







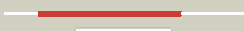


















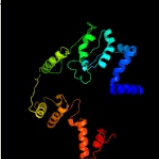
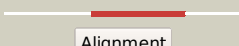

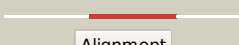
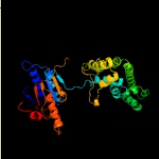
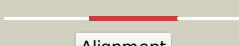






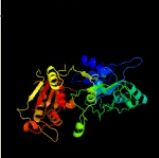
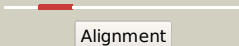
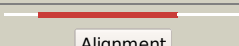

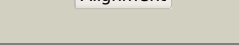
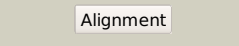

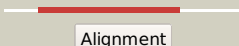



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3201c_(-)_3573728_3577033
Date	Thu Aug 8 16:20:39 BST 2019
Unique Job ID	2c99b5c84a0f80ac

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3u4qA_	 Alignment		100.0	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: atp-dependent helicase/nuclease subunit a; PDBTitle: structure of addab-dna complex at 2.8 angstroms
2	c1w36E_	 Alignment		100.0	21	PDB header: recombination Chain: E: PDB Molecule: exodeoxyribonuclease v beta chain; PDBTitle: recbcd:dna complex
3	c3u44B_	 Alignment		100.0	14	PDB header: hydrolase/dna Chain: B: PDB Molecule: atp-dependent helicase/deoxyribonuclease subunit b; PDBTitle: crystal structure of addab-dna complex
4	c2is6B_	 Alignment		100.0	26	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of uvrd-dna-adpmgf3 ternary complex
5	c1uaaB_	 Alignment		100.0	24	PDB header: hydrolase/dna Chain: B: PDB Molecule: protein (atp-dependent dna helicase rep.); PDBTitle: e. coli rep helicase/dna complex
6	c2pjrF_	 Alignment		100.0	26	PDB header: hydrolase/dna Chain: F: PDB Molecule: protein (helicase pcra); PDBTitle: helicase product complex
7	c4c30I_	 Alignment		100.0	27	PDB header: hydrolase/dna Chain: I: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of deinococcus radiodurans uvrd in2 complex with dna, form 2
8	c3lfuA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of e. coli uvrd
9	c1pjrA_	 Alignment		100.0	29	PDB header: helicase Chain: A: PDB Molecule: pcra; PDBTitle: structure of dna helicase
10	c1w36F_	 Alignment		100.0	16	PDB header: recombination Chain: F: PDB Molecule: exodeoxyribonuclease v gamma chain; PDBTitle: recbcd:dna complex
11	d1w36b1	 Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain

12	d1pjra1	 Alignment		100.0	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
13	d1uaaa1	 Alignment		100.0	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
14	c1qhhB	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
15	d1w36b2	 Alignment		100.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
16	d1uaaa2	 Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
17	d1pjra2	 Alignment		100.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
18	d1w36c2	 Alignment		100.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
19	c4b3gA	 Alignment		100.0	22	PDB header: hydrolase/rna Chain: A: PDB Molecule: dna-binding protein smubp-2; PDBTitle: crystal structure of ighmbp2 helicase in complex with rna
20	c5eaxB	 Alignment		100.0	26	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna replication atp-dependent helicase/nuclease dna2; PDBTitle: crystal structure of dna2 in complex with an ssdna
21	c1qhhA	 Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
22	c2xzIA	 Alignment	not modelled	99.9	28	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent helicase nam7; PDBTitle: upf1-rna complex
23	c2wjyA	 Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: A: PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
24	c2gk7A	 Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: structural and functional insights into the human upf1 helicase core
25	c3upuC	 Alignment	not modelled	99.9	23	PDB header: hydrolase/dna Chain: C: PDB Molecule: atp-dependent dna helicase dda; PDBTitle: crystal structure of the t4 phage sf1b helicase dda
26	c5o6dB	 Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of scpif1 in complex with polydt and atpgs
27	c5wvpA	 Alignment	not modelled	99.9	28	PDB header: hydrolase Chain: A: PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
28	c5ld2D	 Alignment	not modelled	99.9	34	PDB header: hydrolase Chain: D: PDB Molecule: recbcd enzyme subunit recd; PDBTitle: cryo-em structure of recbcd+dna complex revealing activated nuclease2 domain

29	c4pj3A	Alignment	not modelled	99.9	17	PDB header: rna binding protein Chain: A: PDB Molecule: intron-binding protein aquarius; PDBTitle: structural insight into the function and evolution of the spliceosomal2 helicase aquarius, structure of aquarius in complex with amppnp
30	c3gp8A	Alignment	not modelled	99.9	36	PDB header: hydrolase/dna Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd, putative; PDBTitle: crystal structure of the binary complex of recd2 with dna
31	c3e1sA	Alignment	not modelled	99.9	30	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd; PDBTitle: structure of an n-terminal truncation of deinococcus radiodurans recd2
32	c5mznA	Alignment	not modelled	99.9	29	PDB header: hydrolase Chain: A: PDB Molecule: helicase sen1,helicase sen1; PDBTitle: helicase sen1
33	c1w36G	Alignment	not modelled	99.9	28	PDB header: recombination Chain: G: PDB Molecule: exodeoxyribonuclease v alpha chain; PDBTitle: recbcd:dna complex
34	c5wvpB	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
35	c3jb9X	Alignment	not modelled	99.8	13	PDB header: rna binding protein/rna Chain: X: PDB Molecule: pre-mrna-splicing factor cwf11; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
36	d1w36b3	Alignment	not modelled	99.8	21	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Exodeoxyribonuclease V beta chain (RecB), C-terminal domain
37	c5n8oA	Alignment	not modelled	99.7	36	PDB header: transferase Chain: A: PDB Molecule: dna helicase i; PDBTitle: cryo em structure of the conjugative relaxase trai of the f/r1 plasmid2 system
38	c4n0oC	Alignment	not modelled	99.6	41	PDB header: hydrolase/dna Chain: C: PDB Molecule: replicase polyprotein 1ab; PDBTitle: complex structure of arterivirus nonstructural protein 10 (helicase)2 with dna
39	c2pjrB	Alignment	not modelled	99.6	43	PDB header: hydrolase/dna Chain: B: PDB Molecule: protein (helicase pcra); PDBTitle: helicase product complex
40	d1w36d1	Alignment	not modelled	99.6	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
41	c1qhhD	Alignment	not modelled	99.6	43	PDB header: hydrolase Chain: D: PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
42	c3dmnA	Alignment	not modelled	99.5	43	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dna helicase; PDBTitle: the crystal structure of the c-terminal domain of a possibe dna2 helicase from lactobacillus plantarun wcfs1
43	c3vkwA	Alignment	not modelled	99.4	34	PDB header: transferase Chain: A: PDB Molecule: replicase large subunit; PDBTitle: crystal structure of the superfamily 1 helicase from tomato mosaic2 virus
44	c5fhhA	Alignment	not modelled	99.4	30	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of human pif1 helicase domain residues 200-641
45	c3b85A	Alignment	not modelled	99.4	26	PDB header: hydrolase Chain: A: PDB Molecule: phosphate starvation-inducible protein; PDBTitle: crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
46	c5ftbA	Alignment	not modelled	99.4	25	PDB header: hydrolase Chain: A: PDB Molecule: tpr domain protein; PDBTitle: crystal structure of pif1 helicase from bacteroides in2 complex with amppnp
47	c4ic1D	Alignment	not modelled	99.3	21	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of sso0001
48	c5zyuA	Alignment	not modelled	99.3	18	PDB header: dna binding protein/dna Chain: A: PDB Molecule: mitochondrial genome maintenance exonuclease 1; PDBTitle: the crytal struture of humanmgme1 with single strand dna2
49	c4onbA	Alignment	not modelled	99.3	18	PDB header: hydrolase Chain: A: PDB Molecule: crispr-associated exonuclease, cas4 family; PDBTitle: crystal structure of crispr-associated exonuclease (cas4 family) from2 pyrobaculum calidifontis jcm 11548
50	d1w36d2	Alignment	not modelled	99.2	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
51	c3h4rA	Alignment	not modelled	99.0	18	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease 8; PDBTitle: crystal structure of e. coli rece exonuclease
52	c6jimA	Alignment	not modelled	99.0	33	PDB header: viral protein/rna Chain: A: PDB Molecule: helicase; PDBTitle: viral helicase protein
53	c3l0aA	Alignment	not modelled	98.9	12	PDB header: hydrolase Chain: A: PDB Molecule: putative exonuclease; PDBTitle: crystal structure of putative exonuclease (rer070207002219) from2 eubacterium rectale at 2.19 a resolution
54	c4on9B	Alignment	not modelled	98.7	15	PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx58;

						PDBTitle: dech box helicase domain PDB header: hydrolase/rna
55	c3i5yA_	Alignment	not modelled	98.4	21	Chain: A: PDB Molecule: atp-dependent rna helicase mss116; PDBTitle: structure of mss116p bound to ssrna containing a single 5-bru and amp-2 pnp
56	c5v9xA_	Alignment	not modelled	98.2	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: atp-dependent dna helicase; PDBTitle: structure of mycobacterium smegmatis helicase lhr bound to ssdna and2 amp-pnp
57	c4znIB_	Alignment	not modelled	98.2	21	PDB header: viral protein Chain: B: PDB Molecule: phage terminase large subunit; PDBTitle: thermus phage p74-26 large terminase atpase domain bound to adp2 beryllium fluoride
58	d1c4oa1	Alignment	not modelled	98.2	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
59	c5xdrA_	Alignment	not modelled	98.2	15	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase dhx15; PDBTitle: crystal structure of human deah-box rna helicase dhx15 in complex with2 adp
60	c6c90A_	Alignment	not modelled	98.2	17	PDB header: hydrolase/rna binding protein Chain: A: PDB Molecule: exosome rna helicase mtr4,exosome rna helicase mtr4; PDBTitle: human mtr4 helicase in complex with zcchc8-ctd
61	c5ivIA_	Alignment	not modelled	98.1	26	PDB header: hydrolase Chain: A: PDB Molecule: dead-box atp-dependent rna helicase csha; PDBTitle: csha helicase
62	c3dkpA_	Alignment	not modelled	98.1	19	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx52; PDBTitle: human dead-box rna-helicase ddx52, conserved domain i in complex with2 adp
63	c2xgjA_	Alignment	not modelled	98.1	17	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
64	c3tbkA_	Alignment	not modelled	98.1	15	PDB header: hydrolase Chain: A: PDB Molecule: rig-i helicase domain; PDBTitle: mouse rig-i atpase domain
65	c1gm5A_	Alignment	not modelled	98.0	18	PDB header: helicase Chain: A: PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
66	c4xgtA_	Alignment	not modelled	98.0	17	PDB header: hydrolase Chain: A: PDB Molecule: frq-interacting rna helicase; PDBTitle: structure of rna helicase frh a critical component of the neurospora2 crassa circadian clock
67	c2va8A_	Alignment	not modelled	98.0	14	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
68	c5agaA_	Alignment	not modelled	98.0	17	PDB header: transferase Chain: A: PDB Molecule: dna polymerase theta; PDBTitle: crystal structure of the helicase domain of human dna2 polymerase theta in complex with amppnp
69	c3i9oA_	Alignment	not modelled	98.0	17	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: crystal structure of mtr4, a co-factor of the nuclear exosome
70	d1gkub1	Alignment	not modelled	98.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
71	c4ljyA_	Alignment	not modelled	98.0	22	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-processing atp-dependent rna helicase prp5; PDBTitle: crystal structure of rna splicing effector prp5 in complex with adp
72	c4nl4H_	Alignment	not modelled	97.9	27	PDB header: dna binding protein Chain: H: PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to adp
73	c1c4oA_	Alignment	not modelled	97.9	30	PDB header: replication Chain: A: PDB Molecule: dna nucleotide excision repair enzyme uvrB; PDBTitle: crystal structure of the dna nucleotide excision repair enzyme uvrB2 from thermus thermophilus
74	c6iehB_	Alignment	not modelled	97.9	17	PDB header: rna binding protein Chain: B: PDB Molecule: exosome rna helicase mtr4; PDBTitle: crystal structures of the hmtr4-nrde2 complex
75	c5mq0V_	Alignment	not modelled	97.9	20	PDB header: splicing Chain: V: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp22; PDBTitle: structure of a spliceosome remodeled for exon ligation
76	c4qqxA_	Alignment	not modelled	97.9	25	PDB header: hydrolase/dna Chain: A: PDB Molecule: crispr-associated helicase, cas3 family; PDBTitle: crystal structure of t. fusca cas3-atp
77	c2zj8A_	Alignment	not modelled	97.9	13	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
78	c3tmiA_	Alignment	not modelled	97.9	15	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase ddx58; PDBTitle: structural basis for rna recognition and activation of rig-i
79	c2zj2A_	Alignment	not modelled	97.9	14	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 1
						PDB header: hydrolase

80	c4a4zA_	Alignment	not modelled	97.8	15	Chain: A: PDB Molecule: antiviral helicase ski2; PDBTitle: crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
81	c5z58x_	Alignment	not modelled	97.8	17	PDB header: splicing Chain: X: PDB Molecule: smad nuclear-interacting protein 1; PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
82	c3kx2A_	Alignment	not modelled	97.8	17	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp43; PDBTitle: crystal structure of prp43p in complex with adp
83	c4ddvA_	Alignment	not modelled	97.8	22	PDB header: hydrolase Chain: A: PDB Molecule: reverse gyrase; PDBTitle: thermotoga maritima reverse gyrase, triclinic form
84	c6i3oA_	Alignment	not modelled	97.8	21	PDB header: hydrolase Chain: A: PDB Molecule: putative pre-mrna splicing factor; PDBTitle: crystal structure of deah-box atpase prp22
85	c6iczY_	Alignment	not modelled	97.8	19	PDB header: splicing Chain: Y: PDB Molecule: atp-dependent rna helicase dhx8; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
86	c2db3D_	Alignment	not modelled	97.8	26	PDB header: hydrolase/rna Chain: D: PDB Molecule: atp-dependent rna helicase vasa; PDBTitle: structural basis for rna unwinding by the dead-box protein2 drosophila vasa
87	c6jdeB_	Alignment	not modelled	97.8	22	PDB header: hydrolase Chain: B: PDB Molecule: putative dna repair helicase radd; PDBTitle: crystal structure of a dna repair protein
88	c1wp9D_	Alignment	not modelled	97.8	21	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent rna helicase, putative; PDBTitle: crystal structure of pyrococcus furiosus hef helicase domain
89	c6fa5A_	Alignment	not modelled	97.8	16	PDB header: hydrolase Chain: A: PDB Molecule: putative mrna splicing factor; PDBTitle: crystal structure of the deah-box helicase prp2 in complex with adp
90	c1xtkA_	Alignment	not modelled	97.7	22	PDB header: gene regulation Chain: A: PDB Molecule: probable atp-dependent rna helicase p47; PDBTitle: structure of decd to dead mutation of human uap56
91	c4nl8E_	Alignment	not modelled	97.7	27	PDB header: dna binding protein Chain: E: PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to ssb c-terminal tail peptide
92	c2hxC_	Alignment	not modelled	97.7	26	PDB header: hydrolase Chain: C: PDB Molecule: probable atp-dependent rna helicase ddx48; PDBTitle: crystal structure of human apo-eif4aii
93	c6c0fp_	Alignment	not modelled	97.7	23	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: yeast nucleolar pre-60s ribosomal subunit (state 2)
94	c4q2dA_	Alignment	not modelled	97.7	26	PDB header: hydrolase Chain: A: PDB Molecule: crispr-associated helicase cas3; PDBTitle: crystal structure of crispr-associated protein in complex with 2'-2 deoxyadenosine 5'-triphosphate
95	c2z0mA_	Alignment	not modelled	97.7	26	PDB header: rna binding protein Chain: A: PDB Molecule: 337aa long hypothetical atp-dependent rna PDBTitle: crystal structure of hypothetical atp-dependent rna2 helicase from sulfobolus tokodaii
96	d1gl9b1	Alignment	not modelled	97.7	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
97	c3oiyB_	Alignment	not modelled	97.7	21	PDB header: isomerase Chain: B: PDB Molecule: reverse gyrase helicase domain; PDBTitle: helicase domain of reverse gyrase from thermotoga maritima
98	c2vsxA_	Alignment	not modelled	97.7	22	PDB header: translation/hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase eif4a; PDBTitle: crystal structure of a translation initiation complex
99	c4w7sA_	Alignment	not modelled	97.7	22	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing atp-dependent rna helicase prp28; PDBTitle: crystal structure of the yeast dead-box splicing factor prp28 at 2.542 angstroms resolution
100	c3ly5A_	Alignment	not modelled	97.7	18	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx18; PDBTitle: ddx18 dead-domain
101	c5wsge_	Alignment	not modelled	97.7	15	PDB header: rna binding protein/rna Chain: E: PDB Molecule: saccharomyces cerevisiae s288c snr6 snrna; PDBTitle: cryo-em structure of the catalytic step ii spliceosome (c* complex) at2 4.0 angstrom resolution
102	c3bxzA_	Alignment	not modelled	97.7	17	PDB header: transport protein Chain: A: PDB Molecule: preprotein translocase subunit seca; PDBTitle: crystal structure of the isolated dead motor domains from escherichia2 coli seca
103	c5lj5Q_	Alignment	not modelled	97.6	18	PDB header: splicing Chain: Q: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp16; PDBTitle: overall structure of the yeast spliceosome immediately after2 branching.
104	c5supB_	Alignment	not modelled	97.6	18	PDB header: hydrolase/rna Chain: B: PDB Molecule: atp-dependent rna helicase sub2; PDBTitle: structure of mrna export factors
105	c1hv8B_	Alignment	not modelled	97.6	29	PDB header: rna binding protein Chain: B: PDB Molecule: putative atp-dependent rna helicase mj0669;

						PDBTitle: crystal structure of a dead box protein from the2 hyperthermophile methanococcus jannaschii
106	c1ymfA_	Alignment	not modelled	97.6	14	PDB header: hydrolase Chain: A; PDB Molecule: genome polyprotein [contains: flavivirin protease ns3 PDBTitle: crystal structure of yellow fever virus ns3 helicase complexed with2 adp
107	c3fhtA_	Alignment	not modelled	97.6	25	PDB header: hydrolase/rna Chain: A; PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: crystal structure of human dbp5 in complex with amppnp and rna
108	c6iegA_	Alignment	not modelled	97.6	17	PDB header: rna binding protein Chain: A; PDB Molecule: exosome rna helicase mtr4; PDBTitle: crystal structure of human mtr4
109	c4bujA_	Alignment	not modelled	97.6	15	PDB header: hydrolase Chain: A; PDB Molecule: antiviral helicase ski2; PDBTitle: crystal structure of the s. cerevisiae ski2-3-8 complex
110	c2d7dA_	Alignment	not modelled	97.6	22	PDB header: hydrolase/dna Chain: A; PDB Molecule: uvrabc system protein b; PDBTitle: structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc
111	c3pexA_	Alignment	not modelled	97.6	22	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent rna helicase dbp5; PDBTitle: s. cerevisiae dbp5 l327v bound to gle1 h337r and ip6
112	c5oe9C_	Alignment	not modelled	97.6	20	PDB header: viral protein Chain: C; PDB Molecule: large subunit terminase; PDBTitle: structure of large terminase from the thermophilic bacteriophage d6e2 in complex with sulfate (crystal form 2)
113	c3ewsA_	Alignment	not modelled	97.6	25	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: human dead-box rna-helicase ddx19 in complex with adp
114	c2kbeA_	Alignment	not modelled	97.6	24	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent rna helicase dbp5; PDBTitle: solution structure of amino-terminal domain of dbp5p
115	c4d25A_	Alignment	not modelled	97.6	25	PDB header: hydrolase Chain: A; PDB Molecule: bmvlg protein; PDBTitle: crystal structure of the bombyx mori vasa helicase (e339q)2 in complex with rna and amppnp
116	c1s2mA_	Alignment	not modelled	97.6	25	PDB header: rna binding protein Chain: A; PDB Molecule: putative atp-dependent rna helicase dhh1; PDBTitle: crystal structure of the dead box protein dhh1p
117	c6o16A_	Alignment	not modelled	97.6	18	PDB header: hydrolase/rna Chain: A; PDB Molecule: deah (asp-glu-ala-his) box polypeptide 37; PDBTitle: crystal structure of murine dhx37 in complex with rna
118	c2ocaA_	Alignment	not modelled	97.6	17	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent dna helicase uvsw; PDBTitle: the crystal structure of t4 uvsw
119	c4cbhC_	Alignment	not modelled	97.6	19	PDB header: hydrolase Chain: C; PDB Molecule: serine protease ns3; PDBTitle: pestivirus ns3 helicase
120	c4bijD_	Alignment	not modelled	97.5	22	PDB header: hydrolase Chain: D; PDB Molecule: dna maturase b; PDBTitle: threading model of t7 large terminase