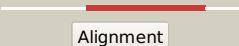





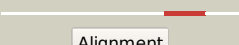



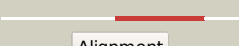






















Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	A2A4P0
Date	Wed Jul 10 14:06:11 BST 2013
Unique Job ID	df13e67bc2946f07

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kx2A_	 Alignment		100.0	47	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing factor atp-dependent rna PDBTitle: crystal structure of prp43p in complex with adp
2	c1cu1B_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: protein (protease/helicase ns3); PDBTitle: crystal structure of an enzyme complex from hepatitis c2 virus
3	c4b6eB_	 Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: non-structural protein 4a, serine protease ns3; PDBTitle: discovery of an allosteric mechanism for the regulation of hcv ns3 protein function
4	c3i4uA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dhx8; PDBTitle: crystal structure analysis of a helicase associated domain
5	c1a1vA_	 Alignment		100.0	18	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein (ns3 protein); PDBTitle: hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
6	c2f55C_	 Alignment		100.0	19	PDB header: hydrolase/dna Chain: C: PDB Molecule: polyprotein; PDBTitle: two hepatitis c virus ns3 helicase domains complexed with2 the same strand of dna
7	c2wv9A_	 Alignment		100.0	17	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
8	c2vbcA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dengue 4 ns3 full-length protein; PDBTitle: crystal structure of the ns3 protease-helicase from dengue2 virus
9	c1ymfA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: genome polyprotein [contains: flavivirin PDBTitle: crystal structure of yellow fever virus ns3 helicase2 complexed with adp
10	c2jlrA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: serine protease subunit ns3; PDBTitle: dengue virus 4 ns3 helicase in complex with amppnp
11	c3rc8A_	 Alignment		100.0	18	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

12	c2z83A_	Alignment		100.0	19	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
13	c3llmB_	Alignment		100.0	31	PDB header: hydrolase Chain: B; PDB Molecule: atp-dependent rna helicase a; PDBTitle: crystal structure analysis of a rna helicase
14	c2va8A_	Alignment		100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
15	c2p6uA_	Alignment		100.0	20	PDB header: dna binding protein Chain: A; PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
16	c2zj8A_	Alignment		100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
17	d8ohma2	Alignment		100.0	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
18	c2zj2A_	Alignment		100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 1
19	c2v6jA_	Alignment		100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: rna helicase; PDBTitle: kokobera virus helicase: mutant met47thr
20	c4f92B_	Alignment		100.0	20	PDB header: hydrolase Chain: B; PDB Molecule: u5 small nuclear ribonucleoprotein 200 kda helicase; PDBTitle: brr2 helicase region s1087l
21	c4bgdA_	Alignment	not modelled	99.9	14	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
22	c2qeqA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A; PDB Molecule: flavivirin protease ns3 catalytic subunit; PDBTitle: crystal structure of kunjin virus ns3 helicase
23	c2xgjA_	Alignment	not modelled	99.9	22	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
24	c4a4zA_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A; PDB Molecule: antiviral helicase ski2; PDBTitle: crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
25	d1yksa2	Alignment	not modelled	99.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
26	c3bxzA_	Alignment	not modelled	99.9	16	PDB header: transport protein Chain: A; PDB Molecule: preprotein translocase subunit seca; PDBTitle: crystal structure of the isolated dead motor domains from2 escherichia coli seca
27	c3l9oA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: crystal structure of mtr4, a co-factor of the nuclear exosome
28	c2v1xB_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B; PDB Molecule: atp-dependent dna helicase q1; PDBTitle: crystal structure of human recq-like dna helicase
29	d2bmfA2	Alianment	not modelled	99.9	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

					Family:RNA helicase
30	c3ewsA	Alignment	not modelled	99.9	14 PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: human dead-box rna-helicase ddx19 in complex with adp
31	c2db3D	Alignment	not modelled	99.9	18 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
32	c2eyqA	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of escherichia coli transcription-repair2 coupling factor
33	c3fhtA	Alignment	not modelled	99.9	14 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
34	c1oywA	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase; PDBTitle: structure of the reqc catalytic core
35	c1gm5A	Alignment	not modelled	99.8	17 PDB header: helicase Chain: A: PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
36	c1xtkA	Alignment	not modelled	99.8	13 PDB header: gene regulation Chain: A: PDB Molecule: probable atp-dependent rna helicase p47; PDBTitle: structure of decd to dead mutation of human uap56
37	c4gl2A	Alignment	not modelled	99.8	19 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
38	c3pexA	Alignment	not modelled	99.8	17 PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dbp5; PDBTitle: s. cerevisiae dbp5 I327v bound to gle1 h337r and ip6
39	c1hv8B	Alignment	not modelled	99.8	15 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
40	c2fsgA	Alignment	not modelled	99.8	21 PDB header: protein transport Chain: A: PDB Molecule: preprotein translocase seca subunit; PDBTitle: complex seca:atp from escherichia coli
41	c1s2mA	Alignment	not modelled	99.8	14 PDB header: rna binding protein Chain: A: PDB Molecule: putative atp-dependent rna helicase dhh1; PDBTitle: crystal structure of the dead box protein dhh1p
42	c1gl9B	Alignment	not modelled	99.7	17 PDB header: topoisomerase Chain: B: PDB Molecule: reverse gyrase; PDBTitle: archaeoglobus fulgidus reverse gyrase complexed with adpnp
43	c3i5yA	Alignment	not modelled	99.7	20 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
44	c2vsxA	Alignment	not modelled	99.7	12 PDB header: translation/hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase eif4a; PDBTitle: crystal structure of a translation initiation complex
45	c4ddvA	Alignment	not modelled	99.7	16 PDB header: hydrolase Chain: A: PDB Molecule: reverse gyrase; PDBTitle: thermotoga maritima reverse gyrase, triclinic form
46	c2z0mA	Alignment	not modelled	99.7	17 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
47	c3tmiA	Alignment	not modelled	99.7	19 PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase ddx58; PDBTitle: structural basis for rna recognition and activation of rig-i
48	c2i4iA	Alignment	not modelled	99.7	17 PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx3x; PDBTitle: crystal structure of human dead-box rna helicase ddx3x
49	c1wp9D	Alignment	not modelled	99.7	19 PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent rna helicase, putative; PDBTitle: crystal structure of pyrococcus furiosus hef helicase domain
50	c2ocaA	Alignment	not modelled	99.7	13 PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase uvsw; PDBTitle: the crystal structure of t4 uvsw
51	c3eiqD	Alignment	not modelled	99.6	15 PDB header: hydrolase/antitumor protein Chain: D: PDB Molecule: eukaryotic initiation factor 4a-i; PDBTitle: crystal structure of pdcd4-eif4a
52	c2hxyC	Alignment	not modelled	99.6	13 PDB header: hydrolase Chain: C: PDB Molecule: probable atp-dependent rna helicase ddx48; PDBTitle: crystal structure of human apo-eif4aiii
53	c2fsgB	Alignment	not modelled	99.6	20 PDB header: protein transport Chain: B: PDB Molecule: preprotein translocase seca subunit; PDBTitle: complex seca:atp from escherichia coli
54	c1c4oA	Alignment	not modelled	99.6	15 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
					PDB header: hydrolase

55	c3tbkA_	Alignment	not modelled	99.6	18	Chain: A: PDB Molecule: rig-i helicase domain; PDBTitle: mouse rig-i atpase domain
56	c3oiyB_	Alignment	not modelled	99.6	15	PDB header: isomerase Chain: B: PDB Molecule: reverse gyrase helicase domain; PDBTitle: helicase domain of reverse gyrase from thermotoga maritima
57	c1tf2A_	Alignment	not modelled	99.6	27	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
58	c2fwrA_	Alignment	not modelled	99.5	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad25; PDBTitle: structure of archaeoglobus fulgidis xpb
59	c3h1tA_	Alignment	not modelled	99.5	18	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
60	c3fhoB_	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase dbp5; PDBTitle: structure of s. pombe dbp5
61	d1a1va1	Alignment	not modelled	99.5	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
62	c3dl8B_	Alignment	not modelled	99.4	25	PDB header: protein transport Chain: B: PDB Molecule: protein translocase subunit seca; PDBTitle: structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
63	d1yksa1	Alignment	not modelled	99.4	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
64	d2p6ra3	Alignment	not modelled	99.3	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
65	d1a1va2	Alignment	not modelled	99.3	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
66	c3cwr1_	Alignment	not modelled	99.3	20	PDB header: hydrolase Chain: 1: PDB Molecule: xpd/rad3 related dna helicase; PDBTitle: "xpd_apo"
67	d1q0ua_	Alignment	not modelled	99.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
68	d1gkub1	Alignment	not modelled	99.2	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
69	c2d7dA_	Alignment	not modelled	99.2	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrbc system protein b; PDBTitle: structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc
70	c3fhcB_	Alignment	not modelled	99.2	17	PDB header: transport protein/hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: crystal structure of human dbp5 in complex with nup214
71	c3fmoB_	Alignment	not modelled	99.2	17	PDB header: oncoprotein/hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: crystal structure of the nucleoporin nup214 in complex with the dead-2 box helicase ddx19
72	d1ql9b1	Alignment	not modelled	99.2	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
73	c2j7pA_	Alignment	not modelled	99.2	20	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
74	c3dkpA_	Alignment	not modelled	99.1	14	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
75	d1veca_	Alignment	not modelled	99.1	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
76	d2eyqa5	Alignment	not modelled	99.1	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
77	d1t6na_	Alignment	not modelled	99.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
78	d1qdea_	Alignment	not modelled	99.1	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
79	c2cnwF_	Alignment	not modelled	99.1	17	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
80	c2vl7A_	Alignment	not modelled	99.1	22	PDB header: unknown function Chain: A: PDB Molecule: xpd; PDBTitle: structure of s. tokodaii xpd4
81	d1hv8a1	Alignment	not modelled	99.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
						PDB header: oncoprotein/hydrolase

82	c3fmpD_	Alignment	not modelled	99.1	15	Chain: D: PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: crystal structure of the nucleoporin nup214 in complex with the dead-2 box helicase ddx19
83	d2eyqa3	Alignment	not modelled	99.1	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
84	c2kbeA_	Alignment	not modelled	99.1	16	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dbp5; PDBTitle: solution structure of amino-terminal domain of dbp5p
85	c2w74B_	Alignment	not modelled	99.1	13	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
86	d1s2ma1	Alignment	not modelled	99.1	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
87	d2p6ra4	Alignment	not modelled	99.1	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
88	c2pl3A_	Alignment	not modelled	99.0	15	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx10; PDBTitle: human dead-box rna helicase ddx10, dead domain in complex with adp
89	c3ly5A_	Alignment	not modelled	99.0	15	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx18; PDBTitle: ddx18 dead-domain
90	c3b6eA_	Alignment	not modelled	99.0	16	PDB header: hydrolase Chain: A: PDB Molecule: interferon-induced helicase c domain-containing protein 1; PDBTitle: crystal structure of human dech-box rna helicase mda5 (melanoma2 differentiation-associated protein 5), dech-domain
91	c2oxcA_	Alignment	not modelled	99.0	15	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx20; PDBTitle: human dead-box rna helicase ddx20, dead domain in complex2 with adp
92	d1wp9a1	Alignment	not modelled	99.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
93	d2g9na1	Alignment	not modelled	99.0	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
94	c4db4A_	Alignment	not modelled	99.0	18	PDB header: rna-binding protein/dna,rna Chain: A: PDB Molecule: atp-dependent rna helicase mss116, mitochondrial; PDBTitle: mss116p dead-box helicase domain 2 bound to a chimaeric rna-dna duplex
95	c3berA_	Alignment	not modelled	99.0	19	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx47; PDBTitle: human dead-box rna-helicase ddx47, conserved domain i in complex with2 amp
96	d2j0sa1	Alignment	not modelled	99.0	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
97	d2j0sa2	Alignment	not modelled	98.9	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
98	c2gxqA_	Alignment	not modelled	98.9	18	PDB header: hydrolase Chain: A: PDB Molecule: heat resistant rna dependent atpase; PDBTitle: hera n-terminal domain in complex with amp, crystal form 1
99	c3iuyB_	Alignment	not modelled	98.9	18	PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx53; PDBTitle: crystal structure of ddx53 dead-box domain
100	d1c4oa2	Alignment	not modelled	98.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
101	c2px0D_	Alignment	not modelled	98.9	21	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
102	d1s2ma2	Alignment	not modelled	98.9	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
103	d1oywa3	Alignment	not modelled	98.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
104	d1wrba1	Alignment	not modelled	98.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
105	c1z3iX_	Alignment	not modelled	98.9	16	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
106	c3mwyW_	Alignment	not modelled	98.9	19	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
107	c2vdaA_	Alignment	not modelled	98.8	24	PDB header: protein transport Chain: A: PDB Molecule: translocase subunit seca;

						PDBTitle: solution structure of the seca-signal peptide complex
108	c3fe2B_	Alignment	not modelled	98.8	17	PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx5; PDBTitle: human dead-box rna helicase ddx5 (p68), conserved domain i in complex2 with adp
109	c2yjtD_	Alignment	not modelled	98.8	16	PDB header: hydrolase inhibitor/hydrolase Chain: D: PDB Molecule: atp-dependent rna helicase srmb; PDBTitle: crystal structure of e. coli dead-box protein srmb bound to2 regulator of ribonuclease activity a (rraa)
110	d1rifa_	Alignment	not modelled	98.8	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: DNA helicase UvsW
111	d1t5la2	Alignment	not modelled	98.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
112	d1jr6a_	Alignment	not modelled	98.8	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
113	c3earA_	Alignment	not modelled	98.8	21	PDB header: hydrolase Chain: A: PDB Molecule: hera; PDBTitle: novel dimerization motif in the dead box rna helicase hera: form 1,2 partial dimer
114	c2p6nA_	Alignment	not modelled	98.8	23	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx41; PDBTitle: human dead-box rna helicase ddx41, helicase domain
115	d1wp9a2	Alignment	not modelled	98.8	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
116	c2hvjB_	Alignment	not modelled	98.8	21	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase dbpa; PDBTitle: structure of the second domain (residues 207-368) of the2 bacillus subtilis yxin protein
117	d1hv8a2	Alignment	not modelled	98.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
118	d1gm5a3	Alignment	not modelled	98.7	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
119	c2w00B_	Alignment	not modelled	98.7	14	PDB header: hydrolase Chain: B: PDB Molecule: hsdr; PDBTitle: crystal structure of the hsdr subunit of the ecor124i2 restriction enzyme in complex with atp
120	d2q2ja1	Alignment	not modelled	98.7	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain