


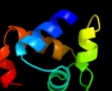
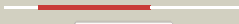

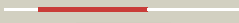


























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1s4ka_</a>	 Alignment		100.0	56	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> YdiL-like
2	<a href="#">c3fmyA_</a>	 Alignment		99.0	18	<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)
3	<a href="#">c3gn5B_</a>	 Alignment		98.8	18	<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)
4	<a href="#">c2ppxA_</a>	 Alignment		98.7	15	<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
5	<a href="#">d2ppxA1</a>	 Alignment		98.7	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
6	<a href="#">c1y9qA_</a>	 Alignment		98.4	18	<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
7	<a href="#">c2ef8A_</a>	 Alignment		98.4	18	<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
8	<a href="#">c3mlfC_</a>	 Alignment		98.4	19	<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.
9	<a href="#">d1rioA_</a>	 Alignment		98.3	10	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
10	<a href="#">c2xcjB_</a>	 Alignment		98.3	13	<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
11	<a href="#">c1b0nA_</a>	 Alignment		98.3	13	<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

12	<a href="#">c3f6wE_</a>	Alignment		98.3	17	<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
13	<a href="#">d1adra_</a>	Alignment		98.2	12	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
14	<a href="#">c3op9A_</a>	Alignment		98.2	12	<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
15	<a href="#">d2icta1</a>	Alignment		98.2	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
16	<a href="#">c2jvIA_</a>	Alignment		98.2	16	<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
17	<a href="#">c3lisB_</a>	Alignment		98.2	23	<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)
18	<a href="#">c3clcC_</a>	Alignment		98.1	14	<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.esp1396i tetramer in complex with its natural 35 base-pair operator
19	<a href="#">c3bs3A_</a>	Alignment		98.1	9	<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
20	<a href="#">c3ivpD_</a>	Alignment		98.1	16	<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.
21	<a href="#">c3f52A_</a>	Alignment	not modelled	98.1	14	<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
22	<a href="#">d2r1j11</a>	Alignment	not modelled	98.1	12	<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="#">d1x57a1</a>	Alignment	not modelled	98.1	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> EDF1-like
24	<a href="#">c3kxAd_</a>	Alignment	not modelled	98.0	24	<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
25	<a href="#">c3eusB_</a>	Alignment	not modelled	98.0	12	<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
26	<a href="#">c3cecA_</a>	Alignment	not modelled	98.0	10	<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
27	<a href="#">d1y9qa1</a>	Alignment	not modelled	98.0	18	<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
28	<a href="#">c3omtA_</a>	Alignment	not modelled	98.0	7	<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.
29	<a href="#">d1y7ya1</a>	Alignment	not modelled	98.0	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
30	<a href="#">d2croa</a>	Alignment	not modelled	98.0	27 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
31	<a href="#">d1b0na2</a>	Alignment	not modelled	98.0	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
32	<a href="#">d1r69a</a>	Alignment	not modelled	98.0	24 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
33	<a href="#">d2b5aa1</a>	Alignment	not modelled	98.0	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
34	<a href="#">d1utxa</a>	Alignment	not modelled	98.0	13 <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="#">d1llib</a>	Alignment	not modelled	98.0	10 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
36	<a href="#">c3dnvB</a>	Alignment	not modelled	98.0	18 <b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator hipb; <b>PDBTitle:</b> mdt protein
37	<a href="#">c3bdnB</a>	Alignment	not modelled	98.0	10 <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
38	<a href="#">d1lmb3</a>	Alignment	not modelled	98.0	10 <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	97.9	23 <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="#">c2ebyA</a>	Alignment	not modelled	97.9	15 <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
41	<a href="#">c3trbA</a>	Alignment	not modelled	97.9	16 <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
42	<a href="#">d2o38a1</a>	Alignment	not modelled	97.8	18 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
43	<a href="#">c2o38A</a>	Alignment	not modelled	97.8	18 <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
44	<a href="#">c3fymA</a>	Alignment	not modelled	97.8	14 <b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the 1a structure of ymfM, a putative dna-binding membrane2 protein from staphylococcus aureus
45	<a href="#">c2axzC</a>	Alignment	not modelled	97.8	8 <b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> prgx; <b>PDBTitle:</b> crystal structure of prgx/ccf10 complex
46	<a href="#">d2a6ca1</a>	Alignment	not modelled	97.8	15 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
47	<a href="#">c2fjrB</a>	Alignment	not modelled	97.8	13 <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
48	<a href="#">c2ewtA</a>	Alignment	not modelled	97.7	14 <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
49	<a href="#">c2kpiA</a>	Alignment	not modelled	97.7	18 <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
50	<a href="#">c2bnoA</a>	Alignment	not modelled	97.7	25 <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. wedmorenisi.
51	<a href="#">c2wusR</a>	Alignment	not modelled	97.6	11 <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
52	<a href="#">c2auwB</a>	Alignment	not modelled	97.6	9 <b>PDB header:</b> unknown function <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
53	<a href="#">c3pxpA</a>	Alignment	not modelled	97.4	24 <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
54	<a href="#">d2ox6a1</a>	Alignment	not modelled	97.3	18 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> YdiL-like

55	<a href="#">c3t76A</a>	Alignment	not modelled	97.3	9	<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
56	<a href="#">d2ofya1</a>	Alignment	not modelled	97.3	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
57	<a href="#">c3b7hA</a>	Alignment	not modelled	97.0	14	<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
58	<a href="#">c2qfcB</a>	Alignment	not modelled	96.9	13	<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
59	<a href="#">d2auwa1</a>	Alignment	not modelled	96.3	9	<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
60	<a href="#">c3bd1B</a>	Alignment	not modelled	95.1	10	<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
61	<a href="#">d2bnma1</a>	Alignment	not modelled	90.2	27	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
62	<a href="#">d1lrza</a>	Alignment	not modelled	86.6	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
63	<a href="#">d1lcda</a>	Alignment	not modelled	84.4	12	<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
64	<a href="#">c2w48D</a>	Alignment	not modelled	83.4	15	<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
65	<a href="#">d2ao9a1</a>	Alignment	not modelled	83.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
66	<a href="#">c3d1nK</a>	Alignment	not modelled	82.9	14	<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
67	<a href="#">d2bjca1</a>	Alignment	not modelled	82.5	12	<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
68	<a href="#">c3mkyP</a>	Alignment	not modelled	82.5	21	<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
69	<a href="#">c3l1pA</a>	Alignment	not modelled	82.2	11	<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
70	<a href="#">c2lcva</a>	Alignment	not modelled	82.1	5	<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
71	<a href="#">d1a04a1</a>	Alignment	not modelled	81.4	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
72	<a href="#">d1zs4a1</a>	Alignment	not modelled	81.2	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Bacteriophage CII protein
73	<a href="#">d1q06a</a>	Alignment	not modelled	80.6	27	<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
74	<a href="#">d1au7a2</a>	Alignment	not modelled	80.5	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
75	<a href="#">c1u78A</a>	Alignment	not modelled	80.1	13	<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
76	<a href="#">d2jn6a1</a>	Alignment	not modelled	80.0	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
77	<a href="#">d2hsga1</a>	Alignment	not modelled	79.9	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
78	<a href="#">d1r71a</a>	Alignment	not modelled	79.8	11	<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
79	<a href="#">d1e3oc2</a>	Alignment	not modelled	79.2	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
80	<a href="#">d1qpza1</a>	Alignment	not modelled	78.8	13	<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="#">c2l8nA</a>	Alignment	not modelled	77.7	5	<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
82	<a href="#">c3mkzU</a>	Alignment	not modelled	76.8	19	<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
83	<a href="#">c3k2zA</a>	Alignment	not modelled	76.4	6	<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
84	<a href="#">c2zhhA</a>	Alignment	not modelled	76.1	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensitive transcriptional activator soxr; <b>PDBTitle:</b> crystal structure of soxr
85	<a href="#">d1ic8a2</a>	Alignment	not modelled	75.8	7	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
86	<a href="#">d1i5za1</a>	Alignment	not modelled	75.7	16	<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
87	<a href="#">d1ft9a1</a>	Alignment	not modelled	75.5	19	<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
88	<a href="#">d1efaa1</a>	Alignment	not modelled	75.3	12	<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
89	<a href="#">c1zljE</a>	Alignment	not modelled	75.1	12	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
90	<a href="#">c1hf0A</a>	Alignment	not modelled	75.1	8	<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
91	<a href="#">d1l3la1</a>	Alignment	not modelled	74.8	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
92	<a href="#">d1biaa1</a>	Alignment	not modelled	74.7	4	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
93	<a href="#">c3r0aB</a>	Alignment	not modelled	74.4	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
94	<a href="#">d1yioa1</a>	Alignment	not modelled	74.4	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
95	<a href="#">d2oz6a1</a>	Alignment	not modelled	74.4	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
96	<a href="#">c3sztB</a>	Alignment	not modelled	73.8	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
97	<a href="#">d1vz0a1</a>	Alignment	not modelled	73.8	20	<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
98	<a href="#">d1p4wa</a>	Alignment	not modelled	73.6	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
99	<a href="#">d2coha1</a>	Alignment	not modelled	73.5	24	<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
100	<a href="#">c2jmlA</a>	Alignment	not modelled	73.3	21	<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
101	<a href="#">d2bgca1</a>	Alignment	not modelled	73.1	15	<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
102	<a href="#">d3e5ua1</a>	Alignment	not modelled	72.4	0	<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
103	<a href="#">c1r71B</a>	Alignment	not modelled	71.8	11	<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
104	<a href="#">c2vz4A</a>	Alignment	not modelled	71.5	5	<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
105	<a href="#">d2h6ca1</a>	Alignment	not modelled	70.8	0	<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
106	<a href="#">d1j9ia</a>	Alignment	not modelled	69.7	7	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Terminase gpNU1 subunit domain
107	<a href="#">c3gp4B</a>	Alignment	not modelled	69.4	18	<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 <b>PDB header:</b> transcription



108	<a href="#">c2krfB_</a>	Alignment	not modelled	68.9	19	<b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein coma; <b>PDBTitle:</b> nmr solution structure of the dna binding domain of competence protein2 a
109	<a href="#">dlj5ya1</a>	Alignment	not modelled	68.9	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
110	<a href="#">dlfsea_</a>	Alignment	not modelled	68.7	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
111	<a href="#">c1x3uA_</a>	Alignment	not modelled	68.4	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein fixj; <b>PDBTitle:</b> solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
112	<a href="#">c3frwF_</a>	Alignment	not modelled	68.2	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> putative trp repressor protein; <b>PDBTitle:</b> crystal structure of putative trpr protein from ruminococcus obeum
113	<a href="#">dluxda_</a>	Alignment	not modelled	67.8	27	<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
114	<a href="#">c2q0oA_</a>	Alignment	not modelled	67.3	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional activator protein trar; <b>PDBTitle:</b> crystal structure of an anti-activation complex in bacterial quorum2 sensing
115	<a href="#">d2gaua1</a>	Alignment	not modelled	66.9	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
116	<a href="#">c3korD_</a>	Alignment	not modelled	66.7	12	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> possible trp repressor; <b>PDBTitle:</b> crystal structure of a putative trp repressor from staphylococcus2 aureus
117	<a href="#">d2cg4a1</a>	Alignment	not modelled	66.0	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
118	<a href="#">c3qaoA_</a>	Alignment	not modelled	66.0	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> merr-like transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
119	<a href="#">clic8B_</a>	Alignment	not modelled	65.7	8	<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
120	<a href="#">dls7oa_</a>	Alignment	not modelled	65.7	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like