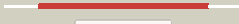



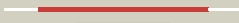


















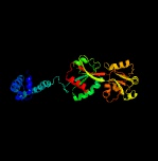

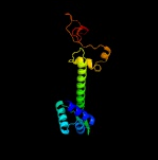
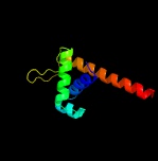
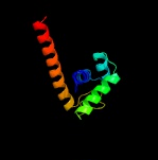
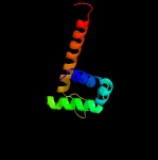

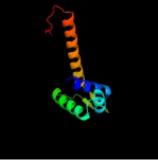


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0117_(oxyS)_141198_142142
Date	Tue Jul 23 14:50:16 BST 2019
Unique Job ID	16165cd17e217b17

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5y2vA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rubisco operon transcriptional regulator; <b>PDBTitle:</b> strcutrue of the full-length ccmr complexed with 2-og from2 synechocystis pcc6803
2	<a href="#">c6g4rE_</a>	 Alignment		100.0	23	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> hydrogen peroxide-inducible genes activator; <b>PDBTitle:</b> corynebacterium glutamicum oxyr c206s mutant, h2o2-bound
3	<a href="#">c1iz1B_</a>	 Alignment		100.0	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> lysr-type regulatory protein; <b>PDBTitle:</b> crystal structure of cbnr, a lysr family transcriptional2 regulator
4	<a href="#">c3fzjC_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> lysr type regulator of tsambcd; <b>PDBTitle:</b> tsar low resolution crystal structure, tetragonal form
5	<a href="#">c2esnC_</a>	 Alignment		100.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa
6	<a href="#">c3k1nB_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of full-length benm
7	<a href="#">c3hhgF_</a>	 Alignment		100.0	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
8	<a href="#">c3t1bB_</a>	 Alignment		100.0	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> crystal structure of the full-length aphb n100e variant
9	<a href="#">c5y9sD_</a>	 Alignment		100.0	16	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> vv2_1132; <b>PDBTitle:</b> crystal structure of vv2_1132, a lysr family transcriptional regulator
10	<a href="#">c5ydwB_</a>	 Alignment		100.0	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell density-dependent motility repressor; <b>PDBTitle:</b> full-length structure of hpyt from salmonella typhimuriuma2 (hypochlorite-specific lysr-type transcriptional regulator)
11	<a href="#">c3fzvC_</a>	 Alignment		100.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of pa01 protein, putative lysr family2 transcriptional regulator from pseudomonas aeruginosa

12	<a href="#">c3ispA_</a>	Alignment		100.0	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator <b>PDBTitle:</b> crystal structure of argp from mycobacterium tuberculosis
13	<a href="#">c5ae5A_</a>	Alignment		100.0	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lysr-type regulatory protein; <b>PDBTitle:</b> structures of inactive and activated dntr provide conclusive evidence2 for the mechanism of action of lysr transcription factors
14	<a href="#">c4x6gG_</a>	Alignment		100.0	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> oxyr; <b>PDBTitle:</b> full-length oxyr c199d from pseudomonas aeruginosa
15	<a href="#">c1b9nA_</a>	Alignment		99.9	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein (mode); <b>PDBTitle:</b> regulator from escherichia coli
16	<a href="#">c5z4yB_</a>	Alignment		99.9	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cys regulon transcriptional activator; <b>PDBTitle:</b> crystal structure of pacysb ntd domain with space group p4
17	<a href="#">c3m1eA_</a>	Alignment		99.9	34	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of benm_dbd
18	<a href="#">c5fo5A_</a>	Alignment		99.9	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator metr; <b>PDBTitle:</b> structure of the dna-binding domain of escherichia coli methionine2 biosynthesis regulator metr
19	<a href="#">d2esna1</a>	Alignment		99.9	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LysR-like transcriptional regulators
20	<a href="#">d1b9ma1</a>	Alignment		99.8	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> N-terminal domain of molybdate-dependent transcriptional regulator ModE
21	<a href="#">d1ixca1</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> LysR-like transcriptional regulators
22	<a href="#">c4pzjA_</a>	Alignment	not modelled	99.8	34	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> 1.60 angstrom resolution crystal structure of a transcriptional2 regulator of the lysr family from eggerthella lenta dsm 2243
23	<a href="#">c5z50A_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cys regulon transcriptional activator; <b>PDBTitle:</b> crystal structure of pacysb regulatory domain
24	<a href="#">c5b70B_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> lysr family transcriptional regulator; <b>PDBTitle:</b> oxyr2 e204g regulatory domain from vibrio vulnificus
25	<a href="#">c2hxrA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator cynr; <b>PDBTitle:</b> structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
26	<a href="#">d2fyia1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
27	<a href="#">c5y2wA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rubisco operon transcriptional regulator; <b>PDBTitle:</b> structure of synechocystis pcc6803 ccmr regulatory domain in complex2 with 2-pg
28	<a href="#">c5tedA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0488 protein; <b>PDBTitle:</b> effector binding domain of quir in complex with shikimate

29	<a href="#">d1a13a_</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
30	<a href="#">c1a13A_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> cys regulon transcriptional activator cysb; <b>PDBTitle:</b> cofactor binding fragment of cysb from klebsiella aerogenes
31	<a href="#">c4rnsA_</a>	Alignment	not modelled	99.7	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pcp degradation transcriptional activation protein; <b>PDBTitle:</b> pcpr inducer binding domain (apo-form)
32	<a href="#">c3oxnD_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator, lysr family; <b>PDBTitle:</b> the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
33	<a href="#">c5z49A_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator cmpr; <b>PDBTitle:</b> crystal structure of the effector-binding domain of synechococcus2 elongatus cmpr in complex with ribulose-1,5-bisphosphate
34	<a href="#">c2ijjB_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> molybdenum-binding transcriptional repressor; <b>PDBTitle:</b> the structure of a putative mode from agrobacterium tumefaciens.
35	<a href="#">d1utha_</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
36	<a href="#">c2ql3G_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> probable transcriptional regulator, lysr family protein; <b>PDBTitle:</b> crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
37	<a href="#">c3jv9B_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> the structure of a reduced form of oxyr from n. meningitidis
38	<a href="#">c5tpiA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator (lysr family); <b>PDBTitle:</b> 1.47 angstrom crystal structure of the c-terminal substrate binding2 domain of lysr family transcriptional regulator from klebsiella3 pneumoniae.
39	<a href="#">c2uyeA_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> double mutant y110s,f111v dntr from burkholderia sp. strain2 dnt in complex with thiocyanate
40	<a href="#">c3ho7A_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> oxyr; <b>PDBTitle:</b> crystal structure of oxyr from porphyromonas gingivalis
41	<a href="#">d1i6aa_</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
42	<a href="#">d1ixca2</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
43	<a href="#">d2esna2</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
44	<a href="#">c2h9qC_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> hth-type transcriptional regulator catm; <b>PDBTitle:</b> crystal structure of the effector binding domain of a catm2 variant (r156h)
45	<a href="#">c4ab6A_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> regulatory domain structure of nmb2055 (metr), c103s c106s mutant, a2 lysr family regulator from n. meningitidis
46	<a href="#">c2f7cA_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator catm; <b>PDBTitle:</b> catm effector binding domain with its effector cis,cis-muconate
47	<a href="#">c3n6uA_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lysr type regulator of tsambcd; <b>PDBTitle:</b> effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
48	<a href="#">c5vvhE_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> octopine catabolism/uptake operon regulatory protein occr; <b>PDBTitle:</b> crystal structure of the effector binding domain of lysr-type2 transcriptional regulator, occr from agrobacterium tumefaciens
49	<a href="#">c3fd3A_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome replication initiation inhibitor protein; <b>PDBTitle:</b> structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
50	<a href="#">c2h9bB_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
51	<a href="#">c2f78A_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> benm effector binding domain with its effector benzoate
52	<a href="#">c4jvcA_</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator mvfr; <b>PDBTitle:</b> crystal structure of pqsr co-inducer binding domain <b>PDB header:</b> transcription

53	<a href="#">c3kosA</a>	Alignment	not modelled	99.6	12	<b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator ampr; <b>PDBTitle:</b> structure of the ampr effector binding domain from <i>citrobacter2 freundii</i>
54	<a href="#">c3hhfB</a>	Alignment	not modelled	99.5	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> structure of crga regulatory domain, a lysr-type transcriptional2 regulator from <i>neisseria meningitidis</i> .
55	<a href="#">c5z72B</a>	Alignment	not modelled	99.5	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> ccpc; <b>PDBTitle:</b> crystal structure of ccpc regulatory domain in complex with citrate2 from <i>bacillus amyloliquefaciens</i>
56	<a href="#">c4qbaB</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> lysr family regulatory protein; <b>PDBTitle:</b> crystal structure of the effector-binding domain of <i>s. aureus ccpe</i>
57	<a href="#">c3mz1D</a>	Alignment	not modelled	99.5	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a possible transcription regulator protein2 from <i>sinorhizobium meliloti 1021</i>
58	<a href="#">c6gz1A</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator leuo; <b>PDBTitle:</b> crystal structure of the leuo effector binding domain
59	<a href="#">c5mmhD</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional activator ampr; <b>PDBTitle:</b> the x-ray structure of the effector domain of the transcriptional2 regulator ampr of <i>pseudomonas aeruginosa</i>
60	<a href="#">c3onmB</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator lrha; <b>PDBTitle:</b> effector binding domain of lysr-type transcription factor rovm from <i>y.2 pseudotuberculosis</i>
61	<a href="#">c5yezD</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> cell density-dependent motility repressor; <b>PDBTitle:</b> regulatory domain of hypt m206q mutant from <i>salmonella typhimurium</i>
62	<a href="#">c2qsxB</a>	Alignment	not modelled	99.1	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator, lysr family; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator lysr from <i>2 vibrio parahaemolyticus</i>
63	<a href="#">c2x4hA</a>	Alignment	not modelled	98.0	14	<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 from <i>2 sulfobolus solfataricus</i>
64	<a href="#">c3boqB</a>	Alignment	not modelled	98.0	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 transcriptional regulator from <i>2 silicibacter pomeroyi</i>
65	<a href="#">c3ctaA</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase; <b>PDBTitle:</b> crystal structure of riboflavin kinase from <i>thermoplasma acidophilum</i>
66	<a href="#">c5zc2B</a>	Alignment	not modelled	97.8	11	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> p-hydroxyphenylacetate 3-hydroxylase, reductase component; <b>PDBTitle:</b> <i>acinetobacter baumannii</i> p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
67	<a href="#">d2fxaa1</a>	Alignment	not modelled	97.8	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
68	<a href="#">c2fa5B</a>	Alignment	not modelled	97.7	16	<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 <i>xanthomonas campestris</i>
69	<a href="#">c3nrvC</a>	Alignment	not modelled	97.7	14	<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 from <i>2 acinetobacter sp. adp1</i>
70	<a href="#">c3bpxB</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
71	<a href="#">c2qxA</a>	Alignment	not modelled	97.6	20	<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 <i>sulfolobus tokodaii strain7</i>
72	<a href="#">c2nnnB</a>	Alignment	not modelled	97.6	8	<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 from <i>2 pseudomonas aeruginosa</i>
73	<a href="#">d2fbha1</a>	Alignment	not modelled	97.6	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
74	<a href="#">d1lnwa</a>	Alignment	not modelled	97.6	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
75	<a href="#">c3cdhB</a>	Alignment	not modelled	97.6	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 the marr family transcriptional regulator spo14532 from <i>silicibacter pomeroyi dss-3</i>
76	<a href="#">c3g3zA</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> the structure of nmb1585, a marr family regulator from <i>neisseria2 meningitidis</i>
77	<a href="#">d2bv6a1</a>	Alignment	not modelled	97.6	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
						<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulatory

78	<a href="#">c2nyxB</a>	Alignment	not modelled	97.6	17	protein, rv1404; <b>PDBTitle:</b> crystal structure of rv1404 from mycobacterium tuberculosis
79	<a href="#">c4xrfA</a>	Alignment	not modelled	97.6	22	<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
80	<a href="#">c3fm5D</a>	Alignment	not modelled	97.6	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> x-ray crystal structure of transcriptional regulator (marr family)2 from rhodococcus sp. rha1
81	<a href="#">d1lj9a</a>	Alignment	not modelled	97.6	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
82	<a href="#">d1jgsa</a>	Alignment	not modelled	97.5	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
83	<a href="#">c3f3xA</a>	Alignment	not modelled	97.5	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family, putative; <b>PDBTitle:</b> crystal structure of the transcriptional regulator bldr from2 sulfobolus solfataricus
84	<a href="#">c2fxaB</a>	Alignment	not modelled	97.5	13	<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.
85	<a href="#">c3ecoB</a>	Alignment	not modelled	97.5	24	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> mepr; <b>PDBTitle:</b> crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
86	<a href="#">c4fhtA</a>	Alignment	not modelled	97.5	16	<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
87	<a href="#">c3e6mD</a>	Alignment	not modelled	97.5	13	<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.
88	<a href="#">c5eriA</a>	Alignment	not modelled	97.5	10	<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
89	<a href="#">c5yhxB</a>	Alignment	not modelled	97.5	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 zitri, wild type
90	<a href="#">d2hr3a1</a>	Alignment	not modelled	97.5	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
91	<a href="#">c2h09A</a>	Alignment	not modelled	97.4	18	<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
92	<a href="#">c3hruA</a>	Alignment	not modelled	97.4	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+
93	<a href="#">c3nqoB</a>	Alignment	not modelled	97.4	21	<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
94	<a href="#">c5e1xA</a>	Alignment	not modelled	97.4	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of the organohalide sensing rdhr-cbdba16252 transcriptional regulator in the 3,4-dichlorophenol bound form
95	<a href="#">c4mnuA</a>	Alignment	not modelled	97.4	20	<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
96	<a href="#">c1f5tA</a>	Alignment	not modelled	97.4	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
97	<a href="#">d1p4xa1</a>	Alignment	not modelled	97.4	10	<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="#">d1s3ja</a>	Alignment	not modelled	97.4	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
99	<a href="#">c2pexA</a>	Alignment	not modelled	97.4	18	<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 xanthamonas campestris
100	<a href="#">c4yifE</a>	Alignment	not modelled	97.4	26	<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
101	<a href="#">d2etha1</a>	Alignment	not modelled	97.4	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
102	<a href="#">c2rdpA</a>	Alignment	not modelled	97.4	14	<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
103	<a href="#">c5aiqD</a>	Alignment	not modelled	97.4	22	<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

104	<a href="#">c3cjnA_</a>	Alignment	not modelled	97.4	13	<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
105	<a href="#">c5hsmA_</a>	Alignment	not modelled	97.3	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator rv2887; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis marr family protein2 rv2887
106	<a href="#">d3broa1</a>	Alignment	not modelled	97.3	11	<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="#">d2fbia1</a>	Alignment	not modelled	97.3	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
108	<a href="#">c5cviB_</a>	Alignment	not modelled	97.3	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> slor; <b>PDBTitle:</b> structure of the manganese regulator slor
109	<a href="#">d1ub9a_</a>	Alignment	not modelled	97.3	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
110	<a href="#">c3bjaA_</a>	Alignment	not modelled	97.3	12	<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
111	<a href="#">c4kd5A_</a>	Alignment	not modelled	97.3	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type transport system, molybdenum-specific <b>PDBTitle:</b> substrate binding domain of putative molybdenum abc transporter from2 clostridium difficile
112	<a href="#">c3hrmA_</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator sarz; <b>PDBTitle:</b> crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form
113	<a href="#">d2fbka1</a>	Alignment	not modelled	97.3	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
114	<a href="#">c4o6jA_</a>	Alignment	not modelled	97.3	12	<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
115	<a href="#">d2frha1</a>	Alignment	not modelled	97.2	7	<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="#">c1fx7C_</a>	Alignment	not modelled	97.2	22	<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
117	<a href="#">c2it0A_</a>	Alignment	not modelled	97.2	24	<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
118	<a href="#">c4b8xB_</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> possible marr-transcriptional regulator; <b>PDBTitle:</b> near atomic resolution crystal structure of sco5413, a marr family2 transcriptional regulator from streptomyces coelicolor
119	<a href="#">d2a61a1</a>	Alignment	not modelled	97.2	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
120	<a href="#">c3oopA_</a>	Alignment	not modelled	97.2	16	<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