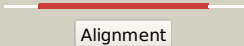

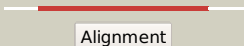

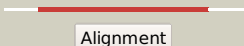







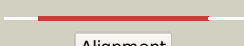




















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1773c_(-)_2007027_2007773
Date	Fri Aug 2 13:30:38 BST 2019
Unique Job ID	c1a9b14aa318f1d4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1mkmA_</a>	 Alignment		100.0	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> iclr transcriptional regulator; <b>PDBTitle:</b> crystal structure of the thermotoga maritima iclr
2	<a href="#">c5y6iB_</a>	 Alignment		100.0	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator kdgr; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa hmgr
3	<a href="#">c2o0yB_</a>	 Alignment		100.0	26	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
4	<a href="#">c2g7uB_</a>	 Alignment		100.0	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
5	<a href="#">c5h1aC_</a>	 Alignment		100.0	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> iclr transcription factor homolog; <b>PDBTitle:</b> crystal structure of an iclr homolog from microbacterium sp. strain2 hm58-2
6	<a href="#">c5whmB_</a>	 Alignment		100.0	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> iclr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of iclr family transcriptional regulator from2 brucella abortus
7	<a href="#">c2xroE_</a>	 Alignment		100.0	29	<b>PDB header:</b> dna-binding protein/dna <b>Chain:</b> E: <b>PDB Molecule:</b> hth-type transcriptional regulator ttgv; <b>PDBTitle:</b> crystal structure of ttgv in complex with its dna operator
8	<a href="#">c5w1eA_</a>	 Alignment		100.0	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> pobr in complex with phb
9	<a href="#">c3mq0A_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription repressor <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor of the blcabc operon; <b>PDBTitle:</b> crystal structure of agobacterium tumefaciens repressor blcr
10	<a href="#">c3r4kD_</a>	 Alignment		100.0	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
11	<a href="#">c2ia2D_</a>	 Alignment		100.0	28	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1

12	<a href="#">c5tjA</a>	Alignment		100.0	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of iclr transcriptional regulator from2 alicyclobacillus acidocaldarius
13	<a href="#">c3bjnA</a>	Alignment		100.0	30	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, putative; <b>PDBTitle:</b> crystal structure of c-terminal domain of putative transcriptional2 regulator from vibrio cholerae, targeted domain 79-240
14	<a href="#">d1tf1a</a>	Alignment		100.0	25	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> lclR ligand-binding domain-like
15	<a href="#">d1mkma2</a>	Alignment		100.0	26	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> lclR ligand-binding domain-like
16	<a href="#">c3d3oA</a>	Alignment		100.0	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of the effector domain of the putative2 transcriptional regulator iclr from acinetobacter sp. adp1
17	<a href="#">d2o9aa1</a>	Alignment		100.0	24	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> lclR ligand-binding domain-like
18	<a href="#">c3obfA</a>	Alignment		100.0	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator, iclr family;2 targeted domain 129...302
19	<a href="#">c1ysqA</a>	Alignment		100.0	26	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator yiaj; <b>PDBTitle:</b> the crystal structure of transcriptional regulator yaij
20	<a href="#">c5hpfA</a>	Alignment		100.0	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> p-hydroxybenzoate hydroxylase transcriptional activator; <b>PDBTitle:</b> crystal structure of the double mutant of pobr transcription factor2 inducer binding domain from acinetobacter
21	<a href="#">c1yspA</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator kdgr; <b>PDBTitle:</b> crystal structure of the c-terminal domain of e. coli transcriptional2 regulator kdgr.
22	<a href="#">d1mkma1</a>	Alignment	not modelled	99.8	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator lclR, N-terminal domain
23	<a href="#">c2qufB</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor pf0095; <b>PDBTitle:</b> crystal structure of transcription factor axxa-pf0095 from pyrococcus2 furiosus
24	<a href="#">d2hr3a1</a>	Alignment	not modelled	98.2	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
25	<a href="#">c2h09A</a>	Alignment	not modelled	98.2	22	<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
26	<a href="#">c1f5tA</a>	Alignment	not modelled	98.2	16	<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
27	<a href="#">c2it0A</a>	Alignment	not modelled	98.1	15	<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
28	<a href="#">c6j05B</a>	Alignment	not modelled	98.1	25	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

29	<a href="#">dlj5ya1</a>	Alignment	not modelled	98.1	14	<b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
30	<a href="#">c6hsdB_</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rff2 family transcriptional regulator; <b>PDBTitle:</b> crystal structure of the oxidized form of the transcription regulator2 rsrr
31	<a href="#">c2oqgA_</a>	Alignment	not modelled	98.0	22	<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
32	<a href="#">c3t8tA_</a>	Alignment	not modelled	98.0	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> staphylococcus aureus cymr (oxidized form); <b>PDBTitle:</b> crystal structure of staphylococcus aureus cymr oxidized form
33	<a href="#">c1fx7C_</a>	Alignment	not modelled	98.0	15	<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) from2 mycobacterium tuberculosis
34	<a href="#">c6cmvA_</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator Irs14-like protein; <b>PDBTitle:</b> crystal structure of archaeal biofilm regulator (abfr2) from2 sulfobolus acidocaldarius
35	<a href="#">d1biaa1</a>	Alignment	not modelled	98.0	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
36	<a href="#">c3r0aB_</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
37	<a href="#">d3ctaa1</a>	Alignment	not modelled	97.9	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
38	<a href="#">c2wteB_</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> antiviral protein <b>Chain:</b> B: <b>PDB Molecule:</b> csa3; <b>PDBTitle:</b> the structure of the crispr-associated protein, csa3, from2 sulfobolus solfataricus at 1.8 angstrom resolution.
39	<a href="#">c1g3wA_</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtxr
40	<a href="#">c2x4hA_</a>	Alignment	not modelled	97.9	13	<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 sulfobolus solfataricus
41	<a href="#">d2d1ha1</a>	Alignment	not modelled	97.9	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
42	<a href="#">c3ctaA_</a>	Alignment	not modelled	97.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase; <b>PDBTitle:</b> crystal structure of riboflavin kinase from thermoplasma acidophilum
43	<a href="#">d1ku9a_</a>	Alignment	not modelled	97.9	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
44	<a href="#">c4o6jA_</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent transcription repressor related protein; <b>PDBTitle:</b> crystal structure of t. acidophilum ider
45	<a href="#">c6j0eB_</a>	Alignment	not modelled	97.8	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> arsenic responsive repressor arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
46	<a href="#">d2fbha1</a>	Alignment	not modelled	97.8	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
47	<a href="#">c3f6vA_</a>	Alignment	not modelled	97.8	25	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> crystal structure of possible transcriptional regulator for arsenical2 resistance
48	<a href="#">c3g3zA_</a>	Alignment	not modelled	97.8	17	<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
49	<a href="#">c4hf1B_</a>	Alignment	not modelled	97.8	38	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator iscr; <b>PDBTitle:</b> crystal structure of iscr bound to its promoter
50	<a href="#">c3cuoB_</a>	Alignment	not modelled	97.8	17	<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
51	<a href="#">c5dukA_</a>	Alignment	not modelled	97.8	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna binding protein; <b>PDBTitle:</b> n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05
52	<a href="#">c6jbxB_</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid biosynthesis transcriptional regulator; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae fabt in complex with dna
53	<a href="#">d1lnwa_</a>	Alignment	not modelled	97.8	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
54	<a href="#">c5ibrA_</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bcav_2135;

54	<a href="#">c3j7A</a>	Alignment	not modelled	97.8	13	<b>PDBTitle:</b> crystal structure of uncharacterized protein bcav_2135 from2 beutenbergia cavernae
55	<a href="#">d1tw3a1</a>	Alignment	not modelled	97.7	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Plant O-methyltransferase, N-terminal domain
56	<a href="#">c3pgkD</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> biofilm growth-associated repressor; <b>PDBTitle:</b> crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
57	<a href="#">c4yifE</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> marr family protein rv0880; <b>PDBTitle:</b> crystal structure of rv0880
58	<a href="#">c5eriA</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> marr family transcriptional regulator; <b>PDBTitle:</b> marr protein from peptoclostridium difficile da00132
59	<a href="#">d1ub9a</a>	Alignment	not modelled	97.7	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
60	<a href="#">c2fa5B</a>	Alignment	not modelled	97.7	11	<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
61	<a href="#">c3lwfD</a>	Alignment	not modelled	97.7	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
62	<a href="#">c4nb5D</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> dna binding protein; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
63	<a href="#">c3jthA</a>	Alignment	not modelled	97.7	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
64	<a href="#">c6iv7B</a>	Alignment	not modelled	97.7	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase lepi; <b>PDBTitle:</b> the crystal structure of a sam-dependent enzyme from aspergillus2 flavus
65	<a href="#">c3f6oB</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator, arsr family <b>PDBTitle:</b> crystal structure of arsr family transcriptional regulator,2 rha00566
66	<a href="#">c5zc2B</a>	Alignment	not modelled	97.7	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> p-hydroxyphenylacetate 3-hydroxylase, reductase component; <b>PDBTitle:</b> acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
67	<a href="#">c3s2wB</a>	Alignment	not modelled	97.7	24	<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 mazeri go1
68	<a href="#">c4cicB</a>	Alignment	not modelled	97.7	27	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, badm/rff2 family; <b>PDBTitle:</b> t. potens iscr
69	<a href="#">c3bj6B</a>	Alignment	not modelled	97.7	17	<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
70	<a href="#">c5cviB</a>	Alignment	not modelled	97.7	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> slor; <b>PDBTitle:</b> structure of the manganese regulator slor
71	<a href="#">c2qwwB</a>	Alignment	not modelled	97.7	24	<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
72	<a href="#">c3deuB</a>	Alignment	not modelled	97.7	24	<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 slya from2 salmonella typhimurium in complex with salicylate ligands
73	<a href="#">c2kkoB</a>	Alignment	not modelled	97.7	18	<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.
74	<a href="#">d1r1ua</a>	Alignment	not modelled	97.7	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArSR-like transcriptional regulators
75	<a href="#">c1r22B</a>	Alignment	not modelled	97.7	28	<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
76	<a href="#">d3deu1</a>	Alignment	not modelled	97.7	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
77	<a href="#">c3fm5D</a>	Alignment	not modelled	97.7	21	<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
78	<a href="#">c4xrfA</a>	Alignment	not modelled	97.7	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of mepr like protein complexed with pseudoligands
						<b>PDB header:</b> transcription

79	<a href="#">c2y75F_</a>	Alignment	not modelled	97.7	25	<b>Chain:</b> F: <b>PDB Molecule:</b> hth-type transcriptional regulator cymr; <b>PDBTitle:</b> the structure of cymr (yrzc) the global cysteine regulator of b.2 subtilis
80	<a href="#">c4fhtA_</a>	Alignment	not modelled	97.7	31	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pcav transcriptional regulator; <b>PDBTitle:</b> crystal structure of the pcav transcriptional regulator from 2 streptomyces coelicolor in complex with its natural ligand
81	<a href="#">d2etha1</a>	Alignment	not modelled	97.7	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
82	<a href="#">c2nyxB_</a>	Alignment	not modelled	97.7	28	<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
83	<a href="#">d2a61a1</a>	Alignment	not modelled	97.6	20	<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="#">c4omzG_</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> nolr; <b>PDBTitle:</b> crystal structure of nolr from sinorhizobium fredii
85	<a href="#">d2isya1</a>	Alignment	not modelled	97.6	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
86	<a href="#">d1sfxa_</a>	Alignment	not modelled	97.6	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
87	<a href="#">d1jhfa1</a>	Alignment	not modelled	97.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LexA repressor, N-terminal DNA-binding domain
88	<a href="#">d2fbia1</a>	Alignment	not modelled	97.6	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
89	<a href="#">c2ev5B_</a>	Alignment	not modelled	97.6	15	<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
90	<a href="#">c3zmdD_</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of absc, a marr family transcriptional 2 regulator from streptomyces coelicolor
91	<a href="#">c3cjnA_</a>	Alignment	not modelled	97.6	29	<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, from 2 silicibacter pomeroyi
92	<a href="#">c5yhXH_</a>	Alignment	not modelled	97.6	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> zinc transport transcriptional regulator; <b>PDBTitle:</b> structure of lactococcus lactis zittr, wild type
93	<a href="#">d1r1ta_</a>	Alignment	not modelled	97.6	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
94	<a href="#">c2rdpA_</a>	Alignment	not modelled	97.6	31	<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 bacillus 2 stearothermophilus
95	<a href="#">d3broa1</a>	Alignment	not modelled	97.6	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
96	<a href="#">c3bddD_</a>	Alignment	not modelled	97.6	25	<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-resistance 2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution
97	<a href="#">c3nqoB_</a>	Alignment	not modelled	97.6	15	<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
98	<a href="#">d1g3wa1</a>	Alignment	not modelled	97.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
99	<a href="#">c5aiqD_</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of ligand-free nadr
100	<a href="#">d1qzza1</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> Plant O-methyltransferase, N-terminal domain
101	<a href="#">d1lj9a_</a>	Alignment	not modelled	97.6	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
102	<a href="#">c3nrvC_</a>	Alignment	not modelled	97.6	18	<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 from 2 acinetobacter sp. adp1
103	<a href="#">c2jscB_</a>	Alignment	not modelled	97.5	30	<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 mycobacterium 2 tuberculosis
104	<a href="#">d1fp2a1</a>	Alignment	not modelled	97.5	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Plant O-methyltransferase, N-terminal domain
						<b>PDB header:</b> transcription

105	<a href="#">c3hruA_</a>	Alignment	not modelled	97.5	11	<b>Chain:</b> A: <b>PDB Molecule:</b> metalloregulator scar; <b>PDBTitle:</b> crystal structure of scar with bound zn2+
106	<a href="#">d1mzba_</a>	Alignment	not modelled	97.5	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FUR-like
107	<a href="#">c4mnuA_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> slya-like transcription regulator; <b>PDBTitle:</b> crystal structure of uncharacterized slya-like transcription regulator2 from listeria monocytogenes
108	<a href="#">c3dp7B_</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent methyltransferase from bacteroides2 vulgatus atcc 8482
109	<a href="#">c4ijaA_</a>	Alignment	not modelled	97.5	25	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> xylr protein; <b>PDBTitle:</b> structure of s. aureus methicillin resistance factor mecR2
110	<a href="#">c2o03A_</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> probable zinc uptake regulation protein furb; <b>PDBTitle:</b> crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
111	<a href="#">d1s3ja_</a>	Alignment	not modelled	97.5	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
112	<a href="#">d1z05a1</a>	Alignment	not modelled	97.5	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
113	<a href="#">c2fe3B_</a>	Alignment	not modelled	97.5	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> peroxide operon regulator; <b>PDBTitle:</b> the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
114	<a href="#">c2lkpB_</a>	Alignment	not modelled	97.5	33	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, arsr family; <b>PDBTitle:</b> solution structure of apo-nmtr
115	<a href="#">c3k0IA_</a>	Alignment	not modelled	97.5	22	<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
116	<a href="#">c6c28C_</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> transcriptional repressor, cour, bound to p-coumaroyl-coa
117	<a href="#">c3zplE_</a>	Alignment	not modelled	97.5	21	<b>PDB header:</b> transcription/dna repressor; <b>Chain:</b> E: <b>PDB Molecule:</b> putative marr-family transcriptional regulator2 from streptomyces coelicolor, in complex with dna
118	<a href="#">d2fxaa1</a>	Alignment	not modelled	97.5	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
119	<a href="#">c3bpxB_</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
120	<a href="#">d2frha1</a>	Alignment	not modelled	97.5	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