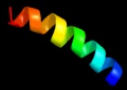
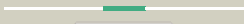
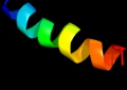
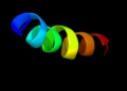
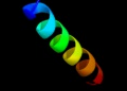
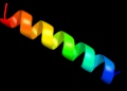
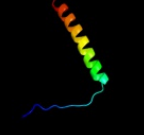
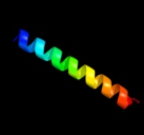
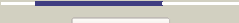


| #  | Template                | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                          |
|----|-------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c2zt9H_</a> | <br>Alignment   |    | 62.0       | 38     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 8;<br><b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120                                                                   |
| 2  | <a href="#">c2e76H_</a> | <br>Alignment   |    | 42.9       | 35     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 8;<br><b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus                                         |
| 3  | <a href="#">c2e74H_</a> | <br>Alignment   |    | 42.9       | 35     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 8;<br><b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from m.laminosus                                                                            |
| 4  | <a href="#">c2e75H_</a> | <br>Alignment   |    | 42.9       | 35     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 8;<br><b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus                           |
| 5  | <a href="#">d2e74h1</a> | <br>Alignment |  | 38.4       | 35     | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> PetN subunit of the cytochrome b6f complex<br><b>Family:</b> PetN subunit of the cytochrome b6f complex                                                                                                        |
| 6  | <a href="#">c2pnvA_</a> | <br>Alignment |  | 35.1       | 29     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> small conductance calcium-activated potassium<br><b>PDBTitle:</b> crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus |
| 7  | <a href="#">c3m9hB_</a> | <br>Alignment |  | 34.9       | 23     | <b>PDB header:</b> chaperone<br><b>Chain:</b> B: <b>PDB Molecule:</b> proteasome-associated atpase;<br><b>PDBTitle:</b> crystal structure of the amino terminal coiled coil domain of the2 mycobacterium tuberculosis proteasomal atpase mpa                                  |
| 8  | <a href="#">c1vf5H_</a> | <br>Alignment |  | 30.6       | 35     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> H: <b>PDB Molecule:</b> protein pet n;<br><b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus                                                                                                    |
| 9  | <a href="#">c1vf5U_</a> | <br>Alignment |  | 27.5       | 35     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> U: <b>PDB Molecule:</b> protein pet n;<br><b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus                                                                                                    |
| 10 | <a href="#">c2d2cU_</a> | <br>Alignment |  | 23.6       | 35     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> U: <b>PDB Molecule:</b> cytochrome b6-f complex subunit viii;<br><b>PDBTitle:</b> crystal structure of cytochrome b6f complex with dbmib from2 m. laminosus                                                                |
| 11 | <a href="#">c2d2cH_</a> | <br>Alignment |  | 23.6       | 35     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome b6-f complex subunit viii;<br><b>PDBTitle:</b> crystal structure of cytochrome b6f complex with dbmib from2 m. laminosus                                                                |

|    |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                   |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c3swfA_</a> | Alignment |    | 21.8 | 37 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cgmp-gated cation channel alpha-1;<br><b>PDBTitle:</b> cnga1 621-690 containing clz domain                                                          |
| 13 | <a href="#">c1ce0B_</a> | Alignment |    | 19.9 | 19 | <b>PDB header:</b> hiv-1 envelope protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein (leucine zipper model h38-p1);<br><b>PDBTitle:</b> trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model |
| 14 | <a href="#">c1ztaA_</a> | Alignment |    | 19.4 | 25 | <b>PDB header:</b> dna-binding motif<br><b>Chain:</b> A: <b>PDB Molecule:</b> leucine zipper monomer;<br><b>PDBTitle:</b> the solution structure of a leucine-zipper motif peptide                                                |
| 15 | <a href="#">c1zmeD_</a> | Alignment |    | 18.0 | 16 | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> D: <b>PDB Molecule:</b> proline utilization transcription activator;<br><b>PDBTitle:</b> crystal structure of put3/dna complex                                              |
| 16 | <a href="#">c1ij2C_</a> | Alignment |    | 17.2 | 25 | <b>PDB header:</b> transcription<br><b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position                                    |
| 17 | <a href="#">c1rb1B_</a> | Alignment |   | 16.9 | 25 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution                            |
| 18 | <a href="#">c3k7zA_</a> | Alignment |  | 16.9 | 25 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution                            |
| 19 | <a href="#">c3k7zB_</a> | Alignment |  | 16.9 | 25 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution                            |
| 20 | <a href="#">c1rb1A_</a> | Alignment |  | 16.9 | 25 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution                            |
| 21 | <a href="#">c1rb6C_</a> | Alignment | not modelled                                                                        | 16.9 | 25 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form                 |
| 22 | <a href="#">c1swiA_</a> | Alignment | not modelled                                                                        | 16.9 | 25 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> A: <b>PDB Molecule:</b> gcn4p1;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a complexed with2 benzene                                                            |
| 23 | <a href="#">c2akfB_</a> | Alignment | not modelled                                                                        | 16.5 | 35 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> coronin-1a;<br><b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1                                                              |
| 24 | <a href="#">c2akfC_</a> | Alignment | not modelled                                                                        | 16.5 | 35 | <b>PDB header:</b> protein binding<br><b>Chain:</b> C: <b>PDB Molecule:</b> coronin-1a;<br><b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1                                                              |
| 25 | <a href="#">c2akfA_</a> | Alignment | not modelled                                                                        | 16.5 | 35 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> coronin-1a;<br><b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1                                                              |
| 26 | <a href="#">c1ij3C_</a> | Alignment | not modelled                                                                        | 16.3 | 25 | <b>PDB header:</b> transcription<br><b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position                                       |
| 27 | <a href="#">c1ij3B_</a> | Alignment | not modelled                                                                        | 16.3 | 25 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position                                       |
| 28 | <a href="#">c1ij2B_</a> | Alignment | not modelled                                                                        | 15.7 | 25 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position                                    |
|    |                         |           |                                                                                     |      |    | <b>PDB header:</b> unknown function                                                                                                                                                                                               |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                                                                                                               |
|----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | <a href="#">c1p9iA_</a> | Alignment | not modelled | 15.6 | 32 | <b>Chain:</b> A: <b>PDB Molecule:</b> cortexillin i/gcn4 hybrid peptide;<br><b>PDBTitle:</b> coiled-coil x-ray structure at 1.17 a resolution                                                                                                                                                                                                                                                 |
| 30 | <a href="#">c1qcrD_</a> | Alignment | not modelled | 14.1 | 17 | <b>PDB header:</b><br><b>PDB COMPND:</b>                                                                                                                                                                                                                                                                                                                                                      |
| 31 | <a href="#">c1junB_</a> | Alignment | not modelled | 13.2 | 40 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> B: <b>PDB Molecule:</b> c-jun homodimer;<br><b>PDBTitle:</b> nmr study of c-jun homodimer                                                                                                                                                                                                                                        |
| 32 | <a href="#">c2ergA_</a> | Alignment | not modelled | 12.5 | 13 | <b>PDB header:</b> transcription activator/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein leu3;<br><b>PDBTitle:</b> crystal structure of leu3 dna-binding domain with a single2 h50c mutation complexed with a 15mer dna duplex                                                                                                                                              |
| 33 | <a href="#">c2k21A_</a> | Alignment | not modelled | 12.0 | 22 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e<br><b>PDBTitle:</b> nmr structure of human kcne1 in Impg micelles at ph 6.0 and2 40 degree c                                                                                                                                                                         |
| 34 | <a href="#">c3ci9B_</a> | Alignment | not modelled | 11.2 | 43 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> heat shock factor-binding protein 1;<br><b>PDBTitle:</b> crystal structure of the human hsbp1                                                                                                                                                                                                                       |
| 35 | <a href="#">c3he5A_</a> | Alignment | not modelled | 11.2 | 37 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> synzip1;<br><b>PDBTitle:</b> heterospecific coiled-coil pair synzip2:synzip1                                                                                                                                                                                                                                      |
| 36 | <a href="#">c2y69Z_</a> | Alignment | not modelled | 11.2 | 25 | <b>PDB header:</b> electron transport<br><b>Chain:</b> Z: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 8h;<br><b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular2 oxygen                                                                                                                                                                                   |
| 37 | <a href="#">c1gk6B_</a> | Alignment | not modelled | 10.4 | 15 | <b>PDB header:</b> vimentin<br><b>Chain:</b> B: <b>PDB Molecule:</b> vimentin;<br><b>PDBTitle:</b> human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)                                                                                                                                                                                                                       |
| 38 | <a href="#">c2o7hF_</a> | Alignment | not modelled | 10.3 | 21 | <b>PDB header:</b> transcription<br><b>Chain:</b> F: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> crystal structure of trimeric coiled coil gcn4 leucine zipper                                                                                                                                                                                                     |
| 39 | <a href="#">c3p8cE_</a> | Alignment | not modelled | 9.9  | 22 | <b>PDB header:</b> protein binding<br><b>Chain:</b> E: <b>PDB Molecule:</b> probable protein brick1;<br><b>PDBTitle:</b> structure and control of the actin regulatory wave complex                                                                                                                                                                                                           |
| 40 | <a href="#">d1v54m_</a> | Alignment | not modelled | 9.9  | 25 | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)<br><b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)                                                                                                                                                                                          |
| 41 | <a href="#">c1u0iA_</a> | Alignment | not modelled | 9.4  | 37 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> iaal-e3;<br><b>PDBTitle:</b> iaal-e3/k3 heterodimer                                                                                                                                                                                                                                                               |
| 42 | <a href="#">c3rylB_</a> | Alignment | not modelled | 8.8  | 45 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein vpa1370;<br><b>PDBTitle:</b> dimerization domain of vibrio parahemolyticus vopl                                                                                                                                                                                                                           |
| 43 | <a href="#">c3nmdA_</a> | Alignment | not modelled | 8.7  | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cgmp dependent protein kinase;<br><b>PDBTitle:</b> crystal structure of the leucine zipper domain of cgmp dependent2 protein kinase i beta                                                                                                                                                                            |
| 44 | <a href="#">c2xzrA_</a> | Alignment | not modelled | 7.8  | 16 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin-binding protein eibd;<br><b>PDBTitle:</b> escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors                                                                                                                                                                       |
| 45 | <a href="#">c2ke4A_</a> | Alignment | not modelled | 7.8  | 15 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cdc42-interacting protein 4;<br><b>PDBTitle:</b> the nmr structure of the tc10 and cdc42 interacting domain2 of cip4                                                                                                                                                                                             |
| 46 | <a href="#">c2xv5A_</a> | Alignment | not modelled | 7.5  | 13 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> lamin-a/c;<br><b>PDBTitle:</b> human lamin a coil 2b fragment                                                                                                                                                                                                                                                  |
| 47 | <a href="#">c1u2uA_</a> | Alignment | not modelled | 7.4  | 40 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> nmr solution structure of a designed heterodimeric leucine2 zipper                                                                                                                                                                                                |
| 48 | <a href="#">d1grja1</a> | Alignment | not modelled | 7.1  | 20 | <b>Fold:</b> Long alpha-hairpin<br><b>Superfamily:</b> GreA transcript cleavage protein, N-terminal domain<br><b>Family:</b> GreA transcript cleavage protein, N-terminal domain                                                                                                                                                                                                              |
| 49 | <a href="#">c1hwtC_</a> | Alignment | not modelled | 7.1  | 39 | <b>PDB header:</b> gene regulation/dna<br><b>Chain:</b> C: <b>PDB Molecule:</b> protein (heme activator protein);<br><b>PDBTitle:</b> structure of a hap1/dna complex reveals dramatically2 asymmetric dna binding by a homodimeric protein                                                                                                                                                   |
| 50 | <a href="#">c2yy0D_</a> | Alignment | not modelled | 7.1  | 3  | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> c-myc-binding protein;<br><b>PDBTitle:</b> crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens                                                                                                                                                                                           |
| 51 | <a href="#">c2lf0A_</a> | Alignment | not modelled | 6.6  | 20 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yibi;<br><b>PDBTitle:</b> 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 |
| 52 | <a href="#">c1dipA_</a> | Alignment | not modelled | 6.5  | 18 | <b>PDB header:</b> acetylation<br><b>Chain:</b> A: <b>PDB Molecule:</b> delta-sleep-inducing peptide immunoreactive<br><b>PDBTitle:</b> the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures                                                                                                                                            |
| 53 | <a href="#">d2f23a1</a> | Alignment | not modelled | 6.0  | 25 | <b>Fold:</b> Long alpha-hairpin<br><b>Superfamily:</b> GreA transcript cleavage protein, N-terminal domain<br><b>Family:</b> GreA transcript cleavage protein, N-terminal domain                                                                                                                                                                                                              |
| 54 | <a href="#">c3n4xB_</a> | Alignment | not modelled | 5.9  | 3  | <b>PDB header:</b> replication<br><b>Chain:</b> B: <b>PDB Molecule:</b> monopolin complex subunit csm1;<br><b>PDBTitle:</b> structure of csm1 full-length                                                                                                                                                                                                                                     |

|    |                         |                                                                                             |              |     |    |                                                                                                                                                                                                                                                                              |
|----|-------------------------|---------------------------------------------------------------------------------------------|--------------|-----|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 55 | <a href="#">c3riaC_</a> |  Alignment  | not modelled | 5.8 | 11 | <b>PDB header:</b> transport protein/immune system<br><b>Chain:</b> C: <b>PDB Molecule:</b> avermectin-sensitive glutamate-gated chloride channel gluc1<br><b>PDBTitle:</b> c. elegans glutamate-gated chloride channel (gluc1) in complex with2 fab, ivermectin and iodide. |
| 56 | <a href="#">d1ioka2</a> |  Alignment | not modelled | 5.4 | 15 | <b>Fold:</b> The "swivelling" beta/beta/alpha domain<br><b>Superfamily:</b> GroEL apical domain-like<br><b>Family:</b> GroEL-like chaperone, apical domain                                                                                                                   |
| 57 | <a href="#">c2zfcB_</a> |  Alignment | not modelled | 5.4 | 44 | <b>PDB header:</b> viral protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> hiv-1 gp41;<br><b>PDBTitle:</b> x-ray crystal structure of an engineered n-terminal hiv-12 gp41 trimer with enhanced stability and potency                                                         |