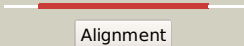

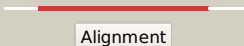

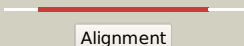







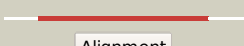











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0586 (- )_684413_685135
Date	Fri Jul 26 01:50:14 BST 2019
Unique Job ID	0ce36dd75507f00a

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4p96B_</a>			100.0	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid metabolism regulator protein; <b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from vibrio cholerae
2	<a href="#">c1e2xA_</a>			100.0	21	<b>PDB header:</b> transcriptional regulation <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid metabolism regulator protein; <b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from e.2 coli
3	<a href="#">c3c7jA_</a>			100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntR family; <b>PDBTitle:</b> crystal structure of transcriptional regulator (gntR family member)2 from pseudomonas syringae pv. tomato str. dc3000
4	<a href="#">c3fmsA_</a>			100.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntR family; <b>PDBTitle:</b> crystal structure of tm0439, a gntR transcriptional regulator
5	<a href="#">c2hs5A_</a>			100.0	18	<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
6	<a href="#">c2di3A_</a>			100.0	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial regulatory proteins, gntR family; <b>PDBTitle:</b> crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
7	<a href="#">c3ihuA_</a>			100.0	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntR family; <b>PDBTitle:</b> crystal structure of dna binding protein (yp_298823.1) from ralstonia2 eutropha jmp134 at 1.92 a resolution
8	<a href="#">c6ep3B_</a>			100.0	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> lmo0651 protein; <b>PDBTitle:</b> lar controls the expression of the listeria monocytogenes agr system2 and mediates virulence.
9	<a href="#">c6az6B_</a>			100.0	24	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> gntR family transcriptional regulator; <b>PDBTitle:</b> streptococcus agalactiae gntR
10	<a href="#">c4p9fA_</a>			100.0	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator mcbr; <b>PDBTitle:</b> e. coli mcbr/yncc
11	<a href="#">c4hamA_</a>			99.9	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo2241 protein; <b>PDBTitle:</b> crystal structure of transcriptional antiterminator from listeria2 monocytogenes egd-e

12	<a href="#">c3by6C_</a>	Alignment		99.8	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> predicted transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator from oenococcus oeni
13	<a href="#">c4r1hA_</a>	Alignment		99.8	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
14	<a href="#">c5kvrA_</a>	Alignment		99.8	41	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase complex repressor; <b>PDBTitle:</b> x-ray crystal structure of a fragment (1-75) of a transcriptional2 regulator pdhr from escherichia coli cft073
15	<a href="#">c2du9A_</a>	Alignment		99.8	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> predicted transcriptional regulators; <b>PDBTitle:</b> crystal structure of the transcriptional factor from c.glutamicum
16	<a href="#">c3bwgA_</a>	Alignment		99.8	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator yydk; <b>PDBTitle:</b> the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
17	<a href="#">c3neuA_</a>	Alignment		99.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin1836 protein; <b>PDBTitle:</b> the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
18	<a href="#">c3edpB_</a>	Alignment		99.8	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lin2111 protein; <b>PDBTitle:</b> the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
19	<a href="#">c4zs8A_</a>	Alignment		99.8	31	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor dasr; <b>PDBTitle:</b> crystal structure of ligand-free, full length dasr
20	<a href="#">c3eetA_</a>	Alignment		99.8	34	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative gntR-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative gntR-family transcriptional2 regulator
21	<a href="#">d1v4ra1</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
22	<a href="#">c3f8mA_</a>	Alignment	not modelled	99.8	34	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gntR-family protein transcriptional regulator; <b>PDBTitle:</b> crystal structure of phnF from mycobacterium smegmatis
23	<a href="#">d1hw1a1</a>	Alignment	not modelled	99.8	36	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
24	<a href="#">c4eqzA_</a>	Alignment	not modelled	99.8	30	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> arabinose metabolism transcriptional repressor; <b>PDBTitle:</b> crystal structure of arar(dbd) in complex with operator orr3
25	<a href="#">d3bwga1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
26	<a href="#">c4n0bA_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulatory protein gabr; <b>PDBTitle:</b> crystal structure of bacillus subtilis gabr, an autorepressor and2 transcriptional activator of gabt
27	<a href="#">d2hs5a1</a>	Alignment	not modelled	99.7	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
28	<a href="#">c3ic7A_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator of qntr family2 from bacteroides thetaiotaomicron

29	<a href="#">d1hw1a2</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> GntR ligand-binding domain-like <b>Superfamily:</b> GntR ligand-binding domain-like <b>Family:</b> GntR ligand-binding domain-like
30	<a href="#">c3tqnC</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, gntR family; <b>PDBTitle:</b> structure of the transcriptional regulator of the gntR family, from2 coxiella burnetii.
31	<a href="#">c5tpmD</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate dehydrogenase complex repressor; <b>PDBTitle:</b> 2.8 angstrom crystal structure of the c-terminal dimerization domain2 of transcriptional regulator pdhr from escherichia coli.
32	<a href="#">d2hs5a2</a>	Alignment	not modelled	99.6	10	<b>Fold:</b> GntR ligand-binding domain-like <b>Superfamily:</b> GntR ligand-binding domain-like <b>Family:</b> GntR ligand-binding domain-like
33	<a href="#">c3sxB</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, gntR family; <b>PDBTitle:</b> zn2+-bound fcd domain of tm0439, a putative transcriptional regulator
34	<a href="#">c2wv0H</a>	Alignment	not modelled	99.5	27	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> hth-type transcriptional repressor yvoa; <b>PDBTitle:</b> crystal structure of the gntR-hutC family member yvoa from2 bacillus subtilis
35	<a href="#">c2h09A</a>	Alignment	not modelled	98.6	21	<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
36	<a href="#">c1f5tA</a>	Alignment	not modelled	98.4	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
37	<a href="#">c2it0A</a>	Alignment	not modelled	98.2	19	<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
38	<a href="#">c3hruA</a>	Alignment	not modelled	98.2	22	<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+
39	<a href="#">d1biaa1</a>	Alignment	not modelled	98.0	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
40	<a href="#">c1g3wA</a>	Alignment	not modelled	98.0	24	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtxr
41	<a href="#">d1jhfa1</a>	Alignment	not modelled	97.9	32	<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
42	<a href="#">d1stza1</a>	Alignment	not modelled	97.8	16	<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
43	<a href="#">c4o6jA</a>	Alignment	not modelled	97.7	15	<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
44	<a href="#">c5cviB</a>	Alignment	not modelled	97.6	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> slor; <b>PDBTitle:</b> structure of the manganese regulator slor
45	<a href="#">d1g3wa1</a>	Alignment	not modelled	97.6	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
46	<a href="#">c3rkaA</a>	Alignment	not modelled	97.6	18	<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
47	<a href="#">c1fx7C</a>	Alignment	not modelled	97.5	23	<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
48	<a href="#">c3ctaA</a>	Alignment	not modelled	97.5	14	<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
49	<a href="#">d2isya1</a>	Alignment	not modelled	97.5	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
50	<a href="#">c2x4hA</a>	Alignment	not modelled	97.5	18	<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
51	<a href="#">c3r0aB</a>	Alignment	not modelled	97.4	12	<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)
52	<a href="#">c3zplE</a>	Alignment	not modelled	97.3	20	<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
53	<a href="#">c3zmdD</a>	Alignment	not modelled	97.3	16	<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
54	<a href="#">d1j5ya1</a>	Alianment	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
55	<a href="#">d3broa1</a>	Alignment	not modelled	97.2	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
56	<a href="#">c3nqoB</a>	Alignment	not modelled	97.1	16	<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
57	<a href="#">d1i5za1</a>	Alignment	not modelled	97.1	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
58	<a href="#">c2y75F</a>	Alignment	not modelled	97.1	14	<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
59	<a href="#">c6cmvA</a>	Alignment	not modelled	97.1	23	<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 sulfolobus acidocaldarius
60	<a href="#">c1j5yA</a>	Alignment	not modelled	97.1	19	<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
61	<a href="#">d3ctaa1</a>	Alignment	not modelled	97.0	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
62	<a href="#">c5ey0A</a>	Alignment	not modelled	97.0	30	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> crystal structure of cody from staphylococcus aureus with gtp and ile
63	<a href="#">c3bj6B</a>	Alignment	not modelled	97.0	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcriptional regulator sp03579
64	<a href="#">c3lwfD</a>	Alignment	not modelled	97.0	16	<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
65	<a href="#">c5jbrA</a>	Alignment	not modelled	96.9	17	<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
66	<a href="#">c3t8tA</a>	Alignment	not modelled	96.9	16	<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
67	<a href="#">c4cicB</a>	Alignment	not modelled	96.9	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, badm/rrf2 family; <b>PDBTitle:</b> t. potens iscr
68	<a href="#">c2ev5B</a>	Alignment	not modelled	96.9	14	<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
69	<a href="#">c2rdpA</a>	Alignment	not modelled	96.8	17	<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
70	<a href="#">d2fbha1</a>	Alignment	not modelled	96.8	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
71	<a href="#">c5bqtC</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative hth-type transcriptional regulator trmbI2; <b>PDBTitle:</b> structure of trmbI2, an archaeal chromatin protein, shows a novel mode2 of dna binding.
72	<a href="#">c4hf1B</a>	Alignment	not modelled	96.8	13	<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
73	<a href="#">c6c28C</a>	Alignment	not modelled	96.8	18	<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
74	<a href="#">c4mnuA</a>	Alignment	not modelled	96.8	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
75	<a href="#">c2fa5B</a>	Alignment	not modelled	96.7	15	<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
76	<a href="#">c5eriA</a>	Alignment	not modelled	96.7	20	<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
77	<a href="#">c2v79B</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna replication protein dnad; <b>PDBTitle:</b> crystal structure of the n-terminal domain of dnad from bacillus2 subtilis
78	<a href="#">c3k69A</a>	Alignment	not modelled	96.7	19	<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
79	<a href="#">c6o5cB</a>	Alignment	not modelled	96.7	20	<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 mtr
80	<a href="#">d2d1ha1</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> TrmB-like
81	<a href="#">c2gxgA</a>	Alignment	not modelled	96.7	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> 146aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
82	<a href="#">c4i2oA</a>	Alignment	not modelled	96.7	22	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> fixk2 protein; <b>PDBTitle:</b> the structure of fixk2 from bradyrhizobium japonicum
83	<a href="#">c3nrvc</a>	Alignment	not modelled	96.7	17	<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
84	<a href="#">c5jlsA</a>	Alignment	not modelled	96.6	22	<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)
85	<a href="#">c2ewnA</a>	Alignment	not modelled	96.6	26	<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="#">c3oopA</a>	Alignment	not modelled	96.6	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
87	<a href="#">d1ft9a1</a>	Alignment	not modelled	96.6	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
88	<a href="#">d2h6ca1</a>	Alignment	not modelled	96.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
89	<a href="#">c4fhtA</a>	Alignment	not modelled	96.5	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pcav transcriptional regulator; <b>PDBTitle:</b> crystal structure of the pcav transcriptional regulator from2 streptomyces coelicolor in complex with its natural ligand
90	<a href="#">c3tgnA</a>	Alignment	not modelled	96.5	24	<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
91	<a href="#">d2oz6a1</a>	Alignment	not modelled	96.5	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
92	<a href="#">c1ft9A</a>	Alignment	not modelled	96.5	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide oxidation system transcription <b>PDBTitle:</b> structure of the reduced (feii) co-sensing protein from r.2 rubrum
93	<a href="#">c5zc2B</a>	Alignment	not modelled	96.5	16	<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)
94	<a href="#">c1zybA</a>	Alignment	not modelled	96.5	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator, crp family; <b>PDBTitle:</b> crystal structure of transcription regulator from bacteroides2 thetaiotaomicron vpi-5482 at 2.15 a resolution
95	<a href="#">d2etha1</a>	Alignment	not modelled	96.5	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
96	<a href="#">c3g3zA</a>	Alignment	not modelled	96.5	20	<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
97	<a href="#">d1lnwa</a>	Alignment	not modelled	96.5	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
98	<a href="#">d1jgsa</a>	Alignment	not modelled	96.5	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
99	<a href="#">c6hsdB</a>	Alignment	not modelled	96.5	33	<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
100	<a href="#">d2coha1</a>	Alignment	not modelled	96.4	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
101	<a href="#">c3d0sA</a>	Alignment	not modelled	96.4	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> camp receptor protein from m.tuberculosis, camp-free form
102	<a href="#">d1xd7a</a>	Alignment	not modelled	96.4	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator Rrf2
103	<a href="#">d1sfxa</a>	Alignment	not modelled	96.4	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
104	<a href="#">d3deua1</a>	Alignment	not modelled	96.4	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

105	<a href="#">d1yifa1</a>	Alignment	not modelled	96.4	14	<b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator Rrf2
106	<a href="#">c5yhxB</a>	Alignment	not modelled	96.3	20	<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 zitr, wild type
107	<a href="#">c3bjaA</a>	Alignment	not modelled	96.3	15	<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
108	<a href="#">c3s2wB</a>	Alignment	not modelled	96.3	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
109	<a href="#">d1s3ja</a>	Alignment	not modelled	96.3	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
110	<a href="#">d2ev0a1</a>	Alignment	not modelled	96.3	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
111	<a href="#">d2gaua1</a>	Alignment	not modelled	96.3	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
112	<a href="#">d1mkma1</a>	Alignment	not modelled	96.2	16	<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
113	<a href="#">d2fbia1</a>	Alignment	not modelled	96.2	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
114	<a href="#">d2b0la1</a>	Alignment	not modelled	96.2	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CodY HTH domain
115	<a href="#">d1lj9a</a>	Alignment	not modelled	96.2	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
116	<a href="#">c3kp3B</a>	Alignment	not modelled	96.2	21	<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
117	<a href="#">d2bv6a1</a>	Alignment	not modelled	96.2	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
118	<a href="#">d2hr3a1</a>	Alignment	not modelled	96.2	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
119	<a href="#">c5e44A</a>	Alignment	not modelled	96.2	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fnr regulator; <b>PDBTitle:</b> crystal structure of holo-fnr of a. fischeri
120	<a href="#">c5aiqD</a>	Alignment	not modelled	96.2	27	<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