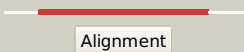

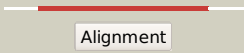



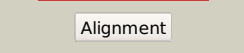



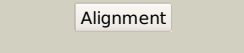

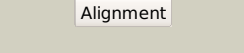



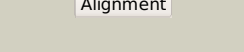

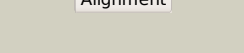

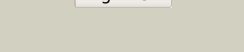

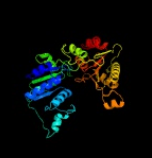



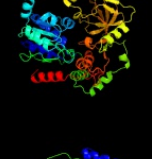

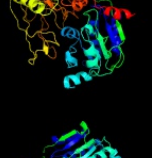
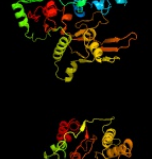
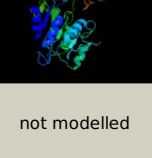


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0629c_(recD)_720008_721735
Date	Fri Jul 26 01:50:19 BST 2019
Unique Job ID	44c504c57012a6c8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ld2D_	 Alignment		100.0	37	PDB header: hydrolase Chain: D; PDB Molecule: recbcd enzyme subunit recd; PDBTitle: cryo-em structure of recbcd+dna complex revealing activated nuclease2 domain
2	c3gp8A_	 Alignment		100.0	29	PDB header: hydrolase/dna Chain: A; PDB Molecule: exodeoxyribonuclease v, subunit recd, putative; PDBTitle: crystal structure of the binary complex of recd2 with dna
3	c1w36G_	 Alignment		100.0	37	PDB header: recombination Chain: G; PDB Molecule: exodeoxyribonuclease v alpha chain; PDBTitle: recbcd:dna complex
4	c3e1sA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A; PDB Molecule: exodeoxyribonuclease v, subunit recd; PDBTitle: structure of an n-terminal truncation of deinococcus radiodurans recd2
5	c5n8oA_	 Alignment		100.0	20	PDB header: transferase Chain: A; PDB Molecule: dna helicase i; PDBTitle: cryo em structure of the conjugative relaxase trai of the f/r1 plasmid2 system
6	d1w36d1	 Alignment		100.0	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
7	c5eaxB_	 Alignment		100.0	23	PDB header: hydrolase/dna Chain: B; PDB Molecule: dna replication atp-dependent helicase/nuclease dna2; PDBTitle: crystal structure of dna2 in complex with an ssdna
8	c2xzlA_	 Alignment		100.0	22	PDB header: hydrolase/rna Chain: A; PDB Molecule: atp-dependent helicase nam7; PDBTitle: upf1-rna complex
9	c5wwpA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
10	c2wjyA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
11	c5wwpB_	 Alignment		100.0	19	PDB header: hydrolase Chain: B; PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)

12	c4b3gA_	Alignment		100.0	23	PDB header: hydrolase/rna Chain: A: PDB Molecule: dna-binding protein smubp-2; PDBTitle: crystal structure of ighmbp2 helicase in complex with rna
13	c2gk7A_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: structural and functional insights into the human upf1 helicase core
14	c5mznA_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: helicase sen1,helicase sen1; PDBTitle: helicase sen1
15	c4pj3A_	Alignment		100.0	18	PDB header: rna binding protein Chain: A: PDB Molecule: intron-binding protein aquarius; PDBTitle: structural insight into the function and evolution of the spliceosomal2 helicase aquarius, structure of aquarius in complex with amppnp
16	c5ftbA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: tpr domain protein; PDBTitle: crystal structure of pif1 helicase from bacteroides in2 complex with amppnp
17	c3upuC_	Alignment		100.0	22	PDB header: hydrolase/dna Chain: C: PDB Molecule: atp-dependent dna helicase dda; PDBTitle: crystal structure of the t4 phage sf1b helicase dda
18	c5fhhA_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of human pif1 helicase domain residues 200-641
19	c5o6dB_	Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of scpif1 in complex with polydt and atpgs
20	c3jb9X_	Alignment		100.0	18	PDB header: rna binding protein/rna Chain: X: PDB Molecule: pre-mrna-splicing factor cwf11; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
21	c4n0oC_	Alignment	not modelled	100.0	28	PDB header: hydrolase/dna Chain: C: PDB Molecule: replicase polyprotein 1ab; PDBTitle: complex structure of arterivirus nonstructural protein 10 (helicase)2 with dna
22	c2is6B_	Alignment	not modelled	100.0	27	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of uvrd-dna-adpmgf3 ternary complex
23	c4c30I_	Alignment	not modelled	100.0	24	PDB header: hydrolase/dna Chain: I: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of deinococcus radiodurans uvrd in2 complex with dna, form 2
24	c1uaaB_	Alignment	not modelled	100.0	30	PDB header: hydrolase/dna Chain: B: PDB Molecule: protein (atp-dependent dna helicase rep.); PDBTitle: e. coli rep helicase/dna complex
25	c1pjrA_	Alignment	not modelled	100.0	22	PDB header: helicase Chain: A: PDB Molecule: pcra; PDBTitle: structure of dna helicase
26	c3ifuA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of e. coli uvrd
27	c3vkwA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: replicase large subunit; PDBTitle: crystal structure of the superfamily 1 helicase from tomato mosaic2 virus
28	d1w36d2	Alignment	not modelled	100.0	37	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
29	c3u4nA_	Alignment	not modelled	100.0	26	PDB header: hydrolase/dna Chain: A: PDB Molecule: atp-dependent helicase/nuclease subunit

29	c3u4qA	Alignment	not modelled	100.0	20	a; PDBTitle: structure of addab-dna complex at 2.8 angstroms
30	c1w36E	Alignment	not modelled	100.0	27	PDB header: recombination Chain: E; PDB Molecule: exodeoxyribonuclease v beta chain; PDBTitle: recbcd:dna complex
31	c2l8bA	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A; PDB Molecule: protein trai; PDBTitle: trai (381-569)
32	d1pja1	Alignment	not modelled	99.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
33	c3b85A	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A; PDB Molecule: phosphate starvation-inducible protein; PDBTitle: crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
34	d1uaaa1	Alignment	not modelled	99.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
35	c2pjrF	Alignment	not modelled	99.9	27	PDB header: hydrolase/dna Chain: F; PDB Molecule: protein (helicase pcra); PDBTitle: helicase product complex
36	d1w36b1	Alignment	not modelled	99.8	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
37	c6jimA	Alignment	not modelled	99.8	21	PDB header: viral protein/rna Chain: A; PDB Molecule: helicase; PDBTitle: viral helicase protein
38	c3u44B	Alignment	not modelled	99.7	19	PDB header: hydrolase/dna Chain: B; PDB Molecule: atp-dependent helicase/deoxyribonuclease subunit b; PDBTitle: crystal structure of addab-dna complex
39	c1qhhA	Alignment	not modelled	99.4	25	PDB header: hydrolase Chain: A; PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
40	c3dmnA	Alignment	not modelled	99.4	27	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative dna helicase; PDBTitle: the crystal structure of the c-terminal domain of a possilbe dna2 helicase from lactobacillus plantarun wcfs1
41	d1w36b2	Alignment	not modelled	99.4	34	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
42	c2pjrB	Alignment	not modelled	99.2	25	PDB header: hydrolase/dna Chain: B; PDB Molecule: protein (helicase pcra); PDBTitle: helicase product complex
43	c1qhhD	Alignment	not modelled	99.2	25	PDB header: hydrolase Chain: D; PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
44	d1pja2	Alignment	not modelled	99.1	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
45	d1uaaa2	Alignment	not modelled	99.1	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
46	c2vbcA	Alignment	not modelled	98.8	21	PDB header: hydrolase Chain: A; PDB Molecule: dengue 4 ns3 full-length protein; PDBTitle: crystal structure of the ns3 protease-helicase from dengue2 virus
47	c6c90A	Alignment	not modelled	98.8	14	PDB header: hydrolase/rna binding protein Chain: A; PDB Molecule: exosome rna helicase mtr4,exosome rna helicase mtr4; PDBTitle: human mtr4 helicase in complex with zcchc8-ctd
48	c5xdrA	Alignment	not modelled	98.7	26	PDB header: hydrolase Chain: A; PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase dhx15; PDBTitle: crystal structure of human deah-box rna helicase dhx15 in complex with2 adp
49	c2wv9A	Alignment	not modelled	98.7	24	PDB header: hydrolase Chain: A; PDB Molecule: flavivirin protease ns2b regulatory subunit, flavivirin PDBTitle: crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus
50	c6iegA	Alignment	not modelled	98.7	13	PDB header: rna binding protein Chain: A; PDB Molecule: exosome rna helicase mtr4; PDBTitle: crystal structure of human mtr4
51	c6jdeB	Alignment	not modelled	98.7	22	PDB header: hydrolase Chain: B; PDB Molecule: putative dna repair helicase radd; PDBTitle: crystal structure of a dna repair protein
52	c5aorA	Alignment	not modelled	98.7	21	PDB header: hydrolase/rna Chain: A; PDB Molecule: dosage compensation regulator; PDBTitle: structure of mle rna adp alf4 complex
53	d1rifa	Alignment	not modelled	98.7	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: DNA helicase UvsW
54	c6iehB	Alignment	not modelled	98.7	14	PDB header: rna binding protein Chain: B; PDB Molecule: exosome rna helicase mtr4; PDBTitle: crystal structures of the hmtr4-nrde2 complex
55	c2xgjA	Alignment	not modelled	98.7	11	PDB header: hydrolase/rna Chain: A; PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance

56	c4bujA_	Alignment	not modelled	98.7	11	PDB header: hydrolase Chain: A: PDB Molecule: antiviral helicase ski2; PDBTitle: crystal structure of the s. cerevisiae ski2-3-8 complex
57	c5vheA_	Alignment	not modelled	98.6	23	PDB header: hydrolase Chain: A: PDB Molecule: deah (asp-glu-ala-his) box polypeptide 36; PDBTitle: dhx36 in complex with the c-myc g-quadruplex
58	c6iczY_	Alignment	not modelled	98.6	23	PDB header: splicing Chain: Y: PDB Molecule: atp-dependent rna helicase dhx8; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at 2 3.0 angstrom
59	d2fwr2	Alignment	not modelled	98.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
60	c5mq0V_	Alignment	not modelled	98.6	27	PDB header: splicing Chain: V: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp22; PDBTitle: structure of a spliceosome remodeled for exon ligation
61	c5mqfq_	Alignment	not modelled	98.6	25	PDB header: splicing Chain: Q: PDB Molecule: protein bud31 homolog; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of 2 splicing (c* complex)
62	c3kx2A_	Alignment	not modelled	98.6	23	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp43; PDBTitle: crystal structure of prp43p in complex with adp
63	c4xgtA_	Alignment	not modelled	98.6	12	PDB header: hydrolase Chain: A: PDB Molecule: frq-interacting rna helicase; PDBTitle: structure of rna helicase frh a critical component of the neurospora2 crassa circadian clock
64	c2ocaA_	Alignment	not modelled	98.6	11	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase uvsw; PDBTitle: the crystal structure of t4 uvsw
65	c6hegA_	Alignment	not modelled	98.6	18	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase hrpb; PDBTitle: crystal structure of escherichia coli deah/rna helicase hrpb
66	d1gkub1	Alignment	not modelled	98.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
67	c2zj2A_	Alignment	not modelled	98.6	13	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 1
68	c2eyqA_	Alignment	not modelled	98.6	17	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of escherichia coli transcription-repair2 coupling factor
69	c5ylzW_	Alignment	not modelled	98.6	24	PDB header: splicing Chain: W: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp22; PDBTitle: cryo-em structure of the post-catalytic spliceosome from saccharomyces2 cerevisiae at 3.6 angstrom
70	c6fa5A_	Alignment	not modelled	98.6	28	PDB header: hydrolase Chain: A: PDB Molecule: putative mrna splicing factor; PDBTitle: crystal structure of the deah-box helicase prp2 in complex with adp
71	c3l9oA_	Alignment	not modelled	98.6	11	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: crystal structure of mtr4, a co-factor of the nuclear exosome
72	c4on9B_	Alignment	not modelled	98.6	11	PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx58; PDBTitle: dech box helicase domain
73	c5z58x_	Alignment	not modelled	98.6	26	PDB header: splicing Chain: X: PDB Molecule: smad nuclear-interacting protein 1; PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
74	c2zj8A_	Alignment	not modelled	98.6	14	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
75	d2fz4a1	Alignment	not modelled	98.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
76	c4qqxA_	Alignment	not modelled	98.5	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: crispr-associated helicase, cas3 family; PDBTitle: crystal structure of t. fusca cas3-atp
77	c6h57A_	Alignment	not modelled	98.5	21	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase dhr1; PDBTitle: crystal structure of s. cerevisiae deah-box rna helicase dhr1,2 essential for small ribosomal subunit biogenesis
78	d2eyqa3	Alignment	not modelled	98.5	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
79	c5lqwO_	Alignment	not modelled	98.5	23	PDB header: splicing Chain: O: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase-like PDBTitle: yeast activated spliceosome
80	c5n8zA_	Alignment	not modelled	98.5	24	PDB header: hydrolase Chain: A: PDB Molecule: cg9323, isoform a; PDBTitle: crystal structure of drosophila dhx36 helicase in complex with 2 ctctccctt
81	c5lj5Q_	Alignment	not modelled	98.5	26	PDB header: splicing Chain: Q: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp16; PDBTitle: overall structure of the yeast spliceosome immediately after 2 branching.

82	c3llmB_	Alignment	not modelled	98.5	18	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase a; PDBTitle: crystal structure analysis of a rna helicase
83	c2fwrA_	Alignment	not modelled	98.5	17	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad25; PDBTitle: structure of archaeoglobus fulgidis xpb
84	c3iuyB_	Alignment	not modelled	98.5	18	PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx53; PDBTitle: crystal structure of ddx53 dead-box domain
85	c2p6uA_	Alignment	not modelled	98.5	16	PDB header: dna binding protein Chain: A: PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
86	c5agaA_	Alignment	not modelled	98.5	19	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
87	c3ly5A_	Alignment	not modelled	98.5	14	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx18; PDBTitle: ddx18 dead-domain
88	c2jlrA_	Alignment	not modelled	98.5	21	PDB header: hydrolase Chain: A: PDB Molecule: serine protease subunit ns3; PDBTitle: dengue virus 4 ns3 helicase in complex with amppnp
89	c4l0jA_	Alignment	not modelled	98.5	24	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase i; PDBTitle: structure of a translocation signal domain mediating conjugative2 transfer by type iv secretion systems
90	c6i3oA_	Alignment	not modelled	98.5	22	PDB header: hydrolase Chain: A: PDB Molecule: putative pre-mrna splicing factor; PDBTitle: crystal structure of deah-box atpase prp22
91	c2ja1A_	Alignment	not modelled	98.5	17	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
92	c5wsge_	Alignment	not modelled	98.5	27	PDB header: rna binding protein/rna Chain: E: PDB Molecule: saccharomyces cerevisiae s288c snr6 snrna; PDBTitle: cryo-em structure of the catalytic step ii spliceosome (c* complex) at2 4.0 angstrom resolution
93	c1ymfA_	Alignment	not modelled	98.4	26	PDB header: hydrolase Chain: A: PDB Molecule: genome polyprotein [contains: flavivirin protease ns3 PDBTitle: crystal structure of yellow fever virus ns3 helicase complexed with2 adp
94	c4nl8E_	Alignment	not modelled	98.4	18	PDB header: dna binding protein Chain: E: PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to ssb c-terminal tail peptide
95	c4a4zA_	Alignment	not modelled	98.4	12	PDB header: hydrolase Chain: A: PDB Molecule: antiviral helicase ski2; PDBTitle: crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
96	d1a1va1	Alignment	not modelled	98.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
97	c1gm5A_	Alignment	not modelled	98.4	14	PDB header: helicase Chain: A: PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
98	c2va8A_	Alignment	not modelled	98.4	17	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
99	c5v9xA_	Alignment	not modelled	98.4	20	PDB header: hydrolase/dna Chain: A: PDB Molecule: atp-dependent dna helicase; PDBTitle: structure of mycobacterium smegmatis helicase lhr bound to ssdna and2 amp-pnp
100	c3fe2B_	Alignment	not modelled	98.4	18	PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx5; PDBTitle: human dead-box rna helicase ddx5 (p68), conserved domain i in complex2 with adp
101	c2qeqA_	Alignment	not modelled	98.4	24	PDB header: hydrolase Chain: A: PDB Molecule: flavivirin protease ns3 catalytic subunit; PDBTitle: crystal structure of kunjin virus ns3 helicase
102	c6nmiA_	Alignment	not modelled	98.4	14	PDB header: transcription Chain: A: PDB Molecule: general transcription and dna repair factor iih helicase PDBTitle: cryo-em structure of the human tfiih core complex
103	c3oiyB_	Alignment	not modelled	98.4	13	PDB header: isomerase Chain: B: PDB Molecule: reverse gyrase helicase domain; PDBTitle: helicase domain of reverse gyrase from thermotoga maritima
104	c4nl4H_	Alignment	not modelled	98.4	19	PDB header: dna binding protein Chain: H: PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to adp
105	c4ddvA_	Alignment	not modelled	98.4	15	PDB header: hydrolase Chain: A: PDB Molecule: reverse gyrase; PDBTitle: thermotoga maritima reverse gyrase, triclinic form
106	c2v6jA_	Alignment	not modelled	98.4	23	PDB header: hydrolase Chain: A: PDB Molecule: rna helicase; PDBTitle: kokobera virus helicase: mutant met47thr
107	c5lkiB_	Alignment	not modelled	98.4	15	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of full-length csfv ns3/4a
						PDB header: hydrolase/rna

108	c6o16A_	Alignment	not modelled	98.4	23	Chain: A: PDB Molecule: deah (asp-glu-ala-his) box polypeptide 37; PDBTitle: crystal structure of murine dhx37 in complex with rna
109	c2z83A_	Alignment	not modelled	98.4	28	PDB header: viral protein Chain: A: PDB Molecule: helicase/nucleoside triphosphatase; PDBTitle: crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8
110	d1gl9b1	Alignment	not modelled	98.4	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
111	c3dkpA_	Alignment	not modelled	98.3	19	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx52; PDBTitle: human dead-box rna-helicase ddx52, conserved domain i in complex with2 adp
112	c4gl2A_	Alignment	not modelled	98.3	18	PDB header: rna binding protein/rna Chain: A: PDB Molecule: interferon-induced helicase c domain-containing protein 1; PDBTitle: structural basis for dsrna duplex backbone recognition by mda5
113	c2db3D_	Alignment	not modelled	98.3	15	PDB header: hydrolase/rna Chain: D: PDB Molecule: atp-dependent rna helicase vasa; PDBTitle: structural basis for rna unwinding by the dead-box protein2 drosophila vasa
114	c6aicA_	Alignment	not modelled	98.3	19	PDB header: structural protein Chain: A: PDB Molecule: dead-box atp-dependent rna helicase csha; PDBTitle: crystal structures of the n-terminal domain of staphylococcus aureus2 dead-box cold shock rna helicase csha in complex with amp
115	c4cbhD_	Alignment	not modelled	98.3	18	PDB header: hydrolase Chain: D: PDB Molecule: serine protease ns3; PDBTitle: pestivirus ns3 helicase
116	c2f55C_	Alignment	not modelled	98.3	19	PDB header: hydrolase/dna Chain: C: PDB Molecule: polyprotein; PDBTitle: two hepatitis c virus ns3 helicase domains complexed with the same2 strand of dna
117	c5gvrA_	Alignment	not modelled	98.3	14	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx41; PDBTitle: crystal structure of the ddx41 dead domain in an apo closed form
118	c4cbhC_	Alignment	not modelled	98.3	14	PDB header: hydrolase Chain: C: PDB Molecule: serine protease ns3; PDBTitle: pestivirus ns3 helicase
119	c4xqkB_	Alignment	not modelled	98.3	19	PDB header: hydrolase/dna Chain: B: PDB Molecule: llabiii; PDBTitle: atp-dependent type isp restriction-modification enzyme llabiii bound2 to dna
120	c2pl3A_	Alignment	not modelled	98.3	15	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx10; PDBTitle: human dead-box rna helicase ddx10, dead domain in complex with adp