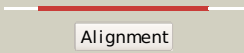
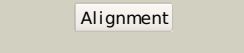
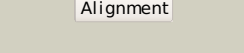
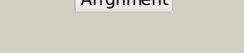
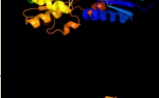
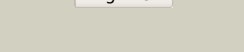


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kjdD_	 Alignment		100.0	30	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
2	c1zvva_	 Alignment		100.0	28	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
3	c1bdhA_	 Alignment		100.0	25	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
4	c3h5tA_	 Alignment		100.0	23	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	d2nzug1	 Alignment		100.0	27	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
6	c3c3kA_	 Alignment		100.0	23	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
7	c2iksA_	 Alignment		100.0	18	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
8	c3h5oB_	 Alignment		100.0	37	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
9	c3e3mA_	 Alignment		100.0	29	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
10	c2o20H_	 Alignment		100.0	24	PDB header: transcription Chain: H: PDB Molecule: catabolite control protein a; PDBTitle: crystal structure of transcription regulator ccpa of lactococcus2 lactis
11	c3k4hA_	 Alignment		100.0	24	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

12	c3k9cA_	Alignment		100.0	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family protein; PDBTitle: crystal structure of laci transcriptional regulator from rhodococcus2 species.
13	c3mizB_	Alignment		100.0	21	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 eti
14	c3qk7C_	Alignment		100.0	17	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
15	c3cs3A_	Alignment		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
16	c3dbiA_	Alignment		100.0	21	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
17	c3hcwB_	Alignment		100.0	15	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
18	c3d8uA_	Alignment		100.0	30	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
19	c3kkeA_	Alignment		100.0	23	PDB header: transcription regulator Chain: A: PDB Molecule: laci family transcriptional regulator; PDBTitle: crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
20	c3gv0A_	Alignment		100.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
21	d1tifa_	Alignment	not modelled	100.0	19	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
22	c3egcF_	Alignment	not modelled	100.0	24	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
23	c3bbiA_	Alignment	not modelled	100.0	24	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
24	c3brqA_	Alignment	not modelled	100.0	19	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator ascg; PDBTitle: crystal structure of the escherichia coli transcriptional repressor2 ascg
25	c3ctpB_	Alignment	not modelled	100.0	23	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
26	c2rgyA_	Alignment	not modelled	100.0	20	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of transcriptional regulator of laci family from2 burkholderia phymatum
27	c3hs3A_	Alignment	not modelled	100.0	17	PDB header: transcription regulator Chain: A: PDB Molecule: ribose operon repressor; PDBTitle: crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
28	c3o74A_	Alignment	not modelled	100.0	15	PDB header: transcription Chain: A: PDB Molecule: fructose transport system repressor frur; PDBTitle: crystal structure of cra transcriptional dual regulator from2 pseudomonas putida

29	d1dbqa_	Alignment	not modelled	100.0	21	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
30	c3huuC_	Alignment	not modelled	100.0	21	PDB header: transcription regulator Chain: C: PDB Molecule: transcription regulator like protein; PDBTitle: crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
31	d1jyea_	Alignment	not modelled	100.0	20	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
32	c1jyeA_	Alignment	not modelled	100.0	20	PDB header: transcription Chain: A: PDB Molecule: lactose operon repressor; PDBTitle: structure of a dimeric lac repressor with c-terminal deletion and k84I2 substitution
33	c3clkB_	Alignment	not modelled	100.0	18	PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from lactobacillus2 plantarum
34	c2qu7B_	Alignment	not modelled	100.0	23	PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
35	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
36	c3jy6B_	Alignment	not modelled	100.0	24	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of laci transcriptional regulator from lactobacillus2 brevis
37	c2ioyB_	Alignment	not modelled	100.0	18	PDB header: sugar binding protein Chain: B: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
38	d1jx6a_	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
39	c3bilA_	Alignment	not modelled	100.0	18	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
40	c3gybB_	Alignment	not modelled	100.0	23	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
41	c3l6uA_	Alignment	not modelled	99.9	15	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 exiguobacterium sibiricum
42	d2dria_	Alignment	not modelled	99.9	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
43	c3jvdA_	Alignment	not modelled	99.9	23	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
44	c2h0aA_	Alignment	not modelled	99.9	25	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of probable transcription regulator from2 thermus thermophilus
45	c2fn9A_	Alignment	not modelled	99.9	15	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	d1guda_	Alignment	not modelled	99.9	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
47	d1byka_	Alignment	not modelled	99.9	20	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
48	c3ma0A_	Alignment	not modelled	99.9	15	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
49	c3g1wB_	Alignment	not modelled	99.9	15	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
50	c3l49D_	Alignment	not modelled	99.9	11	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
51	c3e61A_	Alignment	not modelled	99.9	21	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
52	d8abpa_	Alignment	not modelled	99.9	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
53	c2vk2A_	Alignment	not modelled	99.9	18	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq;

						PDBTitle: crystal structure of a galactofuranose binding protein
54	c3brsA	Alignment	not modelled	99.9	16	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
55	c3ksmA	Alignment	not modelled	99.9	18	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
56	c3gbvB	Alignment	not modelled	99.9	12	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
57	c2rjoA	Alignment	not modelled	99.9	16	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
58	c3h75A	Alignment	not modelled	99.9	14	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
59	c2x7xA	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: fructose binding periplasmic domain of hybrid two component2 system bt1754
60	d1gcaa	Alignment	not modelled	99.8	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
61	c2qvcC	Alignment	not modelled	99.8	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
62	d2fvya1	Alignment	not modelled	99.8	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
63	c3rota	Alignment	not modelled	99.8	9	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
64	c3o1hB	Alignment	not modelled	99.8	13	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
65	c3d02A	Alignment	not modelled	99.8	12	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	44	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
67	d1tjya	Alignment	not modelled	99.8	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
68	d1efaa1	Alignment	not modelled	99.7	42	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	30	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
70	d1qpza1	Alignment	not modelled	99.7	30	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
71	d1lcda	Alignment	not modelled	99.7	48	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
72	d1luxda	Alignment	not modelled	99.6	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
73	c2lcvA	Alignment	not modelled	99.6	43	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
74	d1luxca	Alignment	not modelled	99.6	32	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
75	c2l8nA	Alignment	not modelled	99.5	43	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	c2qh8A	Alignment	not modelled	99.5	11	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
77	c3lftA	Alignment	not modelled	99.5	12	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

78	c2hqbA	Alignment	not modelled	99.5	10	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	99.4	10	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
80	c3s99A	Alignment	not modelled	98.5	11	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	c2ebyA	Alignment	not modelled	97.0	14	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
82	c3trbA	Alignment	not modelled	97.0	9	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
83	c3f8mA	Alignment	not modelled	96.8	27	PDB header: transcription Chain: A: PDB Molecule: gntr-family protein transcriptional regulator; PDBTitle: crystal structure of phnf from mycobacterium smegmatis
84	c3t76A	Alignment	not modelled	96.8	24	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
85	c3bwgA	Alignment	not modelled	96.8	30	PDB header: transcription regulator Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator yydk; PDBTitle: the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
86	c3eetA	Alignment	not modelled	96.6	12	PDB header: transcription regulator Chain: A: PDB Molecule: putative gntr-family transcriptional regulator; PDBTitle: crystal structure of putative gntr-family transcriptional2 regulator
87	c3cecA	Alignment	not modelled	96.5	14	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
88	c3b7hA	Alignment	not modelled	96.5	16	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
89	c2kpiA	Alignment	not modelled	96.4	14	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
90	c3eusB	Alignment	not modelled	96.3	19	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
91	d2icta1	Alignment	not modelled	96.3	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
92	d2o38a1	Alignment	not modelled	96.3	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
93	c2o38A	Alignment	not modelled	96.3	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
94	c3edpB	Alignment	not modelled	96.3	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lin2111 protein; PDBTitle: the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
95	c1y9qA	Alignment	not modelled	96.3	26	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
96	c3clcC	Alignment	not modelled	96.3	16	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
97	d2a6ca1	Alignment	not modelled	96.2	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
98	c3bs3A	Alignment	not modelled	96.2	26	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
99	c2di3A	Alignment	not modelled	96.2	19	PDB header: transcription Chain: A: PDB Molecule: bacterial regulatory proteins, gntr family; PDBTitle: crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
100	c2bnoA	Alignment	not modelled	96.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenii
101	d2b5aa1	Alignment	not modelled	96.1	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
102	d1y9aa1	Alignment	not modelled	96.1	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains

102	dly9qa1	Alignment	not modelled	96.1	20	Family: Probable transcriptional regulator VC1968, N-terminal domain
103	c3neuA	Alignment	not modelled	96.1	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1836 protein; PDBTitle: the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
104	dly7ya1	Alignment	not modelled	96.0	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
105	d1hwl1a1	Alignment	not modelled	96.0	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
106	d1utxa	Alignment	not modelled	96.0	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
107	c3by6C	Alignment	not modelled	96.0	16	PDB header: transcription regulator Chain: C: PDB Molecule: predicted transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator from oenococcus oeni
108	c1u78A	Alignment	not modelled	96.0	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
109	d1v4ra1	Alignment	not modelled	95.9	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
110	c3omtA	Alignment	not modelled	95.9	26	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.
111	c2ef8A	Alignment	not modelled	95.9	9	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
112	d1x57a1	Alignment	not modelled	95.9	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
113	d1b0na2	Alignment	not modelled	95.9	30	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
114	c2du9A	Alignment	not modelled	95.9	15	PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulators; PDBTitle: crystal structure of the transcriptional factor from c.glutamicum
115	d3bwga1	Alignment	not modelled	95.9	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
116	d1rioa	Alignment	not modelled	95.9	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
117	d1adra	Alignment	not modelled	95.8	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
118	d2r1jl1	Alignment	not modelled	95.8	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
119	d2ofya1	Alignment	not modelled	95.8	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
120	c3op9A	Alignment	not modelled	95.8	14	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua