Phyre2

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Description	Undefined
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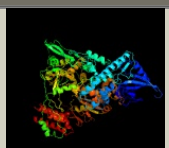
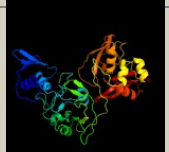
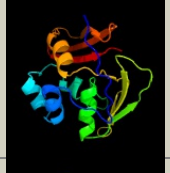
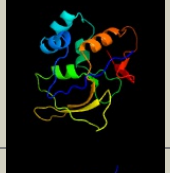
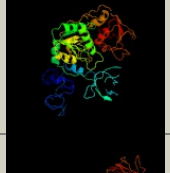
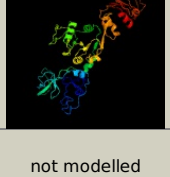
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c7btfA_	Alignment		100.0	100	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nsp12; **PDBTitle:** sars-cov-2 rna-dependent rna polymerase in complex with cofactors in2 reduced condition
2	c6m71A_	Alignment		100.0	100	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sars-cov-2 nsp 12; **PDBTitle:** sars-cov-2 rna-dependent rna polymerase in complex with cofactors
3	c6nusA_	Alignment		100.0	97	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nsp12; **PDBTitle:** sars-coronavirus nsp12 bound to nsp8 co-factor
4	c5c8sD_	Alignment		100.0	95	**PDB header:**transferase **Chain:** D: **PDB Molecule:**guanine-n7 methyltransferase; **PDBTitle:** crystal structure of the sars coronavirus nsp14-nsp10 complex with2 functional ligands sah and gpppa
5	c3r24A_	Alignment		100.0	94	**PDB header:**transferase, viral protein **Chain:** A: **PDB Molecule:**2'-o-methyl transferase; **PDBTitle:** crystal structure of nsp10/nsp16 complex of sars coronavirus
6	c2rhbD_	Alignment		100.0	88	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**uridylate-specific endoribonuclease; **PDBTitle:** crystal structure of nsp15-h234a mutant- hexamer in2 asymmetric unit
7	c5ynpA_	Alignment		100.0	66	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nsp16 protein; **PDBTitle:** crystal structure of mers-cov nsp16/nsp10 complex bound to sinefungin2 and m7gpppa
8	c5yvdA_	Alignment		100.0	52	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nsp15; **PDBTitle:** structural and biochemical characterization of endoribonuclease nsp152 encoded by middle east respiratory syndrome coronavirus
9	c4rs4A_	Alignment		100.0	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uridylate-specific endoribonuclease; **PDBTitle:** crystal structure and mutational analysis of the endoribonuclease from2 human coronavirus 229e
10	c2gtiA_	Alignment		100.0	48	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** mutation of mhv coronavirus non-structural protein nsp15 (f307l)
11	c5wwpA_	Alignment		100.0	73	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**orf1ab; **PDBTitle:** crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)

12	c5wwpB_	Alignment		100.0	72	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**orf1ab; **PDBTitle:** crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
13	d2h85a1	Alignment		100.0	87	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Nsp15 N-terminal domain-like
14	d2h85a2	Alignment		100.0	90	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Nsp15 C-terminal domain-like
15	d2gtia2	Alignment		100.0	55	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Nsp15 C-terminal domain-like
16	d2ozka2	Alignment		100.0	90	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Nsp15 C-terminal domain-like
17	d2ozka1	Alignment		100.0	87	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Nsp15 N-terminal domain-like
18	d2gtia1	Alignment		100.0	42	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Nsp15 N-terminal domain-like
19	c4n0oC_	Alignment		100.0	22	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** complex structure of arterivirus nonstructural protein 10 (helicase)2 with dna
20	c6jdrA_	Alignment		100.0	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**pp1b; **PDBTitle:** crystal structure of methylated prrsv nsp10 (helicase)
21	c2xzlA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent helicase nam7; **PDBTitle:** upf1-rna complex
22	c2wjyA_	Alignment	not modelled	100.0	21	**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
23	c6jdsA_	Alignment	not modelled	100.0	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**pp1b; **PDBTitle:** crystal structure of truncated prrsv nsp10 (helicase)
24	c5mznA_	Alignment	not modelled	100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**helicase sen1,helicase sen1; **PDBTitle:** helicase sen1
25	c2gk7A_	Alignment	not modelled	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
26	c5eaxB_	Alignment	not modelled	100.0	21	**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
27	c4b3gA_	Alignment	not modelled	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
28	c4pj3A_	Alignment	not modelled	100.0	26	**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

29	c3vkwA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**replicase large subunit; **PDBTitle:** crystal structure of the superfamily 1 helicase from tomato mosaic2 virus
30	c3jb9X_	Alignment	not modelled	99.9	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
31	d1xr7a_	Alignment	not modelled	99.9	17	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
32	c3n6mA_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna-dependent rna polymerase; **PDBTitle:** crystal structure of ev71 rdrp in complex with gtp
33	c2uutA_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna-directed rna polymerase; **PDBTitle:** the 2.4 angstrom resolution structure of the d346g mutant of the2 sapporo virus rdrp polymerase
34	c3gp8A_	Alignment	not modelled	99.9	25	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**exodeoxyribonuclease v, subunit recd, putative; **PDBTitle:** crystal structure of the binary complex of recd2 with dna
35	c3e1sA_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease v, subunit recd; **PDBTitle:** structure of an n-terminal truncation of deinococcus radiodurans recd2
36	c1w36G_	Alignment	not modelled	99.9	21	**PDB header:**recombination **Chain:** G: **PDB Molecule:**exodeoxyribonuclease v alpha chain; **PDBTitle:** recbcd:dna complex
37	d1xr6a_	Alignment	not modelled	99.9	19	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
38	c3nahC_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**rna dependent rna polymerase; **PDBTitle:** crystal structures and functional analysis of murine norovirus rna-2 dependent rna polymerase
39	d1ra6a_	Alignment	not modelled	99.9	17	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
40	d1u09a_	Alignment	not modelled	99.9	14	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
41	c5ld2D_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**recbcd enzyme subunit recd; **PDBTitle:** cryo-em structure of recbcd+dna complex revealing activated nuclease2 domain
42	c4nz0F_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** F: **PDB Molecule:**genome polyprotein; **PDBTitle:** the emcv 3dpol structure at 2.8a resolution
43	d1sh0a_	Alignment	not modelled	99.8	13	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
44	c6qwtA_	Alignment	not modelled	99.8	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** sicinivirus 3dpol rna dependent rna polymerase
45	c2b43D_	Alignment	not modelled	99.8	12	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**non-structural polyprotein; **PDBTitle:** crystal structure of the norwalk virus rna dependent rna polymerase2 from strain hu/nlv/dresden174/1997/ge
46	d1khva_	Alignment	not modelled	99.8	15	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
47	d1xr5a_	Alignment	not modelled	99.8	19	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
48	c2ijd1_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase, transferase **Chain:** 1: **PDB Molecule:**picornain 3c, rna-directed rna polymerase; **PDBTitle:** crystal structure of the poliovirus precursor protein 3cd
49	c6r1iB_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**genome polyprotein; **PDBTitle:** structure of porcine aichi virus polymerase
50	c5n8oA_	Alignment	not modelled	99.7	18	**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
51	c6jimA_	Alignment	not modelled	99.7	18	**PDB header:**viral protein/rna **Chain:** A: **PDB Molecule:**helicase; **PDBTitle:** viral helicase protein
52	c5fhhA_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase pif1; **PDBTitle:** structure of human pif1 helicase domain residues 200-641
53	c5ftbA_	Alignment	not modelled	99.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tpr domain protein; **PDBTitle:** crystal structure of pif1 helicase from bacteroides in2 complex with amppnp
54	c3upuC_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**atp-dependent dna helicase dda; **PDBTitle:** crystal structure of the t4 phage sf1b helicase dda
55	d1w36d1	Alignment	not modelled	99.5	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain

56	c2is6B_	Alignment	not modelled	99.4	19	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**dna helicase ii; **PDBTitle:** crystal structure of uvrd-dna-adpmgf3 ternary complex
57	c4c30I_	Alignment	not modelled	99.4	19	**PDB header:**hydrolase/dna **Chain:** I: **PDB Molecule:**dna helicase ii; **PDBTitle:** crystal structure of deinococcus radiodurans uvrd in2 complex with dna, form 2
58	c1pjrA_	Alignment	not modelled	99.3	25	**PDB header:**helicase **Chain:** A: **PDB Molecule:**pcra; **PDBTitle:** structure of dna helicase
59	c3lfuA_	Alignment	not modelled	99.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna helicase ii; **PDBTitle:** crystal structure of e. coli uvrd
60	c1uaaB_	Alignment	not modelled	99.3	20	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**protein (atp-dependent dna helicase rep.); **PDBTitle:** e. coli rep helicase/dna complex
61	d1uaaa1	Alignment	not modelled	99.2	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
62	d1pjra1	Alignment	not modelled	99.2	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
63	c3b85A_	Alignment	not modelled	99.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphate starvation-inducible protein; **PDBTitle:** crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
64	c2pjrF_	Alignment	not modelled	99.1	17	**PDB header:**hydrolase/dna **Chain:** F: **PDB Molecule:**protein (helicase pcra); **PDBTitle:** helicase product complex
65	c5i62A_	Alignment	not modelled	98.8	16	**PDB header:**viral protein, replication **Chain:** A: **PDB Molecule:**potential rna-dependent rna polymerase; **PDBTitle:** crystal structure of the insertion loop deletion mutant of the rna-2 dependent rna polymerase of a human picorbirnavirus
66	d1s48a_	Alignment	not modelled	98.8	16	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
67	c2plwA_	Alignment	not modelled	98.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna methyltransferase, putative; **PDBTitle:** crystal structure of a ribosomal rna methyltransferase, putative, from2 plasmodium falciparum (pf13_0052).
68	c5o6dB_	Alignment	not modelled	98.5	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent dna helicase pif1; **PDBTitle:** structure of scpif1 in complex with polydt and atpgs
69	c5y6rA_	Alignment	not modelled	98.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** crystal structure of csfv ns5b
70	c2l8bA_	Alignment	not modelled	98.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein trai; **PDBTitle:** trai (381-569)
71	c6jp6B_	Alignment	not modelled	98.1	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (cytidine(34)/guanosine(34)-2'-o)-methyltransferase; **PDBTitle:** the x-ray structure of yeast trna methyltransferase complex of trm72 and trm734 essential for 2'-o-methylation at the first position of3 anticodon in specific trnas
72	c3dmnA_	Alignment	not modelled	98.0	15	**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
73	c6em5w_	Alignment	not modelled	97.9	17	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**ribosome assembly factor mrt4; **PDBTitle:** state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
74	c2vbcA_	Alignment	not modelled	97.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dengue 4 ns3 full-length protein; **PDBTitle:** crystal structure of the ns3 protease-helicase from dengue2 virus
75	c3douA_	Alignment	not modelled	97.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase j; **PDBTitle:** crystal structure of methyltransferase involved in cell division from2 thermoplasma volcanicum gss1
76	c3rc8A_	Alignment	not modelled	97.8	24	**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
77	c2cjqA_	Alignment	not modelled	97.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna-directed rna polymerase; **PDBTitle:** bovine viral diarrhea virus cp7-r12 rna-dependent rna2 polymerase
78	d1raja_	Alignment	not modelled	97.8	19	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
79	c1a1vA_	Alignment	not modelled	97.8	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein (ns3 protein); **PDBTitle:** hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
80	c6hegA_	Alignment	not modelled	97.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase hrpb; **PDBTitle:** crystal structure of escherichia coli deah/rha helicase hrpb
81	c6fa5A_	Alignment	not modelled	97.6	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
82	d1ej0a_	Alignment	not modelled	97.6	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**RNA methyltransferase FtsJ
83	c2f55C_	Alignment	not modelled	97.6	23	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**polyprotein; **PDBTitle:** two hepatitis c virus ns3 helicase domains complexed with the same2 strand of dna
84	c5xdrA_	Alignment	not modelled	97.6	16	**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
85	c5mqfq_	Alignment	not modelled	97.6	23	**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)
86	d1a1va1	Alignment	not modelled	97.6	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
87	c2jlrA_	Alignment	not modelled	97.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease subunit ns3; **PDBTitle:** dengue virus 4 ns3 helicase in complex with amppnp
88	c6f4aB_	Alignment	not modelled	97.5	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**suv3 helicase; **PDBTitle:** yeast mitochondrial rna degradosome complex mtexo
89	c5hbzE_	Alignment	not modelled	97.5	27	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**non-structural protein 11; **PDBTitle:** structure of eav nsp11 k170a mutant at 3.10a
90	c5lqwO_	Alignment	not modelled	97.5	17	**PDB header:**splicing **Chain:** O: **PDB Molecule:**pre-mrna-splicing factor atp-dependent rna helicase-like **PDBTitle:** yeast activated spliceosome
91	c6o16A_	Alignment	not modelled	97.5	22	**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
92	c6i3oA_	Alignment	not modelled	97.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative pre-mrna splicing factor; **PDBTitle:** crystal structure of deah-box atpase prp22
93	c2wv9A_	Alignment	not modelled	97.5	18	**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
94	c6iczY_	Alignment	not modelled	97.4	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) at2 3.0 angstrom
95	d1w36d2	Alignment	not modelled	97.4	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
96	c5mq0V_	Alignment	not modelled	97.4	19	**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
97	c5da1B_	Alignment	not modelled	97.4	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoribonuclease; **PDBTitle:** a dimerization-dependent mechanism drives prrsv nsp11 functions as a2 beta interferon antagonist and endoribonuclease
98	c2nyuA_	Alignment	not modelled	97.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative ribosomal rna methyltransferase 2; **PDBTitle:** crystal structure of human ftsj homolog 2 (e.coli) protein in complex2 with s-adenosylmethionine
99	c2z83A_	Alignment	not modelled	97.3	18	**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
100	c5wsge_	Alignment	not modelled	97.3	17	**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
101	c5z58x_	Alignment	not modelled	97.3	13	**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.
102	c5lklB_	Alignment	not modelled	97.3	12	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**genome polyprotein; **PDBTitle:** crystal structure of full-lengh csfv ns3/4a
103	c5ylzW_	Alignment	not modelled	97.3	15	**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
104	c2ja1A_	Alignment	not modelled	97.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from b. cereus with ttp bound as phosphate donor.
105	c6hyuC_	Alignment	not modelled	97.3	19	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**atp-dependent rna helicase dhx8; **PDBTitle:** crystal structure of dhx8 helicase bound to single stranded poly-2 adenine rna
106	c2qeqA_	Alignment	not modelled	97.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns3 catalytic subunit;

						PDBTitle: crystal structure of kunjin virus ns3 helicase
107	c5vheA_	Alignment	not modelled	97.2	15	**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
108	c5lj5Q_	Alignment	not modelled	97.1	17	**PDB header:**splicing **Chain:** Q: **PDB Molecule:**pre-mrna-splicing factor atp-dependent rna helicase prp16; **PDBTitle:** overall structure of the yeast spliceosome immediately after2 branching.
109	c3crw1_	Alignment	not modelled	97.1	14	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**xpd/rad3 related dna helicase; **PDBTitle:** xpd_apo
110	d1w36b1	Alignment	not modelled	97.1	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
111	c3kx2A_	Alignment	not modelled	97.1	13	**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
112	d1gkub1	Alignment	not modelled	97.1	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Helicase-like "domain" of reverse gyrase
113	c6m40A_	Alignment	not modelled	97.0	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**ns3-like protein; **PDBTitle:** crystal structure of the ns3-like helicase from alongshan virus
114	c1ymfA_	Alignment	not modelled	97.0	17	**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
115	c3llmB_	Alignment	not modelled	97.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase a; **PDBTitle:** crystal structure analysis of a rna helicase
116	d1rifa_	Alignment	not modelled	97.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**DNA helicase UvsW
117	c4cbhC_	Alignment	not modelled	96.9	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**serine protease ns3; **PDBTitle:** pestivirus ns3 helicase
118	c4b6eB_	Alignment	not modelled	96.9	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**non-structural protein 4a, serine protease ns3; **PDBTitle:** discovery of an allosteric mechanism for the regulation of2 hcv ns3 protein function
119	c1cu1B_	Alignment	not modelled	96.9	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (protease/helicase ns3); **PDBTitle:** crystal structure of an enzyme complex from hepatitis c virus
120	c6nmiA_	Alignment	not modelled	96.9	16	**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