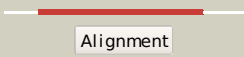

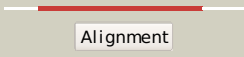

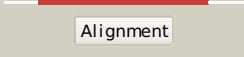
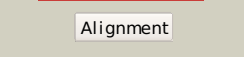

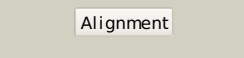
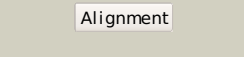

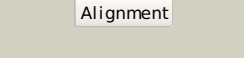

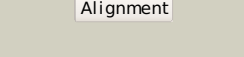


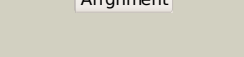
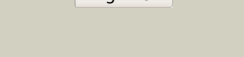












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2db3D_</a>	 Alignment		100.0	34	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent rna helicase vasa; <b>PDBTitle:</b> structural basis for rna unwinding by the dead-box protein2 drosophila vasa
2	<a href="#">c2v1xB_</a>	 Alignment		100.0	18	<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
3	<a href="#">c1s2mA_</a>	 Alignment		100.0	35	<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
4	<a href="#">c1oywA_</a>	 Alignment		100.0	21	<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
5	<a href="#">c3fhtA_</a>	 Alignment		100.0	30	<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
6	<a href="#">c1xtkA_</a>	 Alignment		100.0	30	<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
7	<a href="#">c3ewsA_</a>	 Alignment		100.0	30	<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
8	<a href="#">c2hxyC_</a>	 Alignment		100.0	33	<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
9	<a href="#">c1hv8B_</a>	 Alignment		100.0	33	<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
10	<a href="#">c2i4iA_</a>	 Alignment		100.0	31	<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
11	<a href="#">c3i5yA_</a>	 Alignment		100.0	25	<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

12	<a href="#">c3pexA_</a>	Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dbp5; <b>PDBTitle:</b> s. cerevisiae dbp5 l327v bound to gle1 h337r and ip6
13	<a href="#">c2vsxA_</a>	Alignment		100.0	33	<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
14	<a href="#">c1gl9B_</a>	Alignment		100.0	23	<b>PDB header:</b> topoisomerase <b>Chain:</b> B: <b>PDB Molecule:</b> reverse gyrase; <b>PDBTitle:</b> archaeoglobus fulgidus reverse gyrase complexed with adpnp
15	<a href="#">c2xgjA_</a>	Alignment		100.0	23	<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
16	<a href="#">c2z0mA_</a>	Alignment		100.0	38	<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 sulfolobus tokodaii
17	<a href="#">c2va8A_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
18	<a href="#">c1gm5A_</a>	Alignment		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
19	<a href="#">c3l9oA_</a>	Alignment		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
20	<a href="#">c2zj2A_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ski2-type helicase; <b>PDBTitle:</b> archaeal dna helicase hjm apo state in form 1
21	<a href="#">c4a4zA_</a>	Alignment	not modelled	100.0	21	<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
22	<a href="#">c3bxzA_</a>	Alignment	not modelled	100.0	19	<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
23	<a href="#">c3tmiA_</a>	Alignment	not modelled	100.0	23	<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
24	<a href="#">c2eyqA_</a>	Alignment	not modelled	100.0	21	<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
25	<a href="#">c2p6uA_</a>	Alignment	not modelled	100.0	20	<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
26	<a href="#">c3kx2A_</a>	Alignment	not modelled	100.0	19	<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
27	<a href="#">c1wp9D_</a>	Alignment	not modelled	100.0	25	<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
28	<a href="#">c3oiyB_</a>	Alignment	not modelled	100.0	16	<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
						<b>PDB header:</b> hydrolase

29	<a href="#">c2ocaA_</a>	Alignment	not modelled	100.0	19	<b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase uvsw; <b>PDBTitle:</b> the crystal structure of t4 uvsw
30	<a href="#">c3rc8A_</a>	Alignment	not modelled	100.0	15	<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 suv3 in complex with short rna fragment
31	<a href="#">c2fsgA_</a>	Alignment	not modelled	100.0	20	<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
32	<a href="#">c1c4oA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna nucleotide excision repair enzyme uvrh; <b>PDBTitle:</b> crystal structure of the dna nucleotide excision repair enzyme uvrh2 from thermus thermophilus
33	<a href="#">c2jlrA_</a>	Alignment	not modelled	100.0	16	<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
34	<a href="#">c3tbkA_</a>	Alignment	not modelled	100.0	23	<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
35	<a href="#">c3fe2B_</a>	Alignment	not modelled	100.0	37	<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
36	<a href="#">c2z83A_</a>	Alignment	not modelled	100.0	19	<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
37	<a href="#">c1ymfA_</a>	Alignment	not modelled	100.0	19	<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
38	<a href="#">c2fwrA_</a>	Alignment	not modelled	100.0	22	<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
39	<a href="#">c2v6jA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna helicase; <b>PDBTitle:</b> kokobera virus helicase: mutant met47thr
40	<a href="#">c2d7dA_</a>	Alignment	not modelled	100.0	21	<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 uvrh
41	<a href="#">c1tf2A_</a>	Alignment	not modelled	100.0	17	<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
42	<a href="#">c2vbcA_</a>	Alignment	not modelled	100.0	18	<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
43	<a href="#">c2wv9A_</a>	Alignment	not modelled	100.0	18	<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
44	<a href="#">c2pl3A_</a>	Alignment	not modelled	100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx10; <b>PDBTitle:</b> human dead-box rna helicase ddx10, dead domain in complex with adp
45	<a href="#">c3ly5A_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx18; <b>PDBTitle:</b> ddx18 dead-domain
46	<a href="#">c3dl8B_</a>	Alignment	not modelled	100.0	22	<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="#">d2bmfa2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
48	<a href="#">c2qegA_</a>	Alignment	not modelled	100.0	15	<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
49	<a href="#">d1s2ma1</a>	Alignment	not modelled	100.0	37	<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
50	<a href="#">d1q0ua_</a>	Alignment	not modelled	100.0	33	<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
51	<a href="#">d2j0sa1</a>	Alignment	not modelled	100.0	33	<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
52	<a href="#">c3dkpA_</a>	Alignment	not modelled	100.0	33	<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
53	<a href="#">c1a1vA_</a>	Alignment	not modelled	100.0	16	<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 sdna

54	<a href="#">c2oxcA_</a>	Alignment	not modelled	100.0	30	<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
55	<a href="#">c3iuyB_</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx53; <b>PDBTitle:</b> crystal structure of ddx53 dead-box domain
56	<a href="#">c2gxqA_</a>	Alignment	not modelled	100.0	44	<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
57	<a href="#">c2kbeA_</a>	Alignment	not modelled	100.0	26	<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
58	<a href="#">d1wrba1</a>	Alignment	not modelled	100.0	34	<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
59	<a href="#">d1hv8a1</a>	Alignment	not modelled	100.0	37	<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="#">d1qdea_</a>	Alignment	not modelled	100.0	38	<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
61	<a href="#">c3berA_</a>	Alignment	not modelled	100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx47; <b>PDBTitle:</b> human dead-box rna-helicase ddx47, conserved domain i in complex with2 amp
62	<a href="#">c2f55C_</a>	Alignment	not modelled	100.0	19	<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
63	<a href="#">d1veca_</a>	Alignment	not modelled	100.0	36	<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="#">d1t6na_</a>	Alignment	not modelled	100.0	28	<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
65	<a href="#">c3fmoB_</a>	Alignment	not modelled	100.0	27	<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
66	<a href="#">c3fhcB_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> transport protein/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent rna helicase ddx19b; <b>PDBTitle:</b> crystal structure of human dbp5 in complex with nup214
67	<a href="#">c3h1tA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <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
68	<a href="#">d2j0sa2</a>	Alignment	not modelled	99.9	33	<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
69	<a href="#">c3fmpD_</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> oncoprotein/hydrolase <b>Chain:</b> D: <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
70	<a href="#">d1s2ma2</a>	Alignment	not modelled	99.9	34	<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="#">c3mwyW_</a>	Alignment	not modelled	99.9	18	<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
72	<a href="#">c1z3iX_</a>	Alignment	not modelled	99.9	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
73	<a href="#">c2w74B_</a>	Alignment	not modelled	99.9	14	<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
74	<a href="#">d1hv8a2</a>	Alignment	not modelled	99.9	34	<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
75	<a href="#">d1oywa3</a>	Alignment	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
76	<a href="#">d1oywa2</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
77	<a href="#">c2hjvB_</a>	Alignment	not modelled	99.9	36	<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 the2 bacillus subtilis yxin protein
78	<a href="#">c1cu1B_</a>	Alignment	not modelled	99.9	19	<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
79	<a href="#">c3crw1_</a>	Alignment	not modelled	99.9	18 <b>PDB header:</b> hydrolase <b>Chain:</b> 1: <b>PDB Molecule:</b> xpd/rad3 related dna helicase; <b>PDBTitle:</b> "xpd_apo"
80	<a href="#">c3dmqA_</a>	Alignment	not modelled	99.9	22 <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
81	<a href="#">d2g9na1</a>	Alignment	not modelled	99.9	32 <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
82	<a href="#">d2g2ja1</a>	Alignment	not modelled	99.9	31 <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
83	<a href="#">c3i32A_</a>	Alignment	not modelled	99.9	33 <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
84	<a href="#">c3earA_</a>	Alignment		99.9	25 <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
85	<a href="#">d1t5ia_</a>	Alignment	not modelled	99.9	33 <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="#">c2jgnB_</a>	Alignment	not modelled	99.9	28 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent rna helicase ddx3x; <b>PDBTitle:</b> ddx3 helicase domain
87	<a href="#">c2p6nA_</a>	Alignment	not modelled	99.9	32 <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
88	<a href="#">d1fuka_</a>	Alignment	not modelled	99.9	31 <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
89	<a href="#">c1z63A_</a>	Alignment	not modelled	99.9	16 <b>PDB header:</b> hydrolase/dna complex <b>Chain:</b> A: <b>PDB Molecule:</b> helicase of the snf2/rad54 family; <b>PDBTitle:</b> sulfolobus solfataricus swi2/snf2 atpase core in complex2 with dsdna
90	<a href="#">c2kbFA_</a>	Alignment	not modelled	99.9	34 <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
91	<a href="#">d1gm5a4</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
92	<a href="#">d2eyqa5</a>	Alignment	not modelled	99.8	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
93	<a href="#">d1t5ia2</a>	Alignment	not modelled	99.8	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
94	<a href="#">d1gkub1</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> Helicase-like "domain" of reverse gyrase
95	<a href="#">d1wp9a2</a>	Alignment	not modelled	99.8	27 <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="#">d1c4oa2</a>	Alignment	not modelled	99.8	26 <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="#">d1gl9b1</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 <b>Family:</b> Helicase-like "domain" of reverse gyrase
98	<a href="#">d2p6ra4</a>	Alignment	not modelled	99.8	27 <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="#">d2p6ra3</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 <b>Family:</b> Tandem AAA-ATPase domain
100	<a href="#">d1wp9a1</a>	Alignment	not modelled	99.8	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
101	<a href="#">d2eyqa3</a>	Alignment	not modelled	99.8	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
102	<a href="#">d1tf5a4</a>	Alignment	not modelled	99.8	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
103	<a href="#">c2w00B_</a>	Alignment	not modelled	99.8	17 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hsdr;



103	<a href="#">c2w00b_</a>	Alignment	not modelled	99.8	17	<b>PDBTitle:</b> crystal structure of the hsdR subunit of the ecor124i2 restriction enzyme in complex with atp <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="#">d1nkt4</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent rna helicase a; <b>PDBTitle:</b> crystal structure analysis of a rna helicase
105	<a href="#">c3llmB_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> xpd; <b>PDBTitle:</b> structure of s. tokodaii xpd4
106	<a href="#">c2vl7A_</a>	Alignment	not modelled	99.7	20	<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
107	<a href="#">c3b6eA_</a>	Alignment	not modelled	99.7	20	<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
108	<a href="#">c3juxA_</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
109	<a href="#">d1a1va2</a>	Alignment	not modelled	99.7	20	<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
110	<a href="#">d1gkub2</a>	Alignment	not modelled	99.7	19	<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
111	<a href="#">c1nl3B_</a>	Alignment	not modelled	99.7	19	<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
112	<a href="#">c3dinB_</a>	Alignment	not modelled	99.7	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
113	<a href="#">d1gm5a3</a>	Alignment	not modelled	99.7	18	<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
114	<a href="#">c2vdaA_</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> DNA helicase UvsW
115	<a href="#">d1rifa_</a>	Alignment	not modelled	99.7	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
116	<a href="#">d2fwra1</a>	Alignment	not modelled	99.6	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
117	<a href="#">d1jr6a_</a>	Alignment	not modelled	99.6	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
118	<a href="#">c2fz1A_</a>	Alignment	not modelled	99.6	23	<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
119	<a href="#">c2ipcB_</a>	Alignment	not modelled	99.6	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> preprotein translocase seca subunit; <b>PDBTitle:</b> crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer
120	<a href="#">d1tf5a3</a>	Alignment	not modelled	99.6	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