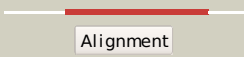

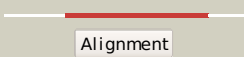

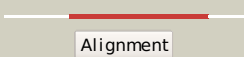

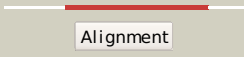

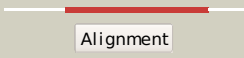
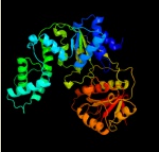
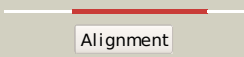

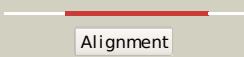
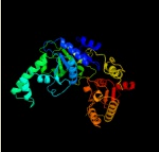
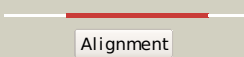

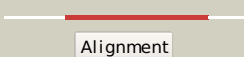

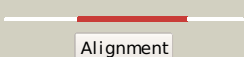

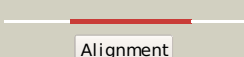










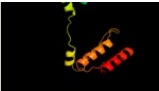


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2is6B_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna helicase ii; <b>PDBTitle:</b> crystal structure of uvrd-dna-adpmgf3 ternary complex
2	<a href="#">c1uaaB_</a>	 Alignment		100.0	30	<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
3	<a href="#">c1w36E_</a>	 Alignment		100.0	24	<b>PDB header:</b> recombination <b>Chain:</b> E: <b>PDB Molecule:</b> exodeoxyribonuclease v beta chain; <b>PDBTitle:</b> recbcd:dna complex
4	<a href="#">c1pjrA_</a>	 Alignment		100.0	28	<b>PDB header:</b> helicase <b>Chain:</b> A: <b>PDB Molecule:</b> pcra; <b>PDBTitle:</b> structure of dna helicase
5	<a href="#">c3lfuA_</a>	 Alignment		100.0	31	<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
6	<a href="#">c2pjrF_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> F: <b>PDB Molecule:</b> protein (helicase pcra); <b>PDBTitle:</b> helicase product complex
7	<a href="#">c2wjyA_</a>	 Alignment		100.0	21	<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
8	<a href="#">c2xzlA_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent helicase nam7; <b>PDBTitle:</b> upf1-rna complex
9	<a href="#">c2gk7A_</a>	 Alignment		100.0	19	<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
10	<a href="#">d1w36b1</a>	 Alignment		100.0	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
11	<a href="#">d1pjr1</a>	 Alignment		100.0	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

12	<a href="#">d1uaaa1</a>	Alignment		100.0	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
13	<a href="#">c3e1sA</a>	Alignment		100.0	23	<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
14	<a href="#">c1w36G</a>	Alignment		100.0	29	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> exodeoxyribonuclease v alpha chain; <b>PDBTitle:</b> recbcd:dna complex
15	<a href="#">c1w36F</a>	Alignment		99.9	16	<b>PDB header:</b> recombination <b>Chain:</b> F: <b>PDB Molecule:</b> exodeoxyribonuclease v gamma chain; <b>PDBTitle:</b> recbcd:dna complex
16	<a href="#">c1qhhA</a>	Alignment		99.9	31	<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
17	<a href="#">c3dmnA</a>	Alignment		99.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna helicase; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of a possilbe dna2 helicase from lactobacillus plantarun wcfs1
18	<a href="#">c1qhhB</a>	Alignment		99.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (pcra (subunit)); <b>PDBTitle:</b> structure of dna helicase with adpnp
19	<a href="#">d1pjra2</a>	Alignment		99.7	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
20	<a href="#">d1uaaa2</a>	Alignment		99.7	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
21	<a href="#">c1qhhD</a>	Alignment	not modelled	99.7	29	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (pcra (subunit)); <b>PDBTitle:</b> structure of dna helicase with adpnp
22	<a href="#">c2pjrB</a>	Alignment	not modelled	99.6	31	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> protein (helicase pcra); <b>PDBTitle:</b> helicase product complex
23	<a href="#">d1w36b2</a>	Alignment	not modelled	99.6	29	<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
24	<a href="#">d1w36d1</a>	Alignment	not modelled	99.5	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
25	<a href="#">d1w36d2</a>	Alignment	not modelled	99.4	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
26	<a href="#">d1w36c2</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
27	<a href="#">c3b85A</a>	Alignment	not modelled	99.3	22	<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 pho2 from corynebacterium glutamicum
28	<a href="#">c2eyqA</a>	Alignment	not modelled	98.7	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
						<b>PDB header:</b> isomerase

29	<a href="#">c3oiyB_</a>	Alignment	not modelled	98.6	19	<b>Chain:</b> B: <b>PDB Molecule:</b> reverse gyrase helicase domain; <b>PDBTitle:</b> helicase domain of reverse gyrase from thermotoga maritima
30	<a href="#">d1gkub1</a>	Alignment		98.5	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
31	<a href="#">c1gm5A_</a>	Alignment	not modelled	98.4	23	<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
32	<a href="#">d1gl9b1</a>	Alignment	not modelled	98.3	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
33	<a href="#">c3i5yA_</a>	Alignment	not modelled	98.2	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
34	<a href="#">c1gl9B_</a>	Alignment	not modelled	98.2	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
35	<a href="#">c2va8A_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
36	<a href="#">c2xgjA_</a>	Alignment	not modelled	98.1	19	<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
37	<a href="#">c2z0mA_</a>	Alignment	not modelled	98.1	22	<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="#">c3l9oA_</a>	Alignment	not modelled	98.1	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
39	<a href="#">c2zj2A_</a>	Alignment	not modelled	98.1	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
40	<a href="#">c2db3D_</a>	Alignment	not modelled	98.1	22	<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
41	<a href="#">c3tbkA_</a>	Alignment	not modelled	98.1	12	<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
42	<a href="#">c1wp9D_</a>	Alignment	not modelled	98.1	19	<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
43	<a href="#">c2p6uA_</a>	Alignment	not modelled	98.0	23	<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
44	<a href="#">c4a4zA_</a>	Alignment	not modelled	98.0	17	<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
45	<a href="#">c2ocaA_</a>	Alignment	not modelled	98.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase uvsw; <b>PDBTitle:</b> the crystal structure of t4 uvsw
46	<a href="#">d2eyqa3</a>	Alignment	not modelled	97.9	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
47	<a href="#">c2hxyC_</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx48; <b>PDBTitle:</b> crystal structure of human apo-eif4aiii
48	<a href="#">c3tmiA_</a>	Alignment	not modelled	97.9	13	<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
49	<a href="#">c1xtkA_</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase p47; <b>PDBTitle:</b> structure of decd to dead mutation of human uap56
50	<a href="#">c3dkpA_</a>	Alignment	not modelled	97.8	20	<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
51	<a href="#">d1rifa_</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> DNA helicase UvsW
52	<a href="#">c2wv9A_</a>	Alignment	not modelled	97.8	23	<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
						<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle receptor;

53	<a href="#">c3dmdA_</a>	Alignment		97.8	12	<b>PDBTitle:</b> structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
54	<a href="#">c1s2mA_</a>	Alignment	not modelled	97.8	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative atp-dependent rna helicase dhh1; <b>PDBTitle:</b> crystal structure of the dead box protein dhh1p
55	<a href="#">c1hv8B_</a>	Alignment	not modelled	97.8	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
56	<a href="#">d1c4oa1</a>	Alignment	not modelled	97.8	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
57	<a href="#">c3ly5A_</a>	Alignment	not modelled	97.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx18; <b>PDBTitle:</b> ddx18 dead-domain
58	<a href="#">c1c4oA_</a>	Alignment	not modelled	97.8	27	<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
59	<a href="#">c3bxzA_</a>	Alignment	not modelled	97.8	12	<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
60	<a href="#">c2vbcA_</a>	Alignment	not modelled	97.7	31	<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
61	<a href="#">c3pexA_</a>	Alignment	not modelled	97.7	22	<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
62	<a href="#">c2d7dA_</a>	Alignment	not modelled	97.7	19	<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
63	<a href="#">c3llmB_</a>	Alignment	not modelled	97.7	16	<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
64	<a href="#">c2qeqA_</a>	Alignment	not modelled	97.7	23	<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
65	<a href="#">d2p6ra3</a>	Alignment	not modelled	97.6	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
66	<a href="#">c3kx2A_</a>	Alignment	not modelled	97.6	16	<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
67	<a href="#">c2fwrA_</a>	Alignment	not modelled	97.6	25	<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
68	<a href="#">c2kbeA_</a>	Alignment	not modelled	97.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dbp5; <b>PDBTitle:</b> solution structure of amino-terminal domain of dbp5p
69	<a href="#">d1gm5a3</a>	Alignment	not modelled	97.6	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
70	<a href="#">c2pl3A_</a>	Alignment	not modelled	97.6	22	<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
71	<a href="#">c2iy3A_</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein ffh; <b>PDBTitle:</b> structure of the e. coli signal recognition particle2 bound to a translating ribosome
72	<a href="#">c2og2A_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative signal recognition particle receptor; <b>PDBTitle:</b> crystal structure of chloroplast ftsy from arabidopsis2 thaliana
73	<a href="#">c2vsxA_</a>	Alignment	not modelled	97.6	25	<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
74	<a href="#">c2z83A_</a>	Alignment	not modelled	97.5	22	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> helicase/nucleoside triphosphatase; <b>PDBTitle:</b> crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8
75	<a href="#">c3fhtA_</a>	Alignment	not modelled	97.5	19	<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
76	<a href="#">c1ymfA_</a>	Alignment	not modelled	97.5	25	<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
77	<a href="#">c2vl7A_</a>	Alignment	not modelled	97.5	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> xpd; <b>PDBTitle:</b> structure of s. tokodaii xpd4

78	<a href="#">c3fe2B_</a>	Alignment	not modelled	97.5	20	<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
79	<a href="#">c3b6eA_</a>	Alignment	not modelled	97.5	19	<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
80	<a href="#">c3ewsA_</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx19b; <b>PDBTitle:</b> human dead-box rna-helicase ddx19 in complex with adp
81	<a href="#">c2v6jA_</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna helicase; <b>PDBTitle:</b> kokobera virus helicase: mutant met47thr
82	<a href="#">d1wp9a1</a>	Alignment	not modelled	97.4	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
83	<a href="#">d1s2ma1</a>	Alignment	not modelled	97.4	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="#">c2w74B_</a>	Alignment	not modelled	97.4	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
85	<a href="#">c2jlrA_</a>	Alignment	not modelled	97.4	28	<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
86	<a href="#">c2v1xB_</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent dna helicase q1; <b>PDBTitle:</b> crystal structure of human recq-like dna helicase
87	<a href="#">c2yhsA_</a>	Alignment	not modelled	97.3	25	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the e. coli srp receptor ftsy
88	<a href="#">c1z63A_</a>	Alignment	not modelled	97.3	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
89	<a href="#">c3iuyB_</a>	Alignment	not modelled	97.3	21	<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
90	<a href="#">c3crw1_</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> 1: <b>PDB Molecule:</b> xpd/rad3 related dna helicase; <b>PDBTitle:</b> "xpd_apo"
91	<a href="#">c3h1tA_</a>	Alignment	not modelled	97.3	22	<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
92	<a href="#">c1oywA_</a>	Alignment	not modelled	97.3	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
93	<a href="#">c2cnwF_</a>	Alignment	not modelled	97.2	23	<b>PDB header:</b> signal recognition <b>Chain:</b> F: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> gdpalf4 complex of the srp gtpases ffh and ftsy
94	<a href="#">c1a1vA_</a>	Alignment	not modelled	97.2	21	<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
95	<a href="#">d2fwra2</a>	Alignment	not modelled	97.2	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
96	<a href="#">c1zu4A_</a>	Alignment	not modelled	97.2	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ftsyl; <b>PDBTitle:</b> crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
97	<a href="#">d1q0ua_</a>	Alignment	not modelled	97.2	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
98	<a href="#">c3b9qA_</a>	Alignment	not modelled	97.2	33	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloroplast srp receptor homolog, alpha subunit <b>PDBTitle:</b> the crystal structure of cpftsyl from arabidopsis thaliana
99	<a href="#">c2w00B_</a>	Alignment	not modelled	97.1	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
100	<a href="#">d1qdea_</a>	Alignment	not modelled	97.1	24	<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="#">c2gxqA_</a>	Alignment	not modelled	97.1	19	<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
102	<a href="#">c2f55C_</a>	Alignment	not modelled	97.1	22	<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
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases



103	<a href="#">d1a1va1</a>	Alignment	not modelled	97.1	21	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
104	<a href="#">c2qy9A</a>	Alignment	not modelled	97.1	27	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsy
105	<a href="#">c1vmaA</a>	Alignment	not modelled	97.0	29	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
106	<a href="#">c1cu1B</a>	Alignment	not modelled	97.0	20	<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
107	<a href="#">d1wrba1</a>	Alignment	not modelled	97.0	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
108	<a href="#">d1oywa2</a>	Alignment	not modelled	97.0	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
109	<a href="#">d2j0sa1</a>	Alignment	not modelled	97.0	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
110	<a href="#">c2j7pA</a>	Alignment	not modelled	96.9	28	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
111	<a href="#">d2fz4a1</a>	Alignment	not modelled	96.9	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
112	<a href="#">d2bmfa2</a>	Alignment	not modelled	96.9	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
113	<a href="#">c3jvva</a>	Alignment	not modelled	96.9	24	<b>PDB header:</b> atp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> twitching mobility protein; <b>PDBTitle:</b> crystal structure of p. aeruginosa pilT with bound amp-pcp
114	<a href="#">c2px0D</a>	Alignment	not modelled	96.9	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> flagellar biosynthesis protein flhf; <b>PDBTitle:</b> crystal structure of flhf complexed with gmppnp/mg(2+)
115	<a href="#">c3ec2A</a>	Alignment	not modelled	96.9	31	<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
116	<a href="#">d1hv8a1</a>	Alignment	not modelled	96.8	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
117	<a href="#">c2j37W</a>	Alignment	not modelled	96.8	19	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
118	<a href="#">c3dm5A</a>	Alignment	not modelled	96.8	27	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
119	<a href="#">c2oxcA</a>	Alignment	not modelled	96.8	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx20; <b>PDBTitle:</b> human dead-box rna helicase ddx20, dead domain in complex2 with adp
120	<a href="#">c3berA</a>	Alignment	not modelled	96.8	22	<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