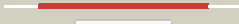



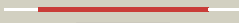



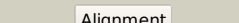
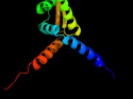


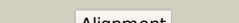






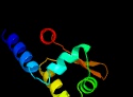













# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3744 (- )_4195618_4195980
Date	Fri Aug 9 18:20:44 BST 2019
Unique Job ID	4008d8be89952f9c

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2lkpB_</a>	 Alignment		100.0	100	<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
2	<a href="#">c1r22B_</a>	 Alignment		99.9	42	<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
3	<a href="#">d1r1ua_</a>	 Alignment		99.9	35	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
4	<a href="#">d1r1ta_</a>	 Alignment		99.9	42	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
5	<a href="#">c2kkoB_</a>	 Alignment		99.9	29	<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.
6	<a href="#">c3pgqD_</a>	 Alignment		99.9	34	<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
7	<a href="#">c6j0eB_</a>	 Alignment		99.9	27	<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
8	<a href="#">c4omzG_</a>	 Alignment		99.9	34	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> nolr; <b>PDBTitle:</b> crystal structure of nolr from sinorhizobium fredii
9	<a href="#">c3jthA_</a>	 Alignment		99.9	31	<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
10	<a href="#">c2zkzC_</a>	 Alignment		99.9	26	<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
11	<a href="#">c2oqgA_</a>	 Alignment		99.9	25	<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

12	<a href="#">d1u2wa1</a>	Alignment		99.9	32	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
13	<a href="#">c6j05B_</a>	Alignment		99.9	35	<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
14	<a href="#">c3cuoB_</a>	Alignment		99.9	29	<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
15	<a href="#">c2jscB_</a>	Alignment		99.9	40	<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
16	<a href="#">c5xpgB_</a>	Alignment		99.9	31	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator rv0081; <b>PDBTitle:</b> crystal structure of m.tuberculosis rv0081
17	<a href="#">c3f6vA_</a>	Alignment		99.9	33	<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
18	<a href="#">c3f6oB_</a>	Alignment		99.9	23	<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
19	<a href="#">d2p4wa1</a>	Alignment		99.8	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
20	<a href="#">d1ulya_</a>	Alignment		99.7	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
21	<a href="#">c4g6qA_</a>	Alignment	not modelled	99.6	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein kfla_6221 from2 kribbella flavida dsm 17836
22	<a href="#">d2d1ha1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
23	<a href="#">c2qufB_</a>	Alignment	not modelled	99.5	15	<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="#">d1ub9a_</a>	Alignment	not modelled	99.5	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
25	<a href="#">c5dukA_</a>	Alignment	not modelled	99.5	21	<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
26	<a href="#">d1y0ua_</a>	Alignment	not modelled	98.8	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
27	<a href="#">d3ctaa1</a>	Alignment	not modelled	98.7	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
28	<a href="#">c3ctaA_</a>	Alignment	not modelled	98.7	18	<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
						<b>PDB header:</b> transcription

29	<a href="#">c4gcvD</a>	Alignment	not modelled	98.7	15	<b>Chain:</b> D: <b>PDB Molecule:</b> putative transcription protein; <b>PDBTitle:</b> structure of a putative transcription factor (pa1374)from pseudomonas2 aeruginosa
30	<a href="#">c6cmvA</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrs14-like protein; <b>PDBTitle:</b> crystal structure of archaeal biofilm regulator (abfr2) from2 sulfolobus acidocaldarius
31	<a href="#">d1sfxa</a>	Alignment	not modelled	98.7	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
32	<a href="#">c4nb5D</a>	Alignment	not modelled	98.7	20	<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
33	<a href="#">c3r0aB</a>	Alignment	not modelled	98.6	14	<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)
34	<a href="#">c5hs9A</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator yodb; <b>PDBTitle:</b> crystal structure of the quinone-bound yodb from b. subtilis
35	<a href="#">c4a5mH</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator yybr; <b>PDBTitle:</b> redox regulator hypr in its oxidized form
36	<a href="#">d2f2ea1</a>	Alignment	not modelled	98.5	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxIR-like
37	<a href="#">d1ku9a</a>	Alignment	not modelled	98.5	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
38	<a href="#">c3f3xA</a>	Alignment	not modelled	98.4	25	<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 bldr from2 sulfolobus solfataricus
39	<a href="#">d2fswa1</a>	Alignment	not modelled	98.4	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxIR-like
40	<a href="#">c4hqeB</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator qsrr; <b>PDBTitle:</b> the crystal structure of qsrr-dna complex
41	<a href="#">d1biaa1</a>	Alignment	not modelled	98.4	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
42	<a href="#">d1z7ua1</a>	Alignment	not modelled	98.4	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxIR-like
43	<a href="#">c2gxgA</a>	Alignment	not modelled	98.4	25	<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
44	<a href="#">c5jlsA</a>	Alignment	not modelled	98.4	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adhesin competence repressor; <b>PDBTitle:</b> crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged)
45	<a href="#">c3df8A</a>	Alignment	not modelled	98.3	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible hxlR family transcriptional factor; <b>PDBTitle:</b> the crystal structure of a possible hxlR family transcriptional factor2 from thermoplasma volcanium gss1
46	<a href="#">d1lnwa</a>	Alignment	not modelled	98.3	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
47	<a href="#">d2a61a1</a>	Alignment	not modelled	98.3	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
48	<a href="#">c5zhcA</a>	Alignment	not modelled	98.3	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of the padr-family transcriptional regulator rv34882 of mycobacterium tuberculosis h37rv
49	<a href="#">c5jbrA</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bcav_2135; <b>PDBTitle:</b> crystal structure of uncharacterized protein bcav_2135 from2 beutenbergia cavernae
50	<a href="#">d2etha1</a>	Alignment	not modelled	98.3	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
51	<a href="#">c3k0IA</a>	Alignment	not modelled	98.3	20	<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
52	<a href="#">d1z05a1</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> ROK associated domain
53	<a href="#">c2rpdA</a>	Alignment	not modelled	98.2	21	<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
54	<a href="#">c4fhtA</a>	Alignment	not modelled	98.2	20	<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 from2 streptomyces coelicolor in complex with its natural ligand
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

55	<a href="#">d1p4xa2</a>	Alignment	not modelled	98.2	18	<b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
56	<a href="#">c4esfA</a>	Alignment	not modelled	98.2	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> padr-like transcriptional regulator; <b>PDBTitle:</b> crystal structure of padr-like transcriptional regulator (bce3449)2 from bacillus cereus strain atcc 10987
57	<a href="#">d2fbia1</a>	Alignment	not modelled	98.2	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
58	<a href="#">d1mkma1</a>	Alignment	not modelled	98.2	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator IclR, N-terminal domain
59	<a href="#">d1yyva1</a>	Alignment	not modelled	98.2	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxIR-like
60	<a href="#">c2nyxB</a>	Alignment	not modelled	98.2	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
61	<a href="#">c6jbxB</a>	Alignment	not modelled	98.2	8	<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
62	<a href="#">c4o6jA</a>	Alignment	not modelled	98.2	16	<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
63	<a href="#">c3bpxB</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
64	<a href="#">c2nnnB</a>	Alignment	not modelled	98.2	21	<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
65	<a href="#">c3bj6B</a>	Alignment	not modelled	98.2	18	<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
66	<a href="#">c3f8fA</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, padr-like family; <b>PDBTitle:</b> crystal structure of multidrug binding transcriptional regulator Imrr2 complexed with daunomycin
67	<a href="#">c3e6mD</a>	Alignment	not modelled	98.1	26	<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.
68	<a href="#">d1lj9a</a>	Alignment	not modelled	98.1	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
69	<a href="#">c2l4aA</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> leucine responsive regulatory protein; <b>PDBTitle:</b> nmr structure of the dna-binding domain of e.coli lrp
70	<a href="#">c3zplE</a>	Alignment	not modelled	98.1	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> E: <b>PDB Molecule:</b> putative marr-family transcriptional repressor; <b>PDBTitle:</b> crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna
71	<a href="#">c4xrfA</a>	Alignment	not modelled	98.1	25	<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
72	<a href="#">c3l7wA</a>	Alignment	not modelled	98.1	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1704; <b>PDBTitle:</b> the crystal structure of smu.1704 from streptococcus mutans ua159
73	<a href="#">d2bv6a1</a>	Alignment	not modelled	98.1	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
74	<a href="#">c4ijaA</a>	Alignment	not modelled	98.1	16	<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
75	<a href="#">c5eriA</a>	Alignment	not modelled	98.1	13	<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
76	<a href="#">d2hr3a1</a>	Alignment	not modelled	98.1	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
77	<a href="#">c4esbA</a>	Alignment	not modelled	98.1	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, padr family; <b>PDBTitle:</b> crystal structure of padr-like transcriptional regulator (bc4206) from2 bacillus cereus strain atcc 14579
78	<a href="#">c3zmdD</a>	Alignment	not modelled	98.1	25	<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 transcriptional2 regulator from streptomyces coelicolor
79	<a href="#">c3hhbA</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, padr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator, a member of padr2 family, from enterococcus faecalis v583
80	<a href="#">c2ewnA</a>	Alignment	not modelled	98.1	29	<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

81	<a href="#">c3g3zA</a>	Alignment	not modelled	98.1	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
82	<a href="#">c3nrvc</a>	Alignment	not modelled	98.1	16	<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
83	<a href="#">c5yhXH</a>	Alignment	not modelled	98.1	17	<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
84	<a href="#">c4em1A</a>	Alignment	not modelled	98.1	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator sar2349; <b>PDBTitle:</b> staphylococcus aureus marr native
85	<a href="#">d1hsja1</a>	Alignment	not modelled	98.1	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
86	<a href="#">c3hrUA</a>	Alignment	not modelled	98.0	20	<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+
87	<a href="#">c5x11G</a>	Alignment	not modelled	98.0	24	<b>PDB header:</b> transcription/dna <b>Chain:</b> G: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of bacillus subtilis padr in complex with operator2 dna
88	<a href="#">c3nqoB</a>	Alignment	not modelled	98.0	12	<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
89	<a href="#">d2frha1</a>	Alignment	not modelled	98.0	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
90	<a href="#">d2cg4a1</a>	Alignment	not modelled	98.0	17	<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
91	<a href="#">c2vbzA</a>	Alignment	not modelled	98.0	26	<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
92	<a href="#">d1s3ja</a>	Alignment	not modelled	98.0	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
93	<a href="#">c6faqA</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding protein; <b>PDBTitle:</b> structure of h. salinarum rosr (vng0258) grown from kbr
94	<a href="#">c2hoeA</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosamine kinase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
95	<a href="#">d3broa1</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> MarR-like transcriptional regulators
96	<a href="#">c1z05A</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, rok family; <b>PDBTitle:</b> crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
97	<a href="#">d2fbha1</a>	Alignment	not modelled	98.0	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
98	<a href="#">c3cjnA</a>	Alignment	not modelled	98.0	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
99	<a href="#">c2xigA</a>	Alignment	not modelled	98.0	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
100	<a href="#">c4mnuA</a>	Alignment	not modelled	98.0	13	<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
101	<a href="#">c2x4hA</a>	Alignment	not modelled	98.0	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
102	<a href="#">c5h20A</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative padr-family transcriptional regulatory protein; <b>PDBTitle:</b> x-ray structure of padr-like transcription factor from bacteroid2 fragilis
103	<a href="#">c2fa5B</a>	Alignment	not modelled	97.9	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
104	<a href="#">c2fxaB</a>	Alignment	not modelled	97.9	12	<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.
105	<a href="#">d2cfxa1</a>	Alignment	not modelled	97.9	22	<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
106	<a href="#">d1jgsa</a>	Alignment	not modelled	97.9	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



107	<a href="#">c2it0A_</a>	Alignment	not modelled	97.9	17	<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
108	<a href="#">c1fx7C_</a>	Alignment	not modelled	97.9	16	<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
109	<a href="#">c1f5tA_</a>	Alignment	not modelled	97.9	20	<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
110	<a href="#">c4rs8A_</a>	Alignment	not modelled	97.9	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> aspa; <b>PDBTitle:</b> apo structure of novel pnob8 plasmid centromere binding protein
111	<a href="#">c4yifE_</a>	Alignment	not modelled	97.9	21	<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
112	<a href="#">c1mkmA_</a>	Alignment	not modelled	97.9	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
113	<a href="#">c4q77B_</a>	Alignment	not modelled	97.9	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> hth-type transcriptional regulator rot; <b>PDBTitle:</b> crystal structure of rot, a global regulator of virulence genes in2 staphylococcus aureus
114	<a href="#">c2qwwB_</a>	Alignment	not modelled	97.9	23	<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
115	<a href="#">d1z91a1</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> MarR-like transcriptional regulators
116	<a href="#">d1okra_</a>	Alignment	not modelled	97.9	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
117	<a href="#">c4b8xB_</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> possible marr-transcriptional regulator; <b>PDBTitle:</b> near atomic resolution crystal structure of sco5413, a marr family2 transcriptional regulator from streptomyces coelicolor
118	<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.
119	<a href="#">c1g3wA_</a>	Alignment	not modelled	97.9	19	<b>PDB header:</b> gene regulation <b>Chain:</b> A; <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtxr
120	<a href="#">c2e7xA_</a>	Alignment	not modelled	97.9	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> A; <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the Irp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand