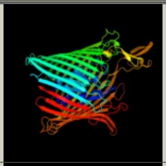
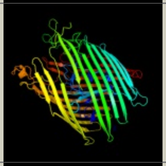
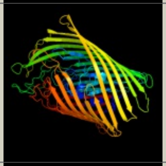
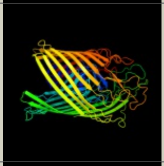
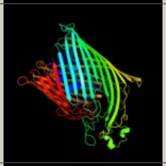
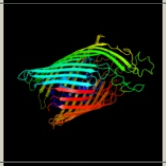
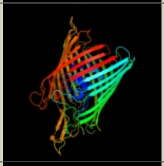
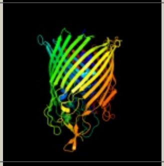
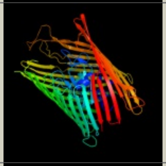
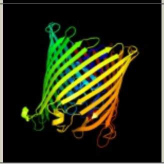
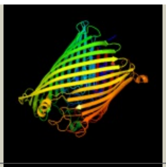
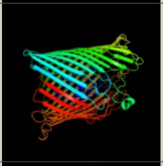
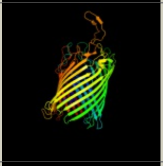
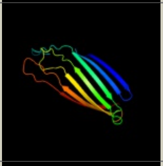
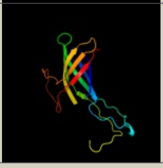
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P17315
Date	Thu Jan 5 11:36:04 GMT 2012
Unique Job ID	c2aea4eb2c01853e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hdiA_	Alignment		100.0	95	**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.
2	c2iahA_	Alignment		100.0	15	**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.
3	c3qlbA_	Alignment		100.0	15	**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
4	c1xkhC_	Alignment		100.0	14	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
5	d1by5a_	Alignment		100.0	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
6	c1xkwA_	Alignment		100.0	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
7	c2grxB_	Alignment		100.0	14	**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
8	c3fhhA_	Alignment		100.0	19	**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	d1fepa_	Alignment		100.0	29	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
10	c3efmA_	Alignment		100.0	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ferric alcaligin siderophore receptor; **PDBTitle:** structure of the alcaligin outer membrane recepteur faua from2 bordetella pertussis
11	d2gufa1	Alignment		100.0	25	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel

12	d1kmoa_	Alignment		100.0	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Ligand-gated protein channel
13	c1po3A_	Alignment		100.0	14	**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
14	c3cslB_	Alignment		100.0	16	**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
15	d1t16a_	Alignment		99.1	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
16	c3dwoX_	Alignment		98.0	8	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
17	c2f1tB_	Alignment		97.4	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
18	c3qraA_	Alignment		97.0	16	**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
19	c3brzA_	Alignment		96.6	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
20	c2k0lA_	Alignment		96.4	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	d1qjpa_	Alignment	not modelled	95.9	15	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
22	d1g90a_	Alignment	not modelled	95.9	11	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
23	c3nb3C_	Alignment	not modelled	95.7	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
24	c2iwvD_	Alignment	not modelled	94.6	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
25	c2wjqA_	Alignment	not modelled	94.5	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
26	c2x27X_	Alignment	not modelled	94.4	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
27	d1p4ta_	Alignment	not modelled	92.4	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
28	d1qj8a_	Alignment	not modelled	91.2	11	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein

29	c2jmmA_	Alignment	not modelled	89.8	12	**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
30	d2fgqx1	Alignment	not modelled	87.8	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
31	d1uynx_	Alignment	not modelled	80.3	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
32	c3bryB_	Alignment	not modelled	77.2	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
33	c2lhfA_	Alignment	not modelled	71.6	9	**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
34	d1osma_	Alignment	not modelled	68.3	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
35	c3nsgA_	Alignment	not modelled	54.5	14	**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	c3kvnA_	Alignment	not modelled	51.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
37	d1phoa_	Alignment	not modelled	50.9	12	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
38	c3qq2C_	Alignment	not modelled	45.5	8	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
39	c2y0kA_	Alignment	not modelled	39.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**pyroglutatmate porin opdo; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
40	d2zfga1	Alignment	not modelled	34.3	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
41	c3a2rX_	Alignment	not modelled	27.0	13	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
42	c3aehB_	Alignment	not modelled	24.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
43	c2qomB_	Alignment	not modelled	22.8	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
44	c3sljA_	Alignment	not modelled	22.6	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
45	c2x4mD_	Alignment	not modelled	22.5	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
46	d2a1ja1	Alignment	not modelled	19.9	50	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
47	c2y0hA_	Alignment	not modelled	17.4	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdl
48	c2eg9B_	Alignment	not modelled	16.3	5	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adp-ribosyl cyclase 1; **PDBTitle:** crystal structure of the truncated extracellular domain of2 mouse cd38
49	c1oy8A_	Alignment	not modelled	14.4	32	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
50	d3prna_	Alignment	not modelled	12.1	20	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
51	d2i4sa1	Alignment	not modelled	11.7	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
52	c2kl1A_	Alignment	not modelled	8.6	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ylbl protein; **PDBTitle:** solution structure of gtr34c from geobacillus thermodenitrificans.2 northeast structural genomics consortium target gtr34c
53	c3k07A_	Alignment	not modelled	8.4	27	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
54	c3lkxB_	Alignment	not modelled	8.3	43	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**nascent polypeptide-associated complex subunit alpha; **PDBTitle:** human nac dimerization domain
						Fold:PDZ domain-like

55	d2i6va1	Alignment	not modelled	7.7	13	**Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
56	c3tdqB_	Alignment	not modelled	7.4	20	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**pily2 protein; **PDBTitle:** crystal structure of a fimbrial biogenesis protein pily22 (pily2_pa4555) from pseudomonas aeruginosa pao1 at 2.10 a resolution
57	d1w0na_	Alignment	not modelled	7.2	29	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 36 carbohydrate binding module, CBM36
58	c2qtkB_	Alignment	not modelled	7.0	10	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable porin; **PDBTitle:** crystal structure of the outer membrane protein opdk from2 pseudomonas aeruginosa
59	c2ihmA_	Alignment	not modelled	6.9	14	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** polymerase mu in ternary complex with gapped 11mer dna2 duplex and bound incoming nucleotide
60	c1wx4B_	Alignment	not modelled	6.7	28	**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
61	d2ef1a1	Alignment	not modelled	6.6	8	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**ADP ribosyl cyclase-like
62	d1isia_	Alignment	not modelled	6.5	16	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**ADP ribosyl cyclase-like
63	d1gm5a2	Alignment	not modelled	6.2	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain
64	c8iczA_	Alignment	not modelled	6.2	12	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (dna polymerase beta (e.c.2.7.7.7)); **PDBTitle:** dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
65	c2y0lA_	Alignment	not modelled	6.0	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cis-aconitate porin opdh; **PDBTitle:** crystal structure of pseudomonas aeruginosa opdo
66	d2aq0a1	Alignment	not modelled	5.8	38	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
67	c3i18A_	Alignment	not modelled	5.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2051 protein; **PDBTitle:** crystal structure of the pdz domain of the sdrc-like protein2 (lmo2051) from listeria monocytogenes, northeast structural3 genomics consortium target lmr166b
68	c2kjpA_	Alignment	not modelled	5.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ylbl; **PDBTitle:** solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
69	d1qw2a_	Alignment	not modelled	5.2	12	**Fold:**Hypothetical protein Ta1206 **Superfamily:**Hypothetical protein Ta1206 **Family:**Hypothetical protein Ta1206