



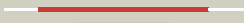

















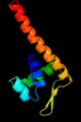










| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c2esnC_ |  Alignment |  | 100.0 | 19 | PDB header: structural genomics, unknown function Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa |
| 2 | c3fzjC_ |  Alignment |  | 100.0 | 18 | PDB header: transcription regulator Chain: C: PDB Molecule: lysr type regulator of tsambcd; PDBTitle: tsar low resolution crystal structure, tetragonal form |
| 3 | c3hhgF_ |  Alignment |  | 100.0 | 21 | PDB header: transcription regulator Chain: F: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga, a lysr-type transcriptional regulator from neisseria meningitidis. |
| 4 | c1iz1B_ |  Alignment |  | 100.0 | 17 | PDB header: dna binding protein Chain: B: PDB Molecule: lysr-type regulatory protein; PDBTitle: crystal structure of cbnr, a lysr family transcriptional2 regulator |
| 5 | c3t1bB_ |  Alignment |  | 100.0 | 15 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: crystal structure of the full-length aphb n100e variant |
| 6 | c3ispA_ |  Alignment |  | 100.0 | 18 | PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator PDBTitle: crystal structure of argp from mycobacterium tuberculosis |
| 7 | c3fzvC_ |  Alignment |  | 100.0 | 18 | PDB header: transcription regulator Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of pa01 protein, putative lysr family2 transcriptional regulator from pseudomonas aeruginosa |
| 8 | c1b9nA_ |  Alignment |  | 99.9 | 14 | PDB header: transcription Chain: A: PDB Molecule: protein (mode); PDBTitle: regulator from escherichia coli |
| 9 | d2esna1 |  Alignment |  | 99.9 | 28 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators |
| 10 | c3m1eA_ |  Alignment |  | 99.9 | 24 | PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd |
| 11 | d1b9ma1 |  Alignment |  | 99.9 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: N-terminal domain of molybdate-dependent transcriptional regulator MoDE |

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|----|-------------------------|-----------|---|------|----|---|
| 12 | dlixca1 | Alignment |  | 99.8 | 28 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators |
| 13 | c2ijlB | Alignment |  | 99.7 | 13 | PDB header: transcription Chain: B: PDB Molecule: molybdenum-binding transcriptional repressor; PDBTitle: the structure of a putative mode from agrobacterium tumefaciens. |
| 14 | d2esna2 | Alignment |  | 99.6 | 15 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 15 | c2hxrA | Alignment |  | 99.6 | 14 | PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator cynr; PDBTitle: structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism |
| 16 | c3kosA | Alignment |  | 99.6 | 16 | PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator ampr; PDBTitle: structure of the ampr effector binding domain from citrobacter2 freundii |
| 17 | c3oxnD | Alignment |  | 99.6 | 11 | PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator, lysr family; PDBTitle: the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus |
| 18 | c3ho7A | Alignment |  | 99.6 | 14 | PDB header: transcription Chain: A: PDB Molecule: oxyr; PDBTitle: crystal structure of oxyr from porphyromonas gingivalis |
| 19 | d2fyia1 | Alignment |  | 99.6 | 17 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 20 | d1utha | Alignment |  | 99.6 | 12 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 21 | c3n6uA | Alignment | not modelled | 99.6 | 15 | PDB header: transcription regulator Chain: A: PDB Molecule: lysr type regulator of tsambcd; PDBTitle: effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate |
| 22 | c2uyeA | Alignment | not modelled | 99.5 | 12 | PDB header: transcription Chain: A: PDB Molecule: regulatory protein; PDBTitle: double mutant y110s,f111v dntR from burkholderia sp. strain2 dnt in complex with thiocyanate |
| 23 | c2h9qC | Alignment | not modelled | 99.5 | 14 | PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: crystal structure of the effector binding domain of a catm2 variant (r156h) |
| 24 | c3fd3A | Alignment | not modelled | 99.5 | 16 | PDB header: transcription regulator Chain: A: PDB Molecule: chromosome replication initiation inhibitor protein; PDBTitle: structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58. |
| 25 | c1al3A | Alignment | not modelled | 99.5 | 13 | PDB header: transcription regulation Chain: A: PDB Molecule: cys regulon transcriptional activator cysb; PDBTitle: cofactor binding fragment of cysb from klebsiella aerogenes |
| 26 | d1al3a | Alignment | not modelled | 99.5 | 13 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 27 | c3jv9B | Alignment | not modelled | 99.5 | 15 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: the structure of a reduced form of oxyr from n. meningitidis |
| 28 | dlixca2 | Alignment | not modelled | 99.5 | 13 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | Family: Phosphate binding protein-like |
| 29 | c2f7cA_ | Alignment | not modelled | 99.5 | 15 | PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: catm effector binding domain with its effector cis,cis-muconate |
| 30 | d1i6aa_ | Alignment | not modelled | 99.5 | 16 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 31 | c2ql3G_ | Alignment | not modelled | 99.5 | 14 | PDB header: transcription Chain: G: PDB Molecule: probable transcriptional regulator, lysr family protein; PDBTitle: crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1 |
| 32 | c2h9bB_ | Alignment | not modelled | 99.5 | 15 | PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s) |
| 33 | c2f78A_ | Alignment | not modelled | 99.4 | 15 | PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: benm effector binding domain with its effector benzoate |
| 34 | c3hhfB_ | Alignment | not modelled | 99.4 | 20 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga regulatory domain, a lysr-type transcriptional2 regulator from neisseria meningitidis. |
| 35 | c3mz1D_ | Alignment | not modelled | 99.3 | 14 | PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: the crystal structure of a possible transcription regulator protein2 from sinorhizobium meliloti 1021 |
| 36 | c3onmB_ | Alignment | not modelled | 99.2 | 14 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator lrrha; PDBTitle: effector binding domain of lysr-type transcription factor rovm from y.2 pseudotuberculosis |
| 37 | c2qsxB_ | Alignment | not modelled | 99.1 | 14 | PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator, lysr family; PDBTitle: crystal structure of putative transcriptional regulator lysr from2 vibrio parahaemolyticus |
| 38 | c2x4hA_ | Alignment | not modelled | 98.0 | 10 | PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus |
| 39 | c3boqB_ | Alignment | not modelled | 97.9 | 9 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi |
| 40 | c3ctaA_ | Alignment | not modelled | 97.8 | 19 | PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase; PDBTitle: crystal structure of riboflavin kinase from thermoplasma2 acidophilum |
| 41 | c3bpxB_ | Alignment | not modelled | 97.6 | 18 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of marr |
| 42 | c3nrvC_ | Alignment | not modelled | 97.6 | 18 | PDB header: transcription regulator Chain: C: PDB Molecule: putative transcriptional regulator (marr/emrr family); PDBTitle: crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1 |
| 43 | c2fa5B_ | Alignment | not modelled | 97.6 | 19 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator marr/emrr family; PDBTitle: the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris |
| 44 | d2fxaa1 | Alignment | not modelled | 97.6 | 11 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 45 | d2fbha1 | Alignment | not modelled | 97.6 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 46 | c2gxgA_ | Alignment | not modelled | 97.6 | 16 | PDB header: transcription Chain: A: PDB Molecule: 146aa long hypothetical transcriptional regulator; PDBTitle: crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7 |
| 47 | d1lnwa_ | Alignment | not modelled | 97.6 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 48 | c2nnnB_ | Alignment | not modelled | 97.5 | 9 | PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa |
| 49 | c3fm5D_ | Alignment | not modelled | 97.5 | 10 | PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of transcriptional regulator (marr family)2 from rhodococcus sp. rha1 |
| 50 | c2nyxB_ | Alignment | not modelled | 97.5 | 18 | PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis |
| 51 | c3g3zA_ | Alignment | not modelled | 97.5 | 18 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis |
| 52 | d1jgsa_ | Alignment | not modelled | 97.5 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| | | | | | | PDB header: transcription Chain: B: PDB Molecule: protease production regulatory protein |

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|----|-------------------------|-----------|--------------|------|----|---|
| 53 | c2fxaB | Alignment | not modelled | 97.5 | 13 | hpr; PDBTitle: structure of the protease production regulatory protein hpr from2 bacillus subtilis. |
| 54 | d1lj9a | Alignment | not modelled | 97.5 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 55 | c3hruA | Alignment | not modelled | 97.4 | 22 | PDB header: transcription Chain: A: PDB Molecule: metalloregulator scar; PDBTitle: crystal structure of scar with bound zn2+ |
| 56 | c3f3xA | Alignment | not modelled | 97.4 | 17 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of the transcriptional regulator bldr2 from sulfolobus solfataricus |
| 57 | d2bv6a1 | Alignment | not modelled | 97.4 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 58 | c3cdhB | Alignment | not modelled | 97.4 | 11 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of the marr family transcriptional regulator spo14532 from silicibacter pomeroyi dss-3 |
| 59 | c3nqoB | Alignment | not modelled | 97.4 | 11 | PDB header: transcription Chain: B: PDB Molecule: marr-family transcriptional regulator; PDBTitle: crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution |
| 60 | c2pexA | Alignment | not modelled | 97.4 | 17 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator ohrr; PDBTitle: structure of reduced c22s ohrr from xanthomonas campestris |
| 61 | c3e6mD | Alignment | not modelled | 97.4 | 18 | PDB header: transcription regulator Chain: D: PDB Molecule: marr family transcriptional regulator; PDBTitle: the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss. |
| 62 | c3ecoB | Alignment | not modelled | 97.4 | 19 | PDB header: transcription Chain: B: PDB Molecule: mepr; PDBTitle: crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa |
| 63 | d2etha1 | Alignment | not modelled | 97.3 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 64 | c1fx7C | Alignment | not modelled | 97.3 | 19 | PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis |
| 65 | c2h09A | Alignment | not modelled | 97.3 | 19 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli |
| 66 | d2hr3a1 | Alignment | not modelled | 97.3 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 67 | c1f5tA | Alignment | not modelled | 97.3 | 18 | PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence |
| 68 | d1s3ja | Alignment | not modelled | 97.3 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 69 | d3broa1 | Alignment | not modelled | 97.3 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 70 | c3bjaA | Alignment | not modelled | 97.2 | 12 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution |
| 71 | c3cjnA | Alignment | not modelled | 97.2 | 13 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi |
| 72 | c2rdpA | Alignment | not modelled | 97.2 | 12 | PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator marr; PDBTitle: the structure of a marr family protein from bacillus2 stearothermophilus |
| 73 | d1p4xa1 | Alignment | not modelled | 97.2 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 74 | d1ub9a | Alignment | not modelled | 97.2 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 75 | c2it0A | Alignment | not modelled | 97.2 | 20 | PDB header: transcription/dna Chain: A: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex crystal2 form ii |
| 76 | d2frha1 | Alignment | not modelled | 97.2 | 11 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 77 | d2fbia1 | Alignment | not modelled | 97.2 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 78 | c3oopA | Alignment | not modelled | 97.1 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2960 protein; PDBTitle: the structure of a protein with unknown function from |

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|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | listeria innocua2 clip11262 |
| 79 | c3hrmA | Alignment | not modelled | 97.1 | 12 | PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator sarz; PDBTitle: crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form |
| 80 | d2fbka1 | Alignment | not modelled | 97.1 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 81 | c1g3wA | Alignment | not modelled | 97.1 | 19 | PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr |
| 82 | d1p4xa2 | Alignment | not modelled | 97.1 | 8 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 83 | c3k0lA | Alignment | not modelled | 97.1 | 18 | PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp |
| 84 | c3bj6B | Alignment | not modelled | 97.1 | 11 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579 |
| 85 | c3kp3B | Alignment | not modelled | 97.0 | 21 | PDB header: transcription regulator/antibiotic Chain: B: PDB Molecule: transcriptional regulator tcar; PDBTitle: staphylococcus epidermidis in complex with ampicillin |
| 86 | c3s2wB | Alignment | not modelled | 97.0 | 16 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the crystal structure of a marr transcriptional regulator from2 methanosarcina mazei go1 |
| 87 | d2a61a1 | Alignment | not modelled | 97.0 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 88 | d1z91a1 | Alignment | not modelled | 97.0 | 11 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 89 | c2qwwB | Alignment | not modelled | 96.9 | 8 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution |
| 90 | d1hsja1 | Alignment | not modelled | 96.9 | 9 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 91 | d3ctaa1 | Alignment | not modelled | 96.9 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 92 | d1twya | Alignment | not modelled | 96.8 | 11 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like |
| 93 | c2ev5B | Alignment | not modelled | 96.7 | 16 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium |
| 94 | d3deua1 | Alignment | not modelled | 96.7 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 95 | c3deuB | Alignment | not modelled | 96.7 | 12 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator slya; PDBTitle: crystal structure of transcription regulatory protein slya2 from salmonella typhimurium in complex with salicylate3 ligands |
| 96 | c3jw4C | Alignment | not modelled | 96.7 | 8 | PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, marr/emrr family; PDBTitle: the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum |
| 97 | c1p4xA | Alignment | not modelled | 96.7 | 15 | PDB header: transcription Chain: A: PDB Molecule: staphylococcal accessory regulator a homologue; PDBTitle: crystal structure of sars protein from staphylococcus aureus |
| 98 | c1twyG | Alignment | not modelled | 96.6 | 11 | PDB header: structural genomics, unknown function Chain: G: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae |
| 99 | c3ongB | Alignment | not modelled | 96.5 | 16 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: regulator of polyketide synthase expression; PDBTitle: crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis |
| 100 | c1r22B | Alignment | not modelled | 96.3 | 17 | PDB header: transcription repressor Chain: B: PDB Molecule: transcriptional repressor smtb; PDBTitle: crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form |
| 101 | c2zkzC | Alignment | not modelled | 96.2 | 21 | PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis |
| 102 | d1rlua | Alignment | not modelled | 96.2 | 12 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators |
| 103 | c2oqgA | Alignment | not modelled | 96.1 | 13 | PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. |

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|-----|-------------------------|-----------|--------------|------|--|
| | | | | | rha1 |
| 104 | c2kkoB | Alignment | not modelled | 96.0 | 15 PDB header: dna binding protein Chain: B: PDB Molecule: possible transcriptional regulatory protein PDBTitle: solution nmr structure of the homodimeric winged helix-turn-2 helix dna-binding domain (fragment 1-100) mb0332 from3 mycobacterium bovis, a possible arsr-family transcriptional4 regulator. northeast structural genomics consortium target5 mbr242e. |
| 105 | d2cg4a1 | Alignment | not modelled | 95.9 | 18 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 106 | d2f2ea1 | Alignment | not modelled | 95.8 | 17 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxlR-like |
| 107 | c3cuoB | Alignment | not modelled | 95.8 | 15 PDB header: transcription regulator Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator ygav; PDBTitle: crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli |
| 108 | d1biaa1 | Alignment | not modelled | 95.8 | 21 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like |
| 109 | d1rlta | Alignment | not modelled | 95.8 | 17 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators |
| 110 | c2cg4B | Alignment | not modelled | 95.6 | 18 PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc |
| 111 | d1u2wa1 | Alignment | not modelled | 95.5 | 15 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators |
| 112 | c3bddD | Alignment | not modelled | 95.5 | 21 PDB header: transcription Chain: D: PDB Molecule: regulatory protein marr; PDBTitle: crystal structure of a putative multiple antibiotic-resistance2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution |
| 113 | c2wteB | Alignment | not modelled | 95.5 | 12 PDB header: antiviral protein Chain: B: PDB Molecule: csa3; PDBTitle: the structure of the crispr-associated protein, csa3, from2 sulfobolus solfataricus at 1.8 angstrom resolution. |
| 114 | c2l4aA | Alignment | not modelled | 95.4 | 15 PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp |
| 115 | d1a04a1 | Alignment | not modelled | 95.3 | 2 Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 116 | c2pijB | Alignment | not modelled | 95.3 | 35 PDB header: transcription Chain: B: PDB Molecule: prophage pfl 6 cro; PDBTitle: structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5 |
| 117 | d1d1la | Alignment | not modelled | 95.3 | 20 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors |
| 118 | c3jthA | Alignment | not modelled | 95.2 | 14 PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6 |
| 119 | c2ewnA | Alignment | not modelled | 95.2 | 22 PDB header: ligase, transcription Chain: A: PDB Molecule: bira bifunctional protein; PDBTitle: ecoli biotin repressor with co-repressor analog |
| 120 | d1sfxa | Alignment | not modelled | 95.2 | 9 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like |