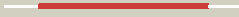
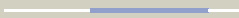
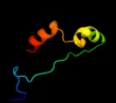
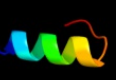
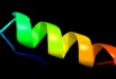
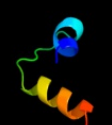


# Phyre2

|               |                             |
|---------------|-----------------------------|
| Email         | I.a.kelley@imperial.ac.uk   |
| Description   | P0ADP9                      |
| Date          | Thu Jan 5 11:21:31 GMT 2012 |
| Unique Job ID | de76755bb9aecb1b            |

Detailed template information

| #  | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                                                                                 |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c2ko6A_</a> |  Alignment   |    | 100.0      | 99     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yihd;<br><b>PDBTitle:</b> solution structure of protein sf3929 from shigella flexneri 2.2a. northeast structural genomics consortium target3 sfr81/ontario center for structural proteomics target4 sf3929 |
| 2  | <a href="#">d2ibge1</a> |  Alignment   |    | 29.6       | 40     | <b>Fold:</b> Hedgehog/DD-peptidase<br><b>Superfamily:</b> Hedgehog/DD-peptidase<br><b>Family:</b> Hedgehog (development protein), N-terminal signaling domain                                                                                                                                                                        |
| 3  | <a href="#">d1ufwa_</a> |  Alignment   |    | 29.3       | 31     | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> RNA-binding domain, RBD<br><b>Family:</b> Canonical RBD                                                                                                                                                                                                                          |
| 4  | <a href="#">c3m1nB_</a> |  Alignment   |    | 25.7       | 40     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> sonic hedgehog protein;<br><b>PDBTitle:</b> crystal structure of human sonic hedgehog n-terminal domain                                                                                                                                                |
| 5  | <a href="#">d3d1ma1</a> |  Alignment |  | 24.7       | 40     | <b>Fold:</b> Hedgehog/DD-peptidase<br><b>Superfamily:</b> Hedgehog/DD-peptidase<br><b>Family:</b> Hedgehog (development protein), N-terminal signaling domain                                                                                                                                                                        |
| 6  | <a href="#">d1iasa_</a> |  Alignment |  | 15.6       | 19     | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit                                                                                                                                                                                 |
| 7  | <a href="#">c1dpuA_</a> |  Alignment |  | 13.9       | 22     | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a (rpa32) c-terminal domain;<br><b>PDBTitle:</b> solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)                                                                                          |
| 8  | <a href="#">d1dpua_</a> |  Alignment |  | 13.9       | 22     | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> C-terminal domain of RPA32                                                                                                                                                                                  |
| 9  | <a href="#">c2kxhB_</a> |  Alignment |  | 10.6       | 54     | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> peptide of far upstream element-binding protein 1;<br><b>PDBTitle:</b> solution structure of the first two rrm domains of fir in the complex2 with fbp nbx peptide                                                                                       |
| 10 | <a href="#">d2cpga_</a> |  Alignment |  | 10.1       | 35     | <b>Fold:</b> Ribbon-helix-helix<br><b>Superfamily:</b> Ribbon-helix-helix<br><b>Family:</b> CopG-like                                                                                                                                                                                                                                |
| 11 | <a href="#">d2ayxa2</a> |  Alignment |  | 10.1       | 32     | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> RcsC linker domain-like                                                                                                                                                                                                                              |

|    |                         |           |                                                                                     |     |    |                                                                                                                                                                                                                                                                                        |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|-----|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c1ygmA_</a> | Alignment |    | 9.1 | 39 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein bsu31320;<br><b>PDBTitle:</b> nmr structure of mistic                                                                                                                                |
| 13 | <a href="#">c2noxP_</a> | Alignment |    | 8.6 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> P: <b>PDB Molecule:</b> tryptophan 2,3-dioxygenase;<br><b>PDBTitle:</b> crystal structure of tryptophan 2,3-dioxygenase from ralstonia2 metallidurans                                                                               |
| 14 | <a href="#">d1bl0a2</a> | Alignment |    | 7.9 | 31 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> AraC type transcriptional activator                                                                                                                                            |
| 15 | <a href="#">c3kzqE_</a> | Alignment |    | 7.7 | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> E: <b>PDB Molecule:</b> putative uncharacterized protein vp2116;<br><b>PDBTitle:</b> the crystal structure of the protein with unknown function from vibrio2 parahaemolyticus rimd 2210633                   |
| 16 | <a href="#">c3db3A_</a> | Alignment |    | 7.5 | 33 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase uhrf1;<br><b>PDBTitle:</b> crystal structure of the tandem tudor domains of the e3 ubiquitin-2 protein ligase uhrf1 in complex with trimethylated histone h3-k93 peptide                |
| 17 | <a href="#">d1r4wa_</a> | Alignment |   | 7.3 | 22 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> DsbA-like                                                                                                                                                                                      |
| 18 | <a href="#">d1kz7a2</a> | Alignment |  | 7.2 | 44 | <b>Fold:</b> PH domain-like barrel<br><b>Superfamily:</b> PH domain-like<br><b>Family:</b> Pleckstrin-homology domain (PH domain)                                                                                                                                                      |
| 19 | <a href="#">d1aopa4</a> | Alignment |  | 6.9 | 18 | <b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like                                                                            |
| 20 | <a href="#">c2in3A_</a> | Alignment |  | 6.9 | 25 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein;<br><b>PDBTitle:</b> crystal structure of a putative protein disulfide isomerase from2 nitrosomonas europaea                                                                                |
| 21 | <a href="#">c1yzxB_</a> | Alignment | not modelled                                                                        | 6.3 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase kappa 1;<br><b>PDBTitle:</b> crystal structure of human kappa class glutathione2 transferase                                                                                         |
| 22 | <a href="#">c2nw7C_</a> | Alignment | not modelled                                                                        | 5.3 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> tryptophan 2,3-dioxygenase;<br><b>PDBTitle:</b> crystal structure of tryptophan 2,3-dioxygenase (tdo) from2 xanthomonas campestris in complex with ferric heme.3 northeast structural genomics target xcr13 |
| 23 | <a href="#">c2htfA_</a> | Alignment | not modelled                                                                        | 5.2 | 50 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase mu;<br><b>PDBTitle:</b> the solution structure of the brct domain from human2 polymerase reveals homology with the tdt brct domain                                                              |
| 24 | <a href="#">d2ivya1</a> | Alignment | not modelled                                                                        | 5.1 | 21 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> TTP0101/SSO1404-like<br><b>Family:</b> TTP0101/SSO1404-like                                                                                                                                                                        |
| 25 | <a href="#">d1d5ya2</a> | Alignment | not modelled                                                                        | 5.1 | 24 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> AraC type transcriptional activator                                                                                                                                            |