

# Phyre2

|               |                             |
|---------------|-----------------------------|
| Email         | I.a.kelley@imperial.ac.uk   |
| Description   | P28246                      |
| Date          | Thu Jan 5 11:44:30 GMT 2012 |
| Unique Job ID | 8d68c86316b499c2            |

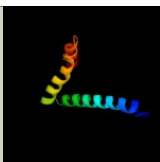
Detailed template information

| # | Template                | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                         |
|---|-------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 | <a href="#">c2gfpA_</a> | <br>Alignment   |    | 100.0      | 21     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein d;<br><b>PDBTitle:</b> structure of the multidrug transporter emrd from2 escherichia coli                                          |
| 2 | <a href="#">d1pw4a_</a> | <br>Alignment   |    | 100.0      | 14     | <b>Fold:</b> MFS general substrate transporter<br><b>Superfamily:</b> MFS general substrate transporter<br><b>Family:</b> Glycerol-3-phosphate transporter                                                                                   |
| 3 | <a href="#">c3o7pA_</a> | <br>Alignment   |    | 100.0      | 13     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-fucose-proton symporter;<br><b>PDBTitle:</b> crystal structure of the e.coli fucose:proton symporter, fucp (n162a)                                           |
| 4 | <a href="#">d1pv7a_</a> | <br>Alignment   |    | 100.0      | 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                                                                                   |
| 5 | <a href="#">c2xutC_</a> | <br>Alignment |  | 100.0      | 14     | <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.                   |
| 6 | <a href="#">c2g9pA_</a> | <br>Alignment |  | 18.8       | 36     | <b>PDB header:</b> antimicrobial protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> antimicrobial peptide laticin 2a;<br><b>PDBTitle:</b> nmr structure of a novel antimicrobial peptide, laticin 2a,2 from spider (lachesana tarabaevi) venom |

7

[d3cx5c2](#)

Alignment



5.9

8

**Fold:** Heme-binding four-helical bundle  
**Superfamily:** Transmembrane di-heme cytochromes  
**Family:** Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)