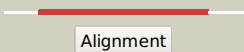

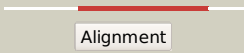



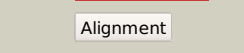
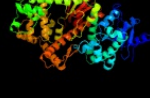


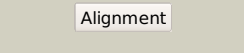

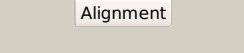



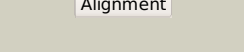

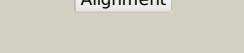

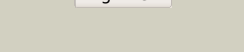


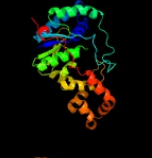
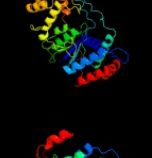





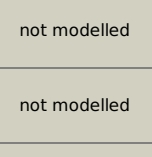


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1629_(polA)_1830672_1833386
Date	Fri Aug 2 13:30:22 BST 2019
Unique Job ID	6686f8aa9529b57f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1cmwA_	 Alignment		100.0	41	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain
2	c4xviA_	 Alignment		100.0	30	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase nu; PDBTitle: binary complex of human polymerase nu and dna with the finger domain2 ajar
3	c1njzA_	 Alignment		100.0	40	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase i; PDBTitle: cytosine-thymine mismatch at the polymerase active site
4	c4x0pB_	 Alignment		100.0	28	PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase theta; PDBTitle: ternary complex of human dna polymerase theta c-terminal domain2 binding ddatp opposite a tetrahydrofuran ap site analog
5	c4ktqA_	 Alignment		100.0	40	PDB header: transferase/dna Chain: A: PDB Molecule: protein (large fragment of dna polymerase i); PDBTitle: binary complex of the large fragment of dna polymerase i2 from t. aquaticus bound to a primer/template dna
6	c2kzzA_	 Alignment		100.0	37	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: klenow fragment with normal substrate and zinc only
7	c5dkuB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: prex dna polymerase; PDBTitle: c-terminal his tagged appol exonuclease mutant
8	d2hhva2	 Alignment		100.0	47	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
9	d1qtma2	 Alignment		100.0	46	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
10	c1tk0A_	 Alignment		100.0	22	PDB header: transferase/electron transport/dna Chain: A: PDB Molecule: dna polymerase; PDBTitle: t7 dna polymerase ternary complex with 8 oxo guanosine and ddctp at2 the insertion site
11	d1kfsa2	 Alignment		100.0	45	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I

12	d1x9ma2	Alignment		100.0	25	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
13	c3zddA	Alignment		100.0	29	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
14	c6c34A	Alignment		100.0	36	PDB header: dna binding protein Chain: A: PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
15	c2ihnA	Alignment		100.0	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
16	c1ut8B	Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
17	c1rxvA	Alignment		100.0	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
18	d1cmwa2	Alignment		100.0	42	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
19	c1a77A	Alignment		100.0	21	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
20	c3q8lA	Alignment		100.0	21	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+
21	c1b43A	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
22	c4wa8A	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: methanopyrus kandleri fen-1 nuclease
23	c3oryA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
24	c2izoA	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
25	c4ztuA	Alignment	not modelled	100.0	21	PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna polymerase subunit gamma-1; PDBTitle: structural basis for processivity and antiviral drug toxicity in human2 mitochondrial dna replicase
26	c1ul1Y	Alignment	not modelled	100.0	21	PDB header: hydrolase/dna binding protein Chain: Y: PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
27	d1xo1a2	Alignment	not modelled	100.0	23	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
28	d1tfra2	Alignment	not modelled	100.0	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
29	c3nea7	Alignment	not modelled	100.0	20	PDB header: hydrolase/dna Chain: Z: PDB Molecule: exonuclease 1;

29	c3qea2_	Alignment	not modelled	100.0	20	PDBTitle: crystal structure of human exonuclease 1 exo1 (wt) in complex with dna2 (complex ii)
30	c4q0rB_	Alignment	not modelled	100.0	20	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna repair protein rad2; PDBTitle: the catalytic core of rad2 (complex i)
31	c1yt3A_	Alignment	not modelled	100.0	13	PDB header: hydrolase,translation Chain: A: PDB Molecule: ribonuclease d; PDBTitle: crystal structure of escherichia coli rnase d, an2 exoribonuclease involved in structured rna processing
32	c5t9jB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: flap endonuclease gen homolog 1; PDBTitle: crystal structure of human gen1 in complex with holliday junction dna2 in the upper interface
33	d1cmwa1	Alignment	not modelled	100.0	36	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
34	c5c0xK_	Alignment	not modelled	100.0	12	PDB header: hydrolase/rna Chain: K: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of a 12-subunit nuclear exosome complex bound to structured2 rna
35	c3ikmD_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: D: PDB Molecule: dna polymerase subunit gamma-1; PDBTitle: crystal structure of human mitochondrial dna polymerase holoenzyme
36	d2hhva1	Alignment	not modelled	99.9	23	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
37	c5zo4B_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: putative 3'-5' exonuclease family protein; PDBTitle: inactive state of the nuclease
38	c4oo1j_	Alignment	not modelled	99.9	10	PDB header: hydrolase/rna Chain: J: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of an rrp6-rna exosome complex bound to poly(a) rna
39	d1xo1a1	Alignment	not modelled	99.9	26	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
40	d1kfsa1	Alignment	not modelled	99.9	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
41	c5cngA_	Alignment	not modelled	99.8	20	PDB header: replication Chain: A: PDB Molecule: nuclease-like protein; PDBTitle: crystal structure of the holliday junction-resolving enzyme gen1 (wt)2 in complex with product dna, mg2+ and mn2+ ions
42	d1yt3a3	Alignment	not modelled	99.8	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
43	d1ul1x1	Alignment	not modelled	99.8	23	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
44	d1a77a1	Alignment	not modelled	99.8	21	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
45	d1b43a1	Alignment	not modelled	99.8	21	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
46	d1mc8a1	Alignment	not modelled	99.7	21	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
47	d1rxwa1	Alignment	not modelled	99.7	27	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
48	c3cymA_	Alignment	not modelled	99.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bad_0989; PDBTitle: crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
49	d2hbka2	Alignment	not modelled	99.7	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
50	d1a77a2	Alignment	not modelled	99.7	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
51	d1rxwa2	Alignment	not modelled	99.7	20	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
52	c5c0wK_	Alignment	not modelled	99.7	14	PDB header: hydrolase/rna Chain: K: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of a 12-subunit nuclear exosome complex bound to single-2 stranded rna substrates
53	c2e6mA_	Alignment	not modelled	99.6	11	PDB header: hydrolase Chain: A: PDB Molecule: werner syndrome atp-dependent helicase homolog; PDBTitle: structure of mouse werner exonuclease domain
54	c2hbka_	Alignment	not modelled	99.6	14	PDB header: hydrolase, gene regulation Chain: A: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of the yeast nuclear exosome component, rrp6p, reveals an2 interplay between the active site and the hrdc domain; protein in3 complex with mn
55	c4nlbA_	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: ribosomal rna processing protein 6; PDBTitle: crystal structure of the catalytic core of rrp6 from trypanosoma2 brucei

56	d1b43a2	Alignment	not modelled	99.6	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
57	d1mc8a2	Alignment	not modelled	99.6	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
58	c3sahA	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: A: PDB Molecule: exosome component 10; PDBTitle: crystal structure of the human rrp6 catalytic domain with y436a2 mutation in the catalytic site
59	d1ul1x2	Alignment	not modelled	99.6	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
60	c6k1dB	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: B: PDB Molecule: exonuclease 3'-5' domain-containing protein 2; PDBTitle: crystal structure of exd2 exonuclease domain soaked in mn and gmp
61	c5fiqE	Alignment	not modelled	99.3	9	PDB header: hydrolase Chain: E: PDB Molecule: exd1; PDBTitle: exonuclease domain-containing 1 (exd1) in the native conformation
62	d1vk0a	Alignment	not modelled	99.1	11	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
63	c5v5fA	Alignment	not modelled	99.0	12	PDB header: transferase Chain: A: PDB Molecule: at3g11770; PDBTitle: crystal structure of rice1 (pnt2)
64	d1x9ma1	Alignment	not modelled	98.7	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
65	c5mq9A	Alignment	not modelled	98.0	19	PDB header: translation Chain: A: PDB Molecule: uncharacterized protein yacp; PDBTitle: crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
66	d1qhta1	Alignment	not modelled	97.9	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
67	d1wn7a1	Alignment	not modelled	97.9	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
68	d1tgoa1	Alignment	not modelled	97.8	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
69	c5z9xA	Alignment	not modelled	97.8	23	PDB header: plant protein/rna Chain: A: PDB Molecule: small rna degrading nuclease 1; PDBTitle: arabidopsis small rna degrading nuclease 1 in complex with an rna2 substrate
70	c2is3B	Alignment	not modelled	97.8	13	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease t; PDBTitle: crystal structure of escherichia coli rnase t
71	d1d5aa1	Alignment	not modelled	97.7	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
72	d2qxfa1	Alignment	not modelled	97.5	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
73	c4rg8A	Alignment	not modelled	97.5	21	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease i; PDBTitle: structural and biochemical studies of a moderately thermophilic2 exonuclease i from methylocaldum szegediense
74	c2p1jB	Alignment	not modelled	97.5	15	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii polc-type; PDBTitle: crystal structure of a polc-type dna polymerase iii exonuclease domain2 from thermotoga maritima
75	c5mdnB	Alignment	not modelled	97.3	17	PDB header: transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: structure of the family b dna polymerase from the hyperthermophilic2 archaeon pyrobaculum calidifontis
76	d1wlja	Alignment	not modelled	97.3	24	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
77	d2f96a1	Alignment	not modelled	97.2	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
78	d1s5ja1	Alignment	not modelled	97.2	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
79	c1d5aA	Alignment	not modelled	97.1	12	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase); PDBTitle: crystal structure of an archaeobacterial dna polymerase2 d.tok. deposition of second native structure at 2.43 angstrom
80	d1x2ia1	Alignment	not modelled	97.1	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
81	d2bgwa1	Alignment	not modelled	97.0	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
82	d1y97a1	Alignment	not modelled	97.0	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease

83	d1noya_	Alignment	not modelled	96.9	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
84	c3u6fA_	Alignment	not modelled	96.8	15	PDB header: hydrolase/dna Chain: A: PDB Molecule: three prime repair exonuclease 1; PDBTitle: mouse trex1 d200n mutant
85	c4czwA_	Alignment	not modelled	96.7	22	PDB header: gene regulation Chain: A: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan2; PDBTitle: structure of the neurospora crassa pan2 catalytic unit (protease and2 nuclease domain)
86	c5fkvD_	Alignment	not modelled	96.7	13	PDB header: transferase Chain: D: PDB Molecule: dna polymerase iii epsilon; PDBTitle: cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
87	c2lyhA_	Alignment	not modelled	96.7	25	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
88	d1dgsa1	Alignment	not modelled	96.6	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
89	d1q8ia1	Alignment	not modelled	96.6	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
90	c2nrzB_	Alignment	not modelled	96.6	32	PDB header: hydrolase Chain: B: PDB Molecule: uvrbc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrC bound to its2 catalytic divalent cation
91	d2a1jb1	Alignment	not modelled	96.6	16	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
92	d1kfta_	Alignment	not modelled	96.5	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
93	c1kftA_	Alignment	not modelled	96.5	23	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
94	c2y35A_	Alignment	not modelled	96.5	21	PDB header: hydrolase/dna Chain: A: PDB Molecule: ld22664p; PDBTitle: crystal structure of xrn1-substrate complex
95	c6r5kA_	Alignment	not modelled	96.4	20	PDB header: rna binding protein Chain: A: PDB Molecule: pan2-pan3 deadenylation complex catalytic subunit pan2; PDBTitle: cryo-em structure of a poly(a) rnp bound to the pan2-pan3 deadenylase
96	c2vwkA_	Alignment	not modelled	96.4	12	PDB header: dna replication Chain: A: PDB Molecule: dna polymerase; PDBTitle: uracil recognition in archaeal dna polymerases captured by2 x-ray crystallography. v93q polymerase variant
97	c5l80B_	Alignment	not modelled	96.4	16	PDB header: rna binding protein Chain: B: PDB Molecule: maternal protein exuperantia,maternal protein exuperantia; PDBTitle: structure of exuperantia exo-like and sam-like domains
98	c2mutA_	Alignment	not modelled	96.3	16	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
99	d1ih7a1	Alignment	not modelled	96.3	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
100	c6fwkB_	Alignment	not modelled	96.2	14	PDB header: dna binding protein Chain: B: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: the crystal structure of pol2core-m644g in complex with dna and an2 incoming nucleotide
101	d1uoca_	Alignment	not modelled	96.2	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF1-like ribonuclease
102	c4wbqA_	Alignment	not modelled	96.2	9	PDB header: rna binding protein Chain: A: PDB Molecule: qde-2-interacting protein; PDBTitle: crystal structure of the exonuclease domain of qip (qde-2 interacting2 protein) solved by native-sad phasing.
103	d3b6oa1	Alignment	not modelled	96.1	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
104	c1s5jA_	Alignment	not modelled	96.1	19	PDB header: transferase Chain: A: PDB Molecule: dna polymerase i; PDBTitle: insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfobolbus solfataricus
105	d1j9aa_	Alignment	not modelled	96.0	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
106	d1cuka2	Alignment	not modelled	95.8	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
107	d2i1qa1	Alignment	not modelled	95.8	21	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
108	c5okiA_	Alignment	not modelled	95.7	15	PDB header: replication Chain: A: PDB Molecule: dna polymerase epsilon catalytic subunit a;

						PDBTitle: crystal structure of the ctf18-1-8 module from ctf18-rfc in complex2 with a 63 kda fragment of dna polymerase epsilon
109	c3iayA_	Alignment	not modelled	95.7	17	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase delta catalytic subunit; PDBTitle: ternary complex of dna polymerase delta
110	c4m8oA_	Alignment	not modelled	95.7	14	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: ternary complex of dna polymerase epsilon with an incoming datp
111	c1ixrB_	Alignment	not modelled	95.6	19	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
112	c1d8iA_	Alignment	not modelled	95.6	27	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
113	c2h5xA_	Alignment	not modelled	95.6	19	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
114	c4qlxA_	Alignment	not modelled	95.5	31	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
115	c2gv9B_	Alignment	not modelled	95.5	12	PDB header: transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the herpes simplex virus type 1 dna polymerase
116	c1q8iA_	Alignment	not modelled	95.3	18	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii; PDBTitle: crystal structure of escherichia coli dna polymerase ii
117	c2p51A_	Alignment	not modelled	95.2	17	PDB header: hydrolase, gene regulation Chain: A: PDB Molecule: spcc18.06c protein; PDBTitle: crystal structure of the s. pombe pop2p deadenylation subunit
118	d1pzna1	Alignment	not modelled	95.2	21	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
119	c1v9pB_	Alignment	not modelled	95.0	29	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
120	c4bxoB_	Alignment	not modelled	95.0	25	PDB header: hydrolase/dna 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