Phyre^2

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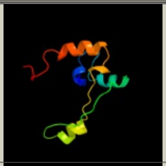
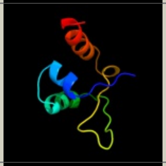
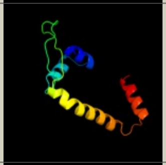
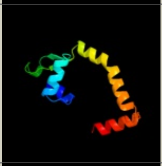
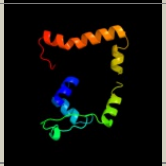
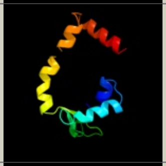
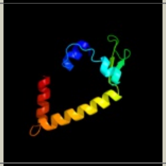
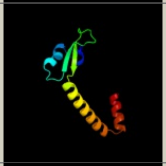
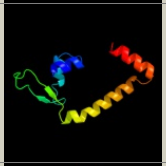
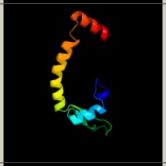
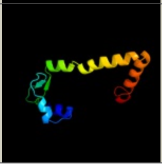
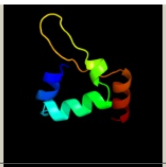
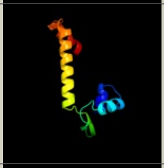
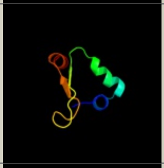
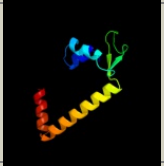
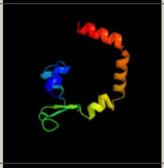
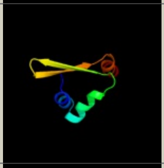
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tnsa_	Alignment		99.8	24	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
2	d1qpma_	Alignment		99.7	21	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
3	c3bpxB_	Alignment		87.4	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of marr
4	c2nnnB_	Alignment		83.5	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
5	c3cjnA_	Alignment		83.3	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
6	d3broa1	Alignment		83.2	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
7	c3k0lA_	Alignment		81.4	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**repressor protein; **PDBTitle:** crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
8	d2etha1	Alignment		81.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
9	d1lj9a_	Alignment		80.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
10	c3bjaA_	Alignment		78.3	12	**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
11	c2qwwB_	Alignment		78.1	14	**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

12	d1ub9a_	Alignment		76.5	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
13	c3nqoB_	Alignment		76.2	18	**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
14	c2rdpA_	Alignment		76.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator marr; **PDBTitle:** the structure of a marr family protein from bacillus2 stearothermophilus
15	c3ctaA_	Alignment		75.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase; **PDBTitle:** crystal structure of riboflavin kinase from thermoplasma2 acidophilum
16	c3bj6B_	Alignment		74.8	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
17	c2nyxB_	Alignment		74.2	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis
18	c3bddD_	Alignment		74.0	22	**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
19	d3ctaa1	Alignment		73.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
20	d2fbka1	Alignment		72.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
21	d1biaa1	Alignment	not modelled	70.8	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
22	d1hsja1	Alignment	not modelled	69.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
23	c3kp3B_	Alignment	not modelled	69.7	22	**PDB header:**transcription regulator/antibiotic **Chain:** B: **PDB Molecule:**transcriptional regulator tcar; **PDBTitle:** staphylococcus epidermidis in complex with ampicillin
24	d1r8ea1	Alignment	not modelled	69.6	7	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
25	d1s3ja_	Alignment	not modelled	69.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
26	c3nrvC_	Alignment	not modelled	68.3	16	**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
27	c2gxgA_	Alignment	not modelled	67.8	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**146aa long hypothetical transcriptional regulator; **PDBTitle:** crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
28	d1lnwa_	Alignment	not modelled	64.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators

29	c3deuB_	Alignment	not modelled	63.9	11	**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
30	d1sfxa_	Alignment	not modelled	63.8	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
31	c3k69A_	Alignment	not modelled	63.8	14	**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
32	c3r0aB_	Alignment	not modelled	63.7	21	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
33	c3g3zA_	Alignment	not modelled	62.5	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
34	c2vz4A_	Alignment	not modelled	59.4	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional activator tipa; **PDBTitle:** the n-terminal domain of merr-like protein tipal bound to2 promoter dna
35	d1p4xa2	Alignment	not modelled	59.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
36	c2jmlA_	Alignment	not modelled	57.5	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor
37	c2kfsA_	Alignment	not modelled	56.4	25	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical regulatory protein; **PDBTitle:** nmr structure of rv2175c
38	d1jgsa_	Alignment	not modelled	55.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
39	c3tgnA_	Alignment	not modelled	54.7	21	**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
40	d2frha1	Alignment	not modelled	54.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
41	d1p4xa1	Alignment	not modelled	53.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
42	c3ezfA_	Alignment	not modelled	46.4	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**para; **PDBTitle:** partition protein
43	d2fbha1	Alignment	not modelled	45.7	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
44	c2oqgA_	Alignment	not modelled	45.4	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
45	d2d1ha1	Alignment	not modelled	44.2	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
46	d1q06a_	Alignment	not modelled	44.0	21	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
47	d3e5ua1	Alignment	not modelled	43.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
48	c2jvfA_	Alignment	not modelled	43.5	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
49	d2fbia1	Alignment	not modelled	43.3	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
50	c3s2wB_	Alignment	not modelled	42.4	17	**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
51	c2fa5B_	Alignment	not modelled	42.0	12	**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
52	c3hh0C_	Alignment	not modelled	41.4	13	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
53	d1j5ya1	Alignment	not modelled	41.4	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
54	c3e6mD_	Alignment	not modelled	41.2	12	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**marr family transcriptional regulator; **PDBTitle:** the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.

55	c2zhhA_	Alignment	not modelled	41.2	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr; **PDBTitle:** crystal structure of soxr
56	c2it0A_	Alignment	not modelled	40.6	9	**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
57	c1qysA_	Alignment	not modelled	40.6	35	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
58	d1xsva_	Alignment	not modelled	39.9	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
59	d2coha1	Alignment	not modelled	39.4	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
60	d2oz6a1	Alignment	not modelled	39.0	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
61	d1z91a1	Alignment	not modelled	38.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
62	d1ft9a1	Alignment	not modelled	37.7	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
63	c3jw4C_	Alignment	not modelled	37.2	16	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, marr/emrr family; **PDBTitle:** the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum
64	c3f6oB_	Alignment	not modelled	36.5	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
65	d1r8da_	Alignment	not modelled	35.4	14	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
66	c2fjrB_	Alignment	not modelled	35.0	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
67	d1i5za1	Alignment	not modelled	34.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
68	d1j9ia_	Alignment	not modelled	33.2	25	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
69	c2ppxA_	Alignment	not modelled	32.7	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1735; **PDBTitle:** crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
70	d2ppxa1	Alignment	not modelled	32.7	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
71	c3lisB_	Alignment	not modelled	32.1	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**csp231i c protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
72	d3deua1	Alignment	not modelled	31.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
73	d2p7vb1	Alignment	not modelled	31.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
74	d2fxaa1	Alignment	not modelled	31.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
75	c3iwfA_	Alignment	not modelled	31.3	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
76	d2cg4a1	Alignment	not modelled	31.0	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
77	c2oz6A_	Alignment	not modelled	30.3	26	**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
78	c3cdhB_	Alignment	not modelled	30.2	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of the marr family transcriptional regulator spo14532 from silicibacter pomeroyi dss-3
79	d2bgca1	Alignment	not modelled	29.8	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
80	d1z05a1	Alignment	not modelled	29.7	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
						Fold:DNA/RNA-binding 3-helical bundle

81	d2gaua1	Alignment	not modelled	29.6	13	**Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
82	c3gp4B_	Alignment	not modelled	29.6	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
83	c3mlfC_	Alignment	not modelled	29.6	25	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** putative transcriptional regulator from staphylococcus aureus.
84	c1j5yA_	Alignment	not modelled	29.1	27	**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
85	c3cuoB_	Alignment	not modelled	29.0	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
86	c2l4aA_	Alignment	not modelled	28.8	17	**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
87	c3ecoB_	Alignment	not modelled	28.5	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mepr; **PDBTitle:** crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
88	c2fxaB_	Alignment	not modelled	28.5	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protease production regulatory protein hpr; **PDBTitle:** structure of the protease production regulatory protein hpr from2 bacillus subtilis.
89	c1r22B_	Alignment	not modelled	28.2	17	**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
90	c3omtA_	Alignment	not modelled	28.1	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
91	d1s7oa_	Alignment	not modelled	28.0	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
92	c3f6vA_	Alignment	not modelled	25.8	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance
93	c3bd1B_	Alignment	not modelled	25.7	35	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cro protein; **PDBTitle:** structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
94	d2ouxa1	Alignment	not modelled	25.5	11	**Fold:**alpha-alpha superhelix **Superfamily:**MgtE N-terminal domain-like **Family:**MgtE N-terminal domain-like
95	c3pqkD_	Alignment	not modelled	25.3	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**biofilm growth-associated repressor; **PDBTitle:** crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
96	c2kpjA_	Alignment	not modelled	25.1	32	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sos-response transcriptional repressor, lexa; **PDBTitle:** solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
97	c2cg4B_	Alignment	not modelled	25.0	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
98	d2ev0a1	Alignment	not modelled	24.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
99	d2h6ca1	Alignment	not modelled	24.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
100	d2a61a1	Alignment	not modelled	24.2	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
101	c1i1gA_	Alignment	not modelled	24.1	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
102	d1ku3a_	Alignment	not modelled	23.8	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
103	c2dbbA_	Alignment	not modelled	23.4	35	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
104	d1i1ga1	Alignment	not modelled	23.3	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
105	c3jthA_	Alignment	not modelled	23.1	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
						Fold:DNA/RNA-binding 3-helical bundle

106	d1ku7a_	Alignment	not modelled	23.1	22	**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
107	d1r1ta_	Alignment	not modelled	22.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
108	c2jpcA_	Alignment	not modelled	22.8	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
109	d2p4wa1	Alignment	not modelled	22.7	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF1790-like
110	d2gxba1	Alignment	not modelled	22.3	37	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
111	d1qbjc_	Alignment	not modelled	22.2	37	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
112	d2cyya1	Alignment	not modelled	22.2	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
113	c1ft9A_	Alignment	not modelled	22.1	26	**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
114	c2e7xA_	Alignment	not modelled	22.0	22	**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
115	c3fmyA_	Alignment	not modelled	21.8	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa **PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
116	d1rz4a1	Alignment	not modelled	21.8	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Eukaryotic translation initiation factor 3 subunit 12, eIF3k, C-terminal domain
117	c3boqB_	Alignment	not modelled	21.7	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
118	c2ia0A_	Alignment	not modelled	21.6	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator pf0864; **PDBTitle:** transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
119	c3iwzB_	Alignment	not modelled	21.6	21	**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
120	d2hr3a1	Alignment	not modelled	21.3	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators