

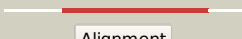

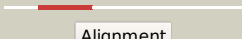
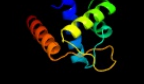
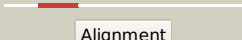
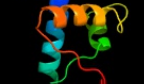
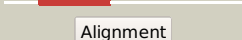

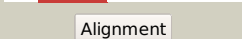

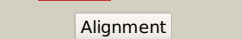

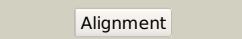
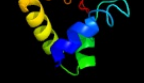
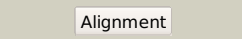

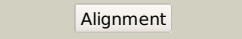

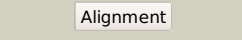



# Phyre2

|               |                                  |
|---------------|----------------------------------|
| Email         | mdejesus@rockefeller.edu         |
| Description   | RVBD2374c_(hrcA)_2654072_2655103 |
| Date          | Mon Aug 5 13:25:53 BST 2019      |
| Unique Job ID | 9182748ee30e2584                 |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|--|---|------------|--------|---|
| 1  | <a href="#">c1stzB_</a> | <br>Alignment   |    | 100.0      | 28     | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> heat-inducible transcription repressor hrcA homolog;<br><b>PDBTitle:</b> crystal structure of a hypothetical protein at 2.2 a resolution                                      |
| 2  | <a href="#">d1stza2</a> | <br>Alignment   |    | 100.0      | 22     | <b>Fold:</b> Profilin-like<br><b>Superfamily:</b> GAF domain-like<br><b>Family:</b> HrcA C-terminal domain-like   |
| 3  | <a href="#">d1stza1</a> | <br>Alignment   |    | 99.9       | 40     | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Heat-inducible transcription repressor HrcA, N-terminal domain   |
| 4  | <a href="#">d1jhfa1</a> | <br>Alignment   |    | 97.9       | 19     | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> LexA repressor, N-terminal DNA-binding domain  |
| 5  | <a href="#">c2x4hA_</a> | <br>Alignment |  | 97.9       | 14     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sso2273;<br><b>PDBTitle:</b> crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus   |
| 6  | <a href="#">c2it0A_</a> | <br>Alignment |  | 97.7       | 21     | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent repressor ider;<br><b>PDBTitle:</b> crystal structure of a two-domain ider-dna complex crystal2 form ii  |
| 7  | <a href="#">c1f5tA_</a> | <br>Alignment |  | 97.7       | 21     | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor;<br><b>PDBTitle:</b> diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence                        |
| 8  | <a href="#">c1j5yA_</a> | <br>Alignment |  | 97.4       | 34     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, biotin repressor family;<br><b>PDBTitle:</b> crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution |
| 9  | <a href="#">c1fx7C_</a> | <br>Alignment |  | 97.4       | 20     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> iron-dependent repressor ider;<br><b>PDBTitle:</b> crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis                              |
| 10 | <a href="#">d1biaa1</a> | <br>Alignment |  | 97.4       | 20     | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Biotin repressor-like  |
| 11 | <a href="#">d1j5ya1</a> | <br>Alignment |  | 97.3       | 31     | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Biotin repressor-like  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 12 | <a href="#">c6sbsB_</a> | Alignment |              | 97.0 | 19 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein;<br><b>PDBTitle:</b> ytra from sulfolobus acidocaldarius, a gntr-family transcription2 factor  |
| 13 | <a href="#">d1in4a1</a> | Alignment |              | 97.0 | 30 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Helicase DNA-binding domain  |
| 14 | <a href="#">d1ixrc1</a> | Alignment |              | 96.9 | 27 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Helicase DNA-binding domain  |
| 15 | <a href="#">c4fx0A_</a> | Alignment |              | 96.9 | 21 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional repressor protein;<br><b>PDBTitle:</b> crystal structure of m. tuberculosis transcriptional regulator mosr   |
| 16 | <a href="#">c2h09A_</a> | Alignment |              | 96.8 | 21 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator mntr;<br><b>PDBTitle:</b> crystal structure of diphtheria toxin repressor like protein2 from e. coli  |
| 17 | <a href="#">c2qxgA_</a> | Alignment |              | 96.8 | 21 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> 146aa long hypothetical transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7  |
| 18 | <a href="#">c6jbxB_</a> | Alignment |              | 96.8 | 19 | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid biosynthesis transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of streptococcus pneumoniae fabt in complex with dna   |
| 19 | <a href="#">d1ixsb1</a> | Alignment |              | 96.8 | 28 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Helicase DNA-binding domain  |
| 20 | <a href="#">c3t8tA_</a> | Alignment |              | 96.8 | 17 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> staphylococcus aureus cymr (oxidized form);<br><b>PDBTitle:</b> crystal structure of staphylococcus aureus cymr oxidized form  |
| 21 | <a href="#">c5w1eA_</a> | Alignment | not modelled | 96.7 | 21 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator;<br><b>PDBTitle:</b> pobr in complex with phb  |
| 22 | <a href="#">c2wteB_</a> | Alignment | not modelled | 96.7 | 25 | <b>PDB header:</b> antiviral protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> csa3;<br><b>PDBTitle:</b> the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.   |
| 23 | <a href="#">c2ev5B_</a> | Alignment | not modelled | 96.7 | 15 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator mntr;<br><b>PDBTitle:</b> bacillus subtilis manganese transport regulator (mntr)2 bound to calcium  |
| 24 | <a href="#">d2g9wa1</a> | Alignment | not modelled | 96.7 | 16 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Penicillinase repressor  |
| 25 | <a href="#">c3bjaA_</a> | Alignment | not modelled | 96.6 | 15 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family, putative;<br><b>PDBTitle:</b> crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution |
| 26 | <a href="#">d2bv6a1</a> | Alignment | not modelled | 96.6 | 22 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> MarR-like transcriptional regulators   |
| 27 | <a href="#">c3oopA_</a> | Alignment | not modelled | 96.5 | 20 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> lin2960 protein;<br><b>PDBTitle:</b> the structure of a protein with unknown function from listeria innocua2 clip11262  |
| 28 | <a href="#">c6cmvA_</a> | Alignment | not modelled | 96.5 | 21 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrs14-like protein;<br><b>PDBTitle:</b> crystal structure of archaeal biofilm regulator (abfr2)   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
|    |                         |           |              |      |    | from2 sulfobolus acidocaldarius  |
| 29 | <a href="#">c4em1A_</a> | Alignment | not modelled | 96.4 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator sar2349;<br><b>PDBTitle:</b> staphylococcus aureus marr native  |
| 30 | <a href="#">c3f3xA_</a> | Alignment | not modelled | 96.4 | 22 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family, putative;<br><b>PDBTitle:</b> crystal structure of the transcriptional regulator bldr from2 sulfobolus solfataricus                                      |
| 31 | <a href="#">c4o6jA_</a> | Alignment | not modelled | 96.4 | 18 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent transcription repressor related protein;<br><b>PDBTitle:</b> crystal structure of t. acidophilum ider   |
| 32 | <a href="#">c3hruA_</a> | Alignment | not modelled | 96.4 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> metalloregulator scar;<br><b>PDBTitle:</b> crystal structure of scar with bound zn2+   |
| 33 | <a href="#">c1g3wA_</a> | Alignment | not modelled | 96.4 | 20 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor;<br><b>PDBTitle:</b> cd-cys102ser dtxr  |
| 34 | <a href="#">d2fbia1</a> | Alignment | not modelled | 96.4 | 25 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> MarR-like transcriptional regulators  |
| 35 | <a href="#">d1lnwa_</a> | Alignment | not modelled | 96.3 | 17 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> MarR-like transcriptional regulators  |
| 36 | <a href="#">c4yifE_</a> | Alignment | not modelled | 96.3 | 19 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> marr family protein rv0880;<br><b>PDBTitle:</b> crystal structure of rv0880  |
| 37 | <a href="#">d2isya1</a> | Alignment | not modelled | 96.2 | 20 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Iron-dependent repressor protein  |
| 38 | <a href="#">c3ic7A_</a> | Alignment | not modelled | 96.2 | 12 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of putative transcriptional regulator of gntr family2 from bacteroides thetaiotaomicron        |
| 39 | <a href="#">c3jsoA_</a> | Alignment | not modelled | 96.2 | 19 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> lexa repressor;<br><b>PDBTitle:</b> classic protein with a new twist: crystal structure of a lexa2 repressor dna complex   |
| 40 | <a href="#">c3by6C_</a> | Alignment | not modelled | 96.1 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> C: <b>PDB Molecule:</b> predicted transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a transcriptional regulator from oenococcus oeni   |
| 41 | <a href="#">c3nqoB_</a> | Alignment | not modelled | 96.1 | 21 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> marr-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution            |
| 42 | <a href="#">d1g3wa1</a> | Alignment | not modelled | 96.0 | 23 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Iron-dependent repressor protein  |
| 43 | <a href="#">c3r0aB_</a> | Alignment | not modelled | 96.0 | 11 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator;<br><b>PDBTitle:</b> possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)  |
| 44 | <a href="#">c3zplE_</a> | Alignment | not modelled | 96.0 | 13 | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> E: <b>PDB Molecule:</b> putative marr-family transcriptional repressor;<br><b>PDBTitle:</b> crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna |
| 45 | <a href="#">c4hf1B_</a> | Alignment | not modelled | 96.0 | 15 | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator iscr;<br><b>PDBTitle:</b> crystal structure of iscr bound to its promoter   |
| 46 | <a href="#">c3bj6B_</a> | Alignment | not modelled | 96.0 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family;<br><b>PDBTitle:</b> crystal structure of marr family transcription regulator sp03579   |
| 47 | <a href="#">d1s3ja_</a> | Alignment | not modelled | 95.9 | 18 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> MarR-like transcriptional regulators  |
| 48 | <a href="#">c4hamA_</a> | Alignment | not modelled | 95.9 | 15 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> lmo2241 protein;<br><b>PDBTitle:</b> crystal structure of transcriptional antiterminator from listeria2 monocytogenes egd-e  |
| 49 | <a href="#">c5xyiT_</a> | Alignment | not modelled | 95.9 | 25 | <b>PDB header:</b> ribosome<br><b>Chain:</b> T: <b>PDB Molecule:</b> ribosomal protein s19e, putative;<br><b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome   |
| 50 | <a href="#">c6hsdB_</a> | Alignment | not modelled | 95.9 | 21 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> rrf2 family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of the oxidized form of the transcription regulator2 rsrr   |
| 51 | <a href="#">c2y75F_</a> | Alignment | not modelled | 95.9 | 15 | <b>PDB header:</b> transcription<br><b>Chain:</b> F: <b>PDB Molecule:</b> hth-type transcriptional regulator cymr;<br><b>PDBTitle:</b> the structure of cymr (yrzc) the global cysteine regulator of b.2 subtilis  |
| 52 | <a href="#">d2etha1</a> | Alignment | not modelled | 95.9 | 29 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> MarR-like transcriptional regulators  |
| 53 | <a href="#">c4fhtA_</a> | Alignment | not modelled | 95.8 | 21 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> pcav transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of the pcav transcriptional regulator from2 streptomyces coelicolor in complex with its natural ligand                     |
| 54 | <a href="#">c3nrvc_</a> | Alignment | not modelled | 95.8 | 19 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative transcriptional regulator (marr/emrr family);   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
|    |                         |           |              |      |    | <b>PDBTitle:</b> crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1  |
| 55 | <a href="#">c5cviB_</a> | Alignment | not modelled | 95.8 | 19 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> slor;<br><b>PDBTitle:</b> structure of the manganese regulator slor  |
| 56 | <a href="#">c4r1hA_</a> | Alignment | not modelled | 95.8 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> lmo0741 protein;<br><b>PDBTitle:</b> gntr family transcriptional regulator from listeria monocytogenes   |
| 57 | <a href="#">c3deuB_</a> | Alignment | not modelled | 95.8 | 13 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator slya;<br><b>PDBTitle:</b> crystal structure of transcription regulatory protein slya from2 salmonella typhimurium in complex with salicylate ligands |
| 58 | <a href="#">d2hs5a1</a> | Alignment | not modelled | 95.8 | 17 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> GntR-like transcriptional regulators  |
| 59 | <a href="#">c2l4aA_</a> | Alignment | not modelled | 95.8 | 22 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> leucine responsive regulatory protein;<br><b>PDBTitle:</b> nmr structure of the dna-binding domain of e.coli lrp   |
| 60 | <a href="#">c3fm5D_</a> | Alignment | not modelled | 95.8 | 17 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> x-ray crystal structure of transcriptional regulator (marr family)2 from rhodococcus sp. rha1                                   |
| 61 | <a href="#">c3k2zA_</a> | Alignment | not modelled | 95.7 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lexa repressor;<br><b>PDBTitle:</b> crystal structure of a lexa protein from thermotoga maritima   |
| 62 | <a href="#">c6ep3B_</a> | Alignment | not modelled | 95.7 | 22 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> lmo0651 protein;<br><b>PDBTitle:</b> lar controls the expression of the listeria monocytogenes agr system2 and mediates virulence.   |
| 63 | <a href="#">c3k69A_</a> | Alignment | not modelled | 95.7 | 23 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription regulator;<br><b>PDBTitle:</b> crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution             |
| 64 | <a href="#">d1okra_</a> | Alignment | not modelled | 95.7 | 15 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Penicillinase repressor   |
| 65 | <a href="#">c3fmsA_</a> | Alignment | not modelled | 95.7 | 22 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntr family;<br><b>PDBTitle:</b> crystal structure of tm0439, a gntr transcriptional regulator  |
| 66 | <a href="#">c2rdpA_</a> | Alignment | not modelled | 95.6 | 19 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator marr;<br><b>PDBTitle:</b> the structure of a marr family protein from bacillus2 stearothermophilus  |
| 67 | <a href="#">c5y6iB_</a> | Alignment | not modelled | 95.6 | 21 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator kdgr;<br><b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa hmgr   |
| 68 | <a href="#">c3tgnA_</a> | Alignment | not modelled | 95.6 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> adc operon repressor adcr;<br><b>PDBTitle:</b> crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state                             |
| 69 | <a href="#">c5h1aC_</a> | Alignment | not modelled | 95.6 | 18 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> C: <b>PDB Molecule:</b> iclr transcription factor homolog;<br><b>PDBTitle:</b> crystal structure of an iclr homolog from microbacterium sp. strain2 hm58-2   |
| 70 | <a href="#">c3bpxB_</a> | Alignment | not modelled | 95.6 | 19 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of marr   |
| 71 | <a href="#">c3cdhB_</a> | Alignment | not modelled | 95.6 | 17 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family;<br><b>PDBTitle:</b> crystal structure of the marr family transcriptional regulator spo14532 from silicibacter pomeroyi dss-3           |
| 72 | <a href="#">c3zmdD_</a> | Alignment | not modelled | 95.6 | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of absc, a marr family transcriptional2 regulator from streptomyces coelicolor                                 |
| 73 | <a href="#">c4xrfA_</a> | Alignment | not modelled | 95.5 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family;<br><b>PDBTitle:</b> crystal structure of mepr like protein complexed with pseudoligands  |
| 74 | <a href="#">c2fxaB_</a> | Alignment | not modelled | 95.5 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> protease production regulatory protein hpr;<br><b>PDBTitle:</b> structure of the protease production regulatory protein hpr from2 bacillus subtilis.                                     |
| 75 | <a href="#">c6az6B_</a> | Alignment | not modelled | 95.5 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> gntr family transcriptional regulator;<br><b>PDBTitle:</b> streptococcus agalactiae gntr   |
| 76 | <a href="#">c5jlsA_</a> | Alignment | not modelled | 95.5 | 12 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> adhesin competence repressor;<br><b>PDBTitle:</b> crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged)                        |
| 77 | <a href="#">c3ihuA_</a> | Alignment | not modelled | 95.5 | 20 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntr family;<br><b>PDBTitle:</b> crystal structure of dna binding protein (yp_298823.1) from ralstonia2 eutropha jmp134 at 1.92 a resolution        |
| 78 | <a href="#">d3bwga1</a> | Alignment | not modelled | 95.5 | 21 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> GntR-like transcriptional regulators  |
| 79 | <a href="#">c6az1X_</a> | Alignment | not modelled | 95.4 | 26 | <b>PDB header:</b> ribosome/antibiotic<br><b>Chain:</b> X: <b>PDB Molecule:</b> ribosomal protein s19e;<br><b>PDBTitle:</b> cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin  |
| 80 | <a href="#">c3f8mA_</a> | Alignment | not modelled | 95.4 | 19 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> gntr-family protein transcriptional  |

|     |                         |           |              |      |    |  |
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| 80  | <a href="#">c3rmaA</a>  | Alignment | not modelled | 95.4 | 19 | regulator;<br><b>PDBTitle:</b> crystal structure of phnf from mycobacterium smegmatis  |
| 81  | <a href="#">d1mkma1</a> | Alignment | not modelled | 95.4 | 24 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Transcriptional regulator IclR, N-terminal domain   |
| 82  | <a href="#">d1ylfa1</a> | Alignment | not modelled | 95.4 | 12 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Transcriptional regulator Rrf2  |
| 83  | <a href="#">c3zeyO</a>  | Alignment | not modelled | 95.3 | 20 | <b>PDB header:</b> ribosome<br><b>Chain:</b> O: <b>PDB Molecule:</b> ribosomal protein s19, putative;<br><b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome   |
| 84  | <a href="#">d2ev0a1</a> | Alignment | not modelled | 95.3 | 16 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Iron-dependent repressor protein  |
| 85  | <a href="#">c2nyxB</a>  | Alignment | not modelled | 95.3 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulatory protein, rv1404;<br><b>PDBTitle:</b> crystal structure of rv1404 from mycobacterium tuberculosis   |
| 86  | <a href="#">c3lwfD</a>  | Alignment | not modelled | 95.2 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution              |
| 87  | <a href="#">d2cfxa1</a> | Alignment | not modelled | 95.2 | 19 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain   |
| 88  | <a href="#">c3neuA</a>  | Alignment | not modelled | 95.1 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> lin1836 protein;<br><b>PDBTitle:</b> the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262                                    |
| 89  | <a href="#">c5eriA</a>  | Alignment | not modelled | 95.1 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> marr family transcriptional regulator;<br><b>PDBTitle:</b> marr protein from peptoclostridium difficile da00132  |
| 90  | <a href="#">c5kvrA</a>  | Alignment | not modelled | 95.1 | 19 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase complex repressor;<br><b>PDBTitle:</b> x-ray crystal structure of a fragment (1-75) of a transcriptional2 regulator pdhr from escherichia coli cft073                       |
| 91  | <a href="#">c4p96B</a>  | Alignment | not modelled | 95.1 | 21 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid metabolism regulator protein;<br><b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from vibrio cholerae   |
| 92  | <a href="#">c3tqnC</a>  | Alignment | not modelled | 95.1 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, gntr family;<br><b>PDBTitle:</b> structure of the transcriptional regulator of the gntr family, from2 coxiella burnetii.  |
| 93  | <a href="#">d2hr3a1</a> | Alignment | not modelled | 95.1 | 18 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> MarR-like transcriptional regulators  |
| 94  | <a href="#">d2frha1</a> | Alignment | not modelled | 95.0 | 21 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> MarR-like transcriptional regulators  |
| 95  | <a href="#">c2nnnB</a>  | Alignment | not modelled | 95.0 | 22 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa   |
| 96  | <a href="#">d1xd7a</a>  | Alignment | not modelled | 95.0 | 16 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Transcriptional regulator Rrf2  |
| 97  | <a href="#">c2p8tA</a>  | Alignment | not modelled | 95.0 | 29 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph0730;<br><b>PDBTitle:</b> hypothetical protein ph0730 from pyrococcus horikoshii ot3  |
| 98  | <a href="#">d1ilga1</a> | Alignment | not modelled | 95.0 | 27 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain   |
| 99  | <a href="#">c2xznT</a>  | Alignment | not modelled | 95.0 | 29 | <b>PDB header:</b> ribosome<br><b>Chain:</b> T: <b>PDB Molecule:</b> rps19e;<br><b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2 |
| 100 | <a href="#">d2cg4a1</a> | Alignment | not modelled | 95.0 | 23 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain   |
| 101 | <a href="#">c3g3zA</a>  | Alignment | not modelled | 94.9 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family;<br><b>PDBTitle:</b> the structure of nmb1585, a marr family regulator from neisseria2 meningitidis   |
| 102 | <a href="#">c3iz6S</a>  | Alignment | not modelled | 94.9 | 30 | <b>PDB header:</b> ribosome<br><b>Chain:</b> S: <b>PDB Molecule:</b> 40s ribosomal protein s19 (s19e);<br><b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome                    |
| 103 | <a href="#">c4cicB</a>  | Alignment | not modelled | 94.9 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, badm/rrf2 family;<br><b>PDBTitle:</b> t. potens iscr  |
| 104 | <a href="#">d1sd4a</a>  | Alignment | not modelled | 94.9 | 12 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Penicillinase repressor   |
| 105 | <a href="#">d1lj9a</a>  | Alignment | not modelled | 94.8 | 22 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> MarR-like transcriptional regulators  |
|     |                         |           |              |      |    | <b>PDB header:</b> transcription regulator   |

|     |                         |           |              |      |    |  |
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| 106 | <a href="#">c3cjnA_</a> | Alignment | not modelled | 94.8 | 18 | <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family;<br><b>PDBTitle:</b> crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi   |
| 107 | <a href="#">c2di3A_</a> | Alignment | not modelled | 94.8 | 31 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> bacterial regulatory proteins, gntr family;<br><b>PDBTitle:</b> crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum             |
| 108 | <a href="#">d1p6ra_</a> | Alignment | not modelled | 94.8 | 13 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Penicillinase repressor   |
| 109 | <a href="#">c1e2xA_</a> | Alignment | not modelled | 94.7 | 21 | <b>PDB header:</b> transcriptional regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid metabolism regulator protein;<br><b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from e.2 coli                             |
| 110 | <a href="#">d1p4xa1</a> | Alignment | not modelled | 94.7 | 17 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> MarR-like transcriptional regulators  |
| 111 | <a href="#">d1hsja1</a> | Alignment | not modelled | 94.7 | 14 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> MarR-like transcriptional regulators  |
| 112 | <a href="#">d1z91a1</a> | Alignment | not modelled | 94.7 | 21 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> MarR-like transcriptional regulators  |
| 113 | <a href="#">c4ijaA_</a> | Alignment | not modelled | 94.6 | 22 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> xylr protein;<br><b>PDBTitle:</b> structure of s. aureus methicillin resistance factor mecrc2  |
| 114 | <a href="#">c5yhxH_</a> | Alignment | not modelled | 94.6 | 17 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> H: <b>PDB Molecule:</b> zinc transport transcriptional regulator;<br><b>PDBTitle:</b> structure of lactococcus lactis zittr, wild type   |
| 115 | <a href="#">d2v7fa1</a> | Alignment | not modelled | 94.6 | 28 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Rps19E-like   |
| 116 | <a href="#">c3j38T_</a> | Alignment | not modelled | 94.6 | 24 | <b>PDB header:</b> ribosome<br><b>Chain:</b> T: <b>PDB Molecule:</b> 40s ribosomal protein s19a;<br><b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins   |
| 117 | <a href="#">c4mnuA_</a> | Alignment | not modelled | 94.6 | 17 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> slya-like transcription regulator;<br><b>PDBTitle:</b> crystal structure of uncharacterized slya-like transcription regulator2 from listeria monocytogenes |
| 118 | <a href="#">c4hblA_</a> | Alignment | not modelled | 94.5 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family;<br><b>PDBTitle:</b> crystal structure of abfr of staphylococcus epidermidis  |
| 119 | <a href="#">c1hqcb_</a> | Alignment | not modelled | 94.5 | 30 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ruvb;<br><b>PDBTitle:</b> structure of ruvb from thermus thermophilus hb8  |
| 120 | <a href="#">c2du9A_</a> | Alignment | not modelled | 94.5 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> predicted transcriptional regulators;<br><b>PDBTitle:</b> crystal structure of the transcriptional factor from c.glutamicum  |