Phyre2

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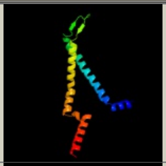
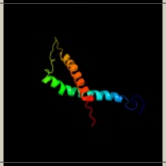
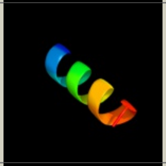
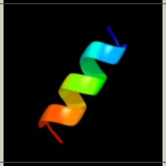
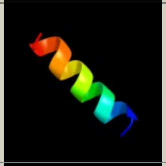
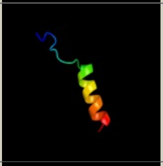
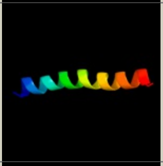
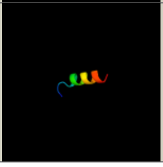
| Email | l.a.kelley@imperial.ac.uk |
| Description | P68805 |
| Date | Tue Jul 17 17:05:13 BST 2012 |
| Unique Job ID | d98c7c601a50ae90 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2oarA_ | Alignment |  | 100.0 | 44 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel;<br>**PDBTitle:** mechanosensitive channel of large conductance (mscl) |
| 2 | c3hzqA_ | Alignment |  | 100.0 | 99 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel;<br>**PDBTitle:** structure of a tetrameric mscl in an expanded intermediate2 state |
| 3 | d2oara1 | Alignment |  | 100.0 | 42 | **Fold:**Gated mechanosensitive channel<br>**Superfamily:**Gated mechanosensitive channel<br>**Family:**Gated mechanosensitive channel |
| 4 | c3qnqD_ | Alignment |  | 81.4 | 20 | **PDB header:**membrane protein, transport protein<br>**Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component;<br>**PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system |
| 5 | d2b3wa1 | Alignment |  | 23.8 | 43 | **Fold:**YbiA-like<br>**Superfamily:**YbiA-like<br>**Family:**YbiA-like |
| 6 | c1vdfB_ | Alignment |  | 21.4 | 38 | **PDB header:**extracellular matrix protein<br>**Chain:** B: **PDB Molecule:**cartilage oligomeric matrix protein;<br>**PDBTitle:** assembly domain of cartilage oligomeric matrix protein |
| 7 | c3t98A_ | Alignment |  | 20.0 | 31 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**nuclear pore complex protein nup54;<br>**PDBTitle:** molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58 |
| 8 | d1q1va_ | Alignment |  | 11.6 | 17 | **Fold:**Another 3-helical bundle<br>**Superfamily:**DEK C-terminal domain<br>**Family:**DEK C-terminal domain |
| 9 | c2rddB_ | Alignment |  | 10.3 | 7 | **PDB header:**membrane protein/transport protein<br>**Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc;<br>**PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix. |
| 10 | d1xpja_ | Alignment |  | 10.1 | 38 | **Fold:**HAD-like<br>**Superfamily:**HAD-like<br>**Family:**Hypothetical protein VC0232 |
| 11 | d1sh0a_ | Alignment |  | 9.9 | 12 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**RNA-dependent RNA-polymerase |

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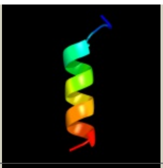
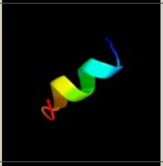
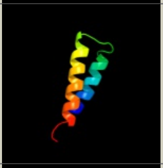
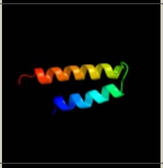
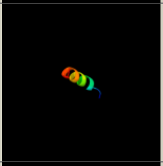
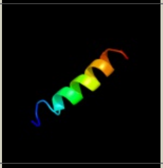
| 12 | c2uutA_ | Alignment |  | 8.7 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**rna-directed rna polymerase;<br>**PDBTitle:** the 2.4 angstrom resolution structure of the d346g mutant2 of the sapporo virus rdrp polymerase |
| 13 | c2lnaA_ | Alignment |  | 8.1 | 38 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**afg3-like protein 2;<br>**PDBTitle:** solution nmr structure of the mitochondrial inner membrane domain2 (residues 164-251), ftsh_ext, from the paraplegin-like protein afg3l23 from homo sapiens, northeast structural genomics consortium target4 hr6741a |
| 14 | d2cazb1 | Alignment |  | 8.0 | 14 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Endosomal sorting complex assembly domain<br>**Family:**VPS28 N-terminal domain |
| 15 | c2cazB_ | Alignment |  | 8.0 | 14 | **PDB header:**protein transport<br>**Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein<br>**PDBTitle:** escrt-i core |
| 16 | c2b43D_ | Alignment |  | 8.0 | 12 | **PDB header:**viral protein<br>**Chain:** D: **PDB Molecule:**non-structural polyprotein;<br>**PDBTitle:** crystal structure of the norwalk virus rna dependent rna polymerase2 from strain hu/nlv/dresden174/1997/ge |
| 17 | c3m91B_ | Alignment |  | 7.4 | 50 | **PDB header:**hydrolase regulator<br>**Chain:** B: **PDB Molecule:**prokaryotic ubiquitin-like protein pup;<br>**PDBTitle:** crystal structure of the prokaryotic ubiquitin-like protein (pup)2 complexed with the amino terminal coiled coil of the mycobacterium3 tuberculosis proteasomal atpase mpa |
| 18 | c3m9dI_ | Alignment |  | 6.8 | 48 | **PDB header:**chaperone<br>**Chain:** I: **PDB Molecule:**prokaryotic ubiquitin-like protein pup;<br>**PDBTitle:** crystal structure of the prokaryotic ubiquitin-like protein pup2 complexed with the hexameric proteasomal atpase mpa which includes3 the amino terminal coiled coil domain and the inter domain |
| 19 | d1khva_ | Alignment |  | 6.8 | 24 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**RNA-dependent RNA-polymerase |
| 20 | c1c94B_ | Alignment |  | 6.7 | 38 | **PDB header:**gene regulation<br>**Chain:** B: **PDB Molecule:**retro-gcn4 leucine zipper;<br>**PDBTitle:** reversing the sequence of the gcn4 leucine zipper does not2 affect its fold. |
| 21 | d2f6mb1 | Alignment | not modelled | 6.7 | 14 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Endosomal sorting complex assembly domain<br>**Family:**VPS28 N-terminal domain |
| 22 | c3p5nA_ | Alignment | not modelled | 6.7 | 14 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**riboflavin uptake protein;<br>**PDBTitle:** structure and mechanism of the s component of a bacterial ecf2 transporter |
| 23 | c3n8uB_ | Alignment | not modelled | 6.1 | 22 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**imelysin peptidase;<br>**PDBTitle:** crystal structure of an imelysin peptidase (bacova_03801) from2 bacteroides ovatus at 1.44 a resolution |
| 24 | c3si5X_ | Alignment | not modelled | 5.8 | 25 | **PDB header:**cell cycle<br>**Chain:** X: **PDB Molecule:**protein casc5;<br>**PDBTitle:** kinetochore-bubr1 kinase complex |
| 25 | c3si5Y_ | Alignment | not modelled | 5.6 | 25 | **PDB header:**cell cycle<br>**Chain:** Y: **PDB Molecule:**protein casc5;<br>**PDBTitle:** kinetochore-bubr1 kinase complex |
| 26 | d2ccqa1 | Alignment | not modelled | 5.4 | 30 | **Fold:**PUG domain-like<br>**Superfamily:**PUG domain-like<br>**Family:**PUG domain |
| 27 | c2l35B_ | Alignment | not modelled | 5.4 | 20 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein;<br>**PDBTitle:** structure of the dap12-nkg2c transmembrane heterotrimer |
| 28 | c2l34B_ | Alignment | not modelled | 5.1 | 20 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein;<br>**PDBTitle:** structure of the dap12 transmembrane homodimer |

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| 29 | c2l34A_ | Alignment | not modelled | 5.1 | 20 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**tyro protein tyrosine kinase-binding protein;<br>**PDBTitle:** structure of the dap12 transmembrane homodimer |