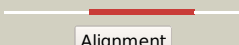



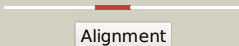

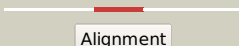
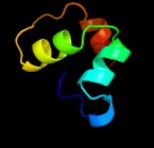


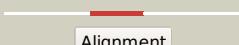

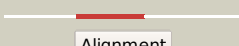

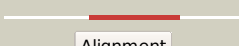













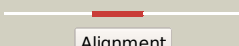

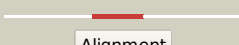









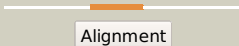
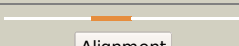
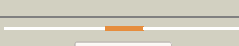
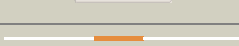
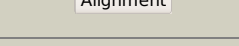
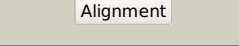
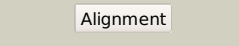




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0348 (-)_418293_418946
Date	Tue Jul 23 14:50:41 BST 2019
Unique Job ID	4e10b7b7876212c5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fkqC_	 Alignment		98.6	20	PDB header: toxin Chain: C; PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
2	c3t76A_	 Alignment		95.3	26	PDB header: transcription regulator Chain: A; PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
3	d1k78a1	 Alignment		94.9	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
4	d2croa_	 Alignment		94.1	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
5	d1a9xa1	 Alignment		94.0	28	Fold: Carbamoyl phosphate synthetase, large subunit connection domain Superfamily: Carbamoyl phosphate synthetase, large subunit connection domain Family: Carbamoyl phosphate synthetase, large subunit connection domain
6	c3fmyA_	 Alignment		93.5	17	PDB header: dna binding protein Chain: A; PDB Molecule: hth-type transcriptional regulator mqsa PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
7	c3gn5B_	 Alignment		93.4	15	PDB header: dna binding protein Chain: B; PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
8	c6gw6B_	 Alignment		93.4	20	PDB header: toxin Chain: B; PDB Molecule: xre antitoxin; PDBTitle: structure of the pseudomonas putida res-xre toxin-antitoxin complex
9	c3op9A_	 Alignment		92.8	20	PDB header: transcription regulator Chain: A; PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
10	c5uk3J_	 Alignment		92.7	17	PDB header: lyase Chain: J; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae
11	d1r69a_	 Alignment		92.7	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors

12	c2kpiA	 Alignment		92.6	26	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
13	c3omtA	 Alignment		92.1	20	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.
14	c4ghjA	 Alignment		91.8	16	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
15	c4pu4C	 Alignment		91.7	19	PDB header: toxin/antitoxin/dna Chain: C: PDB Molecule: toxin-antitoxin system antidote transcriptional repressor PDBTitle: shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21)
16	c2fjrB	 Alignment		91.6	13	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
17	d1qpza1	 Alignment		91.5	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
18	c3bd1B	 Alignment		91.1	31	PDB header: transcription Chain: B: PDB Molecule: cro protein; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
19	d6paxa1	 Alignment		90.5	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
20	c1b0nA	 Alignment		90.4	15	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
21	c5j9iH	 Alignment	not modelled	89.9	14	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
22	c1u78A	 Alignment	not modelled	89.5	16	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
23	d1lcda	 Alignment	not modelled	89.1	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
24	c3bs3A	 Alignment	not modelled	88.8	24	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
25	c2o38A	 Alignment	not modelled	88.4	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
26	d2o38a1	 Alignment	not modelled	88.4	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
27	d2a6ca1	 Alignment	not modelled	88.4	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
28	c2l8nA	 Alignment	not modelled	88.4	15	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
29	c5wqaA	 Alignment	not modelled	87.7	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr;

29	c2w0qa	Alignment	not modelled	87.7	41	PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
30	d1adra	Alignment	not modelled	87.4	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
31	c2ppxA	Alignment	not modelled	87.3	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
32	d2ppxA1	Alignment	not modelled	87.3	6	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
33	d1efaa1	Alignment	not modelled	86.8	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
34	c6paxA	Alignment	not modelled	86.7	32	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
35	d2bjca1	Alignment	not modelled	86.3	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
36	c3eusB	Alignment	not modelled	85.8	18	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
37	d1uxca	Alignment	not modelled	85.8	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
38	c5dotA	Alignment	not modelled	85.7	10	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
39	d1sq8a	Alignment	not modelled	85.6	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
40	c3f52A	Alignment	not modelled	85.2	28	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
41	c5douC	Alignment	not modelled	84.7	10	PDB header: ligase Chain: C: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
42	d1pdnc	Alignment	not modelled	84.4	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
43	c4ybaA	Alignment	not modelled	84.2	18	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
44	c2lcvA	Alignment	not modelled	84.0	15	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
45	c2cfxD	Alignment	not modelled	83.9	24	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
46	d1llib	Alignment	not modelled	83.5	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
47	d2hsqa1	Alignment	not modelled	83.4	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
48	c5jaaB	Alignment	not modelled	82.9	14	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex
49	c2ebyA	Alignment	not modelled	82.5	13	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
50	c3trbA	Alignment	not modelled	82.4	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
51	d1y9qa1	Alignment	not modelled	82.0	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
52	c3mlfC	Alignment	not modelled	80.4	22	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
53	c2k27A	Alignment	not modelled	80.2	32	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
54	c3zhiA	Alignment	not modelled	77.8	17	PDB header: transcription Chain: A: PDB Molecule: ci; PDBTitle: n-terminal domain of the ci repressor from bacteriophage tp901-1
55	c2x48B	Alignment	not modelled	77.7	22	PDB header: viral protein Chain: B: PDB Molecule: cag38821; PDBTitle: orf 55 from sulfolobus islandicus rudivirus 1

56	c5wurB	Alignment	not modelled	77.6	6	PDB header: metal binding protein Chain: B: PDB Molecule: ecf rna polymerase sigma factor sigw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form
57	d1uxda	Alignment	not modelled	77.4	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
58	c2mezA	Alignment	not modelled	77.3	17	PDB header: rna binding protein Chain: A: PDB Molecule: multi-protein bridging factor (mbp-like); PDBTitle: flexible anchoring of archaean mbf1 on ribosomes suggests role as2 recruitment factor
59	c3vdoA	Alignment	not modelled	75.8	13	PDB header: dna binding protein/protein binding Chain: A: PDB Molecule: rna polymerase sigma factor sigk; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
60	c1efaA	Alignment	not modelled	75.7	23	PDB header: transcription/dna Chain: A: PDB Molecule: lac repressor; PDBTitle: crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf
61	d1lutxa	Alignment	not modelled	74.8	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
62	d1y7ya1	Alignment	not modelled	73.7	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
63	c1y9qA	Alignment	not modelled	73.6	15	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
64	c3i4pA	Alignment	not modelled	73.5	31	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
65	d2ofya1	Alignment	not modelled	73.0	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
66	c3ivpD	Alignment	not modelled	72.2	9	PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
67	c6f8sA	Alignment	not modelled	72.1	28	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
68	c3b7hA	Alignment	not modelled	72.1	17	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
69	c1m6vE	Alignment	not modelled	71.8	25	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
70	c2ef8A	Alignment	not modelled	71.8	16	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
71	d2icta1	Alignment	not modelled	71.6	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
72	c5z7iC	Alignment	not modelled	71.6	29	PDB header: dna binding protein/dna Chain: C: PDB Molecule: cell cycle regulatory protein gcra; PDBTitle: caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna
73	c3dnvB	Alignment	not modelled	71.2	19	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
74	c2jvIA	Alignment	not modelled	70.8	15	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
75	c2e1cA	Alignment	not modelled	70.6	19	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
76	c2vbzA	Alignment	not modelled	70.2	29	PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
77	d1rzsA	Alignment	not modelled	69.8	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
78	c3h5tA	Alignment	not modelled	69.4	19	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
79	d1lmb3	Alignment	not modelled	69.0	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
80	c3bdnB	Alignment	not modelled	68.7	17	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
						PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein;

81	c3clcC	Alignment	not modelled	68.7	14	PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
82	c1or7A	Alignment	not modelled	68.6	16	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma-e factor; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
83	c3qyxD	Alignment	not modelled	68.5	18	PDB header: transcription/dna Chain: D: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment
84	c2dbbA	Alignment	not modelled	68.0	14	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
85	d2r1jI1	Alignment	not modelled	67.9	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
86	c3vk0B	Alignment	not modelled	67.2	13	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhtf from2 neisseria
87	c3pxpA	Alignment	not modelled	67.0	18	PDB header: transcription regulator Chain: A: PDB Molecule: helix-turn-helix domain protein; PDBTitle: crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
88	c1i1gA	Alignment	not modelled	66.7	33	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpA; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
89	c2mqkA	Alignment	not modelled	65.7	23	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
90	c4mcxE	Alignment	not modelled	65.5	24	PDB header: toxin Chain: E: PDB Molecule: antidote protein; PDBTitle: p. vulgaris higba structure, crystal form 2
91	c2e7xA	Alignment	not modelled	65.5	19	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
92	c3kxaD	Alignment	not modelled	65.0	20	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
93	d1b0na2	Alignment	not modelled	64.8	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
94	d1rp3a2	Alignment	not modelled	64.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
95	d2b5aa1	Alignment	not modelled	64.3	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
96	c2cg4B	Alignment	not modelled	64.3	29	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
97	c3mzyA	Alignment	not modelled	63.3	14	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
98	c2r0qF	Alignment	not modelled	62.7	16	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
99	c5d50L	Alignment	not modelled	62.2	20	PDB header: dna binding protein Chain: I: PDB Molecule: repressor; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage
100	c1bdhA	Alignment	not modelled	62.1	21	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
101	d1or7a1	Alignment	not modelled	61.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
102	c3hugA	Alignment	not modelled	61.9	17	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigI
103	c2p6tH	Alignment	not modelled	61.4	13	PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
104	c2ia0A	Alignment	not modelled	60.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
105	c3cecA	Alignment	not modelled	60.6	20	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
106	d2cg4a1	Alignment	not modelled	59.2	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
107	c3oioA_	Alignment	not modelled	59.0	22	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (arac-type dna-binding domain- PDBTitle: crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
108	c5zx3F_	Alignment	not modelled	58.9	16	PDB header: transcription Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigh; PDBTitle: mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h
109	c1lbgB_	Alignment	not modelled	58.6	25	PDB header: PDB COMPND:
110	c3vepA_	Alignment	not modelled	58.3	21	PDB header: membrane protein/transcription Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
111	c4czdA_	Alignment	not modelled	58.1	7	PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the Lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
112	c3f6wE_	Alignment	not modelled	57.9	13	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
113	c2gm4B_	Alignment	not modelled	57.8	11	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimera bound to2 cleaved dna
114	c4pccC_	Alignment	not modelled	57.5	19	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
115	c2l4aA_	Alignment	not modelled	57.1	21	PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp
116	c5xe7A_	Alignment	not modelled	56.1	23	PDB header: dna binding protein Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigj; PDBTitle: crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
117	c4j2nB_	Alignment	not modelled	55.5	14	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
118	c3kxD_	Alignment	not modelled	55.4	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
119	c6c03A_	Alignment	not modelled	54.2	23	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
120	c3oouA_	Alignment	not modelled	54.2	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unknwn function from listeria innocua