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| Email | mdejesus@rockefeller.edu |
| Description | RVBD0060 (-) _63906_64964 |
| Date | Tue Jul 23 14:50:09 BST 2019 |
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Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c5m3iB_ |  Alignment |  | 100.0 | 100 | PDB header: antitoxin Chain: B: PDB Molecule: rnase iii inhibitor; PDBTitle: macrodomain of mycobacterium tuberculosis darg |
| 2 | c5m31A_ |  Alignment |  | 100.0 | 56 | PDB header: antitoxin Chain: A: PDB Molecule: appr-1-p processing domain protein; PDBTitle: macrodomain of thermus aquaticus darg |
| 3 | c5e3bA_ |  Alignment |  | 100.0 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: macrodomain protein; PDBTitle: structure of macrodomain protein from streptomyces coelicolor |
| 4 | c2eeeA_ |  Alignment |  | 100.0 | 24 | PDB header: gene regulation Chain: A: PDB Molecule: uncharacterized protein c6orf130; PDBTitle: solution structure of the a1pp domain from human protein2 c6orf130 |
| 5 | d2fg1a1 |  Alignment |  | 100.0 | 22 | Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain |
| 6 | c5iitC_ |  Alignment |  | 100.0 | 18 | PDB header: inositol phosphate binding protein Chain: C: PDB Molecule: vacuolar transporter chaperone 4,core histone macro-h2a.1; PDBTitle: structure of spx domain of the yeast inorganic polyphosphate polymerase2 vtc4 crystallized by carrier-driven crystallization in fusion with3 the macro domain of human histone macroh2a1.1 |
| 7 | c2dx6B_ |  Alignment |  | 100.0 | 23 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ttha0132; PDBTitle: crystal structure of conserved hypothetical protein, ttha0132 from2 thermus thermophilus hb8 |
| 8 | c3q71A_ |  Alignment |  | 100.0 | 17 | PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 14; PDBTitle: human parp14 (artd8) - macro domain 2 in complex with adenosine-5-2 diphosphoribose |
| 9 | c3vfgA_ |  Alignment |  | 100.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 14; PDBTitle: human parp14 (artd8, bal2) - macro domains 1 and 2 in complex with2 adenosine-5-diphosphoribose |
| 10 | d1zr5a1 |  Alignment |  | 100.0 | 16 | Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain |
| 11 | c1zr5B_ |  Alignment |  | 100.0 | 16 | PDB header: gene regulation Chain: B: PDB Molecule: h2afy protein; PDBTitle: crystal structure of the macro-domain of human core histone variant2 macroh2a1.2 |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 12 | d1spva_ | Alignment | | 100.0 | 17 | Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain |
| 13 | d1yd9a1 | Alignment | | 100.0 | 17 | Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain |
| 14 | c2xd7B_ | Alignment | | 100.0 | 16 | PDB header: dna binding protein Chain: B; PDB Molecule: core histone macro-h2a.2; PDBTitle: crystal structure of the macro domain of human core histone h2a |
| 15 | c5l9kB_ | Alignment | | 100.0 | 16 | PDB header: hydrolase Chain: B; PDB Molecule: macrod-type macrodomain; PDBTitle: oceanobacillus iheyensis macrodomain with adpr |
| 16 | c3q6zA_ | Alignment | | 99.9 | 20 | PDB header: transferase Chain: A; PDB Molecule: poly [adp-ribose] polymerase 14; PDBTitle: human parp14 (artd8)-macro domain 1 in complex with adenosine-5-2 diphosphoribose |
| 17 | c5iq5A_ | Alignment | | 99.9 | 24 | PDB header: viral protein Chain: A; PDB Molecule: macro domain; PDBTitle: nmr solution structure of mayaro virus macro domain |
| 18 | c4iqyB_ | Alignment | | 99.9 | 17 | PDB header: hydrolase Chain: B; PDB Molecule: o-acetyl-adp-ribose deacetylase macrod2; PDBTitle: crystal structure of the human protein-proximal adp-ribosyl-hydrolase2 macrod2 |
| 19 | d1vhua_ | Alignment | | 99.9 | 21 | Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain |
| 20 | c5ailA_ | Alignment | | 99.9 | 19 | PDB header: transcription Chain: A; PDB Molecule: poly [adp-ribose] polymerase 9; PDBTitle: human parp9 2nd macrodomain |
| 21 | c2x47A_ | Alignment | not modelled | 99.9 | 18 | PDB header: signaling protein Chain: A; PDB Molecule: macro domain-containing protein 1; PDBTitle: crystal structure of human macrod1 |
| 22 | c3kh6A_ | Alignment | not modelled | 99.9 | 20 | PDB header: transferase Chain: A; PDB Molecule: poly [adp-ribose] polymerase 15; PDBTitle: human poly(adp-ribose) polymerase 15, macro domain 2 in complex with2 adenosine-5-diphosphoribose |
| 23 | c4um1A_ | Alignment | not modelled | 99.9 | 14 | PDB header: signaling protein Chain: A; PDB Molecule: ganglioside-induced differentiation-associated protein 2; PDBTitle: crystal structure of ganglioside induced differentiation2 associated protein 2 (gdap2) macro domain |
| 24 | c4ablA_ | Alignment | not modelled | 99.9 | 18 | PDB header: transferase Chain: A; PDB Molecule: poly [adp-ribose] polymerase 14; PDBTitle: human parp14 (artd8, bal2) - macro domain 3 |
| 25 | c3gpgA_ | Alignment | not modelled | 99.9 | 24 | PDB header: viral protein/rna Chain: A; PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of macro domain of chikungunya virus in complex with2 rna |
| 26 | c5fszA_ | Alignment | not modelled | 99.9 | 12 | PDB header: hydrolase Chain: A; PDB Molecule: macrodomain; PDBTitle: crystal structure of trypanosoma cruzi macrodomain |
| 27 | c3ewqA_ | Alignment | not modelled | 99.9 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: non-structural protein 3; PDBTitle: hcov-229e nsp3 adrp domain |
| 28 | c5fsuA_ | Alignment | not modelled | 99.9 | 12 | PDB header: hydrolase Chain: A; PDB Molecule: macrodomain; PDBTitle: crystal structure of trypanosoma brucei macrodomain2 (crystal form 1) |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c3ejfA_ | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A; PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of ibv x-domain at ph 8.5 |
| 30 | c5kivA_ | Alignment | not modelled | 99.9 | 15 | PDB header: hydrolase Chain: A; PDB Molecule: protein- <i>adp-ribose</i> hydrolase; PDBTitle: crystal structure of saumacro (sav0325) |
| 31 | c5dusA_ | Alignment | not modelled | 99.9 | 19 | PDB header: viral protein Chain: A; PDB Molecule: orf1a; PDBTitle: crystal structure of mers-cov macro domain in complex with <i>adp-ribose</i> |
| 32 | c3ejgA_ | Alignment | not modelled | 99.9 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of hcov-229e x-domain |
| 33 | c3gqeA_ | Alignment | not modelled | 99.9 | 20 | PDB header: viral protein Chain: A; PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of macro domain of venezuelan equine encephalitis2 virus |
| 34 | c3ew5B_ | Alignment | not modelled | 99.9 | 15 | PDB header: rna binding protein Chain: B; PDB Molecule: macro domain of non-structural protein 3; PDBTitle: structure of the tetragonal crystal form of x (adrp) domain2 from fcov |
| 35 | d2acfa1 | Alignment | not modelled | 99.9 | 16 | Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain |
| 36 | c2vriA_ | Alignment | not modelled | 99.9 | 16 | PDB header: viral protein Chain: A; PDB Molecule: non-structural protein 3; PDBTitle: structure of the nsp3 x-domain of human coronavirus n163 |
| 37 | c4guaB_ | Alignment | not modelled | 99.9 | 24 | PDB header: hydrolase Chain: B; PDB Molecule: non-structural polyprotein; PDBTitle: alphavirus p23pro-zbd |
| 38 | d1njra_ | Alignment | not modelled | 99.7 | 21 | Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain |
| 39 | c5lw0A_ | Alignment | not modelled | 99.4 | 17 | PDB header: adp-ribose-binding protein Chain: A; PDB Molecule: basic helix-loop-helix, putative, expressed; PDBTitle: oryza sativa apl macrodomain in complex with <i>adp-ribose</i> |
| 40 | c3siiA_ | Alignment | not modelled | 96.4 | 12 | PDB header: hydrolase/hydrolase inhibitor Chain: A; PDB Molecule: poly(<i>adp-ribose</i>) glycohydrolase; PDBTitle: the x-ray crystal structure of poly(<i>adp-ribose</i>) glycohydrolase bound2 to the inhibitor <i>adp-hpd</i> from <i>thermomonospora curvata</i> |
| 41 | c5zdcL_ | Alignment | not modelled | 96.3 | 10 | PDB header: hydrolase Chain: L; PDB Molecule: poly <i>adp-ribose</i> glycohydrolase; PDBTitle: crystal structure of poly(<i>adp-ribose</i>) glycohydrolase (parg) from2 <i>deinococcus radiodurans</i> in complex with <i>adp-ribose</i> (p32) |
| 42 | d1gyta1 | Alignment | not modelled | 91.3 | 11 | Fold: Macro domain-like Superfamily: Macro domain-like Family: Leucine aminopeptidase (Aminopeptidase A), N-terminal domain |
| 43 | c1gytG_ | Alignment | not modelled | 73.5 | 11 | PDB header: hydrolase Chain: G; PDB Molecule: cytosol aminopeptidase; PDBTitle: e. coli aminopeptidase a (pepa) |
| 44 | c3l7wA_ | Alignment | not modelled | 71.5 | 16 | PDB header: transcription Chain: A; PDB Molecule: putative uncharacterized protein smu.1704; PDBTitle: the crystal structure of smu.1704 from <i>streptococcus mutans</i> ua159 |
| 45 | c6omeA_ | Alignment | not modelled | 63.1 | 11 | PDB header: hydrolase Chain: A; PDB Molecule: probable cytosol aminopeptidase; PDBTitle: crystal structure of a probable cytosol aminopeptidase (leucine2 aminopeptidase, lap) from <i>chlamydia trachomatis</i> d/uw-3/cx |
| 46 | c3r0aB_ | Alignment | not modelled | 62.3 | 10 | PDB header: transcription regulator Chain: B; PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from <i>methanosarcina mazei</i> go1 (gi2 21227196) |
| 47 | c1vqwB_ | Alignment | not modelled | 60.6 | 18 | PDB header: structural genomics, unknown function Chain: B; PDB Molecule: protein with similarity to flavin-containing PDBTitle: crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine3 monooxygenases |
| 48 | c5jlsA_ | Alignment | not modelled | 54.7 | 11 | PDB header: transcription Chain: A; PDB Molecule: adhesin competence repressor; PDBTitle: crystal structure of adhesin competence repressor (adcr) from2 <i>streptococcus pyogenes</i> (c-terminally his tagged) |
| 49 | d2esha1 | Alignment | not modelled | 54.0 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like |
| 50 | c3jruB_ | Alignment | not modelled | 51.8 | 9 | PDB header: hydrolase Chain: B; PDB Molecule: probable cytosol aminopeptidase; PDBTitle: crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 <i>xanthomonas oryzae</i> pv. <i>oryzae</i> kacc10331 |
| 51 | c3h8gC_ | Alignment | not modelled | 48.9 | 13 | PDB header: hydrolase Chain: C; PDB Molecule: cytosol aminopeptidase; PDBTitle: bestatin complex structure of leucine aminopeptidase from <i>pseudomonas2 putida</i> |
| 52 | c5zhcA_ | Alignment | not modelled | 48.2 | 15 | PDB header: dna binding protein Chain: A; PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of the padr-family transcriptional regulator rv34882 of <i>mycobacterium tuberculosis</i> h37rv |
| 53 | c5lw6A_ | Alignment | not modelled | 47.3 | 10 | PDB header: adp-ribose binding protein Chain: A; PDB Molecule: ddb_g0293866; PDBTitle: crystal structure of a se-met substituted dictyostelium discoideum2 <i>adp-ribose</i> binding macrodomain (residues 342-563) of ddb_g0293866 |
| | | | | | | PDB header: dna binding protein |

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| 54 | c4hw0B_ | Alignment | not modelled | 46.6 | 13 | Chain: B: PDB Molecule: dna-binding protein sso10a-2; PDBTitle: crystal structure of sso10a-2, a dna-binding protein from <i>Sulfolobus solfataricus</i> |
| 55 | d1r7ja_ | Alignment | not modelled | 45.6 | 12 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Archaeal DNA-binding protein |
| 56 | c5nmwA_ | Alignment | not modelled | 44.9 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of the pyrrolizidine alkaloid n-oxygenase from <i>Zonocerus variegatus</i> in complex with fad |
| 57 | c5x11G_ | Alignment | not modelled | 44.7 | 14 | PDB header: transcription/dna Chain: G: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of <i>Bacillus subtilis</i> padR in complex with operator2 dna |
| 58 | c1fx7C_ | Alignment | not modelled | 43.1 | 15 | PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ideo; PDBTitle: crystal structure of the iron-dependent regulator (ideo) from <i>Mycobacterium tuberculosis</i> |
| 59 | c5zqhA_ | Alignment | not modelled | 42.2 | 12 | PDB header: dna binding protein Chain: A: PDB Molecule: padR family transcriptional regulator; PDBTitle: crystal structure of <i>Streptococcus</i> transcriptional regulator |
| 60 | c5cviB_ | Alignment | not modelled | 41.8 | 15 | PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor |
| 61 | c2qvoA_ | Alignment | not modelled | 39.9 | 23 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein af_1382; PDBTitle: crystal structure of af1382 from <i>Archaeoglobus fulgidus</i> |
| 62 | c1xmaA_ | Alignment | not modelled | 39.8 | 7 | PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulator; PDBTitle: structure of a transcriptional regulator from <i>Clostridium thermocellum</i> 2 cth-833 |
| 63 | d1xmaa_ | Alignment | not modelled | 39.8 | 7 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like |
| 64 | c3krbB_ | Alignment | not modelled | 39.5 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: aldose reductase; PDBTitle: structure of aldose reductase from <i>Giardia lamblia</i> at 1.75a resolution |
| 65 | c5dymA_ | Alignment | not modelled | 39.3 | 10 | PDB header: dna binding protein Chain: A: PDB Molecule: padR-family transcriptional regulator; PDBTitle: crystal structure of a padR family transcription regulator from <i>Hyperthermus</i> <i>Clostridium difficile</i> r20291 - cdpadr_0991 to 1.893 angstrom resolution |
| 66 | d1vp5a_ | Alignment | not modelled | 39.1 | 23 | Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP) |
| 67 | c5h20A_ | Alignment | not modelled | 35.0 | 12 | PDB header: transcription regulator Chain: A: PDB Molecule: putative padR-family transcriptional regulatory protein; PDBTitle: x-ray structure of padR-like transcription factor from <i>Bacteroides fragilis</i> |
| 68 | d1ixra2 | Alignment | not modelled | 34.8 | 32 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain |
| 69 | d1cuka3 | Alignment | not modelled | 34.1 | 24 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain |
| 70 | c2e1nA_ | Alignment | not modelled | 33.3 | 16 | PDB header: circadian clock protein Chain: A: PDB Molecule: pex; PDBTitle: crystal structure of the cyanobacterium circadian clock modifier pex |
| 71 | c2x4hA_ | Alignment | not modelled | 33.3 | 10 | PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from <i>Sulfolobus solfataricus</i> |
| 72 | c4q3mF_ | Alignment | not modelled | 32.6 | 16 | PDB header: hydrolase Chain: F: PDB Molecule: mgs-m4; PDBTitle: crystal structure of mgs-m4, an aldo-keto reductase enzyme from a2 medee basin deep-sea metagenome library |
| 73 | c4esbA_ | Alignment | not modelled | 31.9 | 15 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, padR family; PDBTitle: crystal structure of padR-like transcriptional regulator (bc4206) from <i>Bacillus cereus</i> strain atcc 14579 |
| 74 | c4otkA_ | Alignment | not modelled | 31.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterial enzyme rv2971; PDBTitle: a structural characterization of the isoniazid <i>Mycobacterium tuberculosis</i> drug target, rv2971, in its unliganded form |
| 75 | c2bgsA_ | Alignment | not modelled | 30.7 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: aldose reductase; PDBTitle: holo aldose reductase from barley |
| 76 | c1g3wA_ | Alignment | not modelled | 30.3 | 15 | PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr |
| 77 | c6bsvB_ | Alignment | not modelled | 30.2 | 11 | PDB header: transferase Chain: B: PDB Molecule: xyloglucan 6-xylosyltransferase 1; PDBTitle: crystal structure of xyloglucan xylosyltransferase binary form |
| 78 | c3f8fA_ | Alignment | not modelled | 30.0 | 16 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, padR-like family; PDBTitle: crystal structure of multidrug binding transcriptional regulator Imrr2 complexed with daunomycin |
| 79 | d1bm9a_ | Alignment | not modelled | 29.8 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Replication terminator protein (RTP) |

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| 80 | c3wbwA_ | Alignment | not modelled | 29.7 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative 2,5-diketo-d-gluconic acid reductase; PDBTitle: crystal structure of gox0644 in complex with nadph |
| 81 | c5yf1A_ | Alignment | not modelled | 29.2 | 50 | PDB header: transferase Chain: A: PDB Molecule: carnosine n-methyltransferase; PDBTitle: crystal structure of carnmt1 bound to carnosine and sfg |
| 82 | c3ri2B_ | Alignment | not modelled | 28.3 | 13 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, padr-like family; PDBTitle: crystal structure of padr family transcriptional regulator from2 eggerthella lenta dsm 2243 |
| 83 | d1mzra_ | Alignment | not modelled | 26.7 | 21 | Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP) |
| 84 | c4ftbD_ | Alignment | not modelled | 26.2 | 22 | PDB header: virus Chain: D: PDB Molecule: capsid protein gamma; PDBTitle: crystal structure of the authentic flock house virus particle |
| 85 | c1ixrB_ | Alignment | not modelled | 25.4 | 32 | PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex |
| 86 | c1ixrA_ | Alignment | not modelled | 25.3 | 32 | PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex |
| 87 | c3df8A_ | Alignment | not modelled | 25.0 | 19 | PDB header: transcription Chain: A: PDB Molecule: possible hxlr family transcriptional factor; PDBTitle: the crystal structure of a possible hxlr family transcriptional factor2 from thermoplasma volcanium gss1 |
| 88 | c2h5xA_ | Alignment | not modelled | 24.3 | 28 | PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis |
| 89 | d2ch5a2 | Alignment | not modelled | 23.8 | 17 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like |
| 90 | d1uh6a_ | Alignment | not modelled | 23.6 | 31 | Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related |
| 91 | d1bvsa3 | Alignment | not modelled | 23.6 | 24 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain |
| 92 | d1hsja1 | Alignment | not modelled | 23.1 | 9 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 93 | d1z7ua1 | Alignment | not modelled | 22.9 | 11 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like |
| 94 | d1hw6a_ | Alignment | not modelled | 22.8 | 19 | Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP) |
| 95 | c3elkA_ | Alignment | not modelled | 22.8 | 12 | PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator ta0346; PDBTitle: crystal structure of putative transcriptional regulator ta0346 from2 thermoplasma acidophilum |
| 96 | c1d8IA_ | Alignment | not modelled | 22.6 | 24 | PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii |
| 97 | c1hjpA_ | Alignment | not modelled | 22.4 | 24 | PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli |
| 98 | c3hhaA_ | Alignment | not modelled | 21.9 | 14 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, padr family; PDBTitle: crystal structure of transcriptional regulator, a member of padr2 family, from enterococcus faecalis v583 |
| 99 | c3m0zD_ | Alignment | not modelled | 21.4 | 15 | PDB header: lyase Chain: D: PDB Molecule: putative aldolase; PDBTitle: crystal structure of putative aldolase from klebsiella pneumoniae. |
| 100 | c3muxB_ | Alignment | not modelled | 20.7 | 10 | PDB header: lyase Chain: B: PDB Molecule: putative 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a |
| 101 | c3m6yA_ | Alignment | not modelled | 20.6 | 10 | PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution. |
| 102 | c4ijrA_ | Alignment | not modelled | 20.5 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: d-arabinose dehydrogenase [nad(p)+] heavy chain; PDBTitle: crystal structure of saccharomyces cerevisiae arabinose dehydrogenase2 ara1 complexed with nadph |