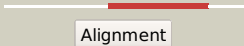



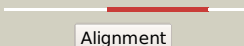







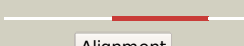











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2101_(helZ)_2360248_2363289
Date	Mon Aug 5 13:25:22 BST 2019
Unique Job ID	ef41c63220ea799a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6g7eB_	 Alignment		100.0	34	PDB header: transcription Chain: B: PDB Molecule: helicase-like protein; PDBTitle: crystal structure of chaetomium thermophilum mot1 (e1434q, 1837-18862 deletion mutant)
2	c5o9gW_	 Alignment		100.0	33	PDB header: dna binding protein Chain: W: PDB Molecule: chromo domain-containing protein 1; PDBTitle: structure of nucleosome-chd1 complex
3	c1z3iX_	 Alignment		100.0	30	PDB header: recombination/dna binding Chain: X: PDB Molecule: similar to rad54-like; PDBTitle: structure of the swi2/snf2 chromatin remodeling domain of eukaryotic2 rad54
4	c6fmIG_	 Alignment		100.0	39	PDB header: dna binding protein Chain: G: PDB Molecule: ino80; PDBTitle: cryoem structure ino80core nucleosome complex
5	c3mwyW_	 Alignment		100.0	33	PDB header: hydrolase Chain: W: PDB Molecule: chromo domain-containing protein 1; PDBTitle: crystal structure of the chromodomain-atpase portion of the yeast chd12 chromatin remodeler
6	c5jxrB_	 Alignment		100.0	30	PDB header: transcription Chain: B: PDB Molecule: chromatin-remodeling complex atpase-like protein; PDBTitle: crystal structure of mtiswi
7	c6gejM_	 Alignment		100.0	33	PDB header: nuclear protein Chain: M: PDB Molecule: helicase swr1; PDBTitle: chromatin remodeller-nucleosome complex at 3.6 a resolution.
8	c6etxG_	 Alignment		100.0	41	PDB header: dna binding protein Chain: G: PDB Molecule: dna helicase ino80; PDBTitle: cryo-em structure of the human ino80 complex bound to nucleosome
9	c5hxrA_	 Alignment		100.0	30	PDB header: transcription Chain: A: PDB Molecule: snf2-family atp dependent chromatin remodeling factor like PDBTitle: crystal structure of mtsnf2
10	c5x0yO_	 Alignment		100.0	32	PDB header: structural protein/hydrolase/dna Chain: O: PDB Molecule: transcription regulatory protein snf2; PDBTitle: complex of snf2-nucleosome complex with snf2 bound to sh2 of the2 nucleosome
11	c3dmqA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: rna polymerase-associated protein rapa; PDBTitle: crystal structure of rapa, a swi2/snf2 protein that recycles rna2 polymerase during transcription

12	c1z63A_	Alignment		100.0	45	PDB header: hydrolase/dna complex Chain: A: PDB Molecule: helicase of the snf2/rad54 family; PDBTitle: sulfolobus solfataricus swi2/snf2 atpase core in complex with dsdna
13	c5vvrM_	Alignment		100.0	33	PDB header: transcription/rna/dna Chain: M: PDB Molecule: dna repair and recombination protein rad26; PDBTitle: ternary complex of rna pol ii, transcription scaffold and rad26
14	c6iroL_	Alignment		100.0	31	PDB header: dna binding protein/dna Chain: L: PDB Molecule: iswi chromatin-remodeling complex atpase isw1; PDBTitle: the crosslinked complex of iswi-nucleosome in the adp-bound state
15	c6ne3W_	Alignment		100.0	36	PDB header: dna binding protein/dna Chain: W: PDB Molecule: swi/snf-related matrix-associated actin-dependent regulator PDBTitle: cryo-em structure of singly-bound snf2h-nucleosome complex with snf2h2 bound at shl-2
16	d1z3ix1	Alignment		100.0	34	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
17	c6eg3A_	Alignment		100.0	30	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: maltose/maltodextrin-binding periplasmic protein,probable PDBTitle: crystal structure of human brm in complex with compound 15
18	c6ro4A_	Alignment		100.0	18	PDB header: translocase Chain: A: PDB Molecule: general transcription and dna repair factor iih helicase PDBTitle: structure of the core tfiih-xpa-dna complex
19	c6nmiA_	Alignment		100.0	18	PDB header: transcription Chain: A: PDB Molecule: general transcription and dna repair factor iih helicase PDBTitle: cryo-em structure of the human tfiih core complex
20	c5of4A_	Alignment		100.0	17	PDB header: transcription Chain: A: PDB Molecule: tfiih basal transcription factor complex helicase xpb PDBTitle: the cryo-em structure of human tfiih
21	c5ivvV_	Alignment	not modelled	100.0	17	PDB header: transcription/dna Chain: V: PDB Molecule: tfiih basal transcription factor complex helicase xpb PDBTitle: human core tfiih bound to dna within the pic
22	c6igmH_	Alignment	not modelled	100.0	38	PDB header: transcription Chain: H: PDB Molecule: helicase srcap; PDBTitle: cryo-em structure of human srcap complex
23	c5jxtB_	Alignment	not modelled	100.0	30	PDB header: transcription Chain: B: PDB Molecule: chromatin-remodeling complex atpase-like protein; PDBTitle: crystal structure of mtiswi bound with histone h4 tail
24	c5fmf1_	Alignment	not modelled	100.0	21	PDB header: transcription Chain: 1: PDB Molecule: dna repair helicase rad25, ssl2; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex
25	d1z3ix2	Alignment	not modelled	100.0	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
26	c5gn1D_	Alignment	not modelled	100.0	32	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent helicase fun30; PDBTitle: crystal structure of the c-terminal part of fun30 atpase domain
27	d1z5za1	Alignment	not modelled	100.0	44	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
28	c5jb2A_	Alignment	not modelled	100.0	18	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. PDB header: immune system

29	c5jcfB_	Alignment	not modelled	100.0	15	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).
30	c1z5zB_	Alignment	not modelled	100.0	44	PDB header: hydrolase/recombination Chain: B: PDB Molecule: helicase of the snf2/rad54 family; PDBTitle: sulfobolus solfataricus swi2/snf2 atpase c-terminal domain
31	d1z63a1	Alignment	not modelled	100.0	45	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
32	c4on9B_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx58; PDBTitle: dech box helicase domain
33	c3tmiA_	Alignment	not modelled	100.0	13	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase ddx58; PDBTitle: structural basis for rna recognition and activation of rig-i
34	c1wp9D_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent rna helicase, putative; PDBTitle: crystal structure of pyrococcus furiosus hef helicase domain
35	c4gl2A_	Alignment	not modelled	100.0	14	PDB header: rna binding protein/rna Chain: A: PDB Molecule: interferon-induced helicase c domain-containing protein 1; PDBTitle: structural basis for dsrna duplex backbone recognition by mda5
36	c2d7dA_	Alignment	not modelled	100.0	18	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
37	c1c4oA_	Alignment	not modelled	100.0	16	PDB header: replication Chain: A: PDB Molecule: dna nucleotide excision repair enzyme uvrbc; PDBTitle: crystal structure of the dna nucleotide excision repair enzyme uvrbc2 from thermus thermophilus
38	c5zamA_	Alignment	not modelled	100.0	18	PDB header: hydrolase/protein binding/rna Chain: A: PDB Molecule: endoribonuclease dicer; PDBTitle: cryo-em structure of human dicer and its complexes with a pre-mirna2 substrate
39	c3tbkA_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: rig-i helicase domain; PDBTitle: mouse rig-i atpase domain
40	c2fwrA_	Alignment	not modelled	100.0	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad25; PDBTitle: structure of archaeoglobus fulgidis xpb
41	c6jdeB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: putative dna repair helicase radd; PDBTitle: crystal structure of a dna repair protein
42	c2ocaA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase uvsw; PDBTitle: the crystal structure of t4 uvsw
43	c3hgtA_	Alignment	not modelled	100.0	10	PDB header: transcription Chain: A: PDB Molecule: hda1 complex subunit 3; PDBTitle: structural and functional studies of the yeast class ii hda12 hdac complex
44	c2eyqA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of escherichia coli transcription-repair2 coupling factor
45	c5v9xA_	Alignment	not modelled	100.0	15	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
46	c6buaA_	Alignment	not modelled	100.0	19	PDB header: rna binding protein Chain: A: PDB Molecule: dicer-2, isoform a; PDBTitle: drosophila dicer-2 apo homology model (helicase, platform-paz,2 rnaseiii domains)
47	c5tnuB_	Alignment	not modelled	100.0	20	PDB header: transcription Chain: B: PDB Molecule: dna-dependent atpase xpbii; PDBTitle: s. tokodaii xpb ii crystal structure at 3.0 angstrom resolution
48	c4xqkB_	Alignment	not modelled	100.0	19	PDB header: hydrolase/dna Chain: B: PDB Molecule: llabiii; PDBTitle: atp-dependent type isp restriction-modification enzyme llabiii bound2 to dna
49	c4ernA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: tfiih basal transcription factor complex helicase xpb PDBTitle: crystal structure of the c-terminal domain of human xpb/ercc-32 excision repair protein at 1.80 a
50	c5agaA_	Alignment	not modelled	100.0	21	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
51	c1gm5A_	Alignment	not modelled	100.0	20	PDB header: helicase Chain: A: PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
52	c1oywA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase; PDBTitle: structure of the recq catalytic core
53	c4cdgA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: bloom syndrome protein; PDBTitle: crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody
54	c3nivB_	Alignment	not modelled	100.0	19	PDB header: isomerase Chain: B: PDB Molecule: reverse gyrase helicase domain;

54	c3vlyB	Alignment	not modelled	100.0	19	PDBTitle: helicase domain of reverse gyrase from thermotoga maritima
55	d1gm5a3	Alignment	not modelled	100.0	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
56	c2fz1A	Alignment	not modelled	100.0	18	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad25, xpb; PDBTitle: structure of c-terminal domain of archaeoglobus fulgidus xpb
57	c2v1xB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent dna helicase q1; PDBTitle: crystal structure of human recq-like dna helicase
58	c2va8A	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
59	d1wp9a2	Alignment	not modelled	100.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
60	c4q47A	Alignment	not modelled	100.0	20	PDB header: dna binding protein Chain: A: PDB Molecule: dna helicase recq; PDBTitle: structure of the drrecq catalytic core in complex with adp
61	d2fwra1	Alignment	not modelled	100.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
62	c4ljyA	Alignment	not modelled	100.0	18	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
63	c4ddvA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: reverse gyrase; PDBTitle: thermotoga maritima reverse gyrase, triclinic form
64	d1rifa	Alignment	not modelled	100.0	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: DNA helicase UvsW
65	c3ewsA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: human dead-box rna-helicase ddx19 in complex with adp
66	d2eyqa3	Alignment	not modelled	99.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
67	d2fwra2	Alignment	not modelled	99.9	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
68	c5lstA	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase q4; PDBTitle: crystal structure of the human recq4 helicase.
69	c2zj8A	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
70	c1q19B	Alignment	not modelled	99.9	20	PDB header: topoisomerase Chain: B: PDB Molecule: reverse gyrase; PDBTitle: archaeoglobus fulgidus reverse gyrase complexed with adpnp
71	c6iehB	Alignment	not modelled	99.9	18	PDB header: rna binding protein Chain: B: PDB Molecule: exosome rna helicase mtr4; PDBTitle: crystal structures of the hmtr4-nrde2 complex
72	c3bxzA	Alignment	not modelled	99.9	20	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
73	c2p6uA	Alignment	not modelled	99.9	23	PDB header: dna binding protein Chain: A: PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
74	d1tf5a3	Alignment	not modelled	99.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
75	c4bujA	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: antiviral helicase ski2; PDBTitle: crystal structure of the s. cerevisiae ski2-3-8 complex
76	c2zj2A	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 1
77	c5m52B	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of yeast brr2 full-length in complex with prp8 jab12 domain
78	c2w74B	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: type i restriction enzyme ecor124ii r protein; PDBTitle: mutant (k220r) of the hsdR subunit of the ecor124ii restriction enzyme in complex with atp
79	c3h1tA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: type i site-specific restriction-modification PDBTitle: the fragment structure of a putative hsdR subunit of a type2 i restriction enzyme from vibrio vulnificus yj016
80	c6iegA	Alignment	not modelled	99.9	17	PDB header: rna binding protein Chain: A: PDB Molecule: exosome rna helicase mtr4; PDBTitle: crystal structure of human mtr4
						PDB header: hydrolase/rna binding protein

81	c6c90A_	Alignment	not modelled	99.9	17	Chain: A: PDB Molecule: exosome rna helicase mtr4,exosome rna helicase mtr4; PDBTitle: human mtr4 helicase in complex with zcchc8-ctd
82	c4xgtA_	Alignment	not modelled	99.9	19	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
83	d2fz4a1	Alignment	not modelled	99.9	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
84	c3i5yA_	Alignment	not modelled	99.9	19	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
85	c6ah0D_	Alignment	not modelled	99.9	24	PDB header: splicing Chain: D: PDB Molecule: u5 small nuclear ribonucleoprotein 200 kda helicase; PDBTitle: the cryo-em structure of the precursor of human pre-catalytic2 spliceosome (pre-b complex)
86	c2db3D_	Alignment	not modelled	99.9	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
87	c5dcaA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of yeast full length brr2 in complex with prp8 jab12 domain
88	c5lqwC_	Alignment	not modelled	99.9	18	PDB header: splicing Chain: C: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: yeast activated spliceosome
89	c2xgjA_	Alignment	not modelled	99.9	18	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
90	c1tf2A_	Alignment	not modelled	99.9	15	PDB header: protein transport Chain: A: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of seca:adp in an open conformation from2 bacillus subtilis
91	c4a4zA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: antiviral helicase ski2; PDBTitle: crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
92	c4bgdA_	Alignment	not modelled	99.9	19	PDB header: transcription Chain: A: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of brr2 in complex with the jab1/mpn domain of prp8
93	c3dl8B_	Alignment	not modelled	99.9	16	PDB header: protein transport Chain: B: PDB Molecule: protein translocase subunit seca; PDBTitle: structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
94	c3i9oA_	Alignment	not modelled	99.9	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
95	c5ib5C_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent dna helicase q5; PDBTitle: crystal structure of human recq15 helicase in complex with adp/mg2 (tricolinc form).
96	c4pxaA_	Alignment	not modelled	99.9	20	PDB header: translation, rna binding protein Chain: A: PDB Molecule: atp-dependent rna helicase ddx3x; PDBTitle: dead-box rna helicase ddx3x cancer-associated mutant d354v
97	c4w7sA_	Alignment	not modelled	99.9	17	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
98	c6c0fp_	Alignment	not modelled	99.9	15	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: yeast nucleolar pre-60s ribosomal subunit (state 2)
99	c5m59C_	Alignment	not modelled	99.9	19	PDB header: splicing Chain: C: PDB Molecule: pre-mrna splicing helicase-like protein; PDBTitle: crystal structure of chaetomium thermophilum brr2 helicase core in2 complex with prp8 jab1 domain
100	c4f92B_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: B: PDB Molecule: u5 small nuclear ribonucleoprotein 200 kda helicase; PDBTitle: brr2 helicase region s1087l
101	c5gi4A_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dead; PDBTitle: dead-box rna helicase
102	c1xtkA_	Alignment	not modelled	99.9	19	PDB header: gene regulation Chain: A: PDB Molecule: probable atp-dependent rna helicase p47; PDBTitle: structure of decd to dead mutation of human uap56
103	c4qqxA_	Alignment	not modelled	99.9	20	PDB header: hydrolase/dna Chain: A: PDB Molecule: crispr-associated helicase, cas3 family; PDBTitle: crystal structure of t. fusca cas3-atp
104	c5supB_	Alignment	not modelled	99.9	21	PDB header: hydrolase/rna Chain: B: PDB Molecule: atp-dependent rna helicase sub2; PDBTitle: structure of mrna export factors
105	c3fhtA_	Alignment	not modelled	99.9	17	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
106	c1s2mA_	Alignment	not modelled	99.9	17	PDB header: rna binding protein Chain: A: PDB Molecule: putative atp-dependent rna helicase dhh1; PDBTitle: crystal structure of the dead box protein dhh1p

107	c3i32A_	 Alignment	not modelled	99.9	22	PDB header: rna binding protein,hydrolase Chain: A: PDB Molecule: heat resistant rna dependent atpase; PDBTitle: dimeric structure of a hera helicase fragment including the c-terminal2 reca domain, the dimerization domain, and the rna binding domain
108	c4d25A_	 Alignment	not modelled	99.9	19	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
109	c6bu9A_	 Alignment	not modelled	99.9	16	PDB header: rna binding protein/rna Chain: A: PDB Molecule: dicer-2, isoform a; PDBTitle: drosophila dicer-2 bound to blunt dsrna
110	c2z0mA_	 Alignment	not modelled	99.9	16	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 sulfolobus tokodaii
111	c2p6nA_	 Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx41; PDBTitle: human dead-box rna helicase ddx41, helicase domain
112	d1t5ia_	 Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
113	c2w00B_	 Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: hsdr; PDBTitle: crystal structure of the hsdR subunit of the ecor124i restriction2 enzyme in complex with atp
114	c3rc8A_	 Alignment	not modelled	99.9	20	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase supv311, mitochondrial; PDBTitle: human mitochondrial helicase suv3 in complex with short rna fragment
115	c1hv8B_	 Alignment	not modelled	99.9	17	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
116	d2j0sa2	 Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
117	c4ct4B_	 Alignment	not modelled	99.9	17	PDB header: rna binding protein Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx6; PDBTitle: cnot1 mif4g domain - ddx6 complex
118	d1s2ma2	 Alignment	not modelled	99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
119	c5ivA_	 Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: dead-box atp-dependent rna helicase csha; PDBTitle: csha helicase
120	c2hxyC_	 Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: C: PDB Molecule: probable atp-dependent rna helicase ddx48; PDBTitle: crystal structure of human apo-eif4aiii