: PDB Molecule: benf-like porin; PDBTitle: crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5