Phyre$^2$

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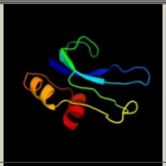
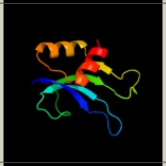
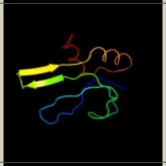
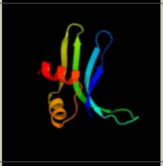
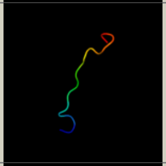
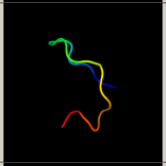
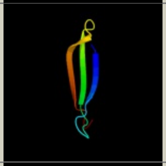
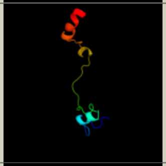
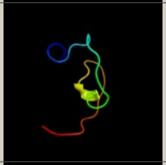
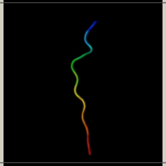
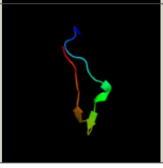
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A7T3 |
| Date | Thu Jan 5 11:06:10 GMT 2012 |
| Unique Job ID | 8a8c7f5a09d526e2 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d2gy9p1 | Alignment |  | 100.0 | 100 | **Fold:**Ribosomal protein S16<br>**Superfamily:**Ribosomal protein S16<br>**Family:**Ribosomal protein S16 |
| 2 | d2uubp1 | Alignment |  | 100.0 | 36 | **Fold:**Ribosomal protein S16<br>**Superfamily:**Ribosomal protein S16<br>**Family:**Ribosomal protein S16 |
| 3 | c3bbnP_ | Alignment |  | 100.0 | 37 | **PDB header:**ribosome<br>**Chain:** P: **PDB Molecule:**ribosomal protein s16;<br>**PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome. |
| 4 | d3bn0a1 | Alignment |  | 100.0 | 29 | **Fold:**Ribosomal protein S16<br>**Superfamily:**Ribosomal protein S16<br>**Family:**Ribosomal protein S16 |
| 5 | d1vbva1 | Alignment |  | 48.4 | 31 | **Fold:**SH3-like barrel<br>**Superfamily:**YccV-like<br>**Family:**YccV-like |
| 6 | c3f62A_ | Alignment |  | 25.7 | 28 | **PDB header:**cytokine<br>**Chain:** A: **PDB Molecule:**interleukin 18 binding protein;<br>**PDBTitle:** crystal structure of human il-18 in complex with ectromelia virus il-2 18 binding protein |
| 7 | c3g0kA_ | Alignment |  | 18.6 | 11 | **PDB header:**ca-binding protein<br>**Chain:** A: **PDB Molecule:**putative membrane protein;<br>**PDBTitle:** crystal structure of a protein of unknown function with a cystatin-2 like fold (saro_2880) from novosphingobium aromaticivorans dsm at3 1.30 a resolution |
| 8 | d1vqol1 | Alignment |  | 10.2 | 28 | **Fold:**Ribosomal proteins L15p and L18e<br>**Superfamily:**Ribosomal proteins L15p and L18e<br>**Family:**Ribosomal proteins L15p and L18e |
| 9 | d2heqa1 | Alignment |  | 10.0 | 37 | **Fold:**SH3-like barrel<br>**Superfamily:**YorP-like<br>**Family:**YorP-like |
| 10 | c3dkxA_ | Alignment |  | 9.7 | 23 | **PDB header:**replication<br>**Chain:** A: **PDB Molecule:**replication protein repb;<br>**PDBTitle:** crystal structure of the replication initiator protein2 encoded on plasmid pmv158 (repb), trigonal form, to 2.7 ang3 resolution |
| 11 | d3cmco2 | Alignment |  | 9.1 | 14 | **Fold:**FwdE/GAPDH domain-like<br>**Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br>**Family:**GAPDH-like |

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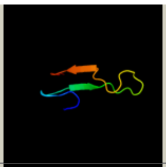
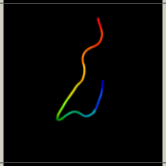
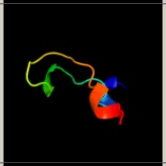
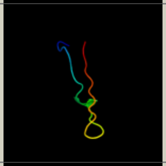
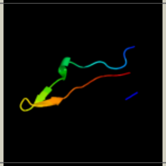
|---|---|---|---|---|---|---|
| 12 | d2dlxa1 | Alignment |  | 8.8 | 10 | **Fold:**Thioredoxin fold<br>**Superfamily:**Thioredoxin-like<br>**Family:**UAS domain |
| 13 | c2v3mF_ | Alignment |  | 7.9 | 36 | **PDB header:**ribosomal protein<br>**Chain:** F: **PDB Molecule:**naf1;<br>**PDBTitle:** structure of the gar1 domain of naf1 |
| 14 | c3ngvA_ | Alignment |  | 7.7 | 24 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**d7 protein;<br>**PDBTitle:** crystal structure of anst-d7l1 |
| 15 | d2pkqo2 | Alignment |  | 7.4 | 11 | **Fold:**FwdE/GAPDH domain-like<br>**Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br>**Family:**GAPDH-like |
| 16 | d1rm4a2 | Alignment |  | 7.1 | 0 | **Fold:**FwdE/GAPDH domain-like<br>**Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br>**Family:**GAPDH-like |
| 17 | c1swiC_ | Alignment |  | 5.9 | 23 | **PDB header:**leucine zipper<br>**Chain:** C: **PDB Molecule:**gcn4p1;<br>**PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene |

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| 18 | c2w2rA_ | Alignment |  | 5.2 | 63 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**matrix protein;<br>**PDBTitle:** structure of the vesicular stomatitis virus matrix protein |