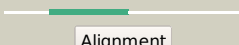
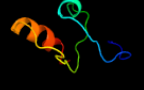
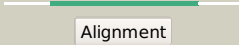

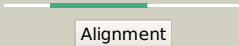

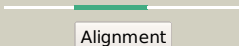

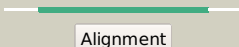

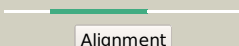

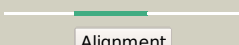
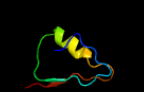
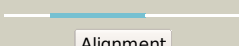

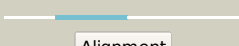

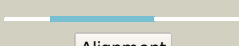
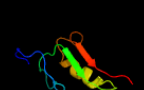


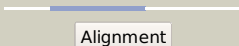
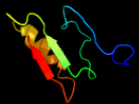
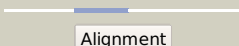

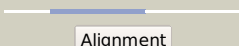

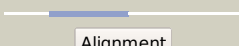

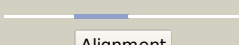

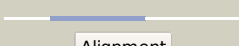
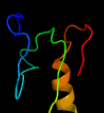

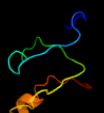
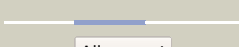


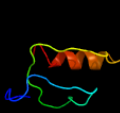
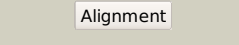

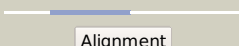
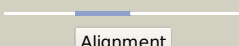
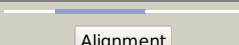
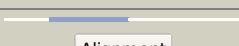




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2360c_(-)_2642160_2642588
Date	Mon Aug 5 13:25:51 BST 2019
Unique Job ID	eb053117e3f4d687

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3earA_</a>	 Alignment		48.9	10	<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
2	<a href="#">c2fzIA_</a>	 Alignment		47.2	14	<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
3	<a href="#">c5jcfB_</a>	 Alignment		45.6	12	<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).
4	<a href="#">c5zamA_</a>	 Alignment		45.5	20	<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
5	<a href="#">d2plga1</a>	 Alignment		42.6	13	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> Type III secretory system chaperone-like <b>Family:</b> TII0839-like
6	<a href="#">c5jb2A_</a>	 Alignment		40.4	15	<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.
7	<a href="#">c4gl2A_</a>	 Alignment		40.0	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
8	<a href="#">c2d7dA_</a>	 Alignment		38.9	18	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> uvrabc system protein b; <b>PDBTitle:</b> structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc
9	<a href="#">c2p6nA_</a>	 Alignment		34.9	7	<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
10	<a href="#">d2fwra1</a>	 Alignment		30.9	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
11	<a href="#">d1s2ma2</a>	 Alignment		28.3	7	<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="#">d1t5la2</a>	 Alignment		24.9	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
13	<a href="#">c2i4iA</a>	 Alignment		24.5	15	<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
14	<a href="#">c1wp9D</a>	 Alignment		24.5	9	<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
15	<a href="#">c2v1xB</a>	 Alignment		24.5	6	<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
16	<a href="#">c4kbfA</a>	 Alignment		24.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> heat resistant rna dependent atpase; <b>PDBTitle:</b> two different open conformations of the helicase core of the rna2 helicase hera
17	<a href="#">d1oywa3</a>	 Alignment		23.7	11	<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
18	<a href="#">c3i32A</a>	 Alignment		23.3	8	<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
19	<a href="#">c4ljyA</a>	 Alignment		22.9	7	<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
20	<a href="#">c4w7sA</a>	 Alignment		22.1	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing atp-dependent rna helicase prp28; <b>PDBTitle:</b> crystal structure of the yeast dead-box splicing factor prp28 at 2.542 angstroms resolution
21	<a href="#">c4d25A</a>	 Alignment	not modelled	21.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bmvlg protein; <b>PDBTitle:</b> crystal structure of the bombyx mori vasa helicase (e339q)2 in complex with rna and amppnp
22	<a href="#">c2z0mA</a>	 Alignment	not modelled	21.4	12	<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 sulfobolus tokodaii
23	<a href="#">c2vjtd</a>	 Alignment	not modelled	21.2	6	<b>PDB header:</b> hydrolase inhibitor/hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent rna helicase srmb; <b>PDBTitle:</b> crystal structure of e. coli dead-box protein srmb bound to regulator2 of ribonuclease activity a (rraa)
24	<a href="#">c6ne3W</a>	 Alignment	not modelled	21.1	14	<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
25	<a href="#">c3tmiA</a>	 Alignment	not modelled	21.0	7	<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
26	<a href="#">c1oywA</a>	 Alignment	not modelled	20.0	13	<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
27	<a href="#">c2hjbB</a>	 Alignment	not modelled	20.0	12	<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
28	<a href="#">d1ikpa3</a>	 Alignment	not modelled	19.7	43	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Exotoxin A, middle domain <b>Family:</b> Exotoxin A, middle domain

29	<a href="#">d2p6ra4</a>	Alignment	not modelled	19.4	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
30	<a href="#">c4pxaA_</a>	Alignment	not modelled	19.4	11	<b>PDB header:</b> translation, rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx3x; <b>PDBTitle:</b> dead-box rna helicase ddx3x cancer-associated mutant d354v
31	<a href="#">c4db4A_</a>	Alignment	not modelled	19.1	8	<b>PDB header:</b> rna-binding protein/dna,rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase mss116, mitochondrial; <b>PDBTitle:</b> mss116p dead-box helicase domain 2 bound to a chimaeric rna-dna duplex
32	<a href="#">c5supB_</a>	Alignment	not modelled	18.8	7	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent rna helicase sub2; <b>PDBTitle:</b> structure of mrna export factors
33	<a href="#">c6iroL_</a>	Alignment	not modelled	18.6	16	<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
34	<a href="#">d1k3ea_</a>	Alignment	not modelled	18.4	10	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> Type III secretory system chaperone-like <b>Family:</b> Type III secretory system chaperone
35	<a href="#">d2j0sa2</a>	Alignment	not modelled	16.5	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
36	<a href="#">c5qi4A_</a>	Alignment	not modelled	15.4	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dead; <b>PDBTitle:</b> dead-box rna helicase
37	<a href="#">c4q47A_</a>	Alignment	not modelled	15.1	15	<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
38	<a href="#">c1c4oA_</a>	Alignment	not modelled	14.9	20	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna nucleotide excision repair enzyme uvrb; <b>PDBTitle:</b> crystal structure of the dna nucleotide excision repair enzyme uvrb2 from thermus thermophilus
39	<a href="#">c6r77B_</a>	Alignment	not modelled	14.3	8	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> proline racemase; <b>PDBTitle:</b> crystal structure of trans-3-hydroxy-l-proline dehydratase in complex2 with substrate - closed conformation
40	<a href="#">c5gn1D_</a>	Alignment	not modelled	13.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent helicase fun30; <b>PDBTitle:</b> crystal structure of the c-terminal part of fun30 atpase domain
41	<a href="#">c5dtuA_</a>	Alignment	not modelled	13.3	4	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prp28; <b>PDBTitle:</b> crystal structure of the rna-helicase prp28 from chaetomium2 thermophilum bound to adp
42	<a href="#">c1s2mA_</a>	Alignment	not modelled	13.2	7	<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="#">c2db3D_</a>	Alignment	not modelled	13.1	7	<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
44	<a href="#">c4ct4B_</a>	Alignment	not modelled	13.0	4	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx6; <b>PDBTitle:</b> cnot1 mif4g domain - ddx6 complex
45	<a href="#">d1ydua1</a>	Alignment	not modelled	12.6	10	<b>Fold:</b> At5g01610-like <b>Superfamily:</b> At5g01610-like <b>Family:</b> At5g01610-like
46	<a href="#">c4nhoA_</a>	Alignment	not modelled	12.6	3	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx23; <b>PDBTitle:</b> structure of the spliceosomal dead-box protein prp28
47	<a href="#">c2xsgB_</a>	Alignment	not modelled	12.3	40	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ccman5; <b>PDBTitle:</b> structure of the gh92 family glycosyl hydrolase ccman5
48	<a href="#">c4cdgA_</a>	Alignment	not modelled	11.8	13	<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
49	<a href="#">c3fhtA_</a>	Alignment	not modelled	11.6	12	<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
50	<a href="#">c5ve9C_</a>	Alignment	not modelled	11.4	20	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> microtubule-actin cross-linking factor 1, isoforms 1/2/3/5; <b>PDBTitle:</b> structure of hacf7 ef1-ef2-gar domains
51	<a href="#">c5lstA_</a>	Alignment	not modelled	11.1	12	<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.
52	<a href="#">c6em3D_</a>	Alignment	not modelled	10.9	15	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent rna helicase has1; <b>PDBTitle:</b> state a architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
53	<a href="#">c1hv8B_</a>	Alignment	not modelled	10.8	7	<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
						<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutative alpha-1.2-mannosidase:

54	<a href="#">c6f92B_</a>	Alignment	not modelled	10.7	30	<b>PDBTitle:</b> structure of the family gh92 alpha-mannosidase bt3965 from bacteroides2 thetaiotaomicron in complex with mannoimidazole (mani)
55	<a href="#">c6iegA_</a>	Alignment	not modelled	10.5	11	<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
56	<a href="#">c5dz8A_</a>	Alignment	not modelled	10.2	35	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> bspa (bspa_v); <b>PDBTitle:</b> streptococcus agalactiae agi/ii polypeptide bspa variable (v) domain
57	<a href="#">c1xtkA_</a>	Alignment	not modelled	10.0	9	<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
58	<a href="#">c3dnfB_</a>	Alignment	not modelled	9.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
59	<a href="#">c6fmIG_</a>	Alignment	not modelled	9.4	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> ino80; <b>PDBTitle:</b> cryoem structure ino80core nucleosome complex
60	<a href="#">c3eiqD_</a>	Alignment	not modelled	8.6	11	<b>PDB header:</b> hydrolase/antitumor protein <b>Chain:</b> D: <b>PDB Molecule:</b> eukaryotic initiation factor 4a-i; <b>PDBTitle:</b> crystal structure of pdcd4-eif4a
61	<a href="#">d1tf5a4</a>	Alignment	not modelled	8.3	9	<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
62	<a href="#">c4n7bA_</a>	Alignment	not modelled	8.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lytb; <b>PDBTitle:</b> structure of the e-1-hydroxy-2-methyl-but-2-enyl-4-diphosphate2 reductase from plasmodium falciparum
63	<a href="#">c4xqkB_</a>	Alignment	not modelled	8.0	11	<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
64	<a href="#">c2fwrA_</a>	Alignment	not modelled	7.8	10	<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
65	<a href="#">c1ikqA_</a>	Alignment	not modelled	7.8	43	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> exotoxin a; <b>PDBTitle:</b> pseudomonas aeruginosa exotoxin a, wild type
66	<a href="#">c2ww1B_</a>	Alignment	not modelled	7.7	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-1,2-mannosidase; <b>PDBTitle:</b> structure of the family gh92 inverting mannosidase bt39902 from bacteroides thetaiotaomicron vpi-5482 in complex with3 thiomannobioside
67	<a href="#">c4a8jA_</a>	Alignment	not modelled	7.5	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> elongator complex protein 4; <b>PDBTitle:</b> crystal structure of the elongator subcomplex elp456
68	<a href="#">c2azpA_</a>	Alignment	not modelled	7.5	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa1268; <b>PDBTitle:</b> crystal structure of pa1268 solved by sulfur sad
69	<a href="#">c2hxyC_</a>	Alignment	not modelled	7.4	16	<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
70	<a href="#">c6f90A_</a>	Alignment	not modelled	7.3	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,2-mannosidase, putative; <b>PDBTitle:</b> structure of the family gh92 alpha-mannosidase bt3130 from bacteroides2 thetaiotaomicron in complex with mannoimidazole (mani)
71	<a href="#">c4kngF_</a>	Alignment	not modelled	7.0	31	<b>PDB header:</b> signaling protein, membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf43; <b>PDBTitle:</b> crystal structure of human lgr5-rspo1-rnf43
72	<a href="#">d1gm5a4</a>	Alignment	not modelled	7.0	4	<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="#">c2vsxA_</a>	Alignment	not modelled	7.0	10	<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="#">d1jx4a1</a>	Alignment	not modelled	6.9	37	<b>Fold:</b> Lesion bypass DNA polymerase (Y-family), little finger domain <b>Superfamily:</b> Lesion bypass DNA polymerase (Y-family), little finger domain <b>Family:</b> Lesion bypass DNA polymerase (Y-family), little finger domain
75	<a href="#">c2wvyA_</a>	Alignment	not modelled	6.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,2-mannosidase; <b>PDBTitle:</b> structure of the family gh92 inverting mannosidase bt21992 from bacteroides thetaiotaomicron vpi-5482
76	<a href="#">c3ke8A_</a>	Alignment	not modelled	6.8	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> crystal structure of isph:hmbpp-complex
77	<a href="#">c3f13A_</a>	Alignment	not modelled	6.8	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nudix hydrolase family member; <b>PDBTitle:</b> crystal structure of putative nudix hydrolase family member from2 chromobacterium violaceum
78	<a href="#">c3ewsA_</a>	Alignment	not modelled	6.7	12	<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
79	<a href="#">c4I92A_</a>	Alignment	not modelled	6.7	57	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor binding protein; <b>PDBTitle:</b> structure of the rbp from lactococcal phage 1358 in

						complex with 22 glcna molecules
80	<a href="#">d1wp9a2</a>	Alignment	not modelled	6.5	9	<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="#">c3urkA</a>	Alignment	not modelled	6.4	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> isph in complex with propynyl diphosphate (1061)
82	<a href="#">c3oiyB</a>	Alignment	not modelled	6.0	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
83	<a href="#">c6c0fp</a>	Alignment	not modelled	5.8	13	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l17-a; <b>PDBTitle:</b> yeast nucleolar pre-60s ribosomal subunit (state 2)
84	<a href="#">c2oo4B</a>	Alignment	not modelled	5.7	21	<b>PDB header:</b> cell cycle,signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> neurogenic locus notch homolog protein 2; <b>PDBTitle:</b> structure of Inr-hd (negative regulatory region) from human notch 2
85	<a href="#">c3epuB</a>	Alignment	not modelled	5.5	15	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> stm2138 virulence chaperone; <b>PDBTitle:</b> crystal structure of stm2138, a novel virulence chaperone in2 salmonella
86	<a href="#">d2g2ja1</a>	Alignment	not modelled	5.4	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
87	<a href="#">c2xvsA</a>	Alignment	not modelled	5.3	25	<b>PDB header:</b> antitumor protein <b>Chain:</b> A: <b>PDB Molecule:</b> tetratricopeptide repeat protein 5; <b>PDBTitle:</b> crystal structure of human ttc5 (strap) c-terminal ob2 domain
88	<a href="#">c5v9xA</a>	Alignment	not modelled	5.2	13	<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
89	<a href="#">c5yvuuA</a>	Alignment	not modelled	5.2	19	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structures of unlinked full length ns3 from dengue virus2 provide insights into dynamics of protease domain
90	<a href="#">c3mx7A</a>	Alignment	not modelled	5.1	20	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> fas apoptotic inhibitory molecule 1; <b>PDBTitle:</b> crystal structure analysis of human faim-ntd