







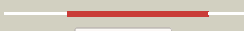


















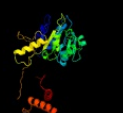





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2024c (- )_2268701_2270248
Date	Mon Aug 5 13:25:13 BST 2019
Unique Job ID	cbf6de575901a6f6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4xqkB_</a>	 Alignment		100.0	42	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> llabiii; <b>PDBTitle:</b> atp-dependent type isp restriction-modification enzyme llabiii bound2 to dna
2	<a href="#">c2w00B_</a>	 Alignment		100.0	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 ecor124i restriction2 enzyme in complex with atp
3	<a href="#">c6h2jB_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> type i restriction enzyme r protein; <b>PDBTitle:</b> crystal structure of the hsdR subunit of the ecor124i restriction2 enzyme with the c-terminal domain
4	<a href="#">c3h1tA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type i site-specific restriction-modification <b>PDBTitle:</b> the fragment structure of a putative hsdR subunit of a type2 i restriction enzyme from vibrio vulnificus yj016
5	<a href="#">c6nmIA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription and dna repair factor iih helicase <b>PDBTitle:</b> cryo-em structure of the human tfiih core complex
6	<a href="#">c2w74B_</a>	 Alignment		100.0	18	<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
7	<a href="#">c5of4A_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tfiih basal transcription factor complex helicase xpb <b>PDBTitle:</b> the cryo-em structure of human tfiih
8	<a href="#">c6jdeB_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dna repair helicase radd; <b>PDBTitle:</b> crystal structure of a dna repair protein
9	<a href="#">c6ro4A_</a>	 Alignment		100.0	19	<b>PDB header:</b> translocase <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription and dna repair factor iih helicase <b>PDBTitle:</b> structure of the core tfiih-xpa-dna complex
10	<a href="#">c5jvwV_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> V: <b>PDB Molecule:</b> tfiih basal transcription factor complex helicase xpb <b>PDBTitle:</b> human core tfiih bound to dna within the pic
11	<a href="#">c5jb2A_</a>	 Alignment		100.0	21	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> lgp2; <b>PDBTitle:</b> crystal structure of chicken lgp2 with 5'ppp 10-mer dsrna and adp-2 alf4-mg2+ at 2.2 a resolution.

12	<a href="#">d2fwra2</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
13	<a href="#">d1rifa_</a>	Alignment		100.0	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> DNA helicase UvsW
14	<a href="#">c6buaA_</a>	Alignment		100.0	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> dicer-2, isoform a; <b>PDBTitle:</b> drosophila dicer-2 apo homology model (helicase, platform-paz,2 rnaseiii domains)
15	<a href="#">c5fmf1_</a>	Alignment		100.0	17	<b>PDB header:</b> transcription <b>Chain:</b> 1; <b>PDB Molecule:</b> dna repair helicase rad25, ssl2; <b>PDBTitle:</b> the p-lobe of rna polymerase ii pre-initiation complex
16	<a href="#">c5x0yO_</a>	Alignment		100.0	16	<b>PDB header:</b> structural protein/hydrolase/dna <b>Chain:</b> O; <b>PDB Molecule:</b> transcription regulatory protein snf2; <b>PDBTitle:</b> complex of snf2-nucleosome complex with snf2 bound to shl2 of the2 nucleosome
17	<a href="#">c4gl2A_</a>	Alignment		100.0	16	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A; <b>PDB Molecule:</b> interferon-induced helicase c domain-containing protein 1; <b>PDBTitle:</b> structural basis for dsrna duplex backbone recognition by mda5
18	<a href="#">c5jcfB_</a>	Alignment		100.0	16	<b>PDB header:</b> immune system <b>Chain:</b> B; <b>PDB Molecule:</b> melanoma differentiation associated protein-5; <b>PDBTitle:</b> crystal structure of chicken mda5 with 5'p 10-mer dsrna and adp-mg2+2 at 2.6 a resolution (orthorhombic form).
19	<a href="#">c5zamA_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase/protein binding/rna <b>Chain:</b> A; <b>PDB Molecule:</b> endoribonuclease dicer; <b>PDBTitle:</b> cryo-em structure of human dicer and its complexes with a pre-mirna2 substrate
20	<a href="#">c3tmiA_</a>	Alignment		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
21	<a href="#">c4zcfC_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase-dna complex <b>Chain:</b> C; <b>PDB Molecule:</b> restriction endonuclease ecop15i, restriction subunit; <b>PDBTitle:</b> structural basis of asymmetric dna methylation and atp-triggered long-2 range diffusion by ecop15i
22	<a href="#">c6iehB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> exosome rna helicase mtr4; <b>PDBTitle:</b> crystal structures of the hmtr4-nrde2 complex
23	<a href="#">c4on9B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx58; <b>PDBTitle:</b> dech box helicase domain
24	<a href="#">c2ocaA_</a>	Alignment	not modelled	100.0	17	<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
25	<a href="#">c5hzaA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> snf2-family atp dependent chromatin remodeling factor like <b>PDBTitle:</b> crystal structure of mtsnf2
26	<a href="#">c2p6uA_</a>	Alignment	not modelled	100.0	18	<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
27	<a href="#">c2xgiA_</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 dob1; <b>PDBTitle:</b> structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
28	<a href="#">c5o9gW_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> W; <b>PDB Molecule:</b> chromo domain-containing protein 1; <b>PDBTitle:</b> structure of nucleosome-chd1 complex

29	<a href="#">d2eyqa3</a>	Alignment	not modelled	100.0	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
30	<a href="#">c5v9xA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase; <b>PDBTitle:</b> structure of mycobacterium smegmatis helicase lhr bound to ssdna and2 amp-pnp
31	<a href="#">c5agaA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase theta; <b>PDBTitle:</b> crystal structure of the helicase domain of human dna2 polymerase theta in complex with amppnp
32	<a href="#">c6c90A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase/rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exosome rna helicase mtr4,exosome rna helicase mtr4; <b>PDBTitle:</b> human mtr4 helicase in complex with zcchc8-ctd
33	<a href="#">c2va8A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
34	<a href="#">c3mwyW</a>	Alignment	not modelled	100.0	17	<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
35	<a href="#">c6iegA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exosome rna helicase mtr4; <b>PDBTitle:</b> crystal structure of human mtr4
36	<a href="#">c3l9oA</a>	Alignment	not modelled	100.0	17	<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
37	<a href="#">d1gm5a3</a>	Alignment	not modelled	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
38	<a href="#">c2zj8A</a>	Alignment	not modelled	100.0	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 2
39	<a href="#">c5jxrB</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> chromatin-remodeling complex atpase-like protein; <b>PDBTitle:</b> crystal structure of mtiswi
40	<a href="#">c4ddvA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> reverse gyrase; <b>PDBTitle:</b> thermotoga maritima reverse gyrase, triclinic form
41	<a href="#">c4a4zA</a>	Alignment	not modelled	99.9	14	<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
42	<a href="#">c2zj2A</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ski2-type helicase; <b>PDBTitle:</b> archaeal dna helicase hjm apo state in form 1
43	<a href="#">c6eg3A</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> maltose/maltodextrin-binding periplasmic protein,probable <b>PDBTitle:</b> crystal structure of human brm in complex with compound 15
44	<a href="#">c4xgtA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> frq-interacting rna helicase; <b>PDBTitle:</b> structure of rna helicase frh a critical component of the neurospora2 crassa circadian clock
45	<a href="#">c6g7eB</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> helicase-like protein; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum mot1 (e1434q, 1837-18862 deletion mutant)
46	<a href="#">c4bujA</a>	Alignment	not modelled	99.9	14	<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 ski2-3-8 complex
47	<a href="#">d2fz4a1</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
48	<a href="#">c3tbkA</a>	Alignment	not modelled	99.9	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
49	<a href="#">c1gm5A</a>	Alignment	not modelled	99.9	18	<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
50	<a href="#">c1z3iX</a>	Alignment	not modelled	99.9	21	<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
51	<a href="#">c1z63A</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase/dna complex <b>Chain:</b> A: <b>PDB Molecule:</b> helicase of the snf2/rad54 family; <b>PDBTitle:</b> sulfobolus solfataricus swi2/snf2 atpase core in complex with dsdna
52	<a href="#">c3dmqA</a>	Alignment	not modelled	99.9	23	<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 that recycles rna2 polymerase during transcription
53	<a href="#">c6irol</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> L: <b>PDB Molecule:</b> iswi chromatin-remodeling complex atpase isw1; <b>PDBTitle:</b> the crosslinked complex of iswi-nucleosome in the adp-bound state
54	<a href="#">c1gl9B</a>	Alignment	not modelled	99.9	16	<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 <b>PDB header:</b> splicing

55	<a href="#">c6ah0D</a>	Alignment	not modelled	99.9	17	<b>Chain:</b> D: <b>PDB Molecule:</b> u5 small nuclear ribonucleoprotein 200 kda helicase; <b>PDBTitle:</b> the cryo-em structure of the precursor of human pre-catalytic2 spliceosome (pre-b complex)
56	<a href="#">d1z3ix2</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
57	<a href="#">c5dcaA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing helicase brr2; <b>PDBTitle:</b> crystal structure of yeast full length brr2 in complex with prp8 jab12 domain
58	<a href="#">c4f92B</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> u5 small nuclear ribonucleoprotein 200 kda helicase; <b>PDBTitle:</b> brr2 helicase region s10871
59	<a href="#">c5m52B</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> pre-mrna-splicing helicase brr2; <b>PDBTitle:</b> crystal structure of yeast brr2 full-lenght in complex with prp8 jab12 domain
60	<a href="#">c2eyqA</a>	Alignment	not modelled	99.9	19	<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
61	<a href="#">c3b6eA</a>	Alignment	not modelled	99.9	21	<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="#">c6gejM</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> nuclear protein <b>Chain:</b> M: <b>PDB Molecule:</b> helicase swr1; <b>PDBTitle:</b> chromatin remodeller-nucleosome complex at 3.6 a resolution.
63	<a href="#">c6etxG</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> dna helicase ino80; <b>PDBTitle:</b> cryo-em structure of the human ino80 complex bound to nucleosome
64	<a href="#">d1wp9a1</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
65	<a href="#">c4bgdA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing helicase brr2; <b>PDBTitle:</b> crystal structure of brr2 in complex with the jab1/mpn domain of prp8
66	<a href="#">c1wp9D</a>	Alignment	not modelled	99.9	23	<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
67	<a href="#">c5vvrM</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transcription/rna/dna <b>Chain:</b> M: <b>PDB Molecule:</b> dna repair and recombination protein rad26; <b>PDBTitle:</b> ternary complex of rna pol ii, transcription scaffold and rad26
68	<a href="#">c5lqwC</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna-splicing helicase brr2; <b>PDBTitle:</b> yeast activated spliceosome
69	<a href="#">c5m59C</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna splicing helicase-like protein; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum brr2 helicase core in2 complex with prp8 jab1 domain
70	<a href="#">c1oywA</a>	Alignment	not modelled	99.9	15	<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
71	<a href="#">c4q47A</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna helicase recq; <b>PDBTitle:</b> structure of the drrecq catalytic core in complex with adp
72	<a href="#">c6fmlG</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> ino80; <b>PDBTitle:</b> cryoem structure ino80core nucleosome complex
73	<a href="#">c3jcrC</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> hbrr2; <b>PDBTitle:</b> 3d structure determination of the human*u4/u6.u5* tri-snnp complex
74	<a href="#">c5lstA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase q4; <b>PDBTitle:</b> crystal structure of the human recq4 helicase.
75	<a href="#">c2v1xB</a>	Alignment	not modelled	99.9	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
76	<a href="#">c4cdgA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bloom syndrome protein; <b>PDBTitle:</b> crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody
77	<a href="#">c3oiyB</a>	Alignment	not modelled	99.9	19	<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
78	<a href="#">c3bxzA</a>	Alignment	not modelled	99.9	13	<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 from escherichia2 coli seca
79	<a href="#">c4n14H</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> primosome assembly protein pria; <b>PDBTitle:</b> pria helicase bound to adp
80	<a href="#">c1c4oA</a>	Alignment	not modelled	99.9	16	<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
81	<a href="#">c6ne3W_</a>	Alignment	not modelled	99.9	18 <b>PDB header:</b> dna binding protein/dna <b>Chain:</b> W: <b>PDB Molecule:</b> swi/snf-related matrix-associated actin-dependent regulator <b>PDBTitle:</b> cryo-em structure of singly-bound snf2h-nucleosome complex with snf2h2 bound at shl-2
82	<a href="#">d2p6ra3</a>	Alignment	not modelled	99.9	22 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
83	<a href="#">c2fwrA_</a>	Alignment	not modelled	99.9	23 <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
84	<a href="#">c5tnuB_</a>	Alignment	not modelled	99.9	24 <b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> dna-dependent atpase xpbii; <b>PDBTitle:</b> s. tokodaii xpb ii crystal structure at 3.0 angstrom resolution
85	<a href="#">c5lb5C_</a>	Alignment	not modelled	99.9	16 <b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent dna helicase q5; <b>PDBTitle:</b> crystal structure of human recq15 helicase in complex with adp/mg2 (triclinc form).
86	<a href="#">c2qeqa_</a>	Alignment	not modelled	99.9	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
87	<a href="#">d1z63a1</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> Tandem AAA-ATPase domain
88	<a href="#">c2d7dA_</a>	Alignment	not modelled	99.8	13 <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 atpase2 activity of uvrB
89	<a href="#">c2v6jA_</a>	Alignment	not modelled	99.8	23 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna helicase; <b>PDBTitle:</b> kokobera virus helicase: mutant met47thr
90	<a href="#">c2z83A_</a>	Alignment	not modelled	99.8	20 <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
91	<a href="#">c3dkpA_</a>	Alignment	not modelled	99.8	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
92	<a href="#">c4qqxA_</a>	Alignment	not modelled	99.8	13 <b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated helicase, cas3 family; <b>PDBTitle:</b> crystal structure of t. fusca cas3-atp
93	<a href="#">c2jlrA_</a>	Alignment	not modelled	99.8	18 <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
94	<a href="#">d1q0ua_</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
95	<a href="#">c4nl8E_</a>	Alignment	not modelled	99.8	22 <b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> primosome assembly protein pria; <b>PDBTitle:</b> pria helicase bound to ssb c-terminal tail peptide
96	<a href="#">c3fe2B_</a>	Alignment	not modelled	99.8	16 <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
97	<a href="#">d1oywa2</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
98	<a href="#">c6aicA_</a>	Alignment	not modelled	99.8	14 <b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> dead-box atp-dependent rna helicase csha; <b>PDBTitle:</b> crystal structures of the n-terminal domain of staphylococcus aureus2 dead-box cold shock rna helicase csha in complex with amp
99	<a href="#">d1gl9b1</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> Helicase-like "domain" of reverse gyrase
100	<a href="#">c3i5yA_</a>	Alignment	not modelled	99.8	17 <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
101	<a href="#">c2wv9A_</a>	Alignment	not modelled	99.8	19 <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
102	<a href="#">d1gkub1</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> Helicase-like "domain" of reverse gyrase
103	<a href="#">c4ljyA_</a>	Alignment	not modelled	99.8	16 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-processing atp-dependent rna helicase prp5; <b>PDBTitle:</b> crystal structure of rna splicing effector prp5 in complex with adp
104	<a href="#">c3kx2A_</a>	Alignment	not modelled	99.8	12 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna helicase prp43; <b>PDBTitle:</b> crystal structure of prp43p in complex with adp <b>PDB header:</b> translation, rna binding protein



105	<a href="#">c4px9C_</a>	Alignment	not modelled	99.8	21	<b>Chain:</b> C; <b>PDB Molecule:</b> atp-dependent rna helicase ddx3x; <b>PDBTitle:</b> dead-box rna helicase ddx3x domain 1 with n-terminal atp-binding loop
106	<a href="#">c2vbcA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dengue 4 ns3 full-length protein; <b>PDBTitle:</b> crystal structure of the ns3 protease-helicase from dengue2 virus
107	<a href="#">c4cbhC_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> serine protease ns3; <b>PDBTitle:</b> pestivirus ns3 helicase
108	<a href="#">d1s2ma1</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
109	<a href="#">c3ewsA_</a>	Alignment	not modelled	99.8	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
110	<a href="#">c2kbeA_</a>	Alignment	not modelled	99.8	16	<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
111	<a href="#">d1tf5a3</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
112	<a href="#">c1ymfA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> genome polyprotein [contains: flavivirin protease ns3 <b>PDBTitle:</b> crystal structure of yellow fever virus ns3 helicase complexed with2 adp
113	<a href="#">c5wsge_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> E; <b>PDB Molecule:</b> saccharomyces cerevisiae s288c snr6 snrna; <b>PDBTitle:</b> cryo-em structure of the catalytic step ii spliceosome (c* complex) at2 4.0 angstrom resolution
114	<a href="#">c3ly5A_</a>	Alignment	not modelled	99.8	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
115	<a href="#">c5gvrA_</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 ddx41; <b>PDBTitle:</b> crystal structure of the ddx41 dead domain in an apo closed form
116	<a href="#">c5mq0V_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> splicing <b>Chain:</b> V; <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna helicase prp22; <b>PDBTitle:</b> structure of a spliceosome remodeled for exon ligation
117	<a href="#">c2pl3A_</a>	Alignment	not modelled	99.8	16	<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
118	<a href="#">c5ivA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dead-box atp-dependent rna helicase csha; <b>PDBTitle:</b> csha helicase
119	<a href="#">c1a1vA_</a>	Alignment	not modelled	99.8	25	<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
120	<a href="#">c6fa5A_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative mrna splicing factor; <b>PDBTitle:</b> crystal structure of the deah-box helicase prp2 in complex with adp