



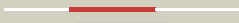
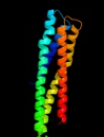



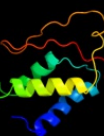





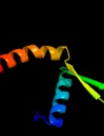












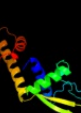
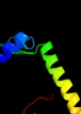


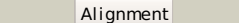
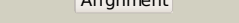


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3euhB_	 Alignment		100.0	100	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of the muke-mukf complex
2	c1t98B_	 Alignment		100.0	98	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of mukf(1-287)
3	d1t98a2	 Alignment		100.0	98	Fold: STAT-like Superfamily: MukF C-terminal domain-like Family: MukF C-terminal domain-like
4	d1t98a1	 Alignment		100.0	98	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MukF N-terminal domain-like
5	c3eujB_	 Alignment		100.0	47	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, symmetric dimer
6	d1fnnal	 Alignment		88.7	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain
7	c1f5ta_	 Alignment		87.8	16	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
8	d2fswa1	 Alignment		81.0	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like
9	c2rqpA_	 Alignment		80.7	12	PDB header: gene regulation Chain: A: PDB Molecule: heterochromatin protein 1-binding protein 3; PDBTitle: the solution structure of heterochromatin protein 1-binding2 protein 74 histone h1 like domain
10	c2v79B_	 Alignment		78.8	19	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
11	c4a5mH_	 Alignment		77.5	12	PDB header: transcription Chain: H: PDB Molecule: uncharacterized hth-type transcriptional regulator yybr; PDBTitle: redox regulator hypr in its oxidized form

12	d1tdpa_	Alignment		74.9	28	Fold: Bromodomain-like Superfamily: Bacteriocin immunity protein-like Family: Carnobacteriocin B2 immunity protein
13	c3g2bA_	Alignment		71.6	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: coenzyme pqq synthesis protein d; PDBTitle: crystal structure of pqqd from xanthomonas campestris
14	c3df8A_	Alignment		71.4	18	PDB header: transcription Chain: A: PDB Molecule: possible hxlR family transcriptional factor; PDBTitle: the crystal structure of a possible hxlR family transcriptional factor2 from thermoplasma volcanium gss1
15	d1z7ua1	Alignment		71.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxlR-like
16	c3e6mD_	Alignment		69.1	21	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.
17	c3hruA_	Alignment		68.0	17	PDB header: transcription Chain: A: PDB Molecule: metalloregulator scar; PDBTitle: crystal structure of scar with bound zn2+
18	c2x4hA_	Alignment		66.0	14	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfobolus solfataricus
19	c2nyxB_	Alignment		63.9	16	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis
20	d2hzta1	Alignment		63.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxlR-like
21	d2p6ra1	Alignment	not modelled	62.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RecQ helicase DNA-binding domain-like
22	d1yyva1	Alignment	not modelled	60.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxlR-like
23	c2h09A_	Alignment	not modelled	59.5	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
24	c3f8fA_	Alignment	not modelled	57.7	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, padr-like family; PDBTitle: crystal structure of multidrug binding transcriptional regulator lmrr2 complexed with daunomycin
25	c3g3zA_	Alignment	not modelled	56.5	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
26	c3odnA_	Alignment	not modelled	55.4	13	PDB header: membrane protein Chain: A: PDB Molecule: dally-like protein; PDBTitle: the crystal structure of drosophila dally-like protein core domain
27	d1hsta_	Alignment	not modelled	55.1	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5
28	c2it0A_	Alignment	not modelled	54.7	18	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

29	c1xmaA_	 Alignment	not modelled	54.4	12	PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulator; PDBTitle: structure of a transcriptional regulator from clostridium thermocellum2 cth-833
30	d1xmaa_	 Alignment	not modelled	54.4	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like
31	c3I09B_	 Alignment	not modelled	54.3	17	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
32	d1i7da_	 Alignment	not modelled	53.8	10	Fold: Prokaryotic type I DNA topoisomerase Superfamily: Prokaryotic type I DNA topoisomerase Family: Prokaryotic type I DNA topoisomerase
33	d1lnwa_	 Alignment	not modelled	52.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
34	d1s3ja_	 Alignment	not modelled	52.5	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
35	d1uhma_	 Alignment	not modelled	52.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5
36	d2f2ea1	 Alignment	not modelled	50.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like
37	c3hhhA_	 Alignment	not modelled	47.3	11	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
38	c3f3xA_	 Alignment	not modelled	47.0	12	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of the transcriptional regulator bldr2 from sulfolobus solfataricus
39	d2juza1	 Alignment	not modelled	45.8	37	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
40	c2gxgA_	 Alignment	not modelled	43.0	11	PDB header: transcription Chain: A: PDB Molecule: 146aa long hypothetical transcriptional regulator; PDBTitle: crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
41	c2o59B_	 Alignment	not modelled	42.6	10	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
42	d1ghca_	 Alignment	not modelled	42.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5
43	d2a61a1	 Alignment	not modelled	40.1	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
44	d2fbha1	 Alignment	not modelled	38.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
45	d1ussa_	 Alignment	not modelled	37.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5
46	c3bpxB_	 Alignment	not modelled	37.7	17	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of marr
47	d1yqaa1	 Alignment	not modelled	36.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5
48	d1ub9a_	 Alignment	not modelled	36.8	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
49	c1fx7C_	 Alignment	not modelled	36.7	18	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
50	d1usta_	 Alignment	not modelled	36.0	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5
51	d2etha1	 Alignment	not modelled	35.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
52	d2qtia1	 Alignment	not modelled	35.2	33	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
53	c3k0IA_	 Alignment	not modelled	34.6	15	PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
54	c3mkyp_	 Alignment	not modelled	33.0	15	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form

55	c3ri2B_		Alignment	not modelled	32.6	17	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
56	c3bj6B_		Alignment	not modelled	32.6	21	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579
57	d2jrxal		Alignment	not modelled	32.5	37	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
58	c3s1bA_		Alignment	not modelled	31.5	31	PDB header: signaling protein Chain: A: PDB Molecule: mini-z; PDBTitle: the development of peptide-based tools for the analysis of2 angiogenesis
59	d1p4xa2		Alignment	not modelled	31.0	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
60	c1fnnB_		Alignment	not modelled	30.7	13	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
61	d2juwal		Alignment	not modelled	30.4	32	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
62	d1qoja_		Alignment	not modelled	29.9	43	Fold: Long alpha-hairpin Superfamily: C-terminal UvrC-binding domain of UvrB Family: C-terminal UvrC-binding domain of UvrB
63	d1lj9a_		Alignment	not modelled	28.2	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
64	d2fbia1		Alignment	not modelled	28.0	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
65	d1jgsa_		Alignment	not modelled	27.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
66	c2fxaB_		Alignment	not modelled	26.3	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.
67	d1lj8a3		Alignment	not modelled	26.3	10	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Mannitol 2-dehydrogenase
68	c3nrvC_		Alignment	not modelled	25.3	8	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
69	c3mkzU_		Alignment	not modelled	24.9	15	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
70	c3bjaa_		Alignment	not modelled	24.7	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
71	c1w0jB_		Alignment	not modelled	24.6	13	PDB header: hydrolase Chain: B: PDB Molecule: atp synthase alpha chain heart isoform, PDBTitle: beryllium fluoride inhibited bovine f1-atpase
72	d2frha1		Alignment	not modelled	24.2	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
73	d2jpqa1		Alignment	not modelled	24.1	26	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
74	d2bv6a1		Alignment	not modelled	23.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
75	d2pv4a1		Alignment	not modelled	23.5	34	Fold: Sama2622-like Superfamily: Sama2622-like Family: Sama2622-like
76	d1hsja1		Alignment	not modelled	22.0	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
77	c2pjha_		Alignment	not modelled	21.8	11	PDB header: transport protein Chain: A: PDB Molecule: nuclear protein localization protein 4 homolog; PDBTitle: strctural model of the p97 n domain- npl4 ubd complex
78	c3fm5D_		Alignment	not modelled	20.8	14	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
79	d2hr3a1		Alignment	not modelled	20.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
80	c2vn2B_		Alignment	not modelled	20.2	17	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
81	d1l4ia2	Alignment	not modelled	20.1	43	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
82	c2ov2O	Alignment	not modelled	19.8	44	PDB header: protein binding/transferase Chain: O: PDB Molecule: serine/threonine-protein kinase pak 4; PDBTitle: the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)
83	c3ls1A	Alignment	not modelled	19.7	12	PDB header: photosynthesis Chain: A: PDB Molecule: sll1638 protein; PDBTitle: crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
84	d1p5va2	Alignment	not modelled	19.3	56	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
85	d1iuga	Alignment	not modelled	19.3	16	Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
86	c1qpxA	Alignment	not modelled	19.0	29	PDB header: chaperone Chain: A: PDB Molecule: papd chaperone; PDBTitle: crystal structures of self-capping papd chaperone homodimers
87	c2qe7C	Alignment	not modelled	18.4	13	PDB header: hydrolase Chain: C: PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
88	c1qunA	Alignment	not modelled	18.1	67	PDB header: chaperone/structural protein Chain: A: PDB Molecule: papd-like chaperone fimc; PDBTitle: x-ray structure of the fimc-fimh chaperone adhesin complex2 from uropathogenic e.coli
89	d3bwuc2	Alignment	not modelled	17.9	47	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
90	d2co7b2	Alignment	not modelled	17.9	44	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
91	c2qenA	Alignment	not modelled	17.6	13	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
92	c2r9vA	Alignment	not modelled	17.5	12	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of atp synthase subunit alpha (tm1612) from2 thermotoga maritima at 2.10 a resolution
93	c3q48B	Alignment	not modelled	17.5	42	PDB header: chaperone Chain: B: PDB Molecule: chaperone cupb2; PDBTitle: crystal structure of pseudomonas aeruginosa cupb2 chaperone
94	d1zara1	Alignment	not modelled	17.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rio2 serine protein kinase N-terminal domain
95	d2otaa1	Alignment	not modelled	17.3	26	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
96	c3l7wA	Alignment	not modelled	17.3	12	PDB header: transcription Chain: A: PDB Molecule: putative uncharacterized protein smu.1704; PDBTitle: the crystal structure of smu.1704 from streptococcus mutans ua159
97	c1g3wA	Alignment	not modelled	17.2	15	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
98	d1p4xa1	Alignment	not modelled	17.1	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
99	d2j2za2	Alignment	not modelled	17.0	42	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain