

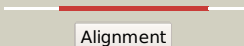
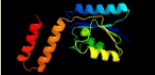
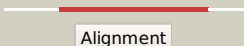
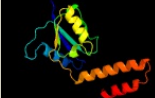














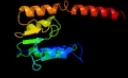





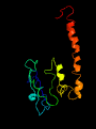




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0921_(-)_1027108_1027689
Date	Fri Jul 26 01:50:51 BST 2019
Unique Job ID	3279f4c7dbe1ebfb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6dgbA_	 Alignment		100.0	100	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		100.0	31	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	35	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	35	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	c3g13B_	 Alignment		99.8	17	PDB header: recombination Chain: B: PDB Molecule: putative conjugative transposon recombinase; PDBTitle: crystal structure of putative conjugative transposon recombinase from2 clostridium difficile
6	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
7	d1gdtA2	 Alignment		99.7	26	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
8	c2mhcA_	 Alignment		99.7	18	PDB header: recombination Chain: A: PDB Molecule: tnpx; PDBTitle: nmr structure of the catalytic domain of the large serine resolvase2 tnpX
9	c3bvpB_	 Alignment		99.7	22	PDB header: recombination Chain: B: PDB Molecule: tp901-1 integrase; PDBTitle: crystal structure of the n-terminal catalytic domain of tp901-12 integrase
10	c4bqqB_	 Alignment		99.7	19	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.
11	c2gm4B_	 Alignment		99.7	24	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

12	d2gm4a2	Alignment		99.7	24	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
13	c3pkzK_	Alignment		99.6	25	PDB header: recombination Chain: K: PDB Molecule: recombinase sin; PDBTitle: structural basis for catalytic activation of a serine recombinase
14	c3ploX_	Alignment		99.6	24	PDB header: recombination Chain: X: PDB Molecule: dna-invertase; PDBTitle: crystal structure of the fis-independent mutant of gin
15	d2rsla_	Alignment		99.6	28	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
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		99.5	31	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
18	c4m6fA_	Alignment		99.4	22	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		98.7	21	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		98.7	23	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
21	c2zhhA_	Alignment	not modelled	98.6	9	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
22	c4r24B_	Alignment	not modelled	98.5	9	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
23	c3qaoA_	Alignment	not modelled	98.4	23	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
24	c3gp4B_	Alignment	not modelled	98.4	21	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
25	c2vz4A_	Alignment	not modelled	98.4	15	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
26	c4r4eA_	Alignment	not modelled	98.3	5	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
27	c4j2nA_	Alignment	not modelled	98.2	14	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
28	d1q06a_	Alignment	not modelled	98.2	14	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	98.2	14	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	c4j2nB_	Alignment	not modelled	98.2	14	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
31	c3hh0C_	Alignment	not modelled	98.2	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	c3gpvA_	Alignment	not modelled	98.2	12	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
33	d1r8da_	Alignment	not modelled	98.2	21	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
34	d1r8ea1	Alignment	not modelled	98.0	5	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
35	c5gpeB_	Alignment	not modelled	97.9	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	c5xqlA_	Alignment	not modelled	97.9	9	PDB header: transcription Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
37	c3d6zA_	Alignment	not modelled	97.8	2	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
38	c3ucsB_	Alignment	not modelled	97.8	9	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
39	c5af3A_	Alignment	not modelled	97.7	19	PDB header: dna binding Chain: A: PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
40	c2jmlA_	Alignment	not modelled	97.7	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	97.2	23	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	d1pm6a_	Alignment	not modelled	96.3	26	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
43	c1z4hA_	Alignment	not modelled	96.2	21	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
44	c2kfsA_	Alignment	not modelled	96.1	26	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
45	c2dg6A_	Alignment	not modelled	95.4	38	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)
46	d1rh6a_	Alignment	not modelled	95.2	26	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
47	c4ua2B_	Alignment	not modelled	93.9	21	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	93.6	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	92.6	14	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex
50	d2jn6a1	Alignment	not modelled	92.5	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
51	c5j9iH_	Alignment	not modelled	92.2	14	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
52	c6fkgC_	Alignment	not modelled	92.1	13	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
53	d2ppxa1	Alignment	not modelled	91.3	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
54	c2ppxA_	Alignment	not modelled	91.3	11	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

55	c2rn7A_	Alignment	not modelled	90.9	23	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
56	c1umqA_	Alignment	not modelled	90.7	19	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
57	d1umqa_	Alignment	not modelled	90.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
58	d1sq8a_	Alignment	not modelled	90.6	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
59	c1zvva_	Alignment	not modelled	90.4	15	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
60	c3bd1B_	Alignment	not modelled	90.4	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
61	c2kpiA_	Alignment	not modelled	90.2	26	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
62	d1fipa_	Alignment	not modelled	89.9	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
63	d1r69a_	Alignment	not modelled	89.8	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
64	d1x57a1	Alignment	not modelled	89.5	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
65	d2croa_	Alignment	not modelled	89.1	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
66	d2ao9a1	Alignment	not modelled	89.0	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
67	d1j9ia_	Alignment	not modelled	88.8	23	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
68	c2fjrB_	Alignment	not modelled	88.8	7	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
69	c3bs3A_	Alignment	not modelled	88.0	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
70	c3omtA_	Alignment	not modelled	87.8	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.
71	c2xcjB_	Alignment	not modelled	87.5	18	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
72	c1y6uA_	Alignment	not modelled	87.5	10	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
73	c3mfc_	Alignment	not modelled	87.2	10	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
74	c1u78A_	Alignment	not modelled	86.8	17	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
75	c3f52A_	Alignment	not modelled	86.8	21	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
76	d1y7ya1	Alignment	not modelled	86.7	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
77	d1etxa_	Alignment	not modelled	86.6	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
78	c3op9A_	Alignment	not modelled	86.4	19	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
79	d1adra_	Alignment	not modelled	86.2	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
						PDB header: gene regulation

80	c4ybaA_	Alignment	not modelled	85.9	16	Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
81	d2r1j1l	Alignment	not modelled	85.8	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
82	c2ebyA_	Alignment	not modelled	85.7	14	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
83	c1b0nA_	Alignment	not modelled	85.7	27	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sinr protein complex
84	c3ezfA_	Alignment	not modelled	85.6	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
85	c3gn5B_	Alignment	not modelled	85.3	14	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)
86	d1j5ya1	Alignment	not modelled	84.9	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
87	c3ivpD_	Alignment	not modelled	84.9	6	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.
88	c2mezA_	Alignment	not modelled	84.7	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
89	c2jvA_	Alignment	not modelled	84.7	16	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
90	c4l5eA_	Alignment	not modelled	84.4	27	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
91	c1g2hA_	Alignment	not modelled	84.1	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
92	d1g2ha_	Alignment	not modelled	84.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
93	c2ef8A_	Alignment	not modelled	84.1	9	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
94	c3e7ID_	Alignment	not modelled	83.9	26	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
95	c3t76A_	Alignment	not modelled	83.8	23	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
96	c2ao9H_	Alignment	not modelled	83.8	30	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: phage protein; PDBTitle: structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
97	d1b0na2	Alignment	not modelled	83.7	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
98	c3vk0B_	Alignment	not modelled	83.4	14	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhf from2 neisseria
99	d1y9qa1	Alignment	not modelled	83.0	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
100	c2m8gX_	Alignment	not modelled	82.5	7	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
101	c5woqA_	Alignment	not modelled	82.4	10	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
102	d2icta1	Alignment	not modelled	82.3	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
103	c3clcC_	Alignment	not modelled	82.2	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
104	c4ghjA_	Alignment	not modelled	82.1	23	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
105	c1bdhA_	Alignment	not modelled	82.0	10	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex

106	c1hlvA_	Alignment	not modelled	81.9	9	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
107	d2coba1	Alignment	not modelled	81.8	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
108	c4lhfA_	Alignment	not modelled	81.7	23	PDB header: viral protein Chain: A: PDB Molecule: regulatory protein cox; PDBTitle: crystal structure of a dna binding protein from phage p2
109	d2b5aa1	Alignment	not modelled	81.6	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
110	d1utxa_	Alignment	not modelled	81.6	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
111	c3dnvB_	Alignment	not modelled	81.5	10	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
112	c3eusB_	Alignment	not modelled	81.3	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
113	c3b7hA_	Alignment	not modelled	81.1	23	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
114	d1rioa_	Alignment	not modelled	80.9	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
115	d1lib_	Alignment	not modelled	80.8	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
116	c1y9qA_	Alignment	not modelled	80.1	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
117	d1rzsA_	Alignment	not modelled	79.8	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
118	c3f6wE_	Alignment	not modelled	79.3	9	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
119	d2bcqa2	Alignment	not modelled	79.0	27	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
120	c3cecA_	Alignment	not modelled	78.9	32	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