Phyre2

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Description	P31453
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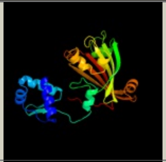
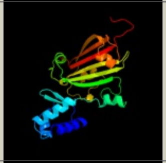
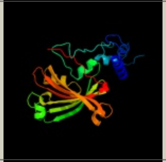
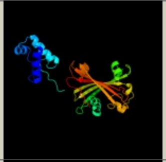
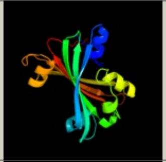
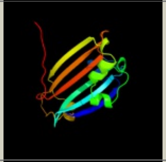
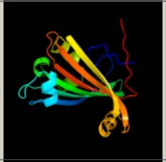
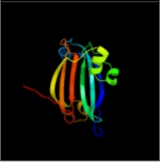
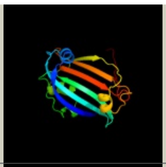
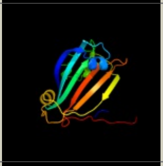
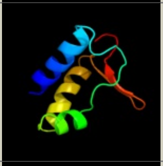
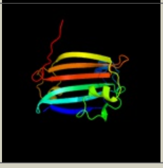
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bwgA_	Alignment		100.0	25	**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
2	c3f8mA_	Alignment		100.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**gntr-family protein transcriptional regulator; **PDBTitle:** crystal structure of phnf from mycobacterium smegmatis
3	c3edpB_	Alignment		100.0	24	**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
4	c2wv0H_	Alignment		100.0	25	**PDB header:**transcription **Chain:** H: **PDB Molecule:**hth-type transcriptional repressor yvoa; **PDBTitle:** crystal structure of the gntr-hutc family member yvoa from2 bacillus subtilis
5	c3eetA_	Alignment		100.0	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative gntr-family transcriptional regulator; **PDBTitle:** crystal structure of putative gntr-family transcriptional2 regulator
6	c3f8lC_	Alignment		99.9	15	**PDB header:**transcription **Chain:** C: **PDB Molecule:**hth-type transcriptional repressor phnf; **PDBTitle:** crystal structure of the effector domain of phnf from mycobacterium2 smegmatis
7	d2ogga1	Alignment		99.9	20	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
8	d2ooia1	Alignment		99.9	18	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
9	d2fa1a1	Alignment		99.9	21	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
10	d3cnva1	Alignment		99.9	23	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
11	d2p19a1	Alignment		99.9	17	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain

12	c2ra5A_	Alignment		99.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of the putative transcriptional regulator2 from streptomyces coelicolor
13	d2ra5a1	Alignment		99.9	19	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
14	d3bwga2	Alignment		99.9	27	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
15	d2ikka1	Alignment		99.9	19	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
16	c3hfiA_	Alignment		99.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative regulator; **PDBTitle:** the crystal structure of the putative regulator from escherichia coli2 cft073
17	c3neuA_	Alignment		99.8	19	**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
18	c2du9A_	Alignment		99.8	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum
19	c3by6C_	Alignment		99.8	21	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator from oenococcus oeni
20	d2pkha1	Alignment		99.8	14	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
21	c3lheA_	Alignment	not modelled	99.8	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**gntr family transcriptional regulator; **PDBTitle:** the crystal structure of the c-terminal domain of a gntr2 family transcriptional regulator from bacillus anthracis3 str. sterne
22	d1v4ra1	Alignment	not modelled	99.8	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
23	c2di3A_	Alignment	not modelled	99.8	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bacterial regulatory proteins, gntr family; **PDBTitle:** crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
24	c1e2xA_	Alignment	not modelled	99.8	23	**PDB header:**transcriptional regulation **Chain:** A: **PDB Molecule:**fatty acid metabolism regulator protein; **PDBTitle:** fadr, fatty acid responsive transcription factor from e.2 coli
25	c3ic7A_	Alignment	not modelled	99.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator of gntr family2 from bacteroides thetaiotaomicron
26	d3bwga1	Alignment	not modelled	99.8	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
27	c3fmsA_	Alignment	not modelled	99.8	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of tm0439, a gntr transcriptional2 regulator
28	c3c7jA_	Alignment	not modelled	99.8	26	**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
						PDB header:transcription regulator

29	c3ihuA_	Alignment	not modelled	99.8	24	**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
30	d1hw1a1	Alignment	not modelled	99.8	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
31	d3ddva1	Alignment	not modelled	99.8	20	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
32	c2hs5A_	Alignment	not modelled	99.7	25	**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
33	d2hs5a1	Alignment	not modelled	99.7	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
34	c3tqnC_	Alignment	not modelled	99.7	14	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** structure of the transcriptional regulator of the gntr family, from2 coxiella burnetii.
35	c2h09A_	Alignment	not modelled	98.1	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
36	d1biaa1	Alignment	not modelled	98.0	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
37	d1stza1	Alignment	not modelled	97.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
38	d1jhfa1	Alignment	not modelled	97.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
39	c1f5tA_	Alignment	not modelled	97.8	21	**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
40	c2it0A_	Alignment	not modelled	97.7	14	**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
41	c3hruA_	Alignment	not modelled	97.5	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
42	c3ctaA_	Alignment	not modelled	97.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase; **PDBTitle:** crystal structure of riboflavin kinase from thermoplasma2 acidophilum
43	d1g3wa1	Alignment	not modelled	97.4	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
44	d1j5ya1	Alignment	not modelled	97.3	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
45	d1i5za1	Alignment	not modelled	97.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
46	c2ewnA_	Alignment	not modelled	97.3	18	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
47	d2isya1	Alignment	not modelled	97.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
48	c2y75F_	Alignment	not modelled	97.2	17	**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
49	c3k69A_	Alignment	not modelled	97.2	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
50	c1g3wA_	Alignment	not modelled	97.2	20	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
51	c2v79B_	Alignment	not modelled	97.2	17	**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
52	c1j5yA_	Alignment	not modelled	97.1	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, biotin repressor family; **PDBTitle:** crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
53	c3r0aB_	Alignment	not modelled	97.1	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
54	c3lwfD_	Alignment	not modelled	97.1	16	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
55	d1xd7a_	Alignment	not modelled	97.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain

						Family: Transcriptional regulator Rrf2
56	d1ft9a1	Alignment	not modelled	96.9	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
57	c1ft9A_	Alignment	not modelled	96.8	22	**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
58	d2gaua1	Alignment	not modelled	96.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
59	c1fx7C_	Alignment	not modelled	96.6	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
60	d2h6ca1	Alignment	not modelled	96.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
61	d2oz6a1	Alignment	not modelled	96.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
62	c2x4hA_	Alignment	not modelled	96.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
63	c2vn2B_	Alignment	not modelled	96.5	19	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
64	d2coha1	Alignment	not modelled	96.5	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
65	c2gauA_	Alignment	not modelled	96.4	10	**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
66	c1zybA_	Alignment	not modelled	96.4	15	**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
67	c2oz6A_	Alignment	not modelled	96.4	17	**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
68	c3d0sA_	Alignment	not modelled	96.3	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** camp receptor protein from m.tuberculosis, camp-free form
69	d2bgca1	Alignment	not modelled	96.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
70	d3e5ua1	Alignment	not modelled	96.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
71	d2d1ha1	Alignment	not modelled	96.2	32	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
72	c3e97A_	Alignment	not modelled	96.1	20	**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
73	c3e6dA_	Alignment	not modelled	96.1	14	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**cyclic nucleotide-binding protein; **PDBTitle:** crystal structure of cprk c200s
74	d1sfxa_	Alignment	not modelled	96.1	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
75	c2zy3A_	Alignment	not modelled	96.1	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
76	d1ylfa1	Alignment	not modelled	96.0	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
77	d3ctaa1	Alignment	not modelled	96.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
78	c2zcwA_	Alignment	not modelled	96.0	25	**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
79	c3kccA_	Alignment	not modelled	96.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**catabolite gene activator; **PDBTitle:** crystal structure of d138l mutant of catabolite gene activator protein
80	d1ku9a_	Alignment	not modelled	96.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
						Fold:DNA/RNA-binding 3-helical bundle

81	d2cg4a1	Alignment	not modelled	95.9	22	**Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
82	c1zreB_	Alignment	not modelled	95.9	14	**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
83	c2zdbA_	Alignment	not modelled	95.8	19	**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
84	c3iwzB_	Alignment	not modelled	95.8	20	**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
85	d3broa1	Alignment	not modelled	95.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
86	c3k2zA_	Alignment	not modelled	95.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
87	c3bj6B_	Alignment	not modelled	95.8	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
88	c2fmyB_	Alignment	not modelled	95.8	14	**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)
89	c2ev5B_	Alignment	not modelled	95.8	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
90	c2fxaB_	Alignment	not modelled	95.7	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protease production regulatory protein hpr; **PDBTitle:** structure of the protease production regulatory protein hpr from2 bacillus subtilis.
91	d2ev0a1	Alignment	not modelled	95.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
92	c3dv8A_	Alignment	not modelled	95.7	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
93	d2nwia1	Alignment	not modelled	95.5	17	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**AF1396-like
94	c2l4aA_	Alignment	not modelled	95.5	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
95	c3nqoB_	Alignment	not modelled	95.5	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
96	d2fxaa1	Alignment	not modelled	95.5	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
97	d1i1ga1	Alignment	not modelled	95.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
98	c2oqgA_	Alignment	not modelled	95.4	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
99	d2fbha1	Alignment	not modelled	95.4	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
100	c2gxgA_	Alignment	not modelled	95.4	30	**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	c2qwwB_	Alignment	not modelled	95.4	20	**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
102	c3tgnA_	Alignment	not modelled	95.4	29	**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
103	d2bv6a1	Alignment	not modelled	95.4	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
104	c3la2A_	Alignment	not modelled	95.3	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**global nitrogen regulator; **PDBTitle:** crystal structure of ntca in complex with 2-oxoglutarate
105	d2cyya1	Alignment	not modelled	95.2	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain

106	d1r1ua_	Alignment	not modelled	95.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
107	d1p4xa2	Alignment	not modelled	95.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
108	c2e7xA_	Alignment	not modelled	95.2	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
109	c3g3zA_	Alignment	not modelled	95.2	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
110	c1r22B_	Alignment	not modelled	95.2	28	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**transcriptional repressor smtb; **PDBTitle:** crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
111	d1mkma1	Alignment	not modelled	95.2	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
112	c2cg4B_	Alignment	not modelled	95.2	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
113	d2cfxa1	Alignment	not modelled	95.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
114	c2bgcA_	Alignment	not modelled	95.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**prfa; **PDBTitle:** prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
115	c3f6tA_	Alignment	not modelled	95.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
116	c3f6vA_	Alignment	not modelled	95.0	32	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance
117	c1stzB_	Alignment	not modelled	95.0	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat-inducible transcription repressor hrca homolog; **PDBTitle:** crystal structure of a hypothetical protein at 2.2 a resolution
118	c3bjaA_	Alignment	not modelled	95.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
119	c2rdpA_	Alignment	not modelled	95.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator marr; **PDBTitle:** the structure of a marr family protein from bacillus2 stearothermophilus
120	c2wteB_	Alignment	not modelled	94.9	24	**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.