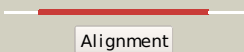
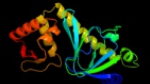
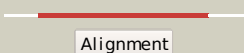
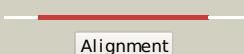
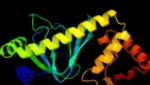
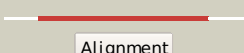
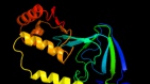
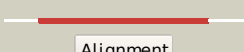
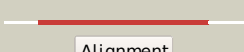
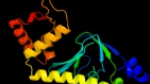
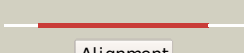
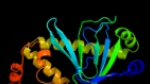
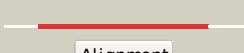
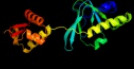
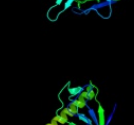
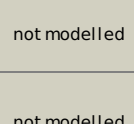
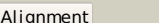
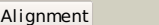
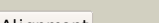
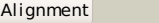
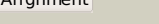
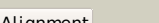
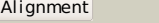
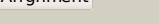
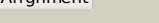
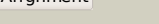
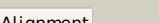
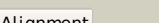


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3iwzB_	 Alignment		100.0	45	PDB header: transcription Chain: B: PDB Molecule: catabolite activation-like protein; PDBTitle: the c-di-gmp responsive global regulator clp links cell-cell signaling2 to virulence gene expression in xanthomonas campestris
2	c3kccA_	 Alignment		100.0	99	PDB header: transcription Chain: A: PDB Molecule: catabolite gene activator; PDBTitle: crystal structure of d138l mutant of catabolite gene activator protein
3	c1zreB_	 Alignment		100.0	100	PDB header: gene regulation/dna Chain: B: PDB Molecule: catabolite gene activator; PDBTitle: 4 crystal structures of cap-dna with all base-pair2 substitutions at position 6, cap-[6g;17c]icap38 dna
4	c1zybA_	 Alignment		100.0	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator, crp family; PDBTitle: crystal structure of transcription regulator from bacteroides2 thetaiotaomicron vpi-5482 at 2.15 a resolution
5	c2oz6A_	 Alignment		100.0	65	PDB header: dna binding protein Chain: A: PDB Molecule: virulence factor regulator; PDBTitle: crystal structure of virulence factor regulator from pseudomonas2 aeruginosa in complex with camp
6	c3dv8A_	 Alignment		100.0	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of a putative transcriptional regulator of the2 crp/fnr family (eubrec_1222) from eubacterium rectale atcc 33656 at3 2.55 a resolution
7	c2bgcA_	 Alignment		100.0	17	PDB header: transcription Chain: A: PDB Molecule: prfa; PDBTitle: prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
8	c3d0sA_	 Alignment		100.0	27	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: camp receptor protein from m.tuberculosis, camp-free form
9	c3fx3A_	 Alignment		100.0	21	PDB header: camp-binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: structure of a putative camp-binding regulatory protein from2 silicibacter pomeroyi dss-3
10	c3dkwB_	 Alignment		100.0	24	PDB header: transcription regulator Chain: B: PDB Molecule: dnr protein; PDBTitle: crystal structure of dnr from pseudomonas aeruginosa.
11	c3la2A_	 Alignment		100.0	26	PDB header: transcription Chain: A: PDB Molecule: global nitrogen regulator; PDBTitle: crystal structure of ntca in complex with 2-oxoglutarate

12	c3e6dA	Alignment		99.9	19	PDB header: transcription regulation Chain: A: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: crystal structure of cpk c200s
13	c3e97A	Alignment		99.9	21	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of transcriptional regulator of crp/fnr2 family (yp_604437.1) from deinococcus geothermalis dsm3 11300 at 1.86 a resolution
14	c2gauA	Alignment		99.9	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of transcriptional regulator of crp/fnr family from2 porphyromonas gingivalis (apc80792), structural genomics, mcsq
15	c2zdbA	Alignment		99.9	24	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, crp family; PDBTitle: crystal structure of tthb099, a transcriptional regulator crp family2 fromthermus thermophilus hb8
16	c1ft9A	Alignment		99.9	20	PDB header: transcription Chain: A: PDB Molecule: carbon monoxide oxidation system transcription PDBTitle: structure of the reduced (feii) co-sensing protein from r.2 rubrum
17	c2fmyB	Alignment		99.9	15	PDB header: dna binding protein Chain: B: PDB Molecule: carbon monoxide oxidation system transcription regulator PDBTitle: co-dependent transcription factor cooa from carboxydotherrnus2 hydrogenoformans (imidazole-bound form)
18	c2zcwA	Alignment		99.9	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, fnr/crp family; PDBTitle: crystal structure of tth1359, a transcriptional regulator,2 crp/fnr family from thermus thermophilus hb8
19	d1zyba2	Alignment		99.8	15	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
20	c3dn7A	Alignment		99.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cyclic nucleotide binding regulatory protein; PDBTitle: cyclic nucleotide binding regulatory protein from cytophaga2 hutchinsonii.
21	d1i5za2	Alignment	not modelled	99.7	100	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
22	c3gydA	Alignment	not modelled	99.7	19	PDB header: dna binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding domain; PDBTitle: crystal structure of a cyclic nucleotide-binding domain (mfla_1926)2 from methylobacillus flagellatus kt at 1.79 a resolution
23	c1o5lA	Alignment	not modelled	99.7	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp family; PDBTitle: crystal structure of transcriptional regulator (tm1171) from2 thermotoga maritima at 2.30 a resolution
24	d1o5la1	Alignment	not modelled	99.7	17	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
25	d2h6ca2	Alignment	not modelled	99.7	16	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
26	c2pqdD	Alignment	not modelled	99.7	24	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: structural genomics, the crystal structure of the n-terminal domain of2 a transcriptional regulator from streptomyces coelicolor a3(2)
27	d3e5ua2	Alignment	not modelled	99.7	17	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
28	d2oz6a2	Alignment	not modelled	99.7	61	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain

29	d2gaua2	Alignment	not modelled	99.6	18	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
30	d1ft9a2	Alignment	not modelled	99.6	22	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: CO-sensing protein CooA, N-terminal domain
31	c2z69A	Alignment	not modelled	99.6	21	PDB header: transcription regulator Chain: A: PDB Molecule: dnr protein; PDBTitle: crystal structure of the sensor domain of the transcriptional2 regulator dnr from pseudomonas aeruginosa
32	d1cx4a2	Alignment	not modelled	99.5	18	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
33	d1cx4a1	Alignment	not modelled	99.5	19	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
34	c3mdpA	Alignment	not modelled	99.5	18	PDB header: nucleotide binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding domain (cnmp-bd) protein; PDBTitle: crystal structure of a putative cyclic nucleotide-binding protein2 (gmet_1532) from geobacter metallireducens gs-15 at 1.90 a resolution
35	d1ne6a2	Alignment	not modelled	99.5	17	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
36	d2coha2	Alignment	not modelled	99.4	24	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
37	d1vp6a	Alignment	not modelled	99.4	25	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
38	d1ne6a1	Alignment	not modelled	99.4	20	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
39	c2ptnA	Alignment	not modelled	99.3	19	PDB header: transport protein Chain: A: PDB Molecule: hyperpolarization-activated (ih) channel; PDBTitle: structure and rearrangements in the carboxy-terminal region of spih2 channels
40	c3idcB	Alignment	not modelled	99.3	19	PDB header: transferase Chain: B: PDB Molecule: camp-dependent protein kinase type ii-beta PDBTitle: crystal structure of (102-265)riib:c holoenzyme of camp-2 dependent protein kinase
41	d1wgpa	Alignment	not modelled	99.3	20	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
42	d2oz6a1	Alignment	not modelled	99.3	76	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
43	c2byvE	Alignment	not modelled	99.3	17	PDB header: regulation Chain: E: PDB Molecule: rap guanine nucleotide exchange factor 4; PDBTitle: structure of the camp responsive exchange factor epac2 in2 its auto-inhibited state
44	c3otfA	Alignment	not modelled	99.3	24	PDB header: transport protein Chain: A: PDB Molecule: potassium/sodium hyperpolarization-activated cyclic PDBTitle: structural basis for the camp-dependent gating in human hcn4 channel
45	c1o7fA	Alignment	not modelled	99.3	17	PDB header: regulation Chain: A: PDB Molecule: camp-dependent rap1 guanine-nucleotide exchange PDBTitle: crystal structure of the regulatory domain of epac2
46	c3ogjD	Alignment	not modelled	99.3	20	PDB header: transferase Chain: D: PDB Molecule: prkg1 protein; PDBTitle: crystal structure of partial apo (92-227) of cgmp-dependent protein2 kinase
47	c3pvbB	Alignment	not modelled	99.3	21	PDB header: transferase Chain: B: PDB Molecule: camp-dependent protein kinase type i-alpha regulatory PDBTitle: crystal structure of (73-244)ria:c holoenzyme of camp-dependent2 protein kinase
48	d1i5za1	Alignment	not modelled	99.2	100	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
49	d1q3ea	Alignment	not modelled	99.2	24	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
50	d1o7fa2	Alignment	not modelled	99.2	14	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
51	d1o7fa3	Alignment	not modelled	99.2	20	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
52	d2gaua1	Alignment	not modelled	99.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
53	c3uknC	Alignment	not modelled	99.2	27	PDB header: transport protein, membrane protein Chain: C: PDB Molecule: novel protein similar to vertebrate potassium voltage-gated PDBTitle: structure of the c-linker/cnbhd of zelk channels in c 2 2 21 space2 group

54	d2coha1	Alignment	not modelled	99.2	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
55	c1cx4A	Alignment	not modelled	99.1	18	PDB header: signaling protein Chain: A: PDB Molecule: camp-dependent protein kinase regulatory subunit PDBTitle: crystal structure of a deletion mutant of the type ii beta2 regulatory subunit of camp-dependent protein kinase
56	c3cf6E	Alignment	not modelled	99.1	22	PDB header: signaling protein/gtp-binding protein Chain: E: PDB Molecule: rap guanine nucleotide exchange factor (gef) 4; PDBTitle: structure of epac2 in complex with cyclic-amp and rap
57	c2d93A	Alignment	not modelled	99.1	12	PDB header: signaling protein Chain: A: PDB Molecule: rap guanine nucleotide exchange factor 6; PDBTitle: solution structure of the cnmp_binding domain of human rap2 guanine nucleotide exchange factor 6
58	c3of1A	Alignment	not modelled	99.1	27	PDB header: transferase Chain: A: PDB Molecule: camp-dependent protein kinase regulatory subunit; PDBTitle: crystal structure of bcy1, the yeast regulatory subunit of pka
59	d2h6ca1	Alignment	not modelled	99.1	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
60	d2bgca1	Alignment	not modelled	99.0	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
61	d1ft9a1	Alignment	not modelled	99.0	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
62	c3shrA	Alignment	not modelled	99.0	23	PDB header: transferase Chain: A: PDB Molecule: cgmmp-dependent protein kinase 1; PDBTitle: crystal structure of cgmmp-dependent protein kinase reveals novel site2 of interchain communication
63	c1rgsA	Alignment	not modelled	98.9	20	PDB header: kinase Chain: A: PDB Molecule: camp dependent protein kinase; PDBTitle: regulatory subunit of camp dependent protein kinase
64	d3e5ua1	Alignment	not modelled	98.8	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
65	d1zyba1	Alignment	not modelled	97.6	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
66	c2x4hA	Alignment	not modelled	97.2	12	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
67	c2it0A	Alignment	not modelled	96.9	19	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
68	d3ctaa1	Alignment	not modelled	96.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
69	c2h09A	Alignment	not modelled	96.9	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
70	c2w48D	Alignment	not modelled	96.9	27	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
71	d2fxaa1	Alignment	not modelled	96.8	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
72	c2rdpA	Alignment	not modelled	96.8	9	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator marr; PDBTitle: the structure of a marr family protein from bacillus2 stearothermophilus
73	c1f5tA	Alignment	not modelled	96.8	17	PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dbxr consensus binding sequence
74	d3broa1	Alignment	not modelled	96.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
75	c2pexA	Alignment	not modelled	96.8	18	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator ohrr; PDBTitle: structure of reduced c22s ohrr from xanthamonas campestris
76	c3ctaA	Alignment	not modelled	96.7	19	PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase; PDBTitle: crystal structure of riboflavin kinase from thermoplasma2 acidophilum
77	c1g3wA	Alignment	not modelled	96.7	17	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dbxr
78	c3s2wB	Alignment	not modelled	96.7	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the crystal structure of a marr transcriptional regulator from2 methanosarcina mazei go1
79	d2isya1	Alignment	not modelled	96.6	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein

80	c2fxaB	 Alignment	not modelled	96.6	12	PDB header: transcription Chain: B: PDB Molecule: protease production regulatory protein hpr; PDBTitle: structure of the protease production regulatory protein hpr from2 bacillus subtilis.
81	c3g3zA	 Alignment	not modelled	96.6	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
82	d1g3wa1	 Alignment	not modelled	96.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
83	c3bddD	 Alignment	not modelled	96.6	19	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
84	c2qwwB	 Alignment	not modelled	96.6	10	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
85	d1s3ja	 Alignment	not modelled	96.5	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
86	d2d1ha1	 Alignment	not modelled	96.5	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
87	c1fx7C	 Alignment	not modelled	96.5	19	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
88	c3edpB	 Alignment	not modelled	96.5	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lin2111 protein; PDBTitle: the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
89	d1z05a1	 Alignment	not modelled	96.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
90	c3kp3B	 Alignment	not modelled	96.4	15	PDB header: transcription regulator/antibiotic Chain: B: PDB Molecule: transcriptional regulator tcar; PDBTitle: staphylococcus epidermidis in complex with ampicillin
91	d1ku9a	 Alignment	not modelled	96.4	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DNA-binding protein Mj223
92	d3deua1	 Alignment	not modelled	96.4	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
93	d2fbha1	 Alignment	not modelled	96.4	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
94	c3k0lA	 Alignment	not modelled	96.4	12	PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
95	c3f3xA	 Alignment	not modelled	96.4	9	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of the transcriptional regulator bldr2 from sulfolobus solfataricus
96	c3hruA	 Alignment	not modelled	96.3	26	PDB header: transcription Chain: A: PDB Molecule: metalloregulator scar; PDBTitle: crystal structure of scar with bound zn2+
97	c3deuB	 Alignment	not modelled	96.3	21	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator slya; PDBTitle: crystal structure of transcription regulatory protein slya2 from salmonella typhimurium in complex with salicylate3 ligands
98	c3ecoB	 Alignment	not modelled	96.3	19	PDB header: transcription Chain: B: PDB Molecule: mepR; PDBTitle: crystal structure of mepR, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepA
99	d2ev0a1	 Alignment	not modelled	96.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
100	c2gxgA	 Alignment	not modelled	96.3	11	PDB header: transcription Chain: A: PDB Molecule: 146aa long hypothetical transcriptional regulator; PDBTitle: crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
101	d1sfxa	 Alignment	not modelled	96.3	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
102	d1lnwa	 Alignment	not modelled	96.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
103	c3r0aB	 Alignment	not modelled	96.3	20	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2_21227196)
104	c3eetA	 Alignment	not modelled	96.2	22	PDB header: transcription regulator Chain: A: PDB Molecule: putative gntR-family transcriptional regulator; PDBTitle: crystal structure of putative gntR-family transcriptional2 regulator

105	d2hr3a1	Alignment	not modelled	96.2	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
106	d1jgsa	Alignment	not modelled	96.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
107	c3bj6B	Alignment	not modelled	96.2	15	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579
108	c3nqoB	Alignment	not modelled	96.1	19	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
109	c3f8mA	Alignment	not modelled	96.1	31	PDB header: transcription Chain: A: PDB Molecule: gntr-family protein transcriptional regulator; PDBTitle: crystal structure of phnf from mycobacterium smegmatis
110	c3oopA	Alignment	not modelled	96.1	16	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
111	d1hw1a1	Alignment	not modelled	96.1	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
112	c2ev5B	Alignment	not modelled	96.1	9	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
113	d1lj9a	Alignment	not modelled	96.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
114	c2nyxB	Alignment	not modelled	96.0	19	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis
115	c3boqB	Alignment	not modelled	96.0	8	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
116	c3tgnA	Alignment	not modelled	96.0	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
117	c3bwgA	Alignment	not modelled	96.0	21	PDB header: transcription regulator Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator yydk; PDBTitle: the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
118	c2du9A	Alignment	not modelled	95.9	11	PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulators; PDBTitle: crystal structure of the transcriptional factor from c.glutamicum
119	c3neuA	Alignment	not modelled	95.9	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1836 protein; PDBTitle: the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
120	c3nrvC	Alignment	not modelled	95.9	31	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