

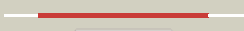




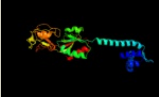







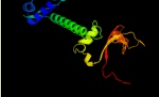
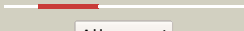






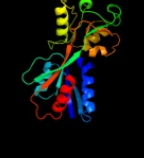
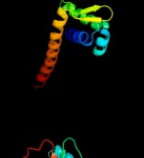
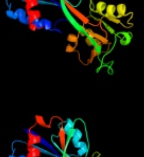
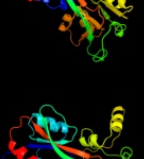
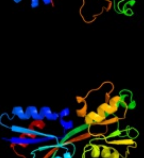


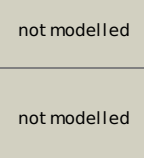


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1iz1B_</a>	 Alignment		100.0	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> lysr-type regulatory protein; <b>PDBTitle:</b> crystal structure of cbnr, a lysr family transcriptional2 regulator
2	<a href="#">c3hhgF_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
3	<a href="#">c2esnC_</a>	 Alignment		100.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa
4	<a href="#">c3fzjC_</a>	 Alignment		100.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> lysr type regulator of tsambcd; <b>PDBTitle:</b> tsar low resolution crystal structure, tetragonal form
5	<a href="#">c3t1bB_</a>	 Alignment		100.0	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> crystal structure of the full-length aphb n100e variant
6	<a href="#">c3fzvC_</a>	 Alignment		100.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of pa01 protein, putative lysr family2 transcriptional regulator from pseudomonas aeruginosa
7	<a href="#">c3ispA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator <b>PDBTitle:</b> crystal structure of argp from mycobacterium tuberculosis
8	<a href="#">c1b9nA_</a>	 Alignment		99.9	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein (mode); <b>PDBTitle:</b> regulator from escherichia coli
9	<a href="#">c3m1eA_</a>	 Alignment		99.9	48	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of benm_dbd
10	<a href="#">d2esna1</a>	 Alignment		99.9	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LysR-like transcriptional regulators
11	<a href="#">d1b9ma1</a>	 Alignment		99.8	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> N-terminal domain of molybdate-dependent transcriptional regulator MoDE

12	<a href="#">c2hxrA_</a>	Alignment		99.8	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator cynr; <b>PDBTitle:</b> structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
13	<a href="#">dlixca2</a>	Alignment		99.8	22	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
14	<a href="#">dlixca1</a>	Alignment		99.8	46	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LysR-like transcriptional regulators
15	<a href="#">c2h9qC_</a>	Alignment		99.8	27	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> hth-type transcriptional regulator catm; <b>PDBTitle:</b> crystal structure of the effector binding domain of a catm2 variant (r156h)
16	<a href="#">c2f7cA_</a>	Alignment		99.8	26	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator catm; <b>PDBTitle:</b> catm effector binding domain with its effector cis,cis-muconate
17	<a href="#">c3jv9B_</a>	Alignment		99.7	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> the structure of a reduced form of oxyr from n. meningitidis
18	<a href="#">c2h9bB_</a>	Alignment		99.7	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
19	<a href="#">d2fyia1</a>	Alignment		99.7	20	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
20	<a href="#">c2ijlB_</a>	Alignment		99.7	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> molybdenum-binding transcriptional repressor; <b>PDBTitle:</b> the structure of a putative mode from agrobacterium tumefaciens.
21	<a href="#">d1i6aa_</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
22	<a href="#">c3oxnD_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator, lysr family; <b>PDBTitle:</b> the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
23	<a href="#">c3ho7A_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> oxyr; <b>PDBTitle:</b> crystal structure of oxyr from porphyromonas gingivalis
24	<a href="#">c3fd3A_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome replication initiation inhibitor protein; <b>PDBTitle:</b> structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
25	<a href="#">c2f78A_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> benm effector binding domain with its effector benzoate
26	<a href="#">d1lutha_</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
27	<a href="#">c2ql3G_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> probable transcriptional regulator, lysr family protein; <b>PDBTitle:</b> crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1 <b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> cvs regulon transcriptional activator

28	<a href="#">c1al3A_</a>	Alignment	not modelled	99.7	20	cysb; <b>PDBTitle:</b> cofactor binding fragment of cysb from klebsiella aerogenes
29	<a href="#">d1al3a_</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
30	<a href="#">c2uyeA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> double mutant y110s,f111v dnt- from burkholderia sp. strain2 dnt in complex with thiocyanate
31	<a href="#">c3n6uA_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lysr type regulator of tsambcd; <b>PDBTitle:</b> effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
32	<a href="#">d2esna2_</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
33	<a href="#">c3kosA_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator ampr; <b>PDBTitle:</b> structure of the ampr effector binding domain from citrobacter2 freundii
34	<a href="#">c3hhfB_</a>	Alignment	not modelled	99.5	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> structure of crga regulatory domain, a lysr-type transcriptional2 regulator from neisseria meningitidis.
35	<a href="#">c3mz1D_</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a possible transcription regulator protein2 from sinorhizobium meliloti 1021
36	<a href="#">c3onmB_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator lrrha; <b>PDBTitle:</b> effector binding domain of lysr-type transcription factor rovm from y.2 pseudotuberculosis
37	<a href="#">c2qsxB_</a>	Alignment	not modelled	99.2	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator, lysr family; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator lysr from2 vibrio parahaemolyticus
38	<a href="#">c2x4hA_</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sso2273; <b>PDBTitle:</b> crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
39	<a href="#">c3boqB_</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
40	<a href="#">c3ctaA_</a>	Alignment	not modelled	97.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase; <b>PDBTitle:</b> crystal structure of riboflavin kinase from thermoplasma2 acidophilum
41	<a href="#">c2gxgA_</a>	Alignment	not modelled	97.7	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> 146aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
42	<a href="#">c2fa5B_</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator marr/emrr family; <b>PDBTitle:</b> the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
43	<a href="#">c3f3xA_</a>	Alignment	not modelled	97.6	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family, putative; <b>PDBTitle:</b> crystal structure of the transcriptional regulator bldr2 from sulfolobus solfataricus
44	<a href="#">d2fxaa1_</a>	Alignment	not modelled	97.6	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
45	<a href="#">d2fbha1_</a>	Alignment	not modelled	97.6	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
46	<a href="#">c3bpxB_</a>	Alignment	not modelled	97.6	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
47	<a href="#">c2nnnB_</a>	Alignment	not modelled	97.6	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
48	<a href="#">c2fxaB_</a>	Alignment	not modelled	97.5	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> protease production regulatory protein hpr; <b>PDBTitle:</b> structure of the protease production regulatory protein hpr from2 bacillus subtilis.
49	<a href="#">c2nyxB_</a>	Alignment	not modelled	97.5	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulatory protein, rv1404; <b>PDBTitle:</b> crystal structure of rv1404 from mycobacterium tuberculosis
50	<a href="#">c3fm5D_</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> x-ray crystal structure of transcriptional regulator (marr family)2 from rhodococcus sp. rha1
51	<a href="#">c3nrvC_</a>	Alignment	not modelled	97.5	12	<b>PDB header:</b> transcription regulator <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
52	<a href="#">d1jgsa_</a>	Alignment	not modelled	97.5	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain

						<b>Family:</b> MarR-like transcriptional regulators
53	<a href="#">c3cjnA</a>	Alignment	not modelled	97.5	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
54	<a href="#">d2bv6a1</a>	Alignment	not modelled	97.4	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
55	<a href="#">d1lj9a</a>	Alignment	not modelled	97.4	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
56	<a href="#">c2h09A</a>	Alignment	not modelled	97.4	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> crystal structure of diphtheria toxin repressor like protein2 from e. coli
57	<a href="#">c1f5tA</a>	Alignment	not modelled	97.4	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
58	<a href="#">c2rdpA</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator marr; <b>PDBTitle:</b> the structure of a marr family protein from bacillus2 stearothermophilus
59	<a href="#">c3cdhB</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of the marr family transcriptional regulator spo14532 from silicibacter pomeroyi dss-3
60	<a href="#">d1lnwa</a>	Alignment	not modelled	97.4	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
61	<a href="#">c3g3zA</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
62	<a href="#">c2pexA</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator ohrr; <b>PDBTitle:</b> structure of reduced c22s ohrr from xanthomonas campestris
63	<a href="#">c3e6mD</a>	Alignment	not modelled	97.3	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> marr family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
64	<a href="#">c1g3wA</a>	Alignment	not modelled	97.3	24	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtxr
65	<a href="#">c3bjaA</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family, putative; <b>PDBTitle:</b> crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
66	<a href="#">c3hrmA</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator sarz; <b>PDBTitle:</b> crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form
67	<a href="#">d2etha1</a>	Alignment	not modelled	97.2	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
68	<a href="#">d1s3ja</a>	Alignment	not modelled	97.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
69	<a href="#">c3ecoB</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> mepR; <b>PDBTitle:</b> crystal structure of mepR, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepA
70	<a href="#">c3hruA</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> metalloregulator scar; <b>PDBTitle:</b> crystal structure of scar with bound zn2+
71	<a href="#">c3bj6B</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcription regulator sp03579
72	<a href="#">d2frha1</a>	Alignment	not modelled	97.2	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
73	<a href="#">d1ub9a</a>	Alignment	not modelled	97.2	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
74	<a href="#">d1p4xa1</a>	Alignment	not modelled	97.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
75	<a href="#">c3nqoB</a>	Alignment	not modelled	97.1	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> marr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
76	<a href="#">c3k0lA</a>	Alignment	not modelled	97.1	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein; <b>PDBTitle:</b> crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
77	<a href="#">c1fx7C</a>	Alignment	not modelled	97.1	24	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

78	<a href="#">d2fbia1</a>	Alignment	not modelled	97.1	16	<b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
79	<a href="#">d3broa1</a>	Alignment	not modelled	97.0	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
80	<a href="#">d1twya</a>	Alignment	not modelled	97.0	10	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
81	<a href="#">c1twyG</a>	Alignment	not modelled	97.0	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein; <b>PDBTitle:</b> crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
82	<a href="#">c2it0A</a>	Alignment	not modelled	97.0	26	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of a two-domain ider-dna complex crystal2 form ii
83	<a href="#">d2fbka1</a>	Alignment	not modelled	97.0	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
84	<a href="#">c3kp3B</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> transcription regulator/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator tcar; <b>PDBTitle:</b> staphylococcus epidermidis in complex with ampicillin
85	<a href="#">c3oopA</a>	Alignment	not modelled	96.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2960 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from listeria innocua2 clip11262
86	<a href="#">d2hr3a1</a>	Alignment	not modelled	96.9	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
87	<a href="#">d1hsja1</a>	Alignment	not modelled	96.9	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
88	<a href="#">d1z91a1</a>	Alignment	not modelled	96.9	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
89	<a href="#">c1p4xA</a>	Alignment	not modelled	96.8	7	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> staphylococcal accessory regulator a homologue; <b>PDBTitle:</b> crystal structure of sars protein from staphylococcus aureus
90	<a href="#">d1p4xa2</a>	Alignment	not modelled	96.8	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
91	<a href="#">d3ctaa1</a>	Alignment	not modelled	96.8	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
92	<a href="#">d2cfxa1</a>	Alignment	not modelled	96.8	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
93	<a href="#">d1biaa1</a>	Alignment	not modelled	96.8	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
94	<a href="#">d2a61a1</a>	Alignment	not modelled	96.7	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
95	<a href="#">c3s2wB</a>	Alignment	not modelled	96.7	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> the crystal structure of a marr transcriptional regulator from2 methanosarcina mazei go1
96	<a href="#">c3deuB</a>	Alignment	not modelled	96.6	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator slya; <b>PDBTitle:</b> crystal structure of transcription regulatory protein slya2 from salmonella typhimurium in complex with salicylate3 ligands
97	<a href="#">c1r22B</a>	Alignment	not modelled	96.6	19	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor smtb; <b>PDBTitle:</b> crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
98	<a href="#">c2zkzC</a>	Alignment	not modelled	96.6	10	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional repressor pagr; <b>PDBTitle:</b> crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
99	<a href="#">c3onqB</a>	Alignment	not modelled	96.5	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> regulator of polyketide synthase expression; <b>PDBTitle:</b> crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
100	<a href="#">c2ev5B</a>	Alignment	not modelled	96.5	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
101	<a href="#">d3deua1</a>	Alignment	not modelled	96.5	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
102	<a href="#">d1r1ua</a>	Alignment	not modelled	96.4	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
103	<a href="#">c2qwwB</a>	Alignment	not modelled	96.4	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <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
						<b>PDB header:</b> transcription regulator



104	<a href="#">c3jw4C_</a>	Alignment	not modelled	96.4	10	<b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, marr/emrr family; <b>PDBTitle:</b> the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum
105	<a href="#">c2kkoB_</a>	Alignment	not modelled	96.3	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulatory protein <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.
106	<a href="#">d1r1ta_</a>	Alignment	not modelled	96.3	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
107	<a href="#">c3cuoB_</a>	Alignment	not modelled	96.2	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
108	<a href="#">c2cfxD_</a>	Alignment	not modelled	96.1	16	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrpc; <b>PDBTitle:</b> structure of b.subtilis lrpc
109	<a href="#">c2ia0A_</a>	Alignment	not modelled	96.1	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator pf0864; <b>PDBTitle:</b> transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
110	<a href="#">c2cg4B_</a>	Alignment	not modelled	96.1	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
111	<a href="#">c2dbbA_</a>	Alignment	not modelled	96.0	16	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph0061; <b>PDBTitle:</b> crystal structure of ph0061
112	<a href="#">c3jthA_</a>	Alignment	not modelled	96.0	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription activator hlyu; <b>PDBTitle:</b> crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
113	<a href="#">c2ewnA_</a>	Alignment	not modelled	95.9	17	<b>PDB header:</b> ligase, transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bira bifunctional protein; <b>PDBTitle:</b> ecoli biotin repressor with co-repressor analog
114	<a href="#">d2cg4a1</a>	Alignment	not modelled	95.9	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
115	<a href="#">c3bddD_</a>	Alignment	not modelled	95.9	19	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein marr; <b>PDBTitle:</b> crystal structure of a putative multiple antibiotic-resistance2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution
116	<a href="#">d1u2wa1</a>	Alignment	not modelled	95.8	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
117	<a href="#">c2vzbA_</a>	Alignment	not modelled	95.7	14	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
118	<a href="#">c3tgnA_</a>	Alignment	not modelled	95.7	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adc operon repressor adcr; <b>PDBTitle:</b> crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
119	<a href="#">c2oqgA_</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> arsr-like transcriptional regulator from rhodococcus sp. rha1
120	<a href="#">c2jscB_</a>	Alignment	not modelled	95.6	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator rv1994c/mt2050; <b>PDBTitle:</b> nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis