Phyre$^2$

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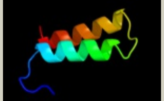
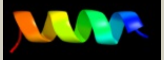
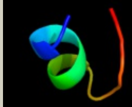
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P52134 |
| Date | Thu Jan 5 12:05:40 GMT 2012 |
| Unique Job ID | aeb84aea492ae7ed |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1ciiA_ | Alignment |  | 64.1 | 20 | **PDB header:**transmembrane protein<br>**Chain:** A: **PDB Molecule:**colicin ia;<br>**PDBTitle:** colicin ia |
| 2 | c3aqpB_ | Alignment |  | 22.1 | 27 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein;<br>**PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus |
| 3 | c1qg9A_ | Alignment |  | 18.9 | 28 | **PDB header:**transmembrane channel<br>**Chain:** A: **PDB Molecule:**protein (sodium channel protein, brain ii alpha<br>**PDBTitle:** second repeat (is2mic) from voltage-gated sodium channel |
| 4 | d1a8ra_ | Alignment |  | 18.0 | 14 | **Fold:**T-fold<br>**Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like<br>**Family:**GTP cyclohydrolase I |
| 5 | d1wpla_ | Alignment |  | 16.3 | 39 | **Fold:**T-fold<br>**Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like<br>**Family:**GTP cyclohydrolase I |
| 6 | c1is7F_ | Alignment |  | 14.7 | 39 | **PDB header:**hydrolase/protein binding<br>**Chain:** F: **PDB Molecule:**gtp cyclohydrolase i;<br>**PDBTitle:** crystal structure of rat gtpchi/gfrp stimulatory complex |
| 7 | c3jzdA_ | Alignment |  | 13.1 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase;<br>**PDBTitle:** crystal structure of putative alcohol dehedrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution |
| 8 | d1jo5a_ | Alignment |  | 13.1 | 18 | **Fold:**Light-harvesting complex subunits<br>**Superfamily:**Light-harvesting complex subunits<br>**Family:**Light-harvesting complex subunits |
| 9 | d1wura1 | Alignment |  | 12.8 | 39 | **Fold:**T-fold<br>**Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like<br>**Family:**GTP cyclohydrolase I |
| 10 | c1wm9D_ | Alignment |  | 12.8 | 39 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**gtp cyclohydrolase i;<br>**PDBTitle:** structure of gtp cyclohydrolase i from thermus thermophilus hb8 |
| 11 | d1ztda1 | Alignment |  | 12.1 | 62 | **Fold:**RNase III domain-like<br>**Superfamily:**RNase III domain-like<br>**Family:**PF0609-like |

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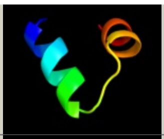
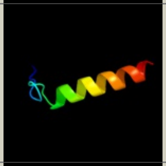
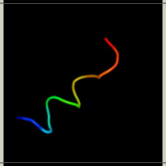
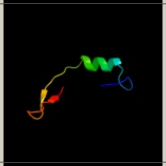
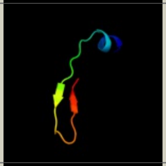
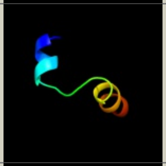
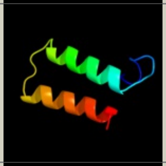
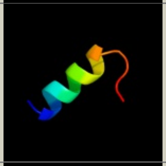
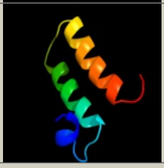
|---|---|---|---|---|---|---|
| 12 | c2xzmO_ | Alignment |  | 9.7 | 27 | **PDB header:**ribosome<br>**Chain:** O: **PDB Molecule:**rps13e;<br>**PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1 |
| 13 | d1rh1a2 | Alignment |  | 9.6 | 20 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Colicin<br>**Family:**Colicin |
| 14 | c2ariA_ | Alignment |  | 9.4 | 58 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**envelope polyprotein gp160;<br>**PDBTitle:** solution structure of micelle-bound fusion domain of hiv-12 gp41 |
| 15 | c1h2dA_ | Alignment |  | 9.2 | 30 | **PDB header:**virus/viral protein<br>**Chain:** A: **PDB Molecule:**matrix protein vp40;<br>**PDBTitle:** ebola virus matrix protein vp40 n-terminal domain in2 complex with rna (low-resolution vp40[31-212] variant). |
| 16 | d1h2ca_ | Alignment |  | 9.0 | 28 | **Fold:**EV matrix protein<br>**Superfamily:**EV matrix protein<br>**Family:**EV matrix protein |
| 17 | c3izbO_ | Alignment |  | 8.6 | 14 | **PDB header:**ribosome<br>**Chain:** O: **PDB Molecule:**40s ribosomal protein rps13 (s15p);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 18 | d1ciia1 | Alignment |  | 7.6 | 18 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Colicin<br>**Family:**Colicin |
| 19 | c1wrgA_ | Alignment |  | 7.1 | 29 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**light-harvesting protein b-880, beta chain;<br>**PDBTitle:** light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum |
| 20 | c2i88A_ | Alignment |  | 6.9 | 15 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**colicin-e1;<br>**PDBTitle:** crystal structure of the channel-forming domain of colicin2 e1 |
| 21 | d2vv5a3 | Alignment | not modelled | 5.8 | 29 | **Fold:**Mechanosensitive channel protein MscS (YggB), transmembrane region<br>**Superfamily:**Mechanosensitive channel protein MscS (YggB), transmembrane region<br>**Family:**Mechanosensitive channel protein MscS (YggB), transmembrane region |