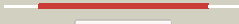



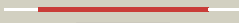


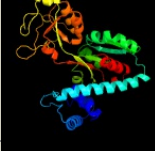



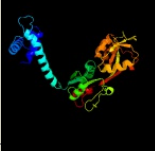












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0377 (-) _454422_455387
Date	Tue Jul 23 14:50:45 BST 2019
Unique Job ID	19d3fe8e2da6692b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5y2vA_</a>	 Alignment		100.0	19	<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="#">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
3	<a href="#">c2esnC_</a>	 Alignment		100.0	20	<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
4	<a href="#">c3hhgF_</a>	 Alignment		100.0	20	<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.
5	<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
6	<a href="#">c5y9sD_</a>	 Alignment		100.0	13	<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
7	<a href="#">c6q4rE_</a>	 Alignment		100.0	16	<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
8	<a href="#">c3k1nB_</a>	 Alignment		100.0	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 full-length benm
9	<a href="#">c1iz1B_</a>	 Alignment		100.0	19	<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
10	<a href="#">c5ydwB_</a>	 Alignment		100.0	13	<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	16	<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="#">c5ae5A_</a>	Alignment		100.0	17	<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
13	<a href="#">c3ispA_</a>	Alignment		100.0	14	<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
14	<a href="#">c4x6gG_</a>	Alignment		100.0	17	<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	18	<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	33	<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	26	<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	29	<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	29	<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		99.9	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="#">c5y2wA_</a>	Alignment	not modelled	99.9	14	<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
22	<a href="#">c2hxrA_</a>	Alignment	not modelled	99.9	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
23	<a href="#">c5z50A_</a>	Alignment	not modelled	99.8	15	<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	15	<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="#">c3oxnD_</a>	Alignment	not modelled	99.8	13	<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
26	<a href="#">c5tpiA_</a>	Alignment	not modelled	99.8	10	<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.
27	<a href="#">c5z49A_</a>	Alignment	not modelled	99.8	16	<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
28	<a href="#">d2fyia1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II

					<b>Family:</b> Phosphate binding protein-like
29	<a href="#">d1ixca1</a>	Alignment	not modelled	99.8	27 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LysR-like transcriptional regulators
30	<a href="#">d1utha</a>	Alignment	not modelled	99.8	14 <b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
31	<a href="#">d1al3a</a>	Alignment	not modelled	99.8	15 <b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
32	<a href="#">c1al3A</a>	Alignment	not modelled	99.8	15 <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
33	<a href="#">c5tedA</a>	Alignment	not modelled	99.8	16 <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
34	<a href="#">c3fd3A</a>	Alignment	not modelled	99.8	15 <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.
35	<a href="#">c4rnsA</a>	Alignment	not modelled	99.8	17 <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)
36	<a href="#">c2uyeA</a>	Alignment	not modelled	99.8	14 <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
37	<a href="#">d1i6aa</a>	Alignment	not modelled	99.8	14 <b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
38	<a href="#">d2esna2</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
39	<a href="#">c4pziA</a>	Alignment	not modelled	99.8	28 <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
40	<a href="#">c3ho7A</a>	Alignment	not modelled	99.8	14 <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="#">c2ql3G</a>	Alignment	not modelled	99.8	16 <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
42	<a href="#">c3jv9B</a>	Alignment	not modelled	99.8	13 <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
43	<a href="#">c3kosA</a>	Alignment	not modelled	99.8	16 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator ampr; <b>PDBTitle:</b> structure of the ampr effector binding domain from citrobacter2 freundii
44	<a href="#">c3n6uA</a>	Alignment	not modelled	99.8	16 <b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lysyr type regulator of tsambcd; <b>PDBTitle:</b> effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
45	<a href="#">c2h9qC</a>	Alignment	not modelled	99.8	14 <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)
46	<a href="#">c4ab6A</a>	Alignment	not modelled	99.7	16 <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
47	<a href="#">c3hhfB</a>	Alignment	not modelled	99.7	18 <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 neisseria meningitidis.
48	<a href="#">c2ijlB</a>	Alignment	not modelled	99.7	20 <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.
49	<a href="#">c2f7cA</a>	Alignment	not modelled	99.7	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
50	<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
51	<a href="#">c4jvcA</a>	Alignment	not modelled	99.7	14 <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
52	<a href="#">c5vvhE</a>	Alignment	not modelled	99.7	16 <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
53	<a href="#">c3h0hB</a>	Alignment	not modelled	99.7	16 <b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator benm;

53	<a href="#">c2190B</a>	Alignment	not modelled	99.7	10	<b>PDBTitle:</b> crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s) <b>PDB header:</b> transcription regulator
54	<a href="#">c4qbaB</a>	Alignment	not modelled	99.7	10	<b>Chain:</b> B: <b>PDB Molecule:</b> lysr family regulatory protein; <b>PDBTitle:</b> crystal structure of the effector-binding domain of s. aureus ccpe
55	<a href="#">c5z72B</a>	Alignment	not modelled	99.7	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 bacillus amyloliquefaciens
56	<a href="#">c3mz1D</a>	Alignment	not modelled	99.7	13	<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 sinorhizobium meliloti 1021
57	<a href="#">c2f78A</a>	Alignment	not modelled	99.7	16	<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
58	<a href="#">c5yezD</a>	Alignment	not modelled	99.6	15	<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 salmonella typhimurium
59	<a href="#">c2qsxB</a>	Alignment	not modelled	99.6	14	<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 from2 vibrio parahaemolyticus
60	<a href="#">c6gz1A</a>	Alignment	not modelled	99.5	10	<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
61	<a href="#">c5mmhD</a>	Alignment	not modelled	99.5	18	<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 pseudomonas aeruginosa
62	<a href="#">c3onmB</a>	Alignment	not modelled	99.5	17	<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 y.2 pseudotuberculosis
63	<a href="#">c4kd5A</a>	Alignment	not modelled	98.3	8	<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
64	<a href="#">c4gd5B</a>	Alignment	not modelled	98.1	10	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphate abc transporter, phosphate-binding protein; <b>PDBTitle:</b> x-ray crystal structure of a putative phosphate abc transporter2 substrate-binding protein with bound phosphate from clostridium3 perfringens
65	<a href="#">c2x4hA</a>	Alignment	not modelled	98.1	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 sulfolobus solfataricus
66	<a href="#">c4n13A</a>	Alignment	not modelled	98.1	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate abc transporter, periplasmic phosphate-binding <b>PDBTitle:</b> crystal structure of psts (bb_0215) from borrelia burgdorferi
67	<a href="#">c3boqB</a>	Alignment	not modelled	98.1	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
68	<a href="#">c4ecfA</a>	Alignment	not modelled	98.0	11	<b>PDB header:</b> phosphate-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type phosphate transport system, periplasmic component; <b>PDBTitle:</b> crystal structure of an abc-type phosphate transport system,2 periplasmic component (Ivis_0633) from lactobacillus brevis atcc 3673 at 1.55 a resolution
69	<a href="#">c5zc2B</a>	Alignment	not modelled	98.0	15	<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)
70	<a href="#">d1twya</a>	Alignment	not modelled	97.9	8	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
71	<a href="#">c2fa5B</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator marr/emrr family; <b>PDBTitle:</b> the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
72	<a href="#">c1twyG</a>	Alignment	not modelled	97.8	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein; <b>PDBTitle:</b> crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
73	<a href="#">c3ctaA</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase; <b>PDBTitle:</b> crystal structure of riboflavin kinase from thermoplasma acidophilum
74	<a href="#">d2fbha1</a>	Alignment	not modelled	97.8	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
75	<a href="#">c2gxgA</a>	Alignment	not modelled	97.8	15	<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
76	<a href="#">c3nrvc</a>	Alignment	not modelled	97.8	18	<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
77	<a href="#">c3bpxB</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
78	<a href="#">c2nnnB</a>	Alignment	not modelled	97.8	16	<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
79	<a href="#">c4xrfA</a>	Alignment	not modelled	97.7	13	<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="#">c2nyxB</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulatory protein, rv1404; <b>PDBTitle:</b> crystal structure of rv1404 from mycobacterium tuberculosis
81	<a href="#">d1lj9a</a>	Alignment	not modelled	97.7	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
82	<a href="#">d1jgsa</a>	Alignment	not modelled	97.7	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
83	<a href="#">c3cdhB</a>	Alignment	not modelled	97.7	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 silicibacter pomeroyi dss-3
84	<a href="#">c3e6mD</a>	Alignment	not modelled	97.7	16	<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.
85	<a href="#">d1lnwa</a>	Alignment	not modelled	97.7	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
86	<a href="#">c3ecoB</a>	Alignment	not modelled	97.6	22	<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
87	<a href="#">d2etha1</a>	Alignment	not modelled	97.6	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
88	<a href="#">c3fm5D</a>	Alignment	not modelled	97.6	21	<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
89	<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
90	<a href="#">c4fhtA</a>	Alignment	not modelled	97.6	22	<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
91	<a href="#">c3nqoB</a>	Alignment	not modelled	97.6	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
92	<a href="#">c3cjinA</a>	Alignment	not modelled	97.6	12	<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
93	<a href="#">d2fxaa1</a>	Alignment	not modelled	97.6	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
94	<a href="#">c3f3xA</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family, putative; <b>PDBTitle:</b> crystal structure of the transcriptional regulator bldr from2 sulfolobus solfataricus
95	<a href="#">c2pexA</a>	Alignment	not modelled	97.6	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator ohrr; <b>PDBTitle:</b> structure of reduced c22s ohrr from xanthomonas campestris
96	<a href="#">d1s3ja</a>	Alignment	not modelled	97.6	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
97	<a href="#">c2h09A</a>	Alignment	not modelled	97.6	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
98	<a href="#">c2rdpA</a>	Alignment	not modelled	97.6	16	<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
99	<a href="#">c4mnuA</a>	Alignment	not modelled	97.5	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
100	<a href="#">c3g3zA</a>	Alignment	not modelled	97.5	14	<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
101	<a href="#">d2fbia1</a>	Alignment	not modelled	97.5	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
102	<a href="#">c3hrmA</a>	Alignment	not modelled	97.5	15	<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
103	<a href="#">c5aiqD_</a>	Alignment	not modelled	97.5	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
104	<a href="#">c4o6jA_</a>	Alignment	not modelled	97.5	13	<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
105	<a href="#">c5e1xA_</a>	Alignment	not modelled	97.5	18	<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
106	<a href="#">c4exlD_</a>	Alignment	not modelled	97.5	10	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> phosphate-binding protein psts 1; <b>PDBTitle:</b> crystal structure of phosphate abc transporter, periplasmic phosphate-2 binding protein psts 1 (pbp1) from streptococcus pneumoniae canada3 mdr_19a
107	<a href="#">c5hsmA_</a>	Alignment	not modelled	97.5	18	<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
108	<a href="#">c4yifE_</a>	Alignment	not modelled	97.5	18	<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
109	<a href="#">d1p4xa1</a>	Alignment	not modelled	97.5	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
110	<a href="#">c5eriA_</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> marr family transcriptional regulator; <b>PDBTitle:</b> marr protein from peptoclostridium difficile da00132
111	<a href="#">c3hruA_</a>	Alignment	not modelled	97.5	21	<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+
112	<a href="#">c2fxaB_</a>	Alignment	not modelled	97.5	12	<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.
113	<a href="#">c3bjaa_</a>	Alignment	not modelled	97.5	8	<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
114	<a href="#">c4jwoA_</a>	Alignment	not modelled	97.5	12	<b>PDB header:</b> phosphate binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate binding protein; <b>PDBTitle:</b> the crystal structure of a possible phosphate binding protein from2 planctomyces limnophilus dsm 3776
115	<a href="#">c5cviB_</a>	Alignment	not modelled	97.4	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> slor; <b>PDBTitle:</b> structure of the manganese regulator slor
116	<a href="#">c3k0lA_</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein; <b>PDBTitle:</b> crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
117	<a href="#">c5yhXH_</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> zinc transport transcriptional regulator; <b>PDBTitle:</b> structure of lactococcus lactis zittr, wild type
118	<a href="#">d2fbka1</a>	Alignment	not modelled	97.4	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
119	<a href="#">c3oopA_</a>	Alignment	not modelled	97.4	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
120	<a href="#">c5jlsA_</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adhesin competence repressor; <b>PDBTitle:</b> crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged)