

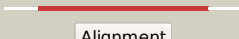

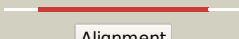












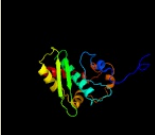






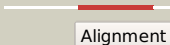

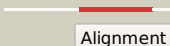







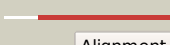





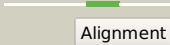
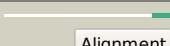
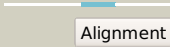

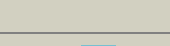
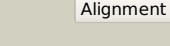

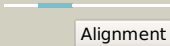


Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1392_(metK)_1566831_1568042 |
| Date | Wed Jul 31 22:05:49 BST 2019 |
| Unique Job ID | ed7a20f0620bd8ff |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c5h9uC_ |  Alignment |  | 100.0 | 59 | PDB header: transferase Chain: C; PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of a thermostable methionine adenosyltransferase |
| 2 | c1rg9D_ |  Alignment |  | 100.0 | 61 | PDB header: transferase Chain: D; PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: s-adenosylmethionine synthetase complexed with sam and ppnp |
| 3 | c3rv2B_ |  Alignment |  | 100.0 | 95 | PDB header: transferase Chain: B; PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum |
| 4 | c2obvA_ |  Alignment |  | 100.0 | 55 | PDB header: transferase Chain: A; PDB Molecule: s-adenosylmethionine synthetase isoform type-1; PDBTitle: crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product |
| 5 | c4odjA_ |  Alignment |  | 100.0 | 51 | PDB header: transferase Chain: A; PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of a putative s-adenosylmethionine synthetase from2 cryptosporidium hominis in complex with s-adenosyl-methionine |
| 6 | c3so4C_ |  Alignment |  | 100.0 | 52 | PDB header: transferase Chain: C; PDB Molecule: methionine-adenosyltransferase; PDBTitle: methionine-adenosyltransferase from entamoeba histolytica |
| 7 | c3imlB_ |  Alignment |  | 100.0 | 60 | PDB header: transferase Chain: B; PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei |
| 8 | c4le5A_ |  Alignment |  | 100.0 | 43 | PDB header: transferase Chain: A; PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: structure of an unusual s-adenosylmethionine synthetase from2 campylobacter jejuni |
| 9 | d1mxaa3 |  Alignment |  | 100.0 | 67 | Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase |
| 10 | d1qm4a3 |  Alignment |  | 100.0 | 62 | Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase |
| 11 | d2p02a3 |  Alignment |  | 100.0 | 61 | Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase |

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|----|-------------------------|---|---|-------|----|---|
| 12 | d1mxaa2 |  Alignment |  | 100.0 | 50 | Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase |
| 13 | d2p02a2 |  Alignment |  | 100.0 | 45 | Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase |
| 14 | d1qm4a2 |  Alignment |  | 100.0 | 49 | Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase |
| 15 | d2p02a1 |  Alignment |  | 100.0 | 56 | Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase |
| 16 | d1mxaa1 |  Alignment |  | 100.0 | 60 | Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase |
| 17 | d1qm4a1 |  Alignment |  | 100.0 | 56 | Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase |
| 18 | c4hpaA |  Alignment |  | 99.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of s-adenosylmethionine synthetase from sulfolobus2 solfataricus |
| 19 | c4l4qa |  Alignment |  | 99.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine synthase; PDBTitle: methionine adenosyltransferase |
| 20 | c2mb1a |  Alignment |  | 52.2 | 21 | PDB header: de novo protein Chain: A: PDB Molecule: top7 fold protein top7m13; PDBTitle: solution nmr structure of de novo designed top7 fold protein top7m13,2 northeast structural genomics consortium (nesg) target or33 |
| 21 | d1w9ha1 |  Alignment | not modelled | 52.0 | 14 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: PIWI domain |
| 22 | c4idxA |  Alignment | not modelled | 44.5 | 43 | PDB header: dna binding protein Chain: A: PDB Molecule: nucleocapsid protein; PDBTitle: hexameric crystal structure of schmallenberg virus nucleoprotein |
| 23 | d1u04a2 |  Alignment | not modelled | 39.8 | 22 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: PIWI domain |
| 24 | c3ho1A |  Alignment | not modelled | 38.6 | 25 | PDB header: nucleic acid binding protein/dna/rna Chain: A: PDB Molecule: argonaute; PDBTitle: crystal structure of t. thermophilus argonaute n546 mutant protein2 complexed with dna guide strand and 12-nt rna target strand |
| 25 | c5guhA |  Alignment | not modelled | 37.6 | 18 | PDB header: hydrolase/rna Chain: A: PDB Molecule: piwi; PDBTitle: crystal structure of silkworm piwi-clade argonaute siwi bound to pirna |
| 26 | c4ijsB |  Alignment | not modelled | 37.4 | 38 | PDB header: rna binding protein/rna Chain: B: PDB Molecule: nucleoprotein; PDBTitle: crystal structure of nucleocapsid protein encoded by the prototypic2 member of orthobunyavirus |
| 27 | d1twfc1 |  Alignment | not modelled | 36.6 | 21 | Fold: DCoH-like Superfamily: RBP11-like subunits of RNA polymerase Family: RNA polymerase alpha subunit dimerisation domain |
| 28 | c4bhhZ |  Alignment | not modelled | 36.6 | 48 | PDB header: viral protein/rna Chain: Z: PDB Molecule: nucleoprotein; PDBTitle: crystal structure of tetramer of la crosse virus nucleoprotein in2 complex with srna |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | d1kjna_ | Alignment | not modelled | 34.3 | 29 | Fold: Hypothetical protein MTH777 (MT0777) Superfamily: Hypothetical protein MTH777 (MT0777) Family: Hypothetical protein MTH777 (MT0777) |
| 30 | c2z51A_ | Alignment | not modelled | 34.0 | 35 | PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 2, chloroplast; PDBTitle: crystal structure of arabidopsis cnfu involved in iron-sulfur cluster2 biosynthesis |
| 31 | c2w42A_ | Alignment | not modelled | 33.7 | 16 | PDB header: protein/dna complex Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the structure of a piwi protein from archaeoglobus fulgidus2 complexed with a 16nt dna duplex. |
| 32 | c2w8iG_ | Alignment | not modelled | 31.4 | 28 | PDB header: membrane protein Chain: G: PDB Molecule: putative outer membrane lipoprotein wza; PDBTitle: crystal structure of wza24-345. |
| 33 | c3lvtA_ | Alignment | not modelled | 31.1 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 38; PDBTitle: the crystal structure of a protein in the glycosyl hydrolase family 382 from enterococcus faecalis to 2.55a |
| 34 | c4j1jA_ | Alignment | not modelled | 29.5 | 33 | PDB header: viral protein/dna Chain: A: PDB Molecule: nucleocapsid; PDBTitle: leanyer orthobunyavirus nucleoprotein-ssdna complex |
| 35 | c2mraA_ | Alignment | not modelled | 29.2 | 23 | PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein or459; PDBTitle: solution nmr structure of de novo designed protein, northeast2 structural genomics consortium (nsg) target or459 |
| 36 | c2gjhA_ | Alignment | not modelled | 24.5 | 21 | PDB header: de novo protein Chain: A: PDB Molecule: designed protein; PDBTitle: nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7) |
| 37 | d1to0a_ | Alignment | not modelled | 24.5 | 50 | Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like |
| 38 | c3k8zD_ | Alignment | not modelled | 23.9 | 21 | PDB header: oxidoreductase Chain: D: PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of gudb1 a decrypted secondary glutamate2 dehydrogenase from b. subtilis |
| 39 | d1vh0a_ | Alignment | not modelled | 23.6 | 63 | Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like |
| 40 | c2inrA_ | Alignment | not modelled | 23.2 | 25 | PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 4 subunit a; PDBTitle: crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus |
| 41 | d2fm8a1 | Alignment | not modelled | 23.2 | 28 | Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone |
| 42 | d1ns5a_ | Alignment | not modelled | 22.6 | 40 | Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like |
| 43 | c3kxyV_ | Alignment | not modelled | 22.3 | 54 | PDB header: chaperone/transcription inhibitor Chain: V: PDB Molecule: exsc; PDBTitle: crystal structure of the exsc-exsc complex |
| 44 | d1o6da_ | Alignment | not modelled | 22.1 | 50 | Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like |
| 45 | d2nrqa1 | Alignment | not modelled | 21.9 | 28 | Fold: RL5-like Superfamily: RL5-like Family: SSO1042-like |
| 46 | d1vkha_ | Alignment | not modelled | 21.3 | 19 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Putative serine hydrolase Ydr428c |
| 47 | c2vofA_ | Alignment | not modelled | 20.6 | 4 | PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-related protein a1; PDBTitle: structure of mouse a1 bound to the puma bh3-domain |
| 48 | c5lqwL_ | Alignment | not modelled | 20.4 | 43 | PDB header: splicing Chain: L: PDB Molecule: pre-mrna-splicing factor cwc26; PDBTitle: yeast activated spliceosome |
| 49 | c2jvfA_ | Alignment | not modelled | 19.9 | 9 | PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein |
| 50 | d1mp9a1 | Alignment | not modelled | 19.7 | 20 | Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain |
| 51 | c4v19T_ | Alignment | not modelled | 19.6 | 22 | PDB header: ribosome Chain: T: PDB Molecule: mitoribosomal protein bl19m, mrp19; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2 |
| 52 | c5i4aC_ | Alignment | not modelled | 18.8 | 18 | PDB header: rna binding protein/rna Chain: C: PDB Molecule: argonaute protein; PDBTitle: x-ray crystal structure of marinitoga piezophila argonaute in complex2 with 5' oh guide rna |
| 53 | c2mcdA_ | Alignment | not modelled | 18.3 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: murine norovirus 1; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for murine2 norovirus ns1/2 d94e mutant |
| 54 | c4e0iA_ | Alignment | not modelled | 18.0 | 69 | PDB header: oxidoreductase Chain: A: PDB Molecule: mitochondrial fad-linked sulfhydryl oxidase erv1; PDBTitle: crystal structure of the c30s/c133s mutant of erv1 from saccharomyces2 cerevisiae PDB header: transferase Chain: D: PDB Molecule: ribosomal rna large subunit |

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|----|-------------------------|-----------|--------------|------|----|---|
| 55 | c5zyoD_ | Alignment | not modelled | 18.0 | 50 | Fold: methyltransferase h; PDBTitle: crystal structure of domain-swapped circular-permuted ybea (cp74) from <i>Escherichia coli</i> |
| 56 | d1azpa_ | Alignment | not modelled | 17.9 | 40 | Fold: SH3-like barrel Superfamily: Chromo domain-like Family: "Histone-like" proteins from archaea |
| 57 | d2fiqa1 | Alignment | not modelled | 17.8 | 32 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like |
| 58 | c5vogA_ | Alignment | not modelled | 17.4 | 19 | PDB header: transferase Chain: A; PDB Molecule: putative phosphoribosyltransferase; PDBTitle: crystal structure of a hypothetical protein from <i>Neisseria gonorrhoeae</i> 2 with bound pppp |
| 59 | d1aisa2 | Alignment | not modelled | 17.4 | 13 | Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain |
| 60 | c1u04A_ | Alignment | not modelled | 17.4 | 31 | PDB header: hydrolase/gene regulation Chain: A; PDB Molecule: hypothetical protein pf0537; PDBTitle: crystal structure of full length argonaute from <i>Pyrococcus furiosus</i> |
| 61 | c5awhA_ | Alignment | not modelled | 17.2 | 21 | PDB header: rna binding protein/dna/rna Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: <i>Rhodobacter sphaeroides</i> argonaute in complex with guide rna/target dna2 heteroduplex |
| 62 | c3d4oA_ | Alignment | not modelled | 16.6 | 44 | PDB header: oxidoreductase Chain: A; PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from <i>Bacillus halodurans</i> at 2.10 Å resolution |
| 63 | c2z8uQ_ | Alignment | not modelled | 16.4 | 27 | PDB header: transcription Chain: Q; PDB Molecule: tata-box-binding protein; PDBTitle: <i>Methanococcus jannaschii</i> tbp |
| 64 | c2jkbB_ | Alignment | not modelled | 15.3 | 40 | PDB header: transferase Chain: B; PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: <i>Saccharomyces cerevisiae</i> hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'-3' monophosphate) (orthorhombic crystal form) |
| 65 | d1q33a_ | Alignment | not modelled | 15.2 | 60 | Fold: Nudix Superfamily: Nudix Family: MutT-like |
| 66 | c5theA_ | Alignment | not modelled | 15.2 | 24 | PDB header: rna binding protein/rna Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the c-terminal lobe of a budding yeast argonaute |
| 67 | c5vidG_ | Alignment | not modelled | 15.0 | 18 | PDB header: toxin Chain: G; PDB Molecule: bot.0671.2; PDBTitle: receptor binding domain of bont/b in complex with mini-protein binder2 bot.0671.2 |
| 68 | c5vidI_ | Alignment | not modelled | 15.0 | 18 | PDB header: toxin Chain: I; PDB Molecule: bot.0671.2; PDBTitle: receptor binding domain of bont/b in complex with mini-protein binder2 bot.0671.2 |
| 69 | c3aoeC_ | Alignment | not modelled | 15.0 | 25 | PDB header: oxidoreductase Chain: C; PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of hetero-hexameric glutamate dehydrogenase from <i>Thermus thermophilus</i> (leu bound form) |
| 70 | c5g5tA_ | Alignment | not modelled | 14.8 | 33 | PDB header: hydrolase/dna Chain: A; PDB Molecule: argonaute; PDBTitle: structure of the argonaute protein from <i>Methanocaldococcus jannaschii</i> in2 complex with guide dna |
| 71 | c2mckA_ | Alignment | not modelled | 14.5 | 28 | PDB header: hydrolase Chain: A; PDB Molecule: polyprotein; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for murine2 norovirus cr6 ns1/2 protein |
| 72 | d2bgxa2 | Alignment | not modelled | 14.5 | 21 | Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like |
| 73 | c5ijzH_ | Alignment | not modelled | 14.4 | 24 | PDB header: oxidoreductase Chain: H; PDB Molecule: nadp-specific glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase (gdh) from <i>Corynebacterium</i> 2 glutamicum |
| 74 | c3aogA_ | Alignment | not modelled | 14.3 | 24 | PDB header: oxidoreductase Chain: A; PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase (gdhb) from <i>Thermus</i> 2 <i>thermophilus</i> (glu bound form) |
| 75 | d1csna_ | Alignment | not modelled | 14.0 | 15 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 76 | c6qzka_ | Alignment | not modelled | 14.0 | 13 | PDB header: hydrolase Chain: A; PDB Molecule: <i>Clostridium butyricum</i> argonaute; PDBTitle: structure of <i>Clostridium butyricum</i> argonaute bound to a guide dna (5'2 deoxycytidine) and a 19-mer target dna |
| 77 | d2f9wa2 | Alignment | not modelled | 13.6 | 43 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like |
| 78 | d1t0ga_ | Alignment | not modelled | 13.4 | 39 | Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Steroid-binding domain |
| 79 | c4m6iA_ | Alignment | not modelled | 13.4 | 15 | PDB header: hydrolase Chain: A; PDB Molecule: peptidoglycan amidase rv3717; PDBTitle: structure of the reduced, zn-bound form of <i>Mycobacterium tuberculosis</i> 2 peptidoglycan amidase rv3717 |
| 80 | c1qysA_ | Alignment | not modelled | 13.2 | 29 | PDB header: de novo protein Chain: A; PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold |

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|----|-------------------------|-----------|--------------|------|----|--|
| 81 | c2j58G_ | Alignment | not modelled | 13.2 | 27 | PDB header: membrane protein Chain: G: PDB Molecule: outer membrane lipoprotein wza; PDBTitle: the structure of wza |
| 82 | d1knga_ | Alignment | not modelled | 13.2 | 16 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like |
| 83 | c1v57A_ | Alignment | not modelled | 12.9 | 25 | PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbg; PDBTitle: crystal structure of the disulfide bond isomerase dsbg |
| 84 | d1nh2a2 | Alignment | not modelled | 12.8 | 20 | Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain |
| 85 | c5b3kA_ | Alignment | not modelled | 12.7 | 19 | PDB header: electron transport Chain: A: PDB Molecule: uncharacterized protein pa3435; PDBTitle: c101a mutant of flavodoxin from pseudomonas aeruginosa |
| 86 | c2bmaA_ | Alignment | not modelled | 12.5 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase (nadp+); PDBTitle: the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs |
| 87 | c5b54D_ | Alignment | not modelled | 12.2 | 28 | PDB header: transferase Chain: D: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of hydrogen sulfide-producing enzyme (fn1055) from2 fusobacterium nucleatum: lysine-dimethylated form |
| 88 | d1yvua2 | Alignment | not modelled | 12.1 | 6 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: PIWI domain |
| 89 | c1wnkA_ | Alignment | not modelled | 12.0 | 43 | PDB header: transcription Chain: A: PDB Molecule: fibroin-modulator-binding-protein-1; PDBTitle: nmr structure of fmbp-1 tandem repeat 3 in 30%(v/v) tfe2 solution |
| 90 | c5ylyB_ | Alignment | not modelled | 11.9 | 6 | PDB header: flavoprotein Chain: B: PDB Molecule: nitrate reductase; PDBTitle: crystal structure of the cytochrome b5 reductase domain of ulva2 prolifera nitrate reductase |
| 91 | c2wl2B_ | Alignment | not modelled | 11.8 | 22 | PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit a; PDBTitle: crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8 |
| 92 | c6qt9Y_ | Alignment | not modelled | 11.8 | 37 | PDB header: virus Chain: Y: PDB Molecule: orf 31; PDBTitle: cryo-em structure of sh1 full particle. |
| 93 | d1aisa1 | Alignment | not modelled | 11.8 | 29 | Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain |
| 94 | c4ediC_ | Alignment | not modelled | 11.7 | 17 | PDB header: transport protein Chain: C: PDB Molecule: ethanolamine utilization protein; PDBTitle: disulfide bonded eutl from clostridium perfringens |
| 95 | c2hnbA_ | Alignment | not modelled | 11.6 | 15 | PDB header: electron transport Chain: A: PDB Molecule: protein mioc; PDBTitle: solution structure of a bacterial holo-flavodoxin |
| 96 | d1mtyd_ | Alignment | not modelled | 11.3 | 59 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 97 | c3u27D_ | Alignment | not modelled | 11.3 | 34 | PDB header: structural protein Chain: D: PDB Molecule: microcompartments protein; PDBTitle: crystal structure of ethanolamine utilization protein eutl from2 leptotrichia buccalis c-1013-b |
| 98 | c6cp8D_ | Alignment | not modelled | 11.3 | 39 | PDB header: toxin/antitoxin Chain: D: PDB Molecule: cdii; PDBTitle: contact-dependent growth inhibition toxin-immunity protein complex2 from from e. coli 3006 |
| 99 | c4fmoB_ | Alignment | not modelled | 11.1 | 32 | PDB header: hydrolase Chain: B: PDB Molecule: dna mismatch repair protein pms1; PDBTitle: structure of the c-terminal domain of the saccharomyces cerevisiae2 mutl alpha (mlh1/pms1) heterodimer bound to a fragment of exo1 |