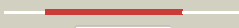












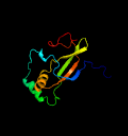










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3917c_(parB)_4405634_4406668
Date	Sat Aug 10 22:05:10 BST 2019
Unique Job ID	77b9cf548bf553f8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vz0B_	 Alignment		100.0	48	PDB header: nuclear protein Chain: B: PDB Molecule: chromosome-partitioning protein spo0j; PDBTitle: chromosome segregation protein spo0j from thermus thermophilus
2	c4umkA_	 Alignment		100.0	40	PDB header: dna binding protein/dna Chain: A: PDB Molecule: probable chromosome-partitioning protein parb; PDBTitle: the complex of spo0j and pars dna in chromosomal partition system
3	c4rsfA_	 Alignment		100.0	13	PDB header: dna binding protein Chain: A: PDB Molecule: parb domain protein nuclease; PDBTitle: structure of pnob8-like parb n-domain
4	d1vk1a_	 Alignment		100.0	17	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Hypothetical protein PF0380
5	c5ujeA_	 Alignment		99.9	13	PDB header: gene regulation Chain: A: PDB Molecule: sbni protein; PDBTitle: sbni with c-terminal truncation from staphylococcus aureus
6	d1vz0a2	 Alignment		99.9	53	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: ParB-like nuclease domain
7	d1xw3a1	 Alignment		99.9	27	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Sulfiredoxin-like
8	d2b6fa1	 Alignment		99.9	24	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Sulfiredoxin-like
9	d1vz0a1	 Alignment		99.8	47	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
10	c5ujdB_	 Alignment		99.8	22	PDB header: gene regulation Chain: B: PDB Molecule: siderophore biosynthesis protein sbni; PDBTitle: sbni from staphylococcus pseudintermedius
11	d1r71a_	 Alignment		99.7	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like

12	c1r71B_	Alignment		99.7	21	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
13	c3mkyP_	Alignment		99.7	25	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
14	c3mkzU_	Alignment		99.7	26	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
15	c5nocA_	Alignment		99.0	35	PDB header: dna binding protein Chain: A: PDB Molecule: stage 0 sporulation protein j; PDBTitle: solution nmr structure of the c-terminal domain of parb (spo0j)
16	c1zx4B_	Alignment		98.5	13	PDB header: cell cycle Chain: B: PDB Molecule: plasmid partition par b protein; PDBTitle: structure of parb bound to dna
17	c3vwbA_	Alignment		97.9	16	PDB header: transcription/dna Chain: A: PDB Molecule: virulence regulon transcriptional activator virb; PDBTitle: crystal structure of virb core domain (se-met derivative) complexed2 with the cis-acting site (5-bru modifications) upstream ic5b promoter
18	d2hwja1	Alignment		97.0	17	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Atu1540-like
19	c4go1A_	Alignment		96.3	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
20	c2w48D_	Alignment		96.1	18	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
21	d1ic8a2	Alignment	not modelled	95.4	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
22	c2mqkA_	Alignment	not modelled	95.4	22	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
23	c2o38A_	Alignment	not modelled	95.2	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
24	d2o38a1	Alignment	not modelled	95.2	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
25	d1rioa_	Alignment	not modelled	95.1	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
26	c2fjrB_	Alignment	not modelled	95.1	11	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
27	c1u78A_	Alignment	not modelled	95.0	24	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
28	d2a6ca1	Alignment	not modelled	95.0	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
29	d1llib_	Alignment	not modelled	94.8	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains

						Family: Phage repressors
30	d1hlva1	Alignment	not modelled	94.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
31	c1y9qA	Alignment	not modelled	94.6	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
32	d1lmb3	Alignment	not modelled	94.5	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
33	c3dnvB	Alignment	not modelled	94.5	31	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
34	c4pu4C	Alignment	not modelled	94.4	15	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)
35	c5d4zF	Alignment	not modelled	94.3	12	PDB header: dna binding protein Chain: F: PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage
36	c3op9A	Alignment	not modelled	94.2	14	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
37	c3ivpD	Alignment	not modelled	94.2	16	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.
38	c5j9iH	Alignment	not modelled	94.2	13	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
39	c3eusB	Alignment	not modelled	94.1	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
40	c2ppxA	Alignment	not modelled	94.1	14	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
41	d2ppxa1	Alignment	not modelled	94.1	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
42	c2kpiA	Alignment	not modelled	94.0	18	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
43	c4mcxE	Alignment	not modelled	94.0	17	PDB header: toxin Chain: E: PDB Molecule: antidote protein; PDBTitle: p. vulgaris higa2 structure, crystal form 2
44	c6fkgC	Alignment	not modelled	94.0	15	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
45	c4ghjA	Alignment	not modelled	93.9	24	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
46	c3fmyA	Alignment	not modelled	93.9	7	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)
47	c5jaaB	Alignment	not modelled	93.8	13	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex
48	c2elhA	Alignment	not modelled	93.7	20	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
49	c3cecA	Alignment	not modelled	93.7	23	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
50	c3omtA	Alignment	not modelled	93.7	16	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.
51	d1y7ya1	Alignment	not modelled	93.5	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
52	c3vk0B	Alignment	not modelled	93.5	24	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhtf from2 neisseria
53	d2d1ha1	Alignment	not modelled	93.4	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
54	d2icta1	Alignment	not modelled	93.4	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains

						Family: SinR domain-like
55	c4wt3A	Alignment	not modelled	93.4	14	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
56	c2ef8A	Alignment	not modelled	93.4	24	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
57	d1y9qa1	Alignment	not modelled	93.4	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
58	d1r69a	Alignment	not modelled	93.3	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
59	d1b0na2	Alignment	not modelled	93.2	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
60	c3f6wE	Alignment	not modelled	93.2	26	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
61	c2xcjB	Alignment	not modelled	93.2	9	PDB header: viral protein Chain: B: PDB Molecule: c protein; PDBTitle: crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
62	d1sq8a	Alignment	not modelled	93.2	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
63	d2b5aa1	Alignment	not modelled	93.2	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
64	c3bs3A	Alignment	not modelled	93.1	26	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
65	c5d50L	Alignment	not modelled	93.1	19	PDB header: dna binding protein Chain: I: PDB Molecule: repressor; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage
66	c3b7hA	Alignment	not modelled	93.1	15	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
67	c3clcC	Alignment	not modelled	93.1	24	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
68	c5uk3L	Alignment	not modelled	93.1	13	PDB header: lyase Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae
69	c2bnoA	Alignment	not modelled	93.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
70	c2wteB	Alignment	not modelled	93.0	16	PDB header: antiviral protein Chain: B: PDB Molecule: csa3; PDBTitle: the structure of the crispr-associated protein, csa3, from2 sulfobolus solfataricus at 1.8 angstrom resolution.
71	d1adra	Alignment	not modelled	93.0	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
72	c3f52A	Alignment	not modelled	93.0	29	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
73	d1x57a1	Alignment	not modelled	92.9	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
74	c3trbA	Alignment	not modelled	92.9	13	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
75	c2mezA	Alignment	not modelled	92.9	12	PDB header: rna binding protein Chain: A: PDB Molecule: multi-protein bridging factor (mbp-like); PDBTitle: flexible anchoring of archaeal mbf1 on ribosomes suggests role as2 recruitment factor
76	c1b0nA	Alignment	not modelled	92.8	18	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
77	d2ofya1	Alignment	not modelled	92.7	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
78	c2ebyA	Alignment	not modelled	92.6	19	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
79	c6f8sA	Alignment	not modelled	92.4	27	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
80	d1lutxa	Alignment	not modelled	92.2	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like

81	c3gn5B	Alignment	not modelled	92.2	6	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)
82	c3bd1B	Alignment	not modelled	92.0	24	PDB header: transcription Chain: B: PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
83	d1bw6a	Alignment	not modelled	91.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
84	d2r1j1	Alignment	not modelled	91.9	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
85	d2croa	Alignment	not modelled	91.6	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
86	c3t76A	Alignment	not modelled	91.5	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
87	c5woqA	Alignment	not modelled	91.4	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
88	c1hlvA	Alignment	not modelled	91.2	18	PDB header: dna binding protein/dna Chain: A: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
89	c3mfc	Alignment	not modelled	91.2	28	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
90	d1trra	Alignment	not modelled	91.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
91	c4ybaA	Alignment	not modelled	90.9	22	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
92	c3kxaD	Alignment	not modelled	90.7	26	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
93	d2cg4a1	Alignment	not modelled	90.7	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
94	c3bdnB	Alignment	not modelled	90.6	18	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
95	d1jhga	Alignment	not modelled	90.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
96	c3zhiA	Alignment	not modelled	90.4	11	PDB header: transcription Chain: A: PDB Molecule: ci; PDBTitle: n-terminal domain of the ci repressor from bacteriophage tp901-1
97	c4nb5D	Alignment	not modelled	90.1	18	PDB header: dna binding protein Chain: D: PDB Molecule: dna binding protein; PDBTitle: crystal structure of a transcriptional regulator
98	c2ewtA	Alignment	not modelled	90.1	11	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bidd
99	d1k78a1	Alignment	not modelled	90.0	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
100	c5dukA	Alignment	not modelled	89.6	13	PDB header: transcription Chain: A: PDB Molecule: putative dna binding protein; PDBTitle: n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05
101	c2ia0A	Alignment	not modelled	89.6	20	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)
102	c5jbrA	Alignment	not modelled	89.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bcav_2135; PDBTitle: crystal structure of uncharacterized protein bcav_2135 from2 beutenbergia cavernae
103	c2vzbA	Alignment	not modelled	89.3	26	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
104	c2jvA	Alignment	not modelled	89.2	22	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
105	d1pdnc	Alignment	not modelled	89.0	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
106	d2cfxa1	Alignment	not modelled	89.0	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
107	c4o8bA	Alignment	not modelled	88.9	9	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein;

						PDBTitle: crystal structure of transcriptional regulator bswr
108	dlilga1	Alignment	not modelled	88.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
109	c6jqsa	Alignment	not modelled	88.8	15	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
110	d2cyya1	Alignment	not modelled	88.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
111	c2dbbA	Alignment	not modelled	88.4	26	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
112	c2cg4B	Alignment	not modelled	88.3	25	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
113	c2p6tH	Alignment	not modelled	88.3	21	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
114	c2e1cA	Alignment	not modelled	88.1	16	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
115	c3k2zA	Alignment	not modelled	88.1	14	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
116	c2wusR	Alignment	not modelled	87.5	9	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz
117	c4pcqC	Alignment	not modelled	87.3	23	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
118	c2h8rA	Alignment	not modelled	87.1	9	PDB header: transcription activator/dna Chain: A: PDB Molecule: hepatocyte nuclear factor 1-beta; PDBTitle: hepatocyte nuclear factor 1b bound to dna: mody5 gene2 product
119	c2l4aA	Alignment	not modelled	87.0	20	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
120	c2e7xA	Alignment	not modelled	86.8	17	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