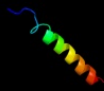
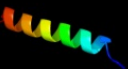
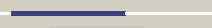
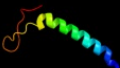


# Phyre2

|               |                             |
|---------------|-----------------------------|
| Email         | l.a.kelley@imperial.ac.uk   |
| Description   | P45566                      |
| Date          | Thu Jan 5 12:03:19 GMT 2012 |
| Unique Job ID | ac56034b96431280            |

Detailed template information

| #  | Template                | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                           |
|----|-------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c1bhbA_</a> | <br>Alignment   |    | 18.9       | 37     | <b>PDB header:</b> photoreceptor<br><b>Chain:</b> A: <b>PDB Molecule:</b> bacteriorhodopsin;<br><b>PDBTitle:</b> three-dimensional structure of (1-71) bacterioopsin2 solubilized in methanol-chloroform and sds micelles3 determined by 15n-1h heteronuclear nmr spectroscopy |
| 2  | <a href="#">c2kv5A_</a> | <br>Alignment   |    | 18.0       | 23     | <b>PDB header:</b> toxin<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein rna1;<br><b>PDBTitle:</b> solution structure of the par toxin fst in dpc micelles                                                                                           |
| 3  | <a href="#">c2kncB_</a> | <br>Alignment   |    | 14.3       | 17     | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3;<br><b>PDBTitle:</b> platelet integrin alfa1iib-beta3 transmembrane-cytoplasmic2 heterocomplex                                                                                       |
| 4  | <a href="#">c2rmzA_</a> | <br>Alignment   |    | 10.9       | 19     | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> integrin beta-3;<br><b>PDBTitle:</b> bicelle-embedded integrin beta3 transmembrane segment                                                                                                           |
| 5  | <a href="#">c2k1aA_</a> | <br>Alignment |  | 10.5       | 20     | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iib;<br><b>PDBTitle:</b> bicelle-embedded integrin alpha(iib) transmembrane segment                                                                                                   |
| 6  | <a href="#">c2kncA_</a> | <br>Alignment |  | 10.1       | 20     | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iib;<br><b>PDBTitle:</b> platelet integrin alfa1iib-beta3 transmembrane-cytoplasmic2 heterocomplex                                                                                    |
| 7  | <a href="#">c3c1iA_</a> | <br>Alignment |  | 8.7        | 20     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ammonia channel;<br><b>PDBTitle:</b> substrate binding, deprotonation and selectivity at the2 periplasmic entrance of the e. coli ammonia channel amtB                                           |
| 8  | <a href="#">d1h5oa_</a> | <br>Alignment |  | 5.9        | 43     | <b>Fold:</b> Defensin-like<br><b>Superfamily:</b> Defensin-like<br><b>Family:</b> Myotoxin                                                                                                                                                                                     |
| 9  | <a href="#">c2d46A_</a> | <br>Alignment |  | 5.8        | 50     | <b>PDB header:</b> metal transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> calcium channel, voltage-dependent, beta 4<br><b>PDBTitle:</b> solution structure of the human beta4a-a domain                                                                                     |
| 10 | <a href="#">d1ehsa_</a> | <br>Alignment |  | 5.6        | 27     | <b>Fold:</b> Toxic hairpin<br><b>Superfamily:</b> Heat-stable enterotoxin B<br><b>Family:</b> Heat-stable enterotoxin B                                                                                                                                                        |
| 11 | <a href="#">c1ufiD_</a> | <br>Alignment |  | 5.5        | 40     | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> major centromere autoantigen b;<br><b>PDBTitle:</b> crystal structure of the dimerization domain of human cenp-b                                                                               |

12

[d1ufia\\_](#)

Alignment



5.2

40

**Fold:**ROP-like  
**Superfamily:**Dimerisation domain of CENP-B  
**Family:**Dimerisation domain of CENP-B