
































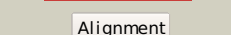





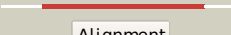
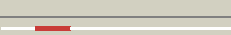

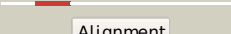
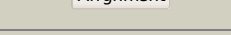
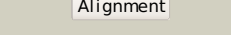

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zvva_	 Alignment		100.0	22	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
2	c3kjd_	 Alignment		100.0	18	PDB header: transcription 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	20	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
4	c3h5tA_	 Alignment		100.0	18	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	c2iksA_	 Alignment		100.0	99	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
6	d2nzug1	 Alignment		100.0	19	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
7	c3c3kA_	 Alignment		100.0	17	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
8	c3k4hA_	 Alignment		100.0	18	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
9	c3dbiA_	 Alignment		100.0	18	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	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
11	c3hcbwB_	 Alignment		100.0	20	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

12	c3kkeA_	Alignment		100.0	15	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	c3h5oB_	Alignment		100.0	21	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
14	d1tfa_	Alignment		100.0	14	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
15	c3brqA_	Alignment		100.0	18	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator ascg; PDBTitle: crystal structure of the escherichia coli transcriptional repressor2 ascg
16	c2o20H_	Alignment		100.0	14	PDB header: transcription Chain: H: PDB Molecule: catabolite control protein a; PDBTitle: crystal structure of transcription regulator ccpa of lactococcus2 lactis
17	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
18	c2rgyA_	Alignment		100.0	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of transcriptional regulator of lacI family from2 burkholderia phymatum
19	c3qk7C_	Alignment		100.0	18	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
20	c3o74A_	Alignment		100.0	42	PDB header: transcription Chain: A: PDB Molecule: fructose transport system repressor frur; PDBTitle: crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
21	c3ctpB_	Alignment	not modelled	100.0	17	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
22	c3cs3A_	Alignment	not modelled	100.0	15	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	c1jyeA_	Alignment	not modelled	100.0	15	PDB header: transcription Chain: A: PDB Molecule: lactose operon repressor; PDBTitle: structure of a dimeric lac repressor with c-terminal deletion and k84I2 substitution
24	d1jyea_	Alignment	not modelled	100.0	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
25	c3mizB_	Alignment	not modelled	100.0	15	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	c3biIA_	Alignment	not modelled	100.0	20	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
27	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

28	c3clkB	Alignment	not modelled	100.0	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from lactobacillus2 plantarum
29	c3k9cA	Alignment	not modelled	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.
30	c3bblA	Alignment	not modelled	100.0	19	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
31	c2qu7B	Alignment	not modelled	100.0	18	PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
32	d1dbqa	Alignment	not modelled	100.0	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
33	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
34	c3gv0A	Alignment	not modelled	100.0	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
35	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
36	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
37	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
38	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
39	c3g85A	Alignment	not modelled	100.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (laci family); PDBTitle: crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
40	d2dria	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
41	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
42	c3gybB	Alignment	not modelled	100.0	20	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	c2h0aA	Alignment	not modelled	100.0	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of probable transcription regulator from2 thermus thermophilus
44	c3l6uA	Alignment	not modelled	100.0	14	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
45	c2fn9A	Alignment	not modelled	100.0	17	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	100.0	13	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	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
48	c3l49D	Alignment	not modelled	99.9	12	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
49	d1byka	Alignment	not modelled	99.9	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
50	c3brsA	Alignment	not modelled	99.9	11	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
51	c3ma0A	Alignment	not modelled	99.9	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
52	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

53	c2vk2A	Alignment	not modelled	99.9	16	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
54	c3gbvB	Alignment	not modelled	99.9	10	PDB header: transcription regulator Chain: B: PDB Molecule: putative lacI-family transcriptional regulator; PDBTitle: crystal structure of a putative lacI transcriptional regulator from <i>Bacteroides fragilis</i>
55	c3ksmA	Alignment	not modelled	99.9	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 <i>Haemaphysalis chejuensis</i>
56	c3e61A	Alignment	not modelled	99.9	20	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 <i>Staphylococcus saprophyticus</i> subsp. <i>saprophyticus</i>
57	c2qvcC	Alignment	not modelled	99.9	14	PDB header: transport protein Chain: C: PDB Molecule: sugar abc transporter, periplasmic sugar-binding PDBTitle: crystal structure of a periplasmic sugar abc transporter2 from <i>Thermotoga maritima</i>
58	c2rjoA	Alignment	not modelled	99.9	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 <i>Burkholderia phytofirmans</i>
59	d1gcaa	Alignment	not modelled	99.9	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
60	d2fvya1	Alignment	not modelled	99.9	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
61	c2x7xA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: fructose binding periplasmic domain of hybrid two component2 system bt1754
62	c3h75A	Alignment	not modelled	99.9	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 <i>Pseudomonas fluorescens</i>
63	c3o1hB	Alignment	not modelled	99.9	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
64	c3rota	Alignment	not modelled	99.9	13	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 <i>Legionella pneumophila</i>
65	d1tjya	Alignment	not modelled	99.9	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
66	c3d02A	Alignment	not modelled	99.9	10	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 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> mgh3 78578 at 1.30 Å resolution
67	c2hqbA	Alignment	not modelled	99.7	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator of comK gene; PDBTitle: crystal structure of a transcriptional activator of comK2 gene from <i>Bacillus halodurans</i>
68	d2bjca1	Alignment	not modelled	99.7	43	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	39	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
70	d1efaa1	Alignment	not modelled	99.7	46	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
71	c3lftA	Alignment	not modelled	99.7	10	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the abc domain in complex with I-trp from <i>Streptococcus pneumoniae</i> to 1.35Å
72	c2qh8A	Alignment	not modelled	99.6	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved domain protein from <i>Vibrio cholerae</i> o1 biovar eltor str. n16961
73	c2fqxA	Alignment	not modelled	99.6	13	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmprc; PDBTitle: pnra from <i>Treponema pallidum</i> complexed with guanosine
74	d1luxda	Alignment	not modelled	99.6	97	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
75	d1qpza1	Alignment	not modelled	99.6	38	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
76	d1luxca	Alignment	not modelled	99.6	100	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator

77	d1lcda_	Alignment	not modelled	99.5	49	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	33	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	c2l8nA_	Alignment	not modelled	99.4	33	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
80	c3s99A_	Alignment	not modelled	99.2	6	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	c3sg0A_	Alignment	not modelled	96.7	17	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
82	c3cecA_	Alignment	not modelled	96.0	24	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
83	c3trbA_	Alignment	not modelled	96.0	11	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
84	d2a6ca1	Alignment	not modelled	96.0	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
85	c2bnoA_	Alignment	not modelled	95.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenisi.
86	c2ebyA_	Alignment	not modelled	95.9	29	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
87	d2icta1	Alignment	not modelled	95.9	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
88	c3eusB_	Alignment	not modelled	95.7	16	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
89	c3b7hA_	Alignment	not modelled	95.7	22	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
90	c2o38A_	Alignment	not modelled	95.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
91	d2o38a1	Alignment	not modelled	95.6	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
92	d1rioa_	Alignment	not modelled	95.6	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
93	c1y9qA_	Alignment	not modelled	95.6	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
94	c1u78A_	Alignment	not modelled	95.5	17	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
95	c3snrA_	Alignment	not modelled	95.5	13	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
96	c1b0nA_	Alignment	not modelled	95.5	20	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
97	d1lmb3_	Alignment	not modelled	95.5	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
98	d2ofya1	Alignment	not modelled	95.4	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
99	c3bs3A_	Alignment	not modelled	95.4	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
100	d2b5aa1	Alignment	not modelled	95.3	34	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
101	d1y9qa1	Alignment	not modelled	95.2	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
102	c3t76A_	Alignment	not modelled	95.2	22	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii

103	c3qi7A_	 Alignment	not modelled	95.2	13	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
104	c3rclC_	 Alignment	not modelled	95.2	21	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
105	d1adra_	 Alignment	not modelled	95.1	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
106	d1utxa_	 Alignment	not modelled	95.1	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
107	d1y7ya1	 Alignment	not modelled	95.0	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
108	d2r1jl1	 Alignment	not modelled	95.0	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
109	c3t0nA_	 Alignment	not modelled	95.0	15	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
110	d1nera_	 Alignment	not modelled	95.0	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
111	c2ef8A_	 Alignment	not modelled	95.0	20	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
112	c3f52A_	 Alignment	not modelled	94.9	26	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
113	c3omtA_	 Alignment	not modelled	94.9	16	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.
114	c2kpiA_	 Alignment	not modelled	94.9	26	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
115	d1v4ra1	 Alignment	not modelled	94.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
116	c3op9A_	 Alignment	not modelled	94.8	24	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
117	c3ip5A_	 Alignment	not modelled	94.7	8	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
118	d2liva_	 Alignment	not modelled	94.7	8	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
119	d1llib_	 Alignment	not modelled	94.7	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
120	d1x57a1	 Alignment	not modelled	94.7	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like