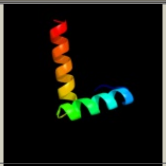
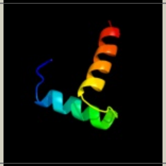
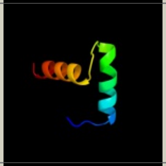
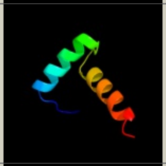
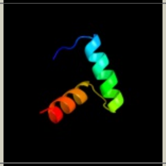
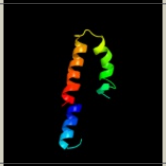
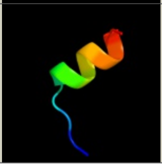
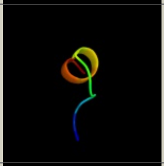
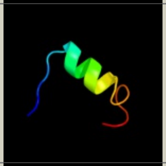
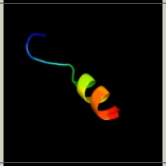
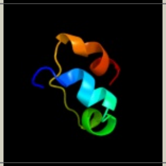
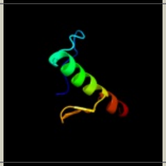
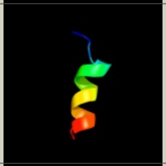
Phyre$^2$

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | Q2EES0 |
| Date | Thu Jan 5 12:33:46 GMT 2012 |
| Unique Job ID | 73c381edb32bc020 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d2bj7a1 | Alignment |  | 70.8 | 20 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**CopG-like |
| 2 | d2hzab1 | Alignment |  | 63.3 | 21 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**CopG-like |
| 3 | d2hzaa1 | Alignment |  | 55.8 | 19 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**CopG-like |
| 4 | c2ca9B_ | Alignment |  | 48.9 | 14 | **PDB header:**transcriptional regulation<br>**Chain:** B: **PDB Molecule:**putative nickel-responsive regulator;<br>**PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation |
| 5 | c2bj3D_ | Alignment |  | 39.6 | 22 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**nickel responsive regulator;<br>**PDBTitle:** nikr-apo |
| 6 | c1q5vB_ | Alignment |  | 33.3 | 20 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**nickel responsive regulator;<br>**PDBTitle:** apo-nikr |
| 7 | d1y9ba1 | Alignment |  | 25.3 | 14 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**VCA0319-like |
| 8 | d2i5ua1 | Alignment |  | 24.0 | 12 | **Fold:**DnaD domain-like<br>**Superfamily:**DnaD domain-like<br>**Family:**DnaD domain |
| 9 | d1qu3a1 | Alignment |  | 21.6 | 12 | **Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br>**Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br>**Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases |
| 10 | c1wn4A_ | Alignment |  | 20.9 | 38 | **PDB header:**plant protein<br>**Chain:** A: **PDB Molecule:**vontr protein;<br>**PDBTitle:** nmr structure of vontr |
| 11 | d1ku2a1 | Alignment |  | 17.9 | 50 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma3 domain |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | c2lf0A_ | Alignment |  | 16.7 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein yibl;<br>**PDBTitle:** solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scatting, nesg4 target sfr339/ocsp target sf3636 |
| 13 | d2c5ra1 | Alignment |  | 16.3 | 50 | **Fold:**Phage replication organizer domain<br>**Superfamily:**Phage replication organizer domain<br>**Family:**Phage replication organizer domain |
| 14 | d1mnta_ | Alignment |  | 15.8 | 27 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**Arc/Mnt-like phage repressors |
| 15 | c2k53A_ | Alignment |  | 14.4 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**a3dk08 protein;<br>**PDBTitle:** nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9 |
| 16 | c2agaA_ | Alignment |  | 14.3 | 38 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**machado-joseph disease protein 1;<br>**PDBTitle:** de-ubiquitinating function of ataxin-3: insights from the2 solution structure of the josephin domain |
| 17 | c2y0fD_ | Alignment |  | 10.7 | 9 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase;<br>**PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27 |
| 18 | c2l3yA_ | Alignment |  | 9.9 | 27 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**interleukin-6;<br>**PDBTitle:** solution structure of mouse il-6 |
| 19 | d1m56d_ | Alignment |  | 8.6 | 27 | **Fold:**Single transmembrane helix<br>**Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV<br>**Family:**Bacterial aa3 type cytochrome c oxidase subunit IV |
| 20 | d1yzma1 | Alignment |  | 8.4 | 18 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Rabenosyn-5 Rab-binding domain-like<br>**Family:**Rabenosyn-5 Rab-binding domain-like |
| 21 | d1pd3a_ | Alignment | not modelled | 8.1 | 60 | **Fold:**ROP-like<br>**Superfamily:**Nonstructural protein ns2, Nep, M1-binding domain<br>**Family:**Nonstructural protein ns2, Nep, M1-binding domain |
| 22 | c2p22D_ | Alignment | not modelled | 8.1 | 22 | **PDB header:**transport protein<br>**Chain:** D: **PDB Molecule:**hypothetical 12.0 kda protein in ade3-ser2<br>**PDBTitle:** structure of the yeast escrt-i heterotetramer core |
| 23 | d1i1rb_ | Alignment | not modelled | 7.8 | 58 | **Fold:**4-helical cytokines<br>**Superfamily:**4-helical cytokines<br>**Family:**Long-chain cytokines |
| 24 | d1mg7a2 | Alignment | not modelled | 7.4 | 25 | **Fold:**Ferredoxin-like<br>**Superfamily:**GHMP Kinase, C-terminal domain<br>**Family:**Early switch protein XOL-1 |
| 25 | d1kkea1 | Alignment | not modelled | 7.2 | 41 | **Fold:**Triple beta-spiral<br>**Superfamily:**Fibre shaft of virus attachment proteins<br>**Family:**Reovirus attachment protein sigma 1 |
| 26 | d1ivsa2 | Alignment | not modelled | 7.1 | 21 | **Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br>**Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br>**Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases |
| 27 | d1z0kb1 | Alignment | not modelled | 6.6 | 25 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Rabenosyn-5 Rab-binding domain-like<br>**Family:**Rabenosyn-5 Rab-binding domain-like |
| 28 | d3saka_ | Alignment | not modelled | 6.4 | 43 | **Fold:**p53 tetramerization domain<br>**Superfamily:**p53 tetramerization domain<br>**Family:**p53 tetramerization domain |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 29 | d1mvfd_ | Alignment | not modelled | 6.4 | 23 | **Fold:**Double-split beta-barrel<br>**Superfamily:**AbrB/MazE/MraZ-like<br>**Family:**Kis/PemI addiction antidote |
| 30 | d1az3a_ | Alignment | not modelled | 6.0 | 42 | **Fold:**Restriction endonuclease-like<br>**Superfamily:**Restriction endonuclease-like<br>**Family:**Restriction endonuclease EcoRV |
| 31 | d1vq3a_ | Alignment | not modelled | 5.8 | 33 | **Fold:**PurS-like<br>**Superfamily:**PurS-like<br>**Family:**PurS subunit of FGAM synthetase |
| 32 | d1ffya1 | Alignment | not modelled | 5.7 | 12 | **Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br>**Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br>**Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases |
| 33 | c3kz5E_ | Alignment | not modelled | 5.7 | 43 | **PDB header:**dna binding protein<br>**Chain:** E: **PDB Molecule:**protein sopb;<br>**PDBTitle:** structure of cdomain |
| 34 | d1gs0a1 | Alignment | not modelled | 5.5 | 20 | **Fold:**Domain of poly(ADP-ribose) polymerase<br>**Superfamily:**Domain of poly(ADP-ribose) polymerase<br>**Family:**Domain of poly(ADP-ribose) polymerase |
| 35 | c1u9pA_ | Alignment | not modelled | 5.3 | 13 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**parc;<br>**PDBTitle:** permuted single-chain arc |
| 36 | c3ostA_ | Alignment | not modelled | 5.2 | 27 | **PDB header:**lipid binding protein<br>**Chain:** A: **PDB Molecule:**serine/threonine-protein kinase kcc4;<br>**PDBTitle:** structure of the kinase associated-1 (ka1) from kcc4p |