

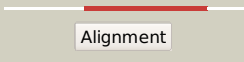

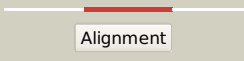

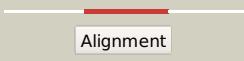

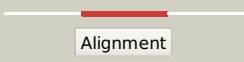
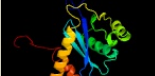
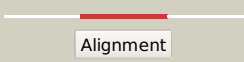

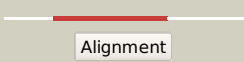

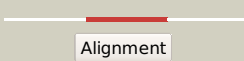

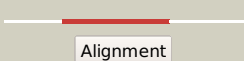

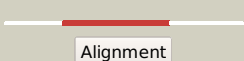

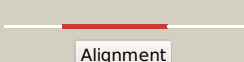












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2812_(-)_3116828_3118237
Date	Wed Aug 7 12:50:47 BST 2019
Unique Job ID	da24ec846017170a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fcyA_	 Alignment		100.0	13	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
2	c1bcoA_	 Alignment		100.0	16	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
3	d1bcoa2	 Alignment		100.0	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
4	c1c0mA_	 Alignment		99.9	21	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
5	d1asua_	 Alignment		99.9	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
6	d1c0ma2	 Alignment		99.9	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
7	c3jcaE_	 Alignment		99.9	20	PDB header: viral protein Chain: E: PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome
8	c5cz1B_	 Alignment		99.9	24	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase
9	c5u1cA_	 Alignment		99.9	17	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
10	c3f9kV_	 Alignment		99.9	15	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
11	c5m0rF_	 Alignment		99.8	16	PDB header: hydrolase Chain: F: PDB Molecule: integrase; PDBTitle: cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex

12	c3hpgC_	Alignment		99.8	16	PDB header: transferase Chain: C: PDB Molecule: integrase; PDBTitle: visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
13	c3nf9A_	Alignment		99.8	20	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: integrase; PDBTitle: structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
14	d1cxqa_	Alignment		99.8	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
15	c3kksB_	Alignment		99.8	21	PDB header: dna binding protein Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of catalytic core domain of biv integrase in crystal2 form ii
16	c4mq3A_	Alignment		99.8	17	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of fiv integrase
17	c1ex4A_	Alignment		99.8	20	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
18	c5ejkG_	Alignment		99.8	16	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome
19	c3l2tB_	Alignment		99.8	17	PDB header: recombination/dna Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
20	d1lexqa_	Alignment		99.8	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
21	c1k6yB_	Alignment	not modelled	99.7	18	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
22	d1hyva_	Alignment	not modelled	99.7	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
23	d1c6va_	Alignment	not modelled	99.7	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
24	c3dlrA_	Alignment	not modelled	99.6	12	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv integrase
25	c3hosA_	Alignment	not modelled	99.6	15	PDB header: transferase, dna binding protein/dna Chain: A: PDB Molecule: transposable element mariner, complete cds; PDBTitle: crystal structure of the mariner mos1 paired end complex with mg
26	c3l2uA_	Alignment	not modelled	99.5	14	PDB header: recombination/dna Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the prototype foamy virus (pfv)2 intasome in complex with magnesium and gs91373 (elvitegravir)
27	c5u1cD_	Alignment	not modelled	99.4	17	PDB header: viral protein Chain: D: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
28	d1bcoa1	Alignment	not modelled	99.1	21	Fold: mu transposase, C-terminal domain Superfamily: mu transposase, C-terminal domain Family: mu transposase, C-terminal domain

29	c6paxA	Alignment	not modelled	98.7	16	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
30	d1pdnc	Alignment	not modelled	98.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
31	c2k27A	Alignment	not modelled	97.9	15	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
32	c1u78A	Alignment	not modelled	97.9	18	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
33	c5cr4B	Alignment	not modelled	97.8	13	PDB header: hydrolase Chain: B: PDB Molecule: sleeping beauty transposase, sb100x; PDBTitle: crystal structure of the sleeping beauty transposase catalytic domain
34	c3f2kB	Alignment	not modelled	97.1	14	PDB header: transferase Chain: B: PDB Molecule: histone-lysine n-methyltransferase setmar; PDBTitle: structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar
35	c2f7tA	Alignment	not modelled	97.0	16	PDB header: dna binding protein Chain: A: PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
36	d2ezla	Alignment	not modelled	96.6	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
37	d2jn6a1	Alignment	not modelled	95.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
38	d2ezia	Alignment	not modelled	95.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
39	d2ezha	Alignment	not modelled	94.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
40	d1k78a1	Alignment	not modelled	93.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
41	c2rn7A	Alignment	not modelled	93.8	21	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
42	d6paxa1	Alignment	not modelled	93.7	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
43	c3hefB	Alignment	not modelled	90.1	20	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
44	d1ntca	Alignment	not modelled	87.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
45	c4j2nB	Alignment	not modelled	83.8	19	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
46	c2elhA	Alignment	not modelled	83.7	10	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
47	c2ao9H	Alignment	not modelled	82.3	24	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
48	c1g2hA	Alignment	not modelled	80.9	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
49	d1g2ha	Alignment	not modelled	80.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
50	c4j2nA	Alignment	not modelled	80.2	14	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
51	d1fipa	Alignment	not modelled	79.9	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
52	d1umqa	Alignment	not modelled	79.4	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
53	c1umqA	Alignment	not modelled	79.4	17	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
54	c6amaO	Alignment	not modelled	78.7	15	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
55	c3e7ID_	Alignment	not modelled	77.7	11	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
56	d1biaa1	Alignment	not modelled	76.9	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
57	c2m8gX_	Alignment	not modelled	76.1	8	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
58	d1etxa_	Alignment	not modelled	75.9	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
59	d2ao9a1	Alignment	not modelled	75.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
60	d1j5ya1	Alignment	not modelled	75.4	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
61	c5m7nA_	Alignment	not modelled	74.9	8	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
62	c4l5eA_	Alignment	not modelled	74.2	8	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
63	c5nwtM_	Alignment	not modelled	74.1	14	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor,rna polymerase sigma-54 PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
64	c2cg4B_	Alignment	not modelled	73.9	15	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
65	c1z4hA_	Alignment	not modelled	72.9	11	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
66	d1etob_	Alignment	not modelled	69.9	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
67	c2p6tH_	Alignment	not modelled	69.4	20	PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
68	c3i4pA_	Alignment	not modelled	68.1	20	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
69	c2ia0A_	Alignment	not modelled	68.1	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
70	c2vzbA_	Alignment	not modelled	67.9	25	PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
71	c2gm4B_	Alignment	not modelled	67.2	15	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
72	c2e7xA_	Alignment	not modelled	67.2	23	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
73	d2cg4a1	Alignment	not modelled	65.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
74	c2r0qF_	Alignment	not modelled	65.8	24	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
75	c4go1A_	Alignment	not modelled	63.3	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
76	c1i1gA_	Alignment	not modelled	62.8	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
77	d1ilga1	Alignment	not modelled	62.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
78	c1h1vA_	Alignment	not modelled	62.3	12	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
79	c1j5yA_	Alignment	not modelled	62.2	24	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
80	d1hlva1	Alignment	not modelled	62.1	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
81	c2vz4A	Alignment	not modelled	61.2	6	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
82	c2e1cA	Alignment	not modelled	59.6	20	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2_complex
83	c5ui5I	Alignment	not modelled	59.2	15	PDB header: transcription/dna Chain: I: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: crystal structure of aquifex aeolicus sigman bound to promoter dna
84	c2l4aA	Alignment	not modelled	58.8	23	PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp
85	c2cfxD	Alignment	not modelled	58.7	20	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
86	c6gh5M	Alignment	not modelled	58.3	14	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
87	c2fjrB	Alignment	not modelled	57.8	7	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
88	c2dbbA	Alignment	not modelled	56.8	23	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
89	c4pcqC	Alignment	not modelled	56.7	20	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
90	c2gqgB	Alignment	not modelled	54.0	23	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
91	d1bw6a	Alignment	not modelled	53.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
92	d2cyya1	Alignment	not modelled	52.7	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
93	c5af3A	Alignment	not modelled	52.0	10	PDB header: dna binding Chain: A: PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
94	c2w48D	Alignment	not modelled	51.9	24	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
95	c5c8eC	Alignment	not modelled	51.1	13	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
96	c6fkqC	Alignment	not modelled	49.6	22	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
97	c4ifuA	Alignment	not modelled	47.0	15	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
98	d1stza1	Alignment	not modelled	46.9	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
99	d2cfxa1	Alignment	not modelled	46.7	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
100	d1mzba	Alignment	not modelled	46.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FUR-like
101	c5byhM	Alignment	not modelled	45.0	20	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor; PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
102	c2q0oA	Alignment	not modelled	44.2	10	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
103	c4czdA	Alignment	not modelled	43.2	14	PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
104	d1i9ia	Alignment	not modelled	43.1	22	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain

						Family: Terminase gpNU1 subunit domain
105	c2zhhA_	Alignment	not modelled	41.7	9	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
106	d1a04a1	Alignment	not modelled	41.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
107	c1ojdD_	Alignment	not modelled	40.6	18	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for the conformational switch necessary for sigma54 binding
108	c5j9iH_	Alignment	not modelled	40.2	24	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
109	c5jaaB_	Alignment	not modelled	39.9	24	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex
110	c3bd1B_	Alignment	not modelled	39.8	6	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
111	c4etsB_	Alignment	not modelled	39.5	11	PDB header: metal binding protein Chain: B: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of campylobacter jejuni ferric uptake regulator
112	c3rkxA_	Alignment	not modelled	39.2	19	PDB header: ligase Chain: A: PDB Molecule: biotin-[acetyl-coa-carboxylase] ligase; PDBTitle: structural characterisation of staphylococcus aureus biotin protein2 ligase
113	c2m8eA_	Alignment	not modelled	37.7	20	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase
114	d1k78a2	Alignment	not modelled	37.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
115	c3fmyA_	Alignment	not modelled	37.2	5	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)
116	c3t76A_	Alignment	not modelled	37.0	12	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
117	d1rzsA_	Alignment	not modelled	36.5	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
118	c2ewnA_	Alignment	not modelled	36.5	25	PDB header: ligase, transcription Chain: A: PDB Molecule: birA bifunctional protein; PDBTitle: ecoli biotin repressor with co-repressor analog
119	d2ppxA1	Alignment	not modelled	36.4	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
120	c2ppxA_	Alignment	not modelled	36.4	24	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