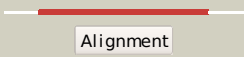
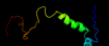
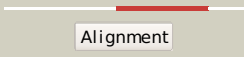

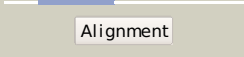

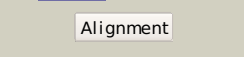

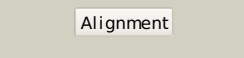

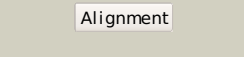

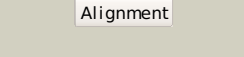

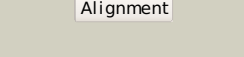


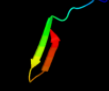


# Phyre2

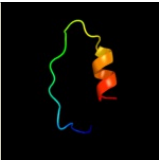
|               |                             |
|---------------|-----------------------------|
| Email         | I.a.kelley@imperial.ac.uk   |
| Description   | P62552                      |
| Date          | Thu Jan 5 12:07:35 GMT 2012 |
| Unique Job ID | 481210cf043dc5f3            |

Detailed template information

| # | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|---|-------------------------|---|---|------------|--------|--|
| 1 | <a href="#">c2adlB_</a> |  Alignment   |    | 100.0      | 96     | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> ccda;<br><b>PDBTitle:</b> solution structure of the bacterial antitoxin ccda:2 implications for dna and toxin binding  |
| 2 | <a href="#">c3g7zD_</a> |  Alignment   |    | 99.8       | 100    | <b>PDB header:</b> toxin/toxin repressor<br><b>Chain:</b> D: <b>PDB Molecule:</b> protein ccda;<br><b>PDBTitle:</b> ccdb dimer in complex with two c-terminal ccda domains   |
| 3 | <a href="#">c2xzmV_</a> |  Alignment   |    | 23.1       | 44     | <b>PDB header:</b> ribosome<br><b>Chain:</b> V: <b>PDB Molecule:</b> rps17e;<br><b>PDBTitle:</b> 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 |
| 4 | <a href="#">c2zouB_</a> |  Alignment   |   | 12.6       | 30     | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> B: <b>PDB Molecule:</b> spondin-1;<br><b>PDBTitle:</b> crystal struture of human f-spondin reeler domain (fragment 2)  |
| 5 | <a href="#">d2db7a1</a> |  Alignment |  | 11.5       | 55     | <b>Fold:</b> Orange domain-like<br><b>Superfamily:</b> Orange domain-like<br><b>Family:</b> Hairy Orange domain  |
| 6 | <a href="#">c3cooB_</a> |  Alignment |  | 10.6       | 30     | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> B: <b>PDB Molecule:</b> spondin-1;<br><b>PDBTitle:</b> the crystal structure of reelin-n domain of f-spondin   |
| 7 | <a href="#">d1qk9a_</a> |  Alignment |  | 9.5        | 24     | <b>Fold:</b> DNA-binding domain<br><b>Superfamily:</b> DNA-binding domain<br><b>Family:</b> Methyl-CpG-binding domain, MBD   |
| 8 | <a href="#">c3d0wD_</a> |  Alignment |  | 6.6        | 22     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> D: <b>PDB Molecule:</b> yflh protein;<br><b>PDBTitle:</b> crystal structure of yflh protein from bacillus subtilis.2 northeast structural genomics consortium target sr326                       |
| 9 | <a href="#">c2i3eA_</a> |  Alignment |  | 5.7        | 30     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> g-rich;<br><b>PDBTitle:</b> solution structure of catalytic domain of goldfish rich2 protein   |

10 [d1wz3a1](#)

Alignment



5.4

24

**Fold:**beta-Grasp (ubiquitin-like)  
**Superfamily:**Ubiquitin-like  
**Family:**APG12-like