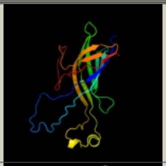
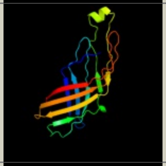
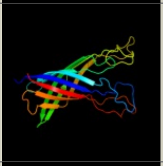
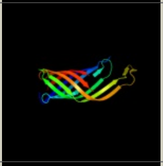
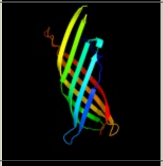
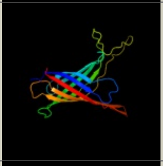
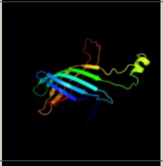
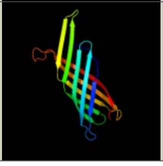
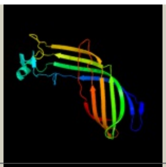
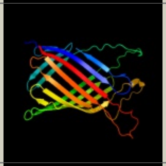
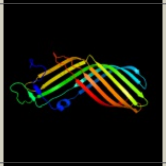
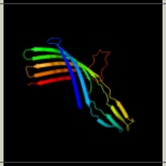
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P37681
Date	Thu Jan 5 11:56:55 GMT 2012
Unique Job ID	0552a630fbc2df8d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k0lA_	Alignment		98.7	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.
2	c2f1tB_	Alignment		98.7	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
3	c2x27X_	Alignment		98.5	17	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
4	d1g90a_	Alignment		98.5	13	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
5	d1qjpa_	Alignment		98.3	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
6	d1p4ta_	Alignment		98.3	10	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
7	c3nb3C_	Alignment		98.2	17	**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
8	c3qraA_	Alignment		98.0	18	**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
9	c2jmmA_	Alignment		97.6	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
10	c2lhfA_	Alignment		97.6	13	**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
11	d1qj8a_	Alignment		97.4	15	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein

12	c2x4mD_	Alignment		97.3	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
13	c2iwvD_	Alignment		96.4	17	**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
14	d1i78a_	Alignment		96.1	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
15	c3sljA_	Alignment		94.7	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
16	c3kvnA_	Alignment		94.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
17	c3aehB_	Alignment		93.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
18	c2wjqA_	Alignment		93.6	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
19	c3dwoX_	Alignment		92.8	15	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
20	c3qq2C_	Alignment		92.6	10	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
21	c2qomB_	Alignment	not modelled	92.0	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
22	d1uynx_	Alignment	not modelled	80.9	19	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
23	c2iahA_	Alignment	not modelled	80.5	11	**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.
24	d1tlya_	Alignment	not modelled	79.9	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Tsx-like channel **Family:**Tsx-like channel
25	c3brzA_	Alignment	not modelled	74.9	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
26	c3a2rX_	Alignment	not modelled	72.6	10	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
27	c3dzmB_	Alignment	not modelled	70.7	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
28	d2fgqx1	Alignment	not modelled	70.4	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin

29	c3bryB_	Alignment	not modelled	62.6	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
30	d3prna_	Alignment	not modelled	55.3	18	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
31	d2zfga1	Alignment	not modelled	54.6	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
32	c1xkhC_	Alignment	not modelled	47.2	11	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
33	d1t16a_	Alignment	not modelled	45.3	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
34	c3efmA_	Alignment	not modelled	45.3	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ferric alcaligin siderophore receptor; **PDBTitle:** structure of the alcaligin outer membrane recepteur faua from2 bordetella pertussis
35	c3cslB_	Alignment	not modelled	43.0	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
36	d1osma_	Alignment	not modelled	39.7	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
37	d2gufa1	Alignment	not modelled	39.1	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
38	c2c4iA_	Alignment	not modelled	28.6	35	**PDB header:**glycoprotein **Chain:** A: **PDB Molecule:**avidin; **PDBTitle:** crystal structure of engineered avidin
39	c3nsgA_	Alignment	not modelled	25.0	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
40	c3qlbA_	Alignment	not modelled	23.4	12	**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
41	c3fhhA_	Alignment	not modelled	17.8	13	**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
42	d1a0tp_	Alignment	not modelled	16.9	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
43	d2vdfa1	Alignment	not modelled	16.6	12	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
44	c3oiqB_	Alignment	not modelled	10.3	27	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**dna polymerase alpha catalytic subunit a; **PDBTitle:** crystal structure of yeast telomere protein cdc13 ob1 and the2 catalytic subunit of dna polymerase alpha pol1
45	d2a6za1	Alignment	not modelled	9.7	14	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Lectin leg-like
46	d1phoa_	Alignment	not modelled	9.2	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
47	c2grxB_	Alignment	not modelled	8.5	13	**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
48	d1thqa_	Alignment	not modelled	8.0	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane enzyme PagP
49	c2hdiA_	Alignment	not modelled	7.5	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.
50	d1fepa_	Alignment	not modelled	5.7	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel