



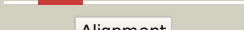
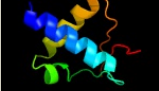
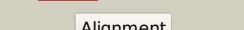

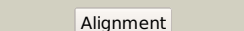





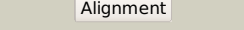

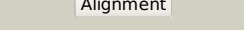

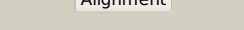

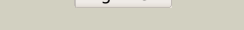











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2095c (-) _2353373_2354323
Date	Mon Aug 5 13:25:21 BST 2019
Unique Job ID	8e2b156c1dc563d8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6oawA</a>	 Alignment		99.3	12	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> wyl1; <b>PDBTitle:</b> crystal structure of a crispr cas-related protein
2	<a href="#">d1biaa1</a>	 Alignment		98.9	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
3	<a href="#">d1j5ya1</a>	 Alignment		98.9	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
4	<a href="#">c1j5ya</a>	 Alignment		98.7	15	<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
5	<a href="#">c3sqnA</a>	 Alignment		98.1	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> putative mga family transcriptional regulator from enterococcus2 faecalis
6	<a href="#">c5wayB</a>	 Alignment		97.9	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional activator; <b>PDBTitle:</b> mgaspn protein, mga regulator from streptococcus pneumoniae
7	<a href="#">c4r6ia</a>	 Alignment		97.6	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> anthrax toxin expression trans-acting positive regulator; <b>PDBTitle:</b> atxa protein, a virulence regulator from bacillus anthracis.
8	<a href="#">c2ewnA</a>	 Alignment		97.6	10	<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
9	<a href="#">c3rkxA</a>	 Alignment		97.5	12	<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
10	<a href="#">c5dukA</a>	 Alignment		97.4	16	<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
11	<a href="#">d1mkma1</a>	 Alignment		97.2	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator IclIR, N-terminal domain

12	<a href="#">d1stza1</a>	Alignment		97.2	9	<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
13	<a href="#">c1mkmA</a>	Alignment		97.0	13	<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
14	<a href="#">c3cuoB</a>	Alignment		96.9	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygvav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
15	<a href="#">d2cg4a1</a>	Alignment		96.9	20	<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
16	<a href="#">c2l4aA</a>	Alignment		96.9	22	<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
17	<a href="#">c2vbzA</a>	Alignment		96.9	22	<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
18	<a href="#">c2oqgA</a>	Alignment		96.8	16	<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
19	<a href="#">c2xroE</a>	Alignment		96.8	14	<b>PDB header:</b> dna-binding protein/dna <b>Chain:</b> E: <b>PDB Molecule:</b> hth-type transcriptional regulator ttgv; <b>PDBTitle:</b> crystal structure of ttgv in complex with its dna operator
20	<a href="#">d2d1ha1</a>	Alignment		96.8	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
21	<a href="#">c5h1aC</a>	Alignment	not modelled	96.8	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> iclr transcription factor homolog; <b>PDBTitle:</b> crystal structure of an iclr homolog from microbacterium sp. strain2 hm58-2
22	<a href="#">c6j05B</a>	Alignment	not modelled	96.8	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
23	<a href="#">c2g7uB</a>	Alignment	not modelled	96.8	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
24	<a href="#">d2p4wa1</a>	Alignment	not modelled	96.7	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
25	<a href="#">c3t8tA</a>	Alignment	not modelled	96.7	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> staphylococcus aureus cymr (oxidized form); <b>PDBTitle:</b> crystal structure of staphylococcus aureus cymr oxidized form
26	<a href="#">d1l1ga1</a>	Alignment	not modelled	96.7	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
27	<a href="#">d2cfxa1</a>	Alignment	not modelled	96.7	18	<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
28	<a href="#">d1r1ua</a>	Alignment	not modelled	96.7	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArSR-like transcriptional regulators

29	<a href="#">d1r1ta_</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
30	<a href="#">d2cyya1</a>	Alignment	not modelled	96.7	15	<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
31	<a href="#">c6hsdB_</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rrf2 family transcriptional regulator; <b>PDBTitle:</b> crystal structure of the oxidized form of the transcription regulator2 rsrr
32	<a href="#">c5tjA_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of icir transcriptional regulator from2 alicyclobacillus acidocaldarius
33	<a href="#">c1r22B_</a>	Alignment	not modelled	96.6	16	<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
34	<a href="#">c2jscB_</a>	Alignment	not modelled	96.6	20	<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
35	<a href="#">d1z05a1</a>	Alignment	not modelled	96.6	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
36	<a href="#">c2x4hA_</a>	Alignment	not modelled	96.6	16	<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
37	<a href="#">c3mq0A_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> transcription repressor <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor of the blcabc operon; <b>PDBTitle:</b> crystal structure of agobacterium tumefaciens repressor blcr
38	<a href="#">c3lmmA_</a>	Alignment	not modelled	96.5	16	<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
39	<a href="#">c5y6iB_</a>	Alignment	not modelled	96.5	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator kdgr; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa hmgr
40	<a href="#">c3i4pA_</a>	Alignment	not modelled	96.5	12	<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
41	<a href="#">c2ia0A_</a>	Alignment	not modelled	96.5	17	<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)
42	<a href="#">c6j0eB_</a>	Alignment	not modelled	96.5	13	<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
43	<a href="#">c2e7xA_</a>	Alignment	not modelled	96.5	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
44	<a href="#">d1xd7a_</a>	Alignment	not modelled	96.5	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator Rrf2
45	<a href="#">c2lkpB_</a>	Alignment	not modelled	96.4	16	<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
46	<a href="#">c4omzG_</a>	Alignment	not modelled	96.4	13	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> nolr; <b>PDBTitle:</b> crystal structure of nolr from sinorhizobium fredii
47	<a href="#">c4pcqC_</a>	Alignment	not modelled	96.4	12	<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)
48	<a href="#">c1f5tA_</a>	Alignment	not modelled	96.4	14	<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
49	<a href="#">c2e1cA_</a>	Alignment	not modelled	96.4	15	<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
50	<a href="#">c2cg4B_</a>	Alignment	not modelled	96.4	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
51	<a href="#">c2y75F_</a>	Alignment	not modelled	96.4	13	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> hth-type transcriptional regulator cymr; <b>PDBTitle:</b> the structure of cymr (yrzc) the global cysteine regulator of b.2 subtilis
52	<a href="#">c4g6qA_</a>	Alignment	not modelled	96.4	14	<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
53	<a href="#">c3pqkD_</a>	Alignment	not modelled	96.3	16	<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 <b>PDB header:</b> transcription

54	<a href="#">c5whmB_</a>	Alignment	not modelled	96.3	17	<b>Chain:</b> B: <b>PDB Molecule:</b> iclr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of iclr family transcriptional regulator from2 brucella abortus
55	<a href="#">c2o0yB_</a>	Alignment	not modelled	96.3	9	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
56	<a href="#">c3eqxB_</a>	Alignment	not modelled	96.3	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> fic domain containing transcriptional regulator; <b>PDBTitle:</b> crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
57	<a href="#">c3jthA_</a>	Alignment	not modelled	96.3	16	<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
58	<a href="#">d1ulya_</a>	Alignment	not modelled	96.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
59	<a href="#">c2kkoB_</a>	Alignment	not modelled	96.2	13	<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.
60	<a href="#">c2cfxD_</a>	Alignment	not modelled	96.2	18	<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
61	<a href="#">c3f6oB_</a>	Alignment	not modelled	96.2	11	<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
62	<a href="#">c2ia2D_</a>	Alignment	not modelled	96.2	24	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
63	<a href="#">c1stzB_</a>	Alignment	not modelled	96.2	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> heat-inducible transcription repressor hrca homolog; <b>PDBTitle:</b> crystal structure of a hypothetical protein at 2.2 a resolution
64	<a href="#">c1fx7C_</a>	Alignment	not modelled	96.2	15	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis
65	<a href="#">c4hf1B_</a>	Alignment	not modelled	96.2	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator iscr; <b>PDBTitle:</b> crystal structure of iscr bound to its promoter
66	<a href="#">c2p6tH_</a>	Alignment	not modelled	96.2	22	<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
67	<a href="#">c1ilgA_</a>	Alignment	not modelled	96.1	17	<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
68	<a href="#">c2dbbA_</a>	Alignment	not modelled	96.1	24	<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
69	<a href="#">c2wteB_</a>	Alignment	not modelled	96.1	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 sulfobolus solfataricus at 1.8 angstrom resolution.
70	<a href="#">c2zkcC_</a>	Alignment	not modelled	96.1	9	<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
71	<a href="#">c6cmvA_</a>	Alignment	not modelled	96.1	13	<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 sulfobolus acidocaldarius
72	<a href="#">d1o57a1</a>	Alignment	not modelled	96.0	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> N-terminal domain of Bacillus PurR
73	<a href="#">c5w1eA_</a>	Alignment	not modelled	96.0	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> pobr in complex with phb
74	<a href="#">c3lmmB_</a>	Alignment	not modelled	96.0	8	<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
75	<a href="#">c3f6vA_</a>	Alignment	not modelled	96.0	15	<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
76	<a href="#">c4cicB_</a>	Alignment	not modelled	96.0	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, badm/rrf2 family; <b>PDBTitle:</b> t. potens iscr
77	<a href="#">c2h09A_</a>	Alignment	not modelled	96.0	20	<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
						<b>PDB header:</b> dna binding protein

78	<a href="#">c3r4kD_</a>	Alignment	not modelled	95.9	13	<b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
79	<a href="#">d1u2wa1</a>	Alignment	not modelled	95.7	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
80	<a href="#">c4ijaA_</a>	Alignment	not modelled	95.7	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
81	<a href="#">c3lwfD_</a>	Alignment	not modelled	95.7	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
82	<a href="#">c4o6jA_</a>	Alignment	not modelled	95.6	14	<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
83	<a href="#">d1ub9a_</a>	Alignment	not modelled	95.6	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
84	<a href="#">c4czdA_</a>	Alignment	not modelled	95.4	15	<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.
85	<a href="#">c2gqqB_</a>	Alignment	not modelled	95.4	22	<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)
86	<a href="#">d1sfxa_</a>	Alignment	not modelled	95.4	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
87	<a href="#">d1g3wa1</a>	Alignment	not modelled	95.4	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
88	<a href="#">d2isyA1</a>	Alignment	not modelled	95.4	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
89	<a href="#">c2it0A_</a>	Alignment	not modelled	95.3	14	<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
90	<a href="#">d2ev0a1</a>	Alignment	not modelled	95.3	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
91	<a href="#">c1z05A_</a>	Alignment	not modelled	95.2	11	<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.
92	<a href="#">c1z6rC_</a>	Alignment	not modelled	95.2	4	<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
93	<a href="#">c3ctaA_</a>	Alignment	not modelled	95.2	13	<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
94	<a href="#">d2p5ka1</a>	Alignment	not modelled	95.2	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
95	<a href="#">d2hs5a1</a>	Alignment	not modelled	95.1	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
96	<a href="#">d1z6ra1</a>	Alignment	not modelled	95.1	4	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
97	<a href="#">c3k69A_</a>	Alignment	not modelled	95.0	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription regulator; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
98	<a href="#">c6jbxB_</a>	Alignment	not modelled	94.9	21	<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
99	<a href="#">c3cjnA_</a>	Alignment	not modelled	94.9	16	<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
100	<a href="#">c6dk4A_</a>	Alignment	not modelled	94.8	15	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> crystal structure of campylobacter jejuni peroxide stress regulator
101	<a href="#">c3oopA_</a>	Alignment	not modelled	94.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2960 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from listeria innocua2 clip11262
102	<a href="#">c3ereD_</a>	Alignment	not modelled	94.8	30	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> D: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
103	<a href="#">c4go1A_</a>	Alignment	not modelled	94.7	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lsrR; <b>PDBTitle:</b> crystal structure of full length transcription repressor lsrR

						from e.2 coli.
104	<a href="#">c4a0zA_</a>	Alignment	not modelled	94.7	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor fapr; <b>PDBTitle:</b> structure of the global transcription regulator fapr from2 staphylococcus aureus in complex with malonyl-coa
105	<a href="#">c2qwwB_</a>	Alignment	not modelled	94.6	19	<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
106	<a href="#">d2etha1</a>	Alignment	not modelled	94.6	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
107	<a href="#">c3g3zA_</a>	Alignment	not modelled	94.6	11	<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
108	<a href="#">c2ev5B_</a>	Alignment	not modelled	94.6	10	<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
109	<a href="#">c5aiqD_</a>	Alignment	not modelled	94.6	16	<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
110	<a href="#">c3r0aB_</a>	Alignment	not modelled	94.5	20	<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)
111	<a href="#">c6c28C_</a>	Alignment	not modelled	94.5	26	<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
112	<a href="#">c2rdpA_</a>	Alignment	not modelled	94.5	8	<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
113	<a href="#">c3nrvC_</a>	Alignment	not modelled	94.5	7	<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
114	<a href="#">c4czdD_</a>	Alignment	not modelled	94.5	32	<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.
115	<a href="#">c3bj6B_</a>	Alignment	not modelled	94.5	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 transcription regulator sp03579
116	<a href="#">c4mnuA_</a>	Alignment	not modelled	94.5	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
117	<a href="#">d2dt5a1</a>	Alignment	not modelled	94.5	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional repressor Rex, N-terminal domain
118	<a href="#">c2nnnB_</a>	Alignment	not modelled	94.4	11	<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
119	<a href="#">c2hs5A_</a>	Alignment	not modelled	94.4	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator gntr; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1
120	<a href="#">c5eriA_</a>	Alignment	not modelled	94.4	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> marr family transcriptional regulator; <b>PDBTitle:</b> marr protein from peptoclostridium difficile da00132