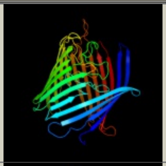
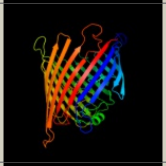
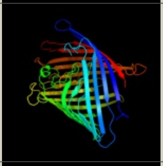
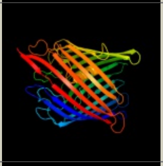
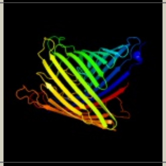
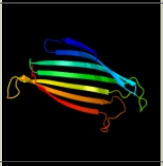
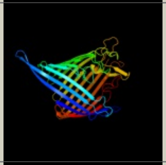
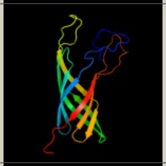
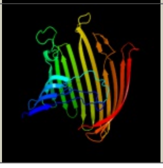
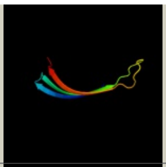
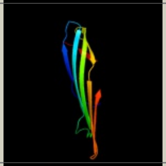
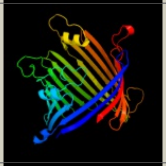
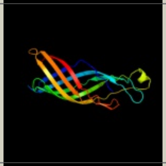
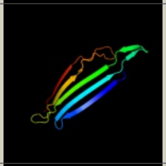
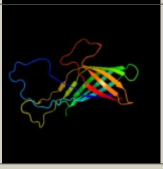
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	Q47706
Date	Thu Jan 5 12:37:07 GMT 2012
Unique Job ID	bf480df354926da9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2y0hA_	Alignment		100.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdl
2	c2odjA_	Alignment		100.0	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**porin d; **PDBTitle:** crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa
3	c2y0lA_	Alignment		100.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cis-aconitate porin opdh; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
4	c2qtkB_	Alignment		100.0	19	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of the outer membrane protein opdk from2 pseudomonas aeruginosa
5	c3jtyB_	Alignment		100.0	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**benf-like porin; **PDBTitle:** crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
6	c2y0kA_	Alignment		100.0	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**pyroglutatmate porin opdo; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
7	c3rbhC_	Alignment		96.9	15	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**alginate production protein alge; **PDBTitle:** structure of alginate export protein alge from pseudomonas aeruginosa
8	c2wjqA_	Alignment		95.8	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
9	c3nsgA_	Alignment		90.3	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
10	d1g90a_	Alignment		87.5	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
11	c3a2rX_	Alignment		83.0	11	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis

12	d1p4ta_	Alignment		79.9	15	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
13	c3qraA_	Alignment		78.6	10	**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
14	c2f1tB_	Alignment		64.4	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
15	d1osma_	Alignment		61.0	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
16	d2pora_	Alignment		50.5	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
17	c2x27X_	Alignment		49.1	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
18	d2fgqx1	Alignment		48.8	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
19	c3fhhA_	Alignment		46.2	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
20	c2k0lA_	Alignment		42.5	15	**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.
21	c2grxB_	Alignment	not modelled	38.3	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
22	d1by5a_	Alignment	not modelled	30.7	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
23	c2iwvD_	Alignment	not modelled	27.7	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
24	c3qlbA_	Alignment	not modelled	26.9	18	**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
25	d2nwaa1	Alignment	not modelled	20.4	17	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YtmB-like
26	c3nb3C_	Alignment	not modelled	16.5	18	**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
27	c2qomB_	Alignment	not modelled	15.8	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
28	c3cslB_	Alignment	not modelled	12.9	10	**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
29	d1qj8a_	Alignment	not modelled	12.1	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
30	c3brzA_	Alignment	not modelled	11.8	6	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
31	d1phoa_	Alignment	not modelled	9.9	9	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin