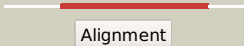

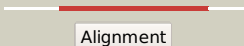

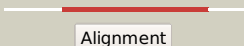







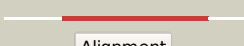






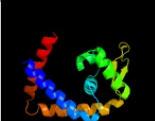













Phyre2

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|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0042c_(-)_46581_47207 |
| Date | Tue Jul 23 14:50:07 BST 2019 |
| Unique Job ID | caa77fcacddd35b5 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | d1s3ja_ |  Alignment |  | 99.9 | 25 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 2 | c3bj6B_ |  Alignment |  | 99.9 | 20 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579 |
| 3 | d2etha1 |  Alignment |  | 99.9 | 24 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 4 | c3k0IA_ |  Alignment |  | 99.9 | 17 | PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp |
| 5 | c3bpxB_ |  Alignment |  | 99.9 | 23 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of marr |
| 6 | c3e6mD_ |  Alignment |  | 99.9 | 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. |
| 7 | c4xrfA_ |  Alignment |  | 99.9 | 27 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of mepr like protein complexed with pseudoligands |
| 8 | c5eriA_ |  Alignment |  | 99.9 | 19 | PDB header: transcription Chain: A: PDB Molecule: marr family transcriptional regulator; PDBTitle: marr protein from peptoclostridium difficile da00132 |
| 9 | c3bjaA_ |  Alignment |  | 99.9 | 16 | 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 |
| 10 | d2fbha1 |  Alignment |  | 99.9 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 11 | d3broa1 |  Alignment |  | 99.9 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |

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|----|-------------------------|-----------|---|------|----|--|
| 12 | c3zplE | Alignment |  | 99.9 | 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 streptomyces coelicolor, in complex with dna |
| 13 | d1lj9a | Alignment |  | 99.9 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 14 | c4fhtA | Alignment |  | 99.9 | 18 | 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 |
| 15 | d2fbia1 | Alignment |  | 99.9 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 16 | c4mnuA | Alignment |  | 99.9 | 18 | PDB header: transcription regulator Chain: A: PDB Molecule: slya-like transcription regulator; PDBTitle: crystal structure of uncharacterized slya-like transcription regulator2 from listeria monocytogenes |
| 17 | d2a61a1 | Alignment |  | 99.9 | 25 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 18 | c3nqoB | Alignment |  | 99.9 | 21 | 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 |
| 19 | c3g3zA | Alignment |  | 99.9 | 15 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis |
| 20 | d1lnwa | Alignment |  | 99.9 | 24 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 21 | c3nrvC | Alignment | not modelled | 99.9 | 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 |
| 22 | c2nyxB | Alignment | not modelled | 99.9 | 25 | PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis |
| 23 | c3zmdD | Alignment | not modelled | 99.9 | 25 | PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of absc, a marr family transcriptional2 regulator from streptomyces coelicolor |
| 24 | c2nnnB | Alignment | not modelled | 99.9 | 33 | PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa |
| 25 | c2gxgA | Alignment | not modelled | 99.9 | 20 | PDB header: transcription Chain: A: PDB Molecule: 146aa long hypothetical transcriptional regulator; PDBTitle: crystal structure of emrr homolog from hyperthermophilic archaea2 sulfobolus tokodaii strain7 |
| 26 | c5e1xA | Alignment | not modelled | 99.9 | 17 | 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 |
| 27 | d2bv6a1 | Alignment | not modelled | 99.9 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 28 | d1z91a1 | Alignment | not modelled | 99.9 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | Family: MarR-like transcriptional regulators |
| 29 | c2rdpA | Alignment | not modelled | 99.9 | 22 | PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator marr; PDBTitle: the structure of a marr family protein from bacillus2 stearothermophilus |
| 30 | c4yifE | Alignment | not modelled | 99.9 | 36 | PDB header: dna binding protein Chain: E: PDB Molecule: marr family protein rv0880; PDBTitle: crystal structure of rv0880 |
| 31 | d1jgsa | Alignment | not modelled | 99.9 | 24 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 32 | c2qwwB | Alignment | not modelled | 99.9 | 19 | 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 |
| 33 | c3cjnA | Alignment | not modelled | 99.9 | 20 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi |
| 34 | c4em1A | Alignment | not modelled | 99.9 | 11 | PDB header: transcription Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator sar2349; PDBTitle: staphylococcus aureus marr native |
| 35 | c3fm5D | Alignment | not modelled | 99.9 | 23 | 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 |
| 36 | c5jlsA | Alignment | not modelled | 99.9 | 25 | 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) |
| 37 | d2hr3a1 | Alignment | not modelled | 99.9 | 30 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 38 | c5zc2B | Alignment | not modelled | 99.9 | 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) |
| 39 | c3oopA | Alignment | not modelled | 99.9 | 20 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2960 protein; PDBTitle: the structure of a protein with unknown function from listeria innocua2 clip11262 |
| 40 | c3f3xA | Alignment | not modelled | 99.8 | 32 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of the transcriptional regulator bldr from2 sulfolobus solfataricus |
| 41 | c2fa5B | Alignment | not modelled | 99.8 | 16 | 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 |
| 42 | c3boqB | Alignment | not modelled | 99.8 | 17 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi |
| 43 | c5aiqD | Alignment | not modelled | 99.8 | 25 | PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of ligand-free nadr |
| 44 | c3cdhB | Alignment | not modelled | 99.8 | 24 | 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 |
| 45 | c5hsmA | Alignment | not modelled | 99.8 | 27 | PDB header: transcription Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator rv2887; PDBTitle: crystal structure of mycobacterium tuberculosis marr family protein2 rv2887 |
| 46 | c3s2wB | Alignment | not modelled | 99.8 | 19 | 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 |
| 47 | c2fxaB | Alignment | not modelled | 99.8 | 15 | PDB header: transcription Chain: B: PDB Molecule: protease production regulatory protein hpr; PDBTitle: structure of the protease production regulatory protein hpr from2 bacillus subtilis. |
| 48 | c3kp3B | Alignment | not modelled | 99.8 | 12 | PDB header: transcription regulator/antibiotic Chain: B: PDB Molecule: transcriptional regulator tcar; PDBTitle: staphylococcus epidermidis in complex with ampicillin |
| 49 | c3jw4C | Alignment | not modelled | 99.8 | 16 | 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 |
| 50 | c6c28C | Alignment | not modelled | 99.8 | 25 | PDB header: dna binding protein Chain: C: PDB Molecule: transcriptional regulator, marr family; PDBTitle: transcriptional repressor, cour, bound to p-coumaroyl-coa |
| 51 | d2fbka1 | Alignment | not modelled | 99.8 | 27 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 52 | c2pexA | Alignment | not modelled | 99.8 | 23 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator ohrr; PDBTitle: structure of reduced c22s ohrr from xanthomonas campestris |
| 53 | c3hrmA | Alignment | not modelled | 99.8 | 16 | PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator sarz; |

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|----|-------------------------|-----------|--------------|------|----|---|
| 53 | c3m11A | Alignment | not modelled | 99.8 | 10 | PDBTitle: crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form PDB header: transcription |
| 54 | c4b8xB | Alignment | not modelled | 99.8 | 20 | Chain: B: PDB Molecule: possible marr-transcriptional regulator; PDBTitle: near atomic resolution crystal structure of sco5413, a marr family2 transcriptional regulator from streptomyces coelicolor |
| 55 | c5yhxB | Alignment | not modelled | 99.8 | 19 | PDB header: metal binding protein Chain: H: PDB Molecule: zinc transport transcriptional regulator; PDBTitle: structure of lactococcus lactis zittr, wild type |
| 56 | c4hblA | Alignment | not modelled | 99.8 | 19 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of abfr of staphylococcus epidermidis |
| 57 | c3deuB | Alignment | not modelled | 99.8 | 21 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator slyA; PDBTitle: crystal structure of transcription regulatory protein slyA from salmonella typhimurium in complex with salicylate ligands |
| 58 | d3deuA1 | Alignment | not modelled | 99.8 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 59 | c3ecoB | Alignment | not modelled | 99.8 | 17 | PDB header: transcription Chain: B: PDB Molecule: mepR; PDBTitle: crystal structure of mepR, a transcription regulator of the 2 staphylococcus aureus multidrug efflux pump mepA |
| 60 | c4q77B | Alignment | not modelled | 99.8 | 14 | 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 |
| 61 | c5jbrA | Alignment | not modelled | 99.7 | 18 | 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 |
| 62 | c3tgnA | Alignment | not modelled | 99.7 | 19 | PDB header: transcription Chain: A: PDB Molecule: adc operon repressor adcr; PDBTitle: crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state |
| 63 | c3bddD | Alignment | not modelled | 99.7 | 23 | 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 |
| 64 | c4fx0A | Alignment | not modelled | 99.7 | 25 | PDB header: transcription regulator Chain: A: PDB Molecule: probable transcriptional repressor protein; PDBTitle: crystal structure of m. tuberculosis transcriptional regulator mosr |
| 65 | d1p4xa1 | Alignment | not modelled | 99.7 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 66 | d2fxaa1 | Alignment | not modelled | 99.7 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 67 | d1ku9a | Alignment | not modelled | 99.7 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DNA-binding protein Mj223 |
| 68 | d2frha1 | Alignment | not modelled | 99.7 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 69 | d1p4xa2 | Alignment | not modelled | 99.7 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 70 | d1hsja1 | Alignment | not modelled | 99.7 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 71 | c1p4xA | Alignment | not modelled | 99.7 | 14 | PDB header: transcription Chain: A: PDB Molecule: staphylococcal accessory regulator a homologue; PDBTitle: crystal structure of sars protein from staphylococcus aureus |
| 72 | c4nb5D | Alignment | not modelled | 99.6 | 21 | PDB header: dna binding protein Chain: D: PDB Molecule: dna binding protein; PDBTitle: crystal structure of a transcriptional regulator |
| 73 | d1sfxa | Alignment | not modelled | 99.6 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like |
| 74 | d1ub9a | Alignment | not modelled | 99.5 | 24 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 75 | d1okra | Alignment | not modelled | 99.4 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor |
| 76 | c3r0aB | Alignment | not modelled | 99.4 | 15 | PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196) |
| 77 | c2x4hA | Alignment | not modelled | 99.4 | 20 | PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfobolus solfataricus |
| 78 | c6cmvA | Alignment | not modelled | 99.3 | 14 | PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulator lrs14-like protein; PDBTitle: crystal structure of archaeal biofilm regulator (abfr2) from2 sulfobolus acidocaldarius |
| 79 | c2it0A | Alignment | not modelled | 99.3 | 23 | PDB header: transcription/dna Chain: A: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex |

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|-----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | crystal2 form ii |
| 80 | d3ctaa1 | Alignment | not modelled | 99.3 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 81 | c1f5tA | Alignment | not modelled | 99.3 | 24 | 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 |
| 82 | c1hsjA | Alignment | not modelled | 99.2 | 18 | PDB header: transcription/sugar binding protein Chain: A: PDB Molecule: fusion protein consisting of staphylococcus accessory PDBTitle: sarr mbp fusion structure |
| 83 | c2wteB | Alignment | not modelled | 99.2 | 19 | 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. |
| 84 | c3ctaA | Alignment | not modelled | 99.2 | 20 | PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase; PDBTitle: crystal structure of riboflavin kinase from thermoplasma acidophilum |
| 85 | c1fx7C | Alignment | not modelled | 99.1 | 22 | PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis |
| 86 | c4o6jA | Alignment | not modelled | 99.0 | 17 | PDB header: metal binding protein Chain: A: PDB Molecule: iron-dependent transcription repressor related protein; PDBTitle: crystal sturcture of t. acidophilum ider |
| 87 | c2h09A | Alignment | not modelled | 99.0 | 22 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli |
| 88 | d1sd4a | Alignment | not modelled | 98.9 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor |
| 89 | c2ev5B | Alignment | not modelled | 98.9 | 12 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium |
| 90 | c5cviB | Alignment | not modelled | 98.9 | 17 | PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor |
| 91 | c1g3wA | Alignment | not modelled | 98.9 | 21 | PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr |
| 92 | d1xmaa | Alignment | not modelled | 98.8 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like |
| 93 | c1xmaA | Alignment | not modelled | 98.8 | 23 | PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulator; PDBTitle: structure of a transcriptional regulator from clostridium thermocellum2 cth-833 |
| 94 | c3hhhA | Alignment | not modelled | 98.8 | 15 | 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 |
| 95 | c3f8fA | Alignment | not modelled | 98.8 | 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 |
| 96 | c3hruA | Alignment | not modelled | 98.8 | 14 | PDB header: transcription Chain: A: PDB Molecule: metalloregulator scar; PDBTitle: crystal structure of scar with bound zn2+ |
| 97 | c5zhcA | Alignment | not modelled | 98.8 | 27 | 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 |
| 98 | c3l7wA | Alignment | not modelled | 98.7 | 14 | PDB header: transcription Chain: A: PDB Molecule: putative uncharacterized protein smu.1704; PDBTitle: the crystal structure of smu.1704 from streptococcus mutans ua159 |
| 99 | d2d1ha1 | Alignment | not modelled | 98.7 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like |
| 100 | c2oqgA | Alignment | not modelled | 98.5 | 17 | PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1 |
| 101 | c3ri2B | Alignment | not modelled | 98.5 | 23 | 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 |
| 102 | c5dymA | Alignment | not modelled | 98.5 | 20 | PDB header: dna binding protein Chain: A: PDB Molecule: padr-family transcriptional regulator; PDBTitle: crystal structure of a padr family transcriptional regulator from2 hypervirulent clostridium difficile r20291 - cdpadr_0991 to 1.893 angstrom resolution |
| 103 | c4esbA | Alignment | not modelled | 98.4 | 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 |
| 104 | d2g9wa1 | Alignment | not modelled | 98.4 | 26 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor |
| | | | | | | PDB header: transcription/dna |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 105 | c4hqeB_ | Alignment | not modelled | 98.4 | 12 | Chain: B: PDB Molecule: transcriptional regulator qsr; PDBTitle: the crystal structure of qsr-dna complex |
| 106 | c3f6vA_ | Alignment | not modelled | 98.4 | 21 | PDB header: transcription regulator Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: crystal structure of possible transcriptional regulator for arsenical2 resistance |
| 107 | d1ulya_ | Alignment | not modelled | 98.4 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein PH1932 |
| 108 | c3f6oB_ | Alignment | not modelled | 98.4 | 19 | PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566 |
| 109 | c6o5cB_ | Alignment | not modelled | 98.3 | 17 | PDB header: dna binding protein Chain: B: PDB Molecule: putative metal-dependent transcriptional regulator; PDBTitle: x-ray crystal structure of metal-dependent transcriptional regulator2 mtsr |
| 110 | c5h20A_ | Alignment | not modelled | 98.3 | 19 | 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 |
| 111 | c5zqhA_ | Alignment | not modelled | 98.3 | 15 | PDB header: dna binding protein Chain: A: PDB Molecule: padr family transcriptional regulator; PDBTitle: crystal structure of streptococcus transcriptional regulator |
| 112 | c2qufB_ | Alignment | not modelled | 98.3 | 14 | PDB header: transcription Chain: B: PDB Molecule: transcription factor pf0095; PDBTitle: crystal structure of transcription factor axxa-pf0095 from pyrococcus2 furiosus |
| 113 | c6faqA_ | Alignment | not modelled | 98.3 | 25 | PDB header: dna binding protein Chain: A: PDB Molecule: dna binding protein; PDBTitle: structure of h. salinarum rosr (vng0258) grown from kbr |
| 114 | d2esha1 | Alignment | not modelled | 98.3 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like |
| 115 | d2f2ea1 | Alignment | not modelled | 98.2 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like |
| 116 | c4a5mH_ | Alignment | not modelled | 98.2 | 19 | PDB header: transcription Chain: H: PDB Molecule: uncharacterized hth-type transcriptional regulator yybr; PDBTitle: redox regulator hypr in its oxidized form |
| 117 | d1z7ua1 | Alignment | not modelled | 98.2 | 27 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like |
| 118 | c4esfA_ | Alignment | not modelled | 98.2 | 16 | 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 |
| 119 | c3cuoB_ | Alignment | not modelled | 98.1 | 20 | 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 |
| 120 | c6j05B_ | Alignment | not modelled | 98.1 | 19 | 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 |