






















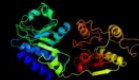









Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3h1tA_</a>	 Alignment		100.0	30	<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
2	<a href="#">c2w00B_</a>	 Alignment		100.0	16	<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
3	<a href="#">c2w74B_</a>	 Alignment		100.0	16	<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
4	<a href="#">c2ocaA_</a>	 Alignment		100.0	19	<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
5	<a href="#">c2xgjA_</a>	 Alignment		100.0	16	<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
6	<a href="#">c3tmiA_</a>	 Alignment		100.0	17	<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
7	<a href="#">c1oywA_</a>	 Alignment		100.0	17	<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
8	<a href="#">c2va8A_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
9	<a href="#">c4a4zA_</a>	 Alignment		100.0	16	<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
10	<a href="#">c3l9oA_</a>	 Alignment		100.0	15	<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
11	<a href="#">c2v1xB_</a>	 Alignment		100.0	19	<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

12	<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
13	<a href="#">c1gm5A_</a>	Alignment		100.0	17 <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
14	<a href="#">c2fwrA_</a>	Alignment		100.0	17 <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
15	<a href="#">c2eyqA_</a>	Alignment		100.0	20 <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
16	<a href="#">c1c4oA_</a>	Alignment		100.0	18 <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
17	<a href="#">c1wp9D_</a>	Alignment		100.0	24 <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
18	<a href="#">c1z3iX_</a>	Alignment		100.0	15 <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
19	<a href="#">c3mwyW_</a>	Alignment		100.0	16 <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
20	<a href="#">c2p6uA_</a>	Alignment		100.0	19 <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
21	<a href="#">c3dmqA_</a>	Alignment	not modelled	100.0	18 <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
22	<a href="#">c1gl9B_</a>	Alignment	not modelled	100.0	22 <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
23	<a href="#">c1z63A_</a>	Alignment	not modelled	100.0	18 <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
24	<a href="#">c3tbkA_</a>	Alignment	not modelled	100.0	18 <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
25	<a href="#">c3i5yA_</a>	Alignment	not modelled	100.0	16 <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
26	<a href="#">c3oiyB_</a>	Alignment	not modelled	100.0	13 <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
27	<a href="#">c2v6jA_</a>	Alignment	not modelled	100.0	20 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna helicase; <b>PDBTitle:</b> kokobera virus helicase: mutant met47thr
28	<a href="#">c3kx2A_</a>	Alignment	not modelled	100.0	17 <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
					<b>PDB header:</b> hydrolase

29	<a href="#">c2jlrA_</a>	Alignment	not modelled	100.0	21	<b>Chain:</b> A: <b>PDB Molecule:</b> serine protease subunit ns3; <b>PDBTitle:</b> dengue virus 4 ns3 helicase in complex with amppnp
30	<a href="#">c3bxzA_</a>	Alignment	not modelled	100.0	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
31	<a href="#">c3ewsA_</a>	Alignment	not modelled	100.0	17	<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
32	<a href="#">c2qeqA_</a>	Alignment	not modelled	100.0	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
33	<a href="#">c2d7dA_</a>	Alignment	not modelled	100.0	23	<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
34	<a href="#">c3rc8A_</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 supv311, mitochondrial; <b>PDBTitle:</b> human mitochondrial helicase suv3 in complex with short rna fragment
35	<a href="#">c2vbcA_</a>	Alignment	not modelled	100.0	22	<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
36	<a href="#">c1hv8B_</a>	Alignment	not modelled	100.0	15	<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
37	<a href="#">c2wv9A_</a>	Alignment	not modelled	100.0	21	<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
38	<a href="#">c2z0mA_</a>	Alignment	not modelled	99.9	17	<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
39	<a href="#">c2db3D_</a>	Alignment	not modelled	99.9	14	<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
40	<a href="#">c2z83A_</a>	Alignment	not modelled	99.9	23	<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
41	<a href="#">c1xtkA_</a>	Alignment	not modelled	99.9	14	<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
42	<a href="#">c1s2mA_</a>	Alignment	not modelled	99.9	15	<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
43	<a href="#">d1rifa_</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> DNA helicase UvsW
44	<a href="#">c3fhtA_</a>	Alignment	not modelled	99.9	16	<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
45	<a href="#">c2vsxA_</a>	Alignment	not modelled	99.9	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
46	<a href="#">c3pexA_</a>	Alignment	not modelled	99.9	18	<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
47	<a href="#">c1ymfA_</a>	Alignment	not modelled	99.9	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
48	<a href="#">d2fwra2</a>	Alignment	not modelled	99.9	25	<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="#">d2bmfa2</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
50	<a href="#">c2hxyC_</a>	Alignment	not modelled	99.9	17	<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
51	<a href="#">d2eyqa3</a>	Alignment	not modelled	99.9	25	<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="#">c2fsgA_</a>	Alignment	not modelled	99.9	17	<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
53	<a href="#">d1gm5a3</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 <b>PDB header:</b> hydrolase/dna

54	<a href="#">c1a1vA</a>	Alignment	not modelled	99.9	17	<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
55	<a href="#">c2i4iA</a>	Alignment	not modelled	99.9	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
56	<a href="#">d2fz4a1</a>	Alignment	not modelled	99.9	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
57	<a href="#">c2f55C</a>	Alignment	not modelled	99.9	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
58	<a href="#">c3crw1</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> 1: <b>PDB Molecule:</b> xpd/rad3 related dna helicase; <b>PDBTitle:</b> "xpd_apo"
59	<a href="#">c1tf2A</a>	Alignment	not modelled	99.8	20	<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
60	<a href="#">d1wp9a1</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
61	<a href="#">c3b6eA</a>	Alignment	not modelled	99.8	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
62	<a href="#">d1z3ix2</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
63	<a href="#">c3dl8B</a>	Alignment	not modelled	99.8	17	<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
64	<a href="#">c1cu1B</a>	Alignment	not modelled	99.8	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
65	<a href="#">d1z63a1</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
66	<a href="#">d2p6ra3</a>	Alignment	not modelled	99.7	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
67	<a href="#">d1oywa2</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
68	<a href="#">c3dkpA</a>	Alignment	not modelled	99.7	19	<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
69	<a href="#">c2vl7A</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> xpd; <b>PDBTitle:</b> structure of s. tokodaii xpd4
70	<a href="#">d1gkub1</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
71	<a href="#">d1gl9b1</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
72	<a href="#">d1tf5a3</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
73	<a href="#">d1a1va1</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
74	<a href="#">c2pl3A</a>	Alignment	not modelled	99.6	17	<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
75	<a href="#">c3fe2B</a>	Alignment	not modelled	99.6	19	<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
76	<a href="#">c3ly5A</a>	Alignment	not modelled	99.6	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
77	<a href="#">d1q0ua</a>	Alignment	not modelled	99.6	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
78	<a href="#">c2kbeA</a>	Alignment	not modelled	99.6	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 amino-terminal domain of dbp5p
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

79	<a href="#">d1yksa1</a>	Alignment	not modelled	99.6	23	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
80	<a href="#">d1hv8a1</a>	Alignment	not modelled	99.6	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
81	<a href="#">c3i32A_</a>	Alignment	not modelled	99.6	19	<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
82	<a href="#">c3llmB_</a>	Alignment	not modelled	99.6	15	<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
83	<a href="#">d1oywa3</a>	Alignment	not modelled	99.6	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
84	<a href="#">d1t5la2</a>	Alignment	not modelled	99.6	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
85	<a href="#">c2oxcA_</a>	Alignment	not modelled	99.6	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
86	<a href="#">d2j0sa1</a>	Alignment	not modelled	99.5	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
87	<a href="#">c2gxqA_</a>	Alignment	not modelled	99.5	18	<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
88	<a href="#">d1s2ma1</a>	Alignment	not modelled	99.5	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
89	<a href="#">d1c4oa2</a>	Alignment	not modelled	99.5	25	<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="#">c3fmoB_</a>	Alignment	not modelled	99.5	17	<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
91	<a href="#">d2fwra1</a>	Alignment	not modelled	99.5	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
92	<a href="#">c3iuyB_</a>	Alignment	not modelled	99.5	20	<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
93	<a href="#">c3berA_</a>	Alignment	not modelled	99.5	19	<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
94	<a href="#">c2fz1A_</a>	Alignment	not modelled	99.5	18	<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
95	<a href="#">d1qdea_</a>	Alignment	not modelled	99.5	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
96	<a href="#">d1c4oa1</a>	Alignment	not modelled	99.5	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
97	<a href="#">d2j0sa2</a>	Alignment	not modelled	99.5	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
98	<a href="#">c3fhcB_</a>	Alignment	not modelled	99.5	18	<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
99	<a href="#">d1t6na_</a>	Alignment	not modelled	99.5	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
100	<a href="#">c2vsfA_</a>	Alignment	not modelled	99.5	23	<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
101	<a href="#">d2eyqa5</a>	Alignment	not modelled	99.4	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
102	<a href="#">c3earA_</a>	Alignment	not modelled	99.4	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
103	<a href="#">d1nkt3</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="#">d1urba1</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate



104	<a href="#">d1wlvda1</a>	Alignment	not modelled	99.4	20	hydrolases <b>Family:</b> Tandem AAA-ATPase domain
105	<a href="#">c2p6nA_</a>	Alignment	not modelled	99.4	21	<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
106	<a href="#">d1veca_</a>	Alignment	not modelled	99.4	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
107	<a href="#">c2vdaA_</a>	Alignment	not modelled	99.4	19	<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
108	<a href="#">d2g9na1</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> Tandem AAA-ATPase domain
109	<a href="#">d1s2ma2</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
110	<a href="#">d1hv8a2</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> Tandem AAA-ATPase domain
111	<a href="#">c3fmpD_</a>	Alignment	not modelled	99.4	16	<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
112	<a href="#">c2hjbB_</a>	Alignment	not modelled	99.4	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
113	<a href="#">d1wp9a2</a>	Alignment	not modelled	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
114	<a href="#">d1fuka_</a>	Alignment	not modelled	99.3	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
115	<a href="#">c1nl3B_</a>	Alignment	not modelled	99.3	16	<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
116	<a href="#">d2p6ra4</a>	Alignment	not modelled	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
117	<a href="#">d1t5ia_</a>	Alignment	not modelled	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
118	<a href="#">d2g2ja1</a>	Alignment	not modelled	99.2	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
119	<a href="#">c3juxA_</a>	Alignment	not modelled	99.2	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
120	<a href="#">d1gm5a4</a>	Alignment	not modelled	99.2	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