Phyre2

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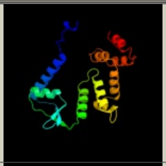
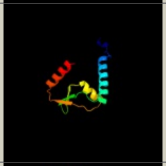
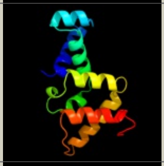
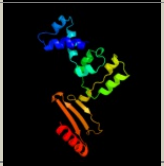
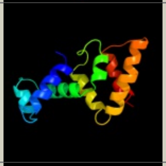
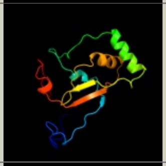
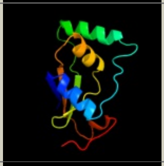
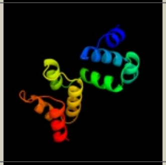
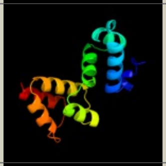
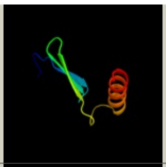
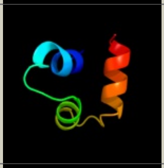
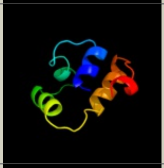
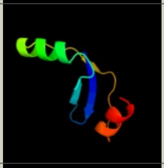
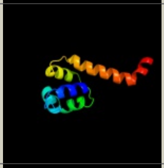
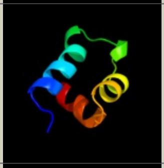
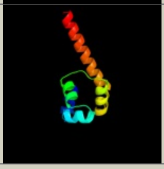
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vz0B_	Alignment		100.0	19	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**chromosome partitioning protein parb; **PDBTitle:** chromosome segregation protein spo0j from thermus2 thermophilus
2	d1vk1a_	Alignment		99.9	12	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**Hypothetical protein PF0380
3	d1vz0a2	Alignment		99.8	22	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**ParB-like nuclease domain
4	c3mkyP_	Alignment		99.8	99	**PDB header:**dna binding protein/dna **Chain:** P: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-323)-18mer dna complex, i23 form
5	c1zx4B_	Alignment		99.8	17	**PDB header:**translation **Chain:** B: **PDB Molecule:**plasmid partition par b protein; **PDBTitle:** structure of parb bound to dna
6	c3mkzU_	Alignment		99.8	99	**PDB header:**dna-binding protein/dna **Chain:** U: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-272)-18mer complex, p21 form
7	d2b6fa1	Alignment		99.6	8	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**Sulfiredoxin-like
8	d1xw3a1	Alignment		99.6	7	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**Sulfiredoxin-like
9	d1r71a_	Alignment		99.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
10	c1r71B_	Alignment		99.4	16	**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
11	d1vz0a1	Alignment		99.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like

12	c3kz5E_	Alignment		97.7	92	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**protein sopb; **PDBTitle:** structure of cdomain
13	c2w48D_	Alignment		95.1	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
14	c2fjrB_	Alignment		93.7	7	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
15	d2hwja1	Alignment		93.7	10	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**Atu1540-like
16	c2ebyA_	Alignment		93.7	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
17	c3trbA_	Alignment		93.7	20	**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
18	c1u78A_	Alignment		93.6	18	**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
19	d2icta1	Alignment		93.6	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
20	c3cecA_	Alignment		92.6	17	**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
21	c3ivpD_	Alignment	not modelled	91.8	12	**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.
22	d1biaa1	Alignment	not modelled	91.5	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
23	c1y9qA_	Alignment	not modelled	91.3	9	**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
24	d2d1ha1	Alignment	not modelled	91.1	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
25	c2wteB_	Alignment	not modelled	90.9	16	**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.
26	c2kpjA_	Alignment	not modelled	90.9	9	**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
27	d1rioa_	Alignment	not modelled	90.7	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
28	c3korD	Alignment	not modelled	90.6	8	**PDB header:**transcription **Chain:** D: **PDB Molecule:**possible trp repressor;

28	[illegible]	Alignment	not modelled	90.6	8	**PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus
29	d1mkma1	Alignment	not modelled	90.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
30	c3frwF_	Alignment	not modelled	90.2	10	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
31	c2o38A_	Alignment	not modelled	90.0	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative xre family transcriptional regulator
32	d2o38a1	Alignment	not modelled	90.0	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
33	d1hlva1	Alignment	not modelled	89.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
34	c3r0aB_	Alignment	not modelled	89.8	7	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
35	d2a6ca1	Alignment	not modelled	89.8	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
36	c3t76A_	Alignment	not modelled	89.3	7	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
37	c3op9A_	Alignment	not modelled	89.1	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
38	c1b0nA_	Alignment	not modelled	88.8	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
39	d1r69a_	Alignment	not modelled	88.4	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
40	c3fmyA_	Alignment	not modelled	88.3	7	**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)
41	c2ef8A_	Alignment	not modelled	88.2	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
42	c2xcjB_	Alignment	not modelled	88.0	8	**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
43	c3f6wE_	Alignment	not modelled	88.0	10	**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
44	d1y9qa1	Alignment	not modelled	87.7	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
45	d1adra_	Alignment	not modelled	87.6	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
46	d1sq8a_	Alignment	not modelled	87.4	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
47	d1ku9a_	Alignment	not modelled	87.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
48	c3dnvB_	Alignment	not modelled	87.0	21	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator hipb; **PDBTitle:** mdt protein
49	d1j5ya1	Alignment	not modelled	87.0	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
50	d2cg4a1	Alignment	not modelled	86.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
51	c2ppxA_	Alignment	not modelled	86.5	9	**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
52	d2ppxa1	Alignment	not modelled	86.5	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
53	d2b5aa1	Alignment	not modelled	86.3	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
54	d1i1ga1	Alignment	not modelled	86.2	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
55	d1x57a1	Alignment	not modelled	86.0	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains

						Family:EDF1-like
56	d1bw6a_	Alignment	not modelled	86.0	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
57	c2g7uB_	Alignment	not modelled	85.9	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
58	c3clcC_	Alignment	not modelled	85.7	12	**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
59	d1lcda_	Alignment	not modelled	85.5	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
60	c3eusB_	Alignment	not modelled	85.5	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
61	d1g3wa1	Alignment	not modelled	85.4	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
62	d2isya1	Alignment	not modelled	85.3	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
63	d1pdnc_	Alignment	not modelled	85.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
64	d1jhfa1	Alignment	not modelled	85.2	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
65	d1b0na2	Alignment	not modelled	85.1	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
66	c3mlfC_	Alignment	not modelled	85.1	11	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** putative transcriptional regulator from staphylococcus aureus.
67	c2it0A_	Alignment	not modelled	84.9	6	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of a two-domain ider-dna complex crystal2 form ii
68	d1ku7a_	Alignment	not modelled	84.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
69	c1mkmA_	Alignment	not modelled	84.6	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iclr transcriptional regulator; **PDBTitle:** crystal structure of the thermotoga maritima iclr
70	c3f52A_	Alignment	not modelled	84.5	18	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
71	c2x4hA_	Alignment	not modelled	84.1	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
72	d2croa_	Alignment	not modelled	84.0	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
73	c1bdhA_	Alignment	not modelled	83.9	29	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
74	c3bdnB_	Alignment	not modelled	83.9	16	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**lambda repressor; **PDBTitle:** crystal structure of the lambda repressor
75	d1i5za1	Alignment	not modelled	83.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
76	d1lmb3_	Alignment	not modelled	83.7	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
77	d1qpza1	Alignment	not modelled	83.5	29	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
78	d1k78a1	Alignment	not modelled	83.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
79	c3omtA_	Alignment	not modelled	83.0	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.
80	d2cfxa1	Alignment	not modelled	83.0	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
81	d2bjca1	Alignment	not modelled	82.8	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
						Fold:DNA/RNA-binding 3-helical bundle

82	d2ev0a1	Alignment	not modelled	82.7	12	**Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
83	d2p7vb1	Alignment	not modelled	82.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
84	c3b7hA_	Alignment	not modelled	82.7	8	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
85	c1f5tA_	Alignment	not modelled	82.6	6	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
86	c2bnoA_	Alignment	not modelled	82.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
87	d1llib_	Alignment	not modelled	82.6	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
88	c3sztB_	Alignment	not modelled	82.3	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**quorum-sensing control repressor; **PDBTitle:** quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
89	d1uxca_	Alignment	not modelled	82.3	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
90	d2hsga1	Alignment	not modelled	82.2	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
91	d1y7ya1	Alignment	not modelled	82.1	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
92	c2h09A_	Alignment	not modelled	81.7	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
93	c2jvlA_	Alignment	not modelled	81.4	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**trmbf1; **PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
94	c3g3zA_	Alignment	not modelled	81.2	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
95	d1ku3a_	Alignment	not modelled	81.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
96	c2ia2D_	Alignment	not modelled	81.0	20	**PDB header:**transcription **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
97	c2l4aA_	Alignment	not modelled	80.9	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
98	d2cyya1	Alignment	not modelled	80.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
99	c2lcvA_	Alignment	not modelled	80.6	15	**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
100	d2oz6a1	Alignment	not modelled	80.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
101	d1sfxa_	Alignment	not modelled	80.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
102	d1ft9a1	Alignment	not modelled	80.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
103	d2gaua1	Alignment	not modelled	80.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
104	c2ev5B_	Alignment	not modelled	80.0	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
105	d1uxda_	Alignment	not modelled	79.7	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
106	c3gn5B_	Alignment	not modelled	79.6	7	**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)
107	c2fa5B_	Alignment	not modelled	79.4	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator marr/emrr family; **PDBTitle:** the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
108	c2q0oA_	Alignment	not modelled	79.4	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar;

						PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
109	c1zgwA_	Alignment	not modelled	79.4	21	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**ada polyprotein; **PDBTitle:** nmr structure of e. coli ada protein in complex with dna
110	c3k2zA_	Alignment	not modelled	79.4	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
111	c3kjxD_	Alignment	not modelled	79.2	14	**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
112	d1efaa1	Alignment	not modelled	79.2	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
113	c3bd1B_	Alignment	not modelled	79.1	24	**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
114	c3h5tA_	Alignment	not modelled	79.0	26	**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
115	d2coha1	Alignment	not modelled	78.9	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
116	d2h6ca1	Alignment	not modelled	78.9	4	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
117	c1zvvA_	Alignment	not modelled	78.8	22	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex
118	c3bs3A_	Alignment	not modelled	78.4	17	**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
119	c2qwwB_	Alignment	not modelled	78.1	6	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
120	d2r1jl1	Alignment	not modelled	78.1	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors