# Phyre$^2$

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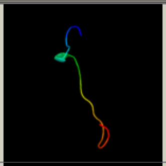
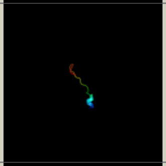
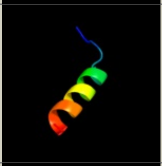
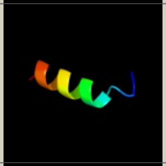
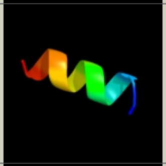
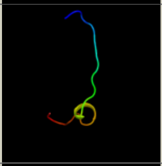
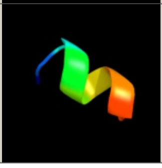
| Email | l.a.kelley@imperial.ac.uk |
| Description | P76157 |
| Date | Thu Jan 5 12:19:49 GMT 2012 |
| Unique Job ID | 399235c9c19b52ac |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1khba1 |  Alignment |  | 42.8 | 65 | **Fold:**PEP carboxykinase-like<br>**Superfamily:**PEP carboxykinase-like<br>**Family:**PEP carboxykinase C-terminal domain |
| 2 | c2qeyA_ |  Alignment |  | 24.5 | 53 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxykinase, cytosolic [gtp];<br>**PDBTitle:** rat cytosolic pepck in complex with gtp |
| 3 | d1pn0a3 |  Alignment |  | 14.5 | 18 | **Fold:**FAD-linked reductases, C-terminal domain<br>**Superfamily:**FAD-linked reductases, C-terminal domain<br>**Family:**PHBH-like |
| 4 | d2gfna1 |  Alignment |  | 8.5 | 17 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 5 | c3bruA_ |  Alignment |  | 7.4 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**regulatory protein, tetr family;<br>**PDBTitle:** crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides |
| 6 | d2g7la1 |  Alignment |  | 7.1 | 21 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 7 | c2zciD_ |  Alignment |  | 7.1 | 53 | **PDB header:**signaling protein, lyase<br>**Chain:** D: **PDB Molecule:**phosphoenolpyruvate carboxykinase [gtp];<br>**PDBTitle:** structure of a gtp-dependent bacterial pep-carboxykinase2 from corynebacterium glutamicum |
| 8 | c2g7lA_ |  Alignment |  | 6.5 | 21 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator;<br>**PDBTitle:** crystal structure of putative transcription regulator sco7704 from2 streptomyces coelicor |
| 9 | c3h4cA_ |  Alignment |  | 6.0 | 33 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription factor tfiib-like;<br>**PDBTitle:** structure of the c-terminal domain of transcription factor iib from2 trypanosoma brucei |
| 10 | c1rqtA_ |  Alignment |  | 5.4 | 44 | **PDB header:**ribosome<br>**Chain:** A: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli |
| 11 | d1rqta_ |  Alignment |  | 5.4 | 44 | **Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain |

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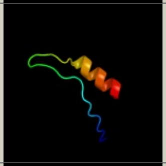
| 12 | c1rqtB_ | Alignment |  | 5.4 | 44 | **PDB header:**ribosome<br>**Chain:** B: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli |
| 13 | d1c4pc_ | Alignment |  | 5.1 | 29 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Staphylokinase/streptokinase<br>**Family:**Staphylokinase/streptokinase |
| 14 | c1bjzA_ | Alignment |  | 5.1 | 36 | **PDB header:**transcription regulation<br>**Chain:** A: **PDB Molecule:**tetracycline repressor;<br>**PDBTitle:** tetracycline chelated mg2+-ion initiates helix unwinding for tet2 repressor induction |

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|---|---|---|---|---|---|---|
| 15 | d2id3a1 | Alignment |  | 5.0 | 38 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |