














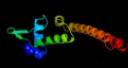












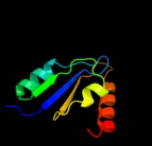




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gpvA_	 Alignment		99.8	19	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
2	d1r8da_	 Alignment		99.8	25	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
3	c2vz4A_	 Alignment		99.8	23	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to2 promoter dna
4	c3hh0C_	 Alignment		99.8	18	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
5	c3gp4B_	 Alignment		99.8	15	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
6	c3qaoA_	 Alignment		99.8	19	PDB header: transcription regulator Chain: A: PDB Molecule: merr-like transcriptional regulator; PDBTitle: the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
7	c2zhhA_	 Alignment		99.8	19	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
8	c3d6zA_	 Alignment		99.8	22	PDB header: transcription regulator/dna Chain: A: PDB Molecule: multi drug-efflux transporter 1 regulator; PDBTitle: crystal structure of r275e mutant of bmrr bound to dna and rhodamine
9	d1q06a_	 Alignment		99.8	14	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
10	d1r8ea1	 Alignment		99.7	19	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
11	c2jmlA_	 Alignment		99.7	28	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor

12	c3ezxA	Alignment		99.6	13	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
13	c2i2xD	Alignment		99.4	9	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
14	c2dg6A	Alignment		99.4	18	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
15	c1bmtB	Alignment		99.4	10	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
16	c1k98A	Alignment		99.0	10	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
17	c2ev2B	Alignment		98.5	15	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenyllyl cylcase rv1264, at ph 8.5
18	c1y80A	Alignment		97.6	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iiii)-binding protein from2 moorella thermoacetica
19	d3bula2	Alignment		97.4	10	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
20	d1q08a	Alignment		97.2	15	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
21	d1ccwa	Alignment	not modelled	96.9	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
22	c3ezfA	Alignment	not modelled	96.6	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
23	c1u78A	Alignment	not modelled	96.5	6	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
24	c2yxB	Alignment	not modelled	96.4	10	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
25	d1xrsb1	Alignment	not modelled	96.2	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
26	c1z4hA	Alignment	not modelled	95.6	12	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
27	d7reqa2	Alignment	not modelled	95.4	9	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
28	c1xrsB	Alignment	not modelled	95.3	14	PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
						Fold: Flavodoxin-like

29	d1fmfa_	Alignment	not modelled	95.2	12	Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
30	c1hlvA_	Alignment	not modelled	95.0	24	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
31	d2jn6a1	Alignment	not modelled	94.3	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
32	c3op9A_	Alignment	not modelled	93.1	11	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
33	c2kfsA_	Alignment	not modelled	92.4	15	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
34	d1pdnc_	Alignment	not modelled	91.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
35	c3fymA_	Alignment	not modelled	90.6	12	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
36	d3bula1	Alignment	not modelled	90.6	8	Fold: Methionine synthase domain-like Superfamily: Methionine synthase domain Family: Methionine synthase domain
37	c2rn7A_	Alignment	not modelled	90.4	29	PDB header: unknown function Chain: A: PDB Molecule: is629 orfA; PDBTitle: nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
38	d1j9ia_	Alignment	not modelled	89.5	19	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
39	d2b5aa1	Alignment	not modelled	89.4	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
40	d1utxa_	Alignment	not modelled	88.4	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
41	c2wusR_	Alignment	not modelled	87.2	27	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape2 protein rodZ
42	c6paxA_	Alignment	not modelled	87.0	14	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
43	d1etxa_	Alignment	not modelled	86.8	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
44	d1fipa_	Alignment	not modelled	86.6	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
45	c2ppxA_	Alignment	not modelled	86.1	32	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
46	d2ppxa1	Alignment	not modelled	86.1	32	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
47	d2bjca1	Alignment	not modelled	86.1	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
48	c3e7lD_	Alignment	not modelled	85.8	14	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
49	c3fmyA_	Alignment	not modelled	85.6	9	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)
50	c3bd1B_	Alignment	not modelled	83.4	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
51	c2kpiA_	Alignment	not modelled	83.2	21	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
52	c3iwfA_	Alignment	not modelled	83.1	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpri family; PDBTitle: the crystal structure of the n-terminal domain of a rpri2 transcriptional regulator from staphylococcus epidermidis to 1.4a
53	c3clcC_	Alignment	not modelled	82.0	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
54	d1adra_	Alignment	not modelled	81.6	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
						Fold: lambda repressor-like DNA-binding domains

55	d1lcda_	Alignment	not modelled	81.5	22	Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
56	c3mklB_	Alignment	not modelled	81.0	15	PDB header: transcription regulator Chain: B: PDB Molecule: hth-type transcriptional regulator gadx; PDBTitle: crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
57	c1bdhA_	Alignment	not modelled	80.3	17	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
58	c1zvva_	Alignment	not modelled	80.3	20	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
59	d1x57a1	Alignment	not modelled	79.9	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
60	c3gn5B_	Alignment	not modelled	79.8	11	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)
61	c3omtA_	Alignment	not modelled	79.8	23	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.
62	c3f52A_	Alignment	not modelled	79.8	27	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
63	c3ivpD_	Alignment	not modelled	79.3	14	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.
64	c3bs3A_	Alignment	not modelled	79.2	18	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
65	c3b7hA_	Alignment	not modelled	79.2	36	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
66	c1umqA_	Alignment	not modelled	79.0	15	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
67	d1umqa_	Alignment	not modelled	79.0	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
68	c3kxaD_	Alignment	not modelled	78.8	17	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
69	d1r69a_	Alignment	not modelled	78.5	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
70	d1qpza1	Alignment	not modelled	78.0	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
71	d1sq8a_	Alignment	not modelled	77.8	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
72	d1b0na2	Alignment	not modelled	77.7	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
73	c2o8xA_	Alignment	not modelled	77.6	21	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
74	c3t76A_	Alignment	not modelled	77.6	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
75	c1y9qA_	Alignment	not modelled	77.6	18	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
76	d2ofya1	Alignment	not modelled	77.4	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
77	d2r1j11	Alignment	not modelled	77.1	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
78	d2croa_	Alignment	not modelled	76.8	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
79	c3h5tA_	Alignment	not modelled	76.6	18	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
80	c3k69A_	Alignment	not modelled	76.6	13	PDB header: transcription Chain: A: PDB Molecule: putative transcription regulator; PDBTitle: crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
						PDB header: transcription regulator

81	c3mlfC_	Alignment	not modelled	76.3	18	Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
82	d1rp3a2	Alignment	not modelled	76.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
83	d1y7ya1	Alignment	not modelled	76.0	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
84	c3dnvB_	Alignment	not modelled	75.6	23	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
85	c1zljE_	Alignment	not modelled	75.0	17	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxiC2 response regulator dosR c-terminal domain
86	c1b0nA_	Alignment	not modelled	75.0	23	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
87	c2ef8A_	Alignment	not modelled	74.5	9	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
88	c2bnoA_	Alignment	not modelled	74.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorensis.
89	c2l8nA_	Alignment	not modelled	74.0	31	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
90	c3mzyA_	Alignment	not modelled	73.8	22	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
91	d1g2ha_	Alignment	not modelled	73.7	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
92	c2xcjB_	Alignment	not modelled	73.6	18	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
93	c1x3uA_	Alignment	not modelled	73.3	23	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
94	d1luxca_	Alignment	not modelled	73.2	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
95	d2hsqa1	Alignment	not modelled	72.9	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
96	d1bw6a_	Alignment	not modelled	72.6	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
97	c2k9sA_	Alignment	not modelled	72.5	22	PDB header: transcription Chain: A: PDB Molecule: arabinose operon regulatory protein; PDBTitle: solution structure of dna binding domain of e. coli arac
98	d1y9qa1	Alignment	not modelled	72.5	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
99	c2jvlA_	Alignment	not modelled	72.1	18	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
100	c3hugA_	Alignment	not modelled	72.0	13	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
101	c3kxD_	Alignment	not modelled	71.9	17	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
102	c2ebyA_	Alignment	not modelled	71.8	23	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
103	c3f6wE_	Alignment	not modelled	71.8	14	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
104	c2fjrB_	Alignment	not modelled	71.7	19	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
105	d1llib_	Alignment	not modelled	71.1	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
106	c3cuoB_	Alignment	not modelled	70.8	21	PDB header: transcription regulator Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator ygav; PDBTitle: crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
						Fold: DNA/RNA-binding 3-helical bundle

107	dlyioa1	Alignment	not modelled	70.5	15	Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
108	dlefaa1	Alignment	not modelled	70.4	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
109	dlfsea_	Alignment	not modelled	70.0	23	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)
110	c3trbA_	Alignment	not modelled	69.9	14	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
111	dlor7a1	Alignment	not modelled	69.5	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
112	dluxda_	Alignment	not modelled	68.9	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
113	c2krfB_	Alignment	not modelled	68.7	13	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
114	d2icta1	Alignment	not modelled	68.6	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
115	dlj5ya1	Alignment	not modelled	68.6	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
116	c2lcvA_	Alignment	not modelled	68.4	26	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
117	dlrioa_	Alignment	not modelled	67.9	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
118	dljt6a1	Alignment	not modelled	67.8	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
119	c2elha_	Alignment	not modelled	67.8	27	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
120	dla04a1	Alignment	not modelled	67.8	17	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)