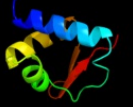
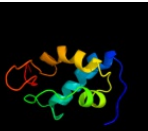
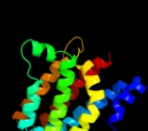


| #  | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                               |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c1e2xA_</a> |  Alignment   |    | 100.0      | 20     | <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                                                                 |
| 2  | <a href="#">c2di3A_</a> |  Alignment   |    | 100.0      | 23     | <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                                                 |
| 3  | <a href="#">c3ihuA_</a> |  Alignment   |    | 100.0      | 25     | <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                        |
| 4  | <a href="#">c3c7jA_</a> |  Alignment   |    | 100.0      | 21     | <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 transcriptional regulator (gntr family member)2 from pseudomonas syringae pv. tomato str. dc3000              |
| 5  | <a href="#">c3fmsA_</a> |  Alignment |  | 100.0      | 19     | <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 transcriptional2 regulator                                                                     |
| 6  | <a href="#">c2hs5A_</a> |  Alignment |  | 100.0      | 20     | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator gntr;<br><b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1                |
| 7  | <a href="#">c3by6C_</a> |  Alignment |  | 99.8       | 18     | <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                                                                 |
| 8  | <a href="#">c2du9A_</a> |  Alignment |  | 99.8       | 19     | <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                                                                             |
| 9  | <a href="#">c3neuA_</a> |  Alignment |  | 99.7       | 22     | <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                                            |
| 10 | <a href="#">c3bwgA_</a> |  Alignment |  | 99.7       | 33     | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator yydk;<br><b>PDBTitle:</b> the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168 |
| 11 | <a href="#">c3edpB_</a> |  Alignment |  | 99.7       | 30     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> lin2111 protein;<br><b>PDBTitle:</b> the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262                                        |

|    |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                                                     |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">dlv4ra1</a> | Alignment |     | 99.7 | 29 | <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                                                                                                       |
| 13 | <a href="#">c3f8mA</a>  | Alignment |    | 99.6 | 31 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> gntR-family protein transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of phnf from mycobacterium smegmatis                                                                 |
| 14 | <a href="#">c3eetA</a>  | Alignment |    | 99.6 | 24 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative gntR-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of putative gntR-family transcriptional2 regulator                                        |
| 15 | <a href="#">dlhwla1</a> | Alignment |    | 99.6 | 33 | <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                                                                                                       |
| 16 | <a href="#">d3bwga1</a> | Alignment |    | 99.6 | 30 | <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                                                                                                       |
| 17 | <a href="#">c3ic7A</a>  | Alignment |    | 99.6 | 18 | <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 |
| 18 | <a href="#">d2hs5a1</a> | Alignment |  | 99.6 | 32 | <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                                                                                                       |
| 19 | <a href="#">dlhwla2</a> | Alignment |  | 99.5 | 16 | <b>Fold:</b> GntR ligand-binding domain-like<br><b>Superfamily:</b> GntR ligand-binding domain-like<br><b>Family:</b> GntR ligand-binding domain-like                                                                                                               |
| 20 | <a href="#">c3tqnC</a>  | Alignment |  | 99.5 | 15 | <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.                                       |
| 21 | <a href="#">d2hs5a2</a> | Alignment | not modelled                                                                        | 99.4 | 16 | <b>Fold:</b> GntR ligand-binding domain-like<br><b>Superfamily:</b> GntR ligand-binding domain-like<br><b>Family:</b> GntR ligand-binding domain-like                                                                                                               |
| 22 | <a href="#">c3sxB</a>   | Alignment | not modelled                                                                        | 99.3 | 15 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, gntR family;<br><b>PDBTitle:</b> zn2+-bound fcd domain of tm0439, a putative transcriptional regulator                                               |
| 23 | <a href="#">c2wv0H</a>  | Alignment | not modelled                                                                        | 99.3 | 28 | <b>PDB header:</b> transcription<br><b>Chain:</b> H: <b>PDB Molecule:</b> hth-type transcriptional repressor yvoa;<br><b>PDBTitle:</b> crystal structure of the gntR-hutC family member yvoa from2 bacillus subtilis                                                |
| 24 | <a href="#">c2h09A</a>  | Alignment | not modelled                                                                        | 98.4 | 17 | <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                                                            |
| 25 | <a href="#">c1f5tA</a>  | Alignment | not modelled                                                                        | 98.1 | 14 | <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                                    |
| 26 | <a href="#">c2it0A</a>  | Alignment | not modelled                                                                        | 98.0 | 15 | <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                                                                |
| 27 | <a href="#">c3hruA</a>  | Alignment | not modelled                                                                        | 97.9 | 20 | <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+                                                                                                      |
| 28 | <a href="#">dlbiaa1</a> | Alignment | not modelled                                                                        | 97.8 | 24 | <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                                                                                                                      |
|    |                         |           |                                                                                     |      |    | <b>PDB header:</b> gene regulation                                                                                                                                                                                                                                  |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                 |
|----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | <a href="#">c1g3wA_</a> | Alignment | not modelled | 97.6 | 15 | <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor;<br><b>PDBTitle:</b> cd-cys102ser dbxr                                                                                                                                                         |
| 30 | <a href="#">d1stza1</a> | Alignment | not modelled | 97.3 | 10 | <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                                                                         |
| 31 | <a href="#">c1fx7C_</a> | Alignment | not modelled | 97.3 | 13 | <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)2 from mycobacterium tuberculosis                                      |
| 32 | <a href="#">d1g3wa1</a> | Alignment | not modelled | 97.3 | 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                                                                                                       |
| 33 | <a href="#">d1jhfa1</a> | Alignment | not modelled | 97.3 | 21 | <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                                                                                          |
| 34 | <a href="#">d2isyA1</a> | Alignment | not modelled | 97.2 | 25 | <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                                                                                                       |
| 35 | <a href="#">c3ctaA_</a> | Alignment | not modelled | 97.1 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase;<br><b>PDBTitle:</b> crystal structure of riboflavin kinase from thermoplasma2 acidophilum                                                                            |
| 36 | <a href="#">c2x4hA_</a> | Alignment | not modelled | 97.1 | 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                                                 |
| 37 | <a href="#">c3r0aB_</a> | Alignment | not modelled | 97.0 | 18 | <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)                                     |
| 38 | <a href="#">c2y75F_</a> | Alignment | not modelled | 96.9 | 19 | <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 regulator2 of b. subtilis                                               |
| 39 | <a href="#">d1j5ya1</a> | Alignment | not modelled | 96.8 | 23 | <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                                                                                                                  |
| 40 | <a href="#">d2hr3a1</a> | Alignment | not modelled | 96.8 | 16 | <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                                                                                                   |
| 41 | <a href="#">c2ev5B_</a> | Alignment | not modelled | 96.7 | 13 | <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                                                          |
| 42 | <a href="#">c3lwfD_</a> | Alignment | not modelled | 96.7 | 16 | <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   |
| 43 | <a href="#">d3broa1</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> MarR-like transcriptional regulators                                                                                                   |
| 44 | <a href="#">d2fbha1</a> | Alignment | not modelled | 96.7 | 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                                                                                                   |
| 45 | <a href="#">d1ylfa1</a> | Alignment | not modelled | 96.6 | 13 | <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                                                                                                         |
| 46 | <a href="#">d3ctaa1</a> | Alignment | not modelled | 96.6 | 15 | <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                                                                                                   |
| 47 | <a href="#">c2rdpA_</a> | Alignment | not modelled | 96.6 | 13 | <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                                                 |
| 48 | <a href="#">c3bj6B_</a> | Alignment | not modelled | 96.5 | 11 | <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                                                |
| 49 | <a href="#">c3cjnA_</a> | Alignment | not modelled | 96.5 | 15 | <b>PDB header:</b> transcription regulator<br><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                        |
| 50 | <a href="#">c3k69A_</a> | Alignment | not modelled | 96.4 | 20 | <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          |
| 51 | <a href="#">c3nqoB_</a> | Alignment | not modelled | 96.4 | 11 | <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 |
| 52 | <a href="#">d1i5za1</a> | Alignment | not modelled | 96.3 | 13 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> CAP C-terminal domain-like                                                                                                             |
| 53 | <a href="#">c3s2wB_</a> | Alignment | not modelled | 96.3 | 13 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family;<br><b>PDBTitle:</b> the crystal structure of a marr transcriptional regulator from2 methanosarcina mazei go1                        |
| 54 | <a href="#">c2ewnA_</a> | Alignment | not modelled | 96.3 | 24 | <b>PDB header:</b> ligase, transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> bira bifunctional protein;<br><b>PDBTitle:</b> ecoli biotin repressor with co-repressor analog                                                                                |
| 55 | <a href="#">d1s3ja_</a> | Alignment | not modelled | 96.3 | 16 | <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                                                                                                   |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                               |
|----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 56 | <a href="#">c2v79B_</a> | Alignment | not modelled | 96.3 | 17 | <b>PDB header:</b> dna-binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna replication protein dnad;<br><b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad from2 bacillus subtilis                                                                                  |
| 57 | <a href="#">c2qwwB_</a> | Alignment | not modelled | 96.3 | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family;<br><b>PDBTitle:</b> crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution          |
| 58 | <a href="#">c2oqgA_</a> | Alignment | not modelled | 96.2 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein;<br><b>PDBTitle:</b> arsr-like transcriptional regulator from rhodococcus sp. rha1                                                                          |
| 59 | <a href="#">c1j5yA_</a> | Alignment | not modelled | 96.2 | 21 | <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                                       |
| 60 | <a href="#">c2gxgA_</a> | Alignment | not modelled | 96.1 | 13 | <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 sulfobus tokodaii strain7                                                  |
| 61 | <a href="#">d2a61a1</a> | Alignment | not modelled | 96.1 | 16 | <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                                                                                                                                 |
| 62 | <a href="#">c3bjaA_</a> | Alignment | not modelled | 96.1 | 9  | <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 |
| 63 | <a href="#">d1sfxa_</a> | Alignment | not modelled | 96.0 | 15 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> TrmB-like                                                                                                                                                            |
| 64 | <a href="#">d1lj9a_</a> | Alignment | not modelled | 96.0 | 13 | <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                                                                                                                                 |
| 65 | <a href="#">c3g3zA_</a> | Alignment | not modelled | 95.9 | 11 | <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                                                                          |
| 66 | <a href="#">d1lnwa_</a> | Alignment | not modelled | 95.9 | 16 | <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                                                                                                                                 |
| 67 | <a href="#">d2d1ha1</a> | Alignment | not modelled | 95.9 | 21 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> TrmB-like                                                                                                                                                            |
| 68 | <a href="#">d1ft9a1</a> | Alignment | not modelled | 95.8 | 19 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> CAP C-terminal domain-like                                                                                                                                           |
| 69 | <a href="#">d2h6ca1</a> | Alignment | not modelled | 95.8 | 10 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> CAP C-terminal domain-like                                                                                                                                           |
| 70 | <a href="#">d2b0la1</a> | Alignment | not modelled | 95.7 | 19 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Cody HTH domain                                                                                                                                                      |
| 71 | <a href="#">d2ev0a1</a> | Alignment | not modelled | 95.7 | 19 | <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                                                                                                                                     |
| 72 | <a href="#">c3f6vA_</a> | Alignment | not modelled | 95.6 | 19 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family<br><b>PDBTitle:</b> crystal structure of possible transcriptional regulator for2 arsenical resistance                                                     |
| 73 | <a href="#">c3e6mD_</a> | Alignment | not modelled | 95.6 | 9  | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> D: <b>PDB Molecule:</b> marr family transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.                                              |
| 74 | <a href="#">d2oz6a1</a> | Alignment | not modelled | 95.5 | 23 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> CAP C-terminal domain-like                                                                                                                                           |
| 75 | <a href="#">c3fm5D_</a> | Alignment | not modelled | 95.5 | 15 | <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                                                              |
| 76 | <a href="#">c1r22B_</a> | Alignment | not modelled | 95.5 | 21 | <b>PDB header:</b> transcription repressor<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor smtb;<br><b>PDBTitle:</b> crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form                              |
| 77 | <a href="#">d2coha1</a> | Alignment | not modelled | 95.5 | 22 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> CAP C-terminal domain-like                                                                                                                                           |
| 78 | <a href="#">c3nrvC_</a> | Alignment | not modelled | 95.4 | 5  | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative transcriptional regulator (marr/emrr family);<br><b>PDBTitle:</b> crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1                                   |
| 79 | <a href="#">c3kp3B_</a> | Alignment | not modelled | 95.4 | 13 | <b>PDB header:</b> transcription regulator/antibiotic<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator tcarr;<br><b>PDBTitle:</b> staphylococcus epidermidis in complex with ampicillin                                                                                     |
|    |                         |           |              |      |    | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulatory                                                                                                                                                                                 |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                                                                                                                        |
|-----|-------------------------|-----------|--------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 80  | <a href="#">c2nyxB</a>  | Alignment | not modelled | 95.4 | 13 | protein, rv1404;<br><b>PDBTitle:</b> crystal structure of rv1404 from mycobacterium tuberculosis                                                                                                                                                                                                                                                                                                       |
| 81  | <a href="#">c1ft9A</a>  | Alignment | not modelled | 95.4 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide oxidation system transcription<br><b>PDBTitle:</b> structure of the reduced (feii) co-sensing protein from r.2 rubrum                                                                                                                                                                                        |
| 82  | <a href="#">d2bv6a1</a> | Alignment | not modelled | 95.4 | 11 | <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                                                                                                                                                                                                                                          |
| 83  | <a href="#">c1stzB</a>  | Alignment | not modelled | 95.4 | 10 | <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                                                                                                                                                                                     |
| 84  | <a href="#">c3oopA</a>  | Alignment | not modelled | 95.3 | 18 | <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 clipl1262                                                                                                                                                                               |
| 85  | <a href="#">d3deua1</a> | Alignment | not modelled | 95.3 | 20 | <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                                                                                                                                                                                                                                          |
| 86  | <a href="#">c3deuB</a>  | Alignment | not modelled | 95.3 | 22 | <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 slya2 from salmonella typhimurium in complex with salicylate3 ligands                                                                                                                                    |
| 87  | <a href="#">c3d0sA</a>  | Alignment | not modelled | 95.3 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein;<br><b>PDBTitle:</b> camp receptor protein from m.tuberculosis, camp-free form                                                                                                                                                                                                            |
| 88  | <a href="#">d1mkma1</a> | Alignment | not modelled | 95.2 | 22 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Transcriptional regulator lclR, N-terminal domain                                                                                                                                                                                                                             |
| 89  | <a href="#">c3boqB</a>  | Alignment | not modelled | 95.2 | 12 | <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 transcriptional regulator from2 silicibacter pomeroyi                                                                                                                                                                 |
| 90  | <a href="#">c2l4aA</a>  | Alignment | not modelled | 95.2 | 27 | <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                                                                                                                                                                                                       |
| 91  | <a href="#">d1r1ua</a>  | Alignment | not modelled | 95.2 | 14 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> ArsR-like transcriptional regulators                                                                                                                                                                                                                                          |
| 92  | <a href="#">c2nnnB</a>  | Alignment | not modelled | 95.2 | 18 | <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                                                                                                                                                                                 |
| 93  | <a href="#">d1xd7a</a>  | Alignment | not modelled | 95.2 | 18 | <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                                                                                                                                                                                                                                                |
| 94  | <a href="#">c3tgnA</a>  | Alignment | not modelled | 95.1 | 23 | <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                                                                                                                                                                 |
| 95  | <a href="#">c1zybA</a>  | Alignment | not modelled | 95.1 | 13 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator, crp family;<br><b>PDBTitle:</b> crystal structure of transcription regulator from bacteroides2 thetaiotaomicron vpi-5482 at 2.15 a resolution                                                                                                                                             |
| 96  | <a href="#">d2etha1</a> | Alignment | not modelled | 95.1 | 16 | <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                                                                                                                                                                                                                                          |
| 97  | <a href="#">c2fa5B</a>  | Alignment | not modelled | 95.1 | 11 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator marr/emrr family;<br><b>PDBTitle:</b> the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris                                                                                                                                         |
| 98  | <a href="#">d2fxaa1</a> | Alignment | not modelled | 95.1 | 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                                                                                                                                                                                                                                          |
| 99  | <a href="#">c3f6oB</a>  | Alignment | not modelled | 95.1 | 24 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator, arsr family<br><b>PDBTitle:</b> crystal structure of arsr family transcriptional regulator,2 rha00566                                                                                                                                                                          |
| 100 | <a href="#">c2kkoB</a>  | Alignment | not modelled | 95.0 | 16 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulatory protein<br><b>PDBTitle:</b> 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. |
| 101 | <a href="#">d1ku9a</a>  | Alignment | not modelled | 95.0 | 15 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> DNA-binding protein Mj223                                                                                                                                                                                                                                                     |
| 102 | <a href="#">d2gava1</a> | Alignment | not modelled | 95.0 | 14 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> CAP C-terminal domain-like                                                                                                                                                                                                                                                    |
| 103 | <a href="#">d1sd4a</a>  | Alignment | not modelled | 94.9 | 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                                                                                                                                                                                                                                                       |
| 104 | <a href="#">c3bddD</a>  | Alignment | not modelled | 94.9 | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein marr;<br><b>PDBTitle:</b> crystal structure of a putative multiple antibiotic-                                                                                                                                                                                                                            |



|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                  |
|-----|-------------------------|-----------|--------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |                         |           |              |      |    | resistance2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution                                                                                                                                                                                                         |
| 105 | <a href="#">d1r1ta_</a> | Alignment | not modelled | 94.8 | 20 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> ArsR-like transcriptional regulators                                                                                                                                    |
| 106 | <a href="#">c3k0lA_</a> | Alignment | not modelled | 94.8 | 11 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein;<br><b>PDBTitle:</b> crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp                                                                       |
| 107 | <a href="#">c2gauA_</a> | Alignment | not modelled | 94.7 | 11 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, crp/fnr family;<br><b>PDBTitle:</b> crystal structure of transcriptional regulator, crp/fnr family from2 porphyromonas gingivalis (apc80792), structural genomics, mcsq                     |
| 108 | <a href="#">c3jthA_</a> | Alignment | not modelled | 94.6 | 19 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcription activator hlyu;<br><b>PDBTitle:</b> crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6                                                                                  |
| 109 | <a href="#">c2jscB_</a> | Alignment | not modelled | 94.6 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator rv1994c/mt2050;<br><b>PDBTitle:</b> nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis                                                                          |
| 110 | <a href="#">c3iwzB_</a> | Alignment | not modelled | 94.6 | 26 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> catabolite activation-like protein;<br><b>PDBTitle:</b> the c-di-gmp responsive global regulator clp links cell-cell signaling2 to virulence gene expression in xanthomonas campestris                                 |
| 111 | <a href="#">c2fmyB_</a> | Alignment | not modelled | 94.6 | 14 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> carbon monoxide oxidation system transcription regulator<br><b>PDBTitle:</b> co-dependent transcription factor cooa from carboxydothermus2 hydrogenoformans (imidazole-bound form)                               |
| 112 | <a href="#">c2vn2B_</a> | Alignment | not modelled | 94.6 | 31 | <b>PDB header:</b> replication<br><b>Chain:</b> B: <b>PDB Molecule:</b> chromosome replication initiation protein;<br><b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426                                                          |
| 113 | <a href="#">c3e6dA_</a> | Alignment | not modelled | 94.5 | 11 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> cyclic nucleotide-binding protein;<br><b>PDBTitle:</b> crystal structure of cprk c200s                                                                                                                      |
| 114 | <a href="#">c3cuoB_</a> | Alignment | not modelled | 94.5 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygav;<br><b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli                                          |
| 115 | <a href="#">c2oz6A_</a> | Alignment | not modelled | 94.5 | 22 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> virulence factor regulator;<br><b>PDBTitle:</b> crystal structure of virulence factor regulator from pseudomonas2 aeruginosa in complex with camp                                                                |
| 116 | <a href="#">c3e97A_</a> | Alignment | not modelled | 94.5 | 18 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, crp/fnr family;<br><b>PDBTitle:</b> crystal structure of transcriptional regulator of crp/fnr2 family (yp_604437.1) from deinococcus geothermalis dsm3 11300 at 1.86 a resolution |
| 117 | <a href="#">c2o0yB_</a> | Alignment | not modelled | 94.4 | 15 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.                                                                |
| 118 | <a href="#">d2cg4a1</a> | Alignment | not modelled | 94.4 | 26 | <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                                                                                                               |
| 119 | <a href="#">c3pqkD_</a> | Alignment | not modelled | 94.4 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> biofilm growth-associated repressor;<br><b>PDBTitle:</b> crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa                                                                              |
| 120 | <a href="#">d1jgsa_</a> | Alignment | not modelled | 94.4 | 16 | <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                                                                                                                                    |