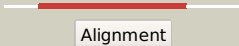



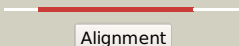

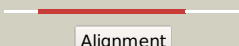

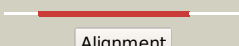

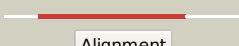

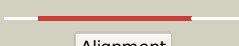

















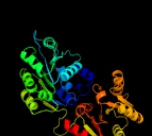


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3211\_(rhE)\_3587794\_3589377  
 Date Thu Aug 8 16:20:41 BST 2019  
 Unique Job ID 9136cc7d2bcb626e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ljyA_</a>	 Alignment		100.0	28	<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
2	<a href="#">c4cdgA_</a>	 Alignment		100.0	21	<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
3	<a href="#">c4w7sA_</a>	 Alignment		100.0	31	<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
4	<a href="#">c2v1xB_</a>	 Alignment		100.0	17	<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
5	<a href="#">c2db3D_</a>	 Alignment		100.0	31	<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
6	<a href="#">c1oywA_</a>	 Alignment		100.0	19	<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
7	<a href="#">c1s2mA_</a>	 Alignment		100.0	32	<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
8	<a href="#">c5lstA_</a>	 Alignment		100.0	19	<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.
9	<a href="#">c4q47A_</a>	 Alignment		100.0	19	<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
10	<a href="#">c4pxaA_</a>	 Alignment		100.0	35	<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
11	<a href="#">c5dtuA_</a>	 Alignment		100.0	35	<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

12	<a href="#">c4ct4B_</a>	Alignment		100.0	30	<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
13	<a href="#">c4d25A_</a>	Alignment		100.0	33	<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
14	<a href="#">c6c0fp_</a>	Alignment		100.0	27	<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)
15	<a href="#">c5supB_</a>	Alignment		100.0	25	<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
16	<a href="#">c5v9xA_</a>	Alignment		100.0	22	<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
17	<a href="#">c4nhoA_</a>	Alignment		100.0	35	<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
18	<a href="#">c3i5yA_</a>	Alignment		100.0	26	<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
19	<a href="#">c1xtkA_</a>	Alignment		100.0	26	<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
20	<a href="#">c1hv8B_</a>	Alignment		100.0	39	<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
21	<a href="#">c3ewsA_</a>	Alignment	not modelled	100.0	29	<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
22	<a href="#">c4kbfA_</a>	Alignment	not modelled	100.0	44	<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
23	<a href="#">c3fhtA_</a>	Alignment	not modelled	100.0	28	<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
24	<a href="#">c2hxyC_</a>	Alignment	not modelled	100.0	33	<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
25	<a href="#">c1gl9B_</a>	Alignment	not modelled	100.0	23	<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
26	<a href="#">c2i4iA_</a>	Alignment	not modelled	100.0	35	<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
27	<a href="#">c2vsxA_</a>	Alignment	not modelled	100.0	31	<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
28	<a href="#">c3pexA_</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent rna helicase dbp5; <b>PDBTitle:</b> s. cerevisiae dbp5 l327v bound to gle1 h337r and ip6
						<b>PDB header:</b> hydrolase/antitumor protein

29	<a href="#">c3eigD_</a>	Alignment	not modelled	100.0	30	<b>Chain:</b> D: <b>PDB Molecule:</b> eukaryotic initiation factor 4a-i; <b>PDBTitle:</b> crystal structure of pdcd4-eif4a
30	<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).
31	<a href="#">c5iv1A_</a>	Alignment	not modelled	100.0	46	<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
32	<a href="#">c5agaA_</a>	Alignment	not modelled	100.0	23	<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
33	<a href="#">c2xgiA_</a>	Alignment	not modelled	100.0	21	<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
34	<a href="#">c6iehB_</a>	Alignment	not modelled	100.0	21	<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
35	<a href="#">c5lqwC_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna-splicing helicase brr2; <b>PDBTitle:</b> yeast activated spliceosome
36	<a href="#">c4xgtA_</a>	Alignment	not modelled	100.0	21	<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
37	<a href="#">c2va8A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
38	<a href="#">c2z0mA_</a>	Alignment	not modelled	100.0	39	<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 sulfobolus tokodaii
39	<a href="#">c6iegA_</a>	Alignment	not modelled	100.0	21	<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
40	<a href="#">c1gm5A_</a>	Alignment	not modelled	100.0	19	<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
41	<a href="#">c6c90A_</a>	Alignment	not modelled	100.0	20	<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
42	<a href="#">c4bgdA_</a>	Alignment	not modelled	100.0	18	<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
43	<a href="#">c3l9oA_</a>	Alignment	not modelled	100.0	21	<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
44	<a href="#">c2zj8A_</a>	Alignment	not modelled	100.0	23	<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
45	<a href="#">c3bxzA_</a>	Alignment	not modelled	100.0	20	<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
46	<a href="#">c4ddvA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> reverse gyrase; <b>PDBTitle:</b> thermotoga maritima reverse gyrase, triclinic form
47	<a href="#">c5dcaA_</a>	Alignment	not modelled	100.0	19	<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
48	<a href="#">c2zj2A_</a>	Alignment	not modelled	100.0	23	<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
49	<a href="#">c5m52B_</a>	Alignment	not modelled	100.0	18	<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-length in complex with prp8 jab12 domain
50	<a href="#">c5m59C_</a>	Alignment	not modelled	100.0	22	<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
51	<a href="#">c6ah0D_</a>	Alignment	not modelled	100.0	19	<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)
52	<a href="#">c4a4zA_</a>	Alignment	not modelled	100.0	20	<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
53	<a href="#">c4f92B_</a>	Alignment	not modelled	100.0	18	<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 s10871
54	<a href="#">c3tmiA_</a>	Alignment	not modelled	100.0	19	<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
						<b>PDB header:</b> hydrolase

55	<a href="#">c4buJA_</a>	Alignment	not modelled	100.0	20	<b>Chain:</b> A: <b>PDB Molecule:</b> antiviral helicase ski2; <b>PDBTitle:</b> crystal structure of the s. cerevisiae ski2-3-8 complex
56	<a href="#">c3jcrC_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> hbrr2; <b>PDBTitle:</b> 3d structure determination of the human*u4/u6.u5* tri-snrrnp complex
57	<a href="#">c5jb2A_</a>	Alignment	not modelled	100.0	25	<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.
58	<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).
59	<a href="#">c2p6uA_</a>	Alignment	not modelled	100.0	22	<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
60	<a href="#">c2eyqA_</a>	Alignment	not modelled	100.0	20	<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
61	<a href="#">c4gl2A_</a>	Alignment	not modelled	100.0	20	<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
62	<a href="#">c3kx2A_</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 prp43; <b>PDBTitle:</b> crystal structure of prp43p in complex with adp
63	<a href="#">c2fsgA_</a>	Alignment	not modelled	100.0	20	<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
64	<a href="#">c1wp9D_</a>	Alignment	not modelled	100.0	24	<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
65	<a href="#">c6iczy_</a>	Alignment	not modelled	100.0	17	<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
66	<a href="#">c3fhoB_</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent rna helicase dbp5; <b>PDBTitle:</b> structure of s. pombe dbp5
67	<a href="#">c2llrA_</a>	Alignment	not modelled	100.0	17	<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
68	<a href="#">c3rc8A_</a>	Alignment	not modelled	100.0	20	<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
69	<a href="#">c5vheA_</a>	Alignment	not modelled	100.0	22	<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
70	<a href="#">c5zamA_</a>	Alignment	not modelled	100.0	20	<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
71	<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
72	<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
73	<a href="#">c5xdrA_</a>	Alignment	not modelled	100.0	17	<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
74	<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
75	<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)
76	<a href="#">c5n8zA_</a>	Alignment	not modelled	100.0	20	<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
77	<a href="#">c6h57A_</a>	Alignment	not modelled	100.0	17	<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
78	<a href="#">c6heqA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase hrpb; <b>PDBTitle:</b> crystal structure of escherichia coli deah/rha helicase hrpb
79	<a href="#">c5mq0V_</a>	Alignment	not modelled	100.0	18	<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

80	<a href="#">c2fsgB_</a>	Alignment	not modelled	100.0	24	<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
81	<a href="#">c2ocaA_</a>	Alignment	not modelled	100.0	17	<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
82	<a href="#">c6fa5A_</a>	Alignment	not modelled	100.0	17	<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
83	<a href="#">c5lqwO_</a>	Alignment	not modelled	100.0	19	<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
84	<a href="#">c5lj5Q_</a>	Alignment	not modelled	100.0	19	<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.
85	<a href="#">c6jdeB_</a>	Alignment	not modelled	100.0	20	<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
86	<a href="#">c1c4oA_</a>	Alignment	not modelled	100.0	18	<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
87	<a href="#">c6f4aB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> suv3 helicase; <b>PDBTitle:</b> yeast mitochondrial rna degradosome complex mtexo
88	<a href="#">c2z83A_</a>	Alignment	not modelled	100.0	18	<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
89	<a href="#">c5z58x_</a>	Alignment	not modelled	100.0	23	<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.
90	<a href="#">c1ymfA_</a>	Alignment	not modelled	100.0	17	<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
91	<a href="#">c1tf2A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> preprotein translocase seca subunit; <b>PDBTitle:</b> crystal structure of seca:adp in an open conformation from2 bacillus subtilis
92	<a href="#">c2v6jA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna helicase; <b>PDBTitle:</b> kokobera virus helicase: mutant met47thr
93	<a href="#">c2wv9A_</a>	Alignment	not modelled	100.0	15	<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
94	<a href="#">c2vbcA_</a>	Alignment	not modelled	100.0	16	<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
95	<a href="#">c3fe2B_</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx5; <b>PDBTitle:</b> human dead-box rna helicase ddx5 (p68), conserved domain i in complex2 with adp
96	<a href="#">c5ivwV_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> V: <b>PDB Molecule:</b> tfiih basal transcription factor complex helicase xpb <b>PDBTitle:</b> human core tfiih bound to dna within the pic
97	<a href="#">c3dl8B_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> protein translocase subunit seca; <b>PDBTitle:</b> structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
98	<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
99	<a href="#">c3tbkA_</a>	Alignment	not modelled	100.0	18	<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
100	<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
101	<a href="#">c4xqkB_</a>	Alignment	not modelled	100.0	15	<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
102	<a href="#">c5gvrA_</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx41; <b>PDBTitle:</b> crystal structure of the ddx41 dead domain in an apo closed form
103	<a href="#">c2fwrA_</a>	Alignment	not modelled	100.0	21	<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
104	<a href="#">c4px9C_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> translation, rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent rna helicase ddx3x; <b>PDBTitle:</b> dead-box rna helicase ddx3x domain 1 with n-terminal

						atp-binding loop
105	<a href="#">c6nmiA_</a>	Alignment	not modelled	100.0	15	<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
106	<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
107	<a href="#">c4nl4H_</a>	Alignment	not modelled	100.0	23	<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
108	<a href="#">c2d7dA_</a>	Alignment	not modelled	100.0	20	<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 uvrbc
109	<a href="#">c5aorA_</a>	Alignment	not modelled	100.0	24	<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
110	<a href="#">c6i3oA_</a>	Alignment	not modelled	100.0	19	<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
111	<a href="#">c2qeqA_</a>	Alignment	not modelled	100.0	15	<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
112	<a href="#">c6ro4A_</a>	Alignment	not modelled	100.0	15	<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
113	<a href="#">c5tnuB_</a>	Alignment	not modelled	100.0	20	<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
114	<a href="#">c1a1vA_</a>	Alignment	not modelled	100.0	18	<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
115	<a href="#">c4q2dA_</a>	Alignment	not modelled	100.0	18	<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
116	<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
117	<a href="#">d2bmfa2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
118	<a href="#">c2f55C_</a>	Alignment	not modelled	100.0	23	<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
119	<a href="#">d2j0sa1</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
120	<a href="#">d1q0ua_</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain