Phyre^2

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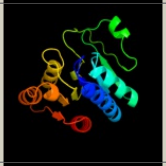
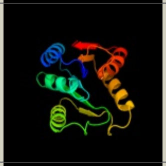
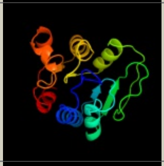
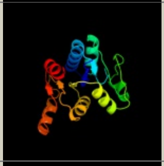
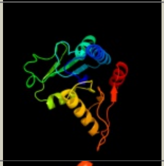
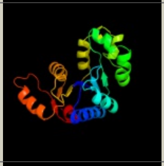
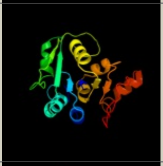
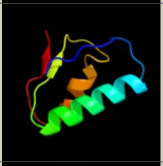
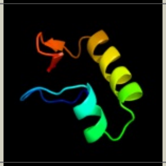
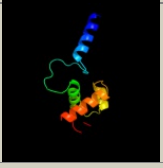
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3majA_	Alignment		100.0	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna processing chain a; **PDBTitle:** crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
2	c2iz6A_	Alignment		99.9	22	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein; **PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein
3	d2nx2a1	Alignment		99.9	15	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**YpsA-like
4	d1weka_	Alignment		99.9	23	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
5	c1rcuB_	Alignment		99.9	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein vt76; **PDBTitle:** x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
6	d1rcua_	Alignment		99.9	17	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
7	c3sbxC_	Alignment		99.8	15	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium marinum bound to adenosine 5'-monophosphate amp
8	d1weha_	Alignment		99.7	18	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
9	c3quaA_	Alignment		99.7	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein and possible2 molybdenum cofactor protein from mycobacterium smegmatis
10	d1t35a_	Alignment		98.6	20	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
11	c2q4oA_	Alignment		98.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein at2g37210/t2n18.3; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210

12	d2q4oa1	Alignment		98.6	16	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
13	d1ydha_	Alignment		98.4	14	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
14	c2q4dB_	Alignment		98.3	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
15	c3imkA_	Alignment		97.1	24	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative molybdenum carrier protein; **PDBTitle:** crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
16	c3bq9A_	Alignment		96.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain- **PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
17	d1mkma1	Alignment		96.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
18	c3gh1A_	Alignment		96.3	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted nucleotide-binding protein; **PDBTitle:** crystal structure of predicted nucleotide-binding protein from vibrio2 cholerae
19	c1mkmA_	Alignment		96.2	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iclr transcriptional regulator; **PDBTitle:** crystal structure of the thermotoga maritima iclr
20	c3tgnA_	Alignment		96.2	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**adc operon repressor adcr; **PDBTitle:** crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
21	d1ku9a_	Alignment	not modelled	95.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
22	c2g7uB_	Alignment	not modelled	95.9	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
23	d1tw3a1	Alignment	not modelled	95.9	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Plant O-methyltransferase, N-terminal domain
24	d2d1ha1	Alignment	not modelled	95.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
25	d1sfxa_	Alignment	not modelled	95.7	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
26	c2it0A_	Alignment	not modelled	95.7	18	**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
27	c3r0aB_	Alignment	not modelled	95.7	10	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
28	c2gxgA_	Alignment	not modelled	95.5	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

29	d2p4wa1	Alignment	not modelled	95.4	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF1790-like
30	c1f5tA_	Alignment	not modelled	95.4	18	**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
31	c2o0yB_	Alignment	not modelled	95.2	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
32	d2dk5a1	Alignment	not modelled	95.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RPO3F domain-like
33	c3i53A_	Alignment	not modelled	95.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o-methyltransferase; **PDBTitle:** crystal structure of an o-methyltransferase (ncsb1) from2 neocarzinostatin biosynthesis in complex with s-adenosyl-l-3 homocysteine (sah)
34	c3r4kD_	Alignment	not modelled	95.1	23	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**transcriptional regulator, iclr family; **PDBTitle:** crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
35	c3bj6B_	Alignment	not modelled	95.1	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
36	d1jhfa1	Alignment	not modelled	95.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
37	d1lnwa_	Alignment	not modelled	95.0	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
38	c2h09A_	Alignment	not modelled	95.0	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
39	c2xroE_	Alignment	not modelled	95.0	22	**PDB header:**dna-binding protein/dna **Chain:** E: **PDB Molecule:**hth-type transcriptional regulator ttgv; **PDBTitle:** crystal structure of ttgv in complex with its dna operator
40	d2hr3a1	Alignment	not modelled	95.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
41	c2ip2B_	Alignment	not modelled	95.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable phenazine-specific methyltransferase; **PDBTitle:** structure of the pyocyanin biosynthetic protein phzm
42	d1okra_	Alignment	not modelled	94.9	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
43	c3kp3B_	Alignment	not modelled	94.9	16	**PDB header:**transcription regulator/antibiotic **Chain:** B: **PDB Molecule:**transcriptional regulator tcar; **PDBTitle:** staphylococcus epidermidis in complex with ampicillin
44	c2x4hA_	Alignment	not modelled	94.9	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
45	d1j5ya1	Alignment	not modelled	94.8	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
46	c1fx7C_	Alignment	not modelled	94.8	17	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
47	c3pqkD_	Alignment	not modelled	94.8	18	**PDB header:**transcription **Chain:** D: **PDB Molecule:**biofilm growth-associated repressor; **PDBTitle:** crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
48	c2wteB_	Alignment	not modelled	94.8	15	**PDB header:**antiviral protein **Chain:** B: **PDB Molecule:**csa3; **PDBTitle:** the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
49	d1r1ta_	Alignment	not modelled	94.8	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
50	c2rdpA_	Alignment	not modelled	94.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator marr; **PDBTitle:** the structure of a marr family protein from bacillus2 stearothermophilus
51	d1dgsa1	Alignment	not modelled	94.7	10	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
52	c1tw3A_	Alignment	not modelled	94.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carminomycin 4-o-methyltransferase; **PDBTitle:** crystal structure of carminomycin-4-o-methyltransferase2 (dnrk) in complex with s-adenosyl-l-homocystein (sah) and3 4-methoxy-e-rhodomycin t (m-et)
53	c3hruA_	Alignment	not modelled	94.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
54	c3g3zA_	Alignment	not modelled	94.6	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis

55	d3broa1	Alignment	not modelled	94.6	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
56	d1biaa1	Alignment	not modelled	94.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
57	c2l4aA_	Alignment	not modelled	94.5	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
58	c1r22B_	Alignment	not modelled	94.2	17	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**transcriptional repressor smtb; **PDBTitle:** crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
59	d1x2ia1	Alignment	not modelled	94.1	7	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
60	c2kkoB_	Alignment	not modelled	94.1	17	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**possible transcriptional regulatory protein **PDBTitle:** 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.
61	c3jthA_	Alignment	not modelled	94.1	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
62	d2fxaa1	Alignment	not modelled	94.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
63	c2fa5B_	Alignment	not modelled	94.0	16	**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
64	d2a61a1	Alignment	not modelled	94.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
65	c3nqoB_	Alignment	not modelled	94.0	15	**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
66	c3bpxB_	Alignment	not modelled	93.9	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of marr
67	d1qzza1	Alignment	not modelled	93.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Plant O-methyltransferase, N-terminal domain
68	c3cuoB_	Alignment	not modelled	93.9	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
69	c3f6oB_	Alignment	not modelled	93.8	21	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
70	c2qwwB_	Alignment	not modelled	93.8	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
71	d2bgwa1	Alignment	not modelled	93.8	11	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
72	c1kftA_	Alignment	not modelled	93.8	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc subunit c; **PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli
73	d1kfta_	Alignment	not modelled	93.8	9	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
74	c2oqgA_	Alignment	not modelled	93.8	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
75	c1x1aA_	Alignment	not modelled	93.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**crtf-related protein; **PDBTitle:** crystal structure of bchu complexed with s-adenosyl-l-methionine
76	d2cyya1	Alignment	not modelled	93.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
77	d1s3ja_	Alignment	not modelled	93.7	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
78	c2nyxB_	Alignment	not modelled	93.7	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis

79	c3cjnA_	Alignment	not modelled	93.7	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
80	c2jscB_	Alignment	not modelled	93.6	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator rv1994c/mt2050; **PDBTitle:** nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
81	d1sd4a_	Alignment	not modelled	93.6	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
82	d2cfxa1	Alignment	not modelled	93.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
83	d2cg4a1	Alignment	not modelled	93.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
84	c3f3xA_	Alignment	not modelled	93.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of the transcriptional regulator bldr2 from sulfolobus solfataricus
85	c3nrvC_	Alignment	not modelled	93.6	12	**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
86	c3oopA_	Alignment	not modelled	93.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2960 protein; **PDBTitle:** the structure of a protein with unknown function from listeria innocua2 clip11262
87	d2fbia1	Alignment	not modelled	93.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
88	d2fbha1	Alignment	not modelled	93.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
89	c2nnnB_	Alignment	not modelled	93.5	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
90	c3mq0A_	Alignment	not modelled	93.4	17	**PDB header:**transcription repressor **Chain:** A: **PDB Molecule:**transcriptional repressor of the blcabc operon; **PDBTitle:** crystal structure of agobacterium tumefaciens repressor blcr
91	c3f6vA_	Alignment	not modelled	93.4	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance
92	c3hrmA_	Alignment	not modelled	93.4	18	**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
93	c2r3sA_	Alignment	not modelled	93.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative o-methyltransferase (npun_r0239) from2 nostoc punctiforme pcc 73102 at 2.15 a resolution
94	d2frha1	Alignment	not modelled	93.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
95	c2qufB_	Alignment	not modelled	93.2	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor pf0095; **PDBTitle:** crystal structure of transcription factor axxa-pf0095 from pyrococcus2 furiosus
96	c3bjaA_	Alignment	not modelled	93.2	10	**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
97	c3bddD_	Alignment	not modelled	93.2	22	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein marr; **PDBTitle:** crystal structure of a putative multiple antibiotic-resistance2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution
98	d1ulya_	Alignment	not modelled	93.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein PH1932
99	d1p4xa2	Alignment	not modelled	93.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
100	d1r1ua_	Alignment	not modelled	93.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
101	c2fxaB_	Alignment	not modelled	93.1	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.
102	c3k0lA_	Alignment	not modelled	93.0	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**repressor protein; **PDBTitle:** crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp

103	d2bv6a1	Alignment	not modelled	93.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
104	d1stza1	Alignment	not modelled	92.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
105	c3lstB_	Alignment	not modelled	92.9	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calo1 methyltransferase; **PDBTitle:** crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form
106	c1g3wA_	Alignment	not modelled	92.8	16	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
107	d1i1ga1	Alignment	not modelled	92.8	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
108	d1p6ra_	Alignment	not modelled	92.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
109	d2isya1	Alignment	not modelled	92.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
110	c3e6mD_	Alignment	not modelled	92.4	15	**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.
111	d2etha1	Alignment	not modelled	92.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
112	d1z6ra1	Alignment	not modelled	92.2	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
113	c3cdhB_	Alignment	not modelled	92.0	16	**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
114	d2aq0a1	Alignment	not modelled	91.9	9	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
115	c2k4bA_	Alignment	not modelled	91.9	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** copr repressor structure
116	d1ub9a_	Alignment	not modelled	91.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
117	c2vbzA_	Alignment	not modelled	91.8	23	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
118	d3ctaa1	Alignment	not modelled	91.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
119	d1g3wa1	Alignment	not modelled	91.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
120	d1lj9a_	Alignment	not modelled	91.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators