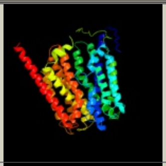
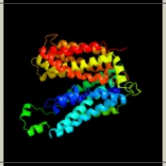
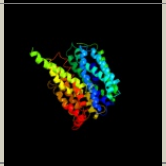
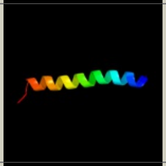
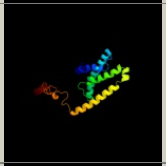
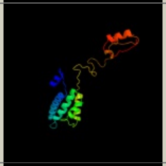
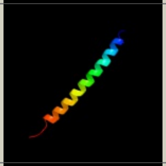
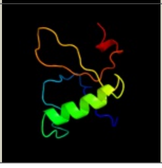
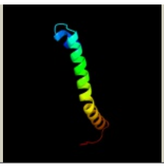
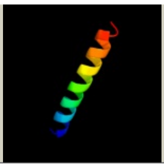
# Phyre2

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0C0L7 |
| Date | Thu Jan 5 11:29:54 GMT 2012 |
| Unique Job ID | 7f08eb684cdf07fd |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1pw4a_ | Alignment |  | 100.0 | 10 | **Fold:**MFS general substrate transporter<br>**Superfamily:**MFS general substrate transporter<br>**Family:**Glycerol-3-phosphate transporter |
| 2 | c3o7pA_ | Alignment |  | 100.0 | 9 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**l-fucose-proton symporter;<br>**PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a) |
| 3 | d1pv7a_ | Alignment |  | 100.0 | 13 | **Fold:**MFS general substrate transporter<br>**Superfamily:**MFS general substrate transporter<br>**Family:**LacY-like proton/sugar symporter |
| 4 | c2gfpA_ | Alignment |  | 100.0 | 13 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**multidrug resistance protein d;<br>**PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli |
| 5 | c2xutC_ | Alignment |  | 99.9 | 9 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**proton/peptide symporter family protein;<br>**PDBTitle:** crystal structure of a proton dependent oligopeptide (pot)2 family transporter. |
| 6 | c1r48A_ | Alignment |  | 97.3 | 100 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**proline/betaine transporter;<br>**PDBTitle:** solution structure of the c-terminal cytoplasmic domain2 residues 468-497 of escherichia coli protein prop |
| 7 | c3b9yA_ | Alignment |  | 50.5 | 13 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein;<br>**PDBTitle:** crystal structure of the nitrosomonas europaea rh protein |
| 8 | c3orgB_ | Alignment |  | 24.5 | 11 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**cmclc;<br>**PDBTitle:** crystal structure of a eukaryotic clc transporter |
| 9 | c2g9pA_ | Alignment |  | 17.1 | 50 | **PDB header:**antimicrobial protein<br>**Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a;<br>**PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom |
| 10 | c2l5gB_ | Alignment |  | 8.6 | 26 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein ncor2;<br>**PDBTitle:** co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207 |
| 11 | d3bz6a2 | Alignment |  | 7.5 | 9 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**PSPTO2686-like |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 12 | c3qnqD_ | Alignment |  | 7.3 | 15 | **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 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 13 | c1a92B_ | Alignment |  | 6.4 | 19 | **PDB header:**leucine zipper<br>**Chain:** B: **PDB Molecule:**delta antigen;<br>**PDBTitle:** oligomerization domain of hepatitis delta antigen |