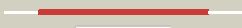




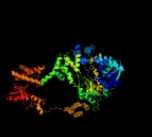



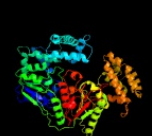







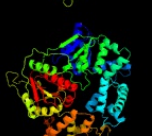




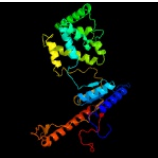

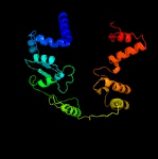
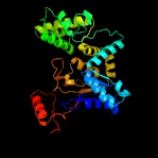

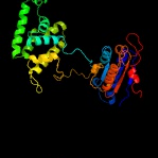





Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0630c_(recB)_721732_725016
 Date Fri Jul 26 01:50:19 BST 2019
 Unique Job ID 84bc22789e6e4a92

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w36E_	 Alignment		100.0	29	PDB header: recombination Chain: E; PDB Molecule: exodeoxyribonuclease v beta chain; PDBTitle: recbcd:dna complex
2	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
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	20	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	22	PDB header: hydrolase/dna Chain: B; PDB Molecule: protein (atp-dependent dna helicase rep.); PDBTitle: e. coli rep helicase/dna complex
6	d1w36b3	 Alignment		100.0	29	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Exodeoxyribonuclease V beta chain (RecB), C-terminal domain
7	c2pjrF_	 Alignment		100.0	20	PDB header: hydrolase/dna Chain: F; PDB Molecule: protein (helicase pcra); PDBTitle: helicase product complex
8	c4c30I_	 Alignment		100.0	23	PDB header: hydrolase/dna Chain: I; PDB Molecule: dna helicase ii; PDBTitle: crystal structure of deinococcus radiodurans uvrd in2 complex with dna, form 2
9	c1pjrA_	 Alignment		100.0	22	PDB header: helicase Chain: A; PDB Molecule: pcra; PDBTitle: structure of dna helicase
10	c3lfuA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: dna helicase ii; PDBTitle: crystal structure of e. coli uvrd
11	d1w36b1	 Alignment		100.0	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain

12	d1w36b2	Alignment		100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
13	c1w36F_	Alignment		100.0	16	PDB header: recombination Chain: F; PDB Molecule: exodeoxyribonuclease v gamma chain; PDBTitle: recbcd:dna complex
14	c1qhhB_	Alignment		100.0	19	PDB header: hydrolase Chain: B; PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
15	d1uaaa1	Alignment		100.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
16	d1pjra1	Alignment		100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
17	d1uaaa2	Alignment		100.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
18	d1pjra2	Alignment		100.0	20	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	24	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	c2wjyA_	Alignment	not modelled	99.9	23	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
22	c2xzlA_	Alignment	not modelled	99.9	20	PDB header: hydrolase/rna Chain: A; PDB Molecule: atp-dependent helicase nam7; PDBTitle: upf1-rna complex
23	d1w36c2	Alignment	not modelled	99.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
24	c3upuC_	Alignment	not modelled	99.9	24	PDB header: hydrolase/dna Chain: C; PDB Molecule: atp-dependent dna helicase dda; PDBTitle: crystal structure of the t4 phage sf1b helicase dda
25	c2gk7A_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A; PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: structural and functional insights into the human upf1 helicase core
26	c5wwpA_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A; PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
27	c3gp8A_	Alignment	not modelled	99.9	33	PDB header: hydrolase/dna Chain: A; PDB Molecule: exodeoxyribonuclease v, subunit recd, putative; PDBTitle: crystal structure of the binary complex of recd2 with dna
28	c5ld2D_	Alignment	not modelled	99.9	30	PDB header: hydrolase Chain: D; PDB Molecule: recbcd enzyme subunit recd; PDBTitle: cryo-em structure of recbcd+dna complex revealing activated nuclease2 domain

29	c3e1sA	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: A; PDB Molecule: exodeoxyribonuclease v, subunit recd; PDBTitle: structure of an n-terminal truncation of deinococcus radiodurans recd2
30	c1w36G	Alignment	not modelled	99.9	27	PDB header: recombination Chain: G; PDB Molecule: exodeoxyribonuclease v alpha chain; PDBTitle: recbcd:dna complex
31	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
32	c5n8oA	Alignment	not modelled	99.9	27	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
33	c5wvpB	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: B; PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
34	c4pj3A	Alignment	not modelled	99.9	15	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
35	c1qhhA	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A; PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
36	c3jb9X	Alignment	not modelled	99.9	11	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
37	c5mznA	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: A; PDB Molecule: helicase sen1,helicase sen1; PDBTitle: helicase sen1
38	c5fhhA	Alignment	not modelled	99.8	27	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of human pif1 helicase domain residues 200-641
39	c4n0oC	Alignment	not modelled	99.7	32	PDB header: hydrolase/dna Chain: C; PDB Molecule: replicase polyprotein 1ab; PDBTitle: complex structure of arterivirus nonstructural protein 10 (helicase)2 with dna
40	c2pjrB	Alignment	not modelled	99.7	30	PDB header: hydrolase/dna Chain: B; PDB Molecule: protein (helicase pcra); PDBTitle: helicase product complex
41	c1qhhD	Alignment	not modelled	99.7	35	PDB header: hydrolase Chain: D; PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
42	d1w36d2	Alignment	not modelled	99.6	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
43	c3dmnA	Alignment	not modelled	99.5	28	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative dna helicase; PDBTitle: the crystal structure of the c-terminal domain of a possilbe dna2 helicase from lactobacillus plantarun wcfs1
44	c3vkwA	Alignment	not modelled	99.4	23	PDB header: transferase Chain: A; PDB Molecule: replicase large subunit; PDBTitle: crystal structure of the superfamily 1 helicase from tomato mosaic2 virus
45	d1w36d1	Alignment	not modelled	99.3	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
46	c3b85A	Alignment	not modelled	99.2	24	PDB header: hydrolase Chain: A; PDB Molecule: phosphate starvation-inducible protein; PDBTitle: crystal structure of predicted phosphate starvation-induced atpase2 pho2 from corynebacterium glutamicum
47	c5ftbA	Alignment	not modelled	99.0	27	PDB header: hydrolase Chain: A; PDB Molecule: tpr domain protein; PDBTitle: crystal structure of pif1 helicase from bacteroides in2 complex with amppnp
48	c6jimA	Alignment	not modelled	98.9	33	PDB header: viral protein/rna Chain: A; PDB Molecule: helicase; PDBTitle: viral helicase protein
49	c5zyuA	Alignment	not modelled	98.5	25	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
50	c4ic1D	Alignment	not modelled	98.3	16	PDB header: structural genomics, unknown function Chain: D; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of sso0001
51	c4on9B	Alignment	not modelled	98.0	16	PDB header: hydrolase Chain: B; PDB Molecule: probable atp-dependent rna helicase ddx58; PDBTitle: dech box helicase domain
52	c4onbA	Alignment	not modelled	97.5	35	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
53	c3l0aA	Alignment	not modelled	97.5	15	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	c2wv9A	Alignment	not modelled	97.3	16	PDB header: hydrolase Chain: A; PDB Molecule: flavivirin protease ns2b regulatory subunit, flavivirin

						PDBTitle: crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus
55	c3i5yA_	Alignment	not modelled	97.3	22	PDB header: hydrolase/rna 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	c2vbcA_	Alignment	not modelled	97.2	19	PDB header: hydrolase Chain: A: PDB Molecule: dengue 4 ns3 full-length protein; PDBTitle: crystal structure of the ns3 protease-helicase from dengue2 virus
57	c1ymfA_	Alignment	not modelled	97.1	27	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
58	c5xdrA_	Alignment	not modelled	97.1	19	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
59	c3h4rA_	Alignment	not modelled	97.0	20	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease 8; PDBTitle: crystal structure of e. coli rece exonuclease
60	d1gkub1	Alignment	not modelled	97.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
61	c5lkIB_	Alignment	not modelled	97.0	22	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of full-length csfv ns3/4a
62	c5v9xA_	Alignment	not modelled	96.9	18	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
63	c2jlrA_	Alignment	not modelled	96.9	23	PDB header: hydrolase Chain: A: PDB Molecule: serine protease subunit ns3; PDBTitle: dengue virus 4 ns3 helicase in complex with amppnp
64	c3tbkA_	Alignment	not modelled	96.9	15	PDB header: hydrolase Chain: A: PDB Molecule: rig-i helicase domain; PDBTitle: mouse rig-i atpase domain
65	c4cbhC_	Alignment	not modelled	96.9	22	PDB header: hydrolase Chain: C: PDB Molecule: serine protease ns3; PDBTitle: pestivirus ns3 helicase
66	d1gl9b1	Alignment	not modelled	96.8	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
67	c5mq0V_	Alignment	not modelled	96.8	17	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
68	c5ivIA_	Alignment	not modelled	96.8	18	PDB header: hydrolase Chain: A: PDB Molecule: dead-box atp-dependent rna helicase csha; PDBTitle: csha helicase
69	c2z83A_	Alignment	not modelled	96.7	21	PDB header: viral protein Chain: A: PDB Molecule: helicase/nucleoside triphosphatase; PDBTitle: crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8
70	c5agaA_	Alignment	not modelled	96.7	23	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
71	c6fwsB_	Alignment	not modelled	96.6	21	PDB header: dna binding protein Chain: B: PDB Molecule: atp-dependent dna helicase ding; PDBTitle: structure of ding in complex with ssdna and adpbf
72	c5lj5Q_	Alignment	not modelled	96.5	22	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.
73	c2qeqA_	Alignment	not modelled	96.5	22	PDB header: hydrolase Chain: A: PDB Molecule: flavivirin protease ns3 catalytic subunit; PDBTitle: crystal structure of kunjin virus ns3 helicase
74	c3tmiA_	Alignment	not modelled	96.5	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
75	c4ddvA_	Alignment	not modelled	96.5	17	PDB header: hydrolase Chain: A: PDB Molecule: reverse gyrase; PDBTitle: thermotoga maritima reverse gyrase, triclinic form
76	c4qqxA_	Alignment	not modelled	96.5	18	PDB header: hydrolase/dna Chain: A: PDB Molecule: crispr-associated helicase, cas3 family; PDBTitle: crystal structure of t. fusca cas3-atp
77	c4ljyA_	Alignment	not modelled	96.5	19	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
78	c3oiyB_	Alignment	not modelled	96.5	17	PDB header: isomerase Chain: B: PDB Molecule: reverse gyrase helicase domain; PDBTitle: helicase domain of reverse gyrase from thermotoga maritima
79	d2bmfa2	Alignment	not modelled	96.5	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase

80	c2db3D_	Alignment	not modelled	96.4	20	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
81	c2w00B_	Alignment	not modelled	96.4	11	PDB header: hydrolase Chain: B: PDB Molecule: hsdr; PDBTitle: crystal structure of the hsdr subunit of the ecor124i restriction2 enzyme in complex with atp
82	c5ylzW_	Alignment	not modelled	96.4	17	PDB header: splicing Chain: W: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp22; PDBTitle: cryo-em structure of the post-catalytic spliceosome from saccharomyces2 cerevisiae at 3.6 angstrom
83	c5aorA_	Alignment	not modelled	96.4	16	PDB header: hydrolase/rna Chain: A: PDB Molecule: dosage compensation regulator; PDBTitle: structure of mle rna adp alf4 complex
84	c6hegA_	Alignment	not modelled	96.4	25	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase hrpb; PDBTitle: crystal structure of escherichia coli deah/rna helicase hrpb
85	c2va8A_	Alignment	not modelled	96.4	22	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
86	c5n8zA_	Alignment	not modelled	96.4	15	PDB header: hydrolase Chain: A: PDB Molecule: cg9323, isoform a; PDBTitle: crystal structure of drosophila dhx36 helicase in complex with2 ctctccctt
87	c1a1vA_	Alignment	not modelled	96.4	20	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein (ns3 protein); PDBTitle: hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
88	c6iczY_	Alignment	not modelled	96.4	15	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
89	c5fmfY_	Alignment	not modelled	96.4	15	PDB header: transcription Chain: Y: PDB Molecule: dna repair helicase rad3; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex
90	c6i3oA_	Alignment	not modelled	96.3	15	PDB header: hydrolase Chain: A: PDB Molecule: putative pre-mrna splicing factor; PDBTitle: crystal structure of deah-box atpase prp22
91	c6fa5A_	Alignment	not modelled	96.3	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
92	c2ocaA_	Alignment	not modelled	96.3	17	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase uvsw; PDBTitle: the crystal structure of t4 uvsw
93	c2w74B_	Alignment	not modelled	96.3	9	PDB header: hydrolase Chain: B: PDB Molecule: type i restriction enzyme ecor124ii r protein; PDBTitle: mutant (k220r) of the hsdr subunit of the ecor124i2 restriction enzyme in complex with atp
94	c4nl8E_	Alignment	not modelled	96.2	20	PDB header: dna binding protein Chain: E: PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to ssb c-terminal tail peptide
95	c6c90A_	Alignment	not modelled	96.2	15	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
96	c4q2dA_	Alignment	not modelled	96.2	23	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
97	c6c0fp_	Alignment	not modelled	96.2	20	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: yeast nucleolar pre-60s ribosomal subunit (state 2)
98	c6nmiB_	Alignment	not modelled	96.2	27	PDB header: transcription Chain: B: PDB Molecule: general transcription and dna repair factor iih helicase PDBTitle: cryo-em structure of the human tfiih core complex
99	c3kx2A_	Alignment	not modelled	96.2	18	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
100	c5z58x_	Alignment	not modelled	96.1	16	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.
101	d1c4oa1	Alignment	not modelled	96.1	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
102	c5vheA_	Alignment	not modelled	96.1	20	PDB header: hydrolase Chain: A: PDB Molecule: deah (asp-glu-ala-his) box polypeptide 36; PDBTitle: dhx36 in complex with the c-myc g-quadruplex
103	c3dkpA_	Alignment	not modelled	96.1	21	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
104	c5wsge_	Alignment	not modelled	96.1	20	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
105	c1w9oD_	Alignment	not modelled	96.0	17	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent rna helicase, putative;

105	c1wp3D_	Alignment	not modelled	96.0	17	PDBTitle: crystal structure of pyrococcus furiosus hef helicase domain PDB header: immune system Chain: A; PDB Molecule: lgp2; PDBTitle: crystal structure of chicken lgp2 with 5'ppp 10-mer dsrna and adp-2 alf4-mg2+ at 2.2 a resolution.
106	c5jb2A_	Alignment	not modelled	96.0	16	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
107	c6o16A_	Alignment	not modelled	96.0	17	PDB header: hydrolase Chain: A; PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
108	c2zj8A_	Alignment	not modelled	96.0	15	PDB header: hydrolase Chain: B; PDB Molecule: protein (protease/helicase ns3); PDBTitle: crystal structure of an enzyme complex from hepatitis c virus
109	c1cu1B_	Alignment	not modelled	96.0	20	PDB header: helicase Chain: A; PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
110	c1gm5A_	Alignment	not modelled	96.0	11	PDB header: hydrolase Chain: A; PDB Molecule: rna helicase; PDBTitle: kokobera virus helicase: mutant met47thr
111	c2v6jA_	Alignment	not modelled	96.0	24	PDB header: hydrolase Chain: B; PDB Molecule: type i restriction enzyme r protein; PDBTitle: crystal structure of the hsdR subunit of the ecor124i restriction2 enzyme with the c-terminal domain
112	c6h2jB_	Alignment	not modelled	95.9	11	PDB header: hydrolase Chain: A; PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 1
113	c2zj2A_	Alignment	not modelled	95.9	16	PDB header: dna binding protein Chain: H; PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to adp
114	c4nl4H_	Alignment	not modelled	95.9	19	PDB header: immune system Chain: B; PDB Molecule: melanoma differentiation associated protein-5; PDBTitle: crystal structure of chicken mda5 with 5'p 10-mer dsrna and adp-mg2+2 at 2.6 a resolution (orthorhombic form).
115	c5jcfB_	Alignment	not modelled	95.9	12	PDB header: hydrolase Chain: A; PDB Molecule: probable atp-dependent rna helicase ddx23; PDBTitle: structure of the spliceosomal dead-box protein prp28
116	c4nhoA_	Alignment	not modelled	95.9	15	PDB header: dna binding protein Chain: A; PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
117	c2p6uA_	Alignment	not modelled	95.9	21	PDB header: unknown function Chain: A; PDB Molecule: xpd; PDBTitle: structure of s. tokodaii xpd4
118	c2vl7A_	Alignment	not modelled	95.9	24	PDB header: hydrolase Chain: C; PDB Molecule: probable atp-dependent rna helicase ddx48; PDBTitle: crystal structure of human apo-eif4aiii
119	c2hxyC_	Alignment	not modelled	95.9	18	PDB header: gene regulation Chain: A; PDB Molecule: probable atp-dependent rna helicase p47; PDBTitle: structure of decd to dead mutation of human uap56
120	c1xtkA_	Alignment	not modelled	95.9	18	