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Email	mdejesus@rockefeller.edu
Description	RVBD1420_(uvrC)_1594048_1595988
Date	Wed Jul 31 22:05:52 BST 2019
Unique Job ID	da41863d3a4b1963

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nrzB_	 Alignment		100.0	46	PDB header: hydrolase Chain: B: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrC bound to its2 catalytic divalent cation
2	c3c65A_	 Alignment		100.0	42	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of bacillus stearothermophilus uvrC 5' endonuclease2 domain
3	c2nrzA_	 Alignment		100.0	50	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal rnahse endonuclease domain of uvrC
4	c1ydzA_	 Alignment		99.9	39	PDB header: dna binding protein Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the giy-yig n-terminal endonuclease domain of2 uvrC from thermotoga maritima: point mutant y19f bound to the3 catalytic divalent cation
5	c2wshC_	 Alignment		99.9	24	PDB header: hydrolase Chain: C: PDB Molecule: endonuclease ii; PDBTitle: structure of bacteriophage t4 endoii e118a mutant
6	c1ydzA_	 Alignment		99.9	42	PDB header: dna binding protein Chain: A: PDB Molecule: uvrC; PDBTitle: crystal structure of the giy-yig n-terminal endonuclease2 domain of uvrC from bacillus caldotenax
7	d1kfta_	 Alignment		99.4	35	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
8	c1kftA_	 Alignment		99.4	35	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
9	d1x2ia1	 Alignment		99.3	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
10	c2lyhA_	 Alignment		99.3	27	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
11	d2aq0a1	 Alignment		99.3	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like

12	d2bgwa1	Alignment		99.3	29	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
13	d2a1jb1	Alignment		99.3	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
14	c2mutA	Alignment		99.2	21	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
15	c4bxoB	Alignment		99.1	20	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
16	d2i1qa1	Alignment		99.0	28	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
17	c4bxoA	Alignment		99.0	12	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
18	d1pzna1	Alignment		98.9	23	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
19	d1mk0a	Alignment		98.9	22	Fold: GIY-YIG endonuclease Superfamily: GIY-YIG endonuclease Family: GIY-YIG endonuclease
20	c2bhnD	Alignment		98.8	30	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
21	d1dgsa1	Alignment	not modelled	98.8	33	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
22	c2zj8A	Alignment	not modelled	98.6	28	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
23	d1szpa1	Alignment	not modelled	98.6	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
24	d1e52a	Alignment	not modelled	98.5	29	Fold: Long alpha-hairpin Superfamily: C-terminal UvrC-binding domain of UvrB Family: C-terminal UvrC-binding domain of UvrB
25	c2owoA	Alignment	not modelled	98.5	27	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
26	c1dgsB	Alignment	not modelled	98.5	33	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filliformis
27	c4glxA	Alignment	not modelled	98.4	27	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
28	c1v9pB	Alignment	not modelled	98.4	33	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
29	c1ixrA	Alignment	not modelled	98.4	23	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva;

						PDBTitle: ruva-ruvb complex
30	c1b22A_	Alignment	not modelled	98.3	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
31	d1b22a_	Alignment	not modelled	98.3	19	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
32	c3c1zA_	Alignment	not modelled	98.2	23	PDB header: dna binding protein Chain: A: PDB Molecule: dna integrity scanning protein disa; PDBTitle: structure of the ligand-free form of a bacterial dna damage sensor2 protein
33	d1cuka2	Alignment	not modelled	98.1	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
34	d1ixra1	Alignment	not modelled	98.0	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
35	c6flqF_	Alignment	not modelled	98.0	17	PDB header: transcription Chain: F: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: cryoem structure of e.coli rna polymerase paused elongation complex2 bound to nusa
36	d1szpb1	Alignment	not modelled	97.8	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
37	c1ixrB_	Alignment	not modelled	97.7	26	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
38	c1hjpA_	Alignment	not modelled	97.7	21	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
39	d1bvsa2	Alignment	not modelled	97.6	30	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
40	c4nspA_	Alignment	not modelled	97.6	21	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: crystal structure of human endov
41	c1d8IA_	Alignment	not modelled	97.6	21	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
42	c2h5xA_	Alignment	not modelled	97.6	32	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
43	c3dlbA_	Alignment	not modelled	97.6	13	PDB header: nucleic acid binding protein/dna Chain: A: PDB Molecule: argonaute; PDBTitle: crystal structure of the guide-strand-containing argonaute2 protein silencing complex
44	d2a1ja1	Alignment	not modelled	97.6	28	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
45	c2w36B_	Alignment	not modelled	97.5	20	PDB header: hydrolase Chain: B: PDB Molecule: endonuclease v; PDBTitle: structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
46	c2va8A_	Alignment	not modelled	97.4	15	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
47	c2p6uA_	Alignment	not modelled	97.4	17	PDB header: dna binding protein Chain: A: PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
48	d1qoja_	Alignment	not modelled	97.2	35	Fold: Long alpha-hairpin Superfamily: C-terminal UvrC-binding domain of UvrB Family: C-terminal UvrC-binding domain of UvrB
49	d2axtu1	Alignment	not modelled	97.1	21	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
50	c1s5lu_	Alignment	not modelled	97.1	16	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
51	c2d7dB_	Alignment	not modelled	97.1	50	PDB header: hydrolase/dna Chain: B: PDB Molecule: 40-mer from uvrabc system protein b; PDBTitle: structural insights into the cryptic dna dependent atp-ase2 activity of uvrB
52	c5agaA_	Alignment	not modelled	97.0	20	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
53	c4xpuA_	Alignment	not modelled	97.0	25	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: the crystal structure of endov from e.coli
54	d2p6ra2	Alignment	not modelled	96.8	18	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Achaeal helicase C-terminal domain
55	c2lwfA_	Alignment	not modelled	96.8	26	PDB header: hydrolase Chain: A: PDB Molecule: monothiol glutaredoxin-s16, chloroplastic; PDBTitle: structure of n-terminal domain of a plant grx
						PDB header: hydrolase

56	c3gocB_	Alignment	not modelled	96.8	27	Chain: B: PDB Molecule: endonuclease v; PDBTitle: crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis, northeast structural genomics consortium target svr196
57	c3ga2A_	Alignment	not modelled	96.7	18	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: crystal structure of the endonuclease_v (bsu36170) from bacillus2 subtilis, northeast structural genomics consortium target sr624
58	c2ziuA_	Alignment	not modelled	96.6	16	PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
59	c3zddA_	Alignment	not modelled	96.6	17	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
60	c2csdB_	Alignment	not modelled	96.5	23	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
61	c2ihmA_	Alignment	not modelled	96.4	23	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
62	d2duya1	Alignment	not modelled	96.4	30	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
63	c2zixA_	Alignment	not modelled	96.3	29	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: crystal structure of the mus81-eme1 complex
64	c3auoB_	Alignment	not modelled	96.2	27	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
65	d1xo1a1	Alignment	not modelled	96.2	23	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
66	c3ho1A_	Alignment	not modelled	96.1	11	PDB header: nucleic acid binding protein/dna/rna Chain: A: PDB Molecule: argonaute; PDBTitle: crystal structure of t. thermophilus argonaute n546 mutant protein2 complexed with dna guide strand and 12-nt rna target strand
67	c2w9mB_	Alignment	not modelled	96.0	16	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
68	c1ut8B_	Alignment	not modelled	96.0	23	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
69	c6qzkA_	Alignment	not modelled	96.0	12	PDB header: hydrolase Chain: A: PDB Molecule: clostridium butyricum argonaute; PDBTitle: structure of clostridium butyricum argonaute bound to a guide dna (5'2 deoxycytidine) and a 19-mer target dna
70	c6c34A_	Alignment	not modelled	95.8	23	PDB header: dna binding protein Chain: A: PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
71	d1a77a1	Alignment	not modelled	95.8	31	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
72	c1kdhA_	Alignment	not modelled	95.8	19	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
73	c3nicA_	Alignment	not modelled	95.8	33	PDB header: hydrolase/dna Chain: A: PDB Molecule: eco29kir; PDBTitle: dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
74	c5o19A_	Alignment	not modelled	95.8	19	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
75	c3mr2A_	Alignment	not modelled	95.7	13	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)
76	d2edua1	Alignment	not modelled	95.7	22	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
77	c5guhA_	Alignment	not modelled	95.5	17	PDB header: hydrolase/rna Chain: A: PDB Molecule: piwi; PDBTitle: crystal structure of silkworm piwi-clade argonaute siwi bound to pirna
78	d1ul1x1	Alignment	not modelled	95.5	25	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
79	d3bzka1	Alignment	not modelled	95.3	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HHH-containing domain-like
80	d1rxwa1	Alignment	not modelled	95.3	22	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
81	c3hcuA_	Alignment	not modelled	95.1	21	PDB header: transferase, lyase/dna Chain: A: PDB Molecule: dna polymerase lambda;

81	c20c0A	Alignment	not modelled	93.1	41	PDBTitle: dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
82	d1u04a2	Alignment	not modelled	95.0	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: PIWI domain
83	c2aq4A	Alignment	not modelled	94.9	29	PDB header: transferase Chain: A: PDB Molecule: dna repair protein rev1; PDBTitle: ternary complex of the catalytic core of rev1 with dna and dctp.
84	c8ic3A	Alignment	not modelled	94.9	21	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)
85	c5zb8B	Alignment	not modelled	94.8	27	PDB header: dna binding protein Chain: B: PDB Molecule: pfluendoq; PDBTitle: crystal structure of the novel lesion-specific endonuclease pfluendoq2 from pyrococcus furiosus
86	d1b43a1	Alignment	not modelled	94.7	12	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
87	d2csba4	Alignment	not modelled	94.6	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
88	c1rxvA	Alignment	not modelled	94.4	21	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
89	c1zq2A	Alignment	not modelled	94.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0213 protein bh0048; PDBTitle: solution nmr structure of the upf0213 protein bh0048 from2 bacillus halodurans. northeast structural genomics target3 bhr2.
90	d1mc8a1	Alignment	not modelled	94.3	17	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
91	c1t4gA	Alignment	not modelled	94.2	26	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: atpase in complex with amp-pnp
92	c4flnA	Alignment	not modelled	94.1	19	PDB header: rna binding protein/rna Chain: A: PDB Molecule: kpaggo; PDBTitle: crystal structure of kluyveromyces polysporus argonaute with a guide2 rna
93	c3q81A	Alignment	not modelled	93.9	26	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+
94	c5i4aC	Alignment	not modelled	93.9	10	PDB header: rna binding protein/rna Chain: C: PDB Molecule: argonaute protein; PDBTitle: x-ray crystal structure of marinitoga piezophila argonaute in complex2 with 5' oh guide rna
95	c4mntA	Alignment	not modelled	93.7	21	PDB header: transcription regulator Chain: A: PDB Molecule: transcription termination factor nusa; PDBTitle: crystal structure of transcription termination factor nusa from2 planctomyces limnophilus dsm 3776
96	c1a77A	Alignment	not modelled	93.6	32	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
97	c3majA	Alignment	not modelled	93.6	25	PDB header: dna binding protein Chain: A: PDB Molecule: dna processing chain a; PDBTitle: crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
98	c1nomA	Alignment	not modelled	93.6	21	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)
99	d2csba3	Alignment	not modelled	93.5	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
100	c1ywlA	Alignment	not modelled	93.1	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0213 protein ef2693; PDBTitle: solution nmr structure of the protein ef2693 from e.2 faecalis: northeast structural genomics consortium target3 efr36
101	c1b43A	Alignment	not modelled	93.0	13	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
102	d1cmwa1	Alignment	not modelled	92.9	31	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
103	d2q0zx1	Alignment	not modelled	92.9	16	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Sec63 N-terminal domain
104	d1t94a2	Alignment	not modelled	92.9	15	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
105	c5theA	Alignment	not modelled	92.8	16	PDB header: rna binding protein/rna Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the c-terminal lobe of a budding yeast argonaute
106	c5lm7A	Alignment	not modelled	92.7	17	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: crystal structure of the lambda n-nus factor complex
						PDB header: hydrolase

107	c4wa8A_	Alignment	not modelled	92.7	41	Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: methanopyrus kandleri fen-1 nuclease
108	c1ul1Y_	Alignment	not modelled	92.7	26	PDB header: hydrolase/dna binding protein Chain: Y: PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
109	c4f92B_	Alignment	not modelled	92.5	16	PDB header: hydrolase Chain: B: PDB Molecule: u5 small nuclear ribonucleoprotein 200 kda helicase; PDBTitle: brr2 helicase region s1087I
110	c4bgdA_	Alignment	not modelled	92.4	7	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
111	c1t3nB_	Alignment	not modelled	92.3	17	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
112	c1pznA_	Alignment	not modelled	92.3	23	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
113	c2izoA_	Alignment	not modelled	92.3	23	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
114	c5m52B_	Alignment	not modelled	92.0	7	PDB header: hydrolase Chain: B: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of yeast brr2 full-lenght in complex with prp8 jab12 domain
115	c5lqwC_	Alignment	not modelled	92.0	7	PDB header: splicing Chain: C: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: yeast activated spliceosome
116	c2r8kB_	Alignment	not modelled	91.9	16	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(gpg)-cisplatin containing dna
117	c4q0rB_	Alignment	not modelled	91.9	19	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna repair protein rad2; PDBTitle: the catalytic core of rad2 (complex i)
118	c4ei3A_	Alignment	not modelled	91.9	19	PDB header: hydrolase/rna Chain: A: PDB Molecule: protein argonaute-2; PDBTitle: crystal structure of human argonaute2
119	c2oceA_	Alignment	not modelled	91.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
120	c3im2A_	Alignment	not modelled	91.7	7	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