



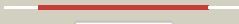









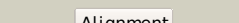

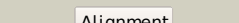



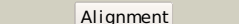






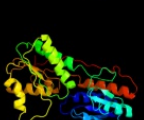





Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0ACP7
Date	Thu Jan 5 11:18:40 GMT 2012
Unique Job ID	9c293121fc7d717e

Detailed template information

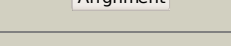
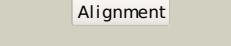
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1bdhA_	 Alignment		100.0	100	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
2	c1zvva_	 Alignment		100.0	30	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
3	c3kjd_	 Alignment		100.0	21	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	21	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	d1dbqa_	 Alignment		100.0	100	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
6	d2nzug1	 Alignment		100.0	25	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
7	c3dbiA_	 Alignment		100.0	22	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
8	c2iksA_	 Alignment		100.0	17	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	c3k4hA_	 Alignment		100.0	25	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	c3kkeA_	 Alignment		100.0	24	PDB header: transcription regulator Chain: A: PDB Molecule: laci family transcriptional regulator; PDBTitle: crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
11	c3e3mA_	 Alignment		100.0	23	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi

12	d1tfa_	Alignment		100.0	23	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
13	c3c3kA_	Alignment		100.0	23	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
14	c3brqA_	Alignment		100.0	22	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator ascg; PDBTitle: crystal structure of the escherichia coli transcriptional repressor2 ascg
15	c2o20H_	Alignment		100.0	24	PDB header: transcription Chain: H: PDB Molecule: catabolite control protein a; PDBTitle: crystal structure of transcription regulator ccpa of lactococcus2 lactis
16	c3qk7C_	Alignment		100.0	21	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
17	c3h5oB_	Alignment		100.0	22	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
18	c3miZB_	Alignment		100.0	24	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
19	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
20	c3k9cA_	Alignment		100.0	19	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family protein; PDBTitle: crystal structure of laci transcriptional regulator from rhodococcus2 species.
21	c3hwcB_	Alignment	not modelled	100.0	17	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
22	c3bblA_	Alignment	not modelled	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
23	c2rgyA_	Alignment	not modelled	100.0	24	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of transcriptional regulator of laci family from2 burkholderia phymatum
24	d1jyea_	Alignment	not modelled	100.0	23	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
25	c1jyeA_	Alignment	not modelled	100.0	23	PDB header: transcription Chain: A: PDB Molecule: lactose operon repressor; PDBTitle: structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
26	c3gv0A_	Alignment	not modelled	100.0	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of a laci family transcription regulator from2 agrobacterium tumefaciens
27	c3ctpB_	Alignment	not modelled	100.0	24	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
						PDB header: transcription

28	c2h0aA_	Alignment	not modelled	100.0	26	Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of probable transcription regulator from2 thermus thermophilus
29	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
30	c3o74A_	Alignment	not modelled	100.0	20	PDB header: transcription Chain: A: PDB Molecule: fructose transport system repressor frur; PDBTitle: crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
31	c3egcF_	Alignment	not modelled	100.0	26	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
32	c3cs3A_	Alignment	not modelled	100.0	21	PDB header: transcription regulator Chain: A: PDB Molecule: sugar-binding transcriptional regulator, laci family; PDBTitle: crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
33	c2qu7B_	Alignment	not modelled	100.0	20	PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
34	c3hs3A_	Alignment	not modelled	100.0	21	PDB header: transcription regulator Chain: A: PDB Molecule: ribose operon repressor; PDBTitle: crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
35	c3g85A_	Alignment	not modelled	100.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (laci family); PDBTitle: crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
36	c3huuC_	Alignment	not modelled	100.0	19	PDB header: transcription regulator Chain: C: PDB Molecule: transcription regulator like protein; PDBTitle: crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
37	c2ioyB_	Alignment	not modelled	100.0	22	PDB header: sugar binding protein Chain: B: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
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	c3bilA_	Alignment	not modelled	100.0	22	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	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
41	c3gybB_	Alignment	not modelled	100.0	26	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	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
43	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
44	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
45	c3l6uA_	Alignment	not modelled	99.9	19	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 exigubacterium sibiricum
46	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
47	c3l49D_	Alignment	not modelled	99.9	14	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
48	d1guda_	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	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
50	c3g1wB_	Alignment	not modelled	99.9	14	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	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
52	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 PDB header: transcription regulator

53	c3gbvB_	Alignment	not modelled	99.9	15	Chain: B: PDB Molecule: putative lacI-family transcriptional regulator; PDBTitle: crystal structure of a putative lacI transcriptional regulator from <i>Bacteroides fragilis</i>
54	c3brsA_	Alignment	not modelled	99.9	14	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/lacI transcriptional regulator; PDBTitle: crystal structure of sugar transporter from <i>Clostridium</i> 2 phytofermentans
55	c3ksmA_	Alignment	not modelled	99.9	18	PDB header: transport protein Chain: A: PDB Molecule: abc-type sugar transport system, periplasmic component; PDBTitle: crystal structure of abc-type sugar transport system, periplasmic2 component from <i>Haella chejuensis</i>
56	c3e61A_	Alignment	not modelled	99.9	24	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	c2rjoA_	Alignment	not modelled	99.9	14	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>
58	d1gcaa_	Alignment	not modelled	99.9	15	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	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
60	c2qvcC_	Alignment	not modelled	99.9	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 <i>Thermotoga maritima</i>
61	c3h75A_	Alignment	not modelled	99.9	19	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 <i>Pseudomonas fluorescens</i>
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	10	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 <i>Legionella pneumophila</i>
65	d1tjya_	Alignment	not modelled	99.9	9	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	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 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> mgh3 78578 at 1.30 Å resolution
67	d2bjca1	Alignment	not modelled	99.7	41	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	46	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	100	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
70	d1lefaa1	Alignment	not modelled	99.7	44	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
71	c2hqbA_	Alignment	not modelled	99.7	14	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>
72	d1luxda_	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
73	c2fqxA_	Alignment	not modelled	99.6	15	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein trmpc; PDBTitle: pnra from <i>Treponema pallidum</i> complexed with guanosine
74	d1lcda_	Alignment	not modelled	99.6	47	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
75	c2qh8A_	Alignment	not modelled	99.5	10	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
76	c2lcvA_	Alignment	not modelled	99.5	48	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

77	d1luxca_	Alignment	not modelled	99.5	36	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
78	c3lftA_	Alignment	not modelled	99.5	9	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
79	c2l8nA_	Alignment	not modelled	99.5	48	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	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	c2w48D_	Alignment	not modelled	96.7	17	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
82	c3trbA_	Alignment	not modelled	96.7	19	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
83	c3cecA_	Alignment	not modelled	96.6	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
84	c2ebyA_	Alignment	not modelled	96.6	24	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
85	c3eusB_	Alignment	not modelled	96.3	24	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
86	c1y9qA_	Alignment	not modelled	96.2	11	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
87	d1rioA_	Alignment	not modelled	96.2	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
88	d2icta1	Alignment	not modelled	96.2	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
89	c3t76A_	Alignment	not modelled	96.2	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
90	d2b5aa1	Alignment	not modelled	96.1	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
91	c3bs3A_	Alignment	not modelled	96.1	16	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	c2bnoA_	Alignment	not modelled	96.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenisi.
93	d2ofya1	Alignment	not modelled	96.0	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
94	d1utxa_	Alignment	not modelled	96.0	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
95	d1adra_	Alignment	not modelled	96.0	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
96	c3clcC_	Alignment	not modelled	96.0	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
97	c2o38A_	Alignment	not modelled	96.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
98	d2o38a1	Alignment	not modelled	96.0	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
99	c3b7hA_	Alignment	not modelled	95.9	24	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
100	d1lmb3_	Alignment	not modelled	95.9	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
101	d1y9qa1	Alignment	not modelled	95.9	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
102	d2a6ca1	Alignment	not modelled	95.9	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354

103	c1u78A_	 Alignment	not modelled	95.8	8	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
104	c2kpiA_	 Alignment	not modelled	95.8	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
105	c3f52A_	 Alignment	not modelled	95.8	24	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
106	c3op9A_	 Alignment	not modelled	95.8	19	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
107	c3iwfA_	 Alignment	not modelled	95.8	20	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
108	d1y7ya1	 Alignment	not modelled	95.7	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
109	d2r1jl1	 Alignment	not modelled	95.7	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
110	c3eetA_	 Alignment	not modelled	95.7	13	PDB header: transcription regulator Chain: A: PDB Molecule: putative gntr-family transcriptional regulator; PDBTitle: crystal structure of putative gntr-family transcriptional2 regulator
111	c3omtA_	 Alignment	not modelled	95.7	22	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	c2ef8A_	 Alignment	not modelled	95.7	11	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
113	d1x57a1	 Alignment	not modelled	95.7	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
114	c3f8mA_	 Alignment	not modelled	95.6	17	PDB header: transcription regulator; Chain: A: PDB Molecule: gntr-family protein transcriptional regulator; PDBTitle: crystal structure of phnf from mycobacterium smegmatis
115	d1llib_	 Alignment	not modelled	95.6	5	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
116	c3f6wE_	 Alignment	not modelled	95.5	22	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
117	d1b0na2	 Alignment	not modelled	95.5	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
118	d1hlva1	 Alignment	not modelled	95.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
119	c3kxaD_	 Alignment	not modelled	95.4	19	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
120	c3bwgA_	 Alignment	not modelled	95.3	13	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