
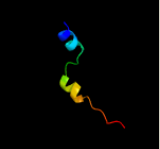





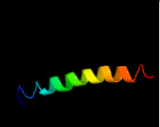

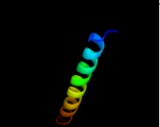





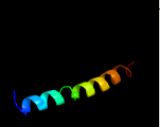

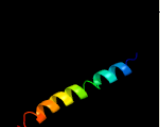











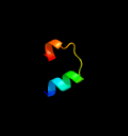



Phyre2

| | |
|---------------|-----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2111c (-) _2370606_2370800 |
| Date | Mon Aug 5 13:25:23 BST 2019 |
| Unique Job ID | 0f65e3e8530472f9 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c4bjrA_ |  Alignment |  | 98.6 | 74 | PDB header: ligase Chain: A: PDB Molecule: pup--protein ligase, prokaryotic ubiquitin-like protein PDBTitle: crystal structure of the complex between prokaryotic2 ubiquitin-like protein pup and its ligase pafa |
| 2 | c3m91B_ |  Alignment |  | 98.5 | 100 | PDB header: hydrolase regulator Chain: B: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein (pup)2 complexed with the amino terminal coiled coil of the mycobacterium3 tuberculosis proteasomal atpase mpa |
| 3 | c3m91D_ |  Alignment |  | 98.5 | 100 | PDB header: hydrolase regulator Chain: D: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein (pup)2 complexed with the amino terminal coiled coil of the mycobacterium3 tuberculosis proteasomal atpase mpa |
| 4 | c3m9dQ_ |  Alignment |  | 98.3 | 100 | PDB header: chaperone Chain: Q: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein pup2 complexed with the hexameric proteasomal atpase mpa which includes3 the amino terminal coiled coil domain and the inter domain |
| 5 | c3m9dP_ |  Alignment |  | 98.3 | 100 | PDB header: chaperone Chain: P: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein pup2 complexed with the hexameric proteasomal atpase mpa which includes3 the amino terminal coiled coil domain and the inter domain |
| 6 | c3m9dR_ |  Alignment |  | 98.3 | 100 | PDB header: chaperone Chain: R: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein pup2 complexed with the hexameric proteasomal atpase mpa which includes3 the amino terminal coiled coil domain and the inter domain |
| 7 | c3m9dG_ |  Alignment |  | 98.3 | 100 | PDB header: chaperone Chain: G: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein pup2 complexed with the hexameric proteasomal atpase mpa which includes3 the amino terminal coiled coil domain and the inter domain |
| 8 | c3m9dl_ |  Alignment |  | 98.3 | 100 | PDB header: chaperone Chain: I: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein pup2 complexed with the hexameric proteasomal atpase mpa which includes3 the amino terminal coiled coil domain and the inter domain |
| 9 | c3m9dH_ |  Alignment |  | 98.2 | 100 | PDB header: chaperone Chain: H: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein pup2 complexed with the hexameric proteasomal atpase mpa which includes3 the amino terminal coiled coil domain and the inter domain |
| 10 | c4me7E_ |  Alignment |  | 54.8 | 25 | PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: antitoxin endoai; PDBTitle: crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze |
| 11 | c3v53E_ |  Alignment |  | 44.5 | 36 | PDB header: rna binding protein Chain: E: PDB Molecule: rna-binding protein 25; PDBTitle: crystal structure of human rbm25 |

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|----|-------------------------|-----------|---|------|----|---|
| 12 | c3ri2B_ | Alignment |  | 42.2 | 24 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, padr-like family; PDBTitle: crystal structure of padr family transcriptional regulator from 2 eggerthella lenta dsm 2243 |
| 13 | d1or4a_ | Alignment |  | 30.8 | 19 | Fold: Globin-like Superfamily: Globin-like Family: Globins |
| 14 | c3lxxA_ | Alignment |  | 27.2 | 32 | PDB header: immune system Chain: A: PDB Molecule: gtpase imap family member 4; PDBTitle: crystal structure of human gtpase imap family member 4 |
| 15 | d2hzab1 | Alignment |  | 25.9 | 36 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 16 | c3j47P_ | Alignment |  | 25.7 | 22 | PDB header: protein binding Chain: P: PDB Molecule: 26s proteasome regulatory subunit rpn5; PDBTitle: formation of an intricate helical bundle dictates the assembly of the 2 26s proteasome lid |
| 17 | c4dvgB_ | Alignment |  | 25.1 | 32 | PDB header: gtp binding/actin binding proteins Chain: B: PDB Molecule: diaphanous protein; PDBTitle: crystal structure of e. histolytica formin1 bound to ehrho1-gtppgammas |
| 18 | d1mpla_ | Alignment |  | 24.1 | 18 | Fold: PWI domain Superfamily: PWI domain Family: PWI domain |
| 19 | c2cazF_ | Alignment |  | 21.6 | 40 | PDB header: protein transport Chain: F: PDB Molecule: protein srn2; PDBTitle: escrt-i core |
| 20 | d2hzaa1 | Alignment |  | 21.1 | 36 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 21 | c2jbxA_ | Alignment | not modelled | 18.5 | 41 | PDB header: apoptosis Chain: A: PDB Molecule: m11l protein; PDBTitle: crystal structure of the myxoma virus anti-apoptotic2 protein m11l |
| 22 | d2bj7a1 | Alignment | not modelled | 15.8 | 32 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like |
| 23 | c2f31A_ | Alignment | not modelled | 15.8 | 29 | PDB header: structural protein Chain: A: PDB Molecule: diaphanous protein homolog 1; PDBTitle: crystal structure of the autoinhibitory switch in formin mdia1; the 2 did/dad complex |
| 24 | c2k5eA_ | Alignment | not modelled | 14.9 | 20 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195 |
| 25 | c3p1jC_ | Alignment | not modelled | 14.9 | 30 | PDB header: hydrolase Chain: C: PDB Molecule: gtpase imap family member 2; PDBTitle: crystal structure of human gtpase imap family member 2 in the 2 nucleotide-free state |
| 26 | d1hx1b_ | Alignment | not modelled | 14.3 | 19 | Fold: Spectrin repeat-like Superfamily: BAG domain Family: BAG domain |
| 27 | d2qtia1 | Alignment | not modelled | 14.0 | 40 | Fold: YejL-like Superfamily: YejL-like Family: YejL-like |
| 28 | d2juwa1 | Alignment | not modelled | 13.5 | 40 | Fold: YejL-like Superfamily: YejL-like Family: YejL-like |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c2o42B | Alignment | not modelled | 13.1 | 41 | PDB header: apoptosis inhibitor Chain: B: PDB Molecule: m11l protein; PDBTitle: crystal structure of m11l, bcl-2 homolog from myxoma virus |
| 30 | c2vcpD | Alignment | not modelled | 12.9 | 56 | PDB header: structural protein Chain: D: PDB Molecule: neural wiskott-aldrich syndrome protein; PDBTitle: crystal structure of n-wasp vc domain in complex with skeletal actin |
| 31 | c2vcpE | Alignment | not modelled | 12.9 | 56 | PDB header: structural protein Chain: E: PDB Molecule: neural wiskott-aldrich syndrome protein; PDBTitle: crystal structure of n-wasp vc domain in complex with skeletal actin |
| 32 | c5us5B | Alignment | not modelled | 12.7 | 25 | PDB header: structural genomics Chain: B: PDB Molecule: upf0297 protein ef_1202; PDBTitle: solution structure of the ireb homodimer |
| 33 | c2k19A | Alignment | not modelled | 12.1 | 43 | PDB header: antimicrobial protein Chain: A: PDB Molecule: putative piscicolin 126 immunity protein; PDBTitle: nmr solution structure of pisi |
| 34 | c3zrjX | Alignment | not modelled | 10.8 | 83 | PDB header: chaperone/peptide Chain: X: PDB Molecule: vipb; PDBTitle: complex of clpv n-domain with vipb peptide |
| 35 | d2jrx1 | Alignment | not modelled | 10.5 | 40 | Fold: YejL-like Superfamily: YejL-like Family: YejL-like |
| 36 | d2jpqa1 | Alignment | not modelled | 10.3 | 33 | Fold: YejL-like Superfamily: YejL-like Family: YejL-like |
| 37 | c1z2tA | Alignment | not modelled | 10.3 | 63 | PDB header: lipid binding protein Chain: A: PDB Molecule: anchor peptide ser65-leu87 of almgs; PDBTitle: nmr structure study of anchor peptide ser65-leu87 of enzyme2 acholeplasma laidlawii monoglycosyldiacyl glycerol3 synthase (almgs) in dhpc micelles |
| 38 | c3m3nW | Alignment | not modelled | 10.0 | 56 | PDB header: structural protein Chain: W: PDB Molecule: neural wiskott-aldrich syndrome protein; PDBTitle: structure of a longitudinal actin dimer assembled by tandem w domains |
| 39 | d1v5sa | Alignment | not modelled | 9.5 | 43 | Fold: TBP-like Superfamily: KA1-like Family: Kinase associated domain 1, KA1 |
| 40 | c4c9yB | Alignment | not modelled | 9.5 | 16 | PDB header: cell cycle Chain: B: PDB Molecule: spindle and kinetochore-associated protein 1; PDBTitle: structural basis for the microtubule binding of the human2 kinetochore ska complex |
| 41 | c4o6bA | Alignment | not modelled | 9.4 | 31 | PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 1; PDBTitle: dengue type2 virus non-structural protein 1 (ns1) form 1 crystal |
| 42 | c3onjA | Alignment | not modelled | 9.3 | 19 | PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain |
| 43 | c4zvbD | Alignment | not modelled | 9.2 | 5 | PDB header: signaling protein Chain: D: PDB Molecule: diguanilate cyclase dosc; PDBTitle: crystal structure of globin domain of the e. coli dosc - form ii2 (ferrous) |
| 44 | c4wfdA | Alignment | not modelled | 9.1 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of the rrp6-rrp47-mtr4 interaction |
| 45 | c3zrjY | Alignment | not modelled | 9.0 | 83 | PDB header: chaperone/peptide Chain: Y: PDB Molecule: vipb; PDBTitle: complex of clpv n-domain with vipb peptide |
| 46 | d1vcsa1 | Alignment | not modelled | 8.6 | 14 | Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins |
| 47 | c4uiqA | Alignment | not modelled | 8.5 | 10 | PDB header: transferase Chain: A: PDB Molecule: globin-coupled sensor with diguanilate cyclase activity; PDBTitle: isolated globin domain of the bordetella pertussis globin-2 coupled sensor with a heme at the dimer interface |
| 48 | c1q5vB | Alignment | not modelled | 8.4 | 28 | PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr |
| 49 | d2bapa1 | Alignment | not modelled | 8.4 | 29 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Diap1 N-terminal region-like |
| 50 | c2lycA | Alignment | not modelled | 8.2 | 21 | PDB header: protein binding Chain: A: PDB Molecule: spindle and kinetochore-associated protein 1 homolog; PDBTitle: structure of c-terminal domain of ska1 |
| 51 | d2plca | Alignment | not modelled | 8.2 | 20 | Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Bacterial PLC |
| 52 | d2g84a1 | Alignment | not modelled | 8.1 | 26 | Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like |
| 53 | d1kwga3 | Alignment | not modelled | 8.0 | 25 | Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: A4 beta-galactosidase middle domain |
| 54 | c2pi9E | Alignment | not modelled | 7.9 | 83 | PDB header: signaling protien Chain: E: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal PDB header: signaling protien |

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|----|-------------------------|-----------|--------------|-----|----|--|
| 55 | c2pl9F_ | Alignment | not modelled | 7.9 | 83 | Chain: F; PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal PDB header: signaling protien |
| 56 | c2pl9D_ | Alignment | not modelled | 7.9 | 83 | Chain: D; PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal PDB header: viral protein |
| 57 | c5k6kB_ | Alignment | not modelled | 7.8 | 38 | Chain: B; PDB Molecule: zika virus protein; PDBTitle: zika virus non-structural protein 1 (ns1) |
| 58 | c2v8sV_ | Alignment | not modelled | 7.8 | 29 | PDB header: protein transport Chain: V; PDB Molecule: vesicle transport through interaction with PDBTitle: vti1b habc domain - epsinr enth domain complex |
| 59 | c2w31A_ | Alignment | not modelled | 7.8 | 26 | PDB header: oxygen transport Chain: A; PDB Molecule: globin; PDBTitle: globin domain of geobacter sulfurreducens globin-coupled sensor |
| 60 | d2juza1 | Alignment | not modelled | 7.6 | 20 | Fold: YejL-like Superfamily: YejL-like Family: YejL-like |
| 61 | c4geqF_ | Alignment | not modelled | 7.5 | 50 | PDB header: cell cycle Chain: F; PDB Molecule: kinetochore-associated protein cnn1; PDBTitle: crystal structure of the spc24-spc25/cnn1 binding interface |
| 62 | c2jpkA_ | Alignment | not modelled | 7.3 | 25 | PDB header: antimicrobial protein Chain: A; PDB Molecule: bacteriocin lactococcin-g subunit beta; PDBTitle: lactococcin g-b in dpc |
| 63 | d1i6pa_ | Alignment | not modelled | 7.2 | 21 | Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab |
| 64 | c2lciA_ | Alignment | not modelled | 7.2 | 47 | PDB header: de novo protein Chain: A; PDB Molecule: protein or36; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or36 (casd3 target) |
| 65 | c3ulpC_ | Alignment | not modelled | 7.2 | 36 | PDB header: dna binding protein/dna Chain: C; PDB Molecule: single-strand binding protein; PDBTitle: plasmodium falciparum ssb complex with ssdna |
| 66 | c4lkuD_ | Alignment | not modelled | 7.1 | 64 | PDB header: transport protein Chain: D; PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance |
| 67 | d3ulla_ | Alignment | not modelled | 7.1 | 36 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB |
| 68 | c3p1jB_ | Alignment | not modelled | 7.0 | 30 | PDB header: hydrolase Chain: B; PDB Molecule: gtpase imap family member 2; PDBTitle: crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state |
| 69 | c4lkuC_ | Alignment | not modelled | 7.0 | 64 | PDB header: transport protein Chain: C; PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance |
| 70 | d2hgka1 | Alignment | not modelled | 6.9 | 21 | Fold: Bromodomain-like Superfamily: YqcC-like Family: YqcC-like |
| 71 | c4lkuE_ | Alignment | not modelled | 6.8 | 64 | PDB header: transport protein Chain: E; PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance |
| 72 | d2ptda_ | Alignment | not modelled | 6.8 | 15 | Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Bacterial PLC |
| 73 | c5j0kA_ | Alignment | not modelled | 6.7 | 37 | PDB header: de novo protein Chain: A; PDB Molecule: designed protein 214hc2_23; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity |
| 74 | d1l5ia_ | Alignment | not modelled | 6.7 | 44 | Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: DNA-binding domain of REP protein |
| 75 | c4lkuB_ | Alignment | not modelled | 6.5 | 64 | PDB header: transport protein Chain: B; PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance |
| 76 | c4lkuA_ | Alignment | not modelled | 6.5 | 64 | PDB header: transport protein Chain: A; PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance |
| 77 | c2bj3D_ | Alignment | not modelled | 6.4 | 32 | PDB header: transcription Chain: D; PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo |
| 78 | c4h62V_ | Alignment | not modelled | 6.3 | 36 | PDB header: transcription Chain: V; PDB Molecule: mediator of rna polymerase ii transcription subunit 22; PDBTitle: structure of the saccharomyces cerevisiae mediator subcomplex2 med17c/med11c/med22c |
| 79 | c6dkmA_ | Alignment | not modelled | 6.2 | 45 | PDB header: de novo protein Chain: A; PDB Molecule: dhd131_a; PDBTitle: dhd131 |

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|----|-------------------------|-----------|--------------|-----|----|--|
| 80 | d2fdoa1 | Alignment | not modelled | 6.0 | 50 | Fold: AF2331-like Superfamily: AF2331-like Family: AF2331-like |
| 81 | c1nzeA | Alignment | not modelled | 5.9 | 8 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxygen-evolving enhancer protein 3; PDBTitle: crystal structure of psbq polypeptide of photosystem ii2 from higher plants |
| 82 | d1nzea | Alignment | not modelled | 5.9 | 8 | Fold: Four-helical up-and-down bundle Superfamily: Oxygen-evolving enhancer protein 3, Family: Oxygen-evolving enhancer protein 3, |
| 83 | c6a6iG | Alignment | not modelled | 5.8 | 42 | PDB header: hydrolase Chain: G: PDB Molecule: excision repair cross-complementing rodent repair PDBTitle: crystal structure of the winged-helix domain of cockayne syndrome2 group b protein in complex with ubiquitin |
| 84 | d2dt5a1 | Alignment | not modelled | 5.8 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional repressor Rex, N-terminal domain |
| 85 | c2xtdB | Alignment | not modelled | 5.7 | 50 | PDB header: transcription Chain: B: PDB Molecule: tbl1 f-box-like/wd repeat-containing protein tbl1x; PDBTitle: structure of the tbl1 tetramerisation domain |
| 86 | c5f9yB | Alignment | not modelled | 5.7 | 21 | PDB header: ligase Chain: B: PDB Molecule: aminoacyl-trna synthetase; PDBTitle: crystal structure of prolyl-trna synthetase from cryptosporidium2 parvum complexed with l-proline and amp |
| 87 | c3j2iQ | Alignment | not modelled | 5.5 | 23 | PDB header: ribosome Chain: Q: PDB Molecule: 50s ribosomal protein l19e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins) |
| 88 | c2xteH | Alignment | not modelled | 5.5 | 50 | PDB header: transcription Chain: H: PDB Molecule: f-box-like/wd repeat-containing protein tbl1x; PDBTitle: structure of the tbl1 tetramerisation domain |
| 89 | c4g0mB | Alignment | not modelled | 5.5 | 18 | PDB header: gene regulation Chain: B: PDB Molecule: protein argonaute 2; PDBTitle: crystal structure of arabidopsis thaliana ago2 mid domain |
| 90 | d1xhja | Alignment | not modelled | 5.5 | 32 | Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like |
| 91 | c4esfA | Alignment | not modelled | 5.3 | 21 | PDB header: transcription Chain: A: PDB Molecule: padr-like transcriptional regulator; PDBTitle: crystal structure of padr-like transcriptional regulator (bce3449)2 from bacillus cereus strain atcc 10987 |
| 92 | d2csba1 | Alignment | not modelled | 5.3 | 31 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain |
| 93 | c4c0nA | Alignment | not modelled | 5.3 | 14 | PDB header: oxygen transport Chain: A: PDB Molecule: 2-on-2 hemoglobin; PDBTitle: crystal structure of non symbiotic plant hemoglobin ahb3 (glb3) from2 arabidopsis thaliana |
| 94 | d2otaa1 | Alignment | not modelled | 5.2 | 20 | Fold: YejL-like Superfamily: YejL-like Family: YejL-like |
| 95 | c6ahrL | Alignment | not modelled | 5.2 | 30 | PDB header: hydrolase/rna Chain: L: PDB Molecule: ribonuclease p protein subunit p40; PDBTitle: cryo-em structure of human ribonuclease p |
| 96 | d1rq8a | Alignment | not modelled | 5.2 | 33 | Fold: IF3-like Superfamily: YhbY-like Family: YhbY-like |
| 97 | c5dolB | Alignment | not modelled | 5.1 | 32 | PDB header: replication Chain: B: PDB Molecule: initiation-control protein yaba; PDBTitle: crystal structure of yaba amino-terminal domain from bacillus subtilis |
| 98 | c3v18A | Alignment | not modelled | 5.1 | 15 | PDB header: lyase Chain: A: PDB Molecule: 1-phosphatidylinositol phosphodiesterase; PDBTitle: structure of the phosphatidylinositol-specific phospholipase c from2 staphylococcus aureus |
| 99 | c5a48B | Alignment | not modelled | 5.1 | 29 | PDB header: protein binding Chain: B: PDB Molecule: maternal effect protein oskar; PDBTitle: crystal structure of the lotus domain (aa 139-240) of drosophila2 oskar in p65 |