

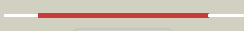
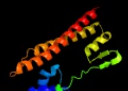





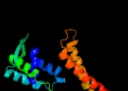














Phyre2

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|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1176c_(-)_1308228_1308797 |
| Date | Wed Jul 31 22:05:26 BST 2019 |
| Unique Job ID | 07839c877b2f0add |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c3l9fD_ |  Alignment |  | 100.0 | 23 | PDB header: transcription regulator Chain: D: PDB Molecule: putative uncharacterized protein smu.1604c; PDBTitle: the crystal structure of smu.1604c from streptococcus mutans ua159 |
| 2 | c5z7bB_ |  Alignment |  | 100.0 | 23 | PDB header: transcription Chain: B: PDB Molecule: padr family transcriptional regulator; PDBTitle: crystal structure of the vanr transcription factor in complex with2 vanillate |
| 3 | d1yg2a_ |  Alignment |  | 100.0 | 34 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like |
| 4 | c5x11G_ |  Alignment |  | 100.0 | 26 | PDB header: transcription/dna Chain: G: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of bacillus subtilis padr in complex with operator2 dna |
| 5 | c6jyiB_ |  Alignment |  | 100.0 | 21 | PDB header: transcription Chain: B: PDB Molecule: transcriptional repressor padr; PDBTitle: crystal structure of the padr-like transcriptional regulator bc17562 from bacillus cereus |
| 6 | d2esha1 |  Alignment |  | 99.9 | 28 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like |
| 7 | c5h20A_ |  Alignment |  | 99.9 | 16 | PDB header: transcription regulator Chain: A: PDB Molecule: putative padr-family transcriptional regulatory protein; PDBTitle: x-ray structure of padr-like transcription factor from bacteroid2 fragilis |
| 8 | c4esbA_ |  Alignment |  | 99.9 | 24 | 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 |
| 9 | c5zqhA_ |  Alignment |  | 99.8 | 23 | PDB header: dna binding protein Chain: A: PDB Molecule: padr family transcriptional regulator; PDBTitle: crystal structure of streptococcus transcriptional regulator |
| 10 | c3f8fA_ |  Alignment |  | 99.8 | 10 | 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 |
| 11 | c3elkA_ |  Alignment |  | 99.8 | 23 | PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator ta0346; PDBTitle: crystal structure of putative transcriptional regulator ta0346 from2 thermoplasma acidophilum |

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|----|-------------------------|-----------|--------------|------|----|---|
| 12 | d1xmaa_ | Alignment | | 99.8 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like |
| 13 | c1xmaA_ | Alignment | | 99.8 | 18 | PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulator; PDBTitle: structure of a transcriptional regulator from clostridium thermocellum2 cth-833 |
| 14 | c5dymA_ | Alignment | | 99.8 | 22 | PDB header: dna binding protein Chain: A: PDB Molecule: padr-family transcriptional regulator; PDBTitle: crystal structure of a padr family transcription regulator from2 hypervirulent clostridium difficile r20291 - cdpadr_0991 to 1.893 angstrom resolution |
| 15 | c6faqA_ | Alignment | | 99.8 | 22 | PDB header: dna binding protein Chain: A: PDB Molecule: dna binding protein; PDBTitle: structure of h. salinarum rosr (vng0258) grown from kbr |
| 16 | c3ri2B_ | Alignment | | 99.8 | 21 | 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 |
| 17 | c3hhhA_ | Alignment | | 99.8 | 28 | 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 |
| 18 | c4esfA_ | Alignment | | 99.8 | 23 | 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 |
| 19 | c2dqlA_ | Alignment | | 99.8 | 15 | PDB header: circadian clock protein Chain: A: PDB Molecule: pex protein; PDBTitle: crystal structure of the circadian clock associated protein pex from2 anabaena |
| 20 | c2e1nA_ | Alignment | | 99.8 | 12 | PDB header: circadian clock protein Chain: A: PDB Molecule: pex; PDBTitle: crystal structure of the cyanobacterium circadian clock modifier pex |
| 21 | c5zhcA_ | Alignment | not modelled | 99.8 | 23 | 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 |
| 22 | c3l7wA_ | Alignment | not modelled | 99.8 | 23 | PDB header: transcription Chain: A: PDB Molecule: putative uncharacterized protein smu.1704; PDBTitle: the crystal structure of smu.1704 from streptococcus mutans ua159 |
| 23 | c2rkhA_ | Alignment | not modelled | 99.3 | 22 | PDB header: transcription Chain: A: PDB Molecule: putative apha-like transcription factor; PDBTitle: crystal structure of a putative apha-like transcription factor2 (zp_00208345.1) from magnetospirillum magnetotacticum ms-1 at 2.00 a3 resolution |
| 24 | d1ub9a_ | Alignment | not modelled | 98.7 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 25 | d1ulya_ | Alignment | not modelled | 98.5 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein PH1932 |
| 26 | d2p4wa1 | Alignment | not modelled | 98.5 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF1790-like |
| 27 | c2gxgA_ | Alignment | not modelled | 98.2 | 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 |
| | | | | | | PDB header: transcription regulator Chain: A: PDB Molecule: possible transcriptional regulator, arsr |

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|----|-------------------------|-----------|--------------|------|----|---|
| 28 | c3f6vA_ | Alignment | not modelled | 98.2 | 23 | family protein; PDBTitle: crystal structure of possible transcriptional regulator for arsenical2 resistance |
| 29 | c3f6oB_ | Alignment | not modelled | 98.2 | 29 | PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566 |
| 30 | c3f3xA_ | Alignment | not modelled | 98.1 | 24 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of the transcriptional regulator bldr from2 sulfolobus solfataricus |
| 31 | c5eriA_ | Alignment | not modelled | 98.1 | 13 | PDB header: transcription Chain: A: PDB Molecule: marr family transcriptional regulator; PDBTitle: marr protein from peptoclostridium difficile da00132 |
| 32 | c3g3zA_ | Alignment | not modelled | 98.1 | 16 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis |
| 33 | c2oqgA_ | Alignment | not modelled | 98.1 | 23 | PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1 |
| 34 | c3bj6B_ | Alignment | not modelled | 98.0 | 19 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579 |
| 35 | d2etha1 | Alignment | not modelled | 98.0 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 36 | d1r1ta_ | Alignment | not modelled | 98.0 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators |
| 37 | d2a61a1 | Alignment | not modelled | 98.0 | 12 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 38 | d1lnwa_ | Alignment | not modelled | 97.9 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 39 | c3pgkD_ | Alignment | not modelled | 97.8 | 17 | PDB header: transcription Chain: D: PDB Molecule: biofilm growth-associated repressor; PDBTitle: crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa |
| 40 | c3zmdD_ | Alignment | not modelled | 97.8 | 18 | PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of absc, a marr family transcriptional2 regulator from streptomyces coelicolor |
| 41 | c4mnuA_ | Alignment | not modelled | 97.8 | 17 | PDB header: transcription regulator Chain: A: PDB Molecule: slya-like transcription regulator; PDBTitle: crystal structure of uncharacterized slya-like transcription regulator2 from listeria monocytogenes |
| 42 | c3jthA_ | Alignment | not modelled | 97.8 | 17 | PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6 |
| 43 | c3zplE_ | Alignment | not modelled | 97.8 | 20 | PDB header: transcription/dna Chain: E: PDB Molecule: putative marr-family transcriptional repressor; PDBTitle: crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna |
| 44 | c3nrvc_ | Alignment | not modelled | 97.8 | 11 | 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 |
| 45 | c6jbxB_ | Alignment | not modelled | 97.8 | 11 | PDB header: transcription/dna Chain: B: PDB Molecule: fatty acid biosynthesis transcriptional regulator; PDBTitle: crystal structure of streptococcus pneumoniae fabt in complex with dna |
| 46 | c2nyxB_ | Alignment | not modelled | 97.8 | 15 | PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis |
| 47 | d1s3ja_ | Alignment | not modelled | 97.8 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 48 | d2bv6a1 | Alignment | not modelled | 97.8 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 49 | c3bjaA_ | Alignment | not modelled | 97.8 | 7 | 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 |
| 50 | c3bpxB_ | Alignment | not modelled | 97.7 | 17 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of marr |
| 51 | c5jlsA_ | Alignment | not modelled | 97.7 | 12 | 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) PDB header: transcription regulator |

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|----|-------------------------|-----------|--------------|------|----|--|
| 52 | c3e6mD_ | Alignment | not modelled | 97.7 | 19 | Chain: D: PDB Molecule: marr family transcriptional regulator; PDBTitle: the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss. |
| 53 | c1r22B_ | Alignment | not modelled | 97.7 | 21 | 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 |
| 54 | d1r1ua_ | Alignment | not modelled | 97.7 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators |
| 55 | c2nnnB_ | Alignment | not modelled | 97.7 | 24 | PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa |
| 56 | d1lj9a_ | Alignment | not modelled | 97.7 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 57 | c4fhtA_ | Alignment | not modelled | 97.7 | 15 | PDB header: transcription Chain: A: PDB Molecule: pcav transcriptional regulator; PDBTitle: crystal structure of the pcav transcriptional regulator from2 streptomyces coelicolor in complex with its natural ligand |
| 58 | c2kkoB_ | Alignment | not modelled | 97.7 | 16 | 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. |
| 59 | d2fbia1 | Alignment | not modelled | 97.7 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 60 | c4xrfA_ | Alignment | not modelled | 97.7 | 17 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of mepr like protein complexed with pseudoligands |
| 61 | c4omzG_ | Alignment | not modelled | 97.6 | 20 | PDB header: transcription Chain: G: PDB Molecule: nolr; PDBTitle: crystal structure of nolr from sinorhizobium fredii |
| 62 | d1p4xa2 | Alignment | not modelled | 97.6 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 63 | d2fbha1 | Alignment | not modelled | 97.6 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 64 | c4a5mH_ | Alignment | not modelled | 97.6 | 20 | PDB header: transcription Chain: H: PDB Molecule: uncharacterized hth-type transcriptional regulator yybr; PDBTitle: redox regulator hypr in its oxidized form |
| 65 | c3k0IA_ | Alignment | not modelled | 97.6 | 20 | PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp |
| 66 | d2frha1 | Alignment | not modelled | 97.6 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 67 | d1jgsa_ | Alignment | not modelled | 97.6 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 68 | c4nb5D_ | Alignment | not modelled | 97.6 | 17 | PDB header: dna binding protein Chain: D: PDB Molecule: dna binding protein; PDBTitle: crystal structure of a transcriptional regulator |
| 69 | c5jbrA_ | Alignment | not modelled | 97.5 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bcav_2135; PDBTitle: crystal structure of uncharacterized protein bcav_2135 from2 beutenbergia cavernae |
| 70 | c4g6qA_ | Alignment | not modelled | 97.5 | 17 | 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 |
| 71 | d3broa1 | Alignment | not modelled | 97.5 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 72 | c5zc2B_ | Alignment | not modelled | 97.5 | 14 | PDB header: flavoprotein Chain: B: PDB Molecule: p-hydroxyphenylacetate 3-hydroxylase, reductase component; PDBTitle: acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1) |
| 73 | c1p4xA_ | Alignment | not modelled | 97.5 | 14 | PDB header: transcription Chain: A: PDB Molecule: staphylococcal accessory regulator a homologue; PDBTitle: crystal structure of sars protein from staphylococcus aureus |
| 74 | d1z7ua1 | Alignment | not modelled | 97.5 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like |
| 75 | c3nqoB_ | Alignment | not modelled | 97.5 | 18 | 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 |
| 76 | c2lqpB_ | Alignment | not modelled | 97.4 | 23 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, arsr family; PDBTitle: solution structure of apo-nmtr |
| 77 | c6j05B_ | Alignment | not modelled | 97.4 | 21 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: |

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|-----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | implications for2 the mechanism of derepression |
| 78 | c2jscB | Alignment | not modelled | 97.4 | 21 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator rv1994c/mt2050; PDBTitle: nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis |
| 79 | c2fxaB | Alignment | not modelled | 97.4 | 19 | PDB header: transcription Chain: B: PDB Molecule: protease production regulatory protein hpr; PDBTitle: structure of the protease production regulatory protein hpr from2 bacillus subtilis. |
| 80 | c6j0eB | Alignment | not modelled | 97.4 | 21 | 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 |
| 81 | d2fswa1 | Alignment | not modelled | 97.4 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like |
| 82 | d1p4xa1 | Alignment | not modelled | 97.4 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 83 | c3cuoB | Alignment | not modelled | 97.4 | 17 | 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 |
| 84 | d1bm9a | Alignment | not modelled | 97.3 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Replication terminator protein (RTP) |
| 85 | c4hqeB | Alignment | not modelled | 97.3 | 16 | PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional regulator qsrq; PDBTitle: the crystal structure of qsrq-dna complex |
| 86 | d1hsja1 | Alignment | not modelled | 97.2 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 87 | c4em1A | Alignment | not modelled | 97.2 | 16 | PDB header: transcription Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator sar2349; PDBTitle: staphylococcus aureus marr native |
| 88 | d2f2ea1 | Alignment | not modelled | 97.1 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like |
| 89 | d1okra | Alignment | not modelled | 97.1 | 3 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor |
| 90 | c2rdpA | Alignment | not modelled | 97.1 | 17 | PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator marr; PDBTitle: the structure of a marr family protein from bacillus2 stearothermophilus |
| 91 | c3r0aB | Alignment | not modelled | 97.1 | 11 | PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196) |
| 92 | d1sfxa | Alignment | not modelled | 97.1 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like |
| 93 | c5xpqB | Alignment | not modelled | 97.1 | 26 | PDB header: transcription Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator rv0081; PDBTitle: crystal structure of m.tuberculosis rv0081 |
| 94 | c4yifE | Alignment | not modelled | 97.1 | 21 | PDB header: dna binding protein Chain: E: PDB Molecule: marr family protein rv0880; PDBTitle: crystal structure of rv0880 |
| 95 | c5i0pA | Alignment | not modelled | 97.0 | 23 | PDB header: de novo protein Chain: A: PDB Molecule: transcription factor etv6, transcription factor etv6, PDBTitle: symmetry-based assembly of a two-dimensional protein lattice |
| 96 | c5e1xA | Alignment | not modelled | 97.0 | 18 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of the organohalide sensing rdhr-cdba16252 transcriptional regulator in the 3,4-dichlorophenol bound form |
| 97 | c3kp3B | Alignment | not modelled | 97.0 | 13 | PDB header: transcription regulator/antibiotic Chain: B: PDB Molecule: transcriptional regulator tcarr; PDBTitle: staphylococcus epidermidis in complex with ampicillin |
| 98 | c3cjnA | Alignment | not modelled | 97.0 | 20 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi |
| 99 | d1z91a1 | Alignment | not modelled | 97.0 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 100 | d1yyva1 | Alignment | not modelled | 96.9 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like |
| 101 | d3ctaa1 | Alignment | not modelled | 96.9 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 102 | c3fm5D | Alignment | not modelled | 96.9 | 25 | 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 |
| 103 | c3hooB | Alignment | not modelled | 96.9 | 14 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 103 | c3u0qB_ | Alignment | not modelled | 96.9 | 14 | PDBTitle: crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi PDB header: transcription |
| 104 | c2xigA_ | Alignment | not modelled | 96.9 | 16 | Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites |
| 105 | d1ku9a_ | Alignment | not modelled | 96.9 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DNA-binding protein Mj223 |
| 106 | d2hr3a1 | Alignment | not modelled | 96.8 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 107 | c3kfwX_ | Alignment | not modelled | 96.8 | 11 | PDB header: structural genomics, unknown function Chain: X: PDB Molecule: uncharacterized protein; PDBTitle: uncharacterized protein rv0674 from mycobacterium tuberculosis |
| 108 | c3b73A_ | Alignment | not modelled | 96.8 | 29 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phih1 repressor-like protein; PDBTitle: crystal structure of the phih1 repressor-like protein from haloarcula2 marismortui |
| 109 | c4razB_ | Alignment | not modelled | 96.8 | 18 | PDB header: metal binding protein Chain: B: PDB Molecule: dna-binding transcriptional dual regulator of siderophore PDBTitle: crystal structure of magnetospirillum gryphiswaldense msr-1 holo-fur |
| 110 | c2fu4B_ | Alignment | not modelled | 96.8 | 23 | PDB header: dna binding protein Chain: B: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator) |
| 111 | d1mzba_ | Alignment | not modelled | 96.8 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FUR-like |
| 112 | c3ctaA_ | Alignment | not modelled | 96.8 | 19 | PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase; PDBTitle: crystal structure of riboflavin kinase from thermoplasma acidophilum |
| 113 | d1sd4a_ | Alignment | not modelled | 96.8 | 7 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor |
| 114 | c3df8A_ | Alignment | not modelled | 96.8 | 11 | 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 |
| 115 | c5hs9A_ | Alignment | not modelled | 96.8 | 19 | PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator yodb; PDBTitle: crystal structure of the quinone-bound yodb from b. subtilis |
| 116 | c2zkzC_ | Alignment | not modelled | 96.8 | 12 | PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis |
| 117 | c5aiqD_ | Alignment | not modelled | 96.7 | 18 | PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of ligand-free nadr |
| 118 | c4etsB_ | Alignment | not modelled | 96.7 | 17 | PDB header: metal binding protein Chain: B: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of campylobacter jejuni ferric uptake regulator |
| 119 | c2o03A_ | Alignment | not modelled | 96.7 | 26 | PDB header: gene regulation Chain: A: PDB Molecule: probable zinc uptake regulation protein furb; PDBTitle: crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator |
| 120 | c2w57A_ | Alignment | not modelled | 96.6 | 26 | PDB header: metal transport Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains |