Phyre2

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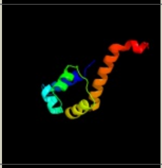
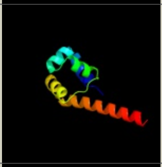
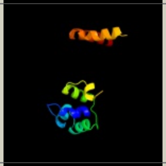
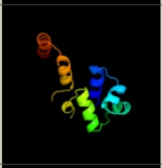
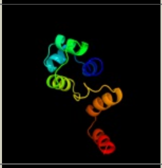
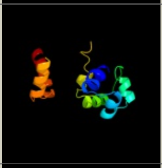
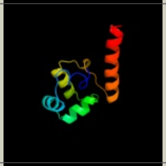
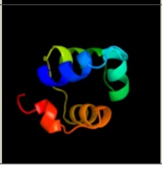
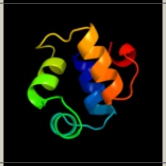
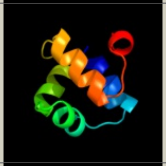
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ebyA_	Alignment		99.9	100	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
2	c3trbA_	Alignment		99.9	38	**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
3	c3cecA_	Alignment		99.9	34	**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
4	d2icta1	Alignment		99.8	35	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
5	c3op9A_	Alignment		99.6	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
6	c3ivpD_	Alignment		99.6	16	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**putative transposon-related dna-binding protein; **PDBTitle:** the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
7	c3lisB_	Alignment		99.6	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**csp231i c protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
8	c1b0nA_	Alignment		99.5	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
9	c3mlfC_	Alignment		99.5	12	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** putative transcriptional regulator from staphylococcus aureus.
10	c1y9qA_	Alignment		99.5	11	**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
11	c2kpjA_	Alignment		99.5	13	**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	c3bs3A_	Alignment		99.5	16	**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
13	c2ewtA_	Alignment		99.5	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd
14	d1rioa_	Alignment		99.4	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
15	c2bnoA_	Alignment		99.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
16	c3f52A_	Alignment		99.4	20	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
17	d2r1jl1	Alignment		99.4	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
18	c3omtA_	Alignment		99.4	22	**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.
19	d1adra_	Alignment		99.4	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
20	d1y9qa1	Alignment		99.4	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
21	d2b5aa1	Alignment	not modelled	99.4	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
22	d1b0na2	Alignment	not modelled	99.4	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
23	c3clcC_	Alignment	not modelled	99.4	15	**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
24	d1x57a1	Alignment	not modelled	99.4	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
25	d1r69a_	Alignment	not modelled	99.4	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
26	d1sq8a_	Alignment	not modelled	99.4	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
27	c3kxaD_	Alignment	not modelled	99.4	15	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
28	d1utxa_	Alignment	not modelled	99.4	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
						Fold:lambda repressor-like DNA-binding domains

29	d2croa_	Alignment	not modelled	99.4	18	**Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
30	d1llib_	Alignment	not modelled	99.4	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
31	c3f6wE_	Alignment	not modelled	99.4	25	**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
32	d1y7ya1	Alignment	not modelled	99.4	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
33	d1lmb3_	Alignment	not modelled	99.4	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
34	c3b7hA_	Alignment	not modelled	99.4	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
35	c2xcjB_	Alignment	not modelled	99.3	16	**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
36	c3dnvB_	Alignment	not modelled	99.3	17	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator hipb; **PDBTitle:** mdt protein
37	c3bdnB_	Alignment	not modelled	99.3	22	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**lambda repressor; **PDBTitle:** crystal structure of the lambda repressor
38	c3eusB_	Alignment	not modelled	99.3	18	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
39	d2ofya1	Alignment	not modelled	99.3	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
40	c2ef8A_	Alignment	not modelled	99.3	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
41	c2jvlA_	Alignment	not modelled	99.3	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**trmbf1; **PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
42	c3t76A_	Alignment	not modelled	99.3	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
43	d2o38a1	Alignment	not modelled	99.2	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
44	c2o38A_	Alignment	not modelled	99.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative xre family transcriptional regulator
45	c2axzC_	Alignment	not modelled	99.2	12	**PDB header:**transcription **Chain:** C: **PDB Molecule:**prgx; **PDBTitle:** crystal structure of prgx/ccf10 complex
46	c2fjrB_	Alignment	not modelled	99.2	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
47	c2qfcB_	Alignment	not modelled	99.2	13	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**plcr protein; **PDBTitle:** crystal structure of bacillus thuringiensis plcr complexed with papr
48	d2a6ca1	Alignment	not modelled	99.1	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
49	c2wusR_	Alignment	not modelled	99.1	10	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz
50	c3pxpA_	Alignment	not modelled	99.1	18	**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
51	c3fymA_	Alignment	not modelled	99.0	21	**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
52	c3fmyA_	Alignment	not modelled	99.0	17	**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)
53	c2ppxA_	Alignment	not modelled	99.0	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
54	d2ppxa1	Alignment	not modelled	99.0	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
55	c3gn5B_	Alignment	not modelled	98.7	17	**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)

56	c3r1fO_	Alignment	not modelled	98.1	21	**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
57	d1nera_	Alignment	not modelled	97.9	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
58	c3bd1B_	Alignment	not modelled	97.7	15	**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
59	d1dwka1	Alignment	not modelled	97.2	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
60	d2hsga1	Alignment	not modelled	96.9	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
61	c2iv1J_	Alignment	not modelled	96.9	25	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cyanate hydratase; **PDBTitle:** site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
62	d1lcda_	Alignment	not modelled	96.9	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
63	d2bjca1	Alignment	not modelled	96.7	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
64	d1efaa1	Alignment	not modelled	96.6	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
65	d1qpza1	Alignment	not modelled	96.6	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
66	d2bnma1	Alignment	not modelled	96.5	30	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
67	d1ic8a2	Alignment	not modelled	96.4	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
68	c1bdhA_	Alignment	not modelled	96.4	24	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
69	d1uxca_	Alignment	not modelled	96.4	29	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
70	c2lcvA_	Alignment	not modelled	96.3	22	**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
71	c2auwB_	Alignment	not modelled	96.3	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
72	c3kjxD_	Alignment	not modelled	96.3	17	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from silicibacter pomeroyi
73	c2l8nA_	Alignment	not modelled	96.2	22	**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	c1zvvA_	Alignment	not modelled	96.0	18	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex
75	c3h5tA_	Alignment	not modelled	96.0	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from corynebacterium glutamicum
76	d1uxda_	Alignment	not modelled	95.9	28	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
77	d2awia1	Alignment	not modelled	95.8	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**PrgX N-terminal domain-like
78	c3k2zA_	Alignment	not modelled	95.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
79	c3mkzU_	Alignment	not modelled	94.6	20	**PDB header:**dna-binding protein/dna **Chain:** U: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-272)-18mer complex, p21 form
80	c3mkyP_	Alignment	not modelled	94.6	20	**PDB header:**dna binding protein/dna **Chain:** P: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-323)-18mer dna complex, i23 form
81	d1rzsa_	Alignment	not modelled	94.2	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
82	c2w48D_	Alignment	not modelled	94.1	26	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2

						regulator sorc from klebsiella pneumoniae
83	d2auwa1	Alignment	not modelled	94.1	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
84	c1ic8B_	Alignment	not modelled	94.0	15	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** hepatocyte nuclear factor 1a bound to dna : mody3 gene2 product
85	c1u78A_	Alignment	not modelled	93.9	7	**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
86	d2csfa1	Alignment	not modelled	93.6	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
87	c2h8rA_	Alignment	not modelled	93.4	13	**PDB header:**transcription activator/dna **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 1-beta; **PDBTitle:** hepatocyte nuclear factor 1b bound to dna: mody5 gene2 product
88	d1vz0a1	Alignment	not modelled	93.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
89	d1r71a_	Alignment	not modelled	92.9	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
90	c2k9qB_	Alignment	not modelled	92.9	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244.
91	c1r71B_	Alignment	not modelled	92.8	7	**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
92	c1zx4B_	Alignment	not modelled	92.4	15	**PDB header:**translation **Chain:** B: **PDB Molecule:**plasmid partition par b protein; **PDBTitle:** structure of parb bound to dna
93	c3iwfA_	Alignment	not modelled	91.3	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
94	d1z05a1	Alignment	not modelled	91.2	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
95	d4croa_	Alignment	not modelled	91.0	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
96	d1i5za1	Alignment	not modelled	90.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
97	d2bgca1	Alignment	not modelled	90.6	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
98	d1hlva1	Alignment	not modelled	90.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
99	d1ku9a_	Alignment	not modelled	90.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
100	d1ft9a1	Alignment	not modelled	90.2	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
101	c2elhA_	Alignment	not modelled	90.1	11	**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
102	d2oz6a1	Alignment	not modelled	90.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
103	d2coha1	Alignment	not modelled	90.1	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
104	d2ao9a1	Alignment	not modelled	90.0	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Nanomeric phage protein-like
105	d2gaua1	Alignment	not modelled	89.8	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
106	d1d1la_	Alignment	not modelled	89.7	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
107	d3orca_	Alignment	not modelled	89.7	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
108	d2jn6a1	Alignment	not modelled	89.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
109	d3e5ua1	Alignment	not modelled	89.0	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain

						Family:CAP C-terminal domain-like
110	d1e3oc2	Alignment	not modelled	88.8	6	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
111	d2h6ca1	Alignment	not modelled	88.6	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
112	d1fipa_	Alignment	not modelled	88.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
113	d1k78a1	Alignment	not modelled	88.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
114	d2d1ha1	Alignment	not modelled	88.4	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
115	d1j5ya1	Alignment	not modelled	88.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
116	c2wteB_	Alignment	not modelled	88.4	27	**PDB header:**antiviral protein **Chain:** B: **PDB Molecule:**csa3; **PDBTitle:** the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
117	c1umqA_	Alignment	not modelled	88.1	22	**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
118	d1umqa_	Alignment	not modelled	88.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
119	d1au7a2	Alignment	not modelled	87.7	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
120	c3l1pA_	Alignment	not modelled	87.6	14	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**pou domain, class 5, transcription factor 1; **PDBTitle:** pou protein:dna complex