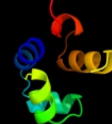
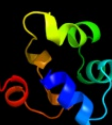


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nera_	 Alignment		100.0	57	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
2	c3b7hA_	 Alignment		97.8	14	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
3	d1lmb3_	 Alignment		97.6	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
4	c3t76A_	 Alignment		97.6	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
5	d1rioa_	 Alignment		97.5	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
6	d1lilib_	 Alignment		97.5	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
7	c2bnoA_	 Alignment		97.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenii.
8	d1b0na2	 Alignment		97.4	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
9	d1sq8a_	 Alignment		97.4	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
10	d1r69a_	 Alignment		97.4	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
11	c2ebyA_	 Alignment		97.4	11	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli

12	dly7ya1	Alignment		97.3	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
13	dly9qa1	Alignment		97.2	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
14	c2ewtA	Alignment		97.1	14	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd
15	d2b5aa1	Alignment		97.1	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
16	c3trbA	Alignment		97.1	21	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
17	c1y9qA	Alignment		97.1	20	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth_3 family; PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
18	d1ladra	Alignment		97.1	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
19	c1b0nA	Alignment		97.1	18	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
20	c3bs3A	Alignment		97.1	25	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
21	c3omtA	Alignment	not modelled	97.1	20	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.
22	d1utxa	Alignment	not modelled	97.1	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
23	d2croa	Alignment	not modelled	97.0	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
24	c3clcC	Alignment	not modelled	97.0	18	PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
25	d2icta1	Alignment	not modelled	97.0	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
26	d2ofya1	Alignment	not modelled	96.9	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
27	c2kpiA	Alignment	not modelled	96.9	11	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
28	c3op9A	Alignment	not modelled	96.9	11	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria

					innocua
29	c3f52A_	Alignment	not modelled	96.9	15 PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
30	c3ivpD_	Alignment	not modelled	96.9	13 PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
31	c3f6wE_	Alignment	not modelled	96.8	16 PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
32	c3cecA_	Alignment	not modelled	96.8	20 PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system; PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
33	d2r1j1l	Alignment	not modelled	96.7	24 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
34	c3bdnB_	Alignment	not modelled	96.6	16 PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
35	c3kxaD_	Alignment	not modelled	96.6	25 PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
36	c2o38A_	Alignment	not modelled	96.3	18 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
37	d2o38a1	Alignment	not modelled	96.3	18 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
38	d2a6ca1	Alignment	not modelled	96.3	12 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
39	c3bd1B_	Alignment	not modelled	96.2	25 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
40	c3mlfC_	Alignment	not modelled	96.0	15 PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
41	c3lisB_	Alignment	not modelled	95.9	13 PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
42	c2wusR_	Alignment	not modelled	95.9	9 PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape2 protein rodz
43	c3eusB_	Alignment	not modelled	95.8	14 PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
44	d2hsga1	Alignment	not modelled	95.6	17 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
45	c2fjrB_	Alignment	not modelled	95.6	15 PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
46	c3h5tA_	Alignment	not modelled	95.6	26 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
47	c2xcjB_	Alignment	not modelled	95.5	20 PDB header: viral protein Chain: B: PDB Molecule: c protein; PDBTitle: crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
48	d1lcda_	Alignment	not modelled	95.4	16 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
49	d2bjca1	Alignment	not modelled	95.2	16 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
50	c3fymA_	Alignment	not modelled	95.0	11 PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of ymfM, a putative dna-binding membrane2 protein from staphylococcus aureus
51	d1x57a1	Alignment	not modelled	94.9	20 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
52	d1efaa1	Alignment	not modelled	94.9	17 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
53	c2l8nA_	Alignment	not modelled	94.8	23 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
54	c2lexA_	Alignment	not modelled	94.7	22 PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr;

54	c2lcva	Alignment	not modelled	94.7	23	PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation
55	dluxca	Alignment	not modelled	94.7	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
56	c2jvlA	Alignment	not modelled	94.6	17	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
57	c3dnvB	Alignment	not modelled	94.3	12	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
58	c1bdhA	Alignment	not modelled	94.2	15	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
59	c3kxD	Alignment	not modelled	94.1	28	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
60	c3fmyA	Alignment	not modelled	94.0	13	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)
61	dluxda	Alignment	not modelled	93.9	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
62	d2ppxa1	Alignment	not modelled	93.9	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
63	c2ppxA	Alignment	not modelled	93.9	21	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
64	d1dwka1	Alignment	not modelled	93.9	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
65	c3pxpA	Alignment	not modelled	93.8	17	PDB header: transcription regulator Chain: A: PDB Molecule: helix-turn-helix domain protein; PDBTitle: crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
66	c1zvva	Alignment	not modelled	93.6	20	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
67	d1qpza1	Alignment	not modelled	93.4	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
68	c2ef8A	Alignment	not modelled	93.3	18	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
69	d1k78a1	Alignment	not modelled	92.9	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
70	c2iv1J	Alignment	not modelled	92.3	22	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
71	c1u78A	Alignment	not modelled	92.1	18	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
72	d1pdnc	Alignment	not modelled	90.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
73	c2gm4B	Alignment	not modelled	90.1	12	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
74	c2elhA	Alignment	not modelled	89.8	28	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
75	d6paxa1	Alignment	not modelled	89.4	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
76	c6paxA	Alignment	not modelled	88.4	24	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
77	d2coba1	Alignment	not modelled	88.0	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
78	d2cg4a1	Alignment	not modelled	86.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
79	d1bw6a	Alignment	not modelled	86.4	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
80	c3gn5B	Alignment	not modelled	86.0	15	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)

81	c2k27A_	Alignment	not modelled	84.8	24	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
82	c3mzyA_	Alignment	not modelled	84.5	14	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
83	d1hlva1	Alignment	not modelled	83.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
84	c2cg4B_	Alignment	not modelled	82.2	21	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
85	c2r0qF_	Alignment	not modelled	82.1	7	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
86	c2vbzA_	Alignment	not modelled	82.1	24	PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
87	c2dbbA_	Alignment	not modelled	81.5	6	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
88	d1ilga1	Alignment	not modelled	80.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
89	c2e1cA_	Alignment	not modelled	79.9	27	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
90	c2l4aA_	Alignment	not modelled	79.8	33	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
91	c2p6tH_	Alignment	not modelled	79.5	27	PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
92	d2obpa1	Alignment	not modelled	79.4	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ReutB4095-like
93	d1r71a_	Alignment	not modelled	79.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
94	d1umqa_	Alignment	not modelled	79.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
95	c1umqA_	Alignment	not modelled	79.2	18	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
96	d2jn6a1	Alignment	not modelled	79.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
97	d1vz0a1	Alignment	not modelled	78.8	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
98	c3e7lD_	Alignment	not modelled	78.3	17	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
99	c2cfxD_	Alignment	not modelled	78.2	25	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
100	c2ia0A_	Alignment	not modelled	78.1	18	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)
101	c3i4pA_	Alignment	not modelled	78.0	18	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
102	c2e7xA_	Alignment	not modelled	77.6	21	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
103	c3m1eA_	Alignment	not modelled	77.5	9	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd
104	c1r71B_	Alignment	not modelled	76.8	19	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional repressor protein korb; PDBTitle: crystal structure of the dna binding domain of korb in2 complex with the operator dna
105	c1ilgA_	Alignment	not modelled	76.3	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpA; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus

106	d1ntca_	Alignment	not modelled	76.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
107	c2oerA_	Alignment	not modelled	75.7	21	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: probable transcriptional regulator from pseudomonas2 aeruginosa
108	d2cyya1	Alignment	not modelled	75.7	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
109	c1or7A_	Alignment	not modelled	75.2	15	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma-e factor; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
110	d1fipa_	Alignment	not modelled	74.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
111	d1xsva_	Alignment	not modelled	74.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
112	c1rr7A_	Alignment	not modelled	74.5	22	PDB header: transcription Chain: A: PDB Molecule: middle operon regulator; PDBTitle: crystal structure of the middle operon regulator protein of2 bacteriophage mu
113	d1rr7a_	Alignment	not modelled	74.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Middle operon regulator, Mor
114	c1s7eA_	Alignment	not modelled	74.2	27	PDB header: transcription Chain: A: PDB Molecule: hepatocyte nuclear factor 6; PDBTitle: solution structure of hnf-6
115	d1mkma1	Alignment	not modelled	74.0	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain
116	c3tgnA_	Alignment	not modelled	71.8	18	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
117	c3hugA_	Alignment	not modelled	71.4	19	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigl
118	d2cfxa1	Alignment	not modelled	71.4	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
119	c2i10A_	Alignment	not modelled	71.3	13	PDB header: transcription Chain: A: PDB Molecule: putative tetr transcriptional regulator; PDBTitle: putative tetr transcriptional regulator from rhodococcus sp. rha1
120	c3k2zA_	Alignment	not modelled	71.1	21	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima