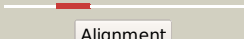

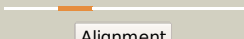

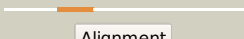
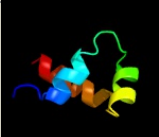


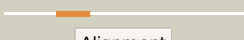


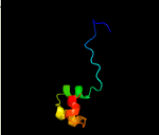

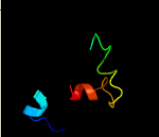










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0883c_(-)_980509_981270
Date	Fri Jul 26 01:50:47 BST 2019
Unique Job ID	71aafd0ce7a228b8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fmyA_	 Alignment		90.0	14	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)
2	c4ybaA_	 Alignment		89.2	18	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
3	d2p7vb1	 Alignment		88.2	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
4	c6jqsA_	 Alignment		85.3	11	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
5	d1l3la1	 Alignment		85.2	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
6	c4lfuA_	 Alignment		83.9	9	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
7	d1rioA_	 Alignment		83.6	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
8	d1ku7a_	 Alignment		83.4	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
9	c5af3A_	 Alignment		83.2	16	PDB header: dna binding Chain: A: PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
10	c1zljE_	 Alignment		83.2	13	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
11	c1y9qA_	 Alignment		82.7	21	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

12	d1ku3a_	Alignment		82.5	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
13	c2q0oA_	Alignment		82.4	20	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
14	d2ppxa1	Alignment		82.3	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
15	c2ppxA_	Alignment		82.3	16	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
16	c4ghjA_	Alignment		82.3	21	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator frm2 vibrio vulnificus.
17	d1fsea_	Alignment		82.2	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
18	c4gysA_	Alignment		82.1	29	PDB header: hydrolase Chain: A: PDB Molecule: allophanate hydrolase; PDBTitle: granulibacter bethesdensis allophanate hydrolase co-crystallized with2 malonate
19	c4pu4C_	Alignment		81.9	16	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)
20	c3fymA_	Alignment		81.6	14	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of ymfm, a putative dna-binding membrane2 protein from staphylococcus aureus
21	c2krfB_	Alignment	not modelled	81.5	21	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
22	c2mezA_	Alignment	not modelled	81.1	29	PDB header: rna binding protein Chain: A: PDB Molecule: multiprotein bridging factor (mbp-like); PDBTitle: flexible anchoring of archaeal mbf1 on ribosomes suggests role as2 recruitment factor
23	d1yioa1	Alignment	not modelled	80.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
24	c3sztB_	Alignment	not modelled	80.4	13	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
25	d1ku2a1	Alignment	not modelled	80.1	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
26	d1a04a1	Alignment	not modelled	80.0	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
27	c2wusR_	Alignment	not modelled	79.3	7	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz
28	c3mfc_	Alignment	not modelled	79.3	11	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.

29	d2ofya1	Alignment	not modelled	78.9	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
30	c5j9iH_	Alignment	not modelled	78.6	10	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
31	c3f6wE_	Alignment	not modelled	78.4	24	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
32	c1h0mD_	Alignment	not modelled	78.0	25	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
33	c3pxpA_	Alignment	not modelled	77.9	30	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
34	c6c05F_	Alignment	not modelled	76.6	20	PDB header: transcription Chain: F: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: mycobacterium tuberculosis rnap holo/rbpa in relaxed state
35	d1y9qa1	Alignment	not modelled	76.3	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
36	d1vz0a1	Alignment	not modelled	75.6	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
37	d1ttya_	Alignment	not modelled	75.4	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
38	c3kxaD_	Alignment	not modelled	75.0	18	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
39	c3eusB_	Alignment	not modelled	73.9	21	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
40	c5uk3J_	Alignment	not modelled	73.1	16	PDB header: lyase Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae
41	c3vk0B_	Alignment	not modelled	73.1	25	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhtf from2 neisseria
42	c1r71B_	Alignment	not modelled	73.0	20	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional repressor protein korb; PDBTitle: crystal structure of the dna binding domain of korb in complex with2 the operator dna
43	c3qp5C_	Alignment	not modelled	72.5	15	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
44	d1r71a_	Alignment	not modelled	72.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
45	c3i71B_	Alignment	not modelled	72.0	32	PDB header: unknown function Chain: B: PDB Molecule: ethanolamine utilization protein eutk; PDBTitle: ethanolamine utilization microcompartment shell subunit, eutk c-2 terminal domain
46	c2ef8A_	Alignment	not modelled	71.9	18	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
47	c4gqmA_	Alignment	not modelled	71.7	18	PDB header: unknown function Chain: A: PDB Molecule: ct009; PDBTitle: crystal structure of a helix-turn-helix containing hypothetical2 protein (ct009) from chlamydia trachomatis in a sub-domain swap3 conformation
48	c3ivpD_	Alignment	not modelled	71.7	29	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.
49	d1p4wa_	Alignment	not modelled	71.4	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
50	c3gn5B_	Alignment	not modelled	71.1	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)
51	c2ewtA_	Alignment	not modelled	70.6	21	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bidd
52	c3omtA_	Alignment	not modelled	70.2	4	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.
53	d1y7ya1	Alignment	not modelled	69.5	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
54	d1r69a_	Alignment	not modelled	69.0	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors

55	c3dnvB_	Alignment	not modelled	68.4	25	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
56	c5tw1F_	Alignment	not modelled	67.9	21	PDB header: transcription activator/transferase/dna Chain: F: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
57	c2bnoA_	Alignment	not modelled	67.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
58	c3clcC_	Alignment	not modelled	67.3	25	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
59	c3bs3A_	Alignment	not modelled	65.8	13	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
60	d2croa_	Alignment	not modelled	65.7	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
61	d1adra_	Alignment	not modelled	65.5	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
62	d2b5aa1	Alignment	not modelled	64.7	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
63	c3f52A_	Alignment	not modelled	64.5	18	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
64	c5woqA_	Alignment	not modelled	64.0	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
65	d1b0na2	Alignment	not modelled	63.9	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
66	d1llib_	Alignment	not modelled	63.5	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
67	d1utxa_	Alignment	not modelled	62.3	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
68	c6diiH_	Alignment	not modelled	61.8	24	PDB header: hydrolase Chain: H: PDB Molecule: fatty acid amide hydrolase; PDBTitle: structure of arabidopsis fatty acid amide hydrolase in complex with2 methyl linolenyl fluorophosphonate
69	c2elhA_	Alignment	not modelled	61.6	29	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
70	d2r1jl1	Alignment	not modelled	60.9	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
71	c1b0nA_	Alignment	not modelled	59.7	18	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
72	c5jpmF_	Alignment	not modelled	59.3	28	PDB header: transcription, transferase/dna/rna Chain: F: PDB Molecule: rna polymerase sigma factor rpos; PDBTitle: sigmas-transcription initiation complex with 4-nt nascent rna
73	d2a6ca1	Alignment	not modelled	59.0	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
74	d1x57a1	Alignment	not modelled	58.7	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
75	c1l9uH_	Alignment	not modelled	58.4	31	PDB header: transcription Chain: H: PDB Molecule: sigma factor siga; PDBTitle: thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
76	c2o38A_	Alignment	not modelled	57.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
77	d2o38a1	Alignment	not modelled	57.3	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
78	d1sq8a_	Alignment	not modelled	57.3	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
79	c3h0rP_	Alignment	not modelled	57.2	19	PDB header: ligase Chain: P: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
80	c3t72o_	Alignment	not modelled	56.8	26	PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex PDB header: oxidoreductase

81	c6b9tH_	Alignment	not modelled	56.8	12	Chain: H: PDB Molecule: methylphosphonate synthase; PDBTitle: crystal structure of mpns with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
82	c5zx3F_	Alignment	not modelled	56.2	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
83	c2jvA_	Alignment	not modelled	56.0	14	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
84	c4o8bA_	Alignment	not modelled	56.0	37	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of transcriptional regulator bswr
85	c3bdnB_	Alignment	not modelled	54.2	23	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
86	d1l0oc_	Alignment	not modelled	53.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
87	c1l0cC_	Alignment	not modelled	53.7	14	PDB header: protein binding Chain: C: PDB Molecule: sigma factor; PDBTitle: crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
88	d1lmb3_	Alignment	not modelled	53.4	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
89	c2rniA_	Alignment	not modelled	53.4	30	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
90	c2ev2B_	Alignment	not modelled	53.3	21	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenyllyl cyclase rv1264, at ph 8.5
91	c6ideA_	Alignment	not modelled	52.8	16	PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional regulator luxr family; PDBTitle: crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design
92	c2lfwA_	Alignment	not modelled	51.7	24	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
93	c1x3uA_	Alignment	not modelled	50.3	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
94	c3op9A_	Alignment	not modelled	49.3	11	PDB header: transcription regulator Chain: A: PDB Molecule: plpI0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
95	c2x48B_	Alignment	not modelled	49.3	38	PDB header: viral protein Chain: B: PDB Molecule: cag38821; PDBTitle: orf 55 from sulfolobus islandicus rudivirus 1
96	c4iqcX_	Alignment	not modelled	49.2	25	PDB header: transcription, transferase Chain: X: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: x-ray crystal structure of escherichia coli sigma70 holoenzyme
97	c4yj6A_	Alignment	not modelled	49.0	23	PDB header: hydrolase Chain: A: PDB Molecule: aryl acylamidase; PDBTitle: the crystal structure of a bacterial aryl acylamidase belonging to the2 amidase signature (as) enzymes family
98	c6f8sA_	Alignment	not modelled	48.8	19	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
99	d2ga1a1	Alignment	not modelled	48.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Alr1493-like
100	c3vdoA_	Alignment	not modelled	48.7	15	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
101	c2o8xA_	Alignment	not modelled	48.0	27	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
102	c2jpcA_	Alignment	not modelled	47.8	12	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
103	c5wurB_	Alignment	not modelled	47.8	9	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
104	c3kfuE_	Alignment	not modelled	46.9	37	PDB header: ligase/rna Chain: E: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: crystal structure of the transamidosome
105	c3cecA_	Alignment	not modelled	46.8	11	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	c3t76A_	Alignment	not modelled	46.8	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form

				ii		
107	d1f44a2	Alignment	not modelled	46.6	21	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
108	c2kpiA	Alignment	not modelled	46.3	7	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
109	c1rr7A	Alignment	not modelled	45.3	14	PDB header: transcription Chain: A: PDB Molecule: middle operon regulator; PDBTitle: crystal structure of the middle operon regulator protein of2 bacteriophage mu
110	d1rr7a	Alignment	not modelled	45.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Middle operon regulator, Mor
111	d1xsva	Alignment	not modelled	45.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
112	c3hefB	Alignment	not modelled	44.7	24	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
113	c5bumA	Alignment	not modelled	44.1	21	PDB header: sugar binding protein Chain: A: PDB Molecule: chitinase a; PDBTitle: crystal structure of lysm domain from equisetum arvense chitinase a
114	c6b9rD	Alignment	not modelled	43.7	18	PDB header: oxidoreductase Chain: D: PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
115	c2ebyA	Alignment	not modelled	43.4	5	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
116	c2dc0A	Alignment	not modelled	43.4	13	PDB header: hydrolase Chain: A: PDB Molecule: probable amidase; PDBTitle: crystal structure of amidase
117	d1rp3a1	Alignment	not modelled	43.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
118	c3mzyA	Alignment	not modelled	42.8	20	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
119	c4wt3A	Alignment	not modelled	42.7	13	PDB header: chaperone Chain: A: PDB Molecule: rubisco accumulation factor 1, isoform 2; PDBTitle: the n-terminal domain of rubisco accumulation factor 1 from2 arabidopsis thaliana
120	c5jaaB	Alignment	not modelled	41.0	8	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex