
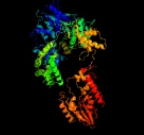



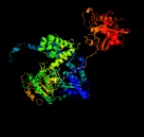



















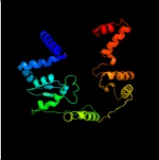







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3202c_(-)_3577030_3580197
Date	Thu Aug 8 16:20:39 BST 2019
Unique Job ID	841eb9773cd51392

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3u44B_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent helicase/deoxyribonuclease subunit b; <b>PDBTitle:</b> crystal structure of addab-dna complex
2	<a href="#">c3u4qA_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent helicase/nuclease subunit a; <b>PDBTitle:</b> structure of addab-dna complex at 2.8 angstroms
3	<a href="#">c1w36E_</a>	 Alignment		100.0	18	<b>PDB header:</b> recombination <b>Chain:</b> E: <b>PDB Molecule:</b> exodeoxyribonuclease v beta chain; <b>PDBTitle:</b> recbcd:dna complex
4	<a href="#">c2is6B_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna helicase ii; <b>PDBTitle:</b> crystal structure of uvrd-dna-adpmgf3 ternary complex
5	<a href="#">c1uaaB_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> protein (atp-dependent dna helicase rep.); <b>PDBTitle:</b> e. coli rep helicase/dna complex
6	<a href="#">c4c30I_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> I: <b>PDB Molecule:</b> dna helicase ii; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans uvrd in2 complex with dna, form 2
7	<a href="#">c1pjrA_</a>	 Alignment		100.0	19	<b>PDB header:</b> helicase <b>Chain:</b> A: <b>PDB Molecule:</b> pcra; <b>PDBTitle:</b> structure of dna helicase
8	<a href="#">c2pjrF_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> F: <b>PDB Molecule:</b> protein (helicase pcra); <b>PDBTitle:</b> helicase product complex
9	<a href="#">c3lfuA_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna helicase ii; <b>PDBTitle:</b> crystal structure of e. coli uvrd
10	<a href="#">c1w36F_</a>	 Alignment		100.0	13	<b>PDB header:</b> recombination <b>Chain:</b> F: <b>PDB Molecule:</b> exodeoxyribonuclease v gamma chain; <b>PDBTitle:</b> recbcd:dna complex
11	<a href="#">d1w36b1</a>	 Alignment		100.0	20	<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

12	<a href="#">d1uaaa1</a>	Alignment		100.0	19	<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
13	<a href="#">d1pjra1</a>	Alignment		100.0	18	<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
14	<a href="#">d1uaaa2</a>	Alignment		100.0	19	<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
15	<a href="#">c1qhhB_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (pcra (subunit)); <b>PDBTitle:</b> structure of dna helicase with adpnp
16	<a href="#">d1w36b2</a>	Alignment		100.0	18	<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
17	<a href="#">d1pjra2</a>	Alignment		100.0	22	<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
18	<a href="#">d1w36c2</a>	Alignment		100.0	15	<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
19	<a href="#">c5eaxB_</a>	Alignment		99.9	26	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna replication atp-dependent helicase/nuclease dna2; <b>PDBTitle:</b> crystal structure of dna2 in complex with an ssdna
20	<a href="#">c1qhhA_</a>	Alignment		99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (pcra (subunit)); <b>PDBTitle:</b> structure of dna helicase with adpnp
21	<a href="#">c4b3gA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein smubp-2; <b>PDBTitle:</b> crystal structure of ighmbp2 helicase in complex with rna
22	<a href="#">c3upuC_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent dna helicase dda; <b>PDBTitle:</b> crystal structure of the t4 phage sf1b helicase dda
23	<a href="#">c2wjyA_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of nonsense transcripts 1; <b>PDBTitle:</b> crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
24	<a href="#">c2xzlA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent helicase nam7; <b>PDBTitle:</b> upf1-rna complex
25	<a href="#">c2gk7A_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of nonsense transcripts 1; <b>PDBTitle:</b> structural and functional insights into the human upf1 helicase core
26	<a href="#">c5wwpA_</a>	Alignment	not modelled	99.8	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> orf1ab; <b>PDBTitle:</b> crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
27	<a href="#">c3e1sA_</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exodeoxyribonuclease v, subunit recd; <b>PDBTitle:</b> structure of an n-terminal truncation of deinococcus radiodurans recd2
28	<a href="#">c1w36G_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> exodeoxyribonuclease v alpha chain; <b>PDBTitle:</b> recbcd:dna complex

29	<a href="#">c3gp8A</a>	Alignment	not modelled	99.8	39	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> exodeoxyribonuclease v, subunit recd, putative; <b>PDBTitle:</b> crystal structure of the binary complex of recd2 with dna
30	<a href="#">c5ld2D</a>	Alignment	not modelled	99.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> recbcd enzyme subunit recd; <b>PDBTitle:</b> cryo-em structure of recbcd+dna complex revealing activated nuclease2 domain
31	<a href="#">c4pj3A</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> intron-binding protein aquarius; <b>PDBTitle:</b> structural insight into the function and evolution of the spliceosomal2 helicase aquarius, structure of aquarius in complex with amppnp
32	<a href="#">c5mznA</a>	Alignment	not modelled	99.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> helicase sen1,helicase sen1; <b>PDBTitle:</b> helicase sen1
33	<a href="#">c4ic1D</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of sso0001
34	<a href="#">c5wvpB</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> orf1ab; <b>PDBTitle:</b> crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
35	<a href="#">c2pjrB</a>	Alignment	not modelled	99.7	31	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> protein (helicase pcra); <b>PDBTitle:</b> helicase product complex
36	<a href="#">c1qhdD</a>	Alignment	not modelled	99.7	30	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (pcra (subunit)); <b>PDBTitle:</b> structure of dna helicase with adpnp
37	<a href="#">c3jb9X</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> X: <b>PDB Molecule:</b> pre-mrna-splicing factor cwf11; <b>PDBTitle:</b> cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
38	<a href="#">c5n8oA</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna helicase i; <b>PDBTitle:</b> cryo em structure of the conjugative relaxase trai of the f/r1 plasmid2 system
39	<a href="#">c4onbA</a>	Alignment	not modelled	99.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated exonuclease, cas4 family; <b>PDBTitle:</b> crystal structure of crispr-associated exonuclease (cas4 family) from2 pyrobaculum calidifontis jcm 11548
40	<a href="#">c5o6dB</a>	Alignment	not modelled	99.6	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent dna helicase pif1; <b>PDBTitle:</b> structure of scpif1 in complex with polydt and atpgs
41	<a href="#">d1w36b3</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Exodeoxyribonuclease V beta chain (RecB), C-terminal domain
42	<a href="#">c4n0oC</a>	Alignment	not modelled	99.5	27	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> C: <b>PDB Molecule:</b> replicase polyprotein 1ab; <b>PDBTitle:</b> complex structure of arterivirus nonstructural protein 10 (helicase)2 with dna
43	<a href="#">d1w36d1</a>	Alignment	not modelled	99.4	21	<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
44	<a href="#">c3l0aA</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative exonuclease; <b>PDBTitle:</b> crystal structure of the c-terminal domain of a putative exonuclease (rer070207002219) from2 eubacterium rectale at 2.19 a resolution
45	<a href="#">d1w36d2</a>	Alignment	not modelled	99.3	29	<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
46	<a href="#">c3dmnA</a>	Alignment	not modelled	99.3	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna helicase; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of a possilbe dna2 helicase from lactobacillus plantarun wcf51
47	<a href="#">c3vkwA</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> replicase large subunit; <b>PDBTitle:</b> crystal structure of the superfamily 1 helicase from tomato mosaïc2 virus
48	<a href="#">c5fhhA</a>	Alignment	not modelled	99.2	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase pif1; <b>PDBTitle:</b> structure of human pif1 helicase domain residues 200-641
49	<a href="#">c5ftbA</a>	Alignment	not modelled	99.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tpr domain protein; <b>PDBTitle:</b> crystal structure of pif1 helicase from bacteroides in2 complex with amppnp
50	<a href="#">c3b85A</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate starvation-inducible protein; <b>PDBTitle:</b> crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
51	<a href="#">c5zyuA</a>	Alignment	not modelled	99.0	16	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial genome maintenance exonuclease 1; <b>PDBTitle:</b> the crytal struture of humanmgme1 with single strand dna2
52	<a href="#">c3h4rA</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exodeoxyribonuclease 8; <b>PDBTitle:</b> crystal structure of e. coli rece exonuclease
53	<a href="#">c6jimA</a>	Alignment	not modelled	98.9	37	<b>PDB header:</b> viral protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> helicase; <b>PDBTitle:</b> viral helicase protein
54	<a href="#">c4on9B</a>	Alignment	not modelled	98.3	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx58;

						<b>PDBTitle:</b> dech box helicase domain <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
55	<a href="#">c3i5yA_</a>	Alignment	not modelled	98.2	7	
56	<a href="#">c5v9xA_</a>	Alignment	not modelled	98.0	16	<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
57	<a href="#">c4cbhC_</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> serine protease ns3; <b>PDBTitle:</b> pestivirus ns3 helicase
58	<a href="#">c5ivIA_</a>	Alignment	not modelled	97.8	13	<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
59	<a href="#">c4ddvA_</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> reverse gyrase; <b>PDBTitle:</b> thermotoga maritima reverse gyrase, triclinic form
60	<a href="#">c4nl4H_</a>	Alignment	not modelled	97.8	17	<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
61	<a href="#">c2wv9A_</a>	Alignment	not modelled	97.7	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
62	<a href="#">c5xdrA_</a>	Alignment	not modelled	97.7	13	<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
63	<a href="#">c6c90A_</a>	Alignment	not modelled	97.7	10	<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
64	<a href="#">c5lklB_</a>	Alignment	not modelled	97.7	11	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of full-lengh csfV ns3/4a
65	<a href="#">c6o16A_</a>	Alignment	not modelled	97.7	13	<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
66	<a href="#">c1gm5A_</a>	Alignment	not modelled	97.7	14	<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
67	<a href="#">d1gkub1</a>	Alignment	not modelled	97.7	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Helicase-like "domain" of reverse gyrase
68	<a href="#">c4ljyA_</a>	Alignment	not modelled	97.7	16	<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
69	<a href="#">c4qqxA_</a>	Alignment	not modelled	97.7	14	<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
70	<a href="#">c4nl8E_</a>	Alignment	not modelled	97.7	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> primosome assembly protein pria; <b>PDBTitle:</b> pria helicase bound to ssb c-terminal tail peptide
71	<a href="#">c6hegA_</a>	Alignment	not modelled	97.6	17	<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/rna helicase hrpb
72	<a href="#">c6iehB_</a>	Alignment	not modelled	97.6	11	<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
73	<a href="#">c2va8A_</a>	Alignment	not modelled	97.6	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
74	<a href="#">c3kx2A_</a>	Alignment	not modelled	97.6	10	<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
75	<a href="#">c1wp9D_</a>	Alignment	not modelled	97.6	12	<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
76	<a href="#">c3tbkA_</a>	Alignment	not modelled	97.6	11	<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
77	<a href="#">c5agaA_</a>	Alignment	not modelled	97.6	11	<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
78	<a href="#">c3pexA_</a>	Alignment	not modelled	97.5	13	<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
79	<a href="#">c6h57A_</a>	Alignment	not modelled	97.5	14	<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
80	<a href="#">c2db3D_</a>	Alignment	not modelled	97.5	10	<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 <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
81	<a href="#">c5mq0V_</a>	Alignment	not modelled	97.5	8	
82	<a href="#">c2zj8A_</a>	Alignment	not modelled	97.5	10	<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
83	<a href="#">c6c0fp_</a>	Alignment	not modelled	97.5	16	<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)
84	<a href="#">c3tmiA_</a>	Alignment	not modelled	97.5	11	<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
85	<a href="#">c1xtkA_</a>	Alignment	not modelled	97.5	18	<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
86	<a href="#">c2xgjA_</a>	Alignment	not modelled	97.5	15	<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
87	<a href="#">c5z58x_</a>	Alignment	not modelled	97.5	10	<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.
88	<a href="#">c1xx6B_</a>	Alignment	not modelled	97.5	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
89	<a href="#">c6iczY_</a>	Alignment	not modelled	97.5	13	<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
90	<a href="#">c6i3oA_</a>	Alignment	not modelled	97.4	11	<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
91	<a href="#">c2hxyC_</a>	Alignment	not modelled	97.4	15	<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
92	<a href="#">c1s2mA_</a>	Alignment	not modelled	97.4	15	<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
93	<a href="#">c6jdeB_</a>	Alignment	not modelled	97.4	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
94	<a href="#">c5supB_</a>	Alignment	not modelled	97.4	13	<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
95	<a href="#">c5lj5Q_</a>	Alignment	not modelled	97.4	17	<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.
96	<a href="#">d1c4oa1</a>	Alignment	not modelled	97.4	21	<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
97	<a href="#">c3ly5A_</a>	Alignment	not modelled	97.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx18; <b>PDBTitle:</b> ddx18 dead-domain
98	<a href="#">c2zj2A_</a>	Alignment	not modelled	97.4	12	<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
99	<a href="#">c6fa5A_</a>	Alignment	not modelled	97.4	9	<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
100	<a href="#">c5n8zA_</a>	Alignment	not modelled	97.4	12	<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
101	<a href="#">c5wsge_</a>	Alignment	not modelled	97.4	13	<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
102	<a href="#">c1a1vA_</a>	Alignment	not modelled	97.4	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
103	<a href="#">c3dkpA_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx52; <b>PDBTitle:</b> human dead-box rna-helicase ddx52, conserved domain i in complex with2 adp
104	<a href="#">c3oiyB_</a>	Alignment	not modelled	97.4	14	<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
105	<a href="#">c4ct4B_</a>	Alignment	not modelled	97.3	13	<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
106	<a href="#">c3l9nA_</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dob1;

106	<a href="#">c390A</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> hydrolase <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
107	<a href="#">c4xgtA</a>	Alignment	not modelled	97.3	14	<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
108	<a href="#">c3ewsA</a>	Alignment	not modelled	97.3	15	<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
109	<a href="#">c1ymfA</a>	Alignment	not modelled	97.3	13	<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
110	<a href="#">c1gl9B</a>	Alignment	not modelled	97.3	11	<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
111	<a href="#">c5aorA</a>	Alignment	not modelled	97.3	14	<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
112	<a href="#">c3bxzA</a>	Alignment	not modelled	97.3	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Helicase-like "domain" of reverse gyrase
113	<a href="#">d1gl9b1</a>	Alignment	not modelled	97.3	9	<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
114	<a href="#">c4a4zA</a>	Alignment	not modelled	97.3	10	<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.
115	<a href="#">c5jb2A</a>	Alignment	not modelled	97.3	21	<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
116	<a href="#">c3fhoB</a>	Alignment	not modelled	97.3	17	<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
117	<a href="#">c4bujA</a>	Alignment	not modelled	97.2	11	<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
118	<a href="#">c3fhtA</a>	Alignment	not modelled	97.2	15	<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
119	<a href="#">c1hv8B</a>	Alignment	not modelled	97.2	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent rna helicase dbp5; <b>PDBTitle:</b> solution structure of amino-terminal domain of dbp5p
120	<a href="#">c2kbeA</a>	Alignment	not modelled	97.2	12	