





















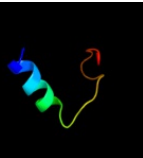




# Phyre2

|               |                              |
|---------------|------------------------------|
| Email         | I.a.kelley@imperial.ac.uk    |
| Description   | P22729                       |
| Date          | Wed Jan 25 15:20:42 GMT 2012 |
| Unique Job ID | bd69bae189549580             |

Detailed template information

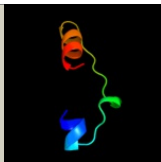
| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c2nq2A_</a> |  Alignment   |    | 97.7       | 13     | <b>PDB header:</b> metal transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical abc transporter permease protein<br><b>PDBTitle:</b> an inward-facing conformation of a putative metal-chelate2 type abc transporter.   |
| 2  | <a href="#">d1l7va_</a> |  Alignment   |    | 96.2       | 17     | <b>Fold:</b> ABC transporter involved in vitamin B12 uptake, BtuC<br><b>Superfamily:</b> ABC transporter involved in vitamin B12 uptake, BtuC<br><b>Family:</b> ABC transporter involved in vitamin B12 uptake, BtuC   |
| 3  | <a href="#">d1pv7a_</a> |  Alignment   |    | 28.8       | 10     | <b>Fold:</b> MFS general substrate transporter<br><b>Superfamily:</b> MFS general substrate transporter<br><b>Family:</b> LacY-like proton/sugar symporter   |
| 4  | <a href="#">d2e74g1</a> |  Alignment   |    | 23.0       | 27     | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> PetG subunit of the cytochrome b6f complex<br><b>Family:</b> PetG subunit of the cytochrome b6f complex   |
| 5  | <a href="#">c3pxpA_</a> |  Alignment |  | 22.3       | 30     | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> helix-turn-helix domain protein;<br><b>PDBTitle:</b> crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution |
| 6  | <a href="#">c2xutC_</a> |  Alignment |  | 13.9       | 6      | <b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> proton/peptide symporter family protein;<br><b>PDBTitle:</b> crystal structure of a proton dependent oligopeptide (pot)2 family transporter.   |
| 7  | <a href="#">c4a18U_</a> |  Alignment |  | 8.1        | 16     | <b>PDB header:</b> ribosome<br><b>Chain:</b> U: <b>PDB Molecule:</b> rpl13;<br><b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1   |
| 8  | <a href="#">c1vf5G_</a> |  Alignment |  | 7.9        | 30     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> G: <b>PDB Molecule:</b> protein pet g;<br><b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.lamosus   |
| 9  | <a href="#">d1vf5g_</a> |  Alignment |  | 7.9        | 30     | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> PetG subunit of the cytochrome b6f complex<br><b>Family:</b> PetG subunit of the cytochrome b6f complex   |
| 10 | <a href="#">c3u5eL_</a> |  Alignment |  | 7.6        | 16     | <b>PDB header:</b> ribosome<br><b>Chain:</b> L: <b>PDB Molecule:</b> 60s ribosomal protein l13-a;<br><b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 resolution   |
| 11 | <a href="#">d1rp1a2</a> |  Alignment |  | 7.2        | 27     | <b>Fold:</b> alpha/beta-Hydrolases<br><b>Superfamily:</b> alpha/beta-Hydrolases<br><b>Family:</b> Pancreatic lipase, N-terminal domain   |

|    |                         |           |   |     |    |   |
|----|-------------------------|-----------|---|-----|----|---|
| 12 | <a href="#">c1y9qA_</a> | Alignment |   | 6.9 | 13 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family;<br><b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae  |
| 13 | <a href="#">c1y6uA_</a> | Alignment |  | 5.7 | 17 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> excisionase from transposon tn916;<br><b>PDBTitle:</b> the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases |
| 14 | <a href="#">d1hpla2</a> | Alignment |  | 5.5 | 23 | <b>Fold:</b> alpha/beta-Hydrolases<br><b>Superfamily:</b> alpha/beta-Hydrolases<br><b>Family:</b> Pancreatic lipase, N-terminal domain  |

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[d1etha2](#)

Alignment



5.2

33

**Fold:**alpha/beta-Hydrolases

**Superfamily:**alpha/beta-Hydrolases

**Family:**Pancreatic lipase, N-terminal domain