



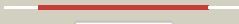









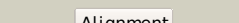

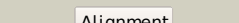



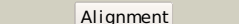












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1zvva_</a>	 Alignment		100.0	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-resistance amylase regulator; <b>PDBTitle:</b> crystal structure of a ccpa-crh-dna complex
2	<a href="#">c3kjd_</a>	 Alignment		100.0	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
3	<a href="#">c1bdhA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (purine repressor); <b>PDBTitle:</b> purine repressor mutant-hypoxanthine-palindromic operator2 complex
4	<a href="#">c3h5tA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
5	<a href="#">d1byka_</a>	 Alignment		100.0	100	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
6	<a href="#">d2nzugl</a>	 Alignment		100.0	20	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
7	<a href="#">c3egcF_</a>	 Alignment		100.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> putative ribose operon repressor; <b>PDBTitle:</b> crystal structure of a putative ribose operon repressor from2 burkholderia thailandensis
8	<a href="#">c2iksA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding transcriptional dual regulator; <b>PDBTitle:</b> crystal structure of n-terminal truncated dna-binding transcriptional2 dual regulator from escherichia coli k12
9	<a href="#">c3brqA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator ascg; <b>PDBTitle:</b> crystal structure of the escherichia coli transcriptional repressor2 ascg
10	<a href="#">c3h5oB_</a>	 Alignment		100.0	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator gntr; <b>PDBTitle:</b> the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
11	<a href="#">c3c3kA_</a>	 Alignment		100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from actinobacillus2 succinogenes

12	<a href="#">c3e3mA_</a>	Alignment		100.0	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
13	<a href="#">c3k4hA_</a>	Alignment		100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator laci from2 bacillus cereus subsp. cytotoxis nvh 391-98
14	<a href="#">c3cs3A_</a>	Alignment		100.0	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sugar-binding transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
15	<a href="#">dljx6a_</a>	Alignment		100.0	12	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
16	<a href="#">c3gv0A_</a>	Alignment		100.0	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
17	<a href="#">c3dbiA_</a>	Alignment		100.0	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sugar-binding transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of sugar-binding transcriptional regulator (laci2 family) from escherichia coli complexed with phosphate
18	<a href="#">c3d8uA_</a>	Alignment		100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> purr transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
19	<a href="#">c2qu7B_</a>	Alignment		100.0	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
20	<a href="#">c2o20H_</a>	Alignment		100.0	17	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> catabolite control protein a; <b>PDBTitle:</b> crystal structure of transcription regulator ccpa of lactococcus2 lactis
21	<a href="#">c3kkeA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> laci family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
22	<a href="#">c3hcvB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> maltose operon transcriptional repressor; <b>PDBTitle:</b> crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus aureus
23	<a href="#">c3jy6B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of laci transcriptional regulator from lactobacillus2 brevis
24	<a href="#">c3bblA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> regulatory protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein of laci family; <b>PDBTitle:</b> crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans
25	<a href="#">c3ctpB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional2 regulator from alkaliphilus metalliredigens qymf complexed with d-3 xylulofuranose
26	<a href="#">c3qk7C_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulators; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
27	<a href="#">c2rgyA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of transcriptional regulator of laci family from2 burkholderia phymatum
						<b>PDB header:</b> transcription regulator

28	<a href="#">c3jvdA_</a>	Alignment	not modelled	100.0	20	<b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulators; <b>PDBTitle:</b> crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
29	<a href="#">d1tifa_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
30	<a href="#">c3g85A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (laci family); <b>PDBTitle:</b> crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
31	<a href="#">c3k9cA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family protein; <b>PDBTitle:</b> crystal structure of laci transcriptional regulator from rhodococcus2 species.
32	<a href="#">c1jyeA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lactose operon repressor; <b>PDBTitle:</b> structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
33	<a href="#">d1jyea_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
34	<a href="#">c3mizB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator protein, laci <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator2 protein, lacI family from rhizobium etli
35	<a href="#">c3o74A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fructose transport system repressor frur; <b>PDBTitle:</b> crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
36	<a href="#">d2dria_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
37	<a href="#">c3clkB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcription regulator; <b>PDBTitle:</b> crystal structure of a transcription regulator from lactobacillus2 plantarum
38	<a href="#">c2ioyB_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic sugar-binding protein; <b>PDBTitle:</b> crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
39	<a href="#">c3bilA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable laci-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a probable laci family transcriptional2 regulator from corynebacterium glutamicum
40	<a href="#">c3hs3A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> ribose operon repressor; <b>PDBTitle:</b> crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
41	<a href="#">c3huuC_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcription regulator like protein; <b>PDBTitle:</b> crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
42	<a href="#">d1dbqa_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
43	<a href="#">c2h0aA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of probable transcription regulator from2 thermus thermophilus
44	<a href="#">c2fn9A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribose abc transporter, periplasmic ribose-binding protein; <b>PDBTitle:</b> thermotoga maritima ribose binding protein unliganded form
45	<a href="#">c3l6uA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type sugar transport system periplasmic <b>PDBTitle:</b> crystal structure of abc-type sugar transport system,2 periplasmic component from exigubacterium sibiricum
46	<a href="#">c3e61A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional repressor of ribose operon; <b>PDBTitle:</b> crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus
47	<a href="#">c3l49D_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> abc sugar (ribose) transporter, periplasmic <b>PDBTitle:</b> crystal structure of abc sugar transporter subunit from2 rhodobacter sphaeroides 2.4.1
48	<a href="#">c3gybB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulators (laci-family) <b>PDBTitle:</b> crystal structure of a laci-family transcriptional2 regulatory protein from corynebacterium glutamicum
49	<a href="#">d1guda_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
50	<a href="#">c3brsA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator; <b>PDBTitle:</b> crystal structure of sugar transporter from clostridium2 phytofermentans
51	<a href="#">c3ksmA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type sugar transport system, periplasmic component; <b>PDBTitle:</b> crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis

52	<a href="#">c3ma0A_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-xylose-binding periplasmic protein; <b>PDBTitle:</b> closed liganded crystal structure of xylose binding protein from <i>Escherichia coli</i>
53	<a href="#">d1gcaa_</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
54	<a href="#">c3g1wB_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sugar abc transporter; <b>PDBTitle:</b> crystal structure of sugar abc transporter (sugar-binding protein)2 from <i>Bacillus halodurans</i>
55	<a href="#">c2rjoA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> twin-arginine translocation pathway signal protein; <b>PDBTitle:</b> crystal structure of twin-arginine translocation pathway signal2 protein from <i>Burkholderia phytofirmans</i>
56	<a href="#">d8abpa_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
57	<a href="#">d2fvya1</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
58	<a href="#">c3o1hB_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic protein tort; <b>PDBTitle:</b> crystal structure of the tors sensor domain - tort complex in the presence of tmao
59	<a href="#">c2vk2A_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter periplasmic-binding protein ytfq; <b>PDBTitle:</b> crystal structure of a galactofuranose binding protein
60	<a href="#">c3h75A_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic sugar-binding domain protein; <b>PDBTitle:</b> crystal structure of a periplasmic sugar-binding protein from <i>Pseudomonas fluorescens</i>
61	<a href="#">c3rotA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc sugar transporter, periplasmic sugar binding protein; <b>PDBTitle:</b> crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from <i>Legionella pneumophila</i>
62	<a href="#">c2x7xA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> fructose binding periplasmic domain of hybrid two component2 system bt1754
63	<a href="#">c3gbvB_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative lacI-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative lacI transcriptional regulator from <i>Bacteroides fragilis</i>
64	<a href="#">c2qvcC_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> sugar abc transporter, periplasmic sugar-binding <b>PDBTitle:</b> crystal structure of a periplasmic sugar abc transporter2 from <i>Thermotoga maritima</i>
65	<a href="#">c3d02A_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative lacI-type transcriptional regulator; <b>PDBTitle:</b> 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
66	<a href="#">d1tjya_</a>	Alignment	not modelled	99.9	8	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
67	<a href="#">c2hqba_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional activator of comK gene; <b>PDBTitle:</b> crystal structure of a transcriptional activator of comK2 gene from <i>Bacillus halodurans</i>
68	<a href="#">d2bjca1</a>	Alignment	not modelled	99.7	43	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
69	<a href="#">c3lftA_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the abc domain in complex with l-trp from <i>Streptococcus pneumoniae</i> to 1.35 Å
70	<a href="#">c2qh8A_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved domain protein from <i>Vibrio cholerae</i> O1 biovar eltor str. n16961
71	<a href="#">d1lefaa1</a>	Alignment	not modelled	99.7	42	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
72	<a href="#">d2hsga1</a>	Alignment	not modelled	99.7	35	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
73	<a href="#">c2fqxA_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> membrane lipoprotein tmprc; <b>PDBTitle:</b> pnra from <i>Treponema pallidum</i> complexed with guanosine
74	<a href="#">d1qpza1</a>	Alignment	not modelled	99.6	38	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
75	<a href="#">d1lcda_</a>	Alignment	not modelled	99.6	46	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
76	<a href="#">d1luxda_</a>	Alianment	not modelled	99.6	39	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains

						<b>Family:</b> GalR/LacI-like bacterial regulator
77	<a href="#">d1luxca_</a>	Alignment	not modelled	99.5	40	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
78	<a href="#">c2lcvA_</a>	Alignment	not modelled	99.5	46	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor cytr; <b>PDBTitle:</b> structure of the cytidine repressor dna-binding domain; an alternate2 calculation
79	<a href="#">c2l8nA_</a>	Alignment	not modelled	99.5	46	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor cytr; <b>PDBTitle:</b> nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
80	<a href="#">c3s99A_</a>	Alignment	not modelled	99.2	8	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> basic membrane lipoprotein; <b>PDBTitle:</b> crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
81	<a href="#">c3sg0A_</a>	Alignment	not modelled	97.1	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular ligand-binding receptor; <b>PDBTitle:</b> the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
82	<a href="#">c3i09A_</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic branched-chain amino acid-binding protein; <b>PDBTitle:</b> crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
83	<a href="#">c3trbA_</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence-associated protein i; <b>PDBTitle:</b> structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
84	<a href="#">c2ebyA_</a>	Alignment	not modelled	96.7	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ybaq; <b>PDBTitle:</b> crystal structure of a hypothetical protein from e. coli
85	<a href="#">c3snrA_</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular ligand-binding receptor; <b>PDBTitle:</b> rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
86	<a href="#">c3t0nA_</a>	Alignment	not modelled	96.5	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> twin-arginine translocation pathway signal; <b>PDBTitle:</b> crystal structure of twin-arginine translocation pathway signal from2 rhodopseudomonas palustris bisb5
87	<a href="#">c3cecA_</a>	Alignment	not modelled	96.4	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative antidote protein of plasmid maintenance system; <b>PDBTitle:</b> crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
88	<a href="#">d2o38a1</a>	Alignment	not modelled	96.4	26	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
89	<a href="#">c2o38A_</a>	Alignment	not modelled	96.4	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> putative xre family transcriptional regulator
90	<a href="#">d1rioa_</a>	Alignment	not modelled	96.3	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
91	<a href="#">c3t76A_</a>	Alignment	not modelled	96.3	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator vanug; <b>PDBTitle:</b> crystal structure of transcriptional regulator vanug, form ii
92	<a href="#">d1qo0a_</a>	Alignment	not modelled	96.2	10	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
93	<a href="#">d2ofya1</a>	Alignment	not modelled	96.2	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
94	<a href="#">c2kpiA_</a>	Alignment	not modelled	96.2	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sos-response transcriptional repressor, lexa; <b>PDBTitle:</b> solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
95	<a href="#">c3f8mA_</a>	Alignment	not modelled	96.2	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gntr-family protein transcriptional regulator; <b>PDBTitle:</b> crystal structure of phnf from mycobacterium smegmatis
96	<a href="#">d2icta1</a>	Alignment	not modelled	96.1	20	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
97	<a href="#">d2a6ca1</a>	Alignment	not modelled	96.1	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
98	<a href="#">c2bnoA_</a>	Alignment	not modelled	96.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase; <b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorensis.
99	<a href="#">c3eusB_</a>	Alignment	not modelled	96.1	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding protein; <b>PDBTitle:</b> the crystal structure of the dna binding protein from silicibacter2 pomeroyi
100	<a href="#">c3clcC_</a>	Alignment	not modelled	96.1	17	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
						<b>PDB header:</b> transcription regulator



101	<a href="#">c1y9qA_</a>	Alignment	not modelled	96.1	22	<b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family; <b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
102	<a href="#">c3bs3A_</a>	Alignment	not modelled	96.0	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of a putative dna-binding protein from bacteroides2 fragilis
103	<a href="#">c3f52A_</a>	Alignment	not modelled	96.0	21	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> clp gene regulator (clgr); <b>PDBTitle:</b> crystal structure of the clp gene regulator clgr from c. glutamicum
104	<a href="#">c3b7hA_</a>	Alignment	not modelled	96.0	32	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> prophage lp1 protein 11; <b>PDBTitle:</b> crystal structure of the prophage lp1 protein 11
105	<a href="#">d2b5aa1</a>	Alignment	not modelled	96.0	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
106	<a href="#">c1b0nA_</a>	Alignment	not modelled	96.0	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> protein (sinr protein); <b>PDBTitle:</b> sinr protein/sini protein complex
107	<a href="#">d1utxa_</a>	Alignment	not modelled	96.0	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
108	<a href="#">d2liva_</a>	Alignment	not modelled	95.9	10	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
109	<a href="#">c3bwgA_</a>	Alignment	not modelled	95.9	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator yydk; <b>PDBTitle:</b> the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
110	<a href="#">c3kxaD_</a>	Alignment	not modelled	95.9	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of ngo0477 from neisseria gonorrhoeae
111	<a href="#">d1lmb3_</a>	Alignment	not modelled	95.9	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
112	<a href="#">d1x57a1</a>	Alignment	not modelled	95.8	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> EDF1-like
113	<a href="#">c3eetA_</a>	Alignment	not modelled	95.8	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative gntr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative gntr-family transcriptional2 regulator
114	<a href="#">d1y9qa1</a>	Alignment	not modelled	95.8	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Probable transcriptional regulator VC1968, N-terminal domain
115	<a href="#">d1y7ya1</a>	Alignment	not modelled	95.7	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
116	<a href="#">d1adra_</a>	Alignment	not modelled	95.7	10	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
117	<a href="#">c2ef8A_</a>	Alignment	not modelled	95.6	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription factor; <b>PDBTitle:</b> crystal structure of c.ecot38is
118	<a href="#">c3omtA_</a>	Alignment	not modelled	95.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
119	<a href="#">d1b0na2</a>	Alignment	not modelled	95.5	29	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
120	<a href="#">c3op9A_</a>	Alignment	not modelled	95.5	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> pli0006 protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator from listeria innocua