Phyre^2

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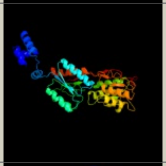
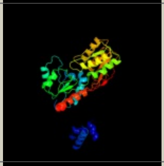
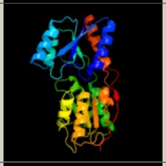
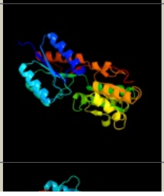
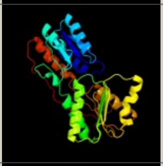
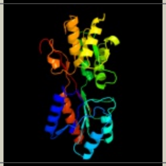
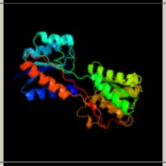
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	c1bdhA_	Alignment		100.0	29	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
3	c3kjxD_	Alignment		100.0	24	**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
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	24	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
6	c3dbiA_	Alignment		100.0	31	**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
7	c3kkeA_	Alignment		100.0	28	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**laci family transcriptional regulator; **PDBTitle:** crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
8	c3qk7C_	Alignment		100.0	22	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
9	c3k4hA_	Alignment		100.0	23	**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
10	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
11	c2o20H_	Alignment		100.0	23	**PDB header:**transcription **Chain:** H: **PDB Molecule:**catabolite control protein a; **PDBTitle:** crystal structure of transcription regulator ccpa of lactococcus2 lactis
						

12	c3mizB_	Alignment		100.0	26	**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
13	d1tlfa_	Alignment		100.0	21	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
14	c3c3kA_	Alignment		100.0	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
15	c3d8uA_	Alignment		100.0	21	**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
16	c3h5oB_	Alignment		100.0	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator gntr; **PDBTitle:** the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
17	c3bblA_	Alignment		100.0	23	**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	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 areus
19	c3brqA_	Alignment		100.0	30	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator ascg; **PDBTitle:** crystal structure of the escherichia coli transcriptional repressor2 ascg
20	c3e3mA_	Alignment		100.0	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
21	d1dbqa_	Alignment	not modelled	100.0	26	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
22	c2rgyA_	Alignment	not modelled	100.0	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of transcriptional regulator of laci family from2 burkhoderia phymatum
23	c3k9cA_	Alignment	not modelled	100.0	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family protein; **PDBTitle:** crystal structure of laci transcriptional regulator from rhodococcus2 species.
24	c1jyeA_	Alignment	not modelled	100.0	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lactose operon repressor; **PDBTitle:** structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
25	d1jyea_	Alignment	not modelled	100.0	22	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
26	c3cs3A_	Alignment	not modelled	100.0	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family; **PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
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	c3gv0A_	Alignment	not modelled	100.0	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens

29	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
30	c2qu7B_	Alignment	not modelled	100.0	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
31	c3huuC_	Alignment	not modelled	100.0	15	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcription regulator like protein; **PDBTitle:** crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
32	c2h0aA_	Alignment	not modelled	100.0	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of probable transcription regulator from2 thermus thermophilus
33	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
34	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
35	c3clkB_	Alignment	not modelled	100.0	22	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcription regulator; **PDBTitle:** crystal structure of a transcription regulator from lactobacillus2 plantarum
36	c3hs3A_	Alignment	not modelled	100.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**ribose operon repressor; **PDBTitle:** crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
37	c3bilA_	Alignment	not modelled	100.0	24	**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
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	c3jvdA_	Alignment	not modelled	100.0	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
40	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
41	c3gybB_	Alignment	not modelled	100.0	24	**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
42	c2ioyB_	Alignment	not modelled	100.0	21	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**periplasmic sugar-binding protein; **PDBTitle:** crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
43	c2fn9A_	Alignment	not modelled	100.0	18	**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	20	**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 exiguobacterium sibiricum
46	d1byka_	Alignment	not modelled	99.9	18	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
47	d1guda_	Alignment	not modelled	99.9	18	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
48	d8abpa_	Alignment	not modelled	99.9	16	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
49	c3l49D_	Alignment	not modelled	99.9	10	**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
50	c3ma0A_	Alignment	not modelled	99.9	18	**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
51	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
52	c3e61A_	Alignment	not modelled	99.9	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

53	c2vk2A_	Alignment	not modelled	99.9	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq; **PDBTitle:** crystal structure of a galactofuranose binding protein
54	c3brsA_	Alignment	not modelled	99.9	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein/laci transcriptional regulator; **PDBTitle:** crystal structure of sugar transporter from clostridium2 phytofermentans
55	c3gbvB_	Alignment	not modelled	99.9	9	**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
56	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 hahella chejuensis
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	d1gcaa_	Alignment	not modelled	99.9	18	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
59	d2fvya1	Alignment	not modelled	99.9	19	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
60	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 the2 pseudomonas fluorescens
61	c2qvcC_	Alignment	not modelled	99.9	13	**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	c2x7xA_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** fructose binding periplasmic domain of hybrid two component2 system bt1754
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	11	**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	d1tjya_	Alignment	not modelled	99.9	12	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
66	c3d02A_	Alignment	not modelled	99.8	11	**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	d2bjca1	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
68	d2hsga1	Alignment	not modelled	99.7	52	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
69	d1qpza1	Alignment	not modelled	99.7	49	**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	d1uxda_	Alignment	not modelled	99.6	41	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
72	c2hqbA_	Alignment	not modelled	99.6	13	**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
73	c2qh8A_	Alignment	not modelled	99.6	14	**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
74	d1lcda_	Alignment	not modelled	99.6	49	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
75	d1uxca_	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	c2lcvA_	Alignment	not modelled	99.6	50	**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
						PDB header:structure genomics, unknown function

77	c3lftA_	Alignment	not modelled	99.6	11	**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	c2l8nA_	Alignment	not modelled	99.6	50	**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
79	c2fqxA_	Alignment	not modelled	99.6	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	99.1	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	c3trbA_	Alignment	not modelled	96.6	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
82	c3cecA_	Alignment	not modelled	96.5	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	c2ebyA_	Alignment	not modelled	96.4	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
84	c3eusB_	Alignment	not modelled	96.1	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
85	c2w48D_	Alignment	not modelled	96.1	28	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
86	d2icta1	Alignment	not modelled	96.0	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
87	c1y9qA_	Alignment	not modelled	96.0	22	**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
88	d1rioa_	Alignment	not modelled	95.9	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
89	d2b5aa1	Alignment	not modelled	95.9	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
90	c2bnoA_	Alignment	not modelled	95.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
91	c3bs3A_	Alignment	not modelled	95.9	27	**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
92	c3t76A_	Alignment	not modelled	95.9	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
93	d2a6ca1	Alignment	not modelled	95.8	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
94	d1adra_	Alignment	not modelled	95.8	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
95	c1u78A_	Alignment	not modelled	95.8	12	**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
96	d2ofya1	Alignment	not modelled	95.8	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
97	d1utxa_	Alignment	not modelled	95.8	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
98	d1lmb3_	Alignment	not modelled	95.7	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
99	d2o38a1	Alignment	not modelled	95.7	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
100	c2o38A_	Alignment	not modelled	95.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative xre family transcriptional regulator
101	d1y9qa1	Alignment	not modelled	95.7	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
102	c3clcC_	Alignment	not modelled	95.6	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

103	c3b7hA_	Alignment	not modelled	95.6	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
104	c3f52A_	Alignment	not modelled	95.5	21	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
105	d1y7ya1	Alignment	not modelled	95.5	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
106	c2ef8A_	Alignment	not modelled	95.5	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
107	c2l0kA_	Alignment	not modelled	95.5	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage iii sporulation protein d; **PDBTitle:** nmr solution structure of a transcription factor spoiiid in complex2 with dna
108	c3op9A_	Alignment	not modelled	95.5	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
109	d2r1jl1	Alignment	not modelled	95.5	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
110	c3iwfA_	Alignment	not modelled	95.5	32	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
111	c3omtA_	Alignment	not modelled	95.4	19	**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.
112	c2kpjA_	Alignment	not modelled	95.4	19	**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
113	c1b0nA_	Alignment	not modelled	95.4	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
114	d1x57a1	Alignment	not modelled	95.4	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
115	d1llib_	Alignment	not modelled	95.2	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
116	d1b0na2	Alignment	not modelled	95.2	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
117	c3f6wE_	Alignment	not modelled	95.1	19	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
118	d1nera_	Alignment	not modelled	95.1	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
119	c3kxaD_	Alignment	not modelled	94.9	21	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
120	d1r69a_	Alignment	not modelled	94.8	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors