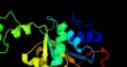
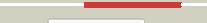
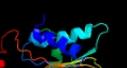


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD1095_(phoH2)_1223002_1224303
Date	Wed Jul 31 22:05:17 BST 2019
Unique Job ID	94940099482bd52f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3b85A</a>			100.0	32	<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
2	<a href="#">c5eaxB</a>			100.0	25	<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
3	<a href="#">c2xzIA</a>			99.9	16	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent helicase nam7; <b>PDBTitle:</b> upf1-rna complex
4	<a href="#">c2wjyA</a>			99.9	18	<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
5	<a href="#">c5mznA</a>			99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> helicase sen1,helicase sen1; <b>PDBTitle:</b> helicase sen1
6	<a href="#">c3gp8A</a>			99.9	27	<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
7	<a href="#">c2gk7A</a>			99.9	18	<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
8	<a href="#">c2hwwC</a>			99.9	25	<b>PDB header:</b> rna binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> telomerase-binding protein est1a; <b>PDBTitle:</b> structure of pin domain of human smg6
9	<a href="#">d1w36d1</a>			99.9	27	<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
10	<a href="#">c4pj3A</a>			99.9	13	<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
11	<a href="#">c3e1sA</a>			99.9	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

12	<a href="#">c4b3gA_</a>			99.9	22	<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
13	<a href="#">c5ld2D_</a>			99.9	19	<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
14	<a href="#">c5wwpB_</a>			99.9	15	<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)
15	<a href="#">c3jb9X_</a>			99.9	24	<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
16	<a href="#">c1w36G_</a>			99.9	22	<b>PDB header:</b> recombination <b>Chain:</b> G; <b>PDB Molecule:</b> exodeoxyribonuclease v alpha chain; <b>PDBTitle:</b> recbcd:dna complex
17	<a href="#">c5wwpA_</a>			99.9	17	<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)
18	<a href="#">c3i8oA_</a>			99.9	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> kh domain-containing protein mj1533; <b>PDBTitle:</b> a domain of a functionally unknown protein from methanocaldococcus jannaschii dsm 2661.
19	<a href="#">d1pjra1</a>			99.9	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
20	<a href="#">c5n8oA_</a>			99.8	16	<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
21	<a href="#">d1uaaa1</a>		not modelled	99.8	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
22	<a href="#">c2pjrf_</a>		not modelled	99.8	19	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> F; <b>PDB Molecule:</b> protein (helicase pcra); <b>PDBTitle:</b> helicase product complex
23	<a href="#">c2is6B_</a>		not modelled	99.8	19	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> dna helicase ii; <b>PDBTitle:</b> crystal structure of uvr-dna-adpmgf3 ternary complex
24	<a href="#">d1w36b1</a>		not modelled	99.7	26	<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
25	<a href="#">c1uaaB_</a>		not modelled	99.7	22	<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
26	<a href="#">c4c30l_</a>		not modelled	99.7	18	<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 uvr in2 complex with dna, form 2
27	<a href="#">c3ix7A_</a>		not modelled	99.7	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein ttha0540; <b>PDBTitle:</b> crystal structure of a domain of functionally unknown protein from2 thermus thermophilus hb8
28	<a href="#">c3u4qA_</a>		not modelled	99.7	18	<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
29	<a href="#">c3u4wA</a>		not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> replicase large subunit;

29	<a href="#">c5ywwA</a>	Alignment	not modelled	99.7	10	<b>PDBTitle:</b> crystal structure of the superfamily 1 helicase from tomato mosaic2 virus
30	<a href="#">c3upuC</a>	Alignment	not modelled	99.7	20	<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
31	<a href="#">c4n0oC</a>	Alignment	not modelled	99.7	14	<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
32	<a href="#">c5f4hF</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> nucleotide binding protein pinc; <b>PDBTitle:</b> archaeal rvrb-like holiday junction helicase
33	<a href="#">c3lfluA</a>	Alignment	not modelled	99.7	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
34	<a href="#">c5o6dB</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent dna helicase pif1; <b>PDBTitle:</b> structure of scipf1 in complex with polydt and atpgs
35	<a href="#">c5ftbA</a>	Alignment	not modelled	99.7	20	<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
36	<a href="#">c2l8bA</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein trai; <b>PDBTitle:</b> trai (381-569)
37	<a href="#">c1pjrA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> helicase <b>Chain:</b> A: <b>PDB Molecule:</b> pcta; <b>PDBTitle:</b> structure of dna helicase
38	<a href="#">c5ywwA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotide binding protein pinc; <b>PDBTitle:</b> archaeal rvrb-like holiday junction helicase
39	<a href="#">c1w36E</a>	Alignment	not modelled	99.6	34	<b>PDB header:</b> recombination <b>Chain:</b> E: <b>PDB Molecule:</b> exodeoxyribonuclease v beta chain; <b>PDBTitle:</b> recbcd:dna complex
40	<a href="#">c5fhhA</a>	Alignment	not modelled	99.6	20	<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
41	<a href="#">c2hwyB</a>	Alignment	not modelled	99.5	28	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein smg5; <b>PDBTitle:</b> structure of pin domain of human smg5.
42	<a href="#">c6jimA</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> viral protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> helicase; <b>PDBTitle:</b> viral helicase protein
43	<a href="#">d1o4wa</a>	Alignment	not modelled	99.2	23	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
44	<a href="#">c6c90A</a>	Alignment	not modelled	99.0	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
45	<a href="#">c4on9B</a>	Alignment	not modelled	99.0	16	<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
46	<a href="#">c5jb2A</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> gp2; <b>PDBTitle:</b> crystal structure of chicken lgp2 with 5'ppp 10-mer dsrna and adp-2 alfp4-mg2+ at 2.2 a resolution.
47	<a href="#">c2xgjA</a>	Alignment	not modelled	98.9	17	<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 dech helicase involved in nuclear rna2 processing and surveillance
48	<a href="#">c4xgtA</a>	Alignment	not modelled	98.9	17	<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="#">c3l9oA</a>	Alignment	not modelled	98.9	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
50	<a href="#">c6iehB</a>	Alignment	not modelled	98.9	20	<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-nrd2 complex
51	<a href="#">c3u44B</a>	Alignment	not modelled	98.9	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
52	<a href="#">c6iegA</a>	Alignment	not modelled	98.8	20	<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
53	<a href="#">d1rifA</a>	Alignment	not modelled	98.8	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> DNA helicase UvsW
54	<a href="#">c2zj8A</a>	Alignment	not modelled	98.8	16	<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
55	<a href="#">d2eyqa3</a>	Alignment	not modelled	98.8	17	<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

56	<a href="#">c2va8A</a>	Alignment	not modelled	98.8	18	<b>Chain: A: PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
57	<a href="#">c2zj2A</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> putative ski2-type helicase; <b>PDBTitle:</b> archaeal dna helicase hjm apo state in form 1
58	<a href="#">c6nmiA</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> transcription <b>Chain: A: PDB Molecule:</b> general transcription and dna repair factor iih helicase <b>PDBTitle:</b> cryo-em structure of the human tfiih core complex
59	<a href="#">c4bgdA</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> transcription <b>Chain: A: PDB Molecule:</b> pre-mrna-splicing helicase brr2; <b>PDBTitle:</b> crystal structure of brr2 in complex with the jab1/mpn domain of prp8
60	<a href="#">c2p6uA</a>	Alignment	not modelled	98.8	22	<b>PDB header:</b> dna binding protein <b>Chain: A: PDB Molecule:</b> afuhel308 helicase; <b>PDBTitle:</b> apo structure of the hel308 superfamily 2 helicase
61	<a href="#">c5agaA</a>	Alignment	not modelled	98.8	24	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> dna polymerase theta; <b>PDBTitle:</b> crystal structure of the helicase domain of human dna2 polymerase theta in complex with amppnp
62	<a href="#">c4f92B</a>	Alignment	not modelled	98.8	22	<b>PDB header:</b> hydrolase <b>Chain: B: PDB Molecule:</b> u5 small nuclear ribonucleoprotein 200 kda helicase; <b>PDBTitle:</b> brr2 helicase region s1087i
63	<a href="#">c5gvrA</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> probable atp-dependent rna helicase ddx41; <b>PDBTitle:</b> crystal structure of the ddx41 dead domain in an apo closed form
64	<a href="#">c5lqwC</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> splicing <b>Chain: C: PDB Molecule:</b> pre-mrna-splicing helicase brr2; <b>PDBTitle:</b> yeast activated spliceosome
65	<a href="#">c4gl2A</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> rna binding protein/rna <b>Chain: A: PDB Molecule:</b> interferon-induced helicase c domain-containing protein 1; <b>PDBTitle:</b> structural basis for dsrna duplex backbone recognition by mda5
66	<a href="#">c5jcfB</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> immune system <b>Chain: 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+ at 2.6 a resolution (orthorhombic form).
67	<a href="#">c3fe2B</a>	Alignment	not modelled	98.7	12	<b>PDB header:</b> hydrolase <b>Chain: 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
68	<a href="#">c4buja</a>	Alignment	not modelled	98.7	24	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> antiviral helicase ski2; <b>PDBTitle:</b> crystal structure of the s. cerevisiae ski2-3-8 complex
69	<a href="#">c3ly5A</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> atp-dependent rna helicase ddx18; <b>PDBTitle:</b> ddx18 dead-domain
70	<a href="#">c5m52B</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> hydrolase <b>Chain: 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
71	<a href="#">c1qhhA</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> protein (pcra (subunit)); <b>PDBTitle:</b> structure of dna helicase with adpnp
72	<a href="#">d2fwra2</a>	Alignment	not modelled	98.7	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
73	<a href="#">c5dcaA</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> pre-mrna-splicing helicase brr2; <b>PDBTitle:</b> crystal structure of yeast full length brr2 in complex with prp8 jab12 domain
74	<a href="#">c6ah0D</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> splicing <b>Chain: D: 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)
75	<a href="#">c5v9xA</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> hydrolase/dna <b>Chain: A: PDB Molecule:</b> atp-dependent dna helicase; <b>PDBTitle:</b> structure of mycobacterium smegmatis helicase lhr bound to ssdna and2 amp-pnp
76	<a href="#">c4q2dA</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> crispr-associated helicase cas3; <b>PDBTitle:</b> crystal structure of crispr-associated protein in complex with 2'-2 deoxyadenosine 5'-triphosphate
77	<a href="#">c3jcrC</a>	Alignment	not modelled	98.7	22	<b>PDB header:</b> splicing <b>Chain: C: PDB Molecule:</b> hbrr2; <b>PDBTitle:</b> 3d structure determination of the human*u4/u6.u5* tri-snrrp complex
78	<a href="#">c2vbcA</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> dengue 4 ns3 full-length protein; <b>PDBTitle:</b> crystal structure of the ns3 protease-helicase from dengue2 virus
79	<a href="#">c2v6jA</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> rna helicase; <b>PDBTitle:</b> kokobera virus helicase: mutant met47thr
80	<a href="#">c4a4za</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> antiviral helicase ski2; <b>PDBTitle:</b> crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
81	<a href="#">c5nf1A</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> transcription <b>Chain: A: PDB Molecule:</b> tfiih basal transcription factor complex

81	<a href="#">c3014A</a>	Alignment	not modelled	98.6	13	helicase xpb <b>PDBTitle:</b> the cryo-em structure of human tfih
82	<a href="#">c2jlrA</a>	Alignment	not modelled	98.6	16	<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
83	<a href="#">c3tmia</a>	Alignment	not modelled	98.6	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
84	<a href="#">c2ocaA</a>	Alignment	not modelled	98.6	11	<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
85	<a href="#">c4nl4H</a>	Alignment	not modelled	98.6	16	<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
86	<a href="#">c2z83A</a>	Alignment	not modelled	98.6	15	<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
87	<a href="#">c4nl8E</a>	Alignment	not modelled	98.6	15	<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
88	<a href="#">c2wv9A</a>	Alignment	not modelled	98.6	14	<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
89	<a href="#">c6jdeB</a>	Alignment	not modelled	98.6	18	<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
90	<a href="#">c3i5yA</a>	Alignment	not modelled	98.6	19	<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 npn
91	<a href="#">c2kbeA</a>	Alignment	not modelled	98.6	19	<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
92	<a href="#">c2oxcA</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx20; <b>PDBTitle:</b> human dead-box rna helicase ddx20, dead domain in complex with adp
93	<a href="#">c5oe9C</a>	Alignment	not modelled	98.6	8	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> large subunit terminase; <b>PDBTitle:</b> structure of large terminase from the thermophilic bacteriophage d6e2 in complex with sulfate (crystal form 2)
94	<a href="#">c2eyqA</a>	Alignment	not modelled	98.6	17	<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
95	<a href="#">d1qoua</a>	Alignment	not modelled	98.5	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
96	<a href="#">c3berA</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx47; <b>PDBTitle:</b> human dead-box rna-helicase ddx47, conserved domain i in complex with2 amp
97	<a href="#">c3dkpA</a>	Alignment	not modelled	98.5	15	<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
98	<a href="#">c5m59C</a>	Alignment	not modelled	98.5	16	<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
99	<a href="#">c1qhhB</a>	Alignment	not modelled	98.5	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
100	<a href="#">c5xdra</a>	Alignment	not modelled	98.5	16	<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="#">c2pl3A</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx10; <b>PDBTitle:</b> human dead-box rna helicase ddx10, dead domain in complex with adp
102	<a href="#">c5gjuA</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dead; <b>PDBTitle:</b> dead-box rna helicase
103	<a href="#">d1s2ma1</a>	Alignment	not modelled	98.5	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
104	<a href="#">c4qqxA</a>	Alignment	not modelled	98.5	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 t. fusca cas3-atp
105	<a href="#">c6md3F</a>	Alignment	not modelled	98.5	20	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> F: <b>PDB Molecule:</b> rrp44p homologue; <b>PDBTitle:</b> structure of t. brucei rrp44 pin domain
106	<a href="#">c29ivR</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> reverse gyrase helicase domain;

100	<a href="#">c2vipy</a>	Alignment	not modelled	98.5	10	<b>PDBTitle:</b> helicase domain of reverse gyrase from thermotoga maritima <b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> dead-box atp-dependent rna helicase csha; <b>PDBTitle:</b> crystal structures of the n-terminal domain of staphylococcus aureus2 dead-box cold shock rna helicase csha in complex with amp
107	<a href="#">c6aicA</a>	Alignment	not modelled	98.5	13	<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
108	<a href="#">c6ro4A</a>	Alignment	not modelled	98.5	14	<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
109	<a href="#">d1qdea</a>	Alignment	not modelled	98.5	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ypf1; <b>PDBTitle:</b> crystal structure of trna(met) cytidine acetyltransferase
110	<a href="#">c2zpaB</a>	Alignment	not modelled	98.5	25	<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
111	<a href="#">c5lqwO</a>	Alignment	not modelled	98.5	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> xpd; <b>PDBTitle:</b> structure of s. tokodaii xpd4
112	<a href="#">c2vl7A</a>	Alignment	not modelled	98.5	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
113	<a href="#">d1gm5a3</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> E: <b>PDB Molecule:</b> saccharomyces cerevisiae s288c snr6 srna; <b>PDBTitle:</b> cryo-em structure of the catalytic step ii spliceosome (c* complex) at 4.0 angstrom resolution
114	<a href="#">d1gkub1</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> hydrolyase <b>Chain:</b> A: <b>PDB Molecule:</b> flavivirin protease ns3 catalytic subunit; <b>PDBTitle:</b> crystal structure of kunjin virus ns3 helicase
115	<a href="#">c5wsge</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> hydrolyase <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
116	<a href="#">c2qeqA</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> hydrolyase <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
117	<a href="#">c3kx2A</a>	Alignment	not modelled	98.5	17	<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
118	<a href="#">c6fa5A</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> hydrolyase <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad25; <b>PDBTitle:</b> structure of archaeoglobus fulgidis xpb
119	<a href="#">c5mq0V</a>	Alignment	not modelled	98.5	14	
120	<a href="#">c2fwrA</a>	Alignment	not modelled	98.4	20	