
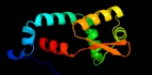
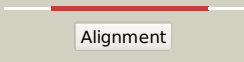

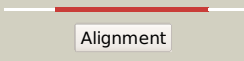

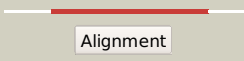

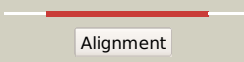

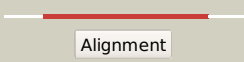

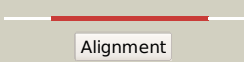

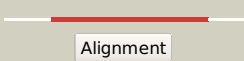

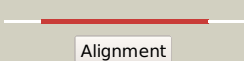

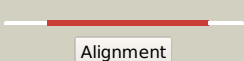
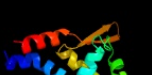
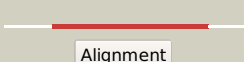



Phyre2

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|---------------|-----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2640c (-) _2965488_2965847 |
| Date | Wed Aug 7 12:50:28 BST 2019 |
| Unique Job ID | 96c152702c9b9649 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c6j0eB_ |  Alignment |  | 100.0 | 35 | PDB header: transcription Chain: B: PDB Molecule: arsenic responsive repressor arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression |
| 2 | c3jthA_ |  Alignment |  | 99.9 | 31 | PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6 |
| 3 | c6j05B_ |  Alignment |  | 99.9 | 33 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression |
| 4 | c2zkzC_ |  Alignment |  | 99.9 | 24 | PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis |
| 5 | c1r22B_ |  Alignment |  | 99.9 | 31 | 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 |
| 6 | d1r1ta_ |  Alignment |  | 99.9 | 31 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators |
| 7 | c3pqkD_ |  Alignment |  | 99.9 | 30 | PDB header: transcription Chain: D: PDB Molecule: biofilm growth-associated repressor; PDBTitle: crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa |
| 8 | c3cuoB_ |  Alignment |  | 99.9 | 31 | 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 |
| 9 | c2lkpB_ |  Alignment |  | 99.9 | 32 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, arsr family; PDBTitle: solution structure of apo-nmtr |
| 10 | c2oqgA_ |  Alignment |  | 99.9 | 27 | PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1 |
| 11 | d1r1ua_ |  Alignment |  | 99.9 | 27 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c4omzG_ | Alignment | | 99.9 | 28 | PDB header: transcription Chain: G: PDB Molecule: nolr; PDBTitle: crystal structure of nolr from sinorhizobium fredii |
| 13 | c2kkoB_ | Alignment | | 99.9 | 29 | 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. |
| 14 | c3f6oB_ | Alignment | | 99.9 | 20 | PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566 |
| 15 | c3f6vA_ | Alignment | | 99.9 | 35 | PDB header: transcription regulator Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: crystal structure of possible transcriptional regulator for arsenical2 resistance |
| 16 | c2jscB_ | Alignment | | 99.9 | 36 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator rv1994c/mt2050; PDBTitle: nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis |
| 17 | c5xpgB_ | Alignment | | 99.9 | 28 | PDB header: transcription Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator rv0081; PDBTitle: crystal structure of m.tuberculosis rv0081 |
| 18 | d1u2wa1 | Alignment | | 99.9 | 27 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators |
| 19 | d2p4wa1 | Alignment | | 99.7 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF1790-like |
| 20 | d1ulya_ | Alignment | | 99.6 | 27 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein PH1932 |
| 21 | d1ub9a_ | Alignment | not modelled | 99.6 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 22 | c4g6qA_ | Alignment | not modelled | 99.5 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of a functionally unknown protein kfla_6221 from2 kribbella flavida dsm 17836 |
| 23 | d2d1ha1 | Alignment | not modelled | 99.5 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like |
| 24 | c2qufB_ | Alignment | not modelled | 99.4 | 22 | PDB header: transcription Chain: B: PDB Molecule: transcription factor pf0095; PDBTitle: crystal structure of transcription factor axxa-pf0095 from pyrococcus2 furiosus |
| 25 | c5dukA_ | Alignment | not modelled | 99.4 | 23 | PDB header: transcription Chain: A: PDB Molecule: putative dna binding protein; PDBTitle: n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05 |
| 26 | c3r0aB_ | Alignment | not modelled | 99.0 | 16 | PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazeri go1 (gi2 21227196) |
| 27 | d3ctaa1 | Alignment | not modelled | 98.9 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 28 | c3ctaA_ | Alignment | not modelled | 98.9 | 19 | PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase; PDBTitle: crystal structure of riboflavin kinase from thermoplasma acidophilum |
| | | | | | | PDB header: dna binding protein |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c4nb5D_ | Alignment | not modelled | 98.8 | 15 | Chain: D: PDB Molecule: dna binding protein; PDBTitle: crystal structure of a transcriptional regulator |
| 30 | c6cmvA_ | Alignment | not modelled | 98.8 | 22 | PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulator Irs14-like protein; PDBTitle: crystal structure of archaeal biofilm regulator (abfr2) from <i>Sulfolobus acidocaldarius</i> |
| 31 | c3zplE_ | Alignment | not modelled | 98.7 | 21 | PDB header: transcription/dna Chain: E: PDB Molecule: putative marr-family transcriptional repressor; PDBTitle: crystal structure of sco3205, a marr family transcriptional regulator2 from <i>Streptomyces coelicolor</i> , in complex with dna |
| 32 | d1y0ua_ | Alignment | not modelled | 98.7 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators |
| 33 | c3zmdD_ | Alignment | not modelled | 98.7 | 21 | PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of absc, a marr family transcriptional2 regulator from <i>Streptomyces coelicolor</i> |
| 34 | d1p4xa2 | Alignment | not modelled | 98.7 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 35 | d1hsja1 | Alignment | not modelled | 98.6 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 36 | d2frha1 | Alignment | not modelled | 98.6 | 12 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 37 | c5jbrA_ | Alignment | not modelled | 98.6 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bcav_2135; PDBTitle: crystal structure of uncharacterized protein bcav_2135 from <i>Beutenbergia cavernae</i> |
| 38 | d2etha1 | Alignment | not modelled | 98.5 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 39 | d1lnwa_ | Alignment | not modelled | 98.5 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 40 | d2a61a1 | Alignment | not modelled | 98.5 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 41 | d3broa1 | Alignment | not modelled | 98.5 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 42 | d1sfxa_ | Alignment | not modelled | 98.5 | 24 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like |
| 43 | c3nqoB_ | Alignment | not modelled | 98.5 | 15 | PDB header: transcription Chain: B: PDB Molecule: marr-family transcriptional regulator; PDBTitle: crystal structure of a marr family transcriptional regulator (cd1569)2 from <i>Clostridium difficile</i> 630 at 2.20 Å resolution |
| 44 | c1p4xA_ | Alignment | not modelled | 98.5 | 12 | PDB header: transcription Chain: A: PDB Molecule: staphylococcal accessory regulator a homologue; PDBTitle: crystal structure of sars protein from <i>Staphylococcus aureus</i> |
| 45 | c3k0IA_ | Alignment | not modelled | 98.5 | 18 | PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from <i>Acinetobacter</i> sp. adp |
| 46 | d1ku9a_ | Alignment | not modelled | 98.5 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DNA-binding protein Mj223 |
| 47 | c4xrfA_ | Alignment | not modelled | 98.5 | 14 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of mepr like protein complexed with pseudoligands |
| 48 | c4hqeB_ | Alignment | not modelled | 98.5 | 14 | PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional regulator qsrr; PDBTitle: the crystal structure of qsrr-dna complex |
| 49 | d1p4xa1 | Alignment | not modelled | 98.5 | 12 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 50 | d2fbia1 | Alignment | not modelled | 98.5 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 51 | d2bv6a1 | Alignment | not modelled | 98.5 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 52 | c4gcvD_ | Alignment | not modelled | 98.5 | 13 | PDB header: transcription Chain: D: PDB Molecule: putative transcription protein; PDBTitle: structure of a putative transcription factor (pa1374)from <i>Pseudomonas aeruginosa</i> |
| 53 | c2nyxB_ | Alignment | not modelled | 98.4 | 13 | PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from <i>Mycobacterium tuberculosis</i> |
| 54 | c4fhtA_ | Alignment | not modelled | 98.4 | 15 | PDB header: transcription Chain: A: PDB Molecule: pcav transcriptional regulator; PDBTitle: crystal structure of the pcav transcriptional regulator from <i>Streptomyces coelicolor</i> in complex with its natural ligand |
| 55 | c2rdaA_ | Alignment | not modelled | 98.4 | 20 | PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator marr; |

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|----|-------------------------|-----------|--------------|------|----|---|
| 55 | c2rupA | Alignment | not modelled | 98.4 | 20 | PDBTitle: the structure of a marr family protein from bacillus2 stearothermophilus PDB header: transcription/dna |
| 56 | c6jbxB | Alignment | not modelled | 98.4 | 16 | Chain: B: PDB Molecule: fatty acid biosynthesis transcriptional regulator; PDBTitle: crystal structure of streptococcus pneumoniae fabt in complex with dna |
| 57 | d1mkma1 | Alignment | not modelled | 98.4 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain |
| 58 | c3bpxB | Alignment | not modelled | 98.4 | 14 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of marr |
| 59 | d1s3ja | Alignment | not modelled | 98.4 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 60 | d1lj9a | Alignment | not modelled | 98.4 | 6 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 61 | c5eriA | Alignment | not modelled | 98.4 | 13 | PDB header: transcription Chain: A: PDB Molecule: marr family transcriptional regulator; PDBTitle: marr protein from peptoclostridium difficile da00132 |
| 62 | c3bj6B | Alignment | not modelled | 98.4 | 19 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579 |
| 63 | c2nnnB | Alignment | not modelled | 98.4 | 19 | PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa |
| 64 | c3f3xA | Alignment | not modelled | 98.4 | 17 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of the transcriptional regulator bldr from2 sulfolobus solfataricus |
| 65 | c3e6mD | Alignment | not modelled | 98.4 | 21 | 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. |
| 66 | d2hr3a1 | Alignment | not modelled | 98.4 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 67 | c2qxA | Alignment | not modelled | 98.3 | 14 | PDB header: transcription Chain: A: PDB Molecule: 146aa long hypothetical transcriptional regulator; PDBTitle: crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7 |
| 68 | c3g3zA | Alignment | not modelled | 98.3 | 14 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis |
| 69 | c5jlsA | Alignment | not modelled | 98.3 | 16 | PDB header: transcription Chain: A: PDB Molecule: adhesin competence repressor; PDBTitle: crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged) |
| 70 | c3nrvc | Alignment | not modelled | 98.3 | 14 | 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 |
| 71 | c2fxaB | Alignment | not modelled | 98.3 | 11 | PDB header: transcription Chain: B: PDB Molecule: protease production regulatory protein hpr; PDBTitle: structure of the protease production regulatory protein hpr from2 bacillus subtilis. |
| 72 | c3cjnA | Alignment | not modelled | 98.3 | 17 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi |
| 73 | d1jgsa | Alignment | not modelled | 98.2 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 74 | c4a5mH | Alignment | not modelled | 98.2 | 14 | PDB header: transcription Chain: H: PDB Molecule: uncharacterized hth-type transcriptional regulator yybr; PDBTitle: redox regulator hyprr in its oxidized form |
| 75 | d2fbha1 | Alignment | not modelled | 98.2 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 76 | c4o6jA | Alignment | not modelled | 98.2 | 17 | PDB header: metal binding protein Chain: A: PDB Molecule: iron-dependent transcription repressor related protein; PDBTitle: crystal sturcture of t. acidophilum ider |
| 77 | c2it0A | Alignment | not modelled | 98.2 | 17 | 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 |
| 78 | c3bjaA | Alignment | not modelled | 98.2 | 10 | 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 |
| 79 | d2f2ea1 | Alignment | not modelled | 98.2 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like PDB header: dna binding protein |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 80 | c5hs9A_ | Alignment | not modelled | 98.2 | 13 | Chain: A: PDB Molecule: hth-type transcriptional regulator yodb; PDBTitle: crystal structure of the quinone-bound yodb from b. subtilis |
| 81 | c4em1A_ | Alignment | not modelled | 98.2 | 11 | PDB header: transcription Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator sar2349; PDBTitle: staphylococcus aureus marr native |
| 82 | c2x4hA_ | Alignment | not modelled | 98.2 | 14 | PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfobolus solfataricus |
| 83 | c1f5tA_ | Alignment | not modelled | 98.2 | 20 | 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 |
| 84 | c4mnuA_ | Alignment | not modelled | 98.2 | 14 | PDB header: transcription regulator Chain: A: PDB Molecule: slya-like transcription regulator; PDBTitle: crystal structure of uncharacterized slya-like transcription regulator2 from listeria monocytogenes |
| 85 | c4b8xB_ | Alignment | not modelled | 98.2 | 17 | PDB header: transcription Chain: B: PDB Molecule: possible marr-transcriptional regulator; PDBTitle: near atomic resolution crystal structure of sco5413, a marr family2 transcriptional regulator from streptomyces coelicolor |
| 86 | c4yifE_ | Alignment | not modelled | 98.2 | 20 | PDB header: dna binding protein Chain: E: PDB Molecule: marr family protein rv0880; PDBTitle: crystal structure of rv0880 |
| 87 | c4esfA_ | Alignment | not modelled | 98.2 | 20 | PDB header: transcription Chain: A: PDB Molecule: padr-like transcriptional regulator; PDBTitle: crystal structure of padr-like transcriptional regulator (bce3449)2 from bacillus cereus strain atcc 10987 |
| 88 | d1z91a1 | Alignment | not modelled | 98.2 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 89 | c1fx7C_ | Alignment | not modelled | 98.2 | 17 | PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis |
| 90 | c3f8fA_ | Alignment | not modelled | 98.1 | 17 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, padr-like family; PDBTitle: crystal structure of multidrug binding transcriptional regulator lmrr2 complexed with daunomycin |
| 91 | c3l7wA_ | Alignment | not modelled | 98.1 | 16 | PDB header: transcription Chain: A: PDB Molecule: putative uncharacterized protein smu.1704; PDBTitle: the crystal structure of smu.1704 from streptococcus mutans ua159 |
| 92 | c5zhcA_ | Alignment | not modelled | 98.1 | 28 | PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of the padr-family transcriptional regulator rv34882 of mycobacterium tuberculosis h37rv |
| 93 | c2fa5B_ | Alignment | not modelled | 98.1 | 15 | 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 |
| 94 | c5tjA_ | Alignment | not modelled | 98.1 | 14 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of icir transcriptional regulator from2 alicyclobacillus acidocaldarius |
| 95 | c1mkmA_ | Alignment | not modelled | 98.1 | 15 | PDB header: transcription Chain: A: PDB Molecule: iclr transcriptional regulator; PDBTitle: crystal structure of the thermotoga maritima iclr |
| 96 | c1g3wA_ | Alignment | not modelled | 98.1 | 20 | PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr |
| 97 | c3bddD_ | Alignment | not modelled | 98.1 | 24 | 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 |
| 98 | c2qwwB_ | Alignment | not modelled | 98.1 | 10 | 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 |
| 99 | d1j5ya1 | Alignment | not modelled | 98.1 | 26 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like |
| 100 | c4q77B_ | Alignment | not modelled | 98.1 | 13 | PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator rot; PDBTitle: crystal structure of rot, a global regulator of virulence genes in2 staphylococcus aureus |
| 101 | d2fxaa1 | Alignment | not modelled | 98.1 | 12 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 102 | d1z7ua1 | Alignment | not modelled | 98.1 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like |
| 103 | d2fswa1 | Alignment | not modelled | 98.1 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like |
| 104 | c2h09A_ | Alignment | not modelled | 98.1 | 25 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli |
| 105 | c3t8tA_ | Alignment | not modelled | 98.1 | 23 | PDB header: unknown function Chain: A: PDB Molecule: staphylococcus aureus cymr (oxidized form); |

| | | | | | |
|-----|-------------------------|-----------|--------------|------|--|
| | | | | | PDBTitle: crystal structure of staphylococcus aureus cymr oxidized form |
| 106 | c5w1eA_ | Alignment | not modelled | 98.1 | 20 PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: pobr in complex with phb |
| 107 | c3hruA_ | Alignment | not modelled | 98.1 | 14 PDB header: transcription Chain: A: PDB Molecule: metalloregulator scar; PDBTitle: crystal structure of scar with bound zn2+ |
| 108 | d1z05a1 | Alignment | not modelled | 98.0 | 13 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain |
| 109 | c4ijaA_ | Alignment | not modelled | 98.0 | 16 PDB header: protein binding Chain: A: PDB Molecule: xylr protein; PDBTitle: structure of s. aureus methicillin resistance factor mecR2 |
| 110 | c5x11G_ | Alignment | not modelled | 98.0 | 17 PDB header: transcription/dna Chain: G: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of bacillus subtilis padr in complex with operator2 dna |
| 111 | d1okra_ | Alignment | not modelled | 98.0 | 11 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor |
| 112 | c3df8A_ | Alignment | not modelled | 98.0 | 18 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 |
| 113 | c4esbA_ | Alignment | not modelled | 98.0 | 16 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, padr family; PDBTitle: crystal structure of padr-like transcriptional regulator (bc4206) from2 bacillus cereus strain atcc 14579 |
| 114 | c2g7uB_ | Alignment | not modelled | 98.0 | 22 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1 |
| 115 | c3u1dA_ | Alignment | not modelled | 98.0 | 19 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the structure of a protein with a gnr superfamily winged-helix-turn-2 helix domain from halomicrobium mukohataei. |
| 116 | c5whmB_ | Alignment | not modelled | 98.0 | 14 PDB header: transcription Chain: B: PDB Molecule: iclr family transcriptional regulator; PDBTitle: crystal structure of iclr family transcriptional regulator from2 brucella abortus |
| 117 | c3hhhA_ | Alignment | not modelled | 98.0 | 19 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 |
| 118 | c5h1aC_ | Alignment | not modelled | 98.0 | 12 PDB header: transcription regulator Chain: C: PDB Molecule: iclr transcription factor homolog; PDBTitle: crystal structure of an iclr homolog from microbacterium sp. strain2 hm58-2 |
| 119 | c5e1xA_ | Alignment | not modelled | 98.0 | 20 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of the organohalide sensing rdhr-cbdba16252 transcriptional regulator in the 3,4-dichlorophenol bound form |
| 120 | c5aiqD_ | Alignment | not modelled | 98.0 | 22 PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of ligand-free nadr |