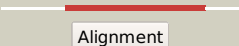



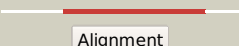





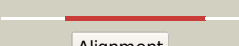










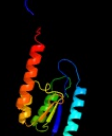


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0605 (-) _701409_702017
Date	Fri Jul 26 01:50:16 BST 2019
Unique Job ID	4ad01c425ae54bc4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6dgbA_	 Alignment		100.0	61	PDB header: hydrolase Chain: A: PDB Molecule: is607 family transposase is1535; PDBTitle: crystal structure of the c-terminal catalytic domain of is1535 tnpa,2 an is607-like serine recombinase
2	c3lhkA_	 Alignment		99.9	27	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna binding protein mj0014; PDBTitle: crystal structure of putative dna binding protein from2 methanocaldococcus jannaschii.
3	c3lhfC_	 Alignment		99.9	36	PDB header: recombination Chain: C: PDB Molecule: serine recombinase; PDBTitle: the crystal structure of a serine recombinase from sulfobolus2 solfataricus to 2.3a
4	c6dgcA_	 Alignment		99.9	32	PDB header: hydrolase Chain: A: PDB Molecule: isc1926 tnpa c-terminal catalytic domain; PDBTitle: crystal structure of the c-terminal catalytic domain of isc1926 tnpa,2 an is607-like serine recombinase
5	c3guvA_	 Alignment		99.8	19	PDB header: recombination Chain: A: PDB Molecule: site-specific recombinase, resolvase family protein; PDBTitle: crystal structure of a resolvase family site-specific recombinase from2 streptococcus pneumoniae
6	c3g13B_	 Alignment		99.8	15	PDB header: recombination Chain: B: PDB Molecule: putative conjugative transposon recombinase; PDBTitle: crystal structure of putative conjugative transposon recombinase from2 clostridium difficile
7	c3bvpB_	 Alignment		99.8	22	PDB header: recombination Chain: B: PDB Molecule: tp901-1 integrase; PDBTitle: crystal structure of the n-terminal catalytic domain of tp901-12 integrase
8	d1gdt2	 Alignment		99.8	21	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
9	d2gm4a2	 Alignment		99.7	20	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
10	c2mhcA_	 Alignment		99.7	17	PDB header: recombination Chain: A: PDB Molecule: tnpx; PDBTitle: nmr structure of the catalytic domain of the large serine resolvase2 tnpa
11	c4bqqB_	 Alignment		99.7	21	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: protein crystal structure of the n-terminal and recombinase domains of2 the streptomyces temperate phage serine recombinase, fc31 integrase.

12	c2gm4B_	Alignment		99.6	22	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
13	c3ploX_	Alignment		99.6	17	PDB header: recombination Chain: X: PDB Molecule: dna-invertase; PDBTitle: crystal structure of the fis-independent mutant of gin
14	d2rsla_	Alignment		99.6	20	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
15	c3pkzK_	Alignment		99.6	25	PDB header: recombination Chain: K: PDB Molecule: recombinase sin; PDBTitle: structural basis for catalytic activation of a serine recombinase
16	c2r0qF_	Alignment		99.5	23	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
17	d1hx7a_	Alignment		99.4	24	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
18	c4m6fA_	Alignment		99.4	18	PDB header: hydrolase/dna Chain: A: PDB Molecule: dna-invertase; PDBTitle: dimer of the g-segment invertase bound to a dna substrate
19	c6amaO_	Alignment		98.8	22	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
20	c5i44E_	Alignment		98.8	27	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
21	c3qaoA_	Alignment	not modelled	98.7	24	PDB header: transcription regulator Chain: A: PDB Molecule: merr-like transcriptional regulator; PDBTitle: the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
22	c4r24B_	Alignment	not modelled	98.7	13	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
23	c2zhhA_	Alignment	not modelled	98.7	16	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
24	c2vz4A_	Alignment	not modelled	98.6	17	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to promoter dna
25	c3gp4B_	Alignment	not modelled	98.5	23	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
26	d1q06a_	Alignment	not modelled	98.5	20	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
27	c4r4eA_	Alignment	not modelled	98.5	7	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
28	d1r8da_	Alignment	not modelled	98.4	22	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators PDB header: transcription regulator/dna

29	c5c8eC_	Alignment	not modelled	98.4	13	Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
30	c3gpvA_	Alignment	not modelled	98.4	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
31	c3hh0C_	Alignment	not modelled	98.3	14	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
32	c4j2nB_	Alignment	not modelled	98.3	16	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
33	c4j2nA_	Alignment	not modelled	98.3	16	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
34	d1r8ea1	Alignment	not modelled	98.2	9	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
35	c5gpeB_	Alignment	not modelled	98.1	15	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, merr-family; PDBTitle: crystal structure of the transcription regulator pbrr691 from2 ralstonia metallidurans ch34 in complex with lead(ii)
36	c3d6zA_	Alignment	not modelled	98.1	6	PDB header: transcription regulator/dna Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of r275e mutant of bmrr bound to dna and rhodamine
37	c3ucsB_	Alignment	not modelled	98.0	12	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
38	c5xqlA_	Alignment	not modelled	97.9	14	PDB header: transcription Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
39	c5af3A_	Alignment	not modelled	97.9	18	PDB header: dna binding Chain: A: PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
40	c2jmlA_	Alignment	not modelled	97.9	14	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
41	c5crlA_	Alignment	not modelled	97.6	19	PDB header: metal binding protein Chain: A: PDB Molecule: mercuric resistance operon regulatory protein; PDBTitle: crystal structure of the transcription activator tn501 merr in complex2 with mercury (ii)
42	c1z4hA_	Alignment	not modelled	96.8	17	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
43	d1pm6a_	Alignment	not modelled	96.6	25	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
44	c2dg6A_	Alignment	not modelled	96.3	31	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
45	c2kfsA_	Alignment	not modelled	95.7	24	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
46	d1rh6a_	Alignment	not modelled	95.6	26	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
47	c4ua2B_	Alignment	not modelled	95.0	17	PDB header: dna binding protein Chain: B: PDB Molecule: regulatory protein; PDBTitle: crystal structure of dual function transcriptional regulator merr from2 bacillus megaterium mb1
48	c3fmyA_	Alignment	not modelled	94.8	19	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)
49	c5jaaB_	Alignment	not modelled	94.0	13	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex
50	c2ppxA_	Alignment	not modelled	93.7	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
51	d2ppxa1	Alignment	not modelled	93.7	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
52	c5j9iH_	Alignment	not modelled	93.6	17	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
53	d2jn6a1	Alignment	not modelled	93.6	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
54	d1sq8a_	Alignment	not modelled	93.4	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors

55	c2kpiA	Alignment	not modelled	93.2	18	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
56	c2ebyA	Alignment	not modelled	93.2	12	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
57	c6fkqC	Alignment	not modelled	92.9	13	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
58	d2croa	Alignment	not modelled	92.1	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
59	d1x57a1	Alignment	not modelled	92.0	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
60	c2rn7A	Alignment	not modelled	91.8	16	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
61	c3mifC	Alignment	not modelled	91.6	9	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
62	d1y7ya1	Alignment	not modelled	91.5	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
63	c3bs3A	Alignment	not modelled	91.4	23	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
64	c2xcjB	Alignment	not modelled	91.3	16	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
65	c1u78A	Alignment	not modelled	91.2	7	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
66	c3bd1B	Alignment	not modelled	91.0	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
67	c3omtA	Alignment	not modelled	90.8	17	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.
68	d2coba1	Alignment	not modelled	90.8	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
69	d1umqa	Alignment	not modelled	90.7	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
70	c1umqA	Alignment	not modelled	90.7	27	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
71	c2fjrB	Alignment	not modelled	90.4	15	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
72	d1r69a	Alignment	not modelled	90.3	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
73	d1fipa	Alignment	not modelled	90.3	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
74	c3f52A	Alignment	not modelled	90.2	15	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
75	c2mezA	Alignment	not modelled	90.2	19	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	c3op9A	Alignment	not modelled	90.1	17	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
77	d1b0na2	Alignment	not modelled	89.9	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
78	d1adra	Alignment	not modelled	89.8	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
79	c2jvIA	Alignment	not modelled	89.8	16	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
80	c3b7hA	Alignment	not modelled	89.8	15	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11;

						PDBTitle: crystal structure of the prophage lp1 protein 11
81	d2r1j1l	Alignment	not modelled	89.8	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
82	c3ivpD	Alignment	not modelled	89.5	10	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.
83	d1j9ia	Alignment	not modelled	89.3	20	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
84	c1b0nA	Alignment	not modelled	89.1	29	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
85	c1y6uA	Alignment	not modelled	89.0	8	PDB header: dna binding protein Chain: A: PDB Molecule: excisionase from transposon tn916; PDBTitle: the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
86	c3t76A	Alignment	not modelled	89.0	21	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	88.9	9	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
88	c3vk0B	Alignment	not modelled	88.8	17	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhtf from2 heisseria
89	d1y9qa1	Alignment	not modelled	88.6	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
90	c3ezfA	Alignment	not modelled	88.4	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
91	c3clcC	Alignment	not modelled	88.2	13	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
92	d1rzsA	Alignment	not modelled	88.1	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
93	d1ntca	Alignment	not modelled	88.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
94	d2ao9a1	Alignment	not modelled	88.0	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
95	d1utxa	Alignment	not modelled	87.9	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
96	d2b5aa1	Alignment	not modelled	87.9	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
97	c3gn5B	Alignment	not modelled	87.8	13	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)
98	d1llib	Alignment	not modelled	87.8	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
99	c1y9qA	Alignment	not modelled	87.8	26	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
100	c4ghjA	Alignment	not modelled	87.6	31	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
101	c2ef8A	Alignment	not modelled	87.6	7	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
102	d1j5ya1	Alignment	not modelled	87.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
103	c4ybaA	Alignment	not modelled	87.4	15	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
104	d1etxa	Alignment	not modelled	87.4	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
105	d1rioA	Alignment	not modelled	87.2	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
106	c3eusB	Alignment	not modelled	87.1	19	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from

					silicibacter2 pomeroyi
107	c3f6wE_	Alignment	not modelled	86.8	15 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
108	c3dvnB_	Alignment	not modelled	86.7	14 PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
109	d2a6ca1	Alignment	not modelled	86.4	27 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
110	c3cecA_	Alignment	not modelled	86.4	26 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
111	d2icta1	Alignment	not modelled	86.3	23 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
112	c2wusR_	Alignment	not modelled	86.2	12 PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz
113	c3trbA_	Alignment	not modelled	86.1	3 PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addition module antidote protein of a higa (higa)2 family from coxiella burnetii
114	d1biaa1	Alignment	not modelled	86.0	11 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
115	c4pu4C_	Alignment	not modelled	86.0	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)
116	c4I5eA_	Alignment	not modelled	85.9	28 PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
117	c4lhfA_	Alignment	not modelled	85.2	21 PDB header: viral protein Chain: A: PDB Molecule: regulatory protein cox; PDBTitle: crystal structure of a dna binding protein from phage p2
118	c1hlvA_	Alignment	not modelled	85.2	15 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
119	c3kxaD_	Alignment	not modelled	85.2	17 PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
120	d2ofya1	Alignment	not modelled	84.9	13 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like