






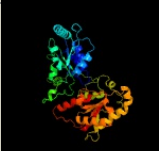

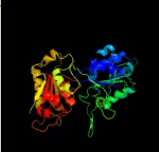

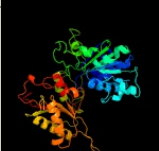

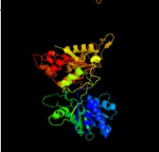





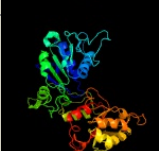




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1251c_(-)_1395827_1399246
Date	Wed Jul 31 22:05:34 BST 2019
Unique Job ID	cb8e1452abc2f40a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wjyA_	 Alignment		100.0	26	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
2	c2xzlA_	 Alignment		100.0	25	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent helicase nam7; PDBTitle: upf1-rna complex
3	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
4	c5mznA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: helicase sen1,helicase sen1; PDBTitle: helicase sen1
5	c4pj3A_	 Alignment		100.0	24	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
6	c2gk7A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: structural and functional insights into the human upf1 helicase core
7	c4b3gA_	 Alignment		100.0	24	PDB header: hydrolase/rna Chain: A: PDB Molecule: dna-binding protein smubp-2; PDBTitle: crystal structure of ighmbp2 helicase in complex with rna
8	c3jb9X_	 Alignment		100.0	17	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
9	c5wvpA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
10	c5wvpB_	 Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
11	c4n0oC_	 Alignment		100.0	25	PDB header: hydrolase/dna Chain: C: PDB Molecule: replicase polyprotein 1ab; PDBTitle: complex structure of arterivirus nonstructural protein 10 (helicase)2 with dna

12	c1w36G_	Alignment		100.0	21	PDB header: recombination Chain: G: PDB Molecule: exodeoxyribonuclease v alpha chain; PDBTitle: recbcd:dna complex
13	c3gp8A_	Alignment		100.0	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd, putative; PDBTitle: crystal structure of the binary complex of recd2 with dna
14	c5ld2D_	Alignment		100.0	21	PDB header: hydrolase Chain: D: PDB Molecule: recbcd enzyme subunit recd; PDBTitle: cryo-em structure of recbcd+dna complex revealing activated nuclease2 domain
15	c3e1sA_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd; PDBTitle: structure of an n-terminal truncation of deinococcus radiodurans recd2
16	c3vkwA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: replicase large subunit; PDBTitle: crystal structure of the superfamily 1 helicase from tomato mosaic2 virus
17	c5n8oA_	Alignment		100.0	17	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
18	c4c30I_	Alignment		100.0	29	PDB header: hydrolase/dna Chain: I: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of deinococcus radiodurans uvrd in2 complex with dna, form 2
19	c2is6B_	Alignment		100.0	26	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of uvrd-dna-adpmgf3 ternary complex
20	c3ifuA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of e. coli uvrd
21	c1pjrA_	Alignment	not modelled	100.0	25	PDB header: helicase Chain: A: PDB Molecule: pcra; PDBTitle: structure of dna helicase
22	c1uaaB_	Alignment	not modelled	100.0	21	PDB header: hydrolase/dna Chain: B: PDB Molecule: protein (atp-dependent dna helicase rep.); PDBTitle: e. coli rep helicase/dna complex
23	c3upuC_	Alignment	not modelled	100.0	18	PDB header: hydrolase/dna Chain: C: PDB Molecule: atp-dependent dna helicase dda; PDBTitle: crystal structure of the t4 phage sf1b helicase dda
24	c5ftbA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: tptr domain protein; PDBTitle: crystal structure of pif1 helicase from bacteroides in2 complex with amppnp
25	c5fhhA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of human pif1 helicase domain residues 200-641
26	c2pjrF_	Alignment	not modelled	100.0	20	PDB header: hydrolase/dna Chain: F: PDB Molecule: protein (helicase pcra); PDBTitle: helicase product complex
27	c3u4qA_	Alignment	not modelled	100.0	28	PDB header: hydrolase/dna Chain: A: PDB Molecule: atp-dependent helicase/nuclease subunit a; PDBTitle: structure of addab-dna complex at 2.8 angstroms
28	d1w36d1	Alignment	not modelled	99.9	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
						PDB header: recombination

29	c1w36E_	Alignment	not modelled	99.9	25	Chain: E; PDB Molecule: exodeoxyribonuclease v beta chain; PDBTitle: recbcd:dna complex
30	c5o6dB_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B; PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of scpif1 in complex with polydt and atpgs
31	d1pjra1	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
32	d1w36b1	Alignment	not modelled	99.9	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
33	d1uaaa1	Alignment	not modelled	99.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
34	c6jimA_	Alignment	not modelled	99.9	25	PDB header: viral protein/rna Chain: A; PDB Molecule: helicase; PDBTitle: viral helicase protein
35	c3b85A_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A; PDB Molecule: phosphate starvation-inducible protein; PDBTitle: crystal structure of predicted phosphate starvation-induced atpase2 pho2 from corynebacterium glutamicum
36	c3dmnA_	Alignment	not modelled	99.6	17	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
37	c3u44B_	Alignment	not modelled	99.5	15	PDB header: hydrolase/dna Chain: B; PDB Molecule: atp-dependent helicase/deoxyribonuclease subunit b; PDBTitle: crystal structure of addab-dna complex
38	c2l8bA_	Alignment	not modelled	99.5	13	PDB header: hydrolase Chain: A; PDB Molecule: protein trai; PDBTitle: trai (381-569)
39	c4onbA_	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: A; PDB Molecule: crispr-associated exonuclease, cas4 family; PDBTitle: crystal structure of crispr-associated exonuclease (cas4 family) from2 pyrobaculum calidifontis jcm 11548
40	c1qhhB_	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: B; PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
41	d1w36d2	Alignment	not modelled	99.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
42	c1qhhA_	Alignment	not modelled	98.9	26	PDB header: hydrolase Chain: A; PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
43	c2vbcA_	Alignment	not modelled	98.9	20	PDB header: hydrolase Chain: A; PDB Molecule: dengue 4 ns3 full-length protein; PDBTitle: crystal structure of the ns3 protease-helicase from dengue2 virus
44	c2wv9A_	Alignment	not modelled	98.8	17	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
45	d1w36b2	Alignment	not modelled	98.8	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
46	c4ddvA_	Alignment	not modelled	98.7	11	PDB header: hydrolase Chain: A; PDB Molecule: reverse gyrase; PDBTitle: thermotoga maritima reverse gyrase, triclinic form
47	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
48	c4xqkB_	Alignment	not modelled	98.7	18	PDB header: hydrolase/dna Chain: B; PDB Molecule: llabiii; PDBTitle: atp-dependent type isp restriction-modification enzyme llabiii bound2 to dna
49	c2jlrA_	Alignment	not modelled	98.7	18	PDB header: hydrolase Chain: A; PDB Molecule: serine protease subunit ns3; PDBTitle: dengue virus 4 ns3 helicase in complex with amppnp
50	c2qeqA_	Alignment	not modelled	98.7	19	PDB header: hydrolase Chain: A; PDB Molecule: flavivirin protease ns3 catalytic subunit; PDBTitle: crystal structure of kunjin virus ns3 helicase
51	c4nl8E_	Alignment	not modelled	98.7	16	PDB header: dna binding protein Chain: E; PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to ssb c-terminal tail peptide
52	c5v9xA_	Alignment	not modelled	98.7	17	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
53	c1ymfA_	Alignment	not modelled	98.7	18	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
54	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
55	c4nl4H_	Alignment	not modelled	98.7	18	PDB header: dna binding protein Chain: H; PDB Molecule: primosome assembly protein pria;

						PDBTitle: pria helicase bound to adp
56	d1gkub1	Alignment	not modelled	98.7	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
57	c2v6jA_	Alignment	not modelled	98.7	17	PDB header: hydrolase Chain: A: PDB Molecule: rna helicase; PDBTitle: kokobera virus helicase: mutant met47thr
58	c1gm5A_	Alignment	not modelled	98.6	15	PDB header: helicase Chain: A: PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
59	c4ic1D_	Alignment	not modelled	98.6	19	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of sso0001
60	c2z83A_	Alignment	not modelled	98.6	22	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
61	d2eyqa3	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
62	c6hegA_	Alignment	not modelled	98.6	17	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase hrpb; PDBTitle: crystal structure of escherichia coli deah/rha helicase hrpb
63	c3l0aA_	Alignment	not modelled	98.5	18	PDB header: hydrolase Chain: A: PDB Molecule: putative exonuclease; PDBTitle: crystal structure of putative exonuclease (rer070207002219) from2 eubacterium rectale at 2.19 a resolution
64	c5mq0V_	Alignment	not modelled	98.5	17	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
65	c3oiyB_	Alignment	not modelled	98.5	14	PDB header: isomerase Chain: B: PDB Molecule: reverse gyrase helicase domain; PDBTitle: helicase domain of reverse gyrase from thermotoga maritima
66	c5okiA_	Alignment	not modelled	98.5	18	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
67	c5l3qB_	Alignment	not modelled	98.5	17	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
68	c2va8A_	Alignment	not modelled	98.5	18	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
69	d1pjra2	Alignment	not modelled	98.5	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
70	c5mqfq_	Alignment	not modelled	98.5	19	PDB header: splicing Chain: Q: PDB Molecule: protein bud31 homolog; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
71	c3rc8A_	Alignment	not modelled	98.5	19	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase supv3l1, mitochondrial; PDBTitle: human mitochondrial helicase suv3 in complex with short rna fragment
72	c2ocaA_	Alignment	not modelled	98.4	12	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase uvsw; PDBTitle: the crystal structure of t4 uvsw
73	d1gl9b1	Alignment	not modelled	98.4	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
74	c5jb2A_	Alignment	not modelled	98.4	25	PDB header: immune system Chain: A: PDB Molecule: lgp2; PDBTitle: crystal structure of chicken lgp2 with 5'ppp 10-mer dsrna and adp-2 alf4-mg2+ at 2.2 a resolution.
75	c5lkiB_	Alignment	not modelled	98.4	12	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of full-length csfv ns3/4a
76	c2eyqA_	Alignment	not modelled	98.4	19	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of escherichia coli transcription-repair2 coupling factor
77	c6i3oA_	Alignment	not modelled	98.4	19	PDB header: hydrolase Chain: A: PDB Molecule: putative pre-mrna splicing factor; PDBTitle: crystal structure of deah-box atpase prp22
78	c5ylzW_	Alignment	not modelled	98.4	16	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
79	c4znlB_	Alignment	not modelled	98.4	13	PDB header: viral protein Chain: B: PDB Molecule: phage terminase large subunit; PDBTitle: thermus phage p74-26 large terminase atpase domain bound to adp2 beryllium fluoride
80	c1gl9B_	Alignment	not modelled	98.4	13	PDB header: topoisomerase Chain: B: PDB Molecule: reverse gyrase; PDBTitle: archaeoglobus fulgidus reverse gyrase complexed with adpnp

81	c6nmiA	Alignment	not modelled	98.4	15	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
82	d1gm5a3	Alignment	not modelled	98.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
83	c5xdrA	Alignment	not modelled	98.4	13	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
84	c6fwsB	Alignment	not modelled	98.4	15	PDB header: dna binding protein Chain: B: PDB Molecule: atp-dependent dna helicase ding; PDBTitle: structure of ding in complex with ssdna and adpbf
85	c2j7pA	Alignment	not modelled	98.4	24	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
86	c4on9B	Alignment	not modelled	98.4	14	PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx58; PDBTitle: dech box helicase domain
87	c2og2A	Alignment	not modelled	98.4	16	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
88	d1yksa1	Alignment	not modelled	98.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
89	c5gafi	Alignment	not modelled	98.3	18	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: rnc in complex with srp
90	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
91	c6cy1B	Alignment	not modelled	98.3	20	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
92	c6iczy	Alignment	not modelled	98.3	18	PDB header: splicing Chain: Y: PDB Molecule: atp-dependent rna helicase dhx8; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
93	c2zj8A	Alignment	not modelled	98.3	19	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
94	c2zj2A	Alignment	not modelled	98.3	17	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 1
95	c3b9qA	Alignment	not modelled	98.3	19	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyl from arabidopsis thaliana
96	c6fa5A	Alignment	not modelled	98.3	18	PDB header: hydrolase Chain: A: PDB Molecule: putative mrna splicing factor; PDBTitle: crystal structure of the deah-box helicase prp2 in complex with adp
97	c4ak9A	Alignment	not modelled	98.3	21	PDB header: protein transport Chain: A: PDB Molecule: cpftsyl; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
98	c5z58x	Alignment	not modelled	98.3	19	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.
99	c6c90A	Alignment	not modelled	98.3	17	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
100	c5agaA	Alignment	not modelled	98.3	17	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
101	c1a1vA	Alignment	not modelled	98.3	15	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein (ns3 protein); PDBTitle: hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
102	c2p6uA	Alignment	not modelled	98.3	14	PDB header: dna binding protein Chain: A: PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
103	c5jpij	Alignment	not modelled	98.3	22	PDB header: ribosome Chain: I: PDB Molecule: u3 small nucleolar rna-associated protein 21; PDBTitle: cryo-em structure of the 90s pre-ribosome
104	c2j37W	Alignment	not modelled	98.3	16	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
105	c4cbhC	Alignment	not modelled	98.3	17	PDB header: hydrolase Chain: C: PDB Molecule: serine protease ns3; PDBTitle: pestivirus ns3 helicase
106	c6o16A	Alignment	not modelled	98.3	18	PDB header: hydrolase/rna Chain: A: PDB Molecule: deah (asp-glu-ala-his) box polypeptide 37; PDBTitle: crystal structure of murine dhx37 in complex with rna

107	c2v17A_	Alignment	not modelled	98.3	21	PDB header: unknown function Chain: A: PDB Molecule: xpd; PDBTitle: structure of s. tokodaii xpd4
108	d1a1va1	Alignment	not modelled	98.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
109	c1zu4A_	Alignment	not modelled	98.3	19	PDB header: protein transport Chain: A: PDB Molecule: ftsy; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
110	c6f4aB_	Alignment	not modelled	98.3	16	PDB header: hydrolase Chain: B: PDB Molecule: suv3 helicase; PDBTitle: yeast mitochondrial rna degradosome complex mtexo
111	c5l3rC_	Alignment	not modelled	98.2	18	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
112	c2iy3A_	Alignment	not modelled	98.2	25	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
113	c2cnwF_	Alignment	not modelled	98.2	20	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
114	c5aorA_	Alignment	not modelled	98.2	15	PDB header: hydrolase/rna Chain: A: PDB Molecule: dosage compensation regulator; PDBTitle: structure of mle rna adp alf4 complex
115	c3dm5A_	Alignment	not modelled	98.2	15	PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
116	c4cbhD_	Alignment	not modelled	98.2	13	PDB header: hydrolase Chain: D: PDB Molecule: serine protease ns3; PDBTitle: pestivirus ns3 helicase
117	c2j289_	Alignment	not modelled	98.2	18	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
118	c1c4oA_	Alignment	not modelled	98.2	14	PDB header: replication Chain: A: PDB Molecule: dna nucleotide excision repair enzyme uvrB; PDBTitle: crystal structure of the dna nucleotide excision repair enzyme uvrB2 from thermus thermophilus
119	d2fwra2	Alignment	not modelled	98.2	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
120	c3dmdA_	Alignment	not modelled	98.2	18	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus