Phyre2

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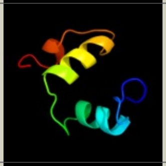
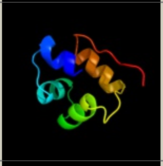
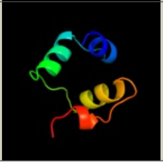
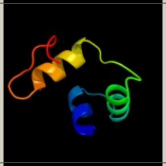
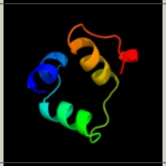
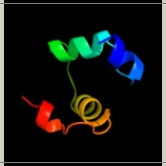
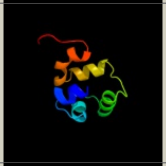
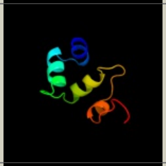
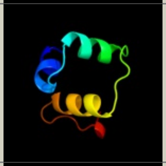
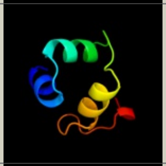
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bd1B_	Alignment		99.7	22	**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
2	d1rioa_	Alignment		98.2	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
3	c3trbA_	Alignment		98.1	18	**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
4	c3cecA_	Alignment		98.1	16	**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
5	d1lmb3_	Alignment		98.1	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
6	d1rzsa_	Alignment		98.0	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
7	d1llib_	Alignment		98.0	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
8	c3bs3A_	Alignment		98.0	13	**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
9	d2icta1	Alignment		98.0	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
10	c2ebyA_	Alignment		98.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
11	c3omtA_	Alignment		97.7	6	**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.

12	c2jvlA_	Alignment		97.7	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**trmbf1; **PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
13	c3op9A_	Alignment		97.7	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
14	d1y7ya1	Alignment		97.6	30	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
15	c2ewtA_	Alignment		97.6	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd
16	c2xcjB_	Alignment		97.6	15	**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
17	d1adra_	Alignment		97.6	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
18	d2b5aa1	Alignment		97.6	27	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
19	d2r1jl1	Alignment		97.5	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
20	c3f52A_	Alignment		97.5	30	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
21	c3kxaD_	Alignment	not modelled	97.5	27	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
22	c3clcC_	Alignment	not modelled	97.5	9	**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
23	d1b0na2	Alignment	not modelled	97.5	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
24	c2kpjA_	Alignment	not modelled	97.5	24	**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
25	c3ivpD_	Alignment	not modelled	97.5	14	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**putative transposon-related dna-binding protein; **PDBTitle:** the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
26	d1utxa_	Alignment	not modelled	97.4	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
27	c1b0nA_	Alignment	not modelled	97.4	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
						PDB header:dna binding protein

28	c3f6wE_	Alignment	not modelled	97.4	18	**Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
29	d1x57a1	Alignment	not modelled	97.4	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
30	c2fjrB_	Alignment	not modelled	97.4	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
31	d1y9qa1	Alignment	not modelled	97.3	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
32	c3mlfC_	Alignment	not modelled	97.3	14	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** putative transcriptional regulator from staphylococcus aureus.
33	c1y9qA_	Alignment	not modelled	97.3	12	**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
34	c3t76A_	Alignment	not modelled	97.3	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
35	d2ofya1	Alignment	not modelled	97.2	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
36	c3eusB_	Alignment	not modelled	97.2	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
37	c2bnoA_	Alignment	not modelled	97.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
38	c3b7hA_	Alignment	not modelled	97.1	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
39	c3bdnB_	Alignment	not modelled	97.1	22	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**lambda repressor; **PDBTitle:** crystal structure of the lambda repressor
40	d2croa_	Alignment	not modelled	97.1	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
41	d1sq8a_	Alignment	not modelled	97.0	28	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
42	d2a6ca1	Alignment	not modelled	97.0	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
43	c3lisB_	Alignment	not modelled	96.9	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**csp231i c protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
44	c3dnvB_	Alignment	not modelled	96.8	24	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator hipb; **PDBTitle:** mdt protein
45	d1r69a_	Alignment	not modelled	96.7	30	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
46	c2ef8A_	Alignment	not modelled	96.7	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
47	d2ppxa1	Alignment	not modelled	96.7	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
48	c2ppxA_	Alignment	not modelled	96.7	19	**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
49	d2o38a1	Alignment	not modelled	96.7	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
50	c2o38A_	Alignment	not modelled	96.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative xre family transcriptional regulator
51	d1lcda_	Alignment	not modelled	96.3	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
52	d2bjca1	Alignment	not modelled	96.2	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
53	d1nera_	Alignment	not modelled	96.1	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
54	d1qpza1	Alignment	not modelled	96.0	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
55	c2lcyA	Alignment	not modelled	95.9	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr;

55	c2icvA_	Alignment	not modelled	95.9	14	**PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
56	d1efaa1	Alignment	not modelled	95.7	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
57	c2l8nA_	Alignment	not modelled	95.7	14	**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
58	c3fmyA_	Alignment	not modelled	95.7	13	**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)
59	c3pxpA_	Alignment	not modelled	95.6	16	**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
60	d2hsga1	Alignment	not modelled	95.6	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
61	d1ic8a2	Alignment	not modelled	95.1	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
62	c1bdhA_	Alignment	not modelled	94.6	9	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
63	d1uxca_	Alignment	not modelled	94.6	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
64	c3h5tA_	Alignment	not modelled	94.4	15	**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
65	c1zvvA_	Alignment	not modelled	94.2	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex
66	c3kjxD_	Alignment	not modelled	93.7	9	**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
67	c2wusR_	Alignment	not modelled	93.5	11	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz
68	d4croa_	Alignment	not modelled	93.0	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
69	d1uxda_	Alignment	not modelled	92.9	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
70	d1d1la_	Alignment	not modelled	92.2	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
71	c2pijB_	Alignment	not modelled	91.7	17	**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
72	d3orca_	Alignment	not modelled	90.0	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
73	c3fymA_	Alignment	not modelled	89.4	18	**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
74	c3gn5B_	Alignment	not modelled	89.0	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)
75	c2axzC_	Alignment	not modelled	88.3	14	**PDB header:**transcription **Chain:** C: **PDB Molecule:**prgx; **PDBTitle:** crystal structure of prgx/ccf10 complex
76	c2h8rA_	Alignment	not modelled	87.7	17	**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
77	d1puza_	Alignment	not modelled	86.6	13	**Fold:**YgfY-like **Superfamily:**YgfY-like **Family:**YgfY-like
78	c3r1fO_	Alignment	not modelled	85.8	20	**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
79	c1x6iB_	Alignment	not modelled	85.2	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ygfy; **PDBTitle:** crystal structure of ygfy from escherichia coli
80	c2qfcB_	Alignment	not modelled	83.4	12	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**plcr protein; **PDBTitle:** crystal structure of bacillus thuringiensis plcr complexed with papr
81	c2jr5A_	Alignment	not modelled	81.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0350 protein vc_2471; **PDBTitle:** solution structure of upf0350 protein vc_2471.

						northeast2 structural genomics target vcr36
82	d1dwka1	Alignment	not modelled	79.2	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
83	c2dmnA_	Alignment	not modelled	78.7	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein tgif2lx; **PDBTitle:** the solution structure of the homeobox domain of human2 homeobox protein tgif2lx
84	d1x2na1	Alignment	not modelled	78.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
85	d1du6a_	Alignment	not modelled	77.9	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
86	d2r5yb1	Alignment	not modelled	76.6	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
87	d1le8b_	Alignment	not modelled	76.5	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
88	c2lm4A_	Alignment	not modelled	75.9	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**succinate dehydrogenase assembly factor 2, mitochondrial; **PDBTitle:** solution nmr structure of mitochondrial succinate dehydrogenase2 assembly factor 2 from saccharomyces cerevisiae, northeast structural3 genomics consortium target yt682a
89	d1pufb_	Alignment	not modelled	75.9	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
90	d1k61a_	Alignment	not modelled	75.7	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
91	c3nzlA_	Alignment	not modelled	75.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding protein satb1; **PDBTitle:** crystal structure of the n-terminal domain of dna-binding protein2 satb1 from homo sapiens, northeast structural genomics consortium3 target hr4435b
92	c2lk2A_	Alignment	not modelled	74.5	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein tgif1; **PDBTitle:** solution nmr structure of homeobox domain (171-248) of human homeobox2 protein tgif1, northeast structural genomics consortium target3 hr4411b
93	c1s7eA_	Alignment	not modelled	74.2	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 6; **PDBTitle:** solution structure of hnf-6
94	c2hinA_	Alignment	not modelled	71.0	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**repressor protein; **PDBTitle:** structure of n15 cro at 1.05 a: an ortholog of lambda cro2 with a completely different but equally effective3 dimerization mechanism
95	c2da4A_	Alignment	not modelled	70.3	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156; **PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
96	d1yrnb_	Alignment	not modelled	69.3	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
97	d1lfup_	Alignment	not modelled	67.6	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
98	c2dmsA_	Alignment	not modelled	67.2	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein otx2; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein otx2
99	c3mkyP_	Alignment	not modelled	67.0	10	**PDB header:**dna binding protein/dna **Chain:** P: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-323)-18mer dna complex, i23 form
100	c1ic8B_	Alignment	not modelled	66.3	17	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** hepatocyte nuclear factor 1a bound to dna : mody3 gene2 product
101	d1fjlb_	Alignment	not modelled	65.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
102	d1mnmc_	Alignment	not modelled	64.5	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
103	d2oz6a1	Alignment	not modelled	63.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
104	d2coha1	Alignment	not modelled	63.6	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
105	d2e1oa1	Alignment	not modelled	62.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
106	d1bw5a_	Alignment	not modelled	62.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
						Fold:DNA/RNA-binding 3-helical bundle

107	d1fjla_	Alignment	not modelled	61.9	16	**Superfamily:**Homeodomain-like **Family:**Homeodomain
108	c3mkzU_	Alignment	not modelled	61.3	15	**PDB header:**dna-binding protein/dna **Chain:** U: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-272)-18mer complex, p21 form
109	d1ftta_	Alignment	not modelled	61.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
110	d1vnda_	Alignment	not modelled	61.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
111	c2l9rA_	Alignment	not modelled	61.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein nkx-3.1; **PDBTitle:** solution nmr structure of homeobox domain of homeobox protein nkx-3.12 from homo sapiens, northeast structural genomics consortium target3 hr6470a
112	d1le8a_	Alignment	not modelled	60.1	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
113	d1octc1	Alignment	not modelled	59.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
114	c3k2zA_	Alignment	not modelled	59.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
115	d2cuea1	Alignment	not modelled	59.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
116	d1ig7a_	Alignment	not modelled	58.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
117	d2craa1	Alignment	not modelled	58.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
118	d1i5za1	Alignment	not modelled	58.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
119	d1z05a1	Alignment	not modelled	58.2	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
120	d2gaua1	Alignment	not modelled	58.1	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like