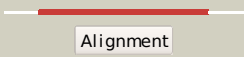

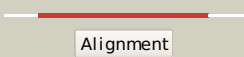

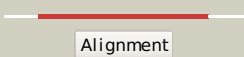

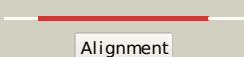

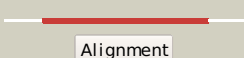

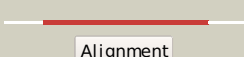

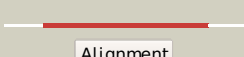

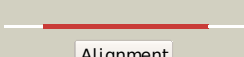

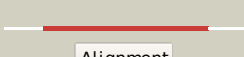

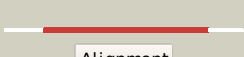














#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zvva_	 Alignment		100.0	27	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
2	c3kjd_	 Alignment		100.0	23	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
3	c1bdhA_	 Alignment		100.0	23	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
4	c3h5tA_	 Alignment		100.0	19	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
5	d1tfa_	 Alignment		100.0	100	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
6	c1jyeA_	 Alignment		100.0	99	PDB header: transcription Chain: A: PDB Molecule: lactose operon repressor; PDBTitle: structure of a dimeric lac repressor with c-terminal deletion and k84I2 substitution
7	d1jyea_	 Alignment		100.0	99	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
8	c2iksA_	 Alignment		100.0	14	PDB header: transcription Chain: A: PDB Molecule: dna-binding transcriptional dual regulator; PDBTitle: crystal structure of n-terminal truncated dna-binding transcriptional2 dual regulator from escherichia coli k12
9	c3dbiA_	 Alignment		100.0	22	PDB header: transcription regulator Chain: A: PDB Molecule: sugar-binding transcriptional regulator, lacI family; PDBTitle: crystal structure of sugar-binding transcriptional regulator (lacI2 family) from escherichia coli complexed with phosphate
10	d2nzug1	 Alignment		100.0	22	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
11	c3c3kA_	 Alignment		100.0	23	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes

12	c3kkeA_	Alignment		100.0	25	PDB header: transcription regulator Chain: A: PDB Molecule: laci family transcriptional regulator; PDBTitle: crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
13	c3qk7C_	Alignment		100.0	20	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
14	c2rgyA_	Alignment		100.0	23	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of transcriptional regulator of laci family from2 burkholderia phymatum
15	c3k4hA_	Alignment		100.0	22	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator laci from2 bacillus cereus subsp. cytotoxis nvh 391-98
16	c3hcbW_	Alignment		100.0	13	PDB header: rna binding protein Chain: B: PDB Molecule: maltose operon transcriptional repressor; PDBTitle: crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus aureus
17	c3brqA_	Alignment		100.0	22	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator ascg; PDBTitle: crystal structure of the escherichia coli transcriptional repressor2 ascg
18	c2o20H_	Alignment		100.0	17	PDB header: transcription Chain: H: PDB Molecule: catabolite control protein a; PDBTitle: crystal structure of transcription regulator ccpa of lactococcus2 lactis
19	c3e3mA_	Alignment		100.0	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
20	c3d8uA_	Alignment		100.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: purr transcriptional regulator; PDBTitle: the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
21	c3k9cA_	Alignment	not modelled	100.0	28	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family protein; PDBTitle: crystal structure of laci transcriptional regulator from rhodococcus2 species.
22	c3cs3A_	Alignment	not modelled	100.0	19	PDB header: transcription regulator Chain: A: PDB Molecule: sugar-binding transcriptional regulator, laci family; PDBTitle: crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
23	c3h5oB_	Alignment	not modelled	100.0	20	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
24	c3hs3A_	Alignment	not modelled	100.0	22	PDB header: transcription regulator Chain: A: PDB Molecule: ribose operon repressor; PDBTitle: crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
25	c3mizB_	Alignment	not modelled	100.0	20	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator protein, laci PDBTitle: crystal structure of a putative transcriptional regulator2 protein, lacI family from rhizobium etli
26	c3egcF_	Alignment	not modelled	100.0	23	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative ribose operon repressor; PDBTitle: crystal structure of a putative ribose operon repressor from2 burkholderia thailandensis
27	c3ctpB_	Alignment	not modelled	100.0	21	PDB header: transcription regulator Chain: B: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of periplasmic binding protein/laci transcriptional2 regulator from alkaliphilus metalliredigens qymf

					complexed with d-3 xylulofuranose
28	d1dbqa_	Alignment	not modelled	100.0	25 Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
29	c3o74A_	Alignment	not modelled	100.0	12 PDB header: transcription Chain: A: PDB Molecule: fructose transport system repressor frur; PDBTitle: crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
30	c3huuC_	Alignment	not modelled	100.0	18 PDB header: transcription regulator Chain: C: PDB Molecule: transcription regulator like protein; PDBTitle: crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
31	c3bblA_	Alignment	not modelled	100.0	22 PDB header: regulatory protein Chain: A: PDB Molecule: regulatory protein of lacI family; PDBTitle: crystal structure of a regulatory protein of lacI family from2 chloroflexus aggregans
32	d1jx6a_	Alignment	not modelled	100.0	13 Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
33	c3gv0A_	Alignment	not modelled	100.0	14 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI family transcription regulator from2 agrobacterium tumefaciens
34	c3bilA_	Alignment	not modelled	100.0	22 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable lacI-family transcriptional regulator; PDBTitle: crystal structure of a probable lacI family transcriptional2 regulator from corynebacterium glutamicum
35	c2qu7B_	Alignment	not modelled	100.0	19 PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
36	c3clkB_	Alignment	not modelled	100.0	24 PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from lactobacillus2 plantarum
37	c2h0aA_	Alignment	not modelled	100.0	20 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of probable transcription regulator from2 thermus thermophilus
38	c2ioyB_	Alignment	not modelled	100.0	19 PDB header: sugar binding protein Chain: B: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
39	c3gybB_	Alignment	not modelled	100.0	25 PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulators (lacI-family) PDBTitle: crystal structure of a lacI-family transcriptional2 regulatory protein from corynebacterium glutamicum
40	c3jvdA_	Alignment	not modelled	100.0	21 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcription regulation repressor (lacI2 family) from corynebacterium glutamicum
41	d2dria_	Alignment	not modelled	100.0	20 Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
42	c3g85A_	Alignment	not modelled	100.0	14 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (lacI family); PDBTitle: crystal structure of lacI family transcription regulator from2 clostridium acetobutylicum
43	c3jy6B_	Alignment	not modelled	100.0	16 PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI transcriptional regulator from lactobacillus2 brevis
44	c3l6uA_	Alignment	not modelled	100.0	13 PDB header: transport protein Chain: A: PDB Molecule: abc-type sugar transport system periplasmic PDBTitle: crystal structure of abc-type sugar transport system,2 periplasmic component from exigobacterium sibiricum
45	c2fn9A_	Alignment	not modelled	99.9	21 PDB header: sugar binding protein Chain: A: PDB Molecule: ribose abc transporter, periplasmic ribose-binding protein; PDBTitle: thermotoga maritima ribose binding protein unliganded form
46	c3l49D_	Alignment	not modelled	99.9	15 PDB header: transport protein Chain: D: PDB Molecule: abc sugar (ribose) transporter, periplasmic PDBTitle: crystal structure of abc sugar transporter subunit from2 rhodobacter sphaeroides 2.4.1
47	d1guda_	Alignment	not modelled	99.9	18 Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
48	d1byka_	Alignment	not modelled	99.9	13 Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
49	c3brsA_	Alignment	not modelled	99.9	13 PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/lacI transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
50	c3g1wB_	Alignment	not modelled	99.9	12 PDB header: transport protein Chain: B: PDB Molecule: sugar abc transporter; PDBTitle: crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans
51	c3ksmA_	Alignment	not modelled	99.9	17 PDB header: transport protein Chain: A: PDB Molecule: abc-type sugar transport system, periplasmic component; PDBTitle: crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
					Fold: Periplasmic binding protein-like I

52	d8abpa_	Alignment	not modelled	99.9	16	Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
53	c3ma0A_	Alignment	not modelled	99.9	19	PDB header: sugar binding protein Chain: A: PDB Molecule: d-xylose-binding periplasmic protein; PDBTitle: closed liganded crystal structure of xylose binding protein from2 escherichia coli
54	c3gbvB_	Alignment	not modelled	99.9	13	PDB header: transcription regulator Chain: B: PDB Molecule: putative lacI-family transcriptional regulator; PDBTitle: crystal structure of a putative lacI transcriptional regulator from2 bacteroides fragilis
55	c3e61A_	Alignment	not modelled	99.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transcriptional repressor of ribose operon; PDBTitle: crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus
56	c2vk2A_	Alignment	not modelled	99.9	17	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
57	c2qvcC_	Alignment	not modelled	99.9	16	PDB header: transport protein Chain: C: PDB Molecule: sugar abc transporter, periplasmic sugar-binding PDBTitle: crystal structure of a periplasmic sugar abc transporter2 from thermotoga maritima
58	c2x7xA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: fructose binding periplasmic domain of hybrid two component2 system bt1754
59	c2rjoA_	Alignment	not modelled	99.9	21	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
60	dlgcaa_	Alignment	not modelled	99.9	18	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
61	c3rotA_	Alignment	not modelled	99.9	12	PDB header: transport protein Chain: A: PDB Molecule: abc sugar transporter, periplasmic sugar binding protein; PDBTitle: crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
62	c3o1hB_	Alignment	not modelled	99.9	10	PDB header: signaling protein Chain: B: PDB Molecule: periplasmic protein tort; PDBTitle: crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
63	d2fvya1	Alignment	not modelled	99.9	18	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
64	c3h75A_	Alignment	not modelled	99.8	16	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic sugar-binding domain protein; PDBTitle: crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
65	c3d02A_	Alignment	not modelled	99.8	14	PDB header: sugar binding protein Chain: A: PDB Molecule: putative lacI-type transcriptional regulator; PDBTitle: crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution
66	d2bjca1	Alignment	not modelled	99.8	93	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
67	dl1jya_	Alignment	not modelled	99.8	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
68	dlefaa1	Alignment	not modelled	99.8	100	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
69	d2hsga1	Alignment	not modelled	99.7	53	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
70	dl1cda_	Alignment	not modelled	99.7	98	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
71	dlqpza1	Alignment	not modelled	99.7	45	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
72	dluxda_	Alignment	not modelled	99.6	46	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
73	dluxca_	Alignment	not modelled	99.6	49	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
74	c21cvA_	Alignment	not modelled	99.6	46	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
75	c218nA_	Alignment	not modelled	99.5	46	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
76	c3lftA_	Alignment	not modelled	99.5	11	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the abc domain in complex with l-

						trp from2 streptococcus pneumonia to 1.35a
77	c2qh8A_	Alignment	not modelled	99.5	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved domain protein from vibrio2 cholerae o1 biovar eltor str. n16961
78	c2hqbA_	Alignment	not modelled	99.5	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator of comk gene; PDBTitle: crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans
79	c2fqxA_	Alignment	not modelled	99.5	12	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
80	c3s99A_	Alignment	not modelled	98.6	9	PDB header: lipid binding protein Chain: A: PDB Molecule: basic membrane lipoprotein; PDBTitle: crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
81	c3trbA_	Alignment	not modelled	96.9	14	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
82	c2ebyA_	Alignment	not modelled	96.8	14	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
83	c3cecA_	Alignment	not modelled	96.7	25	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
84	c3eusB_	Alignment	not modelled	96.5	23	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
85	c3t76A_	Alignment	not modelled	96.5	18	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
86	c2bnoA_	Alignment	not modelled	96.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
87	d2b5aa1	Alignment	not modelled	96.4	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
88	c3bs3A_	Alignment	not modelled	96.3	33	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
89	c3clcC_	Alignment	not modelled	96.3	18	PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.espl3961 tetramer in complex with its natural 35 base-pair operator
90	c1b0nA_	Alignment	not modelled	96.3	26	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
91	d2icta1	Alignment	not modelled	96.3	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
92	d1utxa_	Alignment	not modelled	96.3	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
93	c1y9qA_	Alignment	not modelled	96.3	20	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
94	d2a6ca1	Alignment	not modelled	96.2	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
95	c3b7hA_	Alignment	not modelled	96.2	28	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
96	d1y9qa1	Alignment	not modelled	96.2	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
97	d1y7ya1	Alignment	not modelled	96.2	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
98	c2o38A_	Alignment	not modelled	96.1	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
99	d2o38a1	Alignment	not modelled	96.1	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
100	c2ef8A_	Alignment	not modelled	96.1	14	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
101	d1adra_	Alignment	not modelled	96.1	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
102	d1nera_	Alignment	not modelled	96.1	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains

						Family: Phage repressors
103	c3omtA	Alignment	not modelled	96.1	23	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.
104	d2ofya1	Alignment	not modelled	96.1	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
105	d1rioa	Alignment	not modelled	96.0	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
106	d1x57a1	Alignment	not modelled	96.0	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
107	c2kpiA	Alignment	not modelled	96.0	16	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
108	d2r1j11	Alignment	not modelled	96.0	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
109	c3op9A	Alignment	not modelled	96.0	13	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
110	d1lmb3	Alignment	not modelled	96.0	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
111	d1b0na2	Alignment	not modelled	95.9	33	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
112	c2w48D	Alignment	not modelled	95.9	27	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
113	c3f52A	Alignment	not modelled	95.9	33	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
114	c3iwfA	Alignment	not modelled	95.8	15	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
115	d2croa	Alignment	not modelled	95.7	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
116	c3kxaD	Alignment	not modelled	95.7	30	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
117	d1llib	Alignment	not modelled	95.7	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
118	d1sq8a	Alignment	not modelled	95.7	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
119	c3f6wE	Alignment	not modelled	95.6	15	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
120	c1u78A	Alignment	not modelled	95.6	13	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