Phyre^2

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Description	P0A9E5
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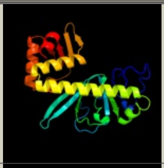
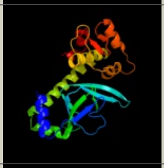
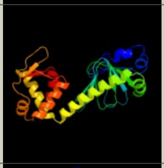
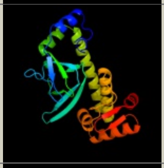
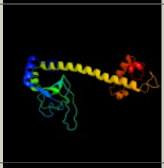
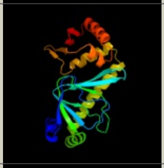
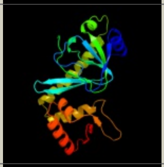
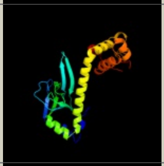
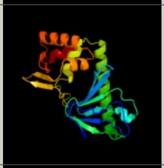
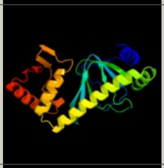
Unique Job ID	cb46dee18dcbb2a1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d0sA_	Alignment		100.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** camp receptor protein from m.tuberculosis, camp-free form
2	c1zybA_	Alignment		100.0	16	**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
3	c3dv8A_	Alignment		100.0	20	**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
4	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
5	c2bgcA_	Alignment		100.0	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**prfa; **PDBTitle:** prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
6	c2fmyB_	Alignment		100.0	20	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**carbon monoxide oxidation system transcription regulator **PDBTitle:** co-dependent transcription factor cooa from carboxydothermus2 hydrogenoformans (imidazole-bound form)
7	c3e97A_	Alignment		100.0	16	**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
8	c3dkwB_	Alignment		100.0	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**dnr protein; **PDBTitle:** crystal structure of dnr from pseudomonas aeruginosa.
9	c3e6dA_	Alignment		100.0	19	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**cyclic nucleotide-binding protein; **PDBTitle:** crystal structure of cprk c200s
10	c2oz6A_	Alignment		100.0	21	**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
11	c2zdbA_	Alignment		100.0	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, crp family; **PDBTitle:** crystal structure of tthb099, a transcriptional regulator crp family2 from thermus thermophilus hb8
						

12	c2gauA_	Alignment		100.0	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, crp/fnr family; **PDBTitle:** crystal structure of transcriptional regulator, crp/fnr family from2 porphyromonas gingivalis (apc80792), structural genomics, mcsg
13	c3la2A_	Alignment		100.0	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**global nitrogen regulator; **PDBTitle:** crystal structure of ntca in complex with 2-oxoglutarate
14	c3iwzB_	Alignment		100.0	19	**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
15	c3kccA_	Alignment		100.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**catabolite gene activator; **PDBTitle:** crystal structure of d138l mutant of catabolite gene activator protein
16	c1ft9A_	Alignment		100.0	16	**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	c2zcwA_	Alignment		99.9	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, fnr/crp family; **PDBTitle:** crystal structure of ttha1359, a transcriptional regulator,2 crp/fnr family from thermus thermophilus hb8
18	c1zreB_	Alignment		99.9	21	**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
19	d1zyba2	Alignment		99.7	14	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
20	c3gydA_	Alignment		99.7	12	**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
21	c2pqqD_	Alignment	not modelled	99.7	17	**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)
22	c3dn7A_	Alignment	not modelled	99.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cyclic nucleotide binding regulatory protein; **PDBTitle:** cyclic nucleotide binding regulatory protein from cytophaga2 hutchinsonii.
23	d3e5ua2	Alignment	not modelled	99.6	15	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
24	d2h6ca2	Alignment	not modelled	99.5	16	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
25	d2oz6a2	Alignment	not modelled	99.5	20	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
26	c3mdpA_	Alignment	not modelled	99.5	17	**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
27	d1ft9a2	Alignment	not modelled	99.5	15	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**CO-sensing protein CooA, N-terminal domain
28	d1i5za2	Alignment	not modelled	99.5	18	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain

29	c2z69A_	Alignment	not modelled	99.5	17	**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
30	d2gaua1	Alignment	not modelled	99.5	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
31	d2bgca1	Alignment	not modelled	99.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
32	d2gaua2	Alignment	not modelled	99.5	26	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
33	c1o5lA_	Alignment	not modelled	99.5	20	**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
34	d1o5la1	Alignment	not modelled	99.5	20	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
35	d2h6ca1	Alignment	not modelled	99.5	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
36	d2coha2	Alignment	not modelled	99.5	15	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
37	d1cx4a2	Alignment	not modelled	99.5	13	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
38	d1ne6a2	Alignment	not modelled	99.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
39	d1wgpa_	Alignment	not modelled	99.4	15	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
40	d1cx4a1	Alignment	not modelled	99.4	14	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
41	c1o7fA_	Alignment	not modelled	99.4	18	**PDB header:**regulation **Chain:** A: **PDB Molecule:**camp-dependent rap1 guanine-nucleotide exchange **PDBTitle:** crystal structure of the regulatory domain of epac2
42	d2coha1	Alignment	not modelled	99.4	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
43	c2byvE_	Alignment	not modelled	99.4	18	**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	d1o7fa2	Alignment	not modelled	99.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
45	d3e5ua1	Alignment	not modelled	99.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
46	c3idcB_	Alignment	not modelled	99.3	13	**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
47	d1ft9a1	Alignment	not modelled	99.3	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
48	d1vp6a_	Alignment	not modelled	99.3	12	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
49	d1ne6a1	Alignment	not modelled	99.3	16	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
50	c3ogjD_	Alignment	not modelled	99.3	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**prkg1 protein; **PDBTitle:** crystal structure of partial apo (92-227) of cgmp-dependent protein2 kinase
51	c3pvbB_	Alignment	not modelled	99.2	16	**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
52	d2oz6a1	Alignment	not modelled	99.2	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
53	c1cx4A_	Alignment	not modelled	99.2	13	**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
54	d1i5za1	Alignment	not modelled	99.1	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like

55	d1o7fa3	Alignment	not modelled	99.1	16	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
56	c3otfA_	Alignment	not modelled	99.1	12	**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
57	c2ptmA_	Alignment	not modelled	99.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hyperpolarization-activated (ih) channel; **PDBTitle:** structure and rearrangements in the carboxy-terminal region of spih2 channels
58	d1q3ea_	Alignment	not modelled	99.1	11	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
59	c3uknC_	Alignment	not modelled	99.0	22	**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
60	c3cf6E_	Alignment	not modelled	99.0	17	**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
61	c1rgsA_	Alignment	not modelled	99.0	15	**PDB header:**kinase **Chain:** A: **PDB Molecule:**camp dependent protein kinase; **PDBTitle:** regulatory subunit of camp dependent protein kinase
62	c3shrA_	Alignment	not modelled	99.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cgmp-dependent protein kinase 1; **PDBTitle:** crystal structure of cgmp-dependent protein kinase reveals novel site2 of interchain communication
63	c2d93A_	Alignment	not modelled	98.9	15	**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
64	c3of1A_	Alignment	not modelled	98.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**camp-dependent protein kinase regulatory subunit; **PDBTitle:** crystal structure of bcy1, the yeast regulatory subunit of pka
65	d1zyba1	Alignment	not modelled	97.9	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
66	d2bgca2	Alignment	not modelled	97.6	14	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**Listeriolysin regulatory protein PrfA, N-terminal domain
67	c2x4hA_	Alignment	not modelled	97.3	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
68	c2w48D_	Alignment	not modelled	97.2	29	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
69	c2h09A_	Alignment	not modelled	97.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
70	c2it0A_	Alignment	not modelled	97.0	17	**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
71	c1f5tA_	Alignment	not modelled	97.0	14	**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
72	d2fxaa1	Alignment	not modelled	96.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
73	d2d1ha1	Alignment	not modelled	96.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
74	d1g3wa1	Alignment	not modelled	96.8	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
75	d3ctaa1	Alignment	not modelled	96.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
76	d2isya1	Alignment	not modelled	96.7	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
77	d1z05a1	Alignment	not modelled	96.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
78	d1hw1a1	Alignment	not modelled	96.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
79	c1fx7C_	Alignment	not modelled	96.7	14	**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
80	c3bj6B_	Alignment	not modelled	96.7	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator

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81	c1g3wA_	Alignment	not modelled	96.7	19	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
82	c3eetA_	Alignment	not modelled	96.6	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative gntr-family transcriptional regulator; **PDBTitle:** crystal structure of putative gntr-family transcriptional2 regulator
83	c2fxaB_	Alignment	not modelled	96.6	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protease production regulatory protein hpr; **PDBTitle:** structure of the protease production regulatory protein hpr from2 bacillus subtilis.
84	c3g3zA_	Alignment	not modelled	96.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
85	c2qwwB_	Alignment	not modelled	96.5	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
86	c3ctaA_	Alignment	not modelled	96.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase; **PDBTitle:** crystal structure of riboflavin kinase from thermoplasma2 acidophilum
87	c2rdpA_	Alignment	not modelled	96.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator marr; **PDBTitle:** the structure of a marr family protein from bacillus2 stearothermophilus
88	d3broa1	Alignment	not modelled	96.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
89	c2pexA_	Alignment	not modelled	96.5	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator ohrr; **PDBTitle:** structure of reduced c22s ohrr from xanthamonas campestris
90	c3nqoB_	Alignment	not modelled	96.5	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
91	d2ev0a1	Alignment	not modelled	96.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
92	d1ku9a_	Alignment	not modelled	96.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
93	c3hruA_	Alignment	not modelled	96.4	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
94	d2hr3a1	Alignment	not modelled	96.4	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
95	d1lnwa_	Alignment	not modelled	96.4	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
96	c3s2wB_	Alignment	not modelled	96.3	10	**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
97	d2etha1	Alignment	not modelled	96.3	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
98	d1s3ja_	Alignment	not modelled	96.3	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
99	c3edpB_	Alignment	not modelled	96.3	14	**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
100	c2du9A_	Alignment	not modelled	96.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum
101	c2nyxB_	Alignment	not modelled	96.3	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis
102	c2ev5B_	Alignment	not modelled	96.3	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
103	c3neuA_	Alignment	not modelled	96.2	17	**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
104	d1sfxa_	Alignment	not modelled	96.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
105	d3deua1	Alignment	not modelled	96.2	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators

106	c2fa5B_	Alignment	not modelled	96.2	9	**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
107	d1z6ra1	Alignment	not modelled	96.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
108	c3r0aB_	Alignment	not modelled	96.2	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
109	c3f8mA_	Alignment	not modelled	96.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**gntr-family protein transcriptional regulator; **PDBTitle:** crystal structure of phnf from mycobacterium smegmatis
110	c3tgnA_	Alignment	not modelled	96.1	18	**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
111	c2hoeA_	Alignment	not modelled	96.1	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetylglucosamine kinase; **PDBTitle:** crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
112	d2fbha1	Alignment	not modelled	96.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
113	c3bddD_	Alignment	not modelled	96.0	17	**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
114	d2hs5a1	Alignment	not modelled	96.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
115	c3deuB_	Alignment	not modelled	96.0	12	**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
116	c3nrvC_	Alignment	not modelled	96.0	22	**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
117	c3by6C_	Alignment	not modelled	96.0	13	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator from oenococcus oeni
118	d2frha1	Alignment	not modelled	96.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
119	d1j5ya1	Alignment	not modelled	96.0	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
120	c2hs5A_	Alignment	not modelled	95.9	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator gntr; **PDBTitle:** structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1