Phyre^2

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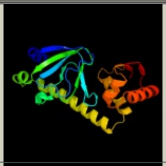
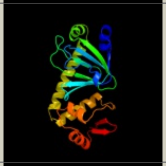
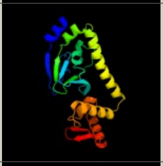
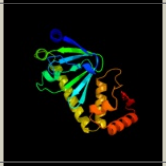
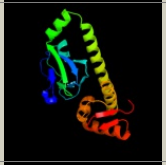
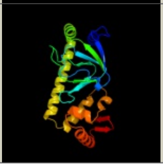
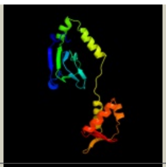
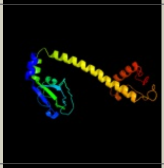
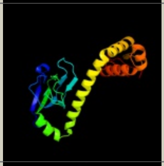
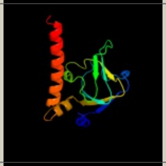
Description	P0AAP5
Date	Thu Jan 5 11:13:26 GMT 2012
Unique Job ID	fa63517e48e1413c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3iwzB_	Alignment		100.0	13	**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	c2bgcA_	Alignment		99.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**prfa; **PDBTitle:** prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
3	c1zybA_	Alignment		99.9	12	**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
4	c3dv8A_	Alignment		99.9	10	**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
5	c3kccA_	Alignment		99.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**catabolite gene activator; **PDBTitle:** crystal structure of d138l mutant of catabolite gene activator protein
6	c3fx3A_	Alignment		99.9	12	**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
7	c3e97A_	Alignment		99.9	14	**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	c1zreB_	Alignment		99.9	13	**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
9	c3la2A_	Alignment		99.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**global nitrogen regulator; **PDBTitle:** crystal structure of ntca in complex with 2-oxoglutarate
10	c3d0sA_	Alignment		99.9	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** camp receptor protein from m.tuberculosis, camp-free form
11	c2oz6A_	Alignment		99.9	16	**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

12	c3e6dA_	Alignment		99.9	12	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**cyclic nucleotide-binding protein; **PDBTitle:** crystal structure of cprk c200s
13	c3dkwB_	Alignment		99.9	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**dnr protein; **PDBTitle:** crystal structure of dnr from pseudomonas aeruginosa.
14	c2gauA_	Alignment		99.9	16	**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
15	c2zdbA_	Alignment		99.9	13	**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
16	c1ft9A_	Alignment		99.9	11	**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	15	**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	c2fmyB_	Alignment		99.8	11	**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)
19	c1o5lA_	Alignment		99.6	16	**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
20	d1o5la1	Alignment		99.6	16	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
21	d2gaua2	Alignment	not modelled	99.6	19	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
22	d2h6ca2	Alignment	not modelled	99.6	10	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
23	d3e5ua2	Alignment	not modelled	99.6	9	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
24	c3gydA_	Alignment	not modelled	99.5	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
25	d1zyba2	Alignment	not modelled	99.5	11	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
26	d2oz6a2	Alignment	not modelled	99.5	14	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
27	c3dn7A_	Alignment	not modelled	99.5	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cyclic nucleotide binding regulatory protein; **PDBTitle:** cyclic nucleotide binding regulatory protein from cytophaga2 hutchinsonii.
28	d1i5za2	Alignment	not modelled	99.5	9	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain

29	c2pqqD_	Alignment	not modelled	99.5	9	**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)
30	d1ft9a2	Alignment	not modelled	99.5	6	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**CO-sensing protein CooA, N-terminal domain
31	c3mdpA_	Alignment	not modelled	99.4	14	**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
32	d1cx4a1	Alignment	not modelled	99.4	9	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
33	d1cx4a2	Alignment	not modelled	99.4	10	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
34	c2z69A_	Alignment	not modelled	99.4	8	**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
35	d2coha2	Alignment	not modelled	99.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
36	c2ptmA_	Alignment	not modelled	99.4	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hyperpolarization-activated (ih) channel; **PDBTitle:** structure and rearrangements in the carboxy-terminal region of spih2 channels
37	d1ne6a1	Alignment	not modelled	99.3	8	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
38	d1o7fa3	Alignment	not modelled	99.3	9	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
39	c1o7fA_	Alignment	not modelled	99.3	9	**PDB header:**regulation **Chain:** A: **PDB Molecule:**camp-dependent rap1 guanine-nucleotide exchange **PDBTitle:** crystal structure of the regulatory domain of epac2
40	d1ne6a2	Alignment	not modelled	99.3	15	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
41	c3otfA_	Alignment	not modelled	99.3	15	**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
42	c3idcB_	Alignment	not modelled	99.3	9	**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
43	c3pvbB_	Alignment	not modelled	99.3	7	**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
44	c3ogjD_	Alignment	not modelled	99.3	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**prkg1 protein; **PDBTitle:** crystal structure of partial apo (92-227) of cgmp-dependent protein2 kinase
45	c2byvE_	Alignment	not modelled	99.3	9	**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
46	c3of1A_	Alignment	not modelled	99.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**camp-dependent protein kinase regulatory subunit; **PDBTitle:** crystal structure of bcy1, the yeast regulatory subunit of pka
47	d1vp6a_	Alignment	not modelled	99.2	10	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
48	d1q3ea_	Alignment	not modelled	99.2	15	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
49	c3cf6E_	Alignment	not modelled	99.2	9	**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
50	d1wgpa_	Alignment	not modelled	99.2	10	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
51	d1o7fa2	Alignment	not modelled	99.2	12	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
52	c3uknC_	Alignment	not modelled	99.2	7	**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
						Fold:DNA/RNA-binding 3-helical bundle

53	d1i5za1	Alignment	not modelled	99.1	21	**Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
54	d2oz6a1	Alignment	not modelled	99.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
55	c3shrA_	Alignment	not modelled	99.1	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
56	c1cx4A_	Alignment	not modelled	99.1	10	**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
57	d2gaua1	Alignment	not modelled	99.0	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
58	d2coha1	Alignment	not modelled	99.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
59	d1ft9a1	Alignment	not modelled	99.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
60	d2h6ca1	Alignment	not modelled	99.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
61	c1rgsA_	Alignment	not modelled	98.9	15	**PDB header:**kinase **Chain:** A: **PDB Molecule:**camp dependent protein kinase; **PDBTitle:** regulatory subunit of camp dependent protein kinase
62	c2d93A_	Alignment	not modelled	98.9	10	**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
63	d2bgca1	Alignment	not modelled	98.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
64	d3e5ua1	Alignment	not modelled	98.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
65	d1zyba1	Alignment	not modelled	98.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
66	c3eetA_	Alignment	not modelled	97.5	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative gntr-family transcriptional regulator; **PDBTitle:** crystal structure of putative gntr-family transcriptional2 regulator
67	c3edpB_	Alignment	not modelled	97.3	13	**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
68	c2hs5A_	Alignment	not modelled	97.3	14	**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
69	d1hw1a1	Alignment	not modelled	97.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
70	c2du9A_	Alignment	not modelled	97.2	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum
71	d2fxaa1	Alignment	not modelled	97.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
72	c3neuA_	Alignment	not modelled	97.1	16	**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
73	c3by6C_	Alignment	not modelled	97.1	14	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator from oenococcus oeni
74	c3ihuA_	Alignment	not modelled	97.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of dna binding protein (yp_298823.1) from ralstonia2 eutropha jmp134 at 1.92 a resolution
75	c2di3A_	Alignment	not modelled	97.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bacterial regulatory proteins, gntr family; **PDBTitle:** crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
76	d2hs5a1	Alignment	not modelled	97.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
77	c2w48D_	Alignment	not modelled	96.9	18	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
78	c3bwgA_	Alignment	not modelled	96.9	17	**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

79	c3f8mA_	Alignment	not modelled	96.9	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**gntr-family protein transcriptional regulator; **PDBTitle:** crystal structure of phnf from mycobacterium smegmatis
80	c3fmsA_	Alignment	not modelled	96.9	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of tm0439, a gntr transcriptional2 regulator
81	c3ctaA_	Alignment	not modelled	96.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase; **PDBTitle:** crystal structure of riboflavin kinase from thermoplasma2 acidophilum
82	d3bwga1	Alignment	not modelled	96.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
83	d1lnwa_	Alignment	not modelled	96.8	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
84	c3c7jA_	Alignment	not modelled	96.8	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of transcriptional regulator (gntr family member)2 from pseudomonas syringae pv. tomato str. dc3000
85	c2it0A_	Alignment	not modelled	96.8	15	**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
86	c2h09A_	Alignment	not modelled	96.8	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
87	c1e2xA_	Alignment	not modelled	96.8	17	**PDB header:**transcriptional regulation **Chain:** A: **PDB Molecule:**fatty acid metabolism regulator protein; **PDBTitle:** fadr, fatty acid responsive transcription factor from e.2 coli
88	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
89	c2x4hA_	Alignment	not modelled	96.7	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
90	c1f5tA_	Alignment	not modelled	96.7	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
91	d2fbha1	Alignment	not modelled	96.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
92	d2isya1	Alignment	not modelled	96.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
93	d3ctaa1	Alignment	not modelled	96.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
94	c2fxaB_	Alignment	not modelled	96.6	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.
95	d3broa1	Alignment	not modelled	96.6	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
96	d1ku9a_	Alignment	not modelled	96.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
97	c3k0lA_	Alignment	not modelled	96.6	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**repressor protein; **PDBTitle:** crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
98	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
99	c3nqoB_	Alignment	not modelled	96.5	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
100	c1g3wA_	Alignment	not modelled	96.5	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
101	d1g3wa1	Alignment	not modelled	96.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
102	c3g3zA_	Alignment	not modelled	96.4	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
103	d1v4ra1	Alignment	not modelled	96.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
104	c3hruA_	Alignment	not modelled	96.4	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+

105	c2nyxB_	Alignment	not modelled	96.4	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis
106	c3nrvC_	Alignment	not modelled	96.4	11	**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
107	c2v79B_	Alignment	not modelled	96.4	14	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
108	d1sfxa_	Alignment	not modelled	96.3	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
109	c1fx7C_	Alignment	not modelled	96.3	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
110	d2d1ha1	Alignment	not modelled	96.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
111	c3r0aB_	Alignment	not modelled	96.2	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
112	d1jhfa1	Alignment	not modelled	96.2	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
113	c3kp3B_	Alignment	not modelled	96.2	9	**PDB header:**transcription regulator/antibiotic **Chain:** B: **PDB Molecule:**transcriptional regulator tcar; **PDBTitle:** staphylococcus epidermidis in complex with ampicillin
114	d1z05a1	Alignment	not modelled	96.2	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
115	c2gxgA_	Alignment	not modelled	96.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**146aa long hypothetical transcriptional regulator; **PDBTitle:** crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
116	c3bj6B_	Alignment	not modelled	96.2	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
117	c3cjnA_	Alignment	not modelled	96.2	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
118	c2y75F_	Alignment	not modelled	96.2	14	**PDB header:**transcription **Chain:** F: **PDB Molecule:**hth-type transcriptional regulator cymr; **PDBTitle:** the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
119	c2rdpA_	Alignment	not modelled	96.1	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator marr; **PDBTitle:** the structure of a marr family protein from bacillus2 stearothermophilus
120	d3deua1	Alignment	not modelled	96.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators