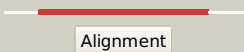

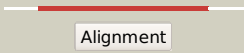

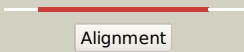

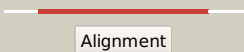

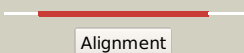

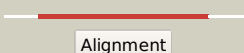

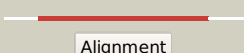





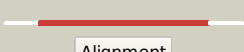

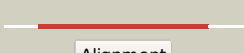



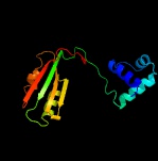
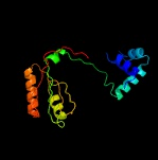
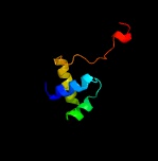
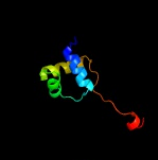
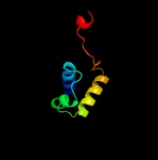
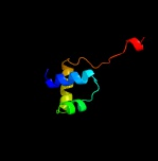
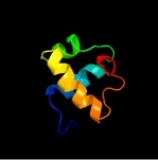


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3291c_(-)_3671842_3672294
Date	Thu Aug 8 16:20:50 BST 2019
Unique Job ID	e88c985261764c6b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2vbzA_</a>			100.0	100	<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
2	<a href="#">c2e1cA_</a>			100.0	27	<b>PDB header:</b> transcription/dna <b>Chain:</b> A; <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
3	<a href="#">c2cg4B_</a>			100.0	26	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
4	<a href="#">c4pccC_</a>			100.0	26	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> possible transcriptional regulatory protein (probably <b>PDBTitle:</b> crystal structure of mtbaldr (rv2779c)
5	<a href="#">c2e7xA_</a>			100.0	22	<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 lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
6	<a href="#">c2cfxD_</a>			100.0	29	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> hth-type transcriptional regulator lrpc; <b>PDBTitle:</b> structure of b.subtilis lrpc
7	<a href="#">c2gqgB_</a>			100.0	34	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> leucine-responsive regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
8	<a href="#">c2p6tH_</a>			100.0	27	<b>PDB header:</b> transcription <b>Chain:</b> H; <b>PDB Molecule:</b> transcriptional regulator, lrp/asnc family; <b>PDBTitle:</b> crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
9	<a href="#">c1i1gA_</a>			100.0	25	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator lrpa; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
10	<a href="#">c3i4pA_</a>			100.0	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
11	<a href="#">c2dbbA_</a>			100.0	19	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A; <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph0061; <b>PDBTitle:</b> crystal structure of ph0061

12	<a href="#">c4czdD</a>	Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
13	<a href="#">c4czdA</a>	Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
14	<a href="#">c2ia0A</a>	Alignment		100.0	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator pf0864; <b>PDBTitle:</b> transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
15	<a href="#">c4ch7A</a>	Alignment		99.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nird-like protein; <b>PDBTitle:</b> crystal structure of the siroheme decarboxylase nirdl
16	<a href="#">d2cg4a1</a>	Alignment		99.7	26	<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
17	<a href="#">d2cfxa1</a>	Alignment		99.7	35	<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
18	<a href="#">d2cyya1</a>	Alignment		99.6	40	<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
19	<a href="#">d1i1ga1</a>	Alignment		99.6	38	<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
20	<a href="#">c2l4aA</a>	Alignment		99.6	47	<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
21	<a href="#">d2cyya2</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
22	<a href="#">d2cg4a2</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
23	<a href="#">d1i1ga2</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
24	<a href="#">c2djwF</a>	Alignment	not modelled	99.2	27	<b>PDB header:</b> unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> probable transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of ttha0845 from thermus thermophilus hb8
25	<a href="#">d2cfxa2</a>	Alignment	not modelled	99.2	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
26	<a href="#">c2zbcH</a>	Alignment	not modelled	99.2	32	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> 83aa long hypothetical transcriptional regulator asnc; <b>PDBTitle:</b> crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
27	<a href="#">c2e1aD</a>	Alignment	not modelled	99.1	23	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> 75aa long hypothetical regulatory protein asnc; <b>PDBTitle:</b> crystal structure of ffrp-dm1
28	<a href="#">d1biaa1</a>	Alignment	not modelled	98.2	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain

						<b>Family:</b> Biotin repressor-like
29	<a href="#">c5dukA</a>	Alignment	not modelled	98.1	18	<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
30	<a href="#">d1ub9a</a>	Alignment	not modelled	98.0	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
31	<a href="#">c2wteB</a>	Alignment	not modelled	98.0	16	<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 sulfolobus solfataricus at 1.8 angstrom resolution.
32	<a href="#">d2d1ha1</a>	Alignment	not modelled	98.0	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
33	<a href="#">d1sfxa</a>	Alignment	not modelled	97.9	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
34	<a href="#">c6cmvA</a>	Alignment	not modelled	97.9	16	<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
35	<a href="#">c3cuoB</a>	Alignment	not modelled	97.9	20	<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
36	<a href="#">d2p4wa1</a>	Alignment	not modelled	97.9	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
37	<a href="#">c1r22B</a>	Alignment	not modelled	97.9	31	<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
38	<a href="#">c1j5yA</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, biotin repressor family; <b>PDBTitle:</b> crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
39	<a href="#">d1r1ta</a>	Alignment	not modelled	97.8	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
40	<a href="#">c2oqgA</a>	Alignment	not modelled	97.8	27	<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
41	<a href="#">d1ulya</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> Hypothetical protein PH1932
42	<a href="#">c2qufB</a>	Alignment	not modelled	97.7	27	<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
43	<a href="#">c3f6vA</a>	Alignment	not modelled	97.7	31	<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
44	<a href="#">c6j0eB</a>	Alignment	not modelled	97.7	22	<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
45	<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
46	<a href="#">c3r0aB</a>	Alignment	not modelled	97.7	19	<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 mazeri go1 (gi2 21227196)
47	<a href="#">c6j05B</a>	Alignment	not modelled	97.7	14	<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
48	<a href="#">c4ijaA</a>	Alignment	not modelled	97.7	12	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> xylyr protein; <b>PDBTitle:</b> structure of s. aureus methicillin resistance factor mecR2
49	<a href="#">c4omzG</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> nolr; <b>PDBTitle:</b> crystal structure of nolr from sinorhizobium fredii
50	<a href="#">c2lkpB</a>	Alignment	not modelled	97.6	27	<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
51	<a href="#">d1u2wa1</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> ArsR-like transcriptional regulators
52	<a href="#">c3f6oB</a>	Alignment	not modelled	97.6	24	<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
53	<a href="#">c2jscB</a>	Alignment	not modelled	97.6	22	<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

54	<a href="#">c2kkoB</a>	Alignment	not modelled	97.6	20	<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.
55	<a href="#">c3bddD</a>	Alignment	not modelled	97.6	16	<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
56	<a href="#">c3pgkD</a>	Alignment	not modelled	97.6	21	<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="#">d1z05a1</a>	Alignment	not modelled	97.5	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
58	<a href="#">c4nb5D</a>	Alignment	not modelled	97.5	25	<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
59	<a href="#">c3jthA</a>	Alignment	not modelled	97.5	21	<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
60	<a href="#">c2zkzC</a>	Alignment	not modelled	97.5	14	<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
61	<a href="#">d1lnwa</a>	Alignment	not modelled	97.5	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
62	<a href="#">c5yhxB</a>	Alignment	not modelled	97.5	15	<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
63	<a href="#">c4yifE</a>	Alignment	not modelled	97.5	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
64	<a href="#">c6c28C</a>	Alignment	not modelled	97.5	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
65	<a href="#">c6jbxB</a>	Alignment	not modelled	97.5	11	<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
66	<a href="#">d1stza1</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> Heat-inducible transcription repressor HrcA, N-terminal domain
67	<a href="#">c3k0IA</a>	Alignment	not modelled	97.5	15	<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
68	<a href="#">c2nnnB</a>	Alignment	not modelled	97.4	18	<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
69	<a href="#">c3lmmB</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the dip2311 protein from corynebacterium2 diphtheriae, northeast structural genomics consortium target cdr35
70	<a href="#">c2nyxB</a>	Alignment	not modelled	97.4	25	<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
71	<a href="#">c3nrnC</a>	Alignment	not modelled	97.4	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
72	<a href="#">c4hblA</a>	Alignment	not modelled	97.4	17	<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
73	<a href="#">c3rkxA</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin-[acetyl-coa-carboxylase] ligase; <b>PDBTitle:</b> structural characterisation of staphylococcus aureus biotin protein2 ligase
74	<a href="#">c3lmmA</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the dip2311 protein from corynebacterium2 diphtheriae, northeast structural genomics consortium target cdr35
75	<a href="#">c1z6rC</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> mlc protein; <b>PDBTitle:</b> crystal structure of mlc from escherichia coli
76	<a href="#">c2rdpA</a>	Alignment	not modelled	97.4	25	<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
77	<a href="#">d2etha1</a>	Alignment	not modelled	97.4	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 <b>PDB header:</b> transcription regulator

78	<a href="#">c3cjnA_</a>	Alignment	not modelled	97.4	18	<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
79	<a href="#">d1z6ra1</a>	Alignment	not modelled	97.3	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
80	<a href="#">c2fa5B_</a>	Alignment	not modelled	97.3	24	<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)2 from xanthomonas campestris
81	<a href="#">c2it0A_</a>	Alignment	not modelled	97.3	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
82	<a href="#">c2qwwB_</a>	Alignment	not modelled	97.3	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
83	<a href="#">c1z05A_</a>	Alignment	not modelled	97.3	12	<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.
84	<a href="#">d1j5ya1</a>	Alignment	not modelled	97.3	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
85	<a href="#">c2ewnA_</a>	Alignment	not modelled	97.3	23	<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
86	<a href="#">c3g3zA_</a>	Alignment	not modelled	97.3	18	<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
87	<a href="#">c3bj6B_</a>	Alignment	not modelled	97.3	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcription regulator sp03579
88	<a href="#">d2bv6a1</a>	Alignment	not modelled	97.3	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
89	<a href="#">d1ku9a_</a>	Alignment	not modelled	97.3	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
90	<a href="#">c3ctaA_</a>	Alignment	not modelled	97.3	27	<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
91	<a href="#">c5jbrA_</a>	Alignment	not modelled	97.3	23	<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
92	<a href="#">d2fxaa1</a>	Alignment	not modelled	97.3	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
93	<a href="#">d2hr3a1</a>	Alignment	not modelled	97.3	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
94	<a href="#">c5f7pA_</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0178 protein; <b>PDBTitle:</b> rok repressor lmo0178 from listeria monocytogenes
95	<a href="#">d1s3ja_</a>	Alignment	not modelled	97.2	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
96	<a href="#">c5jlsA_</a>	Alignment	not modelled	97.2	21	<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)
97	<a href="#">c4q77B_</a>	Alignment	not modelled	97.2	12	<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
98	<a href="#">c3e6mD_</a>	Alignment	not modelled	97.2	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.
99	<a href="#">c5aiqD_</a>	Alignment	not modelled	97.2	26	<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="#">c5zc2B_</a>	Alignment	not modelled	97.2	10	<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)
101	<a href="#">c4xrfA_</a>	Alignment	not modelled	97.2	21	<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
102	<a href="#">c5eriA_</a>	Alignment	not modelled	97.2	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
103	<a href="#">c4fhtA_</a>	Alignment	not modelled	97.2	23	<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>PDB header:</b> structural genomics, unknown function



104	<a href="#">c4g6gA</a>	Alignment	not modelled	97.2	19	<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
105	<a href="#">c3bpxB</a>	Alignment	not modelled	97.2	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
106	<a href="#">d2ev0a1</a>	Alignment	not modelled	97.2	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
107	<a href="#">c3tgnA</a>	Alignment	not modelled	97.2	25	<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
108	<a href="#">c3b73A</a>	Alignment	not modelled	97.2	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phih1 repressor-like protein; <b>PDBTitle:</b> crystal structure of the phih1 repressor-like protein from haloarcula2 marismortui
109	<a href="#">d1z91a1</a>	Alignment	not modelled	97.1	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
110	<a href="#">c2pexA</a>	Alignment	not modelled	97.1	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
111	<a href="#">c2fxaB</a>	Alignment	not modelled	97.1	22	<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.
112	<a href="#">c3bjaA</a>	Alignment	not modelled	97.1	19	<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
113	<a href="#">d1mkma1</a>	Alignment	not modelled	97.1	25	<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
114	<a href="#">d1lj9a</a>	Alignment	not modelled	97.1	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
115	<a href="#">c2h09A</a>	Alignment	not modelled	97.1	23	<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
116	<a href="#">d2a61a1</a>	Alignment	not modelled	97.1	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
117	<a href="#">d1g3wa1</a>	Alignment	not modelled	97.1	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
118	<a href="#">c1f5tA</a>	Alignment	not modelled	97.1	19	<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
119	<a href="#">d2fbia1</a>	Alignment	not modelled	97.1	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
120	<a href="#">c4em1A</a>	Alignment	not modelled	97.1	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