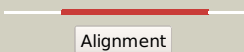

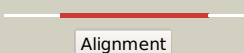

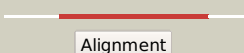

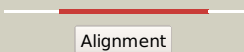
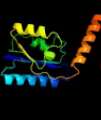


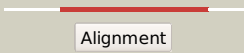

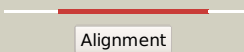

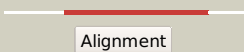

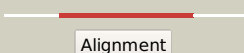



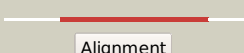



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2792c_(-)_3101591_3102172
Date	Wed Aug 7 12:50:45 BST 2019
Unique Job ID	44384afd6c91c79f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6dgbA_	 Alignment		100.0	62	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	23	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	38	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	34	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	18	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	14	PDB header: recombination Chain: B: PDB Molecule: putative conjugative transposon recombinase; PDBTitle: crystal structure of putative conjugative transposon recombinase from2 clostridium difficile
7	d1gdtA2	 Alignment		99.8	24	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
8	c3bvpB_	 Alignment		99.8	19	PDB header: recombination Chain: B: PDB Molecule: tp901-1 integrase; PDBTitle: crystal structure of the n-terminal catalytic domain of tp901-12 integrase
9	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 tnpX
10	d2gm4a2	 Alignment		99.7	24	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
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	c4bqqB_	Alignment		99.7	18	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.
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	21	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
15	c3pkzK_	Alignment		99.6	23	PDB header: recombination Chain: K: PDB Molecule: recombinase sin; PDBTitle: structural basis for catalytic activation of a serine recombinase
16	d1hx7a_	Alignment		99.5	26	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
17	c2r0qF_	Alignment		99.5	21	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
18	c4m6fA_	Alignment		99.4	19	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	23	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	26	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	98.7	19	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
22	c4r24B_	Alignment	not modelled	98.6	14	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	98.6	26	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	98.5	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	98.5	18	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	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	d1r8da_	Alignment	not modelled	98.4	24	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
28	c4r4eA_	Alignment	not modelled	98.4	7	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
						PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator

29	c5c8eC_	Alignment	not modelled	98.4	12	carh ; PDBTitle : crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
30	c4j2nA_	Alignment	not modelled	98.4	19	PDB header :viral protein Chain : A: PDB Molecule :gp37; PDBTitle : crystal structure of mycobacteriophage pukovnik xis
31	c4j2nB_	Alignment	not modelled	98.4	19	PDB header :viral protein Chain : B: PDB Molecule :gp37; PDBTitle : crystal structure of mycobacteriophage pukovnik xis
32	c3hh0C_	Alignment	not modelled	98.3	17	PDB header :transcription regulator Chain : C: PDB Molecule :transcriptional regulator, merr family; PDBTitle : crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
33	c3gpvA_	Alignment	not modelled	98.3	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
34	d1r8ea1	Alignment	not modelled	98.2	12	Fold :Putative DNA-binding domain Superfamily :Putative DNA-binding domain Family :DNA-binding N-terminal domain of transcription activators
35	c3ucsB_	Alignment	not modelled	98.1	14	PDB header :chaperone Chain : B: PDB Molecule :chaperone-modulator protein cbpm; PDBTitle : crystal structure of the complex between cbpa j-domain and cbpm
36	c5gpeB_	Alignment	not modelled	98.1	18	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)
37	c3d6zA_	Alignment	not modelled	98.1	9	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	c5xqlA_	Alignment	not modelled	98.0	14	PDB header :transcription Chain : A: PDB Molecule :multidrug-efflux transporter 1 regulator; PDBTitle : crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
39	c2jmlA_	Alignment	not modelled	97.9	12	PDB header :transcription Chain : A: PDB Molecule :dna binding domain/transcriptional regulator; PDBTitle : solution structure of the n-terminal domain of cara repressor
40	c5af3A_	Alignment	not modelled	97.7	18	PDB header :dna binding Chain : A: PDB Molecule :vapbc49; PDBTitle : x-ray crystal structure of rv2018 from mycobacterium tuberculosis
41	c5crlA_	Alignment	not modelled	97.4	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	c2kfsA_	Alignment	not modelled	96.5	24	PDB header :dna-binding protein Chain : A: PDB Molecule :conserved hypothetical regulatory protein; PDBTitle : nmr structure of rv2175c
43	d1pm6a_	Alignment	not modelled	96.3	26	Fold :Putative DNA-binding domain Superfamily :Putative DNA-binding domain Family :Excisionase-like
44	c2dg6A_	Alignment	not modelled	95.8	36	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	c1z4hA_	Alignment	not modelled	95.7	19	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
46	c4ua2B_	Alignment	not modelled	95.1	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
47	d1rh6a_	Alignment	not modelled	95.0	26	Fold :Putative DNA-binding domain Superfamily :Putative DNA-binding domain Family :Excisionase-like
48	c3fmyA_	Alignment	not modelled	94.1	19	PDB header :dna binding protein Chain : A: PDB Molecule :hth-type transcriptional regulator mqa PDBTitle : structure of the c-terminal domain of the e. coli protein2 mqa (ygit/b3021)
49	c5jaaB_	Alignment	not modelled	93.7	18	PDB header :toxin Chain : B: PDB Molecule :antitoxin iga-2; PDBTitle : crystal structure of the higa2 toxin-antitoxin complex
50	c5j9iH_	Alignment	not modelled	93.4	21	PDB header :antitoxin Chain : H: PDB Molecule :antitoxin iga-2; PDBTitle : crystal structure of the higa2 antitoxin c-terminal domain
51	d2jn6a1	Alignment	not modelled	93.1	30	Fold :DNA/RNA-binding 3-helical bundle Superfamily :Homeodomain-like Family :Cgl2762-like
52	d2ppxa1	Alignment	not modelled	92.5	14	Fold :lambda repressor-like DNA-binding domains Superfamily :lambda repressor-like DNA-binding domains Family :SinR domain-like
53	c2ppxA_	Alignment	not modelled	92.5	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
54	c6fkgC_	Alignment	not modelled	92.3	10	PDB header :toxin Chain : C: PDB Molecule :rv1990c (mbca); PDBTitle : crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex. PDB header :unknown function

55	c2rn7A_	Alignment	not modelled	92.2	18	Chain: A; PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
56	d1sq8a_	Alignment	not modelled	91.6	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
57	c2kpiA_	Alignment	not modelled	91.6	19	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
58	c2ebyA_	Alignment	not modelled	91.3	15	PDB header: transcription Chain: A; PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
59	c2fjrB_	Alignment	not modelled	91.1	11	PDB header: transcription regulator Chain: B; PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
60	c3bd1B_	Alignment	not modelled	91.0	21	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	d1x57a1	Alignment	not modelled	90.8	6	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
62	d1j9ia_	Alignment	not modelled	90.6	20	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
63	d1r69a_	Alignment	not modelled	90.5	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
64	d2croa_	Alignment	not modelled	90.2	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
65	c3bs3A_	Alignment	not modelled	90.1	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
66	d1biaa1	Alignment	not modelled	89.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
67	c3mifC_	Alignment	not modelled	89.8	6	PDB header: transcription regulator Chain: C; PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
68	c3omtA_	Alignment	not modelled	89.6	13	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.
69	c1umqA_	Alignment	not modelled	89.2	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
70	d1umqa_	Alignment	not modelled	89.2	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
71	c2xcjB_	Alignment	not modelled	89.1	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	d1y7ya1	Alignment	not modelled	89.0	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
73	c3f52A_	Alignment	not modelled	88.9	13	PDB header: transcription activator Chain: A; PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
74	d2ao9a1	Alignment	not modelled	88.6	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
75	c3op9A_	Alignment	not modelled	88.5	16	PDB header: transcription regulator Chain: A; PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
76	d1fipa_	Alignment	not modelled	88.3	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
77	d1adra_	Alignment	not modelled	88.3	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
78	c3ezfA_	Alignment	not modelled	88.2	8	PDB header: biosynthetic protein Chain: A; PDB Molecule: para; PDBTitle: partition protein
79	d2r1jl1	Alignment	not modelled	88.1	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
80	c3t76A_	Alignment	not modelled	88.1	13	PDB header: transcription regulator Chain: A; PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii

81	c1y6uA	Alignment	not modelled	88.0	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
82	c3gn5B	Alignment	not modelled	88.0	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)
83	c1b0nA	Alignment	not modelled	88.0	27	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
84	c2mezA	Alignment	not modelled	87.6	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
85	c4ybaA	Alignment	not modelled	87.4	16	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
86	c2ivA	Alignment	not modelled	87.4	16	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
87	c3ivpD	Alignment	not modelled	87.2	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	c1u78A	Alignment	not modelled	86.8	11	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
89	d1b0na2	Alignment	not modelled	86.6	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
90	c3vk0B	Alignment	not modelled	86.0	10	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhf from2 neisseria
91	c1zvva	Alignment	not modelled	85.8	12	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
92	c4pu4C	Alignment	not modelled	85.7	23	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)
93	d1y9qa1	Alignment	not modelled	85.4	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
94	c2ef8A	Alignment	not modelled	85.2	6	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
95	c5woqA	Alignment	not modelled	85.2	6	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
96	c1hivA	Alignment	not modelled	85.0	13	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
97	c4lhfa	Alignment	not modelled	84.9	22	PDB header: viral protein Chain: A: PDB Molecule: regulatory protein cox; PDBTitle: crystal structure of a dna binding protein from phage p2
98	c4l5eA	Alignment	not modelled	84.9	28	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
99	c3clcC	Alignment	not modelled	84.9	10	PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.espl396i tetramer in complex with its natural 35 base-pair operator
100	d1llib	Alignment	not modelled	84.7	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
101	d2b5aa1	Alignment	not modelled	84.6	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
102	c4ghjA	Alignment	not modelled	84.4	27	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
103	d1etxa	Alignment	not modelled	84.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
104	c2ao9H	Alignment	not modelled	84.1	25	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
105	d1utxa	Alignment	not modelled	84.1	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
106	c3dnvB	Alignment	not modelled	84.0	10	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb;

						PDBTitle: mdt protein
107	c3eusB_	Alignment	not modelled	83.9	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
108	c6hn7A_	Alignment	not modelled	83.4	32	PDB header: dna binding protein Chain: A: PDB Molecule: redirecting phage packaging protein c (rppc); PDBTitle: hijacking the hijackers: escherichia coli pathogenicity islands2 redirect helper phage packaging for their own benefit.
109	d2icta1	Alignment	not modelled	83.4	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
110	d1rioa_	Alignment	not modelled	82.7	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
111	d2coba1	Alignment	not modelled	82.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
112	c3b7hA_	Alignment	not modelled	82.5	18	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
113	d2bcqa2	Alignment	not modelled	82.4	27	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
114	c1y9qA_	Alignment	not modelled	82.1	17	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
115	d1g2ha_	Alignment	not modelled	82.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
116	c1g2hA_	Alignment	not modelled	82.1	18	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
117	c3f6wE_	Alignment	not modelled	81.9	14	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
118	d1jmsa3	Alignment	not modelled	81.6	30	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
119	c6gh5M_	Alignment	not modelled	81.5	26	PDB header: transcription Chain: M: PDB Molecule: rna polymerase sigma-54 factor, rna polymerase sigma-54 PDBTitle: cryo-em structure of bacterial rna polymerase-sigma54 holoenzyme2 transcription open complex
120	d2ofya1	Alignment	not modelled	81.5	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like