




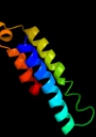



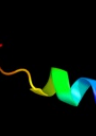

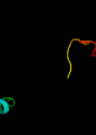

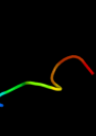

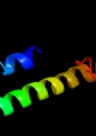




# Phyre2

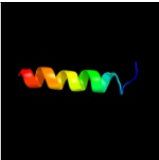
|               |                             |
|---------------|-----------------------------|
| Email         | l.a.kelley@imperial.ac.uk   |
| Description   | P76182                      |
| Date          | Thu Jan 5 12:20:12 GMT 2012 |
| Unique Job ID | 2a3862dcb6c32d9             |

Detailed template information

| # | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|---|-------------------------|---|---|------------|--------|--|
| 1 | <a href="#">c3k3gA_</a> |  Alignment   |    | 27.5       | 24     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> urea transporter;<br><b>PDBTitle:</b> crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea                           |
| 2 | <a href="#">d1iwga8</a> |  Alignment   |    | 23.5       | 9      | <b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain<br><b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain<br><b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain                     |
| 3 | <a href="#">c1oy8A_</a> |  Alignment   |    | 16.5       | 13     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> acriflavine resistance protein b;<br><b>PDBTitle:</b> structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump                       |
| 4 | <a href="#">c2kncA_</a> |  Alignment   |    | 13.2       | 25     | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB;<br><b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex  |
| 5 | <a href="#">c2l0eA_</a> |  Alignment |  | 11.4       | 29     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sodium/hydrogen exchanger 1;<br><b>PDBTitle:</b> structural and functional analysis of tm vi of the nhe1 isoform of the Na <sup>+</sup> /H <sup>+</sup> exchanger |
| 6 | <a href="#">c3knuD_</a> |  Alignment |  | 7.7        | 24     | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> trna (guanine-n(1)-)-methyltransferase;<br><b>PDBTitle:</b> crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum                   |
| 7 | <a href="#">d1jb7a3</a> |  Alignment |  | 6.6        | 67     | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Single strand DNA-binding domain, SSB  |
| 8 | <a href="#">c1ymgA_</a> |  Alignment |  | 5.4        | 21     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> lens fiber major intrinsic protein;<br><b>PDBTitle:</b> the channel architecture of aquaporin o at 2.2 angstrom resolution  |
| 9 | <a href="#">d1ymga1</a> |  Alignment |  | 5.4        | 21     | <b>Fold:</b> Aquaporin-like<br><b>Superfamily:</b> Aquaporin-like<br><b>Family:</b> Aquaporin-like   |

10 [d2axtj1](#)

Alignment



5.3

29

**Fold:**Single transmembrane helix  
**Superfamily:**Photosystem II reaction center protein J, PsbJ  
**Family:**PsbJ-like