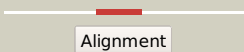

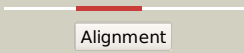



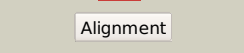



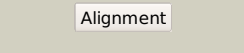

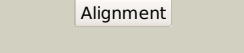



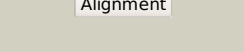
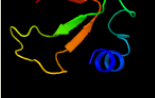
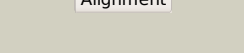
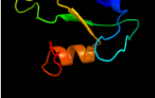
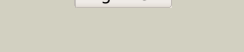












Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1587c_(-)_1788169_1789170 |
| Date | Fri Aug 2 13:30:17 BST 2019 |
| Unique Job ID | 901b180e8e303f7d |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c2qgpA_ |  Alignment |  | 98.8 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: hnh endonuclease; PDBTitle: x-ray structure of the hnh endonuclease from geobacter2 metallireducens. northeast structural genomics consortium target3 gmr87. |
| 2 | c6ghcA_ |  Alignment |  | 98.8 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent ecomcra restriction endonuclease |
| 3 | c5x1hS_ |  Alignment |  | 98.6 | 14 | PDB header: protein transport Chain: S: PDB Molecule: icmj (-dotn); PDBTitle: structure of legionella pneumophila dotn |
| 4 | c5mkwA_ |  Alignment |  | 98.4 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: dna annealing helicase and endonuclease zranb3; PDBTitle: crystal structure of the human zranb3 hnh domain |
| 5 | c5vgbA_ |  Alignment |  | 97.6 | 17 | PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of nmecas9 hnh domain bound to anti-crispr acric1 |
| 6 | c5h0mA_ |  Alignment |  | 97.6 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: hnh endonuclease; PDBTitle: crystal structure of deep-sea thermophilic bacteriophage gve2 hnh2 endonuclease with zinc ion |
| 7 | c4ogeA_ |  Alignment |  | 96.6 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: hnh endonuclease domain protein; PDBTitle: crystal structure of the type ii-c cas9 enzyme from actinomyces2 naeslundii |
| 8 | c5zmmD_ |  Alignment |  | 96.1 | 22 | PDB header: dna binding protein Chain: D: PDB Molecule: uncharacterized protein mcra; PDBTitle: structure of the type iv phosphorothioation-dependent restriction2 endonuclease scomcra |
| 9 | c5axwA_ |  Alignment |  | 95.5 | 13 | PDB header: hydrolase/rna/dna Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of staphylococcus aureus cas9 in complex with sgrna2 and target dna (ttgggt pam) |
| 10 | c6ghsA_ |  Alignment |  | 91.2 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease |
| 11 | d2gykb1 |  Alignment |  | 90.4 | 15 | Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif |

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|----|-------------------------|-----------|---|------|----|---|
| 12 | d2jb0b1 | Alignment |  | 80.5 | 19 | Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif |
| 13 | c4cmqB_ | Alignment |  | 71.8 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9 |
| 14 | c5ew5C_ | Alignment |  | 50.0 | 9 | PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9 |
| 15 | c4qkoH_ | Alignment |  | 49.4 | 16 | PDB header: antimicrobial protein Chain: H: PDB Molecule: pyocin-s2; PDBTitle: the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms |
| 16 | c7ceiB_ | Alignment |  | 41.8 | 13 | PDB header: immune system Chain: B: PDB Molecule: protein (colicin e7 immunity protein); PDBTitle: the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein |
| 17 | c4uhpA_ | Alignment |  | 37.7 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex |
| 18 | d1a1ga1 | Alignment |  | 28.9 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 19 | c2drxA_ | Alignment |  | 28.7 | 73 | PDB header: structural protein Chain: A: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-(log)2-(pog)4 |
| 20 | c2drxB_ | Alignment |  | 28.7 | 80 | PDB header: structural protein Chain: B: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-(log)2-(pog)4 |
| 21 | d2dlka1 | Alignment | not modelled | 28.4 | 50 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 22 | c2drtA_ | Alignment | not modelled | 27.5 | 80 | PDB header: structural protein Chain: A: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5 |
| 23 | c2drtB_ | Alignment | not modelled | 27.5 | 80 | PDB header: structural protein Chain: B: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5 |
| 24 | c2drxC_ | Alignment | not modelled | 27.1 | 80 | PDB header: structural protein Chain: C: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-(log)2-(pog)4 |
| 25 | c2drtC_ | Alignment | not modelled | 27.1 | 80 | PDB header: structural protein Chain: C: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5 |
| 26 | d1zfdA_ | Alignment | not modelled | 24.1 | 36 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 27 | d1a1ia1 | Alignment | not modelled | 23.8 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 28 | c1va1A_ | Alignment | not modelled | 21.4 | 21 | PDB header: transcription Chain: A: PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1) |
| 29 | c2pobC_ | Alignment | not modelled | 20.9 | 67 | PDB header: hydrolase Chain: C: PDB Molecule: mb1 collagen-like peptide; |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c3pobC | Alignment | not modelled | 20.9 | 67 | PDBTitle: crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl |
| 30 | c3ponB | Alignment | not modelled | 20.9 | 67 | PDB header: unknown function Chain: B: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of mbl collagen-like peptide |
| 31 | c3ponA | Alignment | not modelled | 20.9 | 67 | PDB header: unknown function Chain: A: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of mbl collagen-like peptide |
| 32 | c3pobB | Alignment | not modelled | 20.9 | 67 | PDB header: hydrolase Chain: B: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl |
| 33 | c3pobD | Alignment | not modelled | 20.9 | 67 | PDB header: hydrolase Chain: D: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl |
| 34 | d1a1ha1 | Alignment | not modelled | 20.0 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 35 | c2mqcC | Alignment | not modelled | 19.0 | 44 | PDB header: hydrolase Chain: C: PDB Molecule: thp_l_and_m_chain; PDBTitle: transient collagen triple helix binding to a key metalloproteinase in2 invasion and development: spin labels to structure |
| 36 | c2mqcB | Alignment | not modelled | 19.0 | 44 | PDB header: hydrolase Chain: B: PDB Molecule: thp_l_and_m_chain; PDBTitle: transient collagen triple helix binding to a key metalloproteinase in2 invasion and development: spin labels to structure |
| 37 | d1ncsa | Alignment | not modelled | 18.8 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 38 | d1ubdc3 | Alignment | not modelled | 17.6 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 39 | d1sp2a | Alignment | not modelled | 17.6 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 40 | d1u86a1 | Alignment | not modelled | 17.4 | 43 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 41 | c2liyA | Alignment | not modelled | 17.1 | 29 | PDB header: hormone Chain: A: PDB Molecule: epidermal patterning factor-like protein 9; PDBTitle: plant peptide hormone regulating stomatal density |
| 42 | d2glia3 | Alignment | not modelled | 16.1 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 43 | d1aaya1 | Alignment | not modelled | 16.1 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 44 | d1tf3a2 | Alignment | not modelled | 15.5 | 21 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 45 | d2glia4 | Alignment | not modelled | 14.4 | 38 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 46 | c1pxeA | Alignment | not modelled | 14.3 | 45 | PDB header: metal binding protein Chain: A: PDB Molecule: neural zinc finger transcription factor 1; PDBTitle: solution structure of a cchhc domain of neural zinc finger2 factor-1 |
| 47 | c6cd2C | Alignment | not modelled | 14.2 | 43 | PDB header: membrane protein/chaperone Chain: C: PDB Molecule: outer membrane usher protein papc; PDBTitle: crystal structure of the papc usher bound to the chaperone-adhesin2 papd-papg |
| 48 | d1zela1 | Alignment | not modelled | 14.2 | 29 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rv2827c N-terminal domain-like |
| 49 | c1cagC | Alignment | not modelled | 14.1 | 43 | PDB header: collagen Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution |
| 50 | c1cagA | Alignment | not modelled | 14.1 | 43 | PDB header: collagen Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution |
| 51 | d1f2ig1 | Alignment | not modelled | 14.0 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 52 | d1tf6a1 | Alignment | not modelled | 12.7 | 33 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 53 | c1cgdA | Alignment | not modelled | 12.5 | 60 | PDB header: collagen Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide |
| 54 | c1cgdB | Alignment | not modelled | 12.5 | 60 | PDB header: collagen Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide |
| 55 | c1cgdC | Alignment | not modelled | 12.5 | 60 | PDB header: collagen Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide |

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|----|-------------------------|-----------|--------------|------|----|---|
| 56 | c1cagB_ | Alignment | not modelled | 12.5 | 60 | PDB header: collagen Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution |
| 57 | c2i0zA_ | Alignment | not modelled | 12.3 | 29 | PDB header: viral protein Chain: A: PDB Molecule: glycoprotein g2; PDBTitle: solution structure of a zinc-binding domain from the junin virus2 envelope glycoprotein |
| 58 | d2dlka2 | Alignment | not modelled | 11.9 | 38 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 59 | c2e76D_ | Alignment | not modelled | 11.4 | 15 | PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus |
| 60 | c2f6aJ_ | Alignment | not modelled | 11.0 | 60 | PDB header: cell adhesion/structural protein Chain: J: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure |
| 61 | c5anrC_ | Alignment | not modelled | 10.4 | 32 | PDB header: rna binding protein Chain: C: PDB Molecule: eukaryotic translation initiation factor 4e transporter; PDBTitle: structure of a human 4e-t - ddx6 - cnot1 complex |
| 62 | c2f6aG_ | Alignment | not modelled | 9.9 | 60 | PDB header: cell adhesion/structural protein Chain: G: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure |
| 63 | c2f6aI_ | Alignment | not modelled | 9.9 | 60 | PDB header: cell adhesion/structural protein Chain: I: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure |
| 64 | c2f6aE_ | Alignment | not modelled | 9.9 | 60 | PDB header: cell adhesion/structural protein Chain: E: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure |
| 65 | c2f6aH_ | Alignment | not modelled | 9.9 | 60 | PDB header: cell adhesion/structural protein Chain: H: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure |
| 66 | c2f6aF_ | Alignment | not modelled | 9.9 | 60 | PDB header: cell adhesion/structural protein Chain: F: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure |
| 67 | d1ubdc4 | Alignment | not modelled | 9.9 | 33 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 68 | c2lb0A_ | Alignment | not modelled | 9.8 | 17 | PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide |
| 69 | c2lazA_ | Alignment | not modelled | 9.8 | 17 | PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide |
| 70 | d1imta2 | Alignment | not modelled | 9.7 | 16 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Colipase-like Family: Colipase-like |
| 71 | c3le4A_ | Alignment | not modelled | 9.2 | 20 | PDB header: nuclear protein Chain: A: PDB Molecule: microprocessor complex subunit dgcr8; PDBTitle: crystal structure of the dgcr8 dimerization domain |
| 72 | d1tf3a1 | Alignment | not modelled | 9.2 | 38 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 73 | c2kq0A_ | Alignment | not modelled | 9.0 | 21 | PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: human nedd4 3rd ww domain complex with ebola zaire virus matrix2 protein vp40 derived peptide ilptappeynea |
| 74 | c2jydA_ | Alignment | not modelled | 8.7 | 40 | PDB header: metal binding protein Chain: A: PDB Molecule: f5 domain of myelin transcription factor 1; PDBTitle: structure of the fifth zinc finger of myelin transcription2 factor 1 |
| 75 | c5g2xC_ | Alignment | not modelled | 8.6 | 15 | PDB header: transferase Chain: C: PDB Molecule: group ii intron-encoded protein ltra; PDBTitle: structure a of group ii intron complexed with its reverse2 transcriptase |
| 76 | c2mq5D_ | Alignment | not modelled | 8.1 | 42 | PDB header: hydrolase Chain: D: PDB Molecule: thp_t_chain; PDBTitle: transient collagen triple helix binding to a key metalloproteinase in2 invasion and development: spin labels to structure |
| 77 | c1rb8J_ | Alignment | not modelled | 7.9 | 50 | PDB header: virus/dna Chain: J: PDB Molecule: small core protein; PDBTitle: the phix174 dna binding protein j in two different capsid2 environments. |
| 78 | c1zelA_ | Alignment | not modelled | 7.7 | 24 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rv2827c; PDBTitle: crystal structure of rv2827c protein from mycobacterium tuberculosis |
| 79 | d1p9pa_ | Alignment | not modelled | 7.3 | 29 | Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD |
| 80 | d1bhia_ | Alignment | not modelled | 7.0 | 63 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 81 | c1tk7A_ | Alignment | not modelled | 6.8 | 11 | PDB header: signaling protein Chain: A: PDB Molecule: cg4244-pb; PDBTitle: nmr structure of ww domains (ww3-4) from suppressor of2 deltex |

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|----|-------------------------|-----------|--------------|-----|----|---|
| 82 | c6etxR | Alignment | not modelled | 6.5 | 36 | PDB header: dna binding protein Chain: R: PDB Molecule: ino80 complex subunit b; PDBTitle: cryo-em structure of the human ino80 complex bound to nucleosome |
| 83 | c4gyxB | Alignment | not modelled | 6.5 | 75 | PDB header: structural protein, blood clotting Chain: B: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot |
| 84 | c4gyxA | Alignment | not modelled | 6.5 | 75 | PDB header: structural protein, blood clotting Chain: A: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot |
| 85 | c2jtuA | Alignment | not modelled | 6.4 | 58 | PDB header: toxin Chain: A: PDB Molecule: i-superfamily conotoxin r11a; PDBTitle: nmr structure of iota-rxia(38) |
| 86 | c4gyxC | Alignment | not modelled | 6.4 | 67 | PDB header: structural protein, blood clotting Chain: C: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot |
| 87 | c2jryA | Alignment | not modelled | 6.4 | 58 | PDB header: toxin Chain: A: PDB Molecule: i-superfamily conotoxin r11a; PDBTitle: structure and sodium channel activity of an excitatory i1-2 superfamily conotoxin |
| 88 | d1kp0a1 | Alignment | not modelled | 6.3 | 50 | Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain |
| 89 | c1zw8A | Alignment | not modelled | 6.2 | 38 | PDB header: transcription Chain: A: PDB Molecule: zinc-responsive transcriptional regulator zap1; PDBTitle: solution structure of a zap1 zinc-responsive domain2 provides insights into metalloregulatory transcriptional3 repression in saccharomyces cerevisiae |
| 90 | c2y5tG | Alignment | not modelled | 6.0 | 64 | PDB header: immune system Chain: G: PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide |
| 91 | d2evra1 | Alignment | not modelled | 6.0 | 21 | Fold: SH3-like barrel Superfamily: Prokaryotic SH3-related domain Family: Spr N-terminal domain-like |
| 92 | c2v53B | Alignment | not modelled | 6.0 | 62 | PDB header: cell adhesion Chain: B: PDB Molecule: collagen alpha-1(iii) chain; PDBTitle: crystal structure of a sparc-collagen complex |
| 93 | c2v53C | Alignment | not modelled | 6.0 | 62 | PDB header: cell adhesion Chain: C: PDB Molecule: collagen alpha-1(iii) chain; PDBTitle: crystal structure of a sparc-collagen complex |
| 94 | c2v53D | Alignment | not modelled | 6.0 | 62 | PDB header: cell adhesion Chain: D: PDB Molecule: collagen alpha-1(iii) chain; PDBTitle: crystal structure of a sparc-collagen complex |
| 95 | c4zhjA | Alignment | not modelled | 5.9 | 43 | PDB header: metal binding protein Chain: A: PDB Molecule: mg-chelataze subunit chlh; PDBTitle: crystal structure of the catalytic subunit of magnesium chelataze |
| 96 | c5ydyA | Alignment | not modelled | 5.9 | 17 | PDB header: signaling protein Chain: A: PDB Molecule: ww2 domain and ppxy motif complex; PDBTitle: nmr structure of yap1-2 ww2 domain with lats1 ppxy motif complex |
| 97 | c3pg6D | Alignment | not modelled | 5.9 | 27 | PDB header: ligase Chain: D: PDB Molecule: e3 ubiquitin-protein ligase dtx3l; PDBTitle: the carboxyl terminal domain of human deltex 3-like |
| 98 | c1bkvA | Alignment | not modelled | 5.8 | 67 | PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen |
| 99 | d2f21a1 | Alignment | not modelled | 5.5 | 17 | Fold: WW domain-like Superfamily: WW domain Family: WW domain |