



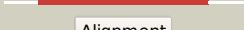

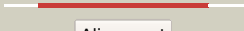





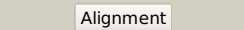

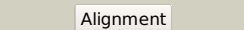

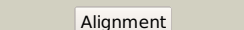

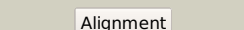

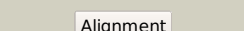





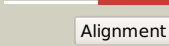
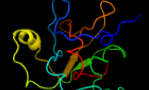


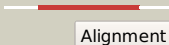










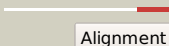
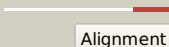
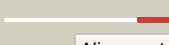


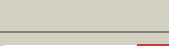


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2711_(ideR)_3023575_3024267
Date	Wed Aug 7 12:50:36 BST 2019
Unique Job ID	cdda670dd5be0403

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1fx7C_</a>	 Alignment		100.0	99	<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
2	<a href="#">c5cviB_</a>	 Alignment		100.0	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> B; <b>PDB Molecule:</b> slor; <b>PDBTitle:</b> structure of the manganese regulator slor
3	<a href="#">c1g3wA_</a>	 Alignment		100.0	57	<b>PDB header:</b> gene regulation <b>Chain:</b> A; <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtxr
4	<a href="#">c4o6jA_</a>	 Alignment		100.0	28	<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 sturcture of t. acidophilum ider
5	<a href="#">c3hruA_</a>	 Alignment		100.0	26	<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+
6	<a href="#">c6o5cB_</a>	 Alignment		100.0	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> putative metal-dependent transcriptional regulator; <b>PDBTitle:</b> x-ray crystal structure of metal-dependent transcriptional regulator2 mtsr
7	<a href="#">c5zr4B_</a>	 Alignment		100.0	28	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> metal-dependent transcriptional regulator; <b>PDBTitle:</b> manganese-dependent transcriptional repressor
8	<a href="#">c2it0A_</a>	 Alignment		100.0	96	<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
9	<a href="#">c2x4hA_</a>	 Alignment		100.0	27	<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
10	<a href="#">c2ev5B_</a>	 Alignment		100.0	24	<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
11	<a href="#">c1f5tA_</a>	 Alignment		100.0	79	<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

12	<a href="#">c2h09A_</a>	 Alignment		100.0	27	<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
13	<a href="#">d1g3wa2</a>	 Alignment		99.9	74	<b>Fold:</b> Iron-dependent repressor protein, dimerization domain <b>Superfamily:</b> Iron-dependent repressor protein, dimerization domain <b>Family:</b> Iron-dependent repressor protein, dimerization domain
14	<a href="#">c1qw1A_</a>	 Alignment		99.9	36	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> solution structure of the c-terminal domain of dtxr2 residues 110-226
15	<a href="#">d2isya2</a>	 Alignment		99.9	100	<b>Fold:</b> Iron-dependent repressor protein, dimerization domain <b>Superfamily:</b> Iron-dependent repressor protein, dimerization domain <b>Family:</b> Iron-dependent repressor protein, dimerization domain
16	<a href="#">d2fxaa1</a>	 Alignment		99.7	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
17	<a href="#">d2ev0a2</a>	 Alignment		99.7	23	<b>Fold:</b> Iron-dependent repressor protein, dimerization domain <b>Superfamily:</b> Iron-dependent repressor protein, dimerization domain <b>Family:</b> Iron-dependent repressor protein, dimerization domain
18	<a href="#">d2isya1</a>	 Alignment		99.6	100	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
19	<a href="#">d1f5ta2</a>	 Alignment		99.6	74	<b>Fold:</b> Iron-dependent repressor protein, dimerization domain <b>Superfamily:</b> Iron-dependent repressor protein, dimerization domain <b>Family:</b> Iron-dependent repressor protein, dimerization domain
20	<a href="#">d1g3wa1</a>	 Alignment		99.6	85	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
21	<a href="#">d2ev0a1</a>	 Alignment	not modelled	99.4	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
22	<a href="#">c2k5fA_</a>	 Alignment	not modelled	99.4	29	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferrous iron transport protein a; <b>PDBTitle:</b> solution nmr structure of feoa protein from chlorobium2 tepidum. northeast structural genomics consortium target3 ctr121
23	<a href="#">c2k4yA_</a>	 Alignment	not modelled	99.4	20	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> feoa-like protein; <b>PDBTitle:</b> nmr structure of feoa-like protein from clostridium2 acetobutylicum: northeast structural genomics consortium3 target car178
24	<a href="#">c2k5iA_</a>	 Alignment	not modelled	99.3	26	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> iron transport protein; <b>PDBTitle:</b> solution structure of iron(ii) transport protein a from2 clostridium thermocellum , northeast structural genomics3 consortium (nesg) target vr131
25	<a href="#">c2fxaB_</a>	 Alignment	not modelled	99.3	19	<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.
26	<a href="#">c2k5iA_</a>	 Alignment	not modelled	99.3	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> feoa; <b>PDBTitle:</b> solution nmr structure of protein feoa from clostridium2 thermocellum, northeast structural genomics consortium3 target cmr17
27	<a href="#">c3e19D_</a>	 Alignment	not modelled	99.3	27	<b>PDB header:</b> transcription regulator, metal binding p <b>Chain:</b> D: <b>PDB Molecule:</b> feoa; <b>PDBTitle:</b> crystal structure of iron uptake regulatory protein (feoa) solved by2 sulfur sad in a monoclinic space group <b>PDB header:</b> metal transport

28	<a href="#">c3mhxB</a>	Alignment	not modelled	99.3	24	<b>Chain:</b> B: <b>PDB Molecule:</b> putative ferrous iron transport protein a; <b>PDBTitle:</b> crystal structure of stentrophomonas maltophilia feoa complexed with2 zinc: a unique prokaryotic sh3 domain protein possibly acting as a3 bacterial ferrous iron transport activating factor
29	<a href="#">d2h3ja1</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> FeoA-like
30	<a href="#">d2hr3a1</a>	Alignment	not modelled	99.1	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
31	<a href="#">d2gcxa1</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> FeoA-like
32	<a href="#">d3broa1</a>	Alignment	not modelled	99.0	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
33	<a href="#">c5jlsA</a>	Alignment	not modelled	99.0	17	<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)
34	<a href="#">d2etha1</a>	Alignment	not modelled	99.0	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
35	<a href="#">c4yifE</a>	Alignment	not modelled	99.0	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
36	<a href="#">c3bj6B</a>	Alignment	not modelled	99.0	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
37	<a href="#">c6jbxB</a>	Alignment	not modelled	99.0	20	<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
38	<a href="#">c3g3zA</a>	Alignment	not modelled	99.0	21	<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
39	<a href="#">c3kp3B</a>	Alignment	not modelled	99.0	14	<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
40	<a href="#">c3bjaA</a>	Alignment	not modelled	99.0	17	<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
41	<a href="#">c3nrvC</a>	Alignment	not modelled	99.0	20	<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
42	<a href="#">c4mnuA</a>	Alignment	not modelled	99.0	21	<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
43	<a href="#">c2fa5B</a>	Alignment	not modelled	99.0	18	<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
44	<a href="#">c3zplE</a>	Alignment	not modelled	99.0	17	<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
45	<a href="#">c2nnnB</a>	Alignment	not modelled	99.0	19	<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
46	<a href="#">d1s3ja</a>	Alignment	not modelled	98.9	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
47	<a href="#">c3nqoB</a>	Alignment	not modelled	98.9	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
48	<a href="#">c2qwwB</a>	Alignment	not modelled	98.9	18	<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
49	<a href="#">d2fbha1</a>	Alignment	not modelled	98.9	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
50	<a href="#">c2qxA</a>	Alignment	not modelled	98.9	22	<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 sulfobolus tokodaii strain7
51	<a href="#">c2rdpA</a>	Alignment	not modelled	98.9	22	<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
52	<a href="#">d1lj9a</a>	Alianment	not modelled	98.9	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain

					Family:MarR-like transcriptional regulators
53	<a href="#">c5eriA_</a>	Alignment	not modelled	98.9	16 <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
54	<a href="#">c4fhtA_</a>	Alignment	not modelled	98.9	19 <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
55	<a href="#">c5yhxB_</a>	Alignment	not modelled	98.9	24 <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 zitri, wild type
56	<a href="#">c3ctaA_</a>	Alignment	not modelled	98.9	19 <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
57	<a href="#">c3zmdD_</a>	Alignment	not modelled	98.9	24 <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
58	<a href="#">d2bv6a1</a>	Alignment	not modelled	98.9	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
59	<a href="#">c3bpxB_</a>	Alignment	not modelled	98.9	20 <b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
60	<a href="#">c2nyxB_</a>	Alignment	not modelled	98.9	16 <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="#">c5zC2B_</a>	Alignment	not modelled	98.9	18 <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)
62	<a href="#">d1lnwa_</a>	Alignment	not modelled	98.9	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
63	<a href="#">c3hrmA_</a>	Alignment	not modelled	98.9	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
64	<a href="#">c5aiqD_</a>	Alignment	not modelled	98.9	20 <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
65	<a href="#">c3k0IA_</a>	Alignment	not modelled	98.9	13 <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
66	<a href="#">c4em1A_</a>	Alignment	not modelled	98.9	18 <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
67	<a href="#">c3boqB_</a>	Alignment	not modelled	98.8	15 <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
68	<a href="#">d2fbia1</a>	Alignment	not modelled	98.8	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
69	<a href="#">d1jgsa_</a>	Alignment	not modelled	98.8	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
70	<a href="#">c3fm5D_</a>	Alignment	not modelled	98.8	20 <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
71	<a href="#">c4xrfA_</a>	Alignment	not modelled	98.8	16 <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="#">d3deua1</a>	Alignment	not modelled	98.8	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
73	<a href="#">c3e6mD_</a>	Alignment	not modelled	98.8	15 <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.
74	<a href="#">c3cjnA_</a>	Alignment	not modelled	98.8	19 <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
75	<a href="#">d2a61a1</a>	Alignment	not modelled	98.8	25 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
76	<a href="#">c3f3xA_</a>	Alignment	not modelled	98.8	19 <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
77	<a href="#">c6c28C_</a>	Alignment	not modelled	98.8	21 <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
78	<a href="#">c3cdhB_</a>	Alignment	not modelled	98.8	23 <b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family;

78	<a href="#">c3cubB</a>	Alignment	not modelled	98.8	23	<b>PDBTitle:</b> crystal structure of the marr family transcriptional regulator spo14532 from silicibacter pomeroyi dss-3 <b>PDB header:</b> transcription
79	<a href="#">c5e1xA</a>	Alignment	not modelled	98.8	22	<b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of the organohalide sensing rdhr-cdba16252 transcriptional regulator in the 3,4-dichlorophenol bound form
80	<a href="#">c3s2wB</a>	Alignment	not modelled	98.7	13	<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
81	<a href="#">c3oopA</a>	Alignment	not modelled	98.7	19	<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
82	<a href="#">c2pexA</a>	Alignment	not modelled	98.7	20	<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
83	<a href="#">c4q77B</a>	Alignment	not modelled	98.7	7	<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
84	<a href="#">c4fx0A</a>	Alignment	not modelled	98.7	28	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of m. tuberculosis transcriptional regulator mosr
85	<a href="#">c3bddD</a>	Alignment	not modelled	98.7	18	<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
86	<a href="#">d3ctaa1</a>	Alignment	not modelled	98.7	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
87	<a href="#">c3deuB</a>	Alignment	not modelled	98.7	21	<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
88	<a href="#">c3ecoB</a>	Alignment	not modelled	98.7	24	<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
89	<a href="#">d1p4xa1</a>	Alignment	not modelled	98.7	9	<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="#">c4b8xB</a>	Alignment	not modelled	98.7	20	<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
91	<a href="#">d2frha1</a>	Alignment	not modelled	98.7	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
92	<a href="#">c5hsmA</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator rv2887; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis marr family protein2 rv2887
93	<a href="#">d1fx7a3</a>	Alignment	not modelled	98.7	100	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> FeoA-like
94	<a href="#">d1z91a1</a>	Alignment	not modelled	98.7	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
95	<a href="#">d1p4xa2</a>	Alignment	not modelled	98.7	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
96	<a href="#">c4nb5D</a>	Alignment	not modelled	98.6	12	<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
97	<a href="#">c3tgnA</a>	Alignment	not modelled	98.6	20	<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
98	<a href="#">d2fbka1</a>	Alignment	not modelled	98.6	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
99	<a href="#">d1qw1a1</a>	Alignment	not modelled	98.5	32	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> FeoA-like
100	<a href="#">d1okra</a>	Alignment	not modelled	98.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
101	<a href="#">c4hblA</a>	Alignment	not modelled	98.5	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of abfr of staphylococcus epidermidis
102	<a href="#">d1hsja1</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> MarR-like transcriptional regulators
103	<a href="#">c5jbrA</a>	Alignment	not modelled	98.5	20	<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
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle



104	<a href="#">d1ub9a_</a>	Alignment	not modelled	98.5	19	<b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
105	<a href="#">c1p4xA_</a>	Alignment	not modelled	98.4	12	<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
106	<a href="#">d1jhfa1</a>	Alignment	not modelled	98.4	23	<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
107	<a href="#">d1mkma1</a>	Alignment	not modelled	98.4	15	<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
108	<a href="#">d1ku9a_</a>	Alignment	not modelled	98.4	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
109	<a href="#">c3r0aB_</a>	Alignment	not modelled	98.4	13	<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)
110	<a href="#">d1sfxa_</a>	Alignment	not modelled	98.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
111	<a href="#">c3jw4C_</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> transcription regulator <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
112	<a href="#">d1stza1</a>	Alignment	not modelled	98.2	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Heat-inducible transcription repressor HrcA, N-terminal domain
113	<a href="#">c2qvoA_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein af_1382; <b>PDBTitle:</b> crystal structure of af1382 from archaeoglobus fulgidus
114	<a href="#">d2d1ha1</a>	Alignment	not modelled	98.1	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
115	<a href="#">c6cmvA_</a>	Alignment	not modelled	98.0	13	<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
116	<a href="#">d1sd4a_</a>	Alignment	not modelled	98.0	11	<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="#">c4r1hA_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0741 protein; <b>PDBTitle:</b> gntR family transcriptional regulator from listeria monocytogenes
118	<a href="#">c2wteB_</a>	Alignment	not modelled	98.0	21	<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="#">c2oqgA_</a>	Alignment	not modelled	98.0	12	<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="#">c3f8fA_</a>	Alignment	not modelled	98.0	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 lmrr2 complexed with daunomycin