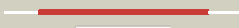





















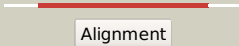

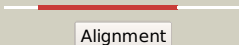

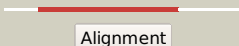



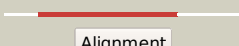

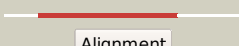

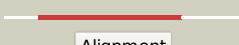





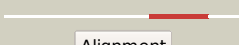
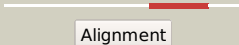


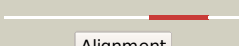




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3056_(dinP)_3416702_3417742
Date	Thu Aug 8 16:20:23 BST 2019
Unique Job ID	39c2573d8ab29f41

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gqcB_	 Alignment		100.0	27	PDB header: transferase/dna Chain: B: PDB Molecule: dna repair protein rev1; PDBTitle: structure of human rev1-dna-dntp ternary complex
2	c4ir1A_	 Alignment		100.0	29	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase iv; PDBTitle: polymerase-dna complex
3	c2oh2B_	 Alignment		100.0	30	PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase kappa; PDBTitle: ternary complex of human dna polymerase
4	c1s97D_	 Alignment		100.0	27	PDB header: transferase/dna Chain: D: PDB Molecule: dna polymerase iv; PDBTitle: dpo4 with gt mismatch
5	c3mr2A_	 Alignment		100.0	27	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
6	c1jihA_	 Alignment		100.0	20	PDB header: translation Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: yeast dna polymerase eta
7	c2r8kB_	 Alignment		100.0	20	PDB header: replication, transferase/dna Chain: B: PDB Molecule: dna polymerase eta; PDBTitle: structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpp)-cisplatin containing dna
8	c1t94B_	 Alignment		100.0	30	PDB header: replication Chain: B: PDB Molecule: polymerase (dna directed) kappa; PDBTitle: crystal structure of the catalytic core of human dna polymerase kappa
9	c2aq4A_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: dna repair protein rev1; PDBTitle: ternary complex of the catalytic core of rev1 with dna and dctp.
10	c1t3nB_	 Alignment		100.0	27	PDB header: replication/dna Chain: B: PDB Molecule: polymerase (dna directed) iota; PDBTitle: structure of the catalytic core of dna polymerase iota in complex with2 dna and dttp
11	c2fiiA_	 Alignment		100.0	29	PDB header: replication/dna Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: ternary complex of human dna polymerase iota with dna and dttp

12	c1k1qA	 Alignment		100.0	26	PDB header: transcription Chain: A: PDB Molecule: dbh protein; PDBTitle: crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
13	d1t94a2	 Alignment		100.0	35	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
14	d1jx4a2	 Alignment		100.0	31	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
15	d1jiha2	 Alignment		100.0	26	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
16	c4dezA	 Alignment		100.0	72	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iv 1; PDBTitle: structure of msdpo4
17	d1k1sa2	 Alignment		100.0	30	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
18	d1zeta2	 Alignment		100.0	30	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
19	d1im4a	 Alignment		100.0	31	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
20	d1unnc	 Alignment		99.6	21	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
21	d1t94a1	 Alignment	not modelled	99.4	24	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
22	d1zeta1	 Alignment	not modelled	99.3	16	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
23	d1jiha1	 Alignment	not modelled	98.9	8	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
24	d1jx4a1	 Alignment	not modelled	98.4	17	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
25	d1k1sa1	 Alignment	not modelled	98.1	22	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
26	d1pzna1	 Alignment	not modelled	96.7	32	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
27	d1szpa1	 Alignment	not modelled	96.6	23	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain

28	d2i1qa1	Alignment	not modelled	96.3	24	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
29	d1gm5a2	Alignment	not modelled	95.9	40	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain
30	c2zj8A	Alignment	not modelled	95.6	17	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
31	d1b22a	Alignment	not modelled	95.6	22	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
32	c1b22A	Alignment	not modelled	95.6	22	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
33	c3bqsB	Alignment	not modelled	95.4	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from2 listeria monocytogenes, trigonal form
34	d1lb2b	Alignment	not modelled	95.3	17	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
35	d1doqa	Alignment	not modelled	95.2	25	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
36	d2p6ra2	Alignment	not modelled	95.1	13	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Achaeal helicase C-terminal domain
37	d1z3eb1	Alignment	not modelled	94.8	23	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
38	c1t4gA	Alignment	not modelled	94.6	31	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: atpase in complex with amp-pnp
39	d1cooa	Alignment	not modelled	94.5	16	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
40	c5agaA	Alignment	not modelled	93.9	15	PDB header: transferase Chain: A: PDB Molecule: dna polymerase theta; PDBTitle: crystal structure of the helicase domain of human dna2 polymerase theta in complex with amppnp
41	c2bcuA	Alignment	not modelled	93.9	20	PDB header: transferase, lyase/dna Chain: A: PDB Molecule: dna polymerase lambda; PDBTitle: dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
42	c1kdhA	Alignment	not modelled	93.7	17	PDB header: transferase/dna Chain: A: PDB Molecule: terminal deoxynucleotidyltransferase short PDBTitle: binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
43	c2ihmA	Alignment	not modelled	93.6	32	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: polymerase mu in ternary complex with gapped 11mer dna duplex and2 bound incoming nucleotide
44	d1jmsa3	Alignment	not modelled	93.2	25	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
45	c1pznA	Alignment	not modelled	93.2	28	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
46	c1nomA	Alignment	not modelled	93.0	29	PDB header: nucleotidyltransferase Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mnc12 (5 millimolar)
47	d2fmpa2	Alignment	not modelled	93.0	25	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
48	d2bcqa2	Alignment	not modelled	92.9	21	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
49	d2vana1	Alignment	not modelled	92.9	29	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
50	c1gm5A	Alignment	not modelled	92.7	43	PDB header: helicase Chain: A: PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
51	d1szpb1	Alignment	not modelled	92.7	24	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
52	d2q0zx1	Alignment	not modelled	92.5	13	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Sec63 N-terminal domain
53	c8iczA	Alignment	not modelled	92.4	25	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase beta (e.c.2.7.7.7)); PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mnc12 (5 millimolar), and lithium sulfate4 (75 millimolar)
						Fold: SAM domain-like

54	d2aq0a1	Alignment	not modelled	92.3	20	Superfamily: RuvA domain 2-like Family: Hef domain-like
55	c2va8A	Alignment	not modelled	92.3	18	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
56	c2w9mB	Alignment	not modelled	92.0	29	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
57	c4p4oA	Alignment	not modelled	91.9	32	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
58	c4bgdA	Alignment	not modelled	91.6	10	PDB header: transcription Chain: A: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of brr2 in complex with the jab1/mpn domain of prp8
59	c2kz3A	Alignment	not modelled	91.6	22	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein rad5113; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
60	c3im2A	Alignment	not modelled	91.4	10	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: structure of the c-terminal sec63 unit of yeast brr2, p41212 form
61	c5m52B	Alignment	not modelled	91.2	10	PDB header: hydrolase Chain: B: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of yeast brr2 full-length in complex with prp8 jab12 domain
62	c5lqwC	Alignment	not modelled	91.0	10	PDB header: splicing Chain: C: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: yeast activated spliceosome
63	c2maxA	Alignment	not modelled	90.9	18	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: nmr structure of the rna polymerase alpha subunit c-terminal domain2 from helicobacter pylori
64	c5dcaA	Alignment	not modelled	90.8	10	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of yeast full length brr2 in complex with prp8 jab12 domain
65	d2a1ja1	Alignment	not modelled	90.7	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
66	d1kfta	Alignment	not modelled	90.5	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
67	c1kftA	Alignment	not modelled	90.5	21	PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc subunit c; PDBTitle: solution structure of the c-terminal domain of uvrc from e-2 coli
68	d1qw2a	Alignment	not modelled	90.0	38	Fold: Hypothetical protein Ta1206 Superfamily: Hypothetical protein Ta1206 Family: Hypothetical protein Ta1206
69	c2lyhA	Alignment	not modelled	90.0	23	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
70	c2dfIA	Alignment	not modelled	89.4	23	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: crystal structure of left-handed rada filament
71	d1ci4a	Alignment	not modelled	88.7	28	Fold: SAM domain-like Superfamily: Barrier-to-autointegration factor, BAF Family: Barrier-to-autointegration factor, BAF
72	c4f92B	Alignment	not modelled	88.5	13	PDB header: hydrolase Chain: B: PDB Molecule: u5 small nuclear ribonucleoprotein 200 kda helicase; PDBTitle: brr2 helicase region s10871
73	c5tw1T	Alignment	not modelled	88.3	19	PDB header: transcription activator/transferase/dna Chain: T: PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
74	c2p6uA	Alignment	not modelled	88.0	14	PDB header: dna binding protein Chain: A: PDB Molecule: afuHel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
75	c3auoB	Alignment	not modelled	87.9	43	PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase beta family (x family); PDBTitle: dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
76	d2bgwa1	Alignment	not modelled	86.4	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
77	d1x2ia1	Alignment	not modelled	86.4	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
78	c1wcnA	Alignment	not modelled	86.1	24	PDB header: rna-binding protein Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: nmr structure of the carboxyterminal domains of escherichia2 coli nusa
79	c5jzcG	Alignment	not modelled	85.9	23	PDB header: dna binding protein Chain: G: PDB Molecule: dna repair protein rad51 homolog 1; PDBTitle: helical filament
						PDB header: signaling protein

80	c1w25B_	Alignment	not modelled	84.5	21	Chain: B; PDB Molecule: staked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp PDB header: signaling protein
81	c3ezuA_	Alignment	not modelled	83.9	23	Chain: A; PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution PDB header: hydrolase/dna
82	c4bxoB_	Alignment	not modelled	83.6	23	Chain: B; PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex PDB header: signaling protein
83	c3i5aA_	Alignment	not modelled	83.4	19	Chain: A; PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae PDB header: transcription/dna/rna
84	c5i2dA_	Alignment	not modelled	82.8	26	Chain: A; PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: crystal structure of t. thermophilus tthb099 class ii transcription2 activation complex: tap-rpo PDB header: hydrolase
85	c2nrzB_	Alignment	not modelled	82.4	18	Chain: B; PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrc bound to its2 catalytic divalent cation
86	d2a1jb1	Alignment	not modelled	81.2	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
87	c2q0zX_	Alignment	not modelled	81.1	12	PDB header: protein transport Chain: X; PDB Molecule: protein pro2281; PDBTitle: crystal structure of q9p172/sec63 from homo sapiens. northeast2 structural genomics target hr1979.
88	c3ldaA_	Alignment	not modelled	80.2	24	PDB header: dna binding protein Chain: A; PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
89	d1dgsa1	Alignment	not modelled	79.8	30	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
90	c6ah0D_	Alignment	not modelled	78.8	13	PDB header: splicing Chain: D; PDB Molecule: u5 small nuclear ribonucleoprotein 200 kda helicase; PDBTitle: the cryo-em structure of the precursor of human pre-catalytic2 spliceosome (pre-b complex) PDB header: transcription
91	c6flqF_	Alignment	not modelled	75.9	19	Chain: F; PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: cryoem structure of e.coli rna polymerase paused elongation complex2 bound to nusa PDB header: structural genomics, unknown function
92	c1wwuA_	Alignment	not modelled	75.6	22	Chain: A; PDB Molecule: hypothetical protein flj21935; PDBTitle: solution structure of the sam_pnt domain of human protein2 flj21935
93	c1szpC_	Alignment	not modelled	74.8	24	PDB header: dna binding protein Chain: C; PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
94	c4qlxA_	Alignment	not modelled	73.9	26	PDB header: ligase/ligase inhibitor/dna Chain: A; PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
95	c2owoA_	Alignment	not modelled	72.9	26	PDB header: ligase/dna Chain: A; PDB Molecule: dna ligase; PDBTitle: last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
96	d1bvsa2	Alignment	not modelled	71.4	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
97	c4bxoA_	Alignment	not modelled	71.2	5	PDB header: hydrolase/dna Chain: A; PDB Molecule: fanconi anemia group m protein; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex PDB header: hydrolase
98	c2mutA_	Alignment	not modelled	71.0	19	Chain: A; PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
99	c2csdB_	Alignment	not modelled	70.3	36	PDB header: isomerase Chain: B; PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
100	c2h5xA_	Alignment	not modelled	68.8	17	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis PDB header: transcription/dna
101	c3iydA_	Alignment	not modelled	68.6	19	Chain: A; PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: three-dimensional em structure of an intact activator-dependent2 transcription initiation complex PDB header: signaling protein
102	c3breA_	Alignment	not modelled	66.3	21	Chain: A; PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702 PDB header: hydrolase
103	c6d9mA_	Alignment	not modelled	65.0	26	Chain: A; PDB Molecule: fusion protein of endolysin,response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef PDB header: gene regulation
104	c1d8IA_	Alignment	not modelled	64.3	21	Chain: A; PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region

						lacking2 domain iii
105	c4mtnA_	Alignment	not modelled	64.1	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcription termination factor nusa; PDBTitle: crystal structure of transcription termination factor nusa from 2 planctomyces limnophilus dsm 3776
106	c1dgsB_	Alignment	not modelled	63.7	30	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
107	c1ixrA_	Alignment	not modelled	59.1	30	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
108	c1ixrB_	Alignment	not modelled	57.5	21	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
109	c5m59C_	Alignment	not modelled	55.8	20	PDB header: splicing Chain: C: PDB Molecule: pre-mrna splicing helicase-like protein; PDBTitle: crystal structure of chaetomium thermophilum brr2 helicase core in2 complex with prp8 jab1 domain
110	c1vddC_	Alignment	not modelled	55.5	47	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
111	c5z2vB_	Alignment	not modelled	52.9	40	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
112	d1vdda_	Alignment	not modelled	52.0	47	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
113	c5zvqA_	Alignment	not modelled	51.9	53	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
114	d2axtu1	Alignment	not modelled	50.9	17	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: PsbU-like
115	c1s5lu_	Alignment	not modelled	49.6	17	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
116	d1ykga1	Alignment	not modelled	49.4	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
117	c2e8mA_	Alignment	not modelled	48.7	19	PDB header: signaling protein Chain: A: PDB Molecule: epidermal growth factor receptor kinase PDBTitle: solution structure of the c-terminal sam-domain of 2 epidermal growth receptor pathway substrate 8
118	c5llxB_	Alignment	not modelled	47.8	20	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase (ggdef) domain-containing protein; PDBTitle: bacteriophytochrome activated diguanylyl cyclase from idiomarina2 species a28l with gtp bound
119	d1d8ba_	Alignment	not modelled	47.5	22	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
120	d2edua1	Alignment	not modelled	43.0	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like