Phyre2

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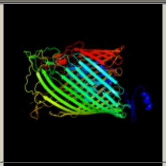
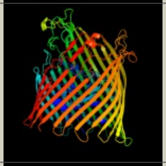
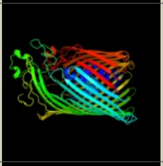
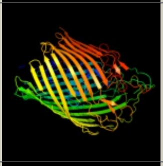
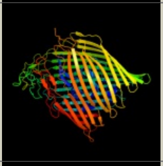
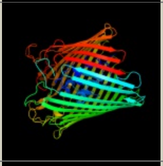
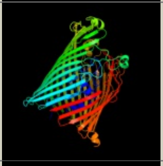
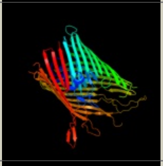
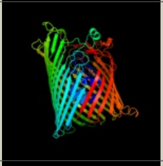
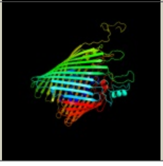
| Email | l.a.kelley@imperial.ac.uk |
| Description | P75780 |
| Date | Thu Jan 5 12:14:03 GMT 2012 |
| Unique Job ID | 7aa9862a22a22ae6 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2iahA_ | Alignment |  | 100.0 | 20 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**ferripyoverdine receptor;<br>**PDBTitle:** crystal structure of the ferripyoverdine receptor of the outer2 membrane of pseudomonas aeruginosa bound to ferripyoverdine. |
| 2 | c3qlbA_ | Alignment |  | 100.0 | 18 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**enantio-pyochelin receptor;<br>**PDBTitle:** enantiopyochelin outer membrane tonb-dependent transporter from2 pseudomonas fluorescens bound to the ferri-enantiopyochelin |
| 3 | c2grxB_ | Alignment |  | 100.0 | 20 | **PDB header:**metal transport<br>**Chain:** B: **PDB Molecule:**ferrichrome-iron receptor;<br>**PDBTitle:** crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome |
| 4 | d1by5a_ | Alignment |  | 100.0 | 20 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Ligand-gated protein channel |
| 5 | c1xkhC_ | Alignment |  | 100.0 | 21 | **PDB header:**membrane protein<br>**Chain:** C: **PDB Molecule:**ferripyoverdine receptor;<br>**PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine |
| 6 | c1xkwA_ | Alignment |  | 100.0 | 21 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor;<br>**PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa |
| 7 | c3fhhA_ | Alignment |  | 100.0 | 18 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane heme receptor shua;<br>**PDBTitle:** crystal structure of the heme/hemoglobin outer membrane2 transporter shua from shigella dysenteriae |
| 8 | d1kmoa_ | Alignment |  | 100.0 | 18 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Ligand-gated protein channel |
| 9 | c3efmA_ | Alignment |  | 100.0 | 20 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**ferric alcaligin siderophore receptor;<br>**PDBTitle:** structure of the alcaligin outer membrane recepteur faua from2 bordetella pertussis |
| 10 | c1po3A_ | Alignment |  | 100.0 | 18 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**iron(iii) dicitrate transport protein feca<br>**PDBTitle:** crystal structure of ferric citrate transporter feca in2 complex with ferric citrate |
| 11 | c3cslB_ | Alignment |  | 100.0 | 17 | **PDB header:**membrane protein/heme binding protein<br>**Chain:** B: **PDB Molecule:**hasr protein;<br>**PDBTitle:** structure of the serratia marcescens hemophore receptor hasr in2 complex with its hemophore hasa and heme |

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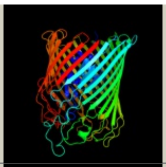
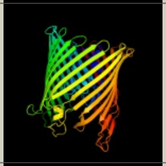
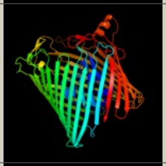
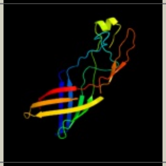
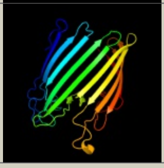
| 12 | d1fepa_ | Alignment |  | 100.0 | 16 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Ligand-gated protein channel |
| 13 | d2gufa1 | Alignment |  | 100.0 | 18 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Ligand-gated protein channel |
| 14 | c2hdiA_ | Alignment |  | 100.0 | 19 | **PDB header:**protein transport,antimicrobial protein<br>**Chain:** A: **PDB Molecule:**colicin i receptor;<br>**PDBTitle:** crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia. |
| 15 | d1t16a_ | Alignment |  | 99.7 | 12 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Outer membrane protein transport protein |
| 16 | c3dwoX_ | Alignment |  | 99.4 | 12 | **PDB header:**membrane protein<br>**Chain:** X: **PDB Molecule:**probable outer membrane protein;<br>**PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue |
| 17 | c3brzA_ | Alignment |  | 98.6 | 12 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**todx;<br>**PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx |
| 18 | c3bryB_ | Alignment |  | 97.0 | 10 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**tbux;<br>**PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux |
| 19 | c2f1tB_ | Alignment |  | 96.4 | 13 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**outer membrane protein w;<br>**PDBTitle:** outer membrane protein ompw |
| 20 | d2fgqx1 | Alignment |  | 96.1 | 12 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 21 | c3qraA_ | Alignment | not modelled | 96.1 | 14 | **PDB header:**cell invasion<br>**Chain:** A: **PDB Molecule:**attachment invasion locus protein;<br>**PDBTitle:** the crystal structure of ail, the attachment invasion locus protein of2 yersinia pestis |
| 22 | d1qjpa_ | Alignment | not modelled | 96.0 | 18 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPA-like<br>**Family:**Outer membrane protein |
| 23 | c3nb3C_ | Alignment | not modelled | 95.9 | 16 | **PDB header:**virus<br>**Chain:** C: **PDB Molecule:**outer membrane protein a;<br>**PDBTitle:** the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components |
| 24 | d1g90a_ | Alignment | not modelled | 95.7 | 13 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPA-like<br>**Family:**Outer membrane protein |
| 25 | c2k0lA_ | Alignment | not modelled | 94.9 | 16 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein a;<br>**PDBTitle:** nmr structure of the transmembrane domain of the outer2 membrane protein a from klebsiella pneumoniae in dhpc3 micelles. |
| 26 | d1qj8a_ | Alignment | not modelled | 92.5 | 13 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPA-like<br>**Family:**Outer membrane protein |
| 27 | c2wjqA_ | Alignment | not modelled | 90.8 | 7 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel<br>**PDBTitle:** nanc porin structure in hexagonal crystal form. |
| 28 | c3sljA_ | Alignment | not modelled | 89.4 | 11 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**serine protease espp;<br>**PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant |

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| 29 | c2x27X_ | Alignment | not modelled | 88.8 | 11 | **PDB header:**membrane protein<br>**Chain:** X: **PDB Molecule:**outer membrane protein oprg;<br>**PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa |
| 30 | c2iwvD_ | Alignment | not modelled | 87.5 | 12 | **PDB header:**ion channel<br>**Chain:** D: **PDB Molecule:**outer membrane protein g;<br>**PDBTitle:** structure of the monomeric outer membrane porin ompg in the2 open and closed conformation |
| 31 | d1osma_ | Alignment | not modelled | 86.1 | 15 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 32 | d1phoa_ | Alignment | not modelled | 86.0 | 8 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 33 | d1uynx_ | Alignment | not modelled | 80.1 | 11 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Autotransporter<br>**Family:**Autotransporter |
| 34 | d2zfga1 | Alignment | not modelled | 75.6 | 12 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 35 | c3kvnA_ | Alignment | not modelled | 73.6 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**esterase esta;<br>**PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa |
| 36 | c2jmmA_ | Alignment | not modelled | 68.3 | 8 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein a;<br>**PDBTitle:** nmr solution structure of a minimal transmembrane beta-2 barrel platform protein |
| 37 | c2lhfA_ | Alignment | not modelled | 66.1 | 15 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein h1;<br>**PDBTitle:** solution structure of outer membrane protein h (oprh) from p.2 aeruginosa in dhpc micelles |
| 38 | d1p4ta_ | Alignment | not modelled | 64.7 | 12 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPA-like<br>**Family:**Outer membrane protein |
| 39 | c3aehB_ | Alignment | not modelled | 47.7 | 13 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter;<br>**PDBTitle:** integral membrane domain of autotransporter hbp |
| 40 | c2x4mD_ | Alignment | not modelled | 33.3 | 16 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**coagulase/fibrinolysin;<br>**PDBTitle:** yersinia pestis plasminogen activator pla |
| 41 | c3a2rX_ | Alignment | not modelled | 28.2 | 8 | **PDB header:**membrane protein<br>**Chain:** X: **PDB Molecule:**outer membrane protein ii;<br>**PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis |
| 42 | c3nsgA_ | Alignment | not modelled | 25.2 | 15 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein f;<br>**PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi |
| 43 | d2a1ja1 | Alignment | not modelled | 23.3 | 50 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Hef domain-like |
| 44 | c2qomB_ | Alignment | not modelled | 19.1 | 10 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**serine protease espp;<br>**PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain. |
| 45 | d2j01t1 | Alignment | not modelled | 18.5 | 8 | **Fold:**SH3-like barrel<br>**Superfamily:**Translation proteins SH3-like domain<br>**Family:**Ribosomal protein L19 |
| 46 | c2w3pB_ | Alignment | not modelled | 16.4 | 13 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**benzoyl-coa-dihydrodiol lyase;<br>**PDBTitle:** boxc crystal structure |
| 47 | c1wx4B_ | Alignment | not modelled | 13.8 | 17 | **PDB header:**oxidoreductase/metal transport<br>**Chain:** B: **PDB Molecule:**melc;<br>**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 |
| 48 | c3k07A_ | Alignment | not modelled | 12.2 | 15 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**cation efflux system protein cusa;<br>**PDBTitle:** crystal structure of cusa |
| 49 | c1oy8A_ | Alignment | not modelled | 12.2 | 14 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**acriflavine resistance protein b;<br>**PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump |
| 50 | c2ftcK_ | Alignment | not modelled | 11.2 | 18 | **PDB header:**ribosome<br>**Chain:** K: **PDB Molecule:**39s ribosomal protein l19, mitochondrial;<br>**PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome |
| 51 | d2gycn1 | Alignment | not modelled | 10.1 | 12 | **Fold:**SH3-like barrel<br>**Superfamily:**Translation proteins SH3-like domain<br>**Family:**Ribosomal protein L19 |
| 52 | c3bboR_ | Alignment | not modelled | 10.1 | 21 | **PDB header:**ribosome<br>**Chain:** R: **PDB Molecule:**ribosomal protein l19;<br>**PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome |
| 53 | c2ai4A_ | Alignment | not modelled | 9.8 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein so1698;<br>**PDBTitle:** structure of protein of unknown function so1698 from shewanella2 oneidensis |
| 54 | c1nwxN_ | Alignment | not modelled | 8.8 | 15 | **PDB header:**ribosome<br>**Chain:** N: **PDB Molecule:**ribosomal protein l19;<br>**PDBTitle:** complex of the large ribosomal subunit from deinococcus2 radiodurans with abt-773 |

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| 55 | d1gm5a2 | Alignment | not modelled | 8.7 | 30 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**RecG "wedge" domain |
| 56 | d2zjrm1 | Alignment | not modelled | 8.6 | 14 | **Fold:**SH3-like barrel<br>**Superfamily:**Translation proteins SH3-like domain<br>**Family:**Ribosomal protein L19 |
| 57 | c3jtyB_ | Alignment | not modelled | 8.4 | 10 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**benf-like porin;<br>**PDBTitle:** crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5 |
| 58 | d1ahsa_ | Alignment | not modelled | 7.8 | 23 | **Fold:**Viral protein domain<br>**Superfamily:**Viral protein domain<br>**Family:**Top domain of virus capsid protein |
| 59 | c3igzB_ | Alignment | not modelled | 7.6 | 13 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase;<br>**PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration |
| 60 | d3prna_ | Alignment | not modelled | 7.5 | 16 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 61 | c3f42A_ | Alignment | not modelled | 7.3 | 7 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**protein hp0035;<br>**PDBTitle:** crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori |
| 62 | c1ybxA_ | Alignment | not modelled | 6.7 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**conserved hypothetical protein;<br>**PDBTitle:** conserved hypothetical protein cth-383 from clostridium thermocellum |
| 63 | d2aq0a1 | Alignment | not modelled | 6.4 | 38 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Hef domain-like |
| 64 | d1pugb_ | Alignment | not modelled | 6.0 | 14 | **Fold:**YbaB-like<br>**Superfamily:**YbaB-like<br>**Family:**YbaB-like |
| 65 | d1bvp12 | Alignment | not modelled | 5.7 | 26 | **Fold:**Viral protein domain<br>**Superfamily:**Viral protein domain<br>**Family:**Top domain of virus capsid protein |
| 66 | c2y0hA_ | Alignment | not modelled | 5.6 | 8 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**probable porin;<br>**PDBTitle:** crystal structure of pseudomonas aeruginosa opdl |
| 67 | c3s93B_ | Alignment | not modelled | 5.5 | 18 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**tudor domain-containing protein 5;<br>**PDBTitle:** crystal structure of conserved motif in tdrd5 |