
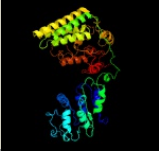





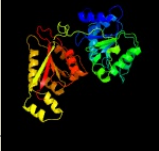








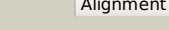

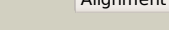

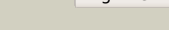
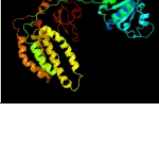


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1179c_(-)_1310485_1313304
Date	Wed Jul 31 22:05:26 BST 2019
Unique Job ID	3b4dfe1e70d5c4a0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5zamA_</a>	 Alignment		100.0	19	<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
2	<a href="#">c5jb2A_</a>	 Alignment		100.0	18	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> Igp2; <b>PDBTitle:</b> crystal structure of chicken Igp2 with 5'ppp 10-mer dsrna and adp-2 alf4-mg2+ at 2.2 a resolution.
3	<a href="#">c4gl2A_</a>	 Alignment		100.0	18	<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
4	<a href="#">c6nmiA_</a>	 Alignment		100.0	24	<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
5	<a href="#">c5jcfB_</a>	 Alignment		100.0	14	<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).
6	<a href="#">c3tmiA_</a>	 Alignment		100.0	15	<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
7	<a href="#">c4xqkB_</a>	 Alignment		100.0	20	<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
8	<a href="#">c5of4A_</a>	 Alignment		100.0	21	<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
9	<a href="#">c5ivwV_</a>	 Alignment		100.0	20	<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
10	<a href="#">c6ro4A_</a>	 Alignment		100.0	23	<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
11	<a href="#">c6buaA_</a>	 Alignment		100.0	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> dicer-2, isoform a; <b>PDBTitle:</b> drosophila dicer-2 apo homology model (helicase, platform-paz,2 rnaseiii domains)

12	<a href="#">c5x0yO_</a>	Alignment		100.0	15	<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 shl2 of the2 nucleosome
13	<a href="#">c3dmqA_</a>	Alignment		100.0	18	<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
14	<a href="#">c3mwyW_</a>	Alignment		100.0	17	<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
15	<a href="#">c1z3iX_</a>	Alignment		100.0	12	<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
16	<a href="#">c5o9gW_</a>	Alignment		100.0	14	<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
17	<a href="#">c6jdeB_</a>	Alignment		100.0	29	<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
18	<a href="#">c5fmf1_</a>	Alignment		100.0	21	<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
19	<a href="#">c1wp9D_</a>	Alignment		100.0	16	<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
20	<a href="#">c6iehB_</a>	Alignment		100.0	17	<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
21	<a href="#">c5vvrM_</a>	Alignment	not modelled	100.0	18	<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
22	<a href="#">c5jxrB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> chromatin-remodeling complex atpase-like protein; <b>PDBTitle:</b> crystal structure of mtiswi
23	<a href="#">c6g7eB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> helicase-like protein; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum mot1 (e1434q, 1837-18862 deletion mutant)
24	<a href="#">c4bujA_</a>	Alignment	not modelled	100.0	15	<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
25	<a href="#">c4on9B_</a>	Alignment	not modelled	100.0	15	<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
26	<a href="#">c2xgjA_</a>	Alignment	not modelled	100.0	16	<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
27	<a href="#">c6iegA_</a>	Alignment	not modelled	100.0	18	<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
28	<a href="#">c6iroL_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> L: <b>PDB Molecule:</b> iswi chromatin-remodeling complex atpase isw1; <b>PDBTitle:</b> the crosslinked complex of iswi-nucleosome in the adp-

						bound state
29	<a href="#">c4a4zA_</a>	Alignment	not modelled	100.0	18	<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
30	<a href="#">c6etxG_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> dna helicase ino80; <b>PDBTitle:</b> cryo-em structure of the human ino80 complex bound to nucleosome
31	<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
32	<a href="#">c6c90A_</a>	Alignment	not modelled	100.0	15	<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
33	<a href="#">c4xgtA_</a>	Alignment	not modelled	100.0	18	<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
34	<a href="#">c6gejM_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> nuclear protein <b>Chain:</b> M: <b>PDB Molecule:</b> helicase swr1; <b>PDBTitle:</b> chromatin remodeller-nucleosome complex at 3.6 a resolution.
35	<a href="#">c6ne3W_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> W: <b>PDB Molecule:</b> swi/snf-related matrix-associated actin-dependent regulator <b>PDBTitle:</b> cryo-em structure of singly-bound snf2h-nucleosome complex with snf2h2 bound at shl-2
36	<a href="#">c2fwrA_</a>	Alignment	not modelled	100.0	25	<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
37	<a href="#">c2ocaA_</a>	Alignment	not modelled	100.0	21	<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
38	<a href="#">c5agaA_</a>	Alignment	not modelled	100.0	18	<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
39	<a href="#">c2d7dA_</a>	Alignment	not modelled	100.0	16	<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
40	<a href="#">c1z63A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase/dna complex <b>Chain:</b> A: <b>PDB Molecule:</b> helicase of the snf2/rad54 family; <b>PDBTitle:</b> sulfobolus solfataricus swi2/snf2 atpase core in complex with dsdna
41	<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 uvrbc; <b>PDBTitle:</b> crystal structure of the dna nucleotide excision repair enzyme uvrbc2 from thermus thermophilus
42	<a href="#">c3l9oA_</a>	Alignment	not modelled	100.0	19	<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
43	<a href="#">c2va8A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
44	<a href="#">c6ah0D_</a>	Alignment	not modelled	100.0	21	<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)
45	<a href="#">c6fmIG_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> ino80; <b>PDBTitle:</b> cryoem structure ino80core nucleosome complex
46	<a href="#">c5v9xA_</a>	Alignment	not modelled	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
47	<a href="#">c5m59C_</a>	Alignment	not modelled	100.0	20	<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
48	<a href="#">c4f92B_</a>	Alignment	not modelled	100.0	22	<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 s1087l
49	<a href="#">c5dcaA_</a>	Alignment	not modelled	100.0	20	<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
50	<a href="#">c5m52B_</a>	Alignment	not modelled	100.0	21	<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
51	<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
52	<a href="#">c3h1tA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type i site-specific restriction-modification <b>PDBTitle:</b> the fragment structure of a putative hsdr subunit of a type2 i restriction enzyme from vibrio vulnificus yj016
53	<a href="#">c1gm5A_</a>	Alignment	not modelled	100.0	26	<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
						<b>PDB header:</b> hydrolase

54	<a href="#">c2zj8A_</a>	Alignment	not modelled	100.0	20	<b>Chain:</b> A: <b>PDB Molecule:</b> putative ski2-type helicase; <b>PDBTitle:</b> archaeal dna helicase hjm apo state in form 2
55	<a href="#">c3jcrC_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> hbr2; <b>PDBTitle:</b> 3d structure determination of the human* <u>4/u6.u5*</u> tri-snrrp complex
56	<a href="#">c4bgdA_</a>	Alignment	not modelled	100.0	22	<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
57	<a href="#">c5hzaA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> snf2-family atp dependent chromatin remodeling factor like <b>PDBTitle:</b> crystal structure of mtsnf2
58	<a href="#">c2v1xB_</a>	Alignment	not modelled	100.0	20	<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
59	<a href="#">c5tnuB_</a>	Alignment	not modelled	100.0	23	<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
60	<a href="#">c4cdgA_</a>	Alignment	not modelled	100.0	18	<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
61	<a href="#">c1oywA_</a>	Alignment	not modelled	100.0	20	<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
62	<a href="#">c2eyqA_</a>	Alignment	not modelled	100.0	23	<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
63	<a href="#">c2zj2A_</a>	Alignment	not modelled	100.0	20	<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
64	<a href="#">c2p6uA_</a>	Alignment	not modelled	100.0	24	<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
65	<a href="#">c4q47A_</a>	Alignment	not modelled	100.0	21	<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
66	<a href="#">c2w74B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> type i restriction enzyme ecor124ii r protein; <b>PDBTitle:</b> mutant (k220r) of the hsdR subunit of the ecor124i2 restriction enzyme in complex with atp
67	<a href="#">c4ddvA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> reverse gyrase; <b>PDBTitle:</b> thermotoga maritima reverse gyrase, triclinic form
68	<a href="#">c3oiyB_</a>	Alignment	not modelled	100.0	20	<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
69	<a href="#">c1q19B_</a>	Alignment	not modelled	100.0	19	<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
70	<a href="#">c51stA_</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 recq14 helicase.
71	<a href="#">c4lijyA_</a>	Alignment	not modelled	100.0	20	<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
72	<a href="#">c51b5C_</a>	Alignment	not modelled	99.9	28	<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).
73	<a href="#">c2db3D_</a>	Alignment	not modelled	99.9	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
74	<a href="#">d2fwra2</a>	Alignment	not modelled	99.9	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
75	<a href="#">c2z0mA_</a>	Alignment	not modelled	99.9	16	<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
76	<a href="#">c4pxaA_</a>	Alignment	not modelled	99.9	20	<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
77	<a href="#">c2w00B_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hsdr; <b>PDBTitle:</b> crystal structure of the hsdR subunit of the ecor124i restriction2 enzyme in complex with atp
78	<a href="#">c6bu9A_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> dicer-2, isoform a; <b>PDBTitle:</b> drosophila dicer-2 bound to blunt dsrna
79	<a href="#">c3i5yA_</a>	Alignment	not modelled	99.9	17	<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

80	<a href="#">c4w7sA</a>	Alignment	not modelled	99.9	14	<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
81	<a href="#">c3ewsA</a>	Alignment	not modelled	99.9	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
82	<a href="#">c1hv8B</a>	Alignment	not modelled	99.9	18	<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
83	<a href="#">c4d25A</a>	Alignment	not modelled	99.9	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
84	<a href="#">c4nl4H</a>	Alignment	not modelled	99.9	24	<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
85	<a href="#">c3bxzA</a>	Alignment	not modelled	99.9	25	<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
86	<a href="#">c3rc8A</a>	Alignment	not modelled	99.9	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
87	<a href="#">c1s2mA</a>	Alignment	not modelled	99.9	19	<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
88	<a href="#">c6c0fp</a>	Alignment	not modelled	99.9	21	<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)
89	<a href="#">c5ivIA</a>	Alignment	not modelled	99.9	17	<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
90	<a href="#">c5wsge</a>	Alignment	not modelled	99.9	17	<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
91	<a href="#">c4zcfC</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase-dna complex <b>Chain:</b> C: <b>PDB Molecule:</b> restriction endonuclease ecop15i, restriction subunit; <b>PDBTitle:</b> structural basis of asymmetric dna methylation and atp-triggered long-2 range diffusion by ecop15i
92	<a href="#">c4ct4B</a>	Alignment	not modelled	99.9	22	<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
93	<a href="#">c1xtkA</a>	Alignment	not modelled	99.9	16	<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
94	<a href="#">c6fa5A</a>	Alignment	not modelled	99.9	21	<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
95	<a href="#">d2eyqa3</a>	Alignment	not modelled	99.9	23	<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
96	<a href="#">c5supB</a>	Alignment	not modelled	99.9	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
97	<a href="#">c6iczy</a>	Alignment	not modelled	99.9	19	<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
98	<a href="#">c6h2jB</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> type i restriction enzyme r protein; <b>PDBTitle:</b> crystal structure of the hsdR subunit of the ecor124i restriction2 enzyme with the c-terminal domain
99	<a href="#">c6f4aB</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> suv3 helicase; <b>PDBTitle:</b> yeast mitochondrial rna degradosome complex mtexo
100	<a href="#">c3fhtA</a>	Alignment	not modelled	99.9	19	<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
101	<a href="#">c2hxyC</a>	Alignment	not modelled	99.9	17	<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
102	<a href="#">c2jlrA</a>	Alignment	not modelled	99.9	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
103	<a href="#">c5mq0V</a>	Alignment	not modelled	99.9	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
104	<a href="#">c5mqfq</a>	Alignment	not modelled	99.9	24	<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) <b>PDB header:</b> hydrolase

105	<a href="#">c5dtuA_</a>	Alignment	not modelled	99.9	21	<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
106	<a href="#">d1rifa_</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> DNA helicase UvsW
107	<a href="#">c2v6jA_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna helicase; <b>PDBTitle:</b> kokobera virus helicase: mutant met47thr
108	<a href="#">c6hegA_</a>	Alignment	not modelled	99.9	22	<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
109	<a href="#">c4qqxA_</a>	Alignment	not modelled	99.9	19	<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
110	<a href="#">c2vbcA_</a>	Alignment	not modelled	99.9	23	<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
111	<a href="#">c5vheA_</a>	Alignment	not modelled	99.9	18	<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
112	<a href="#">c2vsxA_</a>	Alignment	not modelled	99.9	18	<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
113	<a href="#">c5n8zA_</a>	Alignment	not modelled	99.9	21	<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
114	<a href="#">c5lqwO_</a>	Alignment	not modelled	99.9	18	<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
115	<a href="#">d2fz4a1</a>	Alignment	not modelled	99.9	28	<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
116	<a href="#">c4nhoA_</a>	Alignment	not modelled	99.9	20	<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
117	<a href="#">d1gm5a3</a>	Alignment	not modelled	99.9	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
118	<a href="#">c5z58x_</a>	Alignment	not modelled	99.9	25	<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.
119	<a href="#">c3pexA_</a>	Alignment	not modelled	99.9	22	<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
120	<a href="#">c2wv9A_</a>	Alignment	not modelled	99.9	25	<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