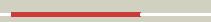
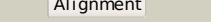
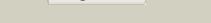
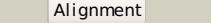
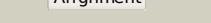
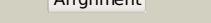
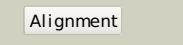
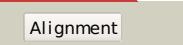


# Phyre<sup>2</sup>

Email	i.a.kelley@imperial.ac.uk
Description	P60240
Date	Thu Jan 5 12:06:41 GMT 2012
Unique Job ID	d3b0cccd5662ca179

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dmqA</a>	 Alignment		100.0	98	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> rna polymerase-associated protein rapa; <b>PDBTitle:</b> crystal structure of rapa, a swi2/snf2 protein that2 recycles rna polymerase during transcription
2	<a href="#">c1z3ix</a>	 Alignment		100.0	17	<b>PDB header:</b> recombination/dna binding <b>Chain:</b> X; <b>PDB Molecule:</b> similar to rad54-like; <b>PDBTitle:</b> structure of the swi2/snf2 chromatin remodeling domain of eukaryotic2 rad54
3	<a href="#">c3mwyW</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> W; <b>PDB Molecule:</b> chromo domain-containing protein 1; <b>PDBTitle:</b> crystal structure of the chromodomain-atpase portion of the yeast chd12 chromatin remodeler
4	<a href="#">c1z63A</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase/dna complex <b>Chain:</b> A; <b>PDB Molecule:</b> helicase of the snf2/rad54 hamily; <b>PDBTitle:</b> sulfolobus solfataricus swi2/snf2 atpase core in complex2 with dsdna
5	<a href="#">c3tmia</a>	 Alignment		100.0	12	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent rna helicase ddx58; <b>PDBTitle:</b> structural basis for rna recognition and activation of rig-i
6	<a href="#">c1wp9D</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> atp-dependent rna helicase, putative; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus hef helicase domain
7	<a href="#">d1z3ix2</a>	 Alignment		100.0	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
8	<a href="#">c2d7dA</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> uvrabc system protein b; <b>PDBTitle:</b> structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc
9	<a href="#">c3tbkA</a>	 Alignment		100.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> rig-i helicase domain; <b>PDBTitle:</b> mouse rig-i atpase domain
10	<a href="#">d1z63a1</a>	 Alignment		100.0	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
11	<a href="#">c1c4oA</a>	 Alignment		100.0	15	<b>PDB header:</b> replication <b>Chain:</b> A; <b>PDB Molecule:</b> dna nucleotide excision repair enzyme uvrbc; <b>PDBTitle:</b> crystal structure of the dna nucleotide excision repair enzyme uvrbc from thermus thermophilus

12	<a href="#">d1z3ix1</a>			100.0	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
13	<a href="#">c2fwrA</a>			100.0	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad25; <b>PDBTitle:</b> structure of archaeoglobus fulgidis xpb
14	<a href="#">c2ocaA</a>			100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase uvsw; <b>PDBTitle:</b> the crystal structure of t4 uvsw
15	<a href="#">cloywA</a>			100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase; <b>PDBTitle:</b> structure of the recq catalytic core
16	<a href="#">d1z5za1</a>			100.0	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
17	<a href="#">c1z5zb</a>			100.0	11	<b>PDB header:</b> hydrolase/recombination <b>Chain:</b> B: <b>PDB Molecule:</b> helicase of the snf2/rad54 family; <b>PDBTitle:</b> sulfolobus solfataricus swi2/snf2 atpase c-terminal domain
18	<a href="#">c2v1xb</a>			100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent dna helicase q1; <b>PDBTitle:</b> crystal structure of human recq-like dna helicase
19	<a href="#">c3oiyB</a>			100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> reverse gyrase helicase domain; <b>PDBTitle:</b> helicase domain of reverse gyrase from thermotoga maritima
20	<a href="#">c2eyqa</a>			100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> transcription-repair coupling factor; <b>PDBTitle:</b> crystal structure of escherichia coli transcription-repair2 coupling factor
21	<a href="#">c1gm5A</a>		not modelled	100.0	20	<b>PDB header:</b> helicase <b>Chain:</b> A: <b>PDB Molecule:</b> recg; <b>PDBTitle:</b> structure of recg bound to three-way dna junction
22	<a href="#">c2va8A</a>		not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
23	<a href="#">c2xgjA</a>		not modelled	100.0	20	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dob1; <b>PDBTitle:</b> structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
24	<a href="#">c3l9oA</a>		not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dob1; <b>PDBTitle:</b> crystal structure of mtr4, a co-factor of the nuclear exosome
25	<a href="#">c4a4zA</a>		not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> antiviral helicase ski2; <b>PDBTitle:</b> crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
26	<a href="#">c3ewsA</a>		not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx19b; <b>PDBTitle:</b> human dead-box rna-helicase ddx19 in complex with adp
27	<a href="#">d1gm5a3</a>		not modelled	99.9	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
28	<a href="#">d1wp9a2</a>		not modelled	99.9	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

29	<a href="#">d2fwra2</a>		Alignment	not modelled	99.9	24	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain <b>PDB header:</b> topoisomerase <b>Chain:</b> B: <b>PDB Molecule:</b> reverse gyrase; <b>PDBTitle:</b> archaeoglobus fulgidus reverse gyrase complexed with adnp
30	<a href="#">c1gl9B</a>		Alignment	not modelled	99.9	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> DNA helicase UvsW
31	<a href="#">d1rifA</a>		Alignment	not modelled	99.9	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> afuhel308 helicase; <b>PDBTitle:</b> apo structure of the hel308 superfamily 2 helicase
32	<a href="#">c2p6uA</a>		Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent rna helicase vasa; <b>PDBTitle:</b> structural basis for rna unwinding by the dead-box protein2 drosophila vasa
33	<a href="#">c2db3D</a>		Alignment	not modelled	99.9	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> preprotein translocase subunit seca; <b>PDBTitle:</b> crystal structure of the isolated dead motor domains from2 escherichia coli seca
34	<a href="#">c3bxzA</a>		Alignment	not modelled	99.9	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
35	<a href="#">d2eyqa3</a>		Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase mss116; <b>PDBTitle:</b> structure of mss116p bound to ssrna containing a single 5-bru and amp-2 pnp
36	<a href="#">c3i5yA</a>		Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ski2-type helicase; <b>PDBTitle:</b> archaeal dna helicase hjm apo state in form 1
37	<a href="#">c2zj2A</a>		Alignment	not modelled	99.9	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
38	<a href="#">d2fwra1</a>		Alignment	not modelled	99.9	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad25, xpb; <b>PDBTitle:</b> structure of c-terminal domain of archaeoglobus fulgidus xpb
39	<a href="#">c2fz1A</a>		Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> type i restriction enzyme ecor124ii r protein; <b>PDBTitle:</b> mutant (k220r) of the hsdr subunit of the ecor124i2 restriction enzyme in complex with atp
40	<a href="#">c2w74B</a>		Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase supv3l1, mitochondrial; <b>PDBTitle:</b> human mitochondrial helicase svu3 in complex with short rna fragment
41	<a href="#">c3rc8A</a>		Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolyase <b>Chain:</b> A: <b>PDB Molecule:</b> type i site-specific restriction-modification <b>PDBTitle:</b> the fragment structure of a putative hsdr subunit of a type2 i restriction enzyme from vibrio vulnificus yj016
42	<a href="#">c3h1tA</a>		Alignment	not modelled	99.9	18	<b>PDB header:</b> rna binding protein,hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> heat resistant rna dependent atpase; <b>PDBTitle:</b> dimeric structure of a hera helicase fragment including the c-terminal2 reca domain, the dimerization domain, and the rna binding domain
43	<a href="#">c3i32A</a>		Alignment	not modelled	99.9	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
44	<a href="#">d2fz4a1</a>		Alignment	not modelled	99.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx41; <b>PDBTitle:</b> human dead-box rna helicase ddx41, helicase domain
45	<a href="#">c2p6nA</a>		Alignment	not modelled	99.9	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative atp-dependent rna helicase dhh1; <b>PDBTitle:</b> crystal structure of the dead box protein dhh1p
46	<a href="#">c1s2mA</a>		Alignment	not modelled	99.9	16	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> protein translocase subunit seca; <b>PDBTitle:</b> structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
47	<a href="#">c3dl8B</a>		Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx19b; <b>PDBTitle:</b> crystal structure of human dbp5 in complex with amppnp and rna
48	<a href="#">c3fhtA</a>		Alignment	not modelled	99.9	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
49	<a href="#">d1t5ia</a>		Alignment	not modelled	99.9	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative atp-dependent rna helicase mj0669; <b>PDBTitle:</b> crystal structure of a dead box protein from the2 hyperthermophile methanococcus jannaschii
50	<a href="#">c1hv8B</a>		Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hera; <b>PDBTitle:</b> novel dimerization motif in the dead box rna helicase hera: form 1,2 partial dimer
51	<a href="#">c3earA</a>		Alignment	not modelled	99.9	19	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase p47; <b>PDBTitle:</b> structure of decd to dead mutation of human uap56
52	<a href="#">c1xtkA</a>		Alignment	not modelled	99.9	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> preprotein translocase seca subunit; <b>PDBTitle:</b> crystal structure of seca:adp in an open conformation from2 bacillus subtilis
53	<a href="#">c1tf2A</a>		Alignment	not modelled	99.9	13	

54	<a href="#">c2z0mA</a>		Alignment	not modelled	99.9	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 337aa long hypothetical atp-dependent rna <b>PDBTitle:</b> crystal structure of hypothetical atp-dependent rna2 helicase from <i>sulfolobus tokodaii</i>
55	<a href="#">d2j0sa2</a>		Alignment	not modelled	99.9	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
56	<a href="#">d1s2ma2</a>		Alignment	not modelled	99.9	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
57	<a href="#">d1tf5a3</a>		Alignment	not modelled	99.9	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
58	<a href="#">c3pexA</a>		Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dbp5; <b>PDBTitle:</b> <i>s. cerevisiae</i> dbp5 l327v bound to gle1 h337r and ip6
59	<a href="#">d1hv8a2</a>		Alignment	not modelled	99.9	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
60	<a href="#">c2hjvB</a>		Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent rna helicase dbpa; <b>PDBTitle:</b> structure of the second domain (residues 207-368) of the <i>bacillus subtilis</i> yxin protein
61	<a href="#">c2w00B</a>		Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hsdr; <b>PDBTitle:</b> crystal structure of the hsdr subunit of the ecor124i2 restriction enzyme in complex with atp
62	<a href="#">c2hxyC</a>		Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx48; <b>PDBTitle:</b> crystal structure of human apo-eif4aiii
63	<a href="#">d1oywa3</a>		Alignment	not modelled	99.9	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
64	<a href="#">c2j1rA</a>		Alignment	not modelled	99.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease subunit ns3; <b>PDBTitle:</b> dengue virus 4 ns3 helicase in complex with amppnp
65	<a href="#">c3kx2A</a>		Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna <b>PDBTitle:</b> crystal structure of prp43p in complex with adp
66	<a href="#">c2v6jA</a>		Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna helicase; <b>PDBTitle:</b> kokobera virus helicase: mutant met47thr
67	<a href="#">c3hgtA</a>		Alignment	not modelled	99.8	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hda1 complex subunit 3; <b>PDBTitle:</b> structural and functional studies of the yeast class ii hda12 hdac complex
68	<a href="#">c2fsgA</a>		Alignment	not modelled	99.8	18	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> preprotein translocase seca subunit; <b>PDBTitle:</b> complex seca:atp from escherichia coli
69	<a href="#">d1tf5a4</a>		Alignment	not modelled	99.8	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
70	<a href="#">d2g2ja1</a>		Alignment	not modelled	99.8	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
71	<a href="#">c2vsxA</a>		Alignment	not modelled	99.8	17	<b>PDB header:</b> translation/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase eif4a; <b>PDBTitle:</b> crystal structure of a translation initiation complex
72	<a href="#">d1fuka</a>		Alignment	not modelled	99.8	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
73	<a href="#">c2vbcA</a>		Alignment	not modelled	99.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dengue 4 ns3 full-length protein; <b>PDBTitle:</b> crystal structure of the ns3 protease-helicase from dengue2 virus
74	<a href="#">c2z83A</a>		Alignment	not modelled	99.8	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> helicase/nucleoside triphosphatase; <b>PDBTitle:</b> crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8
75	<a href="#">c2kbfa</a>		Alignment	not modelled	99.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dbp5; <b>PDBTitle:</b> solution structure of carboxyl-terminal domain of dbp5p
76	<a href="#">d1wp9a1</a>		Alignment	not modelled	99.8	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
77	<a href="#">d1t5la2</a>		Alignment	not modelled	99.8	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
78	<a href="#">c2wv9A</a>		Alignment	not modelled	99.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flavivirin protease ns2b regulatory subunit, flavivirin <b>PDBTitle:</b> crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus
79	<a href="#">d1c4o32</a>		Alignment	not modelled	99.8	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases

79	<a href="#">c1c4y0z</a>	Alignment	not modelled	99.8	20	hydrolases <b>Family:</b> Tandem AAA-ATPase domain <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein [contains: flavivirin <b>PDBTitle:</b> crystal structure of yellow fever virus ns3 helicase2 complexed with adp
80	<a href="#">c1ymfA</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flavivirin protease ns3 catalytic subunit; <b>PDBTitle:</b> crystal structure of kunjin virus ns3 helicase
81	<a href="#">c2qeqA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent rna helicase ddx3x; <b>PDBTitle:</b> ddx3 helicase domain
82	<a href="#">c2jgnB</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (ns3 protein); <b>PDBTitle:</b> hepatitis c virus ns3 helicase domain complexed with single2 stranded dna
83	<a href="#">c1a1vA</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Helicase-like "domain" of reverse gyrase
84	<a href="#">d1gkub2</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Helicase-like "domain" of reverse gyrase
85	<a href="#">d2eyqa5</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
86	<a href="#">d1gl9b1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Helicase-like "domain" of reverse gyrase
87	<a href="#">c2i4iA</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx3x; <b>PDBTitle:</b> crystal structure of human dead-box rna helicase ddx3x
88	<a href="#">c3b6eA</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> interferon-induced helicase c domain-containing protein 1; <b>PDBTitle:</b> crystal structure of human dech-box rna helicase mda5 (melanoma2 differentiation-associated protein 5), dech-domain
89	<a href="#">d2bmfa2</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
90	<a href="#">d1gkub1</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Helicase-like "domain" of reverse gyrase
91	<a href="#">c2f55C</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> C: <b>PDB Molecule:</b> polyprotein; <b>PDBTitle:</b> two hepatitis c virus ns3 helicase domains complexed with2 the same strand of dna
92	<a href="#">d1gm5a4</a>	Alignment	not modelled	99.6	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
93	<a href="#">c3crw1</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> 1: <b>PDB Molecule:</b> xpd/rad3 related dna helicase; <b>PDBTitle:</b> "xpd_apo"
94	<a href="#">c2vl7A</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> xpd; <b>PDBTitle:</b> structure of s. tokodaii xpd4
95	<a href="#">d2p6ra4</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
96	<a href="#">d2p6ra3</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
97	<a href="#">d1nkt4</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
98	<a href="#">d1oywa2</a>	Alignment	not modelled	99.5	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
99	<a href="#">d1yksa1</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
100	<a href="#">c1cu1B</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (protease/helicase ns3); <b>PDBTitle:</b> crystal structure of an enzyme complex from hepatitis c2 virus
101	<a href="#">d1alva1</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
102	<a href="#">d1jr6a</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
103	<a href="#">d1nkt4</a>	Alignment	not modelled	99.4	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
104	<a href="#">d1hv8a1</a>	Alignment	not modelled	99.2	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
						<b>PDB header:</b> hydrolase

105	<a href="#">c3iy5A</a>	Alignment	not modelled	99.1	16	<b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent rna helicase ddx18; <b>PDBTitle:</b> ddx18 dead-domain
106	<a href="#">c2kbeA</a>	Alignment	not modelled	99.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent rna helicase dbp5; <b>PDBTitle:</b> solution structure of amino-terminal domain of dbp5p
107	<a href="#">c3dkpA</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx52; <b>PDBTitle:</b> human dead-box rna-helicase ddx52, conserved domain i in complex with2 adp
108	<a href="#">c3fe2B</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx5; <b>PDBTitle:</b> human dead-box rna helicase ddx5 (p68), conserved domain i in complex2 with adp
109	<a href="#">d1a1va2</a>	Alignment	not modelled	99.1	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
110	<a href="#">d1q0ua</a>	Alignment	not modelled	99.1	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
111	<a href="#">c2vsfA</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dna repair helicase rad3 related protein; <b>PDBTitle:</b> structure of xpd from thermoplasma acidophilum
112	<a href="#">c3juxA</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> protein translocase subunit seca; <b>PDBTitle:</b> structure of the translocation atpase seca from thermotoga2 maritima
113	<a href="#">c1nl3B</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> preprotein translocase seca 1 subunit; <b>PDBTitle:</b> crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
114	<a href="#">c3dinB</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> protein translocase subunit seca; <b>PDBTitle:</b> crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
115	<a href="#">c2vdaA</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> translocase subunit seca; <b>PDBTitle:</b> solution structure of the seca-signal peptide complex
116	<a href="#">c3fmoB</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> oncoprotein/hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> atp-dependent rna helicase ddx19b; <b>PDBTitle:</b> crystal structure of the nucleoporin nup214 in complex with the dead-2 box helicase ddx19
117	<a href="#">d1t6na</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
118	<a href="#">d1s2ma1</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
119	<a href="#">c2oxcA</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx20; <b>PDBTitle:</b> human dead-box rna helicase ddx20, dead domain in complex2 with adp
120	<a href="#">c2gxqA</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> heat resistant rna dependent atpase; <b>PDBTitle:</b> hera n-terminal domain in complex with amp, crystal form 1