Phyre^2

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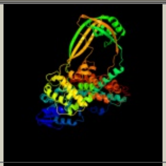
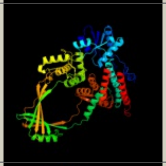
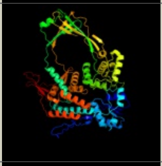
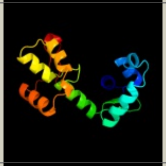
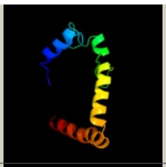
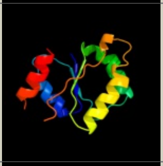
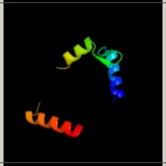
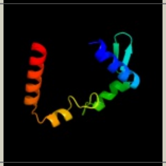
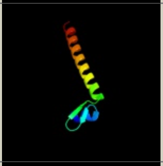
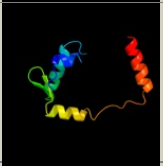
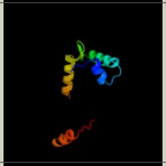
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2o59B_	Alignment		100.0	99	**PDB header:**isomerase/dna **Chain:** B: **PDB Molecule:**dna topoisomerase 3; **PDBTitle:** structure of e. coli topoisomerase iii in complex with an 8-2 base single stranded oligonucleotide. frozen in glycerol3 ph 8.0
2	d1i7da_	Alignment		100.0	100	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
3	d1mw9x_	Alignment		100.0	24	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
4	c2gajA_	Alignment		100.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
5	d1gkub3	Alignment		100.0	21	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
6	c1gl9B_	Alignment		100.0	22	**PDB header:**topoisomerase **Chain:** B: **PDB Molecule:**reverse gyrase; **PDBTitle:** archaeoglobus fulgidus reverse gyrase complexed with adpnp
7	d1cy9a_	Alignment		100.0	24	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
8	d1vdda_	Alignment		98.9	15	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
9	c1vddC_	Alignment		98.6	19	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
10	c2x4hA_	Alignment		95.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
11	d1s3ja_	Alignment		94.7	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators

12	c3boqB_	Alignment		94.3	21	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
13	d2fcja1	Alignment		93.5	19	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
14	c3nrvC_	Alignment		93.4	17	**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
15	c2pexA_	Alignment		93.3	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator ohrr; **PDBTitle:** structure of reduced c22s ohrr from xanthamonas campestris
16	d1r7ja_	Alignment		92.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Archaeal DNA-binding protein
17	d1lnwa_	Alignment		92.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
18	d2etha1	Alignment		92.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
19	c3f3xA_	Alignment		92.1	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of the transcriptional regulator bldr2 from sulfolobus solfataricus
20	c3s2wB_	Alignment		91.6	15	**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
21	c3kp3B_	Alignment	not modelled	91.5	14	**PDB header:**transcription regulator/antibiotic **Chain:** B: **PDB Molecule:**transcriptional regulator tcar; **PDBTitle:** staphylococcus epidermidis in complex with ampicillin
22	c2fa5B_	Alignment	not modelled	91.5	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
23	d3broa1	Alignment	not modelled	91.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
24	c3g3zA_	Alignment	not modelled	91.2	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
25	d1lj9a_	Alignment	not modelled	90.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
26	c3bj6B_	Alignment	not modelled	90.7	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
27	c3e6mD_	Alignment	not modelled	90.6	22	**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.
28	c2rdpA_	Alignment	not modelled	90.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator marr; **PDBTitle:** the structure of a marr family protein from bacillus2 stearothermophilus

29	d2fbka1	Alignment	not modelled	90.3	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
30	c2qwwB_	Alignment	not modelled	90.1	13	**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
31	d3ctaa1	Alignment	not modelled	90.0	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
32	c3bjaA_	Alignment	not modelled	89.6	13	**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
33	d2bv6a1	Alignment	not modelled	89.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
34	d2fxaa1	Alignment	not modelled	89.6	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
35	c3fm5D_	Alignment	not modelled	89.2	20	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator; **PDBTitle:** x-ray crystal structure of transcriptional regulator (marr family)2 from rhodococcus sp. rha1
36	c3hrmA_	Alignment	not modelled	88.8	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator sarz; **PDBTitle:** crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form
37	c2fxaB_	Alignment	not modelled	88.7	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protease production regulatory protein hpr; **PDBTitle:** structure of the protease production regulatory protein hpr from2 bacillus subtilis.
38	c3ecoB_	Alignment	not modelled	88.6	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mepr; **PDBTitle:** crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
39	d2fbia1	Alignment	not modelled	88.3	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
40	c2nyxB_	Alignment	not modelled	88.3	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis
41	c1g3wA_	Alignment	not modelled	87.9	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
42	d1t6t1_	Alignment	not modelled	87.8	15	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
43	d1jgsa_	Alignment	not modelled	87.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
44	c3hruA_	Alignment	not modelled	87.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
45	c3r0aB_	Alignment	not modelled	86.9	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
46	c1f5tA_	Alignment	not modelled	86.6	15	**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
47	d1ub9a_	Alignment	not modelled	86.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
48	d1stza1	Alignment	not modelled	85.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
49	d2hr3a1	Alignment	not modelled	85.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
50	c2ev5B_	Alignment	not modelled	85.4	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
51	d1p4xa1	Alignment	not modelled	85.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
52	c3cjnA_	Alignment	not modelled	85.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
53	d1p4xa2	Alignment	not modelled	84.7	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
54	c1fx7C_	Alignment	not modelled	84.0	20	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**iron-dependent repressor ider;

54	c1fx7C_		Alignment	not modelled	84.0	20	**PDBTitle:** crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
55	c3nqoB_	Alignment	not modelled	83.9	17	**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
56	c2nnnB_	Alignment	not modelled	83.7	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
57	c2gxgA_	Alignment	not modelled	83.7	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**146aa long hypothetical transcriptional regulator; **PDBTitle:** crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
58	c3k0lA_	Alignment	not modelled	83.3	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**repressor protein; **PDBTitle:** crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
59	d1z91a1	Alignment	not modelled	83.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
60	c3tgnA_	Alignment	not modelled	83.1	19	**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
61	c1nuiA_	Alignment	not modelled	83.0	16	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
62	c3bpxB_	Alignment	not modelled	82.6	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of marr
63	d1hsja1	Alignment	not modelled	82.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
64	d2a61a1	Alignment	not modelled	81.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
65	d2fbha1	Alignment	not modelled	81.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
66	c1p4xA_	Alignment	not modelled	81.3	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**staphylococcal accessory regulator a homologue; **PDBTitle:** crystal structure of sars protein from staphylococcus aureus
67	d2fnaa1	Alignment	not modelled	81.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
68	d1nuia1	Alignment	not modelled	80.1	16	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**Primase fragment of primase-helicase protein
69	c2h09A_	Alignment	not modelled	79.7	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
70	c3nuhB_	Alignment	not modelled	79.3	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
71	c3cdhB_	Alignment	not modelled	78.4	28	**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
72	c2it0A_	Alignment	not modelled	77.3	21	**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
73	c3jw4C_	Alignment	not modelled	76.5	19	**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
74	c3ctaA_	Alignment	not modelled	76.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase; **PDBTitle:** crystal structure of riboflavin kinase from thermoplasma2 acidophilum
75	d1olta_	Alignment	not modelled	75.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
76	c1ylmA_	Alignment	not modelled	74.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bsu32300; **PDBTitle:** structure of cytosolic protein of unknown function yute2 from bacillus subtilis
77	c3oopA_	Alignment	not modelled	74.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2960 protein; **PDBTitle:** the structure of a protein with unknown function from listeria innocua2 clip11262
78	c2wteB_	Alignment	not modelled	72.9	29	**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.
79	c1t98B_	Alignment	not modelled	69.0	11	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**chromosome partition protein mukf; **PDBTitle:** crystal structure of mukf(1-287)

80	d1okra_	Alignment	not modelled	68.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
81	d1ku9a_	Alignment	not modelled	67.5	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
82	c3fofD_	Alignment	not modelled	67.1	18	**PDB header:**isomerase/dna **Chain:** D: **PDB Molecule:**dna topoisomerase 4 subunit b; **PDBTitle:** structural insight into the quinolone-dna cleavage complex2 of type iia topoisomerases
83	c1q57G_	Alignment	not modelled	67.0	19	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
84	c3l7wA_	Alignment	not modelled	66.2	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1704; **PDBTitle:** the crystal structure of smu.1704 from streptococcus mutans ua159
85	d2esna1	Alignment	not modelled	66.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LysR-like transcriptional regulators
86	d2isya1	Alignment	not modelled	65.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
87	c3deuB_	Alignment	not modelled	64.5	14	**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
88	d2hyec1	Alignment	not modelled	63.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**SCF ubiquitin ligase complex WHB domain
89	c1byvA_	Alignment	not modelled	62.2	69	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**protein (calcitonin); **PDBTitle:** glycosylated eel calcitonin
90	d1jhfa1	Alignment	not modelled	61.6	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
91	c3bddD_	Alignment	not modelled	61.0	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
92	d1g3wa1	Alignment	not modelled	60.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
93	c3m1eA_	Alignment	not modelled	56.8	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of benm_dbd
94	d1mkma1	Alignment	not modelled	56.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
95	c3u1dA_	Alignment	not modelled	55.2	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the structure of a protein with a gntr superfamily winged-helix-turn-2 helix domain from halomicrobium mukohataei.
96	d1iuya_	Alignment	not modelled	52.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**SCF ubiquitin ligase complex WHB domain
97	d3deua1	Alignment	not modelled	51.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
98	d1q1ha_	Alignment	not modelled	51.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcription factor E/IIe-alpha, N-terminal domain
99	c1q1hA_	Alignment	not modelled	51.0	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor e; **PDBTitle:** an extended winged helix domain in general transcription2 factor e/iie alpha
100	d1ldja1	Alignment	not modelled	50.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**SCF ubiquitin ligase complex WHB domain
101	d2ev0a1	Alignment	not modelled	48.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
102	c2k4bA_	Alignment	not modelled	46.0	7	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** copr repressor structure
103	c2au3A_	Alignment	not modelled	44.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
104	c2vn2B_	Alignment	not modelled	44.6	24	**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
105	d1yg2a_	Alignment	not modelled	44.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PadR-like
						PDB header:isomerase

106	c2zjtB_	Alignment	not modelled	43.1	31	**Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** crystal structure of dna gyrase b' domain sheds lights on2 the mechanism for t-segment navigation
107	c4a0lH_	Alignment	not modelled	42.8	15	**PDB header:**ligase/dna-binding protein/dna **Chain:** H: **PDB Molecule:**cullin-4b; **PDBTitle:** structure of ddb1-ddb2-cul4b-rbx1 bound to a 12 bp abasic2 site containing dna-duplex
108	d2frha1	Alignment	not modelled	42.4	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
109	c3ri2B_	Alignment	not modelled	40.7	22	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, padr-like family; **PDBTitle:** crystal structure of padr family transcriptional regulator from2 eggerthella lenta dsm 2243
110	c3hhhA_	Alignment	not modelled	39.5	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, padr family; **PDBTitle:** crystal structure of transcriptional regulator, a member of padr2 family, from enterococcus faecalis v583
111	c2uvgA_	Alignment	not modelled	39.2	14	**PDB header:**sugar-binding protein **Chain:** A: **PDB Molecule:**abc type periplasmic sugar-binding protein; **PDBTitle:** structure of a periplasmic oligogalacturonide binding2 protein from yersinia enterocolitica
112	d1bjaa_	Alignment	not modelled	37.6	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcription factor MotA, activation domain
113	d2cg4a1	Alignment	not modelled	36.8	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
114	d1p6ra_	Alignment	not modelled	35.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
115	c3l09B_	Alignment	not modelled	35.2	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator2 (jann_22dec04_contig27_revised_gene3569) from jannaschia sp. ccs1 at3 2.81 a resolution
116	d2p6ra1	Alignment	not modelled	34.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RecQ helicase DNA-binding domain-like
117	c2hyeC_	Alignment	not modelled	34.3	13	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**cullin-4a; **PDBTitle:** crystal structure of the ddb1-cul4a-rbx1-sv5v complex
118	c3okqA_	Alignment	not modelled	33.9	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bud site selection protein 6; **PDBTitle:** crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
119	c2x8qA_	Alignment	not modelled	32.7	18	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein p27; **PDBTitle:** cryo-em 3d model of the icosahedral particle2 composed of rous sarcoma virus capsid protein pentamers
120	d2d1ha1	Alignment	not modelled	32.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like