# Phyre$^2$

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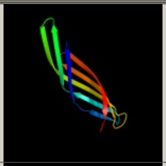
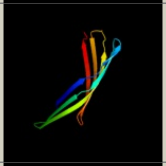
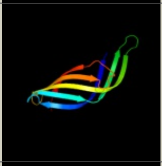
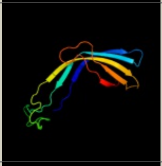
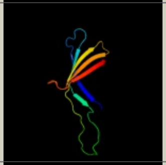
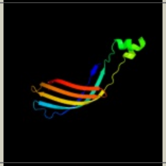
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77184 |
| Date | Thu Jan 5 12:26:08 GMT 2012 |
| Unique Job ID | 000843a6966a4a06 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1qj8a_ | Alignment |  | 99.8 | 36 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPA-like<br>**Family:**Outer membrane protein |
| 2 | c3qraA_ | Alignment |  | 99.7 | 37 | **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 |
| 3 | c3nb3C_ | Alignment |  | 99.3 | 19 | **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 |
| 4 | d1qjpa_ | Alignment |  | 99.2 | 19 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPA-like<br>**Family:**Outer membrane protein |
| 5 | c2k0lA_ | Alignment |  | 99.1 | 17 | **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. |
| 6 | d1g90a_ | Alignment |  | 99.0 | 19 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPA-like<br>**Family:**Outer membrane protein |
| 7 | d1p4ta_ | Alignment |  | 98.9 | 23 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPA-like<br>**Family:**Outer membrane protein |
| 8 | c2f1tB_ | Alignment |  | 98.7 | 17 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**outer membrane protein w;<br>**PDBTitle:** outer membrane protein ompw |
| 9 | c2jmmA_ | Alignment |  | 98.7 | 18 | **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 |
| 10 | c2x27X_ | Alignment |  | 98.6 | 20 | **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 |
| 11 | d1t16a_ | Alignment |  | 98.4 | 14 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Outer membrane protein transport protein |

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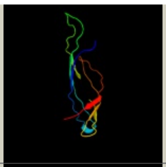
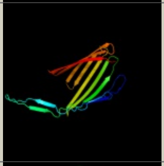
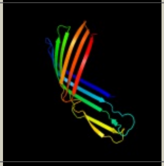
|---|---|---|---|---|---|---|
| 12 | c2lhfA_ | Alignment |  | 98.2 | 18 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein h1;<br>**PDBTitle:** solution structure of outer membrane protein h (oprh) from p.2 aeruginosa in dhpc micelles |
| 13 | c3brzA_ | Alignment |  | 98.0 | 15 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**todx;<br>**PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx |
| 14 | c3bryB_ | Alignment |  | 97.9 | 15 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**tbux;<br>**PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux |
| 15 | d1uynx_ | Alignment |  | 97.9 | 16 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Autotransporter<br>**Family:**Autotransporter |
| 16 | c3dwoX_ | Alignment |  | 97.8 | 19 | **PDB header:**membrane protein<br>**Chain:** X: **PDB Molecule:**probable outer membrane protein;<br>**PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue |
| 17 | c3kvnA_ | Alignment |  | 97.4 | 9 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**esterase esta;<br>**PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa |
| 18 | d2zfga1 | Alignment |  | 97.3 | 14 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 19 | d1osma_ | Alignment |  | 97.3 | 11 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 20 | c3sljA_ | Alignment |  | 97.0 | 15 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**serine protease espp;<br>**PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant |
| 21 | d1phoa_ | Alignment | not modelled | 96.6 | 16 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 22 | c3aehB_ | Alignment | not modelled | 96.5 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter;<br>**PDBTitle:** integral membrane domain of autotransporter hbp |
| 23 | d2fgqx1 | Alignment | not modelled | 95.7 | 15 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 24 | d2vdfa1 | Alignment | not modelled | 95.6 | 24 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPT-like<br>**Family:**Outer membrane adhesin/invasin OpcA |
| 25 | c3nsgA_ | Alignment | not modelled | 95.2 | 17 | **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 |
| 26 | c2qomB_ | Alignment | not modelled | 94.7 | 18 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**serine protease espp;<br>**PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain. |
| 27 | c3qq2C_ | Alignment | not modelled | 93.6 | 16 | **PDB header:**membrane protein/protein transport<br>**Chain:** C: **PDB Molecule:**brka autotransporter;<br>**PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka |
| 28 | d1a0tp_ | Alignment | not modelled | 92.9 | 12 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Maltoporin-like |
| | | | | | | **PDB header:**hydrolase |

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|---|---|---|---|---|---|---|
| 29 | c2x4mD_ | Alignment | not modelled | 86.1 | 24 | **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin;<br>**PDBTitle:** yersinia pestis plasminogen activator pla |
| 30 | d1af6a_ | Alignment | not modelled | 85.4 | 18 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Maltoporin-like |
| 31 | d3prna_ | Alignment | not modelled | 79.1 | 14 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 32 | d2mpra_ | Alignment | not modelled | 78.4 | 20 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Maltoporin-like |
| 33 | d1i78a_ | Alignment | not modelled | 78.1 | 20 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPT-like<br>**Family:**Outer membrane protease OMPT |
| 34 | d2gr7a1 | Alignment | not modelled | 77.9 | 28 | **Fold:**Pili subunits<br>**Superfamily:**Pili subunits<br>**Family:**YadA C-terminal domain-like |
| 35 | c2gr7C_ | Alignment | not modelled | 77.9 | 28 | **PDB header:**membrane protein<br>**Chain:** C: **PDB Molecule:**adhesin;<br>**PDBTitle:** hia 992-1098 |
| 36 | c3a2rX_ | Alignment | not modelled | 66.3 | 13 | **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 |
| 37 | d2gr8a1 | Alignment | not modelled | 58.0 | 26 | **Fold:**Pili subunits<br>**Superfamily:**Pili subunits<br>**Family:**YadA C-terminal domain-like |
| 38 | c2o4vA_ | Alignment | not modelled | 55.2 | 24 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**porin p;<br>**PDBTitle:** an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane |
| 39 | c3emoA_ | Alignment | not modelled | 53.3 | 24 | **PDB header:**membrane protein/cell adhesion<br>**Chain:** A: **PDB Molecule:**hia (adhesin);<br>**PDBTitle:** crystal structure of transmembrane hia 973-1098 |
| 40 | d2pora_ | Alignment | not modelled | 49.2 | 12 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 41 | c3rbhC_ | Alignment | not modelled | 21.3 | 14 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**alginate production protein alge;<br>**PDBTitle:** structure of alginate export protein alge from pseudomonas aeruginosa |
| 42 | d1rl6a2 | Alignment | not modelled | 17.5 | 30 | **Fold:**Ribosomal protein L6<br>**Superfamily:**Ribosomal protein L6<br>**Family:**Ribosomal protein L6 |
| 43 | c2y0lA_ | Alignment | not modelled | 11.0 | 9 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**cis-aconitate porin opdh;<br>**PDBTitle:** crystal structure of pseudomonas aeruginosa opdo |
| 44 | c2iahA_ | Alignment | not modelled | 8.3 | 13 | **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. |
| 45 | d2j01h2 | Alignment | not modelled | 7.9 | 27 | **Fold:**Ribosomal protein L6<br>**Superfamily:**Ribosomal protein L6<br>**Family:**Ribosomal protein L6 |
| 46 | c2zkre_ | Alignment | not modelled | 7.1 | 12 | **PDB header:**ribosomal protein/rna<br>**Chain:** E: **PDB Molecule:**rna expansion segment es7 part ii;<br>**PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map |
| 47 | d2qamg2 | Alignment | not modelled | 7.0 | 46 | **Fold:**Ribosomal protein L6<br>**Superfamily:**Ribosomal protein L6<br>**Family:**Ribosomal protein L6 |
| 48 | d2je6i2 | Alignment | not modelled | 6.8 | 20 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Ribosomal L27 protein-like<br>**Family:**ECR1 N-terminal domain-like |
| 49 | d1osya_ | Alignment | not modelled | 6.1 | 30 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Fungal immunomodulatory protein, FIP<br>**Family:**Fungal immunomodulatory protein, FIP |
| 50 | d1opca_ | Alignment | not modelled | 6.0 | 57 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**C-terminal effector domain of the bipartite response regulators<br>**Family:**PhoB-like |
| 51 | c1xkhC_ | Alignment | not modelled | 5.8 | 13 | **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 |
| 52 | c2e7mA_ | Alignment | not modelled | 5.6 | 27 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**protein kiaa0319;<br>**PDBTitle:** solution structure of the pkd domain (329-428) from human2 kiaa0319 |
| 53 | d2zjre1 | Alignment | not modelled | 5.6 | 55 | **Fold:**Ribosomal protein L6<br>**Superfamily:**Ribosomal protein L6<br>**Family:**Ribosomal protein L6 |
| 54 | c2hqnA_ | Alignment | not modelled | 5.3 | 50 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**putative transcriptional regulator;<br>**PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism |
| 55 | d1c0ma1 | Alignment | not modelled | 5.2 | 22 | **Fold:**SH3-like barrel<br>**Superfamily:**DNA-binding domain of retroviral integrase |

**Family:** DNA-binding domain of retroviral integrase