

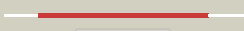


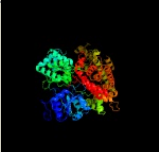
















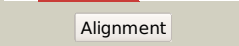




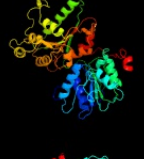


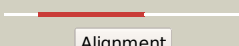

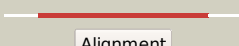

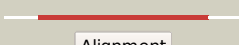







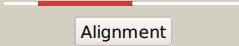
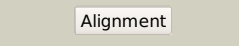
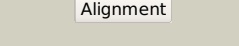
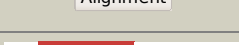




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2092c_(heY)_2349342_2352062
Date	Mon Aug 5 13:25:21 BST 2019
Unique Job ID	73afd02d4542f4bb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4xgtA_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> frq-interacting rna helicase; <b>PDBTitle:</b> structure of rna helicase frh a critical component of the neurospora2 crassa circadian clock
2	<a href="#">c6iehB_</a>	 Alignment		100.0	29	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> exosome rna helicase mtr4; <b>PDBTitle:</b> crystal structures of the hmtr4-nrde2 complex
3	<a href="#">c4a4zA_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> antiviral helicase ski2; <b>PDBTitle:</b> crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
4	<a href="#">c2xgiA_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dob1; <b>PDBTitle:</b> structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
5	<a href="#">c6iegA_</a>	 Alignment		100.0	29	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exosome rna helicase mtr4; <b>PDBTitle:</b> crystal structure of human mtr4
6	<a href="#">c3l9oA_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dob1; <b>PDBTitle:</b> crystal structure of mtr4, a co-factor of the nuclear exosome
7	<a href="#">c4bujA_</a>	 Alignment		100.0	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> antiviral helicase ski2; <b>PDBTitle:</b> crystal structure of the s. cerevisiae ski2-3-8 complex
8	<a href="#">c6c90A_</a>	 Alignment		100.0	35	<b>PDB header:</b> hydrolase/rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exosome rna helicase mtr4,exosome rna helicase mtr4; <b>PDBTitle:</b> human mtr4 helicase in complex with zcchc8-ctd
9	<a href="#">c5m59C_</a>	 Alignment		100.0	26	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna splicing helicase-like protein; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum brr2 helicase core in2 complex with prp8 jab1 domain
10	<a href="#">c5dcaA_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing helicase brr2; <b>PDBTitle:</b> crystal structure of yeast full length brr2 in complex with prp8 jab12 domain
11	<a href="#">c5lqwC_</a>	 Alignment		100.0	28	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna-splicing helicase brr2; <b>PDBTitle:</b> yeast activated spliceosome

12	<a href="#">c4bgdA_</a>	 Alignment		100.0	28	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> pre-mrna-splicing helicase brr2; <b>PDBTitle:</b> crystal structure of brr2 in complex with the jab1/mpn domain of prp8
13	<a href="#">c3jcrC_</a>	 Alignment		100.0	25	<b>PDB header:</b> splicing <b>Chain:</b> C; <b>PDB Molecule:</b> hbr2; <b>PDBTitle:</b> 3d structure determination of the human*u4/u6.u5* tri-snnp complex
14	<a href="#">c4f92B_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> u5 small nuclear ribonucleoprotein 200 kda helicase; <b>PDBTitle:</b> brr2 helicase region s1087I
15	<a href="#">c5m52B_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> pre-mrna-splicing helicase brr2; <b>PDBTitle:</b> crystal structure of yeast brr2 full-lenght in complex with prp8 jab12 domain
16	<a href="#">c6ah0D_</a>	 Alignment		100.0	27	<b>PDB header:</b> splicing <b>Chain:</b> D; <b>PDB Molecule:</b> u5 small nuclear ribonucleoprotein 200 kda helicase; <b>PDBTitle:</b> the cryo-em structure of the precursor of human pre-catalytic2 spliceosome (pre-b complex)
17	<a href="#">c5agaA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> dna polymerase theta; <b>PDBTitle:</b> crystal structure of the helicase domain of human dna2 polymerase theta in complex with amppnp
18	<a href="#">c2zj2A_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative ski2-type helicase; <b>PDBTitle:</b> archaeal dna helicase hjm apo state in form 1
19	<a href="#">c2zj8A_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative ski2-type helicase; <b>PDBTitle:</b> archaeal dna helicase hjm apo state in form 2
20	<a href="#">c2va8A_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
21	<a href="#">c2p6uA_</a>	 Alignment	not modelled	100.0	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> afuhel308 helicase; <b>PDBTitle:</b> apo structure of the hel308 superfamily 2 helicase
22	<a href="#">c3rc8A_</a>	 Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent rna helicase supv311, mitochondrial; <b>PDBTitle:</b> human mitochondrial helicase suv3 in complex with short rna fragment
23	<a href="#">c5v9xA_</a>	 Alignment	not modelled	100.0	30	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent dna helicase; <b>PDBTitle:</b> structure of mycobacterium smegmatis helicase lhr bound to ssdna and2 amp-pnp
24	<a href="#">c6f4aB_</a>	 Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> suv3 helicase; <b>PDBTitle:</b> yeast mitochondrial rna degradosome complex mtexo
25	<a href="#">c4cdgA_</a>	 Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> bloom syndrome protein; <b>PDBTitle:</b> crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody
26	<a href="#">c5lstA_</a>	 Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent dna helicase q4; <b>PDBTitle:</b> crystal structure of the human recq4 helicase.
27	<a href="#">c2v1xB_</a>	 Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> atp-dependent dna helicase q1; <b>PDBTitle:</b> crystal structure of human recq-like dna helicase
28	<a href="#">c1gm5A_</a>	 Alignment	not modelled	100.0	23	<b>PDB header:</b> helicase <b>Chain:</b> A; <b>PDB Molecule:</b> recg; <b>PDBTitle:</b> structure of recg bound to three-way dna junction

29	<a href="#">c1oywA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase; <b>PDBTitle:</b> structure of the recq catalytic core
30	<a href="#">c4q47A</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna helicase recq; <b>PDBTitle:</b> structure of the drrecq catalytic core in complex with adp
31	<a href="#">c2eyqA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> transcription-repair coupling factor; <b>PDBTitle:</b> crystal structure of escherichia coli transcription-repair2 coupling factor
32	<a href="#">c5jb2A</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> lgp2; <b>PDBTitle:</b> crystal structure of chicken lgp2 with 5'ppp 10-mer dsrna and adp-2 alf4-mg2+ at 2.2 a resolution.
33	<a href="#">c3tmiA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx58; <b>PDBTitle:</b> structural basis for rna recognition and activation of rig-i
34	<a href="#">c4ddvA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> reverse gyrase; <b>PDBTitle:</b> thermotoga maritima reverse gyrase, triclinic form
35	<a href="#">c1gl9B</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> topoisomerase <b>Chain:</b> B: <b>PDB Molecule:</b> reverse gyrase; <b>PDBTitle:</b> archaeoglobus fulgidus reverse gyrase complexed with adpnp
36	<a href="#">c5jcfB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> melanoma differentiation associated protein-5; <b>PDBTitle:</b> crystal structure of chicken mda5 with 5'p 10-mer dsrna and adp-mg2+2 at 2.6 a resolution (orthorhombic form).
37	<a href="#">c4gl2A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> interferon-induced helicase c domain-containing protein 1; <b>PDBTitle:</b> structural basis for dsrna duplex backbone recognition by mda5
38	<a href="#">c4llyA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-processing atp-dependent rna helicase prp5; <b>PDBTitle:</b> crystal structure of rna splicing effector prp5 in complex with adp
39	<a href="#">c6jdeB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dna repair helicase radd; <b>PDBTitle:</b> crystal structure of a dna repair protein
40	<a href="#">c3bxzA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> preprotein translocase subunit seca; <b>PDBTitle:</b> crystal structure of the isolated dead motor domains from escherichia2 coli seca
41	<a href="#">c6iczY</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> splicing <b>Chain:</b> Y: <b>PDB Molecule:</b> atp-dependent rna helicase dhx8; <b>PDBTitle:</b> cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
42	<a href="#">c6hegA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase hrbp; <b>PDBTitle:</b> crystal structure of escherichia coli deah/rna helicase hrbp
43	<a href="#">c4w7sA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing atp-dependent rna helicase prp28; <b>PDBTitle:</b> crystal structure of the yeast dead-box splicing factor prp28 at 2.542 angstroms resolution
44	<a href="#">c5lb5C</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent dna helicase q5; <b>PDBTitle:</b> crystal structure of human recq15 helicase in complex with adp/mg2 (triclinic form).
45	<a href="#">c5n8zA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg9323, isoform a; <b>PDBTitle:</b> crystal structure of drosophila dhx36 helicase in complex with2 ctctccctt
46	<a href="#">c2db3D</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent rna helicase vasa; <b>PDBTitle:</b> structural basis for rna unwinding by the dead-box protein2 drosophila vasa
47	<a href="#">c3kx2A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna helicase prp43; <b>PDBTitle:</b> crystal structure of prp43p in complex with adp
48	<a href="#">c5vheA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deah (asp-glu-ala-his) box polypeptide 36; <b>PDBTitle:</b> dhx36 in complex with the c-myc g-quadruplex
49	<a href="#">c6fa5A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mrna splicing factor; <b>PDBTitle:</b> crystal structure of the deah-box helicase prp2 in complex with adp
50	<a href="#">c5mqfq</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> splicing <b>Chain:</b> Q: <b>PDB Molecule:</b> protein bud31 homolog; <b>PDBTitle:</b> cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
51	<a href="#">c5mq0V</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> splicing <b>Chain:</b> V: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna helicase prp22; <b>PDBTitle:</b> structure of a spliceosome remodeled for exon ligation
52	<a href="#">c5ylzW</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> splicing <b>Chain:</b> W: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna helicase prp22; <b>PDBTitle:</b> cryo-em structure of the post-catalytic spliceosome from saccharomyces2 cerevisiae at 3.6 angstrom
53	<a href="#">c5zamA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase/protein binding/rna <b>Chain:</b> A: <b>PDB Molecule:</b> endoribonuclease dicer; <b>PDBTitle:</b> cryo-em structure of human dicer and its complexes with a pre-mirna2 substrate

54	<a href="#">c4d25A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bmvlg protein; <b>PDBTitle:</b> crystal structure of the bombyx mori vasa helicase (e339q)2 in complex with rna and amppnp
55	<a href="#">c5z58x</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> splicing <b>Chain:</b> X: <b>PDB Molecule:</b> smad nuclear-interacting protein 1; <b>PDBTitle:</b> cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
56	<a href="#">c4pxaA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> translation, rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx3x; <b>PDBTitle:</b> dead-box rna helicase ddx3x cancer-associated mutant d354v
57	<a href="#">c5lj5Q</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> splicing <b>Chain:</b> Q: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna helicase prp16; <b>PDBTitle:</b> overall structure of the yeast spliceosome immediately after2 branching.
58	<a href="#">c5wsge</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> E: <b>PDB Molecule:</b> saccharomyces cerevisiae s288c snr6 snrna; <b>PDBTitle:</b> cryo-em structure of the catalytic step ii spliceosome (c* complex) at2 4.0 angstrom resolution
59	<a href="#">c2jlrA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease subunit ns3; <b>PDBTitle:</b> dengue virus 4 ns3 helicase in complex with amppnp
60	<a href="#">c1hv8B</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative atp-dependent rna helicase mj0669; <b>PDBTitle:</b> crystal structure of a dead box protein from the2 hyperthermophile methanococcus jannaschii
61	<a href="#">c1wp9D</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent rna helicase, putative; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus hef helicase domain
62	<a href="#">c5lqwO</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> splicing <b>Chain:</b> O: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna helicase-like <b>PDBTitle:</b> yeast activated spliceosome
63	<a href="#">c5xdrA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna helicase dhx15; <b>PDBTitle:</b> crystal structure of human deah-box rna helicase dhx15 in complex with2 adp
64	<a href="#">c6c0fp</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l17-a; <b>PDBTitle:</b> yeast nucleolar pre-60s ribosomal subunit (state 2)
65	<a href="#">c2v6jA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna helicase; <b>PDBTitle:</b> kokobera virus helicase: mutant met47thr
66	<a href="#">c1s2mA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative atp-dependent rna helicase dhh1; <b>PDBTitle:</b> crystal structure of the dead box protein dhh1p
67	<a href="#">c6h57A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase dhr1; <b>PDBTitle:</b> crystal structure of s. cerevisiae deah-box rna helicase dhr1,2 essential for small ribosomal subunit biogenesis
68	<a href="#">c4ct4B</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx6; <b>PDBTitle:</b> cnot1 mif4g domain - ddx6 complex
69	<a href="#">c3oiyB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> reverse gyrase helicase domain; <b>PDBTitle:</b> helicase domain of reverse gyrase from thermotoga maritima
70	<a href="#">c3ewsA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx19b; <b>PDBTitle:</b> human dead-box rna-helicase ddx19 in complex with adp
71	<a href="#">c2ocaA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase uvsw; <b>PDBTitle:</b> the crystal structure of t4 uvsw
72	<a href="#">c3i5yA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase mss116; <b>PDBTitle:</b> structure of mss116p bound to ssrna containing a single 5-bru and amp-2 pnp
73	<a href="#">c1xtkA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase p47; <b>PDBTitle:</b> structure of decd to dead mutation of human uap56
74	<a href="#">c5dtuA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prp28; <b>PDBTitle:</b> crystal structure of the rna-helicase prp28 from chaetomium2 thermophilum bound to adp
75	<a href="#">c6o16A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> deah (asp-glu-ala-his) box polypeptide 37; <b>PDBTitle:</b> crystal structure of murine dhx37 in complex with rna
76	<a href="#">c3fhtA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx19b; <b>PDBTitle:</b> crystal structure of human dbp5 in complex with amppnp and rna
77	<a href="#">c6nmiA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription and dna repair factor iih helicase <b>PDBTitle:</b> cryo-em structure of the human tfiih core complex
78	<a href="#">c2z0mA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 337aa long hypothetical atp-dependent rna <b>PDBTitle:</b> crystal structure of hypothetical atp-dependent rna2 helicase from sulfolobus tokodaii

79	<a href="#">c4nhoA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx23; <b>PDBTitle:</b> structure of the spliceosomal dead-box protein prp28
80	<a href="#">c5supB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent rna helicase sub2; <b>PDBTitle:</b> structure of mrna export factors
81	<a href="#">c5ivIA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dead-box atp-dependent rna helicase csha; <b>PDBTitle:</b> csha helicase
82	<a href="#">c3pexA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dbp5; <b>PDBTitle:</b> s. cerevisiae dbp5 I327v bound to gle1 h337r and ip6
83	<a href="#">c2vbcA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dengue 4 ns3 full-length protein; <b>PDBTitle:</b> crystal structure of the ns3 protease-helicase from dengue2 virus
84	<a href="#">c2z83A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> helicase/nucleoside triphosphatase; <b>PDBTitle:</b> crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8
85	<a href="#">c2hxyC</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx48; <b>PDBTitle:</b> crystal structure of human apo-eif4aiii
86	<a href="#">c4kbfA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> heat resistant rna dependent atpase; <b>PDBTitle:</b> two different open conformations of the helicase core of the rna2 helicase hera
87	<a href="#">c5aorA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> dosage compensation regulator; <b>PDBTitle:</b> structure of mle rna adp alf4 complex
88	<a href="#">c4qqxA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated helicase, cas3 family; <b>PDBTitle:</b> crystal structure of t. fusca cas3-atp
89	<a href="#">c6i3oA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative pre-mrna splicing factor; <b>PDBTitle:</b> crystal structure of deah-box atpase prp22
90	<a href="#">c4nl4H</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> primosome assembly protein pria; <b>PDBTitle:</b> pria helicase bound to adp
91	<a href="#">c2vsxA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> translation/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase eif4a; <b>PDBTitle:</b> crystal structure of a translation initiation complex
92	<a href="#">c1ymfA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein [contains: flavivirin protease ns3 <b>PDBTitle:</b> crystal structure of yellow fever virus ns3 helicase complexed with2 adp
93	<a href="#">c2fwrA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad25; <b>PDBTitle:</b> structure of archaeoglobus fulgidis xpb
94	<a href="#">c5ivvV</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> V: <b>PDB Molecule:</b> tfiib basal transcription factor complex helicase xpb <b>PDBTitle:</b> human core tfiih bound to dna within the pic
95	<a href="#">c2wv9A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flavivirin protease ns2b regulatory subunit, flavivirin <b>PDBTitle:</b> crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus
96	<a href="#">c3tbkA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rig-i helicase domain; <b>PDBTitle:</b> mouse rig-i atpase domain
97	<a href="#">c3eiqD</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase/antitumor protein <b>Chain:</b> D: <b>PDB Molecule:</b> eukaryotic initiation factor 4a-i; <b>PDBTitle:</b> crystal structure of pdcd4-eif4a
98	<a href="#">c4q2dA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated helicase cas3; <b>PDBTitle:</b> crystal structure of crispr-associated protein in complex with 2'-2 deoxyadenosine 5'-triphosphate
99	<a href="#">c4xqkB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> llabiii; <b>PDBTitle:</b> atp-dependent type isp restriction-modification enzyme llabiii bound2 to dna
100	<a href="#">c2qeQA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flavivirin protease ns3 catalytic subunit; <b>PDBTitle:</b> crystal structure of kunjin virus ns3 helicase
101	<a href="#">c6ro4A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> translocase <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription and dna repair factor iih helicase <b>PDBTitle:</b> structure of the core tfiih-xpa-dna complex
102	<a href="#">c2i4iA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx3x; <b>PDBTitle:</b> crystal structure of human dead-box rna helicase ddx3x
103	<a href="#">c5fmf1</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transcription <b>Chain:</b> 1: <b>PDB Molecule:</b> dna repair helicase rad25, ssl2; <b>PDBTitle:</b> the p-lobe of rna polymerase ii pre-initiation complex
104	<a href="#">c3dmqA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase-associated protein rapa; <b>PDBTitle:</b> crystal structure of rapa, a swi2/snf2 protein that recycles rna2 polymerase during transcription

105	<a href="#">c5of4A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tfiih basal transcription factor complex helicase xpb <b>PDBTitle:</b> the cryo-em structure of human tfiih
106	<a href="#">c2fsgA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> preprotein translocase seca subunit; <b>PDBTitle:</b> complex seca:atp from escherichia coli
107	<a href="#">d2bmfa2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
108	<a href="#">c1c4oA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna nucleotide excision repair enzyme uvrB; <b>PDBTitle:</b> crystal structure of the dna nucleotide excision repair enzyme uvrB2 from thermus thermophilus
109	<a href="#">c1a1vA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (ns3 protein); <b>PDBTitle:</b> hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
110	<a href="#">c5tnuB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> dna-dependent atpase xpbii; <b>PDBTitle:</b> s. tokodaii xpb ii crystal structure at 3.0 angstrom resolution
111	<a href="#">c2d7dA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> uvrabc system protein b; <b>PDBTitle:</b> structural insights into the cryptic dna dependent atp-ase2 activity of uvrB
112	<a href="#">c5x0yO_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> structural protein/hydrolase/dna <b>Chain:</b> O: <b>PDB Molecule:</b> transcription regulatory protein snf2; <b>PDBTitle:</b> complex of snf2-nucleosome complex with snf2 bound to sh2 of the2 nucleosome
113	<a href="#">c5lkIB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of full-length csfv ns3/4a
114	<a href="#">c4cbhC_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> serine protease ns3; <b>PDBTitle:</b> pestivirus ns3 helicase
115	<a href="#">c2f55C_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> C: <b>PDB Molecule:</b> polyprotein; <b>PDBTitle:</b> two hepatitis c virus ns3 helicase domains complexed with the same2 strand of dna
116	<a href="#">c2fsgB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> preprotein translocase seca subunit; <b>PDBTitle:</b> complex seca:atp from escherichia coli
117	<a href="#">c3mwyW_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> W: <b>PDB Molecule:</b> chromo domain-containing protein 1; <b>PDBTitle:</b> crystal structure of the chromodomain-atpase portion of the yeast chd12 chromatin remodeler
118	<a href="#">c5o9gW_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> W: <b>PDB Molecule:</b> chromo domain-containing protein 1; <b>PDBTitle:</b> structure of nucleosome-chd1 complex
119	<a href="#">c1z3iX_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> recombination/dna binding <b>Chain:</b> X: <b>PDB Molecule:</b> similar to rad54-like; <b>PDBTitle:</b> structure of the swi2/snf2 chromatin remodeling domain of eukaryotic2 rad54
120	<a href="#">c5vvrM_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transcription/rna/dna <b>Chain:</b> M: <b>PDB Molecule:</b> dna repair and recombination protein rad26; <b>PDBTitle:</b> ternary complex of rna pol ii, transcription scaffold and rad26