


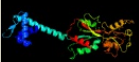




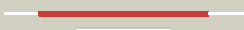













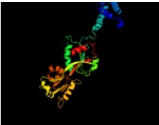










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2282c (-) _2554948_2555886
Date	Mon Aug 5 13:25:42 BST 2019
Unique Job ID	baafda92ca1ab55d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2esnC_	 Alignment		100.0	18	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa
2	c3fzjC_	 Alignment		100.0	19	PDB header: transcription regulator Chain: C: PDB Molecule: lysr type regulator of tsambcd; PDBTitle: tsar low resolution crystal structure, tetragonal form
3	c5y2vA_	 Alignment		100.0	22	PDB header: transcription Chain: A: PDB Molecule: rubisco operon transcriptional regulator; PDBTitle: strcutrue of the full-length ccmr complexed with 2-og from2 synechocystis pcc6803
4	c3hhgF_	 Alignment		100.0	19	PDB header: transcription regulator Chain: F: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
5	c6g4rE_	 Alignment		100.0	22	PDB header: transcription Chain: E: PDB Molecule: hydrogen peroxide-inducible genes activator; PDBTitle: corynebacterium glutamicum oxyr c206s mutant, h2o2-bound
6	c1iz1B_	 Alignment		100.0	20	PDB header: dna binding protein Chain: B: PDB Molecule: lysr-type regulatory protein; PDBTitle: crystal structure of cbnr, a lysr family transcriptional2 regulator
7	c3t1bB_	 Alignment		100.0	18	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: crystal structure of the full-length aphb n100e variant
8	c5y9sD_	 Alignment		100.0	21	PDB header: transcription Chain: D: PDB Molecule: vv2_1132; PDBTitle: crystal structure of vv2_1132, a lysr family transcriptional regulator
9	c3k1nB_	 Alignment		100.0	17	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of full-length benm
10	c3fzvC_	 Alignment		100.0	17	PDB header: transcription regulator Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of pa01 protein, putative lysr family2 transcriptional regulator from pseudomonas aeruginosa
11	c5ydwB_	 Alignment		100.0	16	PDB header: dna binding protein Chain: B: PDB Molecule: cell density-dependent motility repressor; PDBTitle: full-length structure of hypt from salmonella typhimuriuma2 (hypochlorite-specific lysr-type transcriptional regulator)

12	c5ae5A_	Alignment		100.0	16	PDB header: transcription Chain: A: PDB Molecule: lys-r-type regulatory protein; PDBTitle: structures of inactive and activated dntr provide conclusive evidence ² for the mechanism of action of lysr transcription factors
13	c3ispA_	Alignment		100.0	21	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator PDBTitle: crystal structure of argp from mycobacterium tuberculosis
14	c4x6gG_	Alignment		100.0	20	PDB header: dna binding protein Chain: G: PDB Molecule: oxyr; PDBTitle: full-length oxyr c199d from pseudomonas aeruginosa
15	c1b9nA_	Alignment		99.9	13	PDB header: transcription Chain: A: PDB Molecule: protein (mode); PDBTitle: regulator from escherichia coli
16	d2esna1	Alignment		99.9	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators
17	c5fo5A_	Alignment		99.9	25	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator metr; PDBTitle: structure of the dna-binding domain of escherichia coli methionine ² biosynthesis regulator metr
18	c5z4yB_	Alignment		99.9	21	PDB header: dna binding protein Chain: B: PDB Molecule: cys regulon transcriptional activator; PDBTitle: crystal structure of pacysb ntd domain with space group p4
19	c3m1eA_	Alignment		99.9	28	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd
20	d1b9ma1	Alignment		99.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: N-terminal domain of molybdate-dependent transcriptional regulator ModE
21	d1ixca1	Alignment	not modelled	99.8	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators
22	c5z50A_	Alignment	not modelled	99.8	16	PDB header: dna binding protein Chain: A: PDB Molecule: cys regulon transcriptional activator; PDBTitle: crystal structure of pacysb regulatory domain
23	c4pzjA_	Alignment	not modelled	99.8	33	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: 1.60 angstrom resolution crystal structure of a transcriptional ² regulator of the lysr family from eggerthella lenta dsm 2243
24	c5b70B_	Alignment	not modelled	99.8	16	PDB header: transcription Chain: B: PDB Molecule: lys-r family transcriptional regulator; PDBTitle: oxyr ² e204g regulatory domain from vibrio vulnificus
25	c2hxrA_	Alignment	not modelled	99.8	16	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator cynr; PDBTitle: structure of the ligand binding domain of e. coli cynr, a ² transcriptional regulator controlling cyanate metabolism
26	c3oxnD_	Alignment	not modelled	99.8	14	PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator, lysr family; PDBTitle: the crystal structure of a putative transcriptional regulator from ² vibrio parahaemolyticus
27	c5y2wA_	Alignment	not modelled	99.8	21	PDB header: transcription Chain: A: PDB Molecule: rubisco operon transcriptional regulator; PDBTitle: structure of synechocystis pcc6803 cmr regulatory domain in complex ² with 2-pg
28	d1al3a_	Alignment	not modelled	99.8	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like PDB header: transcription regulation

29	c1a13A_	Alignment	not modelled	99.8	17	Chain: A: PDB Molecule: cys regulon transcriptional activator cysb; PDBTitle: cofactor binding fragment of cysb from klebsiella aerogenes
30	c4rnsA_	Alignment	not modelled	99.7	13	PDB header: transcription Chain: A: PDB Molecule: pcp degradation transcriptional activation protein; PDBTitle: pcpr inducer binding domain (apo-form)
31	d1lutha_	Alignment	not modelled	99.7	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
32	c5tpiA_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: putative transcriptional regulator (lysr family); PDBTitle: 1.47 angstrom crystal structure of the c-terminal substrate binding2 domain of lysr family transcriptional regulator from klebsiella3 pneumoniae.
33	d2fyia1	Alignment	not modelled	99.7	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
34	c3fd3A_	Alignment	not modelled	99.7	17	PDB header: transcription regulator Chain: A: PDB Molecule: chromosome replication initiation inhibitor protein; PDBTitle: structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
35	c2ijlB_	Alignment	not modelled	99.7	20	PDB header: transcription Chain: B: PDB Molecule: molybdenum-binding transcriptional repressor; PDBTitle: the structure of a putative mode from agrobacterium tumefaciens.
36	c2uyeA_	Alignment	not modelled	99.7	13	PDB header: transcription Chain: A: PDB Molecule: regulatory protein; PDBTitle: double mutant y110s,f111v dntr from burkholderia sp. strain2 dnt in complex with thiocyanate
37	c5z49A_	Alignment	not modelled	99.7	24	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator cmprr; PDBTitle: crystal structure of the effector-binding domain of synechococcus2 elongatus cmprr in complex with ribulose-1,5-bisphosphate
38	c3jv9B_	Alignment	not modelled	99.7	19	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: the structure of a reduced form of oxyr from n. meningitidis
39	c5tedA_	Alignment	not modelled	99.7	14	PDB header: transcription Chain: A: PDB Molecule: lmo0488 protein; PDBTitle: effector binding domain of quir in complex with shikimate
40	c2ql3G_	Alignment	not modelled	99.7	16	PDB header: transcription Chain: G: PDB Molecule: probable transcriptional regulator, lysr family protein; PDBTitle: crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
41	c3ho7A_	Alignment	not modelled	99.7	15	PDB header: transcription Chain: A: PDB Molecule: oxyr; PDBTitle: crystal structure of oxyr from porphyromonas gingivalis
42	c3n6uA_	Alignment	not modelled	99.7	14	PDB header: transcription regulator Chain: A: PDB Molecule: lysr type regulator of tsambcd; PDBTitle: effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
43	c2h9qC_	Alignment	not modelled	99.7	15	PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: crystal structure of the effector binding domain of a catm2 variant (r156h)
44	d1i6aa_	Alignment	not modelled	99.7	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
45	d2esna2	Alignment	not modelled	99.7	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
46	c4ab6A_	Alignment	not modelled	99.7	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: regulatory domain structure of nmb2055 (metr), c103s c106s mutant, a2 lysr family regulator from n. meningitidis
47	d1ixca2	Alignment	not modelled	99.7	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
48	c2f7cA_	Alignment	not modelled	99.7	14	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: catm effector binding domain with its effector cis,cis-muconate
49	c3kosA_	Alignment	not modelled	99.6	13	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator ampr; PDBTitle: structure of the ampr effector binding domain from citrobacter2 freundii
50	c4jvcA_	Alignment	not modelled	99.6	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator mvfr; PDBTitle: crystal structure of pqsr co-inducer binding domain
51	c2h9bB_	Alignment	not modelled	99.6	14	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
52	c3mz1D_	Alignment	not modelled	99.6	12	PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: the crystal structure of a possible transcription regulator protein2 from sinorhizobium meliloti 1021
53	c2f78A_	Alignment	not modelled	99.6	13	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: benm effector binding domain with its effector benzoate PDB header: transcription

54	c5z72B_	Alignment	not modelled	99.6	11	Chain: B; PDB Molecule: ccpc; PDBTitle: crystal structure of ccpc regulatory domain in complex with citrate2 from bacillus amyloliquefaciens
55	c5vvhE_	Alignment	not modelled	99.6	20	PDB header: transcription Chain: E; PDB Molecule: octopine catabolism/uptake operon regulatory protein occr; PDBTitle: crystal structure of the effector binding domain of lysr-type2 transcriptional regulator, occr from agrobacterium tumefaciens
56	c3hfhB_	Alignment	not modelled	99.6	14	PDB header: transcription regulator Chain: B; PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga regulatory domain, a lysr-type transcriptional2 regulator from neisseria meningitidis.
57	c4qbaB_	Alignment	not modelled	99.5	13	PDB header: transcription regulator Chain: B; PDB Molecule: lysr family regulatory protein; PDBTitle: crystal structure of the effector-binding domain of s. aureus ccpe
58	c6gz1A_	Alignment	not modelled	99.4	8	PDB header: transcription Chain: A; PDB Molecule: hth-type transcriptional regulator leuo; PDBTitle: crystal structure of the leuo effector binding domain
59	c5mmhD_	Alignment	not modelled	99.4	15	PDB header: transcription Chain: D; PDB Molecule: hth-type transcriptional activator ampr; PDBTitle: the x-ray structure of the effector domain of the transcriptional2 regulator ampr of pseudomonas aeruginosa
60	c2qsxB_	Alignment	not modelled	99.4	10	PDB header: transcription Chain: B; PDB Molecule: putative transcriptional regulator, lysr family; PDBTitle: crystal structure of putative transcriptional regulator lysr from2 vibrio parahaemolyticus
61	c5yezD_	Alignment	not modelled	99.3	19	PDB header: dna binding protein Chain: D; PDB Molecule: cell density-dependent motility repressor; PDBTitle: regulatory domain of hypt m206q mutant from salmonella typhimurium
62	c3onmB_	Alignment	not modelled	99.1	16	PDB header: transcription Chain: B; PDB Molecule: transcriptional regulator lrha; PDBTitle: effector binding domain of lysr-type transcription factor rovm from y.2 pseudotuberculosis
63	c2x4hA_	Alignment	not modelled	98.1	14	PDB header: transcription Chain: A; PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
64	c3boqB_	Alignment	not modelled	98.0	21	PDB header: transcription regulator Chain: B; PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
65	c3ctaA_	Alignment	not modelled	97.9	22	PDB header: transferase Chain: A; PDB Molecule: riboflavin kinase; PDBTitle: crystal structure of riboflavin kinase from thermoplasma acidophilum
66	d2fbha1	Alignment	not modelled	97.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
67	c2gxgA_	Alignment	not modelled	97.7	15	PDB header: transcription Chain: A; PDB Molecule: 146aa long hypothetical transcriptional regulator; PDBTitle: crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
68	c3bpxB_	Alignment	not modelled	97.7	13	PDB header: transcription regulator Chain: B; PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of marr
69	c3nrvC_	Alignment	not modelled	97.7	23	PDB header: transcription regulator Chain: C; PDB Molecule: putative transcriptional regulator (marr/emrr family); PDBTitle: crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
70	c4xrfA_	Alignment	not modelled	97.7	15	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of mepr like protein complexed with pseudoligands
71	c5zc2B_	Alignment	not modelled	97.6	16	PDB header: flavoprotein Chain: B; PDB Molecule: p-hydroxyphenylacetate 3-hydroxylase, reductase component; PDBTitle: acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
72	c2nyxB_	Alignment	not modelled	97.6	17	PDB header: transcription Chain: B; PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis
73	c2nnnB_	Alignment	not modelled	97.6	14	PDB header: transcription Chain: B; PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
74	c3hruA_	Alignment	not modelled	97.6	18	PDB header: transcription Chain: A; PDB Molecule: metalloregulator scar; PDBTitle: crystal structure of scar with bound zn2+
75	c2h09A_	Alignment	not modelled	97.6	18	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
76	d1lj9a_	Alignment	not modelled	97.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
77	c3g3zA_	Alignment	not modelled	97.6	21	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
78	d1lnwa_	Alignment	not modelled	97.6	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain

				Family:MarR-like transcriptional regulators		
79	d2fxaa1	Alignment	not modelled	97.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
80	d1jgsa	Alignment	not modelled	97.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
81	d2hr3a1	Alignment	not modelled	97.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
82	d2bv6a1	Alignment	not modelled	97.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
83	c5eriA	Alignment	not modelled	97.5	14	PDB header: transcription Chain: A: PDB Molecule: marr family transcriptional regulator; PDBTitle: marr protein from peptoclostridium difficile da00132
84	c3f3xA	Alignment	not modelled	97.5	28	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of the transcriptional regulator bldr from2 sulfobolus solfataricus
85	c3e6mD	Alignment	not modelled	97.5	16	PDB header: transcription regulator Chain: D: PDB Molecule: marr family transcriptional regulator; PDBTitle: the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
86	c3ecoB	Alignment	not modelled	97.5	20	PDB header: transcription Chain: B: PDB Molecule: mepr; PDBTitle: crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
87	c5yhxB	Alignment	not modelled	97.5	22	PDB header: metal binding protein Chain: H: PDB Molecule: zinc transport transcriptional regulator; PDBTitle: structure of lactococcus lactis zitri, wild type
88	c2fxaB	Alignment	not modelled	97.5	13	PDB header: transcription Chain: B: PDB Molecule: protease production regulatory protein hpr; PDBTitle: structure of the protease production regulatory protein hpr from2 bacillus subtilis.
89	c3nqoB	Alignment	not modelled	97.5	21	PDB header: transcription Chain: B: PDB Molecule: marr-family transcriptional regulator; PDBTitle: crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
90	c4mnuA	Alignment	not modelled	97.5	19	PDB header: transcription regulator Chain: A: PDB Molecule: slya-like transcription regulator; PDBTitle: crystal structure of uncharacterized slya-like transcription regulator2 from listeria monocytogenes
91	c6jxB	Alignment	not modelled	97.5	18	PDB header: transcription/dna Chain: B: PDB Molecule: fatty acid biosynthesis transcriptional regulator; PDBTitle: crystal structure of streptococcus pneumoniae fabt in complex with dna
92	c3fm5D	Alignment	not modelled	97.5	16	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of transcriptional regulator (marr family)2 from rhodococcus sp. rha1
93	c2fa5B	Alignment	not modelled	97.5	25	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator marr/emrr family; PDBTitle: the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
94	c5cviB	Alignment	not modelled	97.5	17	PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor
95	c4o6jA	Alignment	not modelled	97.5	18	PDB header: metal binding protein Chain: A: PDB Molecule: iron-dependent transcription repressor related protein; PDBTitle: crystal structure of t. acidophilum ider
96	c4fhtA	Alignment	not modelled	97.5	11	PDB header: transcription Chain: A: PDB Molecule: pcav transcriptional regulator; PDBTitle: crystal structure of the pcav transcriptional regulator from2 streptomyces coelicolor in complex with its natural ligand
97	c3cdhB	Alignment	not modelled	97.5	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of the marr family transcriptional regulator spo14532 from silicibacter pomeroyi dss-3
98	d1s3ja	Alignment	not modelled	97.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
99	c1f5tA	Alignment	not modelled	97.5	24	PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
100	d2etha1	Alignment	not modelled	97.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
101	d1ub9a	Alignment	not modelled	97.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
102	c2rdaA	Alignment	not modelled	97.4	15	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator marr; PDBTitle: the structure of a marr family protein from bacillus2 stearothermophilus
103	c5e1xA	Alignment	not modelled	97.4	23	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of the organohalide sensing rdhr-cbdba16252 transcriptional regulator in the 3,4-dichlorophenol bound form
						PDB header: transcription regulator

104	c2pexA	Alignment	not modelled	97.4	20	Chain: A: PDB Molecule: transcriptional regulator ohrr; PDBTitle: structure of reduced c22s ohrr from xanthamonas campestris
105	c4yifE	Alignment	not modelled	97.4	17	PDB header: dna binding protein Chain: E: PDB Molecule: marr family protein rv0880; PDBTitle: crystal structure of rv0880
106	d1p4xa1	Alignment	not modelled	97.4	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
107	d3broa1	Alignment	not modelled	97.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
108	c3cjnA	Alignment	not modelled	97.4	19	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
109	c1fx7C	Alignment	not modelled	97.3	21	PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis
110	c3bjaA	Alignment	not modelled	97.3	12	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
111	c5jlsA	Alignment	not modelled	97.3	18	PDB header: transcription Chain: A: PDB Molecule: adhesin competence repressor; PDBTitle: crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged)
112	c5aiqD	Alignment	not modelled	97.3	16	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of ligand-free nadr
113	c3k0A	Alignment	not modelled	97.3	19	PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
114	d2fbka1	Alignment	not modelled	97.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
115	c2it0A	Alignment	not modelled	97.2	24	PDB header: transcription/dna Chain: A: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex crystal2 form ii
116	c1g3wA	Alignment	not modelled	97.2	27	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
117	c4em1A	Alignment	not modelled	97.2	14	PDB header: transcription Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator sar2349; PDBTitle: staphylococcus aureus marr native
118	c5hsmA	Alignment	not modelled	97.2	26	PDB header: transcription Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator rv2887; PDBTitle: crystal structure of mycobacterium tuberculosis marr family protein2 rv2887
119	c3hrmA	Alignment	not modelled	97.2	15	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator sarz; PDBTitle: crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form
120	d2fbia1	Alignment	not modelled	97.2	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators