
















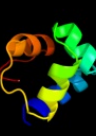








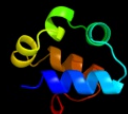






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gn5B_	 Alignment		100.0	100	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
2	c3fmyA_	 Alignment		99.6	100	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
3	c2ppxA_	 Alignment		99.4	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
4	d2ppxA1	 Alignment		99.4	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
5	c1y9qA_	 Alignment		99.2	16	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
6	c3ivpD_	 Alignment		99.1	18	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.
7	c3op9A_	 Alignment		99.1	18	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
8	c3bs3A_	 Alignment		99.1	26	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
9	d1sq8a_	 Alignment		99.1	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
10	c3lisB_	 Alignment		99.0	20	PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
11	d1r69a_	 Alignment		99.0	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors

12	d2croa_	Alignment		99.0	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
13	d1rioa_	Alignment		99.0	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
14	c3mlfC_	Alignment		99.0	19	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
15	c2bnoA_	Alignment		99.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
16	c1b0nA_	Alignment		99.0	24	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
17	c3f52A_	Alignment		99.0	14	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
18	d2icta1	Alignment		99.0	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
19	d1y7ya1	Alignment		99.0	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
20	c3omtA_	Alignment		99.0	15	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.
21	c2kpiA_	Alignment	not modelled	99.0	23	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
22	d2r1jl1	Alignment	not modelled	99.0	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
23	d1adra_	Alignment	not modelled	99.0	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
24	d2b5aa1	Alignment	not modelled	99.0	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
25	c2ewtA_	Alignment	not modelled	99.0	16	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd
26	c3eusB_	Alignment	not modelled	99.0	12	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
27	c3kxaD_	Alignment	not modelled	99.0	21	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
28	c3clcC_	Alignment	not modelled	99.0	16	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
29	d1lIib_	Alignment	not modelled	98.9	18 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
30	d1y9qa1	Alignment	not modelled	98.9	16 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
31	c2fjrB_	Alignment	not modelled	98.9	7 PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
32	c2ebyA_	Alignment	not modelled	98.9	18 PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
33	c3f6wE_	Alignment	not modelled	98.9	19 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
34	c3cecA_	Alignment	not modelled	98.9	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
35	d1b0na2	Alignment	not modelled	98.9	24 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
36	d1x57a1	Alignment	not modelled	98.9	22 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
37	d1lmb3_	Alignment	not modelled	98.9	18 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
38	c2xcjB_	Alignment	not modelled	98.9	25 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
39	d1utxa_	Alignment	not modelled	98.9	19 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
40	c3trbA_	Alignment	not modelled	98.8	10 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
41	c3bdnB_	Alignment	not modelled	98.8	18 PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
42	c2ef8A_	Alignment	not modelled	98.8	25 PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
43	c3dnvB_	Alignment	not modelled	98.8	21 PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
44	c2o38A_	Alignment	not modelled	98.8	19 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
45	d2o38a1	Alignment	not modelled	98.8	19 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
46	c3hi2C_	Alignment	not modelled	98.8	100 PDB header: dna binding protein/toxin Chain: C: PDB Molecule: hth-type transcriptional regulator mqa(ygit); PDBTitle: structure of the n-terminal domain of the e. coli antitoxin mqa2 (ygit/b3021) in complex with the e. coli toxin mqsR (ygiu/b3022)
47	c2jvlA_	Alignment	not modelled	98.8	28 PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
48	c3t76A_	Alignment	not modelled	98.7	13 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
49	c3b7hA_	Alignment	not modelled	98.7	14 PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
50	c2axzC_	Alignment	not modelled	98.6	11 PDB header: transcription Chain: C: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/ccf10 complex
51	d2a6ca1	Alignment	not modelled	98.6	20 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
52	d2ofya1	Alignment	not modelled	98.5	20 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
53	c2wusR_	Alignment	not modelled	98.5	19 PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape2 protein rodZ PDB header: transcription regulator Chain: A: PDB Molecule: helix-turn-helix domain protein;

54	c3pxpA_	Alignment	not modelled	98.5	20	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 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
55	c3fymA_	Alignment	not modelled	98.5	23	PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
56	c2qfcB_	Alignment	not modelled	98.5	27	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
57	c2auwB_	Alignment	not modelled	97.7	17	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
58	c3bd1B_	Alignment	not modelled	96.5	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
59	d2auwa1	Alignment	not modelled	96.3	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
60	d1ic8a2	Alignment	not modelled	95.6	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
61	d1nera_	Alignment	not modelled	95.6	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
62	c3l1pA_	Alignment	not modelled	95.6	24	PDB header: transcription/dna Chain: A: PDB Molecule: pou domain, class 5, transcription factor 1; PDBTitle: pou protein:dna complex
63	clic8B_	Alignment	not modelled	95.4	11	PDB header: transcription/dna Chain: B: PDB Molecule: hepatocyte nuclear factor 1-alpha; PDBTitle: hepatocyte nuclear factor 1a bound to dna : mody3 gene2 product
64	d1r71a_	Alignment	not modelled	95.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
65	d1s4ka_	Alignment	not modelled	95.1	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: YdiL-like
66	d1e3oc2	Alignment	not modelled	95.0	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
67	d1au7a2	Alignment	not modelled	94.9	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
68	c1r71B_	Alignment	not modelled	94.8	15	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
69	c3d1nK_	Alignment	not modelled	94.5	33	PDB header: transcription regulator/dna Chain: K: PDB Molecule: pou domain, class 6, transcription factor 1; PDBTitle: structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter
70	d1rzsa_	Alignment	not modelled	94.1	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
71	d2hsga1	Alignment	not modelled	94.0	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
72	d1lcda_	Alignment	not modelled	93.8	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
73	c3k2zA_	Alignment	not modelled	93.8	15	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
74	d2bnma1	Alignment	not modelled	93.6	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
75	d2ox6a1	Alignment	not modelled	93.5	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: YdiL-like
76	d1dwka1	Alignment	not modelled	93.5	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
77	c2h8rA_	Alignment	not modelled	93.2	13	PDB header: transcription activator/dna Chain: A: PDB Molecule: hepatocyte nuclear factor 1-beta; PDBTitle: hepatocyte nuclear factor 1b bound to dna : mody5 gene2 product
78	d1luxca_	Alignment	not modelled	93.0	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
79	d2bjca1	Alignment	not modelled	92.9	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
80	d1efaa1	Alignment	not modelled	92.1	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator

81	dlvz0a1	Alignment	not modelled	91.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
82	dlqpza1	Alignment	not modelled	91.7	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
83	c1au7B_	Alignment	not modelled	91.5	25	PDB header: transcription/dna Chain: B: PDB Molecule: protein pit-1; PDBTitle: pit-1 mutant/dna complex
84	c3mkyp_	Alignment	not modelled	91.4	4	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
85	c2lcvA_	Alignment	not modelled	91.2	14	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation
86	c1hfoA_	Alignment	not modelled	91.2	28	PDB header: transcription factor Chain: A: PDB Molecule: octamer-binding transcription factor 1; PDBTitle: crystal structure of the dna-binding domain of oct-1 bound2 to dna as a dimer
87	c2xsdC_	Alignment	not modelled	91.1	24	PDB header: transcription/dna Chain: C: PDB Molecule: pou domain, class 3, transcription factor 1; PDBTitle: crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna
88	c3mkzU_	Alignment	not modelled	91.0	4	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
89	dlzs4a1	Alignment	not modelled	90.9	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Bacteriophage CII protein
90	c2l8nA_	Alignment	not modelled	90.6	14	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
91	c3kxD_	Alignment	not modelled	90.5	21	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
92	dluxda_	Alignment	not modelled	90.1	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
93	dlk78a1	Alignment	not modelled	89.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
94	c2w48D_	Alignment	not modelled	89.8	24	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
95	c2iv1J_	Alignment	not modelled	89.7	13	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
96	dlj9ia_	Alignment	not modelled	89.3	20	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
97	c1u78A_	Alignment	not modelled	89.1	23	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
98	c1hlvA_	Alignment	not modelled	88.4	21	PDB header: dna binding protein/dna Chain: A: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
99	c3h5tA_	Alignment	not modelled	88.2	10	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
100	dlhlva1	Alignment	not modelled	88.2	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
101	dl6a_	Alignment	not modelled	88.1	16	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
102	dlrp3a2	Alignment	not modelled	87.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
103	c1zvva_	Alignment	not modelled	87.4	24	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
104	c1bdhA_	Alignment	not modelled	86.9	11	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
105	dlz05a1	Alignment	not modelled	86.7	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
106	d2p7vb1	Alignment	not modelled	86.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
						PDB header: transcription Chain: O: PDB Molecule: esx-1 secretion-associated regulator

107	c3r1fO_	Alignment	not modelled	86.1	12	espr; PDBTitle: crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
108	c2aklA_	Alignment	not modelled	85.9	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phna-like protein pa0128; PDBTitle: solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
109	d2jn6a1	Alignment	not modelled	85.7	3	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
110	d1l3la1	Alignment	not modelled	85.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
111	d1x2la1	Alignment	not modelled	85.7	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
112	d6paxa1	Alignment	not modelled	85.6	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
113	c1rp3G_	Alignment	not modelled	84.9	14	PDB header: transcription Chain: G: PDB Molecule: rna polymerase sigma factor sigma-28 (fliA); PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm
114	c2jmlA_	Alignment	not modelled	84.6	10	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
115	d1z6ra1	Alignment	not modelled	84.3	3	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
116	c2elha_	Alignment	not modelled	84.2	8	PDB header: dna binding protein Chain: A: PDB Molecule: cgl1849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cgl1849-pa
117	d2o4aa1	Alignment	not modelled	83.9	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
118	d1ku3a_	Alignment	not modelled	83.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
119	c3hugA_	Alignment	not modelled	83.6	2	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 sigI
120	c1zx4B_	Alignment	not modelled	83.5	19	PDB header: translation Chain: B: PDB Molecule: plasmid partition par b protein; PDBTitle: structure of parb bound to dna