


















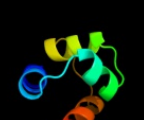




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ppxA_</a>	 Alignment		99.6	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1735; <b>PDBTitle:</b> crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
2	<a href="#">d2ppxA1</a>	 Alignment		99.6	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
3	<a href="#">c3fmyA_</a>	 Alignment		99.6	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
4	<a href="#">c3gn5B_</a>	 Alignment		99.6	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa (ygit/b3021); <b>PDBTitle:</b> structure of the e. coli protein mqsa (ygit/b3021)
5	<a href="#">c1y9gA_</a>	 Alignment		99.4	28	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family; <b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
6	<a href="#">c3ivpD_</a>	 Alignment		99.3	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative transposon-related dna-binding protein; <b>PDBTitle:</b> the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
7	<a href="#">c3bs3A_</a>	 Alignment		99.3	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of a putative dna-binding protein from bacteroides2 fragilis
8	<a href="#">c3lisB_</a>	 Alignment		99.3	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> csp231i c protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
9	<a href="#">c2xcjB_</a>	 Alignment		99.3	20	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> c protein; <b>PDBTitle:</b> crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
10	<a href="#">c3op9A_</a>	 Alignment		99.3	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> pli0006 protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator from listeria innocua
11	<a href="#">c2kpiA_</a>	 Alignment		99.2	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sos-response transcriptional repressor, lexa; <b>PDBTitle:</b> solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a

12	<a href="#">c3mlfC_</a>	Alignment		99.2	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> putative transcriptional regulator from staphylococcus aureus.
13	<a href="#">d1x57a1</a>	Alignment		99.2	20	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> EDF1-like
14	<a href="#">c3eusB_</a>	Alignment		99.2	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding protein; <b>PDBTitle:</b> the crystal structure of the dna binding protein from silicibacter2 pomeroyi
15	<a href="#">c3omtA_</a>	Alignment		99.2	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
16	<a href="#">c3f52A_</a>	Alignment		99.2	20	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> clp gene regulator (clgr); <b>PDBTitle:</b> crystal structure of the clp gene regulator clgr from c. glutamicum
17	<a href="#">d1rioa_</a>	Alignment		99.2	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
18	<a href="#">c2bnoA_</a>	Alignment		99.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase; <b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
19	<a href="#">c2jvlA_</a>	Alignment		99.2	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> trmbf1; <b>PDBTitle:</b> nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
20	<a href="#">c2ewtA_</a>	Alignment		99.2	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of the dna-binding domain of bldd
21	<a href="#">c1b0nA_</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> protein (sinr protein); <b>PDBTitle:</b> sinr protein/sini protein complex
22	<a href="#">d1adra_</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
23	<a href="#">d1y7ya1</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
24	<a href="#">d1utxa_</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
25	<a href="#">d2r1jl1</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
26	<a href="#">d2b5aa1</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
27	<a href="#">c3clcC_</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.esp13961 tetramer in complex with its natural 35 base-pair operator
28	<a href="#">d2icta1</a>	Alignment	not modelled	99.1	10	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
						<b>PDB header:</b> transcription/dna

29	<a href="#">c3dnvB_</a>	Alignment	not modelled	99.1	11	<b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator hipb; <b>PDBTitle:</b> mdt protein
30	<a href="#">d1y9qa1</a>	Alignment	not modelled	99.1	28	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Probable transcriptional regulator VC1968, N-terminal domain
31	<a href="#">c3f6wE_</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> xre-family like protein; <b>PDBTitle:</b> xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
32	<a href="#">c2ebyA_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ybaq; <b>PDBTitle:</b> crystal structure of a hypothetical protein from e. coli
33	<a href="#">c2ef8A_</a>	Alignment	not modelled	99.1	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription factor; <b>PDBTitle:</b> crystal structure of c.ecot38is
34	<a href="#">d1b0na2</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
35	<a href="#">c3kxAd_</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of ngo0477 from neisseria gonorrhoeae
36	<a href="#">d1lmb3_</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
37	<a href="#">d1llib_</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
38	<a href="#">d1r69a_</a>	Alignment	not modelled	99.1	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
39	<a href="#">d1sq8a_</a>	Alignment	not modelled	99.1	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
40	<a href="#">c3cecA_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative antidote protein of plasmid maintenance system; <b>PDBTitle:</b> crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
41	<a href="#">d2o38a1</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
42	<a href="#">c2o38A_</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> putative xre family transcriptional regulator
43	<a href="#">d2croa_</a>	Alignment	not modelled	99.0	12	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
44	<a href="#">d2a6ca1</a>	Alignment	not modelled	99.0	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
45	<a href="#">c2fjrB_</a>	Alignment	not modelled	99.0	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> repressor protein ci; <b>PDBTitle:</b> crystal structure of bacteriophage 186
46	<a href="#">c3trbA_</a>	Alignment	not modelled	99.0	7	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence-associated protein i; <b>PDBTitle:</b> structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
47	<a href="#">c3b7hA_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> prophage lp1 protein 11; <b>PDBTitle:</b> crystal structure of the prophage lp1 protein 11
48	<a href="#">c3bdnB_</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> lambda repressor; <b>PDBTitle:</b> crystal structure of the lambda repressor
49	<a href="#">c3pxpA_</a>	Alignment	not modelled	98.9	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> helix-turn-helix domain protein; <b>PDBTitle:</b> crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
50	<a href="#">c3t76A_</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator vanug; <b>PDBTitle:</b> crystal structure of transcriptional regulator vanug, form ii
51	<a href="#">d2ofya1</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
52	<a href="#">c2axzC_</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> prgx; <b>PDBTitle:</b> crystal structure of prgx/ccf10 complex
53	<a href="#">c2qfcB_</a>	Alignment	not modelled	98.7	25	<b>PDB header:</b> transcription regulation <b>Chain:</b> B: <b>PDB Molecule:</b> plcR protein; <b>PDBTitle:</b> crystal structure of bacillus thuringiensis plcR complexed with papr
54	<a href="#">c2wusR_</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> structural protein <b>Chain:</b> R: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> bacterial actin mreB assembles in complex with cell shape2 protein rodz
55	<a href="#">c3furnA</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;

55	<a href="#">c3ryna</a>	Alignment	not modelled	98.8	13	<b>PDBTitle:</b> the 1a structure of ymfM, a putative dna-binding membrane2 protein from staphylococcus aureus <b>PDB header:</b> unknown function
56	<a href="#">c2auwB</a>	Alignment	not modelled	97.6	20	<b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ne0471; <b>PDBTitle:</b> crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
57	<a href="#">d1s4ka</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> YdiL-like
58	<a href="#">c3bd1B</a>	Alignment	not modelled	96.7	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> cro protein; <b>PDBTitle:</b> structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
59	<a href="#">c3l1pA</a>	Alignment	not modelled	95.8	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> pou domain, class 5, transcription factor 1; <b>PDBTitle:</b> pou protein:dna complex
60	<a href="#">d2auwa1</a>	Alignment	not modelled	95.8	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE0471 C-terminal domain-like
61	<a href="#">d1ic8a2</a>	Alignment	not modelled	95.6	2	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
62	<a href="#">d1e3oc2</a>	Alignment	not modelled	95.6	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
63	<a href="#">d1au7a2</a>	Alignment	not modelled	95.5	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
64	<a href="#">d1nera</a>	Alignment	not modelled	95.5	12	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
65	<a href="#">c1ic8B</a>	Alignment	not modelled	95.5	4	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hepatocyte nuclear factor 1-alpha; <b>PDBTitle:</b> hepatocyte nuclear factor 1a bound to dna : mody3 gene2 product
66	<a href="#">c3k2zA</a>	Alignment	not modelled	95.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lexa repressor; <b>PDBTitle:</b> crystal structure of a lexa protein from thermotoga maritima
67	<a href="#">d1lrza</a>	Alignment	not modelled	95.1	26	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
68	<a href="#">c3d1nK</a>	Alignment	not modelled	95.1	18	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> K: <b>PDB Molecule:</b> pou domain, class 6, transcription factor 1; <b>PDBTitle:</b> structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter
69	<a href="#">d2ox6a1</a>	Alignment	not modelled	95.0	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> YdiL-like
70	<a href="#">d1lcda</a>	Alignment	not modelled	94.9	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
71	<a href="#">d2hsga1</a>	Alignment	not modelled	94.8	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
72	<a href="#">d1r71a</a>	Alignment	not modelled	94.3	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
73	<a href="#">d2bnma1</a>	Alignment	not modelled	94.3	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
74	<a href="#">d2bjca1</a>	Alignment	not modelled	94.3	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
75	<a href="#">c2h8rA</a>	Alignment	not modelled	94.1	7	<b>PDB header:</b> transcription activator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte nuclear factor 1-beta; <b>PDBTitle:</b> hepatocyte nuclear factor 1b bound to dna: mody5 gene2 product
76	<a href="#">d1k78a1</a>	Alignment	not modelled	94.0	32	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
77	<a href="#">c2w48D</a>	Alignment	not modelled	93.9	23	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> sorbitol operon regulator; <b>PDBTitle:</b> crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
78	<a href="#">c1r71B</a>	Alignment	not modelled	93.8	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor protein korb; <b>PDBTitle:</b> crystal structure of the dna binding domain of korb in2 complex with the operator dna
79	<a href="#">d1efaa1</a>	Alignment	not modelled	93.6	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
80	<a href="#">d1qpza1</a>	Alignment	not modelled	93.5	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
81	<a href="#">c1u78A</a>	Alignment	not modelled	93.3	7	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna

82	<a href="#">c3mkyP_</a>	Alignment	not modelled	93.1	14	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> P: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-323)-18mer dna complex, i23 form
83	<a href="#">c2lcvA_</a>	Alignment	not modelled	92.8	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor cytr; <b>PDBTitle:</b> structure of the cytidine repressor dna-binding domain; an alternate2 calculation
84	<a href="#">c3mkzU_</a>	Alignment	not modelled	92.7	14	<b>PDB header:</b> dna-binding protein/dna <b>Chain:</b> U: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-272)-18mer complex, p21 form
85	<a href="#">d1hlva1</a>	Alignment	not modelled	92.4	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
86	<a href="#">d1lv0a1</a>	Alignment	not modelled	92.3	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
87	<a href="#">c2l8nA_</a>	Alignment	not modelled	92.0	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor cytr; <b>PDBTitle:</b> nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
88	<a href="#">c1hf0A_</a>	Alignment	not modelled	92.0	21	<b>PDB header:</b> transcription factor <b>Chain:</b> A: <b>PDB Molecule:</b> octamer-binding transcription factor 1; <b>PDBTitle:</b> crystal structure of the dna-binding domain of oct-1 bound2 to dna as a dimer
89	<a href="#">c2k9qB_</a>	Alignment	not modelled	92.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244.
90	<a href="#">d6paxa1</a>	Alignment	not modelled	91.9	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
91	<a href="#">c2elhA_</a>	Alignment	not modelled	91.9	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cg11849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
92	<a href="#">d2jn6a1</a>	Alignment	not modelled	91.6	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
93	<a href="#">d2csfa1</a>	Alignment	not modelled	91.6	23	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> CUT domain
94	<a href="#">c3kxD_</a>	Alignment	not modelled	91.4	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
95	<a href="#">c1au7B_</a>	Alignment	not modelled	91.2	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> protein pit-1; <b>PDBTitle:</b> pit-1 mutant/dna complex
96	<a href="#">d1luxca_</a>	Alignment	not modelled	91.1	23	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
97	<a href="#">c1bdhA_</a>	Alignment	not modelled	90.9	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (purine repressor); <b>PDBTitle:</b> purine repressor mutant-hypoxanthine-palindromic operator2 complex
98	<a href="#">d1q06a_</a>	Alignment	not modelled	90.8	23	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
99	<a href="#">d1dwka1</a>	Alignment	not modelled	90.5	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Cyanase N-terminal domain
100	<a href="#">c3h5tA_</a>	Alignment	not modelled	90.2	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
101	<a href="#">d1z05a1</a>	Alignment	not modelled	89.9	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
102	<a href="#">d1j9ia_</a>	Alignment	not modelled	89.5	20	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Terminase gpNU1 subunit domain
103	<a href="#">c1hlvA_</a>	Alignment	not modelled	89.3	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> major centromere autoantigen b; <b>PDBTitle:</b> crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
104	<a href="#">c1zvva_</a>	Alignment	not modelled	89.2	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-resistance amylase regulator; <b>PDBTitle:</b> crystal structure of a ccpa-crh-dna complex
105	<a href="#">c3gp4B_</a>	Alignment	not modelled	89.1	27	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
106	<a href="#">d1x2la1</a>	Alignment	not modelled	89.0	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> CUT domain
107	<a href="#">c3r1fO_</a>	Alignment	not modelled	88.8	12	<b>PDB header:</b> transcription <b>Chain:</b> O: <b>PDB Molecule:</b> esx-1 secretion-associated regulator espr; <b>PDBTitle:</b> crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
						<b>Fold:</b> lambda repressor-like DNA-binding domains



108	<a href="#">d1uxda_</a>	Alignment	not modelled	88.8	23	<b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
109	<a href="#">d2a61a1</a>	Alignment	not modelled	88.4	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
110	<a href="#">c2jmlA_</a>	Alignment	not modelled	88.4	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding domain/transcriptional regulator; <b>PDBTitle:</b> solution structure of the n-terminal domain of cara repressor
111	<a href="#">c2xsdC_</a>	Alignment	not modelled	87.9	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> pou domain, class 3, transcription factor 1; <b>PDBTitle:</b> crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna
112	<a href="#">d1bw6a_</a>	Alignment	not modelled	87.8	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
113	<a href="#">d2p7vb1</a>	Alignment	not modelled	87.7	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
114	<a href="#">d2o4aa1</a>	Alignment	not modelled	87.6	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> CUT domain
115	<a href="#">c6paxA_</a>	Alignment	not modelled	87.6	30	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein pax-6; <b>PDBTitle:</b> crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
116	<a href="#">d2ao9a1</a>	Alignment	not modelled	87.5	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
117	<a href="#">c2vz4A_</a>	Alignment	not modelled	87.4	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator tipa; <b>PDBTitle:</b> the n-terminal domain of merr-like protein tipal bound to2 promoter dna
118	<a href="#">d1z6ra1</a>	Alignment	not modelled	87.3	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
119	<a href="#">d2cg4a1</a>	Alignment	not modelled	87.3	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
120	<a href="#">d1ft9a1</a>	Alignment	not modelled	87.3	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like