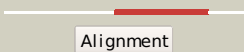

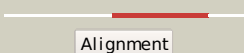









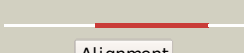
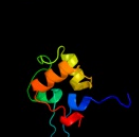
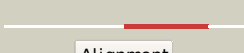



















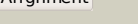



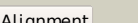

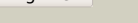



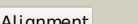
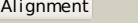
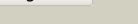



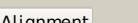

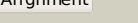



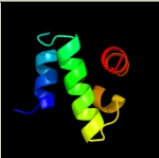


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ebyA_	 Alignment		99.5	23	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
2	c3trbA_	 Alignment		99.4	22	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
3	c3cecA_	 Alignment		99.4	25	PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system; PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
4	d2icta1	 Alignment		99.4	31	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
5	c3bs3A_	 Alignment		99.3	27	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
6	c3op9A_	 Alignment		99.3	24	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
7	c3ivpD_	 Alignment		99.3	19	PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
8	c1y9qA_	 Alignment		99.2	23	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth_3 family; PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
9	c2kpiA_	 Alignment		99.2	18	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
10	c1b0nA_	 Alignment		99.2	23	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
11	c3f52A_	 Alignment		99.2	25	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum

12	c3omtA_	Alignment		99.2	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
13	c2ewtA_	Alignment		99.2	27	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd
14	d1rioa_	Alignment		99.2	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
15	c3clcC_	Alignment		99.2	21	PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
16	d2r1j11	Alignment		99.2	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
17	c3mlfC_	Alignment		99.2	17	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
18	d2b5aa1	Alignment		99.2	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
19	d1b0na2	Alignment		99.2	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
20	d1llib_	Alignment		99.2	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
21	c3f6wE_	Alignment	not modelled	99.2	19	PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
22	c2bnoA_	Alignment	not modelled	99.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
23	c3lisB_	Alignment	not modelled	99.1	18	PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
24	d1utxa_	Alignment	not modelled	99.1	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
25	d1adra_	Alignment	not modelled	99.1	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
26	d1y9qa1	Alignment	not modelled	99.1	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
27	d1lmb3_	Alignment	not modelled	99.1	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
28	c2axzC_	Alignment	not modelled	99.1	23	PDB header: transcription Chain: C: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/ccf10 complex
						Fold: lambda repressor-like DNA-binding domains

29	d1y7ya1	Alignment	not modelled	99.1	33	Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
30	c3kxaD	Alignment	not modelled	99.1	30	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
31	d1r69a	Alignment	not modelled	99.1	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
32	c3b7hA	Alignment	not modelled	99.0	26	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
33	d1sq8a	Alignment	not modelled	99.0	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
34	c2o38A	Alignment	not modelled	99.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
35	d2o38a1	Alignment	not modelled	99.0	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
36	d1x57a1	Alignment	not modelled	99.0	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
37	d2croa	Alignment	not modelled	99.0	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
38	c2qfcB	Alignment	not modelled	99.0	28	PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
39	c3t76A	Alignment	not modelled	99.0	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
40	c2ef8A	Alignment	not modelled	99.0	23	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
41	c3eusB	Alignment	not modelled	99.0	25	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
42	c3dnvB	Alignment	not modelled	98.9	24	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
43	c3bdnB	Alignment	not modelled	98.9	23	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
44	c2xcjB	Alignment	not modelled	98.9	14	PDB header: viral protein Chain: B: PDB Molecule: c protein; PDBTitle: crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
45	d2a6ca1	Alignment	not modelled	98.9	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
46	c2jvlA	Alignment	not modelled	98.9	16	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
47	d2ofya1	Alignment	not modelled	98.8	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
48	c2fjrB	Alignment	not modelled	98.7	16	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
49	d2ppxa1	Alignment	not modelled	98.6	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
50	c2ppxA	Alignment	not modelled	98.6	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
51	c2wusR	Alignment	not modelled	98.5	19	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape2 protein rodZ
52	c3fmyA	Alignment	not modelled	98.5	25	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator mqsa PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
53	c3fymA	Alignment	not modelled	98.5	18	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of ymfM, a putative dna-binding membrane2 protein from staphylococcus aureus
54	c3pxpA	Alignment	not modelled	98.4	19	PDB header: transcription regulator Chain: A: PDB Molecule: helix-turn-helix domain protein; PDBTitle: crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
55	c3gn5B	Alignment	not modelled	98.3	19	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)

56	c3r1fO	 Alignment	not modelled	98.1	30	PDB header: transcription Chain: O: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
57	d1ic8a2	 Alignment	not modelled	96.0	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
58	d2awia1	 Alignment	not modelled	95.7	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: PrgX N-terminal domain-like
59	d1nera	 Alignment	not modelled	95.6	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
60	d1dwka1	 Alignment	not modelled	95.5	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
61	c3bd1B	 Alignment	not modelled	95.3	17	PDB header: transcription Chain: B: PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
62	d2bnma1	 Alignment	not modelled	95.2	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
63	d1lcda	 Alignment	not modelled	94.8	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
64	c2iv1J	 Alignment	not modelled	94.6	14	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
65	d2hsga1	 Alignment	not modelled	94.4	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
66	d2bjca1	 Alignment	not modelled	94.4	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
67	d1luxca	 Alignment	not modelled	93.5	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
68	c3kxD	 Alignment	not modelled	93.4	28	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
69	d2csfa1	 Alignment	not modelled	93.4	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
70	c2lcvA	 Alignment	not modelled	93.1	23	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation
71	d1efaa1	 Alignment	not modelled	92.8	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
72	d1luxda	 Alignment	not modelled	92.6	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
73	d1qpza1	 Alignment	not modelled	92.5	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
74	c2l8nA	 Alignment	not modelled	92.4	23	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
75	c3h5tA	 Alignment	not modelled	91.3	21	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
76	c1zvva	 Alignment	not modelled	91.1	28	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
77	c3mkyP	 Alignment	not modelled	90.4	21	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
78	c2h8rA	 Alignment	not modelled	89.6	18	PDB header: transcription activator/dna Chain: A: PDB Molecule: hepatocyte nuclear factor 1-beta; PDBTitle: hepatocyte nuclear factor 1b bound to dna : mody5 gene2 product
79	d2o4aa1	 Alignment	not modelled	89.3	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
80	c2auwB	 Alignment	not modelled	89.3	16	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
81	clic8B	Alignment	not modelled	89.0	19	PDB header: transcription/dna Chain: B: PDB Molecule: hepatocyte nuclear factor 1-alpha; PDBTitle: hepatocyte nuclear factor 1a bound to dna : mody3 gene2 product
82	d1r71a	Alignment	not modelled	88.7	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like

83	dlvz0a1	Alignment	not modelled	88.3	34	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
84	dlwiza	Alignment	not modelled	87.5	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
85	dlx2la1	Alignment	not modelled	85.9	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
86	dls7ea2	Alignment	not modelled	84.4	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
87	clr71B	Alignment		84.2	22	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional repressor protein korb; PDBTitle: crystal structure of the dna binding domain of korb in2 complex with the operator dna
88	c3k2zA	Alignment	not modelled	83.9	9	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
89	dlwh6a	Alignment	not modelled	83.7	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
90	c3mkzU	Alignment	not modelled	83.7	18	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
91	dlhlva1	Alignment	not modelled	83.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
92	dlz6ra1	Alignment	not modelled	82.5	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
93	dlz05a1	Alignment	not modelled	82.3	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
94	dls4ka	Alignment	not modelled	81.5	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: YdiL-like
95	dle3oc2	Alignment	not modelled	81.2	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
96	dlwh8a	Alignment	not modelled	80.1	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
97	clz6rC	Alignment	not modelled	79.5	23	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
98	dlau7a2	Alignment	not modelled	79.0	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
99	clyseA	Alignment	not modelled	79.0	10	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein satb1; PDBTitle: solution structure of the mar-binding domain of satb1
100	c3g3zA	Alignment	not modelled	78.4	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
101	c3tgnA	Alignment	not modelled	78.1	17	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
102	c3nzla	Alignment	not modelled	77.7	21	PDB header: transcription Chain: A: PDB Molecule: dna-binding protein satb1; PDBTitle: crystal structure of the n-terminal domain of dna-binding protein2 satb1 from homo sapiens, northeast structural genomics consortium3 target hr4435b
103	clz05A	Alignment	not modelled	75.2	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, rok family; PDBTitle: crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
104	c2w48D	Alignment	not modelled	74.8	26	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
105	cls7eA	Alignment	not modelled	74.8	17	PDB header: transcription Chain: A: PDB Molecule: hepatocyte nuclear factor 6; PDBTitle: solution structure of hnf-6
106	c2elhA	Alignment	not modelled	74.6	19	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
107	c2qwwB	Alignment	not modelled	70.5	18	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
						Fold: DNA/RNA-binding 3-helical bundle

108	d1lj9a_	Alignment	not modelled	70.4	11	Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
109	c2wteB_	Alignment	not modelled	69.3	13	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.
110	d2etha1	Alignment	not modelled	69.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
111	c3k0lA_	Alignment	not modelled	69.3	14	PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
112	c1bdhA_	Alignment	not modelled	68.8	22	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
113	d1s3ja_	Alignment	not modelled	68.4	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
114	d2hr3a1	Alignment	not modelled	68.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
115	d2bgca1	Alignment	not modelled	68.0	43	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
116	d1sfxa_	Alignment	not modelled	68.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
117	c2fa5B_	Alignment	not modelled	68.0	30	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
118	c3r0aB_	Alignment	not modelled	66.4	16	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
119	d2fbia1	Alignment	not modelled	65.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
120	c3bj6B_	Alignment	not modelled	65.3	19	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579