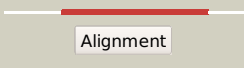

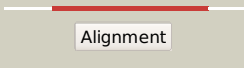

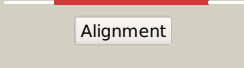

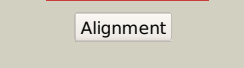
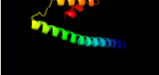
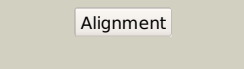
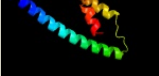
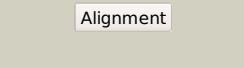

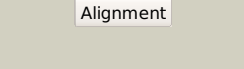

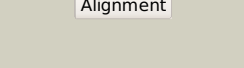

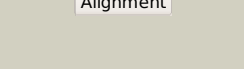

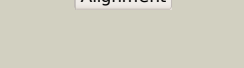

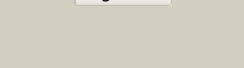

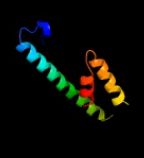


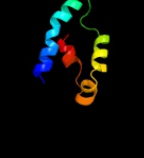

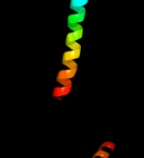

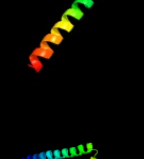



Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0948c_(-)_1057650_1057967 |
| Date | Fri Jul 26 01:50:54 BST 2019 |
| Unique Job ID | 124df60d45b964a3 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c2qbvA_ |  Alignment |  | 99.8 | 100 | PDB header: isomerase Chain: A: PDB Molecule: chorismate mutase; PDBTitle: crystal structure of intracellular chorismate mutase from2 mycobacterium tuberculosis |
| 2 | c5hubA_ |  Alignment |  | 99.8 | 56 | PDB header: isomerase Chain: A: PDB Molecule: chorismate mutase; PDBTitle: high-resolution structure of chorismate mutase from corynebacterium2 glutamicum |
| 3 | c5go2D_ |  Alignment |  | 99.7 | 28 | PDB header: isomerase Chain: D: PDB Molecule: protein aroa(g); PDBTitle: crystal structure of chorismate mutase like domain of bifunctional2 dahp synthase of bacillus subtilis in complex with citrate |
| 4 | c3rmiA_ |  Alignment |  | 99.6 | 25 | PDB header: isomerase Chain: A: PDB Molecule: chorismate mutase protein; PDBTitle: crystal structure of chorismate mutase from bartonella henselae str.2 houston-1 in complex with malate |
| 5 | d1ybza1 |  Alignment |  | 99.6 | 30 | Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Dimeric chorismate mutase |
| 6 | d2d8da1 |  Alignment |  | 99.6 | 25 | Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Dimeric chorismate mutase |
| 7 | d1ecma_ |  Alignment |  | 99.6 | 32 | Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Dimeric chorismate mutase |
| 8 | d2gtvx1 |  Alignment |  | 99.6 | 22 | Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: monomeric chorismate mutase |
| 9 | c6a19A_ |  Alignment |  | 99.6 | 25 | PDB header: isomerase Chain: A: PDB Molecule: chorismate mutase; PDBTitle: crystal structure of chorismate mutase from helicobacter pylori in2 complex with prephenate |
| 10 | c3nvtA_ |  Alignment |  | 99.4 | 23 | PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e |
| 11 | c4qj7E_ |  Alignment |  | 99.2 | 13 | PDB header: isomerase Chain: E: PDB Molecule: chorismate mutase; PDBTitle: crystal structure of chorismate mutase from burkholderia thailandensis |

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|----|-------------------------|-----------|---|------|----|---|
| 12 | d2h9da1 | Alignment |  | 99.2 | 22 | Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Dimeric chorismate mutase |
| 13 | d2fp1a1 | Alignment |  | 99.0 | 14 | Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Secreted chorismate mutase-like |
| 14 | c5ts9H_ | Alignment |  | 98.9 | 16 | PDB header: isomerase Chain: H: PDB Molecule: chorismate mutase; PDBTitle: crystal structure of chorismate mutase from burkholderia phymatum |
| 15 | c2gbbA_ | Alignment |  | 98.9 | 19 | PDB header: isomerase Chain: A: PDB Molecule: putative chorismate mutase; PDBTitle: crystal structure of secreted chorismate mutase from yersinia pestis |
| 16 | c1r48A_ | Alignment |  | 86.0 | 30 | PDB header: transport protein Chain: A: PDB Molecule: proline/betaine transporter; PDBTitle: solution structure of the c-terminal cytoplasmic domain2 residues 468-497 of escherichia coli protein prop |
| 17 | c1r48B_ | Alignment |  | 85.5 | 30 | PDB header: transport protein Chain: B: PDB Molecule: proline/betaine transporter; PDBTitle: solution structure of the c-terminal cytoplasmic domain2 residues 468-497 of escherichia coli protein prop |
| 18 | c3ssuB_ | Alignment |  | 83.8 | 23 | PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment |
| 19 | c2xu6B_ | Alignment |  | 53.2 | 17 | PDB header: protein binding Chain: B: PDB Molecule: mdv1 coiled coil; PDBTitle: mdv1 coiled coil domain |
| 20 | c6cg8A_ | Alignment |  | 45.3 | 15 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: upf0335 protein b7z12_12435; PDBTitle: structure of c. crescentus gapr-dna |
| 21 | c3uuxD_ | Alignment | not modelled | 44.8 | 19 | PDB header: apoptosis Chain: D: PDB Molecule: mitochondrial division protein 1; PDBTitle: crystal structure of yeast fis1 in complex with mdv1 fragment2 containing n-terminal extension and coiled coil domains |
| 22 | c3swkB_ | Alignment | not modelled | 41.6 | 22 | PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1b fragment |
| 23 | c1gk4A_ | Alignment | not modelled | 40.7 | 25 | PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment (cys2) |
| 24 | c3s4rB_ | Alignment | not modelled | 38.9 | 23 | PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment with a stabilizing2 mutation |
| 25 | c1piqA_ | Alignment | not modelled | 35.6 | 10 | PDB header: dna binding protein Chain: A: PDB Molecule: protein (general control protein gcn4-piq); PDBTitle: crystal structure of gcn4-piq, a trimeric coiled coil with buried2 polar residues |
| 26 | c3tnuA_ | Alignment | not modelled | 34.4 | 19 | PDB header: cytosolic protein Chain: A: PDB Molecule: keratin, type i cytoskeletal 14; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14) |
| 27 | c3r84O_ | Alignment | not modelled | 33.4 | 13 | PDB header: transcription Chain: O: PDB Molecule: mediator of rna polymerase ii transcription subunit 11; PDBTitle: structure of the mediator head subcomplex med11/22 |
| 28 | c6fpgG_ | Alignment | not modelled | 31.0 | 33 | PDB header: cell invasion Chain: G: PDB Molecule: chromosome 16, whole genome shotgun sequence; PDBTitle: structure of the ustilago maydis chorismate mutase 1 in complex with a2 zea mays kiwellin |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c3tnuB | Alignment | not modelled | 30.7 | 18 | PDB header: cytosolic protein Chain: B: PDB Molecule: keratin, type ii cytoskeletal 5; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14) |
| 30 | c3movB | Alignment | not modelled | 30.0 | 14 | PDB header: structural protein Chain: B: PDB Molecule: lamin-b1; PDBTitle: crystal structure of human lamin-b1 coil 2 segment |
| 31 | d1gxha | Alignment | not modelled | 29.9 | 33 | Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins |
| 32 | c6h9mA | Alignment | not modelled | 29.9 | 13 | PDB header: membrane protein Chain: A: PDB Molecule: coiled-coil domain-containing protein 90b, mitochondrial, PDBTitle: coiled-coil domain-containing protein 90b residues 43-125 from homo2 sapiens fused to a gcn4 adaptor |
| 33 | c2yy0D | Alignment | not modelled | 29.6 | 21 | PDB header: transcription Chain: D: PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens |
| 34 | c2xv5A | Alignment | not modelled | 29.3 | 17 | PDB header: structural protein Chain: A: PDB Molecule: lamin-a/c; PDBTitle: human lamin a coil 2b fragment |
| 35 | c1gk6B | Alignment | not modelled | 29.2 | 19 | PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment linked to gcn4 leucine zipper (z2b) |
| 36 | d1ayia | Alignment | not modelled | 28.1 | 29 | Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins |
| 37 | c1gcmA | Alignment | not modelled | 27.6 | 10 | PDB header: transcription regulation Chain: A: PDB Molecule: gcn4p-ii; PDBTitle: gcn4 leucine zipper core mutant p-li |
| 38 | d2vlqa1 | Alignment | not modelled | 27.3 | 18 | Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins |
| 39 | c6e2jB | Alignment | not modelled | 27.2 | 19 | PDB header: protein fibril Chain: B: PDB Molecule: keratin, type i cytoskeletal 10; PDBTitle: crystal structure of the heterocomplex between human keratin 1 coil 1b2 containing s233l mutation and wild-type human keratin 10 coil 1b |
| 40 | c4c46B | Alignment | not modelled | 27.1 | 14 | PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4, general control protein gcn4; PDBTitle: andrei-n-lvpas fused to gcn4 adaptors |
| 41 | c4qkaA | Alignment | not modelled | 27.0 | 24 | PDB header: antimicrobial protein Chain: A: PDB Molecule: pyocin-s2 immunity protein; PDBTitle: the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms |
| 42 | c2cceA | Alignment | not modelled | 26.8 | 7 | PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: parallel configuration of pli e20s |
| 43 | c2cceB | Alignment | not modelled | 26.8 | 7 | PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: parallel configuration of pli e20s |
| 44 | c2dq3A | Alignment | not modelled | 26.7 | 20 | PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298 |
| 45 | c1gcmB | Alignment | not modelled | 26.7 | 10 | PDB header: transcription regulation Chain: B: PDB Molecule: gcn4p-ii; PDBTitle: gcn4 leucine zipper core mutant p-li |
| 46 | c4czdD | Alignment | not modelled | 26.5 | 16 | PDB header: lyase Chain: D: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway. |
| 47 | c2ia0A | Alignment | not modelled | 26.4 | 42 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864) |
| 48 | c4wxaE | Alignment | not modelled | 26.2 | 24 | PDB header: transcription Chain: E: PDB Molecule: ekc/keops complex subunit gon7; PDBTitle: crystal structure of binary complex gon7-pcc1 |
| 49 | c1x8yA | Alignment | not modelled | 26.0 | 17 | PDB header: structural protein Chain: A: PDB Molecule: lamin a/c; PDBTitle: human lamin coil 2b |
| 50 | c4uhpB | Alignment | not modelled | 26.0 | 24 | PDB header: hydrolase Chain: B: PDB Molecule: bacteriocin immunity protein; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex |
| 51 | c2ccfA | Alignment | not modelled | 25.9 | 7 | PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: antiparallel configuration of pli e20s |
| 52 | c1gcmC | Alignment | not modelled | 25.8 | 10 | PDB header: transcription regulation Chain: C: PDB Molecule: gcn4p-ii; PDBTitle: gcn4 leucine zipper core mutant p-li |
| 53 | c2no8A | Alignment | not modelled | 25.5 | 29 | PDB header: immune system Chain: A: PDB Molecule: colicin-e2 immunity protein; PDBTitle: nmr structure analysis of the colicin immunity protein im2 |
| | | | | | | PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc |

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|----|-------------------------|-----------|--------------|------|----|--|
| 54 | c4czdA_ | Alignment | not modelled | 25.3 | 29 | family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway. |
| 55 | c1wleB_ | Alignment | not modelled | 21.7 | 20 | PDB header: ligase Chain: B: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate |
| 56 | c1w5jD_ | Alignment | not modelled | 21.4 | 7 | PDB header: four helix bundle Chain: D: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle |
| 57 | c1w5jC_ | Alignment | not modelled | 21.4 | 7 | PDB header: four helix bundle Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle |
| 58 | c1w5jB_ | Alignment | not modelled | 21.4 | 7 | PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle |
| 59 | c1w5jA_ | Alignment | not modelled | 21.4 | 7 | PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle |
| 60 | c2vbzA_ | Alignment | not modelled | 20.3 | 22 | PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan |
| 61 | c6ec0A_ | Alignment | not modelled | 19.6 | 19 | PDB header: protein fibril Chain: A: PDB Molecule: keratin 1; PDBTitle: crystal structure of the wild-type heterocomplex between coil 1b2 domains of human intermediate filament proteins keratin 1 (krt1) and3 keratin 10 (krt10) |
| 62 | c4c1aC_ | Alignment | not modelled | 19.4 | 29 | PDB header: hydrolase Chain: C: PDB Molecule: orf1-encoded protein; PDBTitle: coiled coil domain of the zfl2-1 orf1 protein from the2 zebrafish zfl2-1 retrotransposon |
| 63 | c4c1aB_ | Alignment | not modelled | 19.4 | 29 | PDB header: hydrolase Chain: B: PDB Molecule: orf1-encoded protein; PDBTitle: coiled coil domain of the zfl2-1 orf1 protein from the2 zebrafish zfl2-1 retrotransposon |
| 64 | c4c1aA_ | Alignment | not modelled | 19.4 | 29 | PDB header: hydrolase Chain: A: PDB Molecule: orf1-encoded protein; PDBTitle: coiled coil domain of the zfl2-1 orf1 protein from the2 zebrafish zfl2-1 retrotransposon |
| 65 | c1w5kD_ | Alignment | not modelled | 17.3 | 7 | PDB header: four helix bundle Chain: D: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle |
| 66 | c1w5kC_ | Alignment | not modelled | 17.3 | 7 | PDB header: four helix bundle Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle |
| 67 | c1w5kA_ | Alignment | not modelled | 17.3 | 7 | PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle |
| 68 | c1w5kB_ | Alignment | not modelled | 17.3 | 7 | PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle |
| 69 | c6a9pD_ | Alignment | not modelled | 16.8 | 24 | PDB header: structural protein Chain: D: PDB Molecule: glial fibrillary acidic protein; PDBTitle: crystal structure of the human glial fibrillary acidic protein 1b2 domain |
| 70 | c1usdA_ | Alignment | not modelled | 16.6 | 14 | PDB header: signaling protein Chain: A: PDB Molecule: vasodilator-stimulated phosphoprotein; PDBTitle: human vasp tetramerisation domain l352m |
| 71 | c2dbbA_ | Alignment | not modelled | 15.5 | 20 | PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061 |
| 72 | c2l5gB_ | Alignment | not modelled | 14.7 | 18 | PDB header: transcription regulator Chain: B: PDB Molecule: putative uncharacterized protein ncor2; PDBTitle: co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207 |
| 73 | c2cg4B_ | Alignment | not modelled | 14.5 | 43 | PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc |
| 74 | c1ce9B_ | Alignment | not modelled | 14.2 | 10 | PDB header: helix capping Chain: B: PDB Molecule: protein (gcn4-pmse); PDBTitle: helix capping in the gcn4 leucine zipper |
| 75 | c1ce9A_ | Alignment | not modelled | 14.2 | 10 | PDB header: helix capping Chain: A: PDB Molecule: protein (gcn4-pmse); PDBTitle: helix capping in the gcn4 leucine zipper |
| 76 | c1ce9D_ | Alignment | not modelled | 14.2 | 10 | PDB header: helix capping Chain: D: PDB Molecule: protein (gcn4-pmse); PDBTitle: helix capping in the gcn4 leucine zipper |
| 77 | c1ce9C_ | Alignment | not modelled | 14.2 | 10 | PDB header: helix capping Chain: C: PDB Molecule: protein (gcn4-pmse); PDBTitle: helix capping in the gcn4 leucine zipper |
| 78 | c4dzlE_ | Alignment | not modelled | 14.2 | 33 | PDB header: de novo protein Chain: E: PDB Molecule: coiled-coil peptide cc-tri; PDBTitle: a de novo designed coiled coil cc-tri |
| 79 | c1gclD_ | Alignment | not modelled | 14.2 | 4 | PDB header: leucine zipper Chain: D: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li |
| 80 | c1zimB_ | Alignment | not modelled | 14.1 | 10 | PDB header: leucine zipper Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant asn16gln in the trimeric2 |

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|----|-------------------------|-----------|--------------|------|--|
| | | | | | state |
| 81 | c1zimC_ | Alignment | not modelled | 14.1 | 10 PDB header: leucine zipper Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant asn16gln in the trimeric2 state |
| 82 | d2cfxa1 | Alignment | not modelled | 14.1 | 27 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 83 | c4zryA_ | Alignment | not modelled | 14.0 | 17 PDB header: protein fibril Chain: A: PDB Molecule: keratin, type i cytoskeletal 10; PDBTitle: crystal structure of the heterocomplex between coil 2b domains of2 human intermediate filament proteins keratin 1 (krt1) and keratin 103 (krt10) |
| 84 | c6co6B_ | Alignment | not modelled | 13.9 | 22 PDB header: hydrolase Chain: B: PDB Molecule: probable coa-transferase beta subunit; PDBTitle: crystal structure of rhodococcus jostii rha1 ipdab |
| 85 | c4dzlF_ | Alignment | not modelled | 13.9 | 33 PDB header: de novo protein Chain: F: PDB Molecule: coiled-coil peptide cc-tri; PDBTitle: a de novo designed coiled coil cc-tri |
| 86 | c4dzlB_ | Alignment | not modelled | 13.9 | 33 PDB header: de novo protein Chain: B: PDB Molecule: coiled-coil peptide cc-tri; PDBTitle: a de novo designed coiled coil cc-tri |
| 87 | c4dzlC_ | Alignment | not modelled | 13.9 | 33 PDB header: de novo protein Chain: C: PDB Molecule: coiled-coil peptide cc-tri; PDBTitle: a de novo designed coiled coil cc-tri |
| 88 | c2dq0A_ | Alignment | not modelled | 13.8 | 23 PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog |
| 89 | c1gclA_ | Alignment | not modelled | 13.8 | 3 PDB header: leucine zipper Chain: A: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li |
| 90 | c1gclB_ | Alignment | not modelled | 13.8 | 3 PDB header: leucine zipper Chain: B: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li |
| 91 | c1gclC_ | Alignment | not modelled | 13.8 | 3 PDB header: leucine zipper Chain: C: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li |
| 92 | c3m48A_ | Alignment | not modelled | 13.7 | 14 PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4 leucine zipper peptide mutant |
| 93 | c3utmC_ | Alignment | not modelled | 13.6 | 21 PDB header: transferase/signaling protein Chain: C: PDB Molecule: axin-1; PDBTitle: crystal structure of a mouse tankyrase-axin complex |
| 94 | c1zimA_ | Alignment | not modelled | 13.6 | 11 PDB header: leucine zipper Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant asn16gln in the trimeric2 state |
| 95 | d1ugoa_ | Alignment | not modelled | 13.6 | 9 Fold: Spectrin repeat-like Superfamily: BAG domain Family: BAG domain |
| 96 | c2kogA_ | Alignment | not modelled | 13.6 | 6 PDB header: membrane protein Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: lipid-bound synaptobrevin solution nmr structure |
| 97 | c3i1gA_ | Alignment | not modelled | 13.5 | 14 PDB header: metal binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: crystal structure of a gcn4 leucine zipper mutant at 1.6 a2 resolution |
| 98 | c1uo2A_ | Alignment | not modelled | 13.2 | 3 PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces of four2 helix bundles |
| 99 | c1w5iA_ | Alignment | not modelled | 13.2 | 3 PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: aba does not affect topology of pli. |