Phyre2

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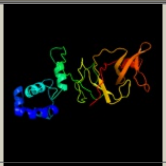
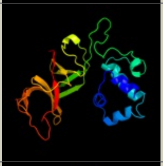
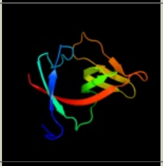
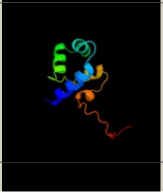
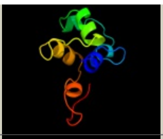
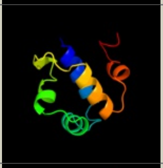
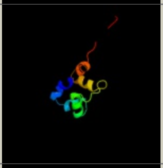
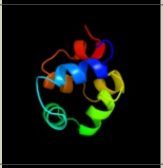
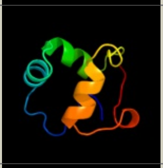
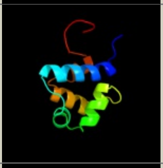
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bdnB_	Alignment		100.0	25	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**lambda repressor; **PDBTitle:** crystal structure of the lambda repressor
2	c3k2zA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
3	c2hnfA_	Alignment		99.9	33	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**repressor protein ci101-229dm-k192a; **PDBTitle:** structure of a hyper-cleavable monomeric fragment of phage2 lambda repressor containing the cleavage site region
4	c2fjrB_	Alignment		99.9	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
5	d1jhfa2	Alignment		99.9	22	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**LexA-related
6	c1jhhB_	Alignment		99.9	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lexa repressor; **PDBTitle:** lexa s119a mutant
7	d1f39a_	Alignment		99.9	39	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**LexA-related
8	d1umua_	Alignment		99.8	31	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**LexA-related
9	c1y9qA_	Alignment		99.4	13	**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
10	c2bnoA_	Alignment		99.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
11	c2kpjA_	Alignment		99.1	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sos-response transcriptional repressor, lexa; **PDBTitle:** solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a

12	c3ivpD_	Alignment		99.0	8	**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.
13	c3b7hA_	Alignment		99.0	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
14	c3op9A_	Alignment		99.0	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
15	d2croa_	Alignment		99.0	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
16	c3mlfC_	Alignment		99.0	12	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** putative transcriptional regulator from staphylococcus aureus.
17	c3bs3A_	Alignment		98.9	9	**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
18	d1y9qa1	Alignment		98.9	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
19	d1adra_	Alignment		98.9	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
20	d2b5aa1	Alignment		98.9	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
21	c3omtA_	Alignment	not modelled	98.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
22	c1b0nA_	Alignment	not modelled	98.9	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
23	d1b0na2	Alignment	not modelled	98.9	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
24	c3f52A_	Alignment	not modelled	98.9	11	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
25	c3lisB_	Alignment	not modelled	98.9	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**csp231i c protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
26	d1rioa_	Alignment	not modelled	98.9	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
27	d2r1jl1	Alignment	not modelled	98.9	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
28	d1y7ya1	Alignment	not modelled	98.9	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
29	d1r69a_	Alignment	not modelled	98.9	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors

30	d1sq8a_	Alignment	not modelled	98.8	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
31	c2jvlA_	Alignment	not modelled	98.8	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**trmbf1; **PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
32	c2ewtA_	Alignment	not modelled	98.8	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd
33	d1x57a1	Alignment	not modelled	98.8	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
34	d1lmb3_	Alignment	not modelled	98.8	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
35	c2ebyA_	Alignment	not modelled	98.8	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
36	d1llib_	Alignment	not modelled	98.8	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
37	d1utxa_	Alignment	not modelled	98.8	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
38	c3cecA_	Alignment	not modelled	98.7	11	**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
39	c3clcC_	Alignment	not modelled	98.7	14	**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
40	d2icta1	Alignment	not modelled	98.7	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
41	c2xcjB_	Alignment	not modelled	98.7	12	**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
42	c3f6wE_	Alignment	not modelled	98.7	9	**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
43	c3trbA_	Alignment	not modelled	98.7	13	**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
44	c2o38A_	Alignment	not modelled	98.7	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative xre family transcriptional regulator
45	d2o38a1	Alignment	not modelled	98.7	7	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
46	c3eusB_	Alignment	not modelled	98.6	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
47	c3kxaD_	Alignment	not modelled	98.6	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
48	c3dnvB_	Alignment	not modelled	98.6	15	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator hipb; **PDBTitle:** mdt protein
49	c3t76A_	Alignment	not modelled	98.6	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
50	d2ofya1	Alignment	not modelled	98.6	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
51	d2a6ca1	Alignment	not modelled	98.5	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
52	c2ef8A_	Alignment	not modelled	98.4	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
53	c3fmyA_	Alignment	not modelled	98.4	15	**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)
54	c2fkdK_	Alignment	not modelled	98.4	18	**PDB header:**transcription regulator **Chain:** K: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of the c-terminal domain of bacteriophage2 186 repressor
55	c2wusR_	Alignment	not modelled	98.4	12	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz

56	d1b12a_	Alignment	not modelled	98.4	24	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**Type 1 signal peptidase
57	d2ppxa1	Alignment	not modelled	98.3	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
58	c2ppxA_	Alignment	not modelled	98.3	11	**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
59	c3fymA_	Alignment	not modelled	98.3	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
60	c3pxpA_	Alignment	not modelled	98.1	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**helix-turn-helix domain protein; **PDBTitle:** crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
61	c3bd1B_	Alignment	not modelled	98.0	13	**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
62	c3gn5B_	Alignment	not modelled	98.0	15	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator mqsa (ygit/b3021); **PDBTitle:** structure of the e. coli protein mqsa (ygit/b3021)
63	c2axzC_	Alignment	not modelled	97.8	7	**PDB header:**transcription **Chain:** C: **PDB Molecule:**prgx; **PDBTitle:** crystal structure of prgx/ccf10 complex
64	c2qfcB_	Alignment	not modelled	97.7	16	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**plcr protein; **PDBTitle:** crystal structure of bacillus thuringiensis plcr complexed with papr
65	c3r1fO_	Alignment	not modelled	96.9	13	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
66	d1nera_	Alignment	not modelled	96.4	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
67	d1ic8a2	Alignment	not modelled	95.9	5	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
68	d1lcda_	Alignment	not modelled	95.9	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
69	d2bjca1	Alignment	not modelled	95.4	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
70	d2hsga1	Alignment	not modelled	95.4	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
71	d1qpza1	Alignment	not modelled	95.4	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
72	d1uxca_	Alignment	not modelled	95.4	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
73	c2l8nA_	Alignment	not modelled	95.3	13	**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
74	d1rzsa_	Alignment	not modelled	95.2	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
75	d1uxda_	Alignment	not modelled	95.0	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
76	c2lcvA_	Alignment	not modelled	95.0	13	**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
77	d1efaa1	Alignment	not modelled	94.9	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
78	c1bdhA_	Alignment	not modelled	94.8	11	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
79	c3kjxD_	Alignment	not modelled	94.7	7	**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
80	c3h5tA_	Alignment	not modelled	94.6	14	**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
81	d1hlva1	Alignment	not modelled	94.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
						PDB header:dna binding protein/dna

82	c3mkyP_	Alignment	not modelled	94.3	15	**Chain:** P: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-323)-18mer dna complex, i23 form
83	c1r71B_	Alignment	not modelled	94.2	8	**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
84	d1r71a_	Alignment	not modelled	94.2	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
85	c3mkzU_	Alignment	not modelled	93.9	15	**PDB header:**dna-binding protein/dna **Chain:** U: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-272)-18mer complex, p21 form
86	c2elhA_	Alignment	not modelled	93.8	13	**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
87	c1zvvA_	Alignment	not modelled	93.6	13	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex
88	c1zx4B_	Alignment	not modelled	93.4	8	**PDB header:**translation **Chain:** B: **PDB Molecule:**plasmid partition par b protein; **PDBTitle:** structure of parb bound to dna
89	d1vz0a1	Alignment	not modelled	93.0	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
90	d1bw6a_	Alignment	not modelled	91.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
91	d1z05a1	Alignment	not modelled	91.7	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
92	c1ic8B_	Alignment	not modelled	91.5	4	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** hepatocyte nuclear factor 1a bound to dna : mody3 gene2 product
93	d1biaa1	Alignment	not modelled	91.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
94	d1r1ua_	Alignment	not modelled	91.4	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
95	c2w48D_	Alignment	not modelled	91.3	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
96	c1u78A_	Alignment	not modelled	90.8	12	**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
97	d1z6ra1	Alignment	not modelled	90.6	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
98	c2pijB_	Alignment	not modelled	90.5	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**prophage pfl 6 cro; **PDBTitle:** structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
99	c1z6rC_	Alignment	not modelled	90.2	6	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
100	d1k78a1	Alignment	not modelled	90.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
101	c2oqgA_	Alignment	not modelled	90.1	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
102	c2h8rA_	Alignment	not modelled	90.0	4	**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
103	c2dt5A_	Alignment	not modelled	89.9	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**at-rich dna-binding protein; **PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
104	c2p6tH_	Alignment	not modelled	89.8	13	**PDB header:**transcription **Chain:** H: **PDB Molecule:**transcriptional regulator, lrp/asnc family; **PDBTitle:** crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
105	c1z05A_	Alignment	not modelled	89.7	3	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, rok family; **PDBTitle:** crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
106	d2jn6a1	Alignment	not modelled	89.6	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
107	c1hlvA_	Alignment	not modelled	89.4	10	**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
108	d1pdnc_	Alignment	not modelled	89.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like

						Family: Paired domain
109	c3cuoB_	Alignment	not modelled	88.7	14	**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
110	c1r22B_	Alignment	not modelled	88.6	14	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**transcriptional repressor smtb; **PDBTitle:** crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
111	d6paxa1	Alignment	not modelled	88.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
112	c2zkzC_	Alignment	not modelled	88.2	9	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional repressor pagr; **PDBTitle:** crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
113	c2jscB_	Alignment	not modelled	88.1	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator rv1994c/mt2050; **PDBTitle:** nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
114	d1zs4a1	Alignment	not modelled	87.8	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Bacteriophage CII protein
115	c2kkoB_	Alignment	not modelled	87.7	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**possible transcriptional regulatory protein **PDBTitle:** solution nmr structure of the homodimeric winged helix-turn-2 helix dna-binding domain (fragment 1-100) mb0332 from3 mycobacterium bovis, a possible arsr-family transcriptional4 regulator. northeast structural genomics consortium target5 mbr242e.
116	d1j5ya1	Alignment	not modelled	87.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
117	c3pqkD_	Alignment	not modelled	87.7	17	**PDB header:**transcription **Chain:** D: **PDB Molecule:**biofilm growth-associated repressor; **PDBTitle:** crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
118	d1r1ta_	Alignment	not modelled	87.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
119	d3orca_	Alignment	not modelled	86.9	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
120	d2cg4a1	Alignment	not modelled	86.6	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain