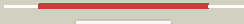



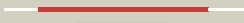



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3240c_(secA1)_3617679_3620528
Date	Thu Aug 8 16:20:44 BST 2019
Unique Job ID	b2171ae55cc8561f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1nl3B_</a>	 Alignment		100.0	100	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> preprotein translocase seca 1 subunit; <b>PDBTitle:</b> crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
2	<a href="#">c2ipcB_</a>	 Alignment		100.0	53	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> preprotein translocase seca subunit; <b>PDBTitle:</b> crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer
3	<a href="#">c2vdaA_</a>	 Alignment		100.0	51	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> translocase subunit seca; <b>PDBTitle:</b> solution structure of the seca-signal peptide complex
4	<a href="#">c3juxA_</a>	 Alignment		100.0	50	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein translocase subunit seca; <b>PDBTitle:</b> structure of the translocation atpase seca from thermotoga2 maritima
5	<a href="#">c3dinB_</a>	 Alignment		100.0	50	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> protein translocase subunit seca; <b>PDBTitle:</b> crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
6	<a href="#">c1tf2A_</a>	 Alignment		100.0	52	<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
7	<a href="#">c3dl8B_</a>	 Alignment		100.0	52	<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
8	<a href="#">c4uaqA_</a>	 Alignment		100.0	39	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein translocase subunit seca 2; <b>PDBTitle:</b> crystal structure of the accessory translocation atpase, seca2, from2 mycobacterium tuberculosis
9	<a href="#">c2fsgB_</a>	 Alignment		100.0	48	<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
10	<a href="#">c2fsgA_</a>	 Alignment		100.0	51	<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
11	<a href="#">d1nka3</a>	 Alignment		100.0	100	<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="#">c3bxzA_</a>	Alignment		100.0	61	<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
13	<a href="#">d1tf5a3</a>	Alignment		100.0	65	<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="#">d1nkt4</a>	Alignment		100.0	100	<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="#">d1tf5a2</a>	Alignment		100.0	35	<b>Fold:</b> Helical scaffold and wing domains of SecA <b>Superfamily:</b> Helical scaffold and wing domains of SecA <b>Family:</b> Helical scaffold and wing domains of SecA
16	<a href="#">d1nkt2</a>	Alignment		100.0	100	<b>Fold:</b> Helical scaffold and wing domains of SecA <b>Superfamily:</b> Helical scaffold and wing domains of SecA <b>Family:</b> Helical scaffold and wing domains of SecA
17	<a href="#">d1nkt1</a>	Alignment		100.0	100	<b>Fold:</b> Pre-protein crosslinking domain of SecA <b>Superfamily:</b> Pre-protein crosslinking domain of SecA <b>Family:</b> Pre-protein crosslinking domain of SecA
18	<a href="#">d1tf5a1</a>	Alignment		100.0	41	<b>Fold:</b> Pre-protein crosslinking domain of SecA <b>Superfamily:</b> Pre-protein crosslinking domain of SecA <b>Family:</b> Pre-protein crosslinking domain of SecA
19	<a href="#">d1tf5a4</a>	Alignment		100.0	63	<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
20	<a href="#">c2v1xB_</a>	Alignment		99.8	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
21	<a href="#">c4cdgA_</a>	Alignment	not modelled	99.8	19	<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
22	<a href="#">c1oywA_</a>	Alignment	not modelled	99.7	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
23	<a href="#">c1gm5A_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> helicase <b>Chain:</b> A: <b>PDB Molecule:</b> recq; <b>PDBTitle:</b> structure of recq bound to three-way dna junction
24	<a href="#">c5v9xA_</a>	Alignment	not modelled	99.7	21	<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 lh bound to ssdna and2 amp-pnp
25	<a href="#">c4q47A_</a>	Alignment	not modelled	99.7	20	<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
26	<a href="#">c4ljyA_</a>	Alignment	not modelled	99.7	19	<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
27	<a href="#">c5lstA_</a>	Alignment	not modelled	99.7	21	<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.
28	<a href="#">c4ddvA_</a>	Alignment	not modelled	99.7	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
						<b>PDB header:</b> hydrolase

29	<a href="#">c5lb5C_</a>	Alignment	not modelled	99.6	23	<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).
30	<a href="#">c1gl9B_</a>	Alignment	not modelled	99.6	22	<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
31	<a href="#">c2db3D_</a>	Alignment	not modelled	99.6	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
32	<a href="#">c4pxaA_</a>	Alignment	not modelled	99.6	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
33	<a href="#">c1c4oA_</a>	Alignment	not modelled	99.6	16	<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
34	<a href="#">c2eyqA_</a>	Alignment	not modelled	99.6	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
35	<a href="#">c5lqwC_</a>	Alignment	not modelled	99.6	22	<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="#">c2d7dA_</a>	Alignment	not modelled	99.5	15	<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
37	<a href="#">c3oiyB_</a>	Alignment	not modelled	99.5	19	<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
38	<a href="#">c4d25A_</a>	Alignment	not modelled	99.5	18	<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
39	<a href="#">c1hv8B_</a>	Alignment	not modelled	99.5	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
40	<a href="#">c6c0fp_</a>	Alignment	not modelled	99.5	17	<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)
41	<a href="#">c5dtuA_</a>	Alignment	not modelled	99.5	21	<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
42	<a href="#">c5jcfB_</a>	Alignment	not modelled	99.5	16	<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).
43	<a href="#">c4gl2A_</a>	Alignment	not modelled	99.5	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
44	<a href="#">c5m52B_</a>	Alignment	not modelled	99.4	23	<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
45	<a href="#">c2xgjA_</a>	Alignment	not modelled	99.4	23	<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
46	<a href="#">c4w7sA_</a>	Alignment	not modelled	99.4	20	<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
47	<a href="#">c4bgdA_</a>	Alignment	not modelled	99.4	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
48	<a href="#">c4xgtA_</a>	Alignment	not modelled	99.4	19	<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
49	<a href="#">c1xtkA_</a>	Alignment	not modelled	99.4	21	<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
50	<a href="#">c5z58x_</a>	Alignment	not modelled	99.4	29	<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.
51	<a href="#">c3i5yA_</a>	Alignment	not modelled	99.4	21	<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
52	<a href="#">c3tmiA_</a>	Alignment	not modelled	99.4	14	<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
53	<a href="#">c1s2mA_</a>	Alignment	not modelled	99.4	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

54	<a href="#">c4kbfA</a>	Alignment	not modelled	99.4	25	<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
55	<a href="#">c4ct4B</a>	Alignment	not modelled	99.4	17	<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
56	<a href="#">c2va8A</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
57	<a href="#">c6c90A</a>	Alignment	not modelled	99.3	23	<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
58	<a href="#">c2jlrA</a>	Alignment	not modelled	99.3	19	<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
59	<a href="#">c6jdeB</a>	Alignment	not modelled	99.3	17	<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
60	<a href="#">c6iczY</a>	Alignment	not modelled	99.3	21	<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) at 2.3.0 angstrom
61	<a href="#">c4nhoA</a>	Alignment	not modelled	99.3	17	<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
62	<a href="#">c5jb2A</a>	Alignment	not modelled	99.3	15	<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.
63	<a href="#">c6o16A</a>	Alignment	not modelled	99.3	23	<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
64	<a href="#">c5agaA</a>	Alignment	not modelled	99.3	21	<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
65	<a href="#">c5mq0V</a>	Alignment	not modelled	99.3	23	<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
66	<a href="#">c4f92B</a>	Alignment	not modelled	99.3	16	<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
67	<a href="#">c4a4zA</a>	Alignment	not modelled	99.3	21	<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
68	<a href="#">c6ah0D</a>	Alignment	not modelled	99.3	23	<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)
69	<a href="#">c5mqfq</a>	Alignment	not modelled	99.3	21	<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)
70	<a href="#">c6iehB</a>	Alignment	not modelled	99.3	19	<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
71	<a href="#">c3eiqD</a>	Alignment	not modelled	99.3	16	<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
72	<a href="#">c2v6jA</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna helicase; <b>PDBTitle:</b> kokobera virus helicase: mutant met47thr
73	<a href="#">c3jcrC</a>	Alignment	not modelled	99.3	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
74	<a href="#">c6h57A</a>	Alignment	not modelled	99.3	19	<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
75	<a href="#">c6hegA</a>	Alignment	not modelled	99.3	19	<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
76	<a href="#">c2ocaA</a>	Alignment	not modelled	99.3	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
77	<a href="#">c5wsge</a>	Alignment	not modelled	99.3	22	<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) at 2.4.0 angstrom resolution
78	<a href="#">c1wp9D</a>	Alignment	not modelled	99.3	18	<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
79	<a href="#">c3rc8A</a>	Alignment	not modelled	99.3	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
80	<a href="#">c3l9oA</a>	Alignment	not modelled	99.3	20	<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
81	<a href="#">c2hxyC</a>	Alignment	not modelled	99.2	14	<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
82	<a href="#">c5dcaA</a>	Alignment	not modelled	99.2	21	<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
83	<a href="#">c3kx2A</a>	Alignment	not modelled	99.2	22	<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
84	<a href="#">c5ivA</a>	Alignment	not modelled	99.2	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
85	<a href="#">c3fhtA</a>	Alignment	not modelled	99.2	18	<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
86	<a href="#">c5zamA</a>	Alignment	not modelled	99.2	17	<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
87	<a href="#">c3pexA</a>	Alignment	not modelled	99.2	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
88	<a href="#">c5supB</a>	Alignment	not modelled	99.2	20	<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
89	<a href="#">c5ylzW</a>	Alignment	not modelled	99.2	21	<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
90	<a href="#">c6fa5A</a>	Alignment	not modelled	99.2	22	<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
91	<a href="#">c2vsxA</a>	Alignment	not modelled	99.2	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="#">c3ewsA</a>	Alignment	not modelled	99.2	21	<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
93	<a href="#">c5n8zA</a>	Alignment	not modelled	99.2	24	<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
94	<a href="#">c5m59C</a>	Alignment	not modelled	99.2	15	<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
95	<a href="#">d1oywa3</a>	Alignment	not modelled	99.2	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
96	<a href="#">c5fmf1</a>	Alignment	not modelled	99.2	17	<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
97	<a href="#">c2p6uA</a>	Alignment	not modelled	99.2	19	<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
98	<a href="#">c2i4iA</a>	Alignment	not modelled	99.2	16	<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
99	<a href="#">c5lqwO</a>	Alignment	not modelled	99.2	21	<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
100	<a href="#">c5xdrA</a>	Alignment	not modelled	99.2	22	<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
101	<a href="#">c2zj8A</a>	Alignment	not modelled	99.2	18	<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
102	<a href="#">c5lj5Q</a>	Alignment	not modelled	99.1	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.
103	<a href="#">c2z83A</a>	Alignment	not modelled	99.1	21	<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
104	<a href="#">c5vheA</a>	Alignment	not modelled	99.1	24	<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



105	<a href="#">c2i9wA_</a>	Alignment	not modelled	99.1	24	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a sec-c motif containing protein (psyc_2064) from <i>psychrobacter arcticus</i> at 1.75 a resolution
106	<a href="#">c2z0mA_</a>	Alignment	not modelled	99.1	22	<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 <i>sulfolobus tokodaii</i>
107	<a href="#">c6nmiA_</a>	Alignment	not modelled	99.1	20	<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
108	<a href="#">c4bujA_</a>	Alignment	not modelled	99.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> antiviral helicase ski2; <b>PDBTitle:</b> crystal structure of the <i>s. cerevisiae</i> ski2-3-8 complex
109	<a href="#">c4qqxA_</a>	Alignment	not modelled	99.1	23	<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 <i>t. fusca</i> cas3-atp
110	<a href="#">c6f4aB_</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> svu3 helicase; <b>PDBTitle:</b> yeast mitochondrial rna degradosome complex mtexo
111	<a href="#">c6i3oA_</a>	Alignment	not modelled	99.1	26	<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
112	<a href="#">d1t5la2</a>	Alignment	not modelled	99.1	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
113	<a href="#">c1ymfA_</a>	Alignment	not modelled	99.1	25	<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
114	<a href="#">c2zj2A_</a>	Alignment	not modelled	99.1	19	<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
115	<a href="#">c6iegA_</a>	Alignment	not modelled	99.0	23	<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
116	<a href="#">d1c4oa2</a>	Alignment	not modelled	99.0	25	<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
117	<a href="#">c5ivwV_</a>	Alignment	not modelled	99.0	17	<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
118	<a href="#">c2vbcA_</a>	Alignment	not modelled	99.0	18	<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
119	<a href="#">d2j0sa2</a>	Alignment	not modelled	99.0	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
120	<a href="#">c2wv9A_</a>	Alignment	not modelled	99.0	18	<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