





















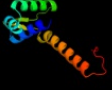










#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ispA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator <b>PDBTitle:</b> crystal structure of argp from mycobacterium tuberculosis
2	<a href="#">c3hhgF_</a>	 Alignment		100.0	15	<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.
3	<a href="#">c2esnC_</a>	 Alignment		100.0	16	<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="#">c1iz1B_</a>	 Alignment		100.0	12	<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
5	<a href="#">c3t1bB_</a>	 Alignment		100.0	11	<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="#">c3fzjC_</a>	 Alignment		100.0	15	<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
7	<a href="#">c3fzvC_</a>	 Alignment		100.0	17	<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
8	<a href="#">c1b9nA_</a>	 Alignment		99.9	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein (mode); <b>PDBTitle:</b> regulator from escherichia coli
9	<a href="#">c3fd3A_</a>	 Alignment		99.9	30	<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.
10	<a href="#">d2esna1</a>	 Alignment		99.9	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LysR-like transcriptional regulators
11	<a href="#">c3m1eA_</a>	 Alignment		99.8	27	<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

12	<a href="#">dlb9ma1</a>	Alignment		99.8	15	<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
13	<a href="#">dlixca1</a>	Alignment		99.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LysR-like transcriptional regulators
14	<a href="#">c2ijlB_</a>	Alignment		99.7	17	<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.
15	<a href="#">c3oxnD_</a>	Alignment		99.7	11	<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
16	<a href="#">c2hxrA_</a>	Alignment		99.7	16	<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
17	<a href="#">d2fyia1</a>	Alignment		99.7	13	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
18	<a href="#">dlutha_</a>	Alignment		99.7	8	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
19	<a href="#">c2uyeA_</a>	Alignment		99.7	8	<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
20	<a href="#">dlal3a_</a>	Alignment		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
21	<a href="#">c1al3A_</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
22	<a href="#">c2h9qC_</a>	Alignment	not modelled	99.6	12	<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)
23	<a href="#">c2ql3G_</a>	Alignment	not modelled	99.6	15	<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
24	<a href="#">c3kosA_</a>	Alignment	not modelled	99.6	15	<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
25	<a href="#">c3jv9B_</a>	Alignment	not modelled	99.6	14	<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
26	<a href="#">dlixca2</a>	Alignment	not modelled	99.6	9	<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="#">c3hhfB_</a>	Alignment	not modelled	99.6	16	<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.
28	<a href="#">d2esna2</a>	Alignment	not modelled	99.6	10	<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="#">c2f7cA_</a>	Alignment	not modelled	99.6	12	<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
30	<a href="#">c3ho7A_</a>	Alignment	not modelled	99.6	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
31	<a href="#">d1i6aa_</a>	Alignment	not modelled	99.6	11	<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="#">c2h9bB_</a>	Alignment	not modelled	99.5	12	<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)
33	<a href="#">c3n6uA_</a>	Alignment	not modelled	99.5	11	<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
34	<a href="#">c2f78A_</a>	Alignment	not modelled	99.5	12	<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
35	<a href="#">c3mz1D_</a>	Alignment	not modelled	99.4	16	<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
36	<a href="#">c3onmB_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator lrrha; <b>PDBTitle:</b> effector binding domain of lysr-type transcription factor rovm from y.2 pseudotuberculosis
37	<a href="#">c2qsxB_</a>	Alignment	not modelled	98.9	13	<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
38	<a href="#">c3ctaA_</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase; <b>PDBTitle:</b> crystal structure of riboflavin kinase from thermoplasma2 acidophilum
39	<a href="#">c2x4hA_</a>	Alignment	not modelled	97.4	17	<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
40	<a href="#">c3boqB_</a>	Alignment	not modelled	97.3	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 from2 silicibacter pomeroyi
41	<a href="#">c2fa5B_</a>	Alignment	not modelled	97.0	10	<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
42	<a href="#">c3onqB_</a>	Alignment	not modelled	96.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> regulator of polyketide synthase expression; <b>PDBTitle:</b> crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
43	<a href="#">c3nrvC_</a>	Alignment	not modelled	96.9	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 from2 acinetobacter sp. adp1
44	<a href="#">c2nyxB_</a>	Alignment	not modelled	96.8	10	<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
45	<a href="#">d2fbha1</a>	Alignment	not modelled	96.8	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
46	<a href="#">c3bpxB_</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
47	<a href="#">d1jgsa_</a>	Alignment	not modelled	96.6	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
48	<a href="#">c2h09A_</a>	Alignment	not modelled	96.5	24	<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
49	<a href="#">d1lnwa_</a>	Alignment	not modelled	96.5	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
50	<a href="#">d2fxaa1</a>	Alignment	not modelled	96.5	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
51	<a href="#">c2gxgA_</a>	Alignment	not modelled	96.5	19	<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
52	<a href="#">c3fm5D_</a>	Alignment	not modelled	96.5	15	<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
53	<a href="#">d1ub9a_</a>	Alignment	not modelled	96.5	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
54	<a href="#">c3cdhB</a>	Alignment	not modelled	96.5	11	<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
55	<a href="#">d2hr3a1</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> MarR-like transcriptional regulators
56	<a href="#">d1lj9a</a>	Alignment	not modelled	96.3	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
57	<a href="#">c2fxaB</a>	Alignment	not modelled	96.3	10	<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.
58	<a href="#">c3f3xA</a>	Alignment	not modelled	96.3	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 bldr2 from sulfobolus solfataricus
59	<a href="#">d2bv6a1</a>	Alignment	not modelled	96.3	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
60	<a href="#">c3e6mD</a>	Alignment	not modelled	96.3	15	<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.
61	<a href="#">d1s3ja</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
62	<a href="#">d1p4xa1</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
63	<a href="#">c2zkzC</a>	Alignment	not modelled	96.2	13	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional repressor pagr; <b>PDBTitle:</b> crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
64	<a href="#">c2dbbA</a>	Alignment	not modelled	96.0	23	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph0061; <b>PDBTitle:</b> crystal structure of ph0061
65	<a href="#">c3hrmA</a>	Alignment	not modelled	96.0	19	<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
66	<a href="#">c3cuoB</a>	Alignment	not modelled	96.0	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
67	<a href="#">d2frha1</a>	Alignment	not modelled	96.0	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
68	<a href="#">c2nnnB</a>	Alignment	not modelled	95.9	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 from2 pseudomonas aeruginosa
69	<a href="#">c3bddD</a>	Alignment	not modelled	95.9	25	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein marr; <b>PDBTitle:</b> crystal structure of a putative multiple antibiotic-resistance2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution
70	<a href="#">c2pexA</a>	Alignment	not modelled	95.9	13	<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
71	<a href="#">d3deva1</a>	Alignment	not modelled	95.9	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
72	<a href="#">c2kkoB</a>	Alignment	not modelled	95.9	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulatory protein <b>PDBTitle:</b> solution nmr structure of the homodimeric winged helix-turn-2 helix dna-binding domain (fragment 1-100) mb0332 from3 mycobacterium bovis, a possible arsr-family transcriptional4 regulator. northeast structural genomics consortium target5 mbr242e.
73	<a href="#">d2fbka1</a>	Alignment	not modelled	95.9	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
74	<a href="#">d3ctaa1</a>	Alignment	not modelled	95.8	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
75	<a href="#">c3nqoB</a>	Alignment	not modelled	95.8	13	<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
76	<a href="#">c2pijB</a>	Alignment	not modelled	95.8	27	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> prophage pfl 6 cro; <b>PDBTitle:</b> structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
77	<a href="#">c3cjnA</a>	Alignment	not modelled	95.7	10	<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
78	<a href="#">c3jthA_</a>	Alignment	not modelled	95.7	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription activator hlyu; <b>PDBTitle:</b> crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
79	<a href="#">c2ia0A_</a>	Alignment	not modelled	95.7	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator pf0864; <b>PDBTitle:</b> transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
80	<a href="#">c3bjaA_</a>	Alignment	not modelled	95.7	5	<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
81	<a href="#">c3g3zA_</a>	Alignment	not modelled	95.7	19	<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
82	<a href="#">c2oqgA_</a>	Alignment	not modelled	95.7	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> arsr-like transcriptional regulator from rhodococcus sp. rha1
83	<a href="#">d1d1la_</a>	Alignment	not modelled	95.7	32	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
84	<a href="#">c2e1cA_</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
85	<a href="#">c2rdpA_</a>	Alignment	not modelled	95.6	11	<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
86	<a href="#">d1u2wa1</a>	Alignment	not modelled	95.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
87	<a href="#">c3ecoB_</a>	Alignment	not modelled	95.6	20	<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
88	<a href="#">d2cg4a1</a>	Alignment	not modelled	95.6	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
89	<a href="#">d4croa_</a>	Alignment	not modelled	95.5	32	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
90	<a href="#">c1ilgA_</a>	Alignment	not modelled	95.5	34	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrpA; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
91	<a href="#">d1ilga1</a>	Alignment	not modelled	95.5	34	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
92	<a href="#">c2e7xA_</a>	Alignment	not modelled	95.5	32	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
93	<a href="#">d2cyya1</a>	Alignment	not modelled	95.4	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
94	<a href="#">d1sfxa_</a>	Alignment	not modelled	95.4	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
95	<a href="#">c3hruA_</a>	Alignment	not modelled	95.4	20	<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+
96	<a href="#">d1rlua_</a>	Alignment	not modelled	95.4	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
97	<a href="#">c2cg4B_</a>	Alignment	not modelled	95.4	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
98	<a href="#">c1g3wA_</a>	Alignment	not modelled	95.4	22	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtxr
99	<a href="#">c2vbzA_</a>	Alignment	not modelled	95.2	25	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
100	<a href="#">c1zljE_</a>	Alignment	not modelled	95.2	10	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
101	<a href="#">d1p4xa2</a>	Alignment	not modelled	95.2	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
102	<a href="#">d2d1ha1</a>	Alignment	not modelled	95.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like



103	<a href="#">c2wteB</a>	Alignment	not modelled	95.2	14	<b>PDB header:</b> antiviral protein <b>Chain:</b> B: <b>PDB Molecule:</b> csa3; <b>PDBTitle:</b> the structure of the crispr-associated protein, csa3, from2 sulfobolus solfataricus at 1.8 angstrom resolution.
104	<a href="#">c1f5tA</a>	Alignment	not modelled	95.1	20	<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
105	<a href="#">c3oopA</a>	Alignment	not modelled	95.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2960 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from listeria innocua2 clip11262
106	<a href="#">d1g2ha</a>	Alignment	not modelled	95.1	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
107	<a href="#">c3s2wB</a>	Alignment	not modelled	95.1	21	<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 maezi go1
108	<a href="#">d1ntca</a>	Alignment	not modelled	95.1	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
109	<a href="#">d2fbia1</a>	Alignment	not modelled	95.1	9	<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="#">c2cfxD</a>	Alignment	not modelled	95.1	20	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrpC; <b>PDBTitle:</b> structure of b.subtilis lrpC
111	<a href="#">d1biaa1</a>	Alignment	not modelled	95.0	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
112	<a href="#">d3orca</a>	Alignment	not modelled	95.0	32	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
113	<a href="#">c2gqgB</a>	Alignment	not modelled	95.0	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> leucine-responsive regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
114	<a href="#">c3f6vA</a>	Alignment	not modelled	94.9	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family <b>PDBTitle:</b> crystal structure of possible transcriptional regulator for2 arsenical resistance
115	<a href="#">c2l4aA</a>	Alignment	not modelled	94.9	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> leucine responsive regulatory protein; <b>PDBTitle:</b> nmr structure of the dna-binding domain of e.coli lrp
116	<a href="#">d2cfxa1</a>	Alignment	not modelled	94.8	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
117	<a href="#">c1r22B</a>	Alignment	not modelled	94.8	33	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor smtb; <b>PDBTitle:</b> crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
118	<a href="#">c3f6oB</a>	Alignment	not modelled	94.8	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator, arsr family <b>PDBTitle:</b> crystal structure of arsr family transcriptional regulator,2 rha00566
119	<a href="#">c3k0lA</a>	Alignment	not modelled	94.8	15	<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
120	<a href="#">c3kp3B</a>	Alignment	not modelled	94.8	16	<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