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1	<a href="#">c3b85A_</a>	 Alignment		100.0	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate starvation-inducible protein; <b>PDBTitle:</b> crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
2	<a href="#">dlw36d1</a>	 Alignment		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
3	<a href="#">clw36G_</a>	 Alignment		99.7	20	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> exodeoxyribonuclease v alpha chain; <b>PDBTitle:</b> recbcd:dna complex
4	<a href="#">c3e1sA_</a>	 Alignment		99.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exodeoxyribonuclease v, subunit recd; <b>PDBTitle:</b> structure of an n-terminal truncation of deinococcus radiodurans recd2
5	<a href="#">c2wjyA_</a>	 Alignment		99.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of nonsense transcripts 1; <b>PDBTitle:</b> crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
6	<a href="#">c2xzlA_</a>	 Alignment		99.6	22	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent helicase nam7; <b>PDBTitle:</b> upf1-rna complex
7	<a href="#">c2l8bA_</a>	 Alignment		99.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein trai; <b>PDBTitle:</b> trai (381-569)
8	<a href="#">c2gk7A_</a>	 Alignment		99.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of nonsense transcripts 1; <b>PDBTitle:</b> structural and functional insights into the human upf1 helicase core
9	<a href="#">dluaaa1</a>	 Alignment		99.3	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
10	<a href="#">dlpjra1</a>	 Alignment		99.3	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
11	<a href="#">c2is6B_</a>	 Alignment		99.3	18	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna helicase ii; <b>PDBTitle:</b> crystal structure of uvrd-dna-adpmgf3 ternary complex

12	<a href="#">c2pjrF_</a>	Alignment		99.2	17	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> F: <b>PDB Molecule:</b> protein (helicase pcra); <b>PDBTitle:</b> helicase product complex
13	<a href="#">c1uaaB_</a>	Alignment		99.2	19	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> protein (atp-dependent dna helicase rep.); <b>PDBTitle:</b> e. coli rep helicase/dna complex
14	<a href="#">c3lfuA_</a>	Alignment		99.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna helicase ii; <b>PDBTitle:</b> crystal structure of e. coli uvrD
15	<a href="#">c3l9oA_</a>	Alignment		99.0	23	<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
16	<a href="#">d1w36b1</a>	Alignment		98.9	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
17	<a href="#">c1pjrA_</a>	Alignment		98.9	23	<b>PDB header:</b> helicase <b>Chain:</b> A: <b>PDB Molecule:</b> pcra; <b>PDBTitle:</b> structure of dna helicase
18	<a href="#">c2xqiA_</a>	Alignment		98.8	18	<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
19	<a href="#">c4a4zA_</a>	Alignment		98.7	23	<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
20	<a href="#">d2eyqa3</a>	Alignment		98.6	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
21	<a href="#">d1rifa_</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> DNA helicase UvsW
22	<a href="#">c3kx2A_</a>	Alignment	not modelled	98.5	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
23	<a href="#">c1w36E_</a>	Alignment	not modelled	98.5	33	<b>PDB header:</b> recombination <b>Chain:</b> E: <b>PDB Molecule:</b> exodeoxyribonuclease v beta chain; <b>PDBTitle:</b> recbcd:dna complex
24	<a href="#">c2zj2A_</a>	Alignment	not modelled	98.5	15	<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
25	<a href="#">c2eyqA_</a>	Alignment	not modelled	98.5	18	<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
26	<a href="#">c3ezkB_</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna packaging protein gp17; <b>PDBTitle:</b> bacteriophage t4 gp17 motor assembly based on crystal2 structures and cryo-em reconstructions
27	<a href="#">c2ja1A_</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
28	<a href="#">c2ocaA_</a>	Alignment	not modelled	98.5	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
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

29	<a href="#">d2fwra2</a>	Alignment	not modelled	98.4	14	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
30	<a href="#">c1gm5A</a>	Alignment	not modelled	98.4	21	<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
31	<a href="#">c2fwrA</a>	Alignment	not modelled	98.4	15	<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
32	<a href="#">c2jlrA</a>	Alignment	not modelled	98.4	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
33	<a href="#">c2vbCA</a>	Alignment	not modelled	98.4	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
34	<a href="#">d1gkub1</a>	Alignment	not modelled	98.4	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
35	<a href="#">c2z83A</a>	Alignment	not modelled	98.3	21	<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
36	<a href="#">c2va8A</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
37	<a href="#">d2j0sa1</a>	Alignment		98.3	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
38	<a href="#">c2p6uA</a>	Alignment	not modelled	98.3	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
39	<a href="#">c3llmB</a>	Alignment	not modelled	98.3	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
40	<a href="#">c3ly5A</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx18; <b>PDBTitle:</b> ddx18 dead-domain
41	<a href="#">c3rc8A</a>	Alignment	not modelled	98.3	16	<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
42	<a href="#">c3fe2B</a>	Alignment	not modelled	98.3	14	<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
43	<a href="#">c2vl7A</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> xpd; <b>PDBTitle:</b> structure of s. tokodaii xpd4
44	<a href="#">c3crw1</a>	Alignment	not modelled	98.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> 1: <b>PDB Molecule:</b> xpd/rad3 related dna helicase; <b>PDBTitle:</b> "xpd_apo"
45	<a href="#">d1gm5a3</a>	Alignment	not modelled	98.2	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
46	<a href="#">c3ec2A</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna replication protein dnaC; <b>PDBTitle:</b> crystal structure of the dnaC helicase loader
47	<a href="#">c2kbeA</a>	Alignment	not modelled	98.2	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
48	<a href="#">c2pl3A</a>	Alignment	not modelled	98.2	13	<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
49	<a href="#">c2oxcA</a>	Alignment	not modelled	98.2	15	<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
50	<a href="#">c3tmiA</a>	Alignment	not modelled	98.2	18	<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
51	<a href="#">d1gl9b1</a>	Alignment	not modelled	98.2	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
52	<a href="#">c1qhha</a>	Alignment	not modelled	98.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (pcra (subunit)); <b>PDBTitle:</b> structure of dna helicase with adpnp
53	<a href="#">c2wv9A</a>	Alignment	not modelled	98.1	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
54	<a href="#">c3hu2C_</a>	Alignment	not modelled	98.1	23	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97 n-d1 r86a mutant in complex with atpgs
55	<a href="#">c2v6jA_</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna helicase; <b>PDBTitle:</b> kokobera virus helicase: mutant met47thr
56	<a href="#">d2fz4a1</a>	Alignment	not modelled	98.1	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
57	<a href="#">c3dkpA_</a>	Alignment	not modelled	98.1	13	<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
58	<a href="#">d1hv8a1</a>	Alignment	not modelled	98.1	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
59	<a href="#">c3iuyB_</a>	Alignment	not modelled	98.1	15	<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
60	<a href="#">c3b6eA_</a>	Alignment	not modelled	98.1	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
61	<a href="#">c3cf1C_</a>	Alignment	not modelled	98.1	21	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/adp.alfx
62	<a href="#">c2o0hA_</a>	Alignment	not modelled	98.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna packaging protein gp17; <b>PDBTitle:</b> t4 gp17 atpase domain mutant complexed with atp
63	<a href="#">d1a1va1</a>	Alignment	not modelled	98.1	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
64	<a href="#">c1gl9B_</a>	Alignment	not modelled	98.1	20	<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
65	<a href="#">d2p6ra3</a>	Alignment	not modelled	98.0	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
66	<a href="#">c3berA_</a>	Alignment	not modelled	98.0	16	<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
67	<a href="#">d1q0ua_</a>	Alignment	not modelled	98.0	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="#">c2qgzA_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative primosome component; <b>PDBTitle:</b> crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58
69	<a href="#">d1yksa1</a>	Alignment	not modelled	98.0	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
70	<a href="#">c2qeqA_</a>	Alignment	not modelled	98.0	18	<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
71	<a href="#">d1s2ma1</a>	Alignment	not modelled	98.0	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
72	<a href="#">d1fnna2</a>	Alignment	not modelled	98.0	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
73	<a href="#">d1wp9a1</a>	Alignment	not modelled	98.0	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
74	<a href="#">c3b9pA_</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
75	<a href="#">c1sxiC_</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> activator 1 40 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
76	<a href="#">c1a1vA_</a>	Alignment	not modelled	97.9	18	<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
77	<a href="#">c1sxiD_</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> activator 1 41 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)

78	<a href="#">dlqdea_</a>	Alignment	not modelled	97.9	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
79	<a href="#">clymfA_</a>	Alignment	not modelled	97.9	17	<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="#">c3bxzA_</a>	Alignment	not modelled	97.9	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
81	<a href="#">c3tbkA_</a>	Alignment	not modelled	97.9	21	<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
82	<a href="#">c3i5yA_</a>	Alignment	not modelled	97.9	19	<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
83	<a href="#">c1z63A_</a>	Alignment	not modelled	97.8	17	<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
84	<a href="#">dlz3ix2</a>	Alignment	not modelled	97.8	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
85	<a href="#">c3h1tA_</a>	Alignment	not modelled	97.8	18	<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
86	<a href="#">dl1t6na_</a>	Alignment	not modelled	97.8	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
87	<a href="#">c2w74B_</a>	Alignment	not modelled	97.8	17	<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
88	<a href="#">c1xxhB_</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase iii subunit gamma; <b>PDBTitle:</b> atpgs bound e. coli clamp loader complex
89	<a href="#">c3fmoB_</a>	Alignment	not modelled	97.8	14	<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
90	<a href="#">dlveca_</a>	Alignment	not modelled	97.8	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
91	<a href="#">c2chvE_</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> dna-binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> replication factor c small subunit; <b>PDBTitle:</b> replication factor c adpnp complex
92	<a href="#">c3pfiB_</a>	Alignment	not modelled	97.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruvb; <b>PDBTitle:</b> 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
93	<a href="#">c3oiyB_</a>	Alignment	not modelled	97.8	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
94	<a href="#">c3nbxX_</a>	Alignment	not modelled	97.7	29	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> atpase rava; <b>PDBTitle:</b> crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
95	<a href="#">c1xx6B_</a>	Alignment	not modelled	97.7	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
96	<a href="#">c2gxqA_</a>	Alignment	not modelled	97.7	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
97	<a href="#">c3dmqA_</a>	Alignment	not modelled	97.7	17	<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
98	<a href="#">dlwrba1</a>	Alignment	not modelled	97.7	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
99	<a href="#">dl1tf5a3</a>	Alignment	not modelled	97.7	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
100	<a href="#">c3pxiB_</a>	Alignment	not modelled	97.6	31	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mecb; <b>PDBTitle:</b> structure of meca108:clpc
101	<a href="#">c1z3iX_</a>	Alignment	not modelled	97.6	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
102	<a href="#">c3te6A_</a>	Alignment	not modelled	97.6	9	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sir3; <b>PDBTitle:</b> crystal structure of the s. cerevisiae sir3 aaa+ domain



103	<a href="#">c3u5zM_</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> M: <b>PDB Molecule:</b> dna polymerase accessory protein 44; <b>PDBTitle:</b> structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
104	<a href="#">c2w00B_</a>	Alignment	not modelled	97.6	18	<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
105	<a href="#">c1hv8B_</a>	Alignment	not modelled	97.6	18	<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
106	<a href="#">c1iqpF_</a>	Alignment	not modelled	97.6	15	<b>PDB header:</b> replication <b>Chain:</b> F: <b>PDB Molecule:</b> rfcs; <b>PDBTitle:</b> crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
107	<a href="#">c2chgB_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> dna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> replication factor c small subunit; <b>PDBTitle:</b> replication factor c domains 1 and 2
108	<a href="#">c2r44A_</a>	Alignment	not modelled	97.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
109	<a href="#">c2db3D_</a>	Alignment	not modelled	97.6	12	<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
110	<a href="#">c1xtkA_</a>	Alignment	not modelled	97.6	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
111	<a href="#">c1s2mA_</a>	Alignment	not modelled	97.5	17	<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
112	<a href="#">d2ce7a2</a>	Alignment	not modelled	97.5	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
113	<a href="#">d1r6bx2</a>	Alignment	not modelled	97.5	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
114	<a href="#">d1r6bx3</a>	Alignment	not modelled	97.5	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
115	<a href="#">c3fhtA_</a>	Alignment	not modelled	97.5	14	<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
116	<a href="#">c2qq0B_</a>	Alignment	not modelled	97.5	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> thymidine kinase from thermotoga maritima in complex with2 thymidine + appnhp
117	<a href="#">d2bmfa2</a>	Alignment	not modelled	97.5	14	<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="#">c3k1jA_</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent protease lon; <b>PDBTitle:</b> crystal structure of lon protease from thermococcus onnurineus na1
119	<a href="#">d1iqa2</a>	Alignment	not modelled	97.5	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
120	<a href="#">c3h4mC_</a>	Alignment	not modelled	97.5	27	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> aaa atpase domain of the proteasome- activating nucleotidase