

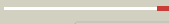




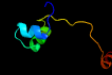




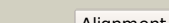

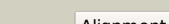









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1051c_(-)_1173950_1174705
Date	Wed Jul 31 22:05:12 BST 2019
Unique Job ID	bde8497469c9900a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ok0B_	 Alignment		99.6	18	PDB header: transferase Chain: B: PDB Molecule: putative; PDBTitle: crystal structure of putative nucleotidyltransferase from h. pylori
2	c1z4hA_	 Alignment		99.2	15	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of 2 atypical excisionase
3	c4j2nA_	 Alignment		99.1	22	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
4	c4j2nB_	 Alignment		99.0	20	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
5	c6amaO_	 Alignment		98.8	25	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
6	c4r24B_	 Alignment		98.0	18	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
7	c4r4eA_	 Alignment		98.0	19	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
8	c1y6uA_	 Alignment		97.9	14	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
9	c5i44E_	 Alignment		97.9	19	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
10	c2zhbA_	 Alignment		97.9	23	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxR; PDBTitle: crystal structure of soxR
11	c5c8eC_	 Alignment		97.8	19	PDB header: transcription regulator/dna 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

12	d1q06a_	Alignment		97.8	9	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
13	c3gp4B_	Alignment		97.7	20	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
14	c5af3A_	Alignment		97.7	22	PDB header: dna binding Chain: A: PDB Molecule: vpapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
15	c3qaoA_	Alignment		97.7	20	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
16	c2vz4A_	Alignment		97.6	24	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
17	d1j9ia_	Alignment		97.5	24	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
18	d1r8da_	Alignment		97.5	26	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
19	c3gpvA_	Alignment		97.5	8	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
20	c3hh0C_	Alignment		97.4	18	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
21	d1r8ea1	Alignment	not modelled	97.2	19	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
22	c5gpeB_	Alignment	not modelled	97.1	16	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)
23	c2jmlA_	Alignment	not modelled	97.0	26	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
24	c3d6zA_	Alignment	not modelled	96.6	17	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
25	c3ucsB_	Alignment	not modelled	96.5	9	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
26	c2kfsA_	Alignment	not modelled	96.4	21	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
27	c5crlA_	Alignment	not modelled	95.8	26	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)
28	c2kvvA_	Alignment	not modelled	95.5	16	PDB header: hydrolase Chain: A: PDB Molecule: putative excisionase; PDBTitle: solution nmr of putative excisionase from klebsiella

						pneumoniae,2 northeast structural genomics consortium target target kpr49
29	c6fkqC	Alignment	not modelled	93.6	14	PDB header: toxin Chain: C; PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
30	d1rh6a	Alignment	not modelled	92.1	24	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
31	d2ao9a1	Alignment	not modelled	92.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
32	d1pm6a	Alignment	not modelled	91.9	19	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
33	c3ezfA	Alignment	not modelled	91.8	11	PDB header: biosynthetic protein Chain: A; PDB Molecule: para; PDBTitle: partition protein
34	d2jn6a1	Alignment	not modelled	91.6	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
35	c5jaaB	Alignment	not modelled	91.4	14	PDB header: toxin Chain: B; PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higba2 toxin-antitoxin complex
36	c5j9iH	Alignment	not modelled	90.4	15	PDB header: antitoxin Chain: H; PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higA2 antitoxin c-terminal domain
37	d2ppxa1	Alignment	not modelled	90.1	33	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
38	c2ppxA	Alignment	not modelled	90.1	33	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
39	c2ebyA	Alignment	not modelled	89.9	15	PDB header: transcription Chain: A; PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
40	c2fjrB	Alignment	not modelled	89.9	7	PDB header: transcription regulator Chain: B; PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
41	c3bd1B	Alignment	not modelled	89.8	22	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
42	c2kpiA	Alignment	not modelled	89.8	21	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	c2rn7A	Alignment	not modelled	89.4	27	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
44	c3omtA	Alignment	not modelled	89.3	18	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.
45	d1j5ya1	Alignment	not modelled	89.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
46	c1hlvA	Alignment	not modelled	88.9	14	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
47	d1biaa1	Alignment	not modelled	88.7	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
48	c3trbA	Alignment	not modelled	88.1	18	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
49	c3bs3A	Alignment	not modelled	87.6	18	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
50	c3t76A	Alignment	not modelled	87.5	14	PDB header: transcription regulator Chain: A; PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
51	c2ao9H	Alignment	not modelled	87.5	17	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
52	c3fmyA	Alignment	not modelled	87.2	22	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)
53	d2croa	Alignment	not modelled	87.0	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
54	c3op9A	Alignment	not modelled	86.8	21	PDB header: transcription regulator Chain: A; PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria

						innocua
55	c3mfc_	Alignment	not modelled	86.7	14	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
56	c1umqA_	Alignment	not modelled	86.6	9	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	86.6	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
58	d1adra_	Alignment	not modelled	86.5	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
59	c1y9qA_	Alignment	not modelled	86.5	19	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
60	c6f8sA_	Alignment	not modelled	86.2	21	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
61	c5d4zF_	Alignment	not modelled	86.0	15	PDB header: dna binding protein Chain: F: PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage
62	c2xcjB_	Alignment	not modelled	85.7	32	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
63	d1sq8a_	Alignment	not modelled	85.5	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
64	c3eqxB_	Alignment	not modelled	85.5	10	PDB header: dna binding protein Chain: B: PDB Molecule: fic domain containing transcriptional regulator; PDBTitle: crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
65	d1fipa_	Alignment	not modelled	85.0	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
66	d1y7ya1	Alignment	not modelled	84.7	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
67	c1b0nA_	Alignment	not modelled	84.5	14	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
68	d1x57a1	Alignment	not modelled	84.4	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
69	c3ivpD_	Alignment	not modelled	84.1	21	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.
70	c4lhfA_	Alignment	not modelled	83.9	20	PDB header: viral protein Chain: A: PDB Molecule: regulatory protein cox; PDBTitle: crystal structure of a dna binding protein from phage p2
71	d1lutxa_	Alignment	not modelled	83.8	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
72	d1r69a_	Alignment	not modelled	83.8	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
73	d1y9qa1	Alignment	not modelled	83.8	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
74	c1g2hA_	Alignment	not modelled	83.7	11	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
75	d1g2ha_	Alignment	not modelled	83.7	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
76	d1b0na2	Alignment	not modelled	83.6	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
77	c2mqkA_	Alignment	not modelled	83.5	23	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
78	d2icta1	Alignment	not modelled	83.1	4	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
79	c3f52A_	Alignment	not modelled	82.9	14	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
						PDB header: dna binding protein

80	c3vk0B_	Alignment	not modelled	82.8	4	Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhft from2 neisseria
81	d1ntca_	Alignment	not modelled	82.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
82	c3clcC_	Alignment	not modelled	82.6	0	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
83	d1etxa_	Alignment	not modelled	82.6	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
84	d2r1j1_	Alignment	not modelled	82.5	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
85	c4ybaA_	Alignment	not modelled	82.3	21	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
86	c1j5yA_	Alignment	not modelled	82.2	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, biotin repressor family; PDBTitle: crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
87	c4l5eA_	Alignment	not modelled	82.0	39	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
88	c3dnvB_	Alignment	not modelled	81.9	11	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
89	c1u78A_	Alignment	not modelled	81.8	15	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
90	d1llib_	Alignment	not modelled	81.6	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
91	c5woqA_	Alignment	not modelled	81.2	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
92	c2jvIA_	Alignment	not modelled	80.6	14	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
93	c4ghjA_	Alignment	not modelled	80.2	25	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
94	c2ef8A_	Alignment	not modelled	80.1	7	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
95	c2m8gX_	Alignment	not modelled	79.9	14	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
96	d2b5aa1	Alignment	not modelled	79.7	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
97	c4pu4C_	Alignment	not modelled	79.4	18	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)
98	c3cecA_	Alignment	not modelled	79.2	15	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
99	c3gn5B_	Alignment	not modelled	79.0	21	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)
100	c1ojID_	Alignment	not modelled	78.8	17	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
101	c5chhA_	Alignment	not modelled	77.8	22	PDB header: transcription Chain: A: PDB Molecule: arac family transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
102	c2ev2B_	Alignment	not modelled	77.6	23	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenylyl cylcase rv1264, at ph 8.5
103	c5wayB_	Alignment	not modelled	77.5	4	PDB header: transcription Chain: B: PDB Molecule: transcriptional activator; PDBTitle: mgaspn protein, mga regulator from streptococcus pneumoniae
104	d2ezla_	Alignment	not modelled	77.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain PDB header: signaling protein

105	c5m7nA_	Alignment	not modelled	77.3	18	Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystal direct automated mounting and cryo-cooling3 technology
106	c3eusB_	Alignment	not modelled	77.2	11	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	d1rtoa_	Alignment	not modelled	77.2	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
108	d1etob_	Alignment	not modelled	77.1	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
109	c3e7ID_	Alignment	not modelled	77.0	29	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
110	c2mezA_	Alignment	not modelled	76.8	11	PDB header: rna binding protein Chain: A: PDB Molecule: multiprotein bridging factor (mbp-like); PDBTitle: flexible anchoring of archaeal mbf1 on ribosomes suggests role as2 recruitment factor
111	d1rzsA_	Alignment	not modelled	76.7	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
112	c3b7hA_	Alignment	not modelled	76.7	20	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
113	c2auwB_	Alignment	not modelled	76.2	22	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
114	c2oqgA_	Alignment	not modelled	75.7	16	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
115	c3kxaD_	Alignment	not modelled	75.5	14	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
116	d1lmb3_	Alignment	not modelled	75.3	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
117	d2ofya1	Alignment	not modelled	75.2	31	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
118	c5uk3J_	Alignment	not modelled	74.8	18	PDB header: lyase Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae
119	c4fcyA_	Alignment	not modelled	74.8	25	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
120	d1vz0a1	Alignment	not modelled	73.7	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like