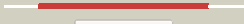



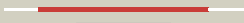


















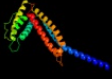
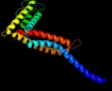








Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	O06446
Date	Tue Jul 17 17:05:02 BST 2012
Unique Job ID	963cd0d565b47ac7


Detailed template information






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ipcB_	 Alignment		100.0	51	PDB header: transport protein Chain: B; PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer
2	c1nl3B_	 Alignment		100.0	50	PDB header: protein transport Chain: B; PDB Molecule: preprotein translocase seca 1 subunit; PDBTitle: crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
3	c2vdaA_	 Alignment		100.0	50	PDB header: protein transport Chain: A; PDB Molecule: translocase subunit seca; PDBTitle: solution structure of the seca-signal peptide complex
4	c3juxA_	 Alignment		100.0	48	PDB header: protein transport Chain: A; PDB Molecule: protein translocase subunit seca; PDBTitle: structure of the translocation atpase seca from thermotoga2 maritima
5	c3dinB_	 Alignment		100.0	48	PDB header: membrane protein, protein transport Chain: B; PDB Molecule: protein translocase subunit seca; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
6	c1tf2A_	 Alignment		100.0	63	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
7	c3dl8B_	 Alignment		100.0	63	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
8	c2fsgA_	 Alignment		100.0	48	PDB header: protein transport Chain: A; PDB Molecule: preprotein translocase seca subunit; PDBTitle: complex seca:atp from escherichia coli
9	d1nka3	 Alignment		100.0	59	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
10	c3bxzA_	 Alignment		100.0	62	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
11	d1tf5a3	 Alignment		100.0	68	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain

12	d1nкта4	Alignment		100.0	65	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
13	d1tf5a2	Alignment		100.0	50	Fold: Helical scaffold and wing domains of SecA Superfamily: Helical scaffold and wing domains of SecA Family: Helical scaffold and wing domains of SecA
14	d1nкта2	Alignment		100.0	30	Fold: Helical scaffold and wing domains of SecA Superfamily: Helical scaffold and wing domains of SecA Family: Helical scaffold and wing domains of SecA
15	d1tf5a4	Alignment		100.0	73	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
16	d1nкта1	Alignment		100.0	44	Fold: Pre-protein crosslinking domain of SecA Superfamily: Pre-protein crosslinking domain of SecA Family: Pre-protein crosslinking domain of SecA
17	d1tf5a1	Alignment		100.0	65	Fold: Pre-protein crosslinking domain of SecA Superfamily: Pre-protein crosslinking domain of SecA Family: Pre-protein crosslinking domain of SecA
18	c2v1xB	Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent dna helicase q1; PDBTitle: crystal structure of human recq-like dna helicase
19	c1oywA	Alignment		99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase; PDBTitle: structure of the recq catalytic core
20	c1gm5A	Alignment		99.9	21	PDB header: helicase Chain: A: PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
21	c1gl9B	Alignment	not modelled	99.9	26	PDB header: topoisomerase Chain: B: PDB Molecule: reverse gyrase; PDBTitle: archaeoglobus fulgidus reverse gyrase complexed with adpnp
22	c2db3D	Alignment	not modelled	99.9	19	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
23	c2eyqA	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of escherichia coli transcription-repair2 coupling factor
24	c2xgjA	Alignment	not modelled	99.9	19	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
25	c3tmiA	Alignment	not modelled	99.9	14	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase ddx58; PDBTitle: structural basis for rna recognition and activation of rig-i
26	c1c4oA	Alignment	not modelled	99.9	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
27	c3i5yA	Alignment	not modelled	99.9	15	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
28	c3kx2A	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing factor atp-dependent rna PDBTitle: crystal structure of prp43p in complex with adp

29	c3l9oA	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: crystal structure of mtr4, a co-factor of the nuclear exosome
30	c2va8A	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
31	c1hv8B	Alignment	not modelled	99.9	19	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
32	c3rc8A	Alignment	not modelled	99.9	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
33	c1xtkA	Alignment	not modelled	99.9	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
34	c3oiyB	Alignment	not modelled	99.9	17	PDB header: isomerase Chain: B: PDB Molecule: reverse gyrase helicase domain; PDBTitle: helicase domain of reverse gyrase from thermotoga maritima
35	c1s2mA	Alignment	not modelled	99.8	20	PDB header: rna binding protein Chain: A: PDB Molecule: putative atp-dependent rna helicase dhh1; PDBTitle: crystal structure of the dead box protein dhh1p
36	c2jlrA	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: serine protease subunit ns3; PDBTitle: dengue virus 4 ns3 helicase in complex with amppnp
37	c3ewsA	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: human dead-box rna-helicase ddx19 in complex with adp
38	c2d7dA	Alignment	not modelled	99.8	16	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
39	c4a4zA	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: antiviral helicase ski2; PDBTitle: crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
40	c3fhtA	Alignment	not modelled	99.8	16	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
41	c2z83A	Alignment	not modelled	99.8	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
42	c2v6jA	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: A: PDB Molecule: rna helicase; PDBTitle: kokobera virus helicase: mutant met47thr
43	c3pexA	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dbp5; PDBTitle: s. cerevisiae dbp5 I327v bound to gle1 h337r and ip6
44	c2hxyC	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: C: PDB Molecule: probable atp-dependent rna helicase ddx48; PDBTitle: crystal structure of human apo-eif4aiii
45	c2ocaA	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase uvsw; PDBTitle: the crystal structure of t4 uvsw
46	c2wv9A	Alignment	not modelled	99.8	20	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
47	c2p6uA	Alignment	not modelled	99.8	20	PDB header: dna binding protein Chain: A: PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
48	c1wp9D	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent rna helicase, putative; PDBTitle: crystal structure of pyrococcus furiosus hef helicase domain
49	c2zj2A	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 1
50	c2vbcA	Alignment	not modelled	99.8	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
51	c2vsxA	Alignment	not modelled	99.8	17	PDB header: translation/hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase eif4a; PDBTitle: crystal structure of a translation initiation complex
52	c2z0mA	Alignment	not modelled	99.8	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
53	c1ymfA	Alignment	not modelled	99.7	23	PDB header: hydrolase Chain: A: PDB Molecule: genome polyprotein [contains: flavivirin PDBTitle: crystal structure of yellow fever virus ns3 helicase2 complexed with adp

54	c2i4iA_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx3x; PDBTitle: crystal structure of human dead-box rna helicase ddx3x
55	c3tbkA_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: A: PDB Molecule: rig-i helicase domain; PDBTitle: mouse rig-i atpase domain
56	c1a1vA_	Alignment	not modelled	99.7	21	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein (ns3 protein); PDBTitle: hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
57	c2qeqA_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: A: PDB Molecule: flavivirin protease ns3 catalytic subunit; PDBTitle: crystal structure of kunjin virus ns3 helicase
58	c2f55C_	Alignment	not modelled	99.7	22	PDB header: hydrolase/dna Chain: C: PDB Molecule: polyprotein; PDBTitle: two hepatitis c virus ns3 helicase domains complexed with2 the same strand of dna
59	c3fe2B_	Alignment	not modelled	99.6	21	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
60	d1oywa3	Alignment	not modelled	99.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
61	d2bmfA2	Alignment	not modelled	99.6	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
62	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
63	c3ly5A_	Alignment	not modelled	99.5	23	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx18; PDBTitle: ddx18 dead-domain
64	d2j0sa1	Alignment	not modelled	99.5	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
65	c2pl3A_	Alignment	not modelled	99.5	22	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
66	d2j0sa2	Alignment	not modelled	99.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
67	c2vl7A_	Alignment	not modelled	99.5	16	PDB header: unknown function Chain: A: PDB Molecule: xpd; PDBTitle: structure of s. tokodaii xpd4
68	c3dkpA_	Alignment	not modelled	99.5	18	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
69	d1t5la2	Alignment	not modelled	99.5	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
70	c1z3iX_	Alignment	not modelled	99.4	15	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
71	c2vjtd_	Alignment	not modelled	99.4	19	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)
72	d1gl9b1	Alignment	not modelled	99.4	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like " domain" of reverse gyrase
73	d1s2ma1	Alignment	not modelled	99.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
74	d1s2ma2	Alignment	not modelled	99.4	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
75	c3mwyW_	Alignment	not modelled	99.4	14	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
76	d1hv8a2	Alignment	not modelled	99.4	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
77	c3iuyB_	Alignment	not modelled	99.4	25	PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx53; PDBTitle: crystal structure of ddx53 dead-box domain
78	c3crw1_	Alignment	not modelled	99.4	12	PDB header: hydrolase Chain: 1: PDB Molecule: xpd/rad3 related dna helicase; PDBTitle: " xpd_ apo"
79	c2hivB_	Alignment	not modelled	99.4	22	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase dbpa;

79	c2ijvb_	Alignment	not modelled	99.4	22	PDBTitle: structure of the second domain (residues 207-368) of the2 bacillus subtilis yxin protein Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
80	d1c4oa2	Alignment	not modelled	99.4	20	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
81	c3berA_	Alignment	not modelled	99.4	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
82	d2eyqa5	Alignment	not modelled	99.4	22	PDB header: hydrolase Chain: A: PDB Molecule: rna polymerase-associated protein rapa; PDBTitle: crystal structure of rapa, a swi2/snf2 protein that2 recycles rna polymerase during transcription
83	c3dmqA_	Alignment	not modelled	99.4	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
84	d1wrba1	Alignment	not modelled	99.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
85	d1q0ua_	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: B: PDB Molecule: protein (protease/helicase ns3); PDBTitle: crystal structure of an enzyme complex from hepatitis c2 virus
86	c1cu1B_	Alignment	not modelled	99.3	22	PDB header: hydrolase Chain: A: PDB Molecule: heat resistant rna dependent atpase; PDBTitle: hera n-terminal domain in complex with amp, crystal form 1
87	c2gxqA_	Alignment	not modelled	99.3	22	PDB header: metal binding protein Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a sec-c motif containing protein (psyc_2064) from2 psychrobacter arcticus at 1.75 a resolution
88	c2i9wA_	Alignment		99.3	46	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
89	d1qdea_	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna heli case dbp5; PDBTitle: solution structure of amino-terminal domain of dbp5p
90	c2kbeA_	Alignment	not modelled	99.3	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
91	d1hv8a1	Alignment	not modelled	99.3	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
92	d1veca_	Alignment	not modelled	99.3	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
93	d1gkub1	Alignment	not modelled	99.3	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like " domain" of reverse gyrase
94	c3earA_	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: A: PDB Molecule: hera; PDBTitle: novel dimerization motif in the dead box rna helicase hera: form 1,2 partial dimer
95	d1gm5a4	Alignment	not modelled	99.3	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
96	d1gm5a3	Alignment	not modelled	99.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
97	c1z63A_	Alignment	not modelled	99.3	16	PDB header: hydrolase/dna complex Chain: A: PDB Molecule: helicase of the snf2/rad54 hamily; PDBTitle: sulfobolus solfataricus swi2/snf2 atpase core in complex2 with dsdna
98	c2w74B_	Alignment	not modelled	99.2	18	PDB header: hydrolase Chain: B: PDB Molecule: type i restriction enzyme ecor124ii r protein; PDBTitle: mutant (k220r) of the hsr subunit of the ecor124i2 restriction enzyme in complex with atp
99	d2eyqa3	Alignment	not modelled	99.2	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
100	c2oxcA_	Alignment	not modelled	99.2	17	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
101	c3fhcB_	Alignment	not modelled	99.2	13	PDB header: transport protein/hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: crystal structure of human dbp5 in complex with nup214
102	d1t5ia_	Alignment	not modelled	99.2	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
103	d2g9na1	Alignment	not modelled	99.2	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

						Family: Tandem AAA-ATPase domain
104	c2kbfA	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dbp5; PDBTitle: solution structure of carboxyl-terminal domain of dbp5p
105	d2g2ja1	Alignment	not modelled	99.2	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
106	c3i32A	Alignment	not modelled	99.2	21	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
107	c3fmoB	Alignment	not modelled	99.2	14	PDB header: oncprotein/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
108	c2p6nA	Alignment	not modelled	99.2	22	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx41; PDBTitle: human dead-box rna helicase ddx41, helicase domain
109	d1a1va2	Alignment	not modelled	99.1	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
110	c3h1tA	Alignment	not modelled	99.1	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
111	c1ozbj	Alignment		99.1	71	PDB header: protein transport Chain: J: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of secb complexed with seca c-terminus
112	d1ozbi	Alignment		99.1	71	Fold: Sec-C motif Superfamily: Sec-C motif Family: Sec-C motif
113	c1ozbj	Alignment		99.1	71	PDB header: protein transport Chain: I: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of secb complexed with seca c-terminus
114	c3fmpD	Alignment	not modelled	99.1	14	PDB header: oncprotein/hydrolase 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
115	d1t6na	Alignment	not modelled	99.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
116	d1oywa2	Alignment	not modelled	99.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
117	c1tm6A	Alignment		99.0	80	PDB header: protein transport Chain: A: PDB Molecule: preprotein translocase seca subunit; PDBTitle: nmr structure of the free zinc binding c-terminal domain of2 seca
118	d1tm6a	Alignment		99.0	80	Fold: Sec-C motif Superfamily: Sec-C motif Family: Sec-C motif
119	c2jgnB	Alignment	not modelled	99.0	16	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase ddx3x; PDBTitle: ddx3 helicase domain
120	d2p6ra4	Alignment	not modelled	99.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain