



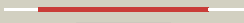



















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zvva_	 Alignment		100.0	35	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
2	c3kjd_	 Alignment		100.0	22	PDB header: transcription 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	33	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
4	c3h5tA_	 Alignment		100.0	22	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	36	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
6	c3k4hA_	 Alignment		100.0	30	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
7	c3qk7C_	 Alignment		100.0	23	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
8	c2iksA_	 Alignment		100.0	19	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	25	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	c2o20H_	 Alignment		100.0	30	PDB header: transcription Chain: H: PDB Molecule: catabolite control protein a; PDBTitle: crystal structure of transcription regulator ccpa of lactococcus2 lactis
11	c3kkeA_	 Alignment		100.0	30	PDB header: transcription regulator Chain: A: PDB Molecule: laci family transcriptional regulator; PDBTitle: crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis

12	c3c3kA_	Alignment		100.0	29	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
13	c3h5oB_	Alignment		100.0	27	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
14	c3d8uA_	Alignment		100.0	22	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
15	c3e3mA_	Alignment		100.0	24	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a lacI family transcriptional2 regulator from silicibacter pomeroyi
16	c2rgyA_	Alignment		100.0	25	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of transcriptional regulator of lacI family from2 burkholderia phymatum
17	c3bblA_	Alignment		100.0	31	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
18	c3hcbW_	Alignment		100.0	19	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
19	c3miZB_	Alignment		100.0	27	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
20	c3brqA_	Alignment		100.0	26	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator ascg; PDBTitle: crystal structure of the escherichia coli transcriptional repressor2 ascg
21	c3k9cA_	Alignment	not modelled	100.0	26	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family protein; PDBTitle: crystal structure of lacI transcriptional regulator from rhodococcus2 species.
22	c3gv0A_	Alignment	not modelled	100.0	18	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI family transcriptional regulator from2 agrobacterium tumefaciens
23	c3egcF_	Alignment	not modelled	100.0	30	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
24	c3cs3A_	Alignment	not modelled	100.0	27	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
25	c3clkB_	Alignment	not modelled	100.0	25	PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from lactobacillus2 plantarum
26	d1tfa_	Alignment	not modelled	100.0	25	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
27	d1dbqa_	Alignment	not modelled	100.0	35	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
28	c3g85A_	Alignment	not modelled	100.0	21	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (lacI family); PDBTitle: crystal structure of lacI family transcription regulator

					from2 clostridium acetobutylicum
29	d1jyea_	Alignment	not modelled	100.0	26 Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
30	c1jyeA_	Alignment	not modelled	100.0	26 PDB header: transcription Chain: A: PDB Molecule: lactose operon repressor; PDBTitle: structure of a dimeric lac repressor with c-terminal deletion and k84I2 substitution
31	c2qu7B_	Alignment	not modelled	100.0	25 PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
32	c3ctpB_	Alignment	not modelled	100.0	26 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
33	c2h0aA_	Alignment	not modelled	100.0	26 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of probable transcription regulator from2 thermus thermophilus
34	c3huuC_	Alignment	not modelled	100.0	20 PDB header: transcription regulator Chain: C: PDB Molecule: transcription regulator like protein; PDBTitle: crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
35	c3o74A_	Alignment	not modelled	100.0	22 PDB header: transcription Chain: A: PDB Molecule: fructose transport system repressor frur; PDBTitle: crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
36	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
37	c3jy6B_	Alignment	not modelled	100.0	21 PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of laci transcriptional regulator from lactobacillus2 brevis
38	d1jx6a_	Alignment	not modelled	100.0	11 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	23 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	c3hs3A_	Alignment	not modelled	100.0	23 PDB header: transcription regulator Chain: A: PDB Molecule: ribose operon repressor; PDBTitle: crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
41	c3jvdA_	Alignment	not modelled	100.0	25 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
42	c3gybB_	Alignment	not modelled	100.0	28 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
43	c2fn9A_	Alignment	not modelled	100.0	16 PDB header: sugar binding protein Chain: A: PDB Molecule: ribose abc transporter, periplasmic ribose-binding protein; PDBTitle: thermotoga maritima ribose binding protein unliganded form
44	d2dria_	Alignment	not modelled	100.0	21 Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
45	c3l6uA_	Alignment	not modelled	100.0	16 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
46	d1guda_	Alignment	not modelled	100.0	17 Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
47	d8abpa_	Alignment	not modelled	100.0	14 Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
48	d1byka_	Alignment	not modelled	100.0	19 Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
49	c3ma0A_	Alignment	not modelled	100.0	14 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
50	c3g1wB_	Alignment	not modelled	100.0	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
51	c3e61A_	Alignment	not modelled	100.0	23 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	c3l49D_	Alignment	not modelled	100.0	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

53	c2vk2A	Alignment	not modelled	100.0	15	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
54	c3ksmA	Alignment	not modelled	100.0	16	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
55	c3brsA	Alignment	not modelled	100.0	16	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
56	c2rjoA	Alignment	not modelled	100.0	12	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
57	c3h75A	Alignment	not modelled	100.0	17	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
58	dlgcaa	Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
59	d2fvya1	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
60	c3gbvB	Alignment	not modelled	100.0	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
61	c2x7xA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: fructose binding periplasmic domain of hybrid two component2 system bt1754
62	c2qvcC	Alignment	not modelled	100.0	15	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
63	dl1tja	Alignment	not modelled	100.0	9	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
64	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
65	c3o1hB	Alignment	not modelled	99.9	14	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
66	c3d02A	Alignment	not modelled	99.9	13	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
67	c2hqbA	Alignment	not modelled	99.9	12	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
68	c2fqxA	Alignment	not modelled	99.8	14	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
69	c2qh8A	Alignment	not modelled	99.8	10	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
70	c3lftA	Alignment	not modelled	99.8	10	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
71	d2bjca1	Alignment	not modelled	99.7	38	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
72	dl1efaa1	Alignment	not modelled	99.7	36	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
73	d2hsqa1	Alignment	not modelled	99.6	36	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
74	dlqpza1	Alignment	not modelled	99.6	45	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
75	c3s99A	Alignment	not modelled	99.6	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
76	dl1cda	Alignment	not modelled	99.5	41	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator

77	dluxda_	Alignment	not modelled	99.5	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
78	c2lcvA_	Alignment	not modelled	99.5	100	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
79	dluxca_	Alignment	not modelled	99.4	30	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
80	c2l8nA_	Alignment	not modelled	99.4	100	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
81	c3qi7A_	Alignment	not modelled	98.2	9	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
82	d1qo0a_	Alignment	not modelled	97.9	9	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
83	c3sg0A_	Alignment	not modelled	97.8	10	PDB header: signaling protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
84	c3t0nA_	Alignment	not modelled	97.8	12	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal; PDBTitle: crystal structure of twin-arginine translocation pathway signal from2 rhodopseudomonas palustris bisb5
85	c3snrA_	Alignment	not modelled	97.8	11	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
86	d3ckma1	Alignment	not modelled	97.7	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
87	c3n0wA_	Alignment	not modelled	97.6	11	PDB header: transport protein Chain: A: PDB Molecule: abc branched chain amino acid family transporter, PDBTitle: crystal structure of a branched chain amino acid abc transporter2 periplasmic ligand-binding protein (bx_e_c0949) from burkholderia3 xenovorans lb400 at 1.88 a resolution
88	d2liva_	Alignment	not modelled	97.5	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
89	c3i09A_	Alignment	not modelled	97.4	13	PDB header: transport protein Chain: A: PDB Molecule: periplasmic branched-chain amino acid-binding protein; PDBTitle: crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
90	c3i45A_	Alignment	not modelled	97.4	10	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of putative twin-arginine translocation pathway2 signal protein from rhodospirillum rubrum atcc 11170
91	c3eafA_	Alignment	not modelled	97.4	13	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
92	c3hutA_	Alignment	not modelled	97.3	12	PDB header: transport protein Chain: A: PDB Molecule: putative branched-chain amino acid abc PDBTitle: crystal structure of a putative branched-chain amino acid2 abc transporter from rhodospirillum rubrum
93	d1usga_	Alignment	not modelled	97.2	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
94	c3ip5A_	Alignment	not modelled	97.2	15	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein (amino acid); PDBTitle: structure of atu2422-gaba receptor in complex with alanine
95	c3f8mA_	Alignment	not modelled	96.6	21	PDB header: transcription Chain: A: PDB Molecule: gntr-family protein transcriptional regulator; PDBTitle: crystal structure of phnf from mycobacterium smegmatis
96	c3lopA_	Alignment	not modelled	96.5	14	PDB header: substrate binding protein Chain: A: PDB Molecule: substrate binding periplasmic protein; PDBTitle: crystal structure of substrate-binding periplasmic protein2 (pbp) from ralstonia solanacearum
97	c3td9A_	Alignment	not modelled	96.4	14	PDB header: transport protein Chain: A: PDB Molecule: branched chain amino acid abc transporter, periplasmic PDBTitle: crystal structure of a leucine binding protein livk (tm1135) from2 thermotoga maritima msb8 at 1.90 a resolution
98	c3lkbB_	Alignment	not modelled	96.3	12	PDB header: transport protein Chain: B: PDB Molecule: probable branched-chain amino acid abc PDBTitle: crystal structure of a branched chain amino acid abc2 transporter from thermus thermophilus with bound valine
99	c3bwgA_	Alignment	not modelled	96.3	14	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
100	c3trbA_	Alignment	not modelled	96.2	16	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
101	c2ebyA_	Alignment	not modelled	96.2	19	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
102	c3eetA_	Alignment	not modelled	96.2	11	PDB header: transcription regulator Chain: A: PDB Molecule: putative gntr-family transcriptional regulator; PDBTitle: crystal structure of putative gntr-family transcriptional2 regulator
103	c3cecA_	Alignment	not modelled	96.0	19	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
104	c3h5lB_	Alignment	not modelled	95.9	10	PDB header: transport protein Chain: B: PDB Molecule: putative branched-chain amino acid abc PDBTitle: crystal structure of a putative branched-chain amino acid2 abc transporter from silicibacter pomeroyi
105	d1ewka_	Alignment	not modelled	95.9	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
106	d1rioA_	Alignment	not modelled	95.8	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
107	c3neuA_	Alignment	not modelled	95.8	29	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
108	c2di3A_	Alignment	not modelled	95.8	18	PDB header: transcription Chain: A: PDB Molecule: bacterial regulatory proteins, gntr family; PDBTitle: crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
109	c1y9qA_	Alignment	not modelled	95.8	14	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
110	c3q41B_	Alignment	not modelled	95.8	10	PDB header: transport protein Chain: B: PDB Molecule: glutamate [nmda] receptor subunit zeta-1; PDBTitle: crystal structure of the glun1 n-terminal domain (ntd)
111	c2bnoA_	Alignment	not modelled	95.7	9	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenisi.
112	c3by6C_	Alignment	not modelled	95.7	21	PDB header: transcription regulator Chain: C: PDB Molecule: predicted transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator from oenococcus oeni
113	c3eusB_	Alignment	not modelled	95.7	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
114	c2w48D_	Alignment	not modelled	95.6	20	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
115	d3bwga1	Alignment	not modelled	95.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
116	c3bs3A_	Alignment	not modelled	95.5	23	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
117	d2icta1	Alignment	not modelled	95.5	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
118	d2b5aa1	Alignment	not modelled	95.5	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
119	c3clcC_	Alignment	not modelled	95.5	19	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
120	c3t76A_	Alignment	not modelled	95.5	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii