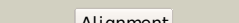
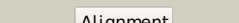
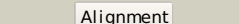
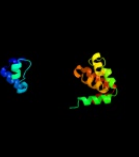


Detailed template information

| #  | Template                | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                          |
|----|-------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c3hjlA_</a> | <br>Alignment   |    | 100.0      | 28     | <b>PDB header:</b> proton transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> flagellar motor switch protein flig;<br><b>PDBTitle:</b> the structure of full-length flig from aquifex aeolicus |
| 2  | <a href="#">c3pl4A_</a> | <br>Alignment   |    | 100.0      | 31     | <b>PDB header:</b> motor protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> flagellar motor switch protein;<br><b>PDBTitle:</b> crystal structure of flig (residue 116-343) from h. pylori      |
| 3  | <a href="#">c3pkrA_</a> | <br>Alignment   |    | 100.0      | 33     | <b>PDB header:</b> motor protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> flagellar motor switch protein;<br><b>PDBTitle:</b> crystal structure of flig (residue 86-343) from h. pylori       |
| 4  | <a href="#">d1lkvx_</a> | <br>Alignment   |    | 100.0      | 42     | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> FlIG<br><b>Family:</b> FlIG                                                                                                        |
| 5  | <a href="#">d1qc7a_</a> | <br>Alignment |  | 100.0      | 53     | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> FlIG<br><b>Family:</b> FlIG                                                                                                        |
| 6  | <a href="#">d1qc7b_</a> | <br>Alignment |  | 100.0      | 54     | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> FlIG<br><b>Family:</b> FlIG                                                                                                        |
| 7  | <a href="#">c3sohB_</a> | <br>Alignment |  | 99.8       | 29     | <b>PDB header:</b> motor protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> flagellar motor switch protein flig;<br><b>PDBTitle:</b> architecture of the flagellar rotor                        |
| 8  | <a href="#">d2ouxal</a> | <br>Alignment |  | 98.5       | 15     | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> MgtE N-terminal domain-like<br><b>Family:</b> MgtE N-terminal domain-like                                                          |
| 9  | <a href="#">c2ouxB_</a> | <br>Alignment |  | 98.3       | 15     | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> magnesium transporter;<br><b>PDBTitle:</b> crystal structure of the soluble part of a magnesium transporter     |
| 10 | <a href="#">d2yvxa1</a> | <br>Alignment |  | 98.1       | 14     | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> MgtE N-terminal domain-like<br><b>Family:</b> MgtE N-terminal domain-like                                                          |
| 11 | <a href="#">c2vxD_</a>  | <br>Alignment |  | 96.7       | 21     | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> mg2+ transporter mgte;<br><b>PDBTitle:</b> crystal structure of magnesium transporter mgte                      |

|    |                         |           |                                                                                     |                                      |    |                                                                                                                                                                                                                                                      |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|--------------------------------------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c2yvzA_</a> | Alignment |     | 96.6                                 | 17 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> mg2+ transporter mgte;<br><b>PDBTitle:</b> crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form                                           |
| 13 | <a href="#">c3b37A_</a> | Alignment |    | 94.3                                 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n;<br><b>PDBTitle:</b> crystal structure of e. coli aminopeptidase n in complex with tyrosine                                                                   |
| 14 | <a href="#">c2kn6A_</a> | Alignment |    | 87.2                                 | 13 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> apoptosis-associated speck-like protein containing a card;<br><b>PDBTitle:</b> structure of full-length human asc (apoptosis-associated speck-like2 protein containing a card) |
| 15 | <a href="#">c3ebhA_</a> | Alignment |    | 78.2                                 | 8  | <b>PDB header:</b> hydrolase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> m1 family aminopeptidase;<br><b>PDBTitle:</b> structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin                                         |
| 16 | <a href="#">c1hjpA_</a> | Alignment |    | 76.2                                 | 12 | <b>PDB header:</b> dna recombination<br><b>Chain:</b> A: <b>PDB Molecule:</b> ruva;<br><b>PDBTitle:</b> holliday junction binding protein ruva from e. coli                                                                                          |
| 17 | <a href="#">c1d8lA_</a> | Alignment |   | 72.0                                 | 13 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (holliday junction dna helicase ruva);<br><b>PDBTitle:</b> e. coli holliday junction binding protein ruva nh2 region2 lacking domain iii                         |
| 18 | <a href="#">d1cuka2</a> | Alignment |  | 70.9                                 | 13 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> RuvA domain 2-like<br><b>Family:</b> DNA helicase RuvA subunit, middle domain                                                                                                                    |
| 19 | <a href="#">d1ixra1</a> | Alignment |  | 56.9                                 | 16 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> RuvA domain 2-like<br><b>Family:</b> DNA helicase RuvA subunit, middle domain                                                                                                                    |
| 20 | <a href="#">c2h5xA_</a> | Alignment |  | 56.6                                 | 12 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruva;<br><b>PDBTitle:</b> ruva from mycobacterium tuberculosis                                                          |
| 21 | <a href="#">d1bvsa2</a> | Alignment | not modelled                                                                        | 56.3                                 | 14 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> RuvA domain 2-like<br><b>Family:</b> DNA helicase RuvA subunit, middle domain                                                                                                                    |
| 22 | <a href="#">c2x49A_</a> | Alignment | not modelled                                                                        | 49.4                                 | 18 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> invasion protein inva;<br><b>PDBTitle:</b> crystal structure of the c-terminal domain of inva                                                                          |
| 23 | <a href="#">c1ixrA_</a> | Alignment | not modelled                                                                        | 49.4                                 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction dna helicase ruva;<br><b>PDBTitle:</b> ruva-ruvb complex                                                                                                     |
| 24 | <a href="#">d1bh9b_</a> | Alignment | not modelled                                                                        | 46.4                                 | 20 | <b>Fold:</b> Histone-fold<br><b>Superfamily:</b> Histone-fold<br><b>Family:</b> TBP-associated factors, TAFs                                                                                                                                         |
| 25 | <a href="#">c3lk2B_</a> | Alignment | not modelled                                                                        | 38.7                                 | 14 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> f-actin-capping protein subunit beta isoforms 1 and 2;<br><b>PDBTitle:</b> crystal structure of capz bound to the uncapping motif from carmil                            |
| 26 | <a href="#">d1iznb_</a> | Alignment | not modelled                                                                        | 34.2                                 | 14 | <b>Fold:</b> Subunits of heterodimeric actin filament capping protein Capz<br><b>Superfamily:</b> Subunits of heterodimeric actin filament capping protein Capz<br><b>Family:</b> Capz beta-1 subunit                                                |
| 27 | <a href="#">d2af7a1</a> | Alignment | not modelled                                                                        | 33.6                                 | 18 | <b>Fold:</b> AhpD-like<br><b>Superfamily:</b> AhpD-like<br><b>Family:</b> CMD-like                                                                                                                                                                   |
| 28 | <a href="#">d1szaa_</a> | Alignment | not modelled                                                                        | 28.0                                 | 8  | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> ENTH/VHS domain<br><b>Family:</b> RPR domain (SMART 00582 )                                                                                                                               |
|    |                         |           |                                                                                     | <b>PDB header:</b> transport protein |    |                                                                                                                                                                                                                                                      |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                                                                |
|----|-------------------------|-----------|--------------|------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | <a href="#">c3kxrA</a>  | Alignment | not modelled | 27.6 | 22 | <b>Chain:</b> A: <b>PDB Molecule:</b> magnesium transporter, putative;<br><b>PDBTitle:</b> structure of the cystathionine beta-synthase pair domain of the2 putative mg2+ transporter so5017 from shewanella oneidensis mr-1.                                                                                                                  |
| 30 | <a href="#">c1lj2B</a>  | Alignment | not modelled | 26.2 | 21 | <b>PDB header:</b> viral protein/ translation<br><b>Chain:</b> B: <b>PDB Molecule:</b> nonstructural rna-binding protein 34;<br><b>PDBTitle:</b> recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization                                                                                                              |
| 31 | <a href="#">c2w9yA</a>  | Alignment | not modelled | 24.7 | 9  | <b>PDB header:</b> lipid transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid/retinol binding protein protein 7,<br><b>PDBTitle:</b> the structure of the lipid binding protein ce-far-7 from2 caenorhabditis elegans                                                                                                                 |
| 32 | <a href="#">d1x2ia1</a> | Alignment | not modelled | 24.2 | 18 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> RuvA domain 2-like<br><b>Family:</b> Hef domain-like                                                                                                                                                                                                                                       |
| 33 | <a href="#">c2kvcA</a>  | Alignment | not modelled | 23.8 | 18 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a                 |
| 34 | <a href="#">c2lkyA</a>  | Alignment | not modelled | 23.7 | 6  | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution structure of msme_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target myma.17112.b |
| 35 | <a href="#">d1mpga1</a> | Alignment | not modelled | 23.5 | 13 | <b>Fold:</b> DNA-glycosylase<br><b>Superfamily:</b> DNA-glycosylase<br><b>Family:</b> DNA repair glycosylase, 2 C-terminal domains                                                                                                                                                                                                             |
| 36 | <a href="#">d2i0za2</a> | Alignment | not modelled | 23.4 | 16 | <b>Fold:</b> HI0933 insert domain-like<br><b>Superfamily:</b> HI0933 insert domain-like<br><b>Family:</b> HI0933 insert domain-like                                                                                                                                                                                                            |
| 37 | <a href="#">c3thgA</a>  | Alignment | not modelled | 20.8 | 3  | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> ribulose biphosphate carboxylase/oxygenase activase 1,<br><b>PDBTitle:</b> crystal structure of the creosote rubisco activase c-domain                                                                                                                             |
| 38 | <a href="#">c3dadA</a>  | Alignment | not modelled | 19.6 | 15 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> fh1/fh2 domain-containing protein 1;<br><b>PDBTitle:</b> crystal structure of the n-terminal regulatory domains of2 the formin fhod1                                                                                                                             |
| 39 | <a href="#">d2bgwa1</a> | Alignment | not modelled | 19.3 | 17 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> RuvA domain 2-like<br><b>Family:</b> Hef domain-like                                                                                                                                                                                                                                       |
| 40 | <a href="#">c8icZA</a>  | Alignment | not modelled | 19.3 | 17 | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase beta (e.c.2.7.7.7));<br><b>PDBTitle:</b> dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)  |
| 41 | <a href="#">d2peoa1</a> | Alignment | not modelled | 18.9 | 16 | <b>Fold:</b> RbcX-like<br><b>Superfamily:</b> RbcX-like<br><b>Family:</b> RbcX-like                                                                                                                                                                                                                                                            |
| 42 | <a href="#">c2peoA</a>  | Alignment | not modelled | 18.9 | 16 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> rbcx protein;<br><b>PDBTitle:</b> crystal structure of rbcx from anabaena ca                                                                                                                                                                                             |
| 43 | <a href="#">c2l0kA</a>  | Alignment | not modelled | 18.5 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> stage iii sporulation protein d;<br><b>PDBTitle:</b> nmr solution structure of a transcription factor spoiiiid in complex2 with dna                                                                                                                                  |
| 44 | <a href="#">d2d1ha1</a> | Alignment | not modelled | 18.3 | 11 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> TrmB-like                                                                                                                                                                                                             |
| 45 | <a href="#">c2ihmA</a>  | Alignment | not modelled | 17.4 | 19 | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase mu;<br><b>PDBTitle:</b> polymerase mu in ternary complex with gapped 11mer dna2 duplex and bound incoming nucleotide                                                                                                                                |
| 46 | <a href="#">d1bh9a</a>  | Alignment | not modelled | 16.9 | 15 | <b>Fold:</b> Histone-fold<br><b>Superfamily:</b> Histone-fold<br><b>Family:</b> TBP-associated factors, TAFs                                                                                                                                                                                                                                   |
| 47 | <a href="#">d1nxb1</a>  | Alignment | not modelled | 16.7 | 10 | <b>Fold:</b> F-box domain<br><b>Superfamily:</b> F-box domain<br><b>Family:</b> F-box domain                                                                                                                                                                                                                                                   |
| 48 | <a href="#">d2efva1</a> | Alignment | not modelled | 15.6 | 19 | <b>Fold:</b> Ribbon-helix-helix<br><b>Superfamily:</b> Ribbon-helix-helix<br><b>Family:</b> MJ0366-like                                                                                                                                                                                                                                        |
| 49 | <a href="#">d2a0ma1</a> | Alignment | not modelled | 15.4 | 15 | <b>Fold:</b> Arginase/deacetylase<br><b>Superfamily:</b> Arginase/deacetylase<br><b>Family:</b> Arginase-like amidino hydrolases                                                                                                                                                                                                               |
| 50 | <a href="#">d1y0na</a>  | Alignment | not modelled | 14.5 | 19 | <b>Fold:</b> YehU-like<br><b>Superfamily:</b> YehU-like<br><b>Family:</b> YehU-like                                                                                                                                                                                                                                                            |
| 51 | <a href="#">d1pzna1</a> | Alignment | not modelled | 14.4 | 12 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> Rad51 N-terminal domain-like<br><b>Family:</b> DNA repair protein Rad51, N-terminal domain                                                                                                                                                                                                 |
| 52 | <a href="#">d1dgna</a>  | Alignment | not modelled | 14.3 | 18 | <b>Fold:</b> DEATH domain<br><b>Superfamily:</b> DEATH domain<br><b>Family:</b> Caspase recruitment domain, CARD                                                                                                                                                                                                                               |
| 53 | <a href="#">d1i5za1</a> | Alignment | not modelled | 13.8 | 12 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain                                                                                                                                                                                                                                         |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                     |
|----|-------------------------|-----------|--------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |                         |           |              |      |    | <b>Family:</b> CAP C-terminal domain-like                                                                                                                                                                                                                           |
| 54 | <a href="#">c2d0sA</a>  | Alignment | not modelled | 13.7 | 0  | <b>PDB header:</b> electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c;<br><b>PDBTitle:</b> crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus                                     |
| 55 | <a href="#">d1dgsa1</a> | Alignment | not modelled | 13.2 | 20 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> RuvA domain 2-like<br><b>Family:</b> NAD+-dependent DNA ligase, domain 3                                                                                                                                        |
| 56 | <a href="#">c1qzeA</a>  | Alignment | not modelled | 13.1 | 15 | <b>PDB header:</b> replication<br><b>Chain:</b> A: <b>PDB Molecule:</b> uv excision repair protein rad23 homolog a;<br><b>PDBTitle:</b> hhr23a protein structure based on residual dipolar coupling2 data                                                           |
| 57 | <a href="#">d1cc5a</a>  | Alignment | not modelled | 12.4 | 17 | <b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> monodomain cytochrome c                                                                                                                                                             |
| 58 | <a href="#">c2jxuA</a>  | Alignment | not modelled | 12.3 | 13 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> terb;<br><b>PDBTitle:</b> nmr solution structure of kp-terb, a tellurite resistance2 protein from klebsiella pneumoniae                                                                |
| 59 | <a href="#">c2kwuA</a>  | Alignment | not modelled | 12.1 | 9  | <b>PDB header:</b> protein binding/signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iota;<br><b>PDBTitle:</b> solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin                                              |
| 60 | <a href="#">c3hjbA</a>  | Alignment | not modelled | 11.9 | 8  | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.                                                     |
| 61 | <a href="#">d1m8za</a>  | Alignment | not modelled | 11.6 | 9  | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> ARM repeat<br><b>Family:</b> Pumilio repeat                                                                                                                                                              |
| 62 | <a href="#">d1htaa</a>  | Alignment | not modelled | 11.3 | 15 | <b>Fold:</b> Histone-fold<br><b>Superfamily:</b> Histone-fold<br><b>Family:</b> Archaeal histone                                                                                                                                                                    |
| 63 | <a href="#">c2gtqA</a>  | Alignment | not modelled | 11.3 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase n;<br><b>PDBTitle:</b> crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis                                                                       |
| 64 | <a href="#">d1y6xa1</a> | Alignment | not modelled | 11.1 | 12 | <b>Fold:</b> all-alpha NTP pyrophosphatases<br><b>Superfamily:</b> all-alpha NTP pyrophosphatases<br><b>Family:</b> HisE-like (PRA-PH)                                                                                                                              |
| 65 | <a href="#">d1tuza</a>  | Alignment | not modelled | 11.0 | 20 | <b>Fold:</b> EF Hand-like<br><b>Superfamily:</b> EF-hand<br><b>Family:</b> EF-hand modules in multidomain proteins                                                                                                                                                  |
| 66 | <a href="#">c2qezC</a>  | Alignment | not modelled | 10.8 | 11 | <b>PDB header:</b> lyase<br><b>Chain:</b> C: <b>PDB Molecule:</b> ethanolamine ammonia-lyase heavy chain;<br><b>PDBTitle:</b> crystal structure of ethanolamine ammonia-lyase heavy chain2 (yp_013784.1) from listeria monocytogenes 4b f2365 at 2.15 a3 resolution |
| 67 | <a href="#">d1ffgb</a>  | Alignment | not modelled | 10.2 | 18 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> CheY-binding domain of CheA<br><b>Family:</b> CheY-binding domain of CheA                                                                                                                                       |
| 68 | <a href="#">c2krcA</a>  | Alignment | not modelled | 10.2 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase subunit delta;<br><b>PDBTitle:</b> solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase                          |
| 69 | <a href="#">c2l6aA</a>  | Alignment | not modelled | 10.0 | 13 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nacht, lrr and pyd domains-containing protein 12;<br><b>PDBTitle:</b> three-dimensional structure of the n-terminal effector pyrin domain of2 nlrp12                                  |
| 70 | <a href="#">d2b0la1</a> | Alignment | not modelled | 10.0 | 22 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Cody HTH domain                                                                                                                            |
| 71 | <a href="#">c3nbuC</a>  | Alignment | not modelled | 10.0 | 8  | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> crystal structure of pgi glucosephosphate isomerase                                                                                        |
| 72 | <a href="#">d2a7wa1</a> | Alignment | not modelled | 10.0 | 11 | <b>Fold:</b> all-alpha NTP pyrophosphatases<br><b>Superfamily:</b> all-alpha NTP pyrophosphatases<br><b>Family:</b> HisE-like (PRA-PH)                                                                                                                              |
| 73 | <a href="#">c2a7wF</a>  | Alignment | not modelled | 10.0 | 11 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> F: <b>PDB Molecule:</b> phosphoribosyl-atp pyrophosphatase;<br><b>PDBTitle:</b> crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7               |
| 74 | <a href="#">c1a0oH</a>  | Alignment | not modelled | 9.9  | 18 | <b>PDB header:</b> chemotaxis<br><b>Chain:</b> H: <b>PDB Molecule:</b> chea;<br><b>PDBTitle:</b> chey-binding domain of chea in complex with chey                                                                                                                   |
| 75 | <a href="#">c3g2bA</a>  | Alignment | not modelled | 9.9  | 14 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme pqq synthesis protein d;<br><b>PDBTitle:</b> crystal structure of pqqd from xanthomonas campestris                                                                        |
| 76 | <a href="#">d1nira1</a> | Alignment | not modelled | 9.7  | 9  | <b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite reductase                                                                                                                      |
| 77 | <a href="#">c2jmkA</a>  | Alignment | not modelled | 9.7  | 20 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0956;<br><b>PDBTitle:</b> solution structure of ta0956                                                                                                           |
| 78 | <a href="#">c3ka1A</a>  | Alignment | not modelled | 9.7  | 16 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> rbcx protein;<br><b>PDBTitle:</b> crystal structure of rbcx from thermosynechococcus elongatus                                                                                                |

|    |                         |           |              |     |    |                                                                                                                                                                                                                                                                                                                 |
|----|-------------------------|-----------|--------------|-----|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 79 | <a href="#">d1dvha_</a> | Alignment | not modelled | 9.6 | 28 | <b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> monodomain cytochrome c                                                                                                                                                                                                         |
| 80 | <a href="#">c2vckC_</a> | Alignment | not modelled | 9.5 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> cyanobacterial phycoerythrobilin;<br><b>PDBTitle:</b> structure of phycoerythrobilin synthase pebs from the2 cyanophage p-ssm2 in complex with the bound substrate3 biliverdin ixa                                                   |
| 81 | <a href="#">d1hiob_</a> | Alignment | not modelled | 9.3 | 15 | <b>Fold:</b> Histone-fold<br><b>Superfamily:</b> Histone-fold<br><b>Family:</b> Nucleosome core histones                                                                                                                                                                                                        |
| 82 | <a href="#">d1a56a_</a> | Alignment | not modelled | 9.2 | 11 | <b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> monodomain cytochrome c                                                                                                                                                                                                         |
| 83 | <a href="#">d1p3mh_</a> | Alignment | not modelled | 9.1 | 17 | <b>Fold:</b> Histone-fold<br><b>Superfamily:</b> Histone-fold<br><b>Family:</b> Nucleosome core histones                                                                                                                                                                                                        |
| 84 | <a href="#">c2km6A_</a> | Alignment | not modelled | 9.0 | 4  | <b>PDB header:</b> signaling protein, protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> nacht, lrr and pyd domains-containing protein 7;<br><b>PDBTitle:</b> nmr structure of the nlrp7 pyrin domain                                                                                                     |
| 85 | <a href="#">d1c53a_</a> | Alignment | not modelled | 8.9 | 22 | <b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> monodomain cytochrome c                                                                                                                                                                                                         |
| 86 | <a href="#">c1cauB_</a> | Alignment | not modelled | 8.8 | 11 | <b>PDB header:</b> seed storage protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> canavalin;<br><b>PDBTitle:</b> determination of three crystal structures of canavalin by molecular2 replacement                                                                                                                |
| 87 | <a href="#">d2h6ca1</a> | Alignment | not modelled | 8.6 | 18 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> CAP C-terminal domain-like                                                                                                                                                             |
| 88 | <a href="#">d1uija1</a> | Alignment | not modelled | 8.6 | 11 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                |
| 89 | <a href="#">c2qwwB_</a> | Alignment | not modelled | 8.5 | 24 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family;<br><b>PDBTitle:</b> crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution                            |
| 90 | <a href="#">c1qlaA_</a> | Alignment | not modelled | 8.3 | 33 | <b>PDB header:</b> membrane proteins<br><b>Chain:</b> A: <b>PDB Molecule:</b> herpes simplex virus protein icp47;<br><b>PDBTitle:</b> structure of the active domain of the herpes simplex virus2 protein icp47 in water/sodium dodecyl sulfate solution3 determined by nuclear magnetic resonance spectroscopy |
| 91 | <a href="#">c2k4bA_</a> | Alignment | not modelled | 8.2 | 15 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> copr repressor structure                                                                                                                                                         |
| 92 | <a href="#">d1huua_</a> | Alignment | not modelled | 8.2 | 19 | <b>Fold:</b> IHF-like DNA-binding proteins<br><b>Superfamily:</b> IHF-like DNA-binding proteins<br><b>Family:</b> Prokaryotic DNA-bending protein                                                                                                                                                               |
| 93 | <a href="#">c2zzsW_</a> | Alignment | not modelled | 8.1 | 22 | <b>PDB header:</b> electron transport<br><b>Chain:</b> W: <b>PDB Molecule:</b><br><b>PDBTitle:</b> crystal structure of cytochrome c554 from vibrio2 parahaemolyticus strain rimd2210633                                                                                                                        |
| 94 | <a href="#">c1dgrW_</a> | Alignment | not modelled | 8.1 | 7  | <b>PDB header:</b> plant protein<br><b>Chain:</b> W: <b>PDB Molecule:</b> canavalin;<br><b>PDBTitle:</b> refined crystal structure of canavalin from jack bean                                                                                                                                                  |
| 95 | <a href="#">d2phla1</a> | Alignment | not modelled | 8.0 | 19 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                |
| 96 | <a href="#">c3fgxA_</a> | Alignment | not modelled | 7.8 | 4  | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> rbstp2171;<br><b>PDBTitle:</b> structure of uncharacterised protein rbstp2171 from bacillus2 stearothermophilus                                                                                               |
| 97 | <a href="#">d1m70a2</a> | Alignment | not modelled | 7.7 | 22 | <b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> Two-domain cytochrome c                                                                                                                                                                                                         |
| 98 | <a href="#">d1k1va_</a> | Alignment | not modelled | 7.7 | 22 | <b>Fold:</b> A DNA-binding domain in eukaryotic transcription factors<br><b>Superfamily:</b> A DNA-binding domain in eukaryotic transcription factors<br><b>Family:</b> A DNA-binding domain in eukaryotic transcription factors                                                                                |
| 99 | <a href="#">d1cora_</a> | Alignment | not modelled | 7.5 | 11 | <b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> monodomain cytochrome c                                                                                                                                                                                                         |