



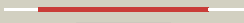








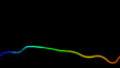

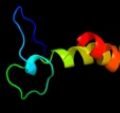

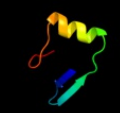



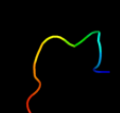




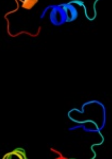


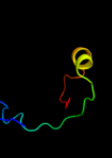
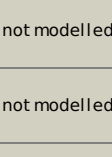


| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c2eeyA_</a> |  Alignment   |    | 100.0      | 50     | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis;<br><b>PDBTitle:</b> structure of gk0241 protein from geobacillus kaustophilus   |
| 2  | <a href="#">c2ideE_</a> |  Alignment   |    | 100.0      | 54     | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> molybdenum cofactor biosynthesis protein c;<br><b>PDBTitle:</b> crystal structure of the molybdenum cofactor biosynthesis protein c2 (ttha1789) from thermus thermophilus hb8   |
| 3  | <a href="#">d1ekra_</a> |  Alignment   |    | 100.0      | 100    | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> Molybdenum cofactor biosynthesis protein C, MoaC<br><b>Family:</b> Molybdenum cofactor biosynthesis protein C, MoaC  |
| 4  | <a href="#">c2eknC_</a> |  Alignment   |   | 100.0      | 41     | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> probable molybdenum cofactor biosynthesis protein c;<br><b>PDBTitle:</b> structure of ph1811 protein from pyrococcus horikoshii   |
| 5  | <a href="#">c2ohdB_</a> |  Alignment |  | 100.0      | 45     | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable molybdenum cofactor biosynthesis protein c;<br><b>PDBTitle:</b> crystal structure of hypothetical molybdenum cofactor biosynthesis2 protein c from sulfolobus tokodaii |
| 6  | <a href="#">c1sfeA_</a> |  Alignment |  | 37.0       | 15     | <b>PDB header:</b> dna-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ada o6-methylguanine-dna methyltransferase;<br><b>PDBTitle:</b> ada o6-methylguanine-dna methyltransferase from escherichia coli   |
| 7  | <a href="#">d1oh4a_</a> |  Alignment |  | 33.7       | 43     | <b>Fold:</b> Galactose-binding domain-like<br><b>Superfamily:</b> Galactose-binding domain-like<br><b>Family:</b> Family 27 carbohydrate binding module, CBM27   |
| 8  | <a href="#">c3ct5A_</a> |  Alignment |  | 31.7       | 30     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> morphogenesis protein 1;<br><b>PDBTitle:</b> crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail  |
| 9  | <a href="#">d2cqaa1</a> |  Alignment |  | 22.5       | 15     | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> TIP49 domain   |
| 10 | <a href="#">d1bu2a2</a> |  Alignment |  | 14.8       | 47     | <b>Fold:</b> Cyclin-like<br><b>Superfamily:</b> Cyclin-like<br><b>Family:</b> Cyclin   |
| 11 | <a href="#">c2b5IC_</a> |  Alignment |  | 13.0       | 31     | <b>PDB header:</b> protein binding/viral protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> nonstructural protein v;<br><b>PDBTitle:</b> crystal structure of ddb1 in complex with simian virus 5 v2 protein   |

|    |                         |           |   |   |    |  |
|----|-------------------------|-----------|---|---|----|--|
| 12 | <a href="#">dlvqon1</a> | Alignment |     | 11.1  | 15 | <b>Fold:</b> Ribonuclease H-like motif<br><b>Superfamily:</b> Translational machinery components<br><b>Family:</b> Ribosomal protein L18 and S11   |
| 13 | <a href="#">c3pn1A</a>  | Alignment |    | 10.3  | 19 | <b>PDB header:</b> ligase/ligase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase;<br><b>PDBTitle:</b> novel bacterial nad+-dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo |
| 14 | <a href="#">c2p0xA</a>  | Alignment |    | 9.2   | 75 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> abiotic atp-binding, folding optimized protein;<br><b>PDBTitle:</b> solution structure of a non-biological atp-binding protein                               |
| 15 | <a href="#">c3bdqB</a>  | Alignment |    | 9.0   | 24 | <b>PDB header:</b> lipid transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> sterol carrier protein 2-like 2;<br><b>PDBTitle:</b> room tempreture crystal structure of sterol carrier protein-2 2 like-2                                  |
| 16 | <a href="#">c2xuvB</a>  | Alignment |    | 8.8   | 22 | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> hdeb;<br><b>PDBTitle:</b> the structure of hdeb   |
| 17 | <a href="#">d1lka</a>   | Alignment |   | 8.1   | 14 | <b>Fold:</b> SCP-like<br><b>Superfamily:</b> SCP-like<br><b>Family:</b> Sterol carrier protein, SCP  |
| 18 | <a href="#">d2f1fa2</a> | Alignment |  | 7.9   | 20 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> IlvH-like   |
| 19 | <a href="#">c2xskA</a>  | Alignment |  | 7.7   | 28 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> csgc;<br><b>PDBTitle:</b> e. coli curli protein csgc - secys   |
| 20 | <a href="#">d2gp4a1</a> | Alignment |  | 7.6   | 25 | <b>Fold:</b> The "swivelling" beta/beta/alpha domain<br><b>Superfamily:</b> LeuD/IlvD-like<br><b>Family:</b> IlvD/EDD C-terminal domain-like   |
| 21 | <a href="#">d2bbya</a>  | Alignment | not modelled  | 7.1   | 4  | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> DNA-binding domain from rap30   |
| 22 | <a href="#">c2ketA</a>  | Alignment | not modelled  | 7.1   | 45 | <b>PDB header:</b> antibiotic<br><b>Chain:</b> A: <b>PDB Molecule:</b> cathelicidin-6;<br><b>PDBTitle:</b> solution structure of bmap-27   |
| 23 | <a href="#">c2kc5A</a>  | Alignment | not modelled  | 7.0   | 13 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase-2 operon protein hybe;<br><b>PDBTitle:</b> solution structure of hybe from escherichia coli  |
| 24 | <a href="#">d1pz4a</a>  | Alignment | not modelled  | 6.9   | 23 | <b>Fold:</b> SCP-like<br><b>Superfamily:</b> SCP-like<br><b>Family:</b> Sterol carrier protein, SCP  |
| 25 | <a href="#">c1z4hA</a>  | Alignment | not modelled  | 6.9   | 32 | <b>PDB header:</b> protein binding, dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> tor inhibition protein;<br><b>PDBTitle:</b> the response regulator tori belongs to a new family of2 atypical excisionase                |
| 26 | <a href="#">d1vlfn1</a> | Alignment | not modelled  | 6.8   | 29 | <b>Fold:</b> Prealbumin-like<br><b>Superfamily:</b> Cna protein B-type domain<br><b>Family:</b> Cna protein B-type domain  |
| 27 | <a href="#">c2p09A</a>  | Alignment | not modelled  | 6.7   | 75 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> a non-biological atp binding protein with two mutations<br><b>PDBTitle:</b> structural insights into the evolution of a non-biological protein               |
| 28 | <a href="#">d1wzua1</a> | Alignment | not modelled  | 6.4   | 38 | <b>Fold:</b> NadA-like<br><b>Superfamily:</b> NadA-like<br><b>Family:</b> NadA-like  |
|    |                         |           |   | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains |    |  |

|    |                         |           |              |     |    |   |
|----|-------------------------|-----------|--------------|-----|----|---|
| 29 | <a href="#">d1uufa2</a> | Alignment | not modelled | 6.1 | 20 | <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain  |
| 30 | <a href="#">d4bcla</a>  | Alignment | not modelled | 5.9 | 23 | <b>Fold:</b> Bacteriochlorophyll A protein<br><b>Superfamily:</b> Bacteriochlorophyll A protein<br><b>Family:</b> Bacteriochlorophyll A protein   |
| 31 | <a href="#">c2gp4A</a>  | Alignment | not modelled | 5.8 | 25 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydratase;<br><b>PDBTitle:</b> structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis |
| 32 | <a href="#">d1juva</a>  | Alignment | not modelled | 5.7 | 9  | <b>Fold:</b> Dihydrofolate reductase-like<br><b>Superfamily:</b> Dihydrofolate reductase-like<br><b>Family:</b> Dihydrofolate reductases  |
| 33 | <a href="#">d1cq3a</a>  | Alignment | not modelled | 5.2 | 83 | <b>Fold:</b> Soluble secreted chemokine inhibitor, VCCI<br><b>Superfamily:</b> Soluble secreted chemokine inhibitor, VCCI<br><b>Family:</b> Soluble secreted chemokine inhibitor, VCCI                                      |