



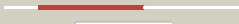









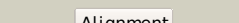

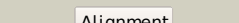



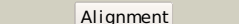












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3kx2A_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna <b>PDBTitle:</b> crystal structure of prp43p in complex with adp
2	<a href="#">c1cu1B_</a>	 Alignment		100.0	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
3	<a href="#">c2wv9A_</a>	 Alignment		100.0	17	<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
4	<a href="#">c2vbcA_</a>	 Alignment		100.0	14	<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
5	<a href="#">c2f55C_</a>	 Alignment		100.0	21	<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
6	<a href="#">c1a1vA_</a>	 Alignment		100.0	19	<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
7	<a href="#">c2jlrA_</a>	 Alignment		100.0	14	<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
8	<a href="#">c1ymfA_</a>	 Alignment		100.0	15	<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
9	<a href="#">c2z83A_</a>	 Alignment		100.0	17	<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
10	<a href="#">c3rc8A_</a>	 Alignment		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
11	<a href="#">c2p6uA_</a>	 Alignment		100.0	22	<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

12	<a href="#">c2va8A_</a>	Alignment		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
13	<a href="#">c2xgjA_</a>	Alignment		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
14	<a href="#">c4a4zA_</a>	Alignment		100.0	19 <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
15	<a href="#">c2zj2A_</a>	Alignment		100.0	19 <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
16	<a href="#">c3l9oA_</a>	Alignment		100.0	19 <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
17	<a href="#">c2v6jA_</a>	Alignment		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
18	<a href="#">c2eyqA_</a>	Alignment		100.0	16 <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
19	<a href="#">c1gm5A_</a>	Alignment		100.0	19 <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
20	<a href="#">c2v1xB_</a>	Alignment		100.0	17 <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
21	<a href="#">c1oywA_</a>	Alignment	not modelled	100.0	18 <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
22	<a href="#">c3bxzA_</a>	Alignment	not modelled	100.0	15 <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="#">d8ohma2</a>	Alignment	not modelled	100.0	16 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
24	<a href="#">c2qeqA_</a>	Alignment	not modelled	100.0	17 <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
25	<a href="#">c1gl9B_</a>	Alignment	not modelled	100.0	17 <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
26	<a href="#">c3ewsA_</a>	Alignment	not modelled	100.0	15 <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="#">c2db3D_</a>	Alignment	not modelled	100.0	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
28	<a href="#">c3l1mB_</a>	Alignment	not modelled	100.0	32 <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
					<b>PDB header:</b> hydrolase/rna

29	<a href="#">c3fhtA</a>	Alignment	not modelled	100.0	14	<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
30	<a href="#">c2fsgA</a>	Alignment	not modelled	100.0	16	<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
31	<a href="#">c3tmiA</a>	Alignment	not modelled	100.0	19	<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
32	<a href="#">d2bmfa2</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
33	<a href="#">c3i5yA</a>	Alignment	not modelled	100.0	18	<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
34	<a href="#">c1hv8B</a>	Alignment	not modelled	100.0	23	<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
35	<a href="#">c1xtkA</a>	Alignment	not modelled	100.0	13	<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
36	<a href="#">c1s2mA</a>	Alignment	not modelled	100.0	14	<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
37	<a href="#">c2z0mA</a>	Alignment	not modelled	100.0	18	<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
38	<a href="#">c3pexA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dbp5; <b>PDBTitle:</b> s. cerevisiae dbp5 I327v bound to gle1 h337r and ip6
39	<a href="#">c2ocaA</a>	Alignment	not modelled	100.0	15	<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
40	<a href="#">c1wp9D</a>	Alignment	not modelled	100.0	26	<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
41	<a href="#">c2vsxA</a>	Alignment	not modelled	100.0	15	<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
42	<a href="#">c1c4oA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna nucleotide excision repair enzyme uvrB; <b>PDBTitle:</b> crystal structure of the dna nucleotide excision repair enzyme uvrB2 from thermus thermophilus
43	<a href="#">d1yksa2</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
44	<a href="#">c2i4iA</a>	Alignment	not modelled	100.0	18	<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
45	<a href="#">c1tf2A</a>	Alignment	not modelled	100.0	21	<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
46	<a href="#">c2hxyC</a>	Alignment	not modelled	100.0	15	<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
47	<a href="#">c3oiyB</a>	Alignment	not modelled	100.0	17	<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
48	<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
49	<a href="#">c3i4uA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dhx8; <b>PDBTitle:</b> crystal structure analysis of a helicase associated domain
50	<a href="#">c2fwrA</a>	Alignment	not modelled	100.0	16	<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
51	<a href="#">c3tbkA</a>	Alignment	not modelled	100.0	19	<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
52	<a href="#">c2d7dA</a>	Alignment	not modelled	99.9	18	<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 uvrB
53	<a href="#">c3h1tA</a>	Alignment	not modelled	99.9	14	<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
54	<a href="#">c3crw1</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> 1: <b>PDB Molecule:</b> xpd/rad3 related dna helicase;

						<b>PDBTitle:</b> "xpd_apo"
55	<a href="#">c2w74B_</a>	Alignment	not modelled	99.9	11	<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
56	<a href="#">d1a1va2</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> RNA helicase
57	<a href="#">c3dmqA_</a>	Alignment	not modelled	99.9	20	<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
58	<a href="#">c3dkpA_</a>	Alignment	not modelled	99.9	17	<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
59	<a href="#">c3fe2B_</a>	Alignment	not modelled	99.9	22	<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
60	<a href="#">d2p6ra3</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
61	<a href="#">c1z3iX_</a>	Alignment	not modelled	99.9	22	<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
62	<a href="#">d1a1va1</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> RNA helicase
63	<a href="#">d1q0ua_</a>	Alignment	not modelled	99.8	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
64	<a href="#">c3mwyW_</a>	Alignment	not modelled	99.8	14	<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
65	<a href="#">c2vl7A_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> xpd; <b>PDBTitle:</b> structure of s. tokodaii xpd4
66	<a href="#">c3ly5A_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx18; <b>PDBTitle:</b> ddx18 dead-domain
67	<a href="#">d2eyqa3</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
68	<a href="#">c2pl3A_</a>	Alignment	not modelled	99.8	18	<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
69	<a href="#">d1oywa3</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
70	<a href="#">c3fmoB_</a>	Alignment	not modelled	99.8	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
71	<a href="#">c2kbeA_</a>	Alignment	not modelled	99.8	20	<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
72	<a href="#">c3iuyB_</a>	Alignment	not modelled	99.8	17	<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
73	<a href="#">d2eyqa5</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
74	<a href="#">d2j0sa1</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
75	<a href="#">d1gkub1</a>	Alignment	not modelled	99.8	18	<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
76	<a href="#">c3fhcB_</a>	Alignment	not modelled	99.8	15	<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
77	<a href="#">d1yksa1</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> RNA helicase
78	<a href="#">d1hv8a1</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
79	<a href="#">c2oxcA_</a>	Alignment	not modelled	99.8	19	<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
80	<a href="#">dlqdea</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
81	<a href="#">c2gxqA</a>	Alignment	not modelled	99.8	20	<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
82	<a href="#">d2p6ra4</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
83	<a href="#">dls2ma1</a>	Alignment	not modelled	99.8	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
84	<a href="#">c1z63A</a>	Alignment	not modelled	99.8	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> sulfobolus solfataricus swi2/snf2 atpase core in complex2 with dsdna
85	<a href="#">d2j0sa2</a>	Alignment	not modelled	99.8	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
86	<a href="#">dlgl9b1</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> Helicase-like "domain" of reverse gyrase
87	<a href="#">c3i32A</a>	Alignment	not modelled	99.8	20	<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
88	<a href="#">dlwrbal</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
89	<a href="#">dlt6na</a>	Alignment	not modelled	99.8	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
90	<a href="#">c3berA</a>	Alignment	not modelled	99.8	18	<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
91	<a href="#">d1t5la2</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
92	<a href="#">dlc4oa2</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="#">c3fmpD</a>	Alignment	not modelled	99.8	17	<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
94	<a href="#">dlveca</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
95	<a href="#">dls2ma2</a>	Alignment	not modelled	99.8	12	<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="#">dlloywa2</a>	Alignment	not modelled	99.8	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
97	<a href="#">c3b6eA</a>	Alignment	not modelled	99.8	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
98	<a href="#">dlgm5a3</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
99	<a href="#">c3earA</a>	Alignment	not modelled	99.8	21	<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
100	<a href="#">c2p6nA</a>	Alignment	not modelled	99.7	24	<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
101	<a href="#">c2w00B</a>	Alignment	not modelled	99.7	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
102	<a href="#">dlwp9a1</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
103	<a href="#">d2g2ja1</a>	Alignment	not modelled	99.7	14	<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="#">dlhy8a2</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate



104	<a href="#">d1trv8a2</a>	Alignment	not modelled	99.7	20	hydrolases <b>Family:</b> Tandem AAA-ATPase domain
105	<a href="#">d2g9na1</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> Tandem AAA-ATPase domain
106	<a href="#">c2vdaA</a>	Alignment	not modelled	99.7	25	<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
107	<a href="#">d1gm5a4</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> Tandem AAA-ATPase domain
108	<a href="#">c2hjbB</a>	Alignment	not modelled	99.7	18	<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
109	<a href="#">d1rifa</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> DNA helicase UvsW
110	<a href="#">d1t5ia</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> Tandem AAA-ATPase domain
111	<a href="#">c1nl3B</a>	Alignment	not modelled	99.7	25	<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
112	<a href="#">c2vsfA</a>	Alignment	not modelled	99.7	20	<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
113	<a href="#">c2kbfA</a>	Alignment	not modelled	99.7	19	<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
114	<a href="#">d1fuka</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> Tandem AAA-ATPase domain
115	<a href="#">d1wp9a2</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="#">c3juxA</a>	Alignment	not modelled	99.7	21	<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
117	<a href="#">d1jr6a</a>	Alignment	not modelled	99.6	26	<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="#">c3dinB</a>	Alignment	not modelled	99.6	22	<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
119	<a href="#">d1nkt4</a>	Alignment	not modelled	99.6	30	<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
120	<a href="#">c2jgnB</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent rna helicase ddx3x; <b>PDBTitle:</b> ddx3 helicase domain