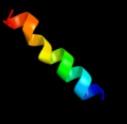


# Phyre<sup>2</sup>

|               |                             |
|---------------|-----------------------------|
| Email         | i.a.kelley@imperial.ac.uk   |
| Description   | P76505                      |
| Date          | Thu Jan 5 12:23:42 GMT 2012 |
| Unique Job ID | 60e608cf0891a7c5            |

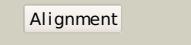
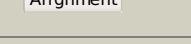
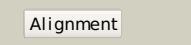
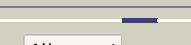
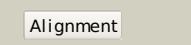
Detailed template information

| #  | Template | Alignment Coverage | 3D Model  | Confidence | % i.d. | Template Information  |
|----|----------|--------------------|---|------------|--------|---|
| 1  | d1u7la_  | Alignment          |    | 37.4       | 17     | <b>Fold:</b> Vacuolar ATP synthase subunit C<br><b>Superfamily:</b> Vacuolar ATP synthase subunit C<br><b>Family:</b> Vacuolar ATP synthase subunit C   |
| 2  | c2ahpB_  | Alignment          |    | 32.5       | 50     | <b>PDB header:</b> de novo protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper, mutation of lys15 to epsilon-azido-lys   |
| 3  | c2ahpA_  | Alignment          |    | 32.1       | 50     | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper, mutation of lys15 to epsilon-azido-lys   |
| 4  | c3etoB_  | Alignment          |   | 27.3       | 24     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> neurogenic locus notch homolog protein 1;<br><b>PDBTitle:</b> 2 angstrom xray structure of the notch1 negative regulatory region2 (nrr)             |
| 5  | c1ce0B_  | Alignment          |  | 26.3       | 35     | <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 |
| 6  | c1ij2C_  | Alignment          |  | 21.9       | 41     | <b>PDB header:</b> transcription<br><b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-pvt coiled-coil trimer with threonine at the a(16)2 position                                     |
| 7  | c1ij1B_  | Alignment          |  | 21.9       | 58     | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-pvt coiled-coil trimer with threonine at the d(12)2 position                                     |
| 8  | c1ij1C_  | Alignment          |  | 21.9       | 58     | <b>PDB header:</b> transcription<br><b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-pvt coiled-coil trimer with threonine at the d(12)2 position                                     |
| 9  | c1ij1A_  | Alignment          |  | 21.9       | 58     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-pvt coiled-coil trimer with threonine at the d(12)2 position                                     |
| 10 | c3k7zA_  | Alignment          |  | 21.8       | 41     | <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                            |
| 11 | c1rb1A_  | Alignment          |  | 21.8       | 41     | <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                            |

|    |                         |  |              |      |    |  |
|----|-------------------------|--|--------------|------|----|--|
| 12 | <a href="#">c1rb6C_</a> |  |              | 21.8 | 41 | <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  |
| 13 | <a href="#">c1swiA_</a> |  |              | 21.8 | 41 | <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   |
| 14 | <a href="#">c1rb1B_</a> |  |              | 21.8 | 41 | <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   |
| 15 | <a href="#">c3k7zB_</a> |  |              | 21.8 | 41 | <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   |
| 16 | <a href="#">c1ij3C_</a> |  |              | 21.8 | 41 | <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  |
| 17 | <a href="#">c1ij3B_</a> |  |              | 21.8 | 41 | <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  |
| 18 | <a href="#">c2wpzA_</a> |  |              | 21.3 | 58 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper mutant with two vxnxxxx motifs2 coordinating chloride  |
| 19 | <a href="#">c1ij0B_</a> |  |              | 21.2 | 58 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> coiled coil trimer gcn4-pvls ser at buried d position  |
| 20 | <a href="#">c1ij0A_</a> |  |              | 21.2 | 58 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> coiled coil trimer gcn4-pvls ser at buried d position  |
| 21 | <a href="#">c1ij0C_</a> |  | not modelled | 21.2 | 58 | <b>PDB header:</b> transcription<br><b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> coiled coil trimer gcn4-pvls ser at buried d position  |
| 22 | <a href="#">c2wq1A_</a> |  | not modelled | 20.5 | 58 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper mutant with three ixxnbxx motifs2 coordinating bromide   |
| 23 | <a href="#">c2wq3A_</a> |  | not modelled | 20.5 | 58 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper mutant with three ixxnbxx motifs2 coordinating chloride and nitrate  |
| 24 | <a href="#">c2wpzB_</a> |  | not modelled | 20.1 | 58 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper mutant with two vxnxxxx motifs2 coordinating chloride  |
| 25 | <a href="#">c2wpzC_</a> |  | not modelled | 19.8 | 58 | <b>PDB header:</b> transcription<br><b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper mutant with two vxnxxxx motifs2 coordinating chloride  |
| 26 | <a href="#">c2o7hF_</a> |  | not modelled | 19.1 | 36 | <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  |
| 27 | <a href="#">c1ij2B_</a> |  | not modelled | 19.1 | 41 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-pvt coiled-coil trimer with threonine at the a(16)2 position  |
| 28 | <a href="#">c2dalA_</a> |  | not modelled | 19.0 | 38 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein kiaa0794;<br><b>PDBTitle:</b> solution structure of the novel identified uba-like domain2 in the n-terminal of human fas associated factor 1 protein |
|    |                         |  |              |      |    | <b>PDB header:</b> dna binding protein   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | <a href="#">c1piqA</a>  | Alignment | not modelled | 18.4 | 50 | <b>Chain:</b> A: <b>PDB Molecule:</b> protein (general control protein gcn4-piq);<br><b>PDBTitle:</b> crystal structure of gcn4-piq, a trimeric coiled coil with buried2 polar residues<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the dimeric2 state<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the dimeric2 state<br><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 automatic solution |
| 30 | <a href="#">c1zilA</a>  | Alignment | not modelled | 17.7 | 45 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the dimeric2 state<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the dimeric2 state<br><b>PDB header:</b> leucine zipper<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 automatic solution   |
| 31 | <a href="#">c1zilB</a>  | Alignment | not modelled | 17.7 | 45 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the dimeric2 state<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the dimeric2 state<br><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 automatic solution  |
| 32 | <a href="#">c1rb4C</a>  | Alignment | not modelled | 17.3 | 58 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal automatic solution  |
| 33 | <a href="#">c1rb4A</a>  | Alignment | not modelled | 16.6 | 58 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal automatic solution<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> gcn4p1;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a complexed with2 benzene  |
| 34 | <a href="#">c1swiB</a>  | Alignment | not modelled | 16.6 | 58 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-ptv coiled-coil trimer with threonine at the a(16)2 position<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> gcn4 leucine zipper;<br><b>PDBTitle:</b> x-ray structure of the gcn4 leucine zipper, a two-stranded,2 parallel coiled coil   |
| 35 | <a href="#">c1ij2A</a>  | Alignment | not modelled | 16.6 | 58 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-ptv coiled-coil trimer with threonine at the a(16)2 position<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> gcn4 leucine zipper;<br><b>PDBTitle:</b> x-ray structure of the gcn4 leucine zipper, a two-stranded,2 parallel coiled coil  |
| 36 | <a href="#">c2ztaB</a>  | Alignment | not modelled | 16.5 | 58 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> A: <b>PDB Molecule:</b> gcn4 leucine zipper;<br><b>PDBTitle:</b> x-ray structure of the gcn4 leucine zipper, a two-stranded,2 parallel coiled coil<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> gcn4 leucine zipper;<br><b>PDBTitle:</b> x-ray structure of the gcn4 leucine zipper, a two-stranded,2 parallel coiled coil   |
| 37 | <a href="#">c2ztaA</a>  | Alignment | not modelled | 16.5 | 58 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> gcn4p-ii;<br><b>PDBTitle:</b> gcn4 leucine zipper core mutant p-ii  |
| 38 | <a href="#">c1gcmA</a>  | Alignment | not modelled | 16.3 | 58 | <b>PDB header:</b> replication/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> replication protein b;<br><b>PDBTitle:</b> crystal structure of the catalytic domain of primase repb' in complex2 with initiator dna   |
| 39 | <a href="#">c3h25A</a>  | Alignment | not modelled | 16.3 | 25 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the trimeric2 state   |
| 40 | <a href="#">c1zimC</a>  | Alignment | not modelled | 16.1 | 45 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the trimeric2 state   |
| 41 | <a href="#">c1zimB</a>  | Alignment | not modelled | 16.1 | 45 | <b>PDB header:</b> leucine zipper<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   |
| 42 | <a href="#">c2xzrA</a>  | Alignment | not modelled | 15.9 | 37 | <b>Fold:</b> Non-globular all-alpha subunits of globular proteins<br><b>Superfamily:</b> Transducin (heterotrimeric G protein), gamma chain<br><b>Family:</b> Transducin (heterotrimeric G protein), gamma chain   |
| 43 | <a href="#">d1xhmB1</a> | Alignment | not modelled | 15.8 | 33 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16lys in the dimeric2 state<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16lys in the dimeric2 state   |
| 44 | <a href="#">c1zikA</a>  | Alignment | not modelled | 15.8 | 58 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16lys in the dimeric2 state<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16lys in the dimeric2 state   |
| 45 | <a href="#">c1zikB</a>  | Alignment | not modelled | 15.8 | 58 | <b>PDB header:</b> helix capping<br><b>Chain:</b> C: <b>PDB Molecule:</b> protein (gcn4-pmse);<br><b>PDBTitle:</b> helix capping in the gcn4 leucine zipper  |
| 46 | <a href="#">c1ce9C</a>  | Alignment | not modelled | 15.8 | 64 | <b>PDB header:</b> helix capping<br><b>Chain:</b> D: <b>PDB Molecule:</b> protein (gcn4-pmse);<br><b>PDBTitle:</b> helix capping in the gcn4 leucine zipper  |
| 47 | <a href="#">c1ce9D</a>  | Alignment | not modelled | 15.8 | 64 | <b>PDB header:</b> helix capping<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (gcn4-pmse);<br><b>PDBTitle:</b> helix capping in the gcn4 leucine zipper  |
| 48 | <a href="#">c1ce9A</a>  | Alignment | not modelled | 15.8 | 64 | <b>PDB header:</b> helix capping<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein (gcn4-pmse);<br><b>PDBTitle:</b> helix capping in the gcn4 leucine zipper  |
| 49 | <a href="#">c1ce9B</a>  | Alignment | not modelled | 15.8 | 64 | <b>PDB header:</b> helix capping<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein (gcn4-pmse);<br><b>PDBTitle:</b> helix capping in the gcn4 leucine zipper  |
| 50 | <a href="#">c1xhmB</a>  | Alignment | not modelled | 15.5 | 33 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> guanine nucleotide-binding protein g(i)/g(s)<br><b>PDBTitle:</b> the crystal structure of a biologically active peptide2 (sigk) bound to a g protein beta:gamma heterodimer  |
| 51 | <a href="#">c1ld4E</a>  | Alignment | not modelled | 15.5 | 64 | <b>PDB header:</b> virus<br><b>Chain:</b> E: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> placement of the structural proteins in sindbis virus  |
| 52 | <a href="#">c2wpyA</a>  | Alignment | not modelled | 15.4 | 58 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper mutant with one vxnnxxx motif2 coordinating chloride   |
| 53 | <a href="#">c1ij3A</a>  | Alignment | not modelled | 15.2 | 58 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-ptv coiled-coil trimer with serine at the a(16)2 position   |
| 54 | <a href="#">c1rb4B</a>  | Alignment | not modelled | 15.2 | 58 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal automatic solution  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 55 | <a href="#">c1rb6B</a>  | Alignment | not modelled | 15.2 | 58 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form   |
| 56 | <a href="#">c1rb5C</a>  | Alignment | not modelled | 15.2 | 58 | <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 trigonal form   |
| 57 | <a href="#">c1rb5B</a>  | Alignment | not modelled | 14.8 | 58 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a trigonal form   |
| 58 | <a href="#">c1rb6A</a>  | Alignment | not modelled | 14.8 | 58 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form   |
| 59 | <a href="#">c1rb5A</a>  | Alignment | not modelled | 14.8 | 58 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a trigonal form   |
| 60 | <a href="#">c1gcmB</a>  | Alignment | not modelled | 14.5 | 58 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> B: <b>PDB Molecule:</b> gcn4p-ii;<br><b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li   |
| 61 | <a href="#">c1gcmC</a>  | Alignment | not modelled | 14.1 | 58 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> C: <b>PDB Molecule:</b> gcn4p-ii;<br><b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li   |
| 62 | <a href="#">c1ziiA</a>  | Alignment | not modelled | 14.1 | 44 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16aba in the dimeric2 state   |
| 63 | <a href="#">c1ziiB</a>  | Alignment | not modelled | 14.1 | 44 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16aba in the dimeric2 state   |
| 64 | <a href="#">d1pzra</a>  | Alignment | not modelled | 14.0 | 45 | <b>Fold:</b> HLH-like<br><b>Superfamily:</b> Docking domain B of the erythromycin polyketide synthase (DEBS)<br><b>Family:</b> Docking domain B of the erythromycin polyketide synthase (DEBS)  |
| 65 | <a href="#">c1zimA</a>  | Alignment | not modelled | 13.9 | 48 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the trimeric2 state  |
| 66 | <a href="#">c3p8mD</a>  | Alignment | not modelled | 13.8 | 58 | <b>PDB header:</b> protein binding<br><b>Chain:</b> D: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> human dynein light chain (dynl12) in complex with an in vitro evolved2 peptide dimerized by leucine zipper                              |
| 67 | <a href="#">c3k7zC</a>  | Alignment | not modelled | 13.6 | 64 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution  |
| 68 | <a href="#">c1rb1C</a>  | Alignment | not modelled | 13.6 | 64 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution  |
| 69 | <a href="#">d1qm4a2</a> | Alignment | not modelled | 13.6 | 31 | <b>Fold:</b> S-adenosylmethionine synthetase<br><b>Superfamily:</b> S-adenosylmethionine synthetase<br><b>Family:</b> S-adenosylmethionine synthetase   |
| 70 | <a href="#">d1mxaa2</a> | Alignment | not modelled | 13.1 | 33 | <b>Fold:</b> S-adenosylmethionine synthetase<br><b>Superfamily:</b> S-adenosylmethionine synthetase<br><b>Family:</b> S-adenosylmethionine synthetase   |
| 71 | <a href="#">c1ztaA</a>  | Alignment | not modelled | 12.7 | 42 | <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  |
| 72 | <a href="#">c2r9iA</a>  | Alignment | not modelled | 12.6 | 33 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative phage capsid protein;<br><b>PDBTitle:</b> crystal structure of putative phage capsid protein domain from2 corynebacterium diphtheriae                      |
| 73 | <a href="#">c1zijB</a>  | Alignment | not modelled | 12.4 | 44 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16aba in the trimeric2 state  |
| 74 | <a href="#">c1zijA</a>  | Alignment | not modelled | 12.4 | 44 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16aba in the trimeric2 state  |
| 75 | <a href="#">c1zijC</a>  | Alignment | not modelled | 12.4 | 44 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16aba in the trimeric2 state  |
| 76 | <a href="#">c1swiC</a>  | Alignment | not modelled | 12.0 | 64 | <b>PDB header:</b> leucine zipper<br><b>Chain:</b> C: <b>PDB Molecule:</b> gcn4p1;<br><b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a complexed with2 benzene  |
| 77 | <a href="#">c1qeyA</a>  | Alignment | not modelled | 12.0 | 50 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (regulatory protein mnt);<br><b>PDBTitle:</b> nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange |
| 78 | <a href="#">c1qeyB</a>  | Alignment | not modelled | 12.0 | 50 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein (regulatory protein mnt);<br><b>PDBTitle:</b> nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange |
| 79 | <a href="#">c1qeyC</a>  | Alignment | not modelled | 12.0 | 50 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> C: <b>PDB Molecule:</b> protein (regulatory protein mnt);<br><b>PDBTitle:</b> nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange |

|    |                         |   |           |              |      |   |
|----|-------------------------|---|-----------|--------------|------|---|
|    |                         |   |           |              |      |   |
| 80 | <a href="#">c1qeyD_</a> |     | Alignment | not modelled | 12.0 | 50<br><b>PDB header:</b> gene regulation<br><b>Chain:</b> D: <b>PDB Molecule:</b> protein (regulatory protein mnt);<br><b>PDBTitle:</b> nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange |
| 81 | <a href="#">c3e9eB_</a> |    | Alignment | not modelled | 11.7 | 18<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> zgc:56074;<br><b>PDBTitle:</b> structure of full-length h11a mutant form of tigar from danio rerio  |
| 82 | <a href="#">c2wq2A_</a> |    | Alignment | not modelled | 11.4 | 78<br><b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper mutant with three ixxnbxx motifs2 coordinating iodide   |
| 83 | <a href="#">c2ccfA_</a> |    | Alignment | not modelled | 10.5 | 50<br><b>PDB header:</b> four helix bundle<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> antiparallel configuration of pli e20s  |
| 84 | <a href="#">c2wg0A_</a> |    | Alignment | not modelled | 10.3 | 78<br><b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper mutant with three ixxnbxx motifs2 coordinating chloride   |
| 85 | <a href="#">c1u9fA_</a> |    | Alignment | not modelled | 10.2 | 50<br><b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)                                     |
| 86 | <a href="#">c1unwB_</a> |    | Alignment | not modelled | 9.8  | 50<br><b>PDB header:</b> four helix bundle<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles   |
| 87 | <a href="#">c1unxA_</a> |    | Alignment | not modelled | 9.7  | 50<br><b>PDB header:</b> four helix bundle<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles   |
| 88 | <a href="#">c1unyB_</a> |    | Alignment | not modelled | 9.7  | 50<br><b>PDB header:</b> four helix bundle<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles   |
| 89 | <a href="#">c2cceA_</a> |    | Alignment | not modelled | 9.7  | 50<br><b>PDB header:</b> four helix bundle<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> parallel configuration of pli e20s  |
| 90 | <a href="#">c2cceB_</a> |   | Alignment | not modelled | 9.7  | 50<br><b>PDB header:</b> four helix bundle<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> parallel configuration of pli e20s  |
| 91 | <a href="#">c1uo0A_</a> |  | Alignment | not modelled | 9.6  | 50<br><b>PDB header:</b> four helix bundle<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles   |
| 92 | <a href="#">c1uo0B_</a> |  | Alignment | not modelled | 9.6  | 50<br><b>PDB header:</b> four helix bundle<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles   |
| 93 | <a href="#">c1uo1B_</a> |  | Alignment | not modelled | 9.6  | 50<br><b>PDB header:</b> four helix bundle<br><b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles   |
| 94 | <a href="#">c1u9hA_</a> |  | Alignment | not modelled | 9.6  | 50<br><b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of e(22)l(23)                                     |
| 95 | <a href="#">c1gclA_</a> |  | Alignment | not modelled | 9.5  | 50<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> A: <b>PDB Molecule:</b> gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li   |
| 96 | <a href="#">c1gclC_</a> |  | Alignment | not modelled | 9.5  | 50<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> C: <b>PDB Molecule:</b> gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li   |
| 97 | <a href="#">c3f1bA_</a> |  | Alignment | not modelled | 9.3  | 10<br><b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetr-like transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of a tetr-like transcriptional regulator from2 rhodococcus sp. rha1.                               |
| 98 | <a href="#">c1gclB_</a> |  | Alignment | not modelled | 9.2  | 50<br><b>PDB header:</b> leucine zipper<br><b>Chain:</b> B: <b>PDB Molecule:</b> gcn4;<br><b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li   |
| 99 | <a href="#">c1u9fC_</a> |  | Alignment | not modelled | 9.1  | 50<br><b>PDB header:</b> transcription<br><b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4;<br><b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)                                     |