
















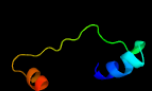

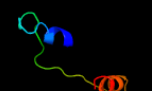

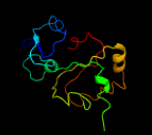
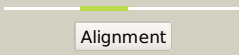
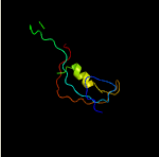
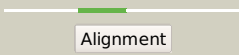
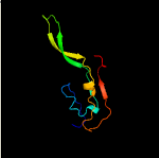
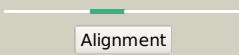
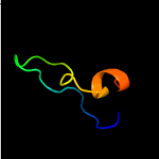
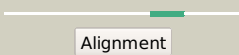

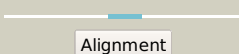
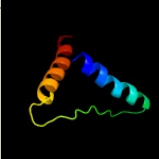
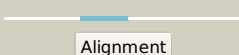
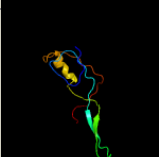
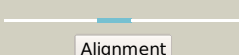
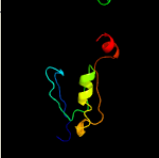

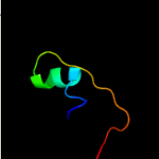
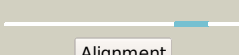


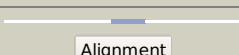
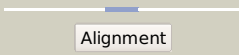
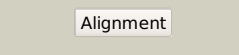
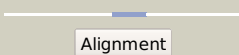

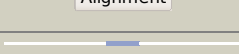



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2529_(-)_2852885_2854276
Date	Wed Aug 7 12:50:16 BST 2019
Unique Job ID	852e58d8b3d58fbf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1j23a_</a>	 Alignment		99.9	29	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> XPF/Rad1/Mus81 nuclease
2	<a href="#">d2bgwa2</a>	 Alignment		99.9	20	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> XPF/Rad1/Mus81 nuclease
3	<a href="#">c2bhnD_</a>	 Alignment		99.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> xpf endonuclease; <b>PDBTitle:</b> xpf from aeropyrum pernix
4	<a href="#">c4bxoA_</a>	 Alignment		99.8	24	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> fanconi anemia group m protein; <b>PDBTitle:</b> architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
5	<a href="#">c2ziuA_</a>	 Alignment		99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mus81 protein; <b>PDBTitle:</b> crystal structure of the mus81-eme1 complex
6	<a href="#">c2zixA_</a>	 Alignment		99.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crossover junction endonuclease mus81; <b>PDBTitle:</b> crystal structure of the mus81-eme1 complex
7	<a href="#">c4bxoB_</a>	 Alignment		99.8	15	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> fanconi anemia-associated protein of 24 kda; <b>PDBTitle:</b> architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
8	<a href="#">c2kngA_</a>	 Alignment		98.1	39	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein lsr2; <b>PDBTitle:</b> solution structure of c-domain of lsr2
9	<a href="#">d1wp9a2</a>	 Alignment		96.5	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
10	<a href="#">c1wp9D_</a>	 Alignment		95.8	21	<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
11	<a href="#">c2zixB_</a>	 Alignment		94.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> crossover junction endonuclease eme1; <b>PDBTitle:</b> crystal structure of the mus81-eme1 complex

12	<a href="#">c1a1vA</a>	 Alignment		66.0	20	<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
13	<a href="#">d8ohma2</a>	 Alignment		53.6	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
14	<a href="#">d1zaka2</a>	 Alignment		48.0	23	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Microbial and mitochondrial ADK, insert "zinc finger" domain <b>Family:</b> Microbial and mitochondrial ADK, insert "zinc finger" domain
15	<a href="#">c5vfkA</a>	 Alignment		45.0	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of an archaeal duf61 family protein sso0941
16	<a href="#">c4gl2A</a>	 Alignment		38.4	28	<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
17	<a href="#">d1a1va2</a>	 Alignment		37.4	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
18	<a href="#">c5n8zA</a>	 Alignment		34.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg9323, isoform a; <b>PDBTitle:</b> crystal structure of drosophila dhx36 helicase in complex with2 ctctccctt
19	<a href="#">c2f55C</a>	 Alignment		33.7	30	<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 with the same2 strand of dna
20	<a href="#">d2hg7a1</a>	 Alignment		32.9	27	<b>Fold:</b> gpW/XkdW-like <b>Superfamily:</b> XkdW-like <b>Family:</b> XkdW-like
21	<a href="#">c2hg7A</a>	 Alignment	not modelled	32.9	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phage-like element pbsx protein xkdw; <b>PDBTitle:</b> solution nmr structure of phage-like element pbsx protein2 xkdw, northeast structural genomics consortium target sr355
22	<a href="#">c5uc0B</a>	 Alignment	not modelled	29.7	35	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein cog5400; <b>PDBTitle:</b> crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus
23	<a href="#">c5vheA</a>	 Alignment	not modelled	28.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deah (asp-glu-ala-his) box polypeptide 36; <b>PDBTitle:</b> dhx36 in complex with the c-myc g-quadruplex
24	<a href="#">c4cbmA</a>	 Alignment	not modelled	24.8	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease ns3; <b>PDBTitle:</b> pestivirus ns3 helicase
25	<a href="#">c1ymfA</a>	 Alignment	not modelled	24.6	11	<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
26	<a href="#">c3gzub</a>	 Alignment	not modelled	24.6	41	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> inner capsid protein vp2; <b>PDBTitle:</b> vp7 reconstituted rotavirus dlp
27	<a href="#">c3crw1</a>	 Alignment	not modelled	23.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> 1: <b>PDB Molecule:</b> xpd/rad3 related dna helicase; <b>PDBTitle:</b> xpd_apo
28	<a href="#">c1cu1B</a>	 Alignment	not modelled	22.4	26	<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 c virus

29	<a href="#">d2d9qb1</a>	Alignment	not modelled	21.9	39	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
30	<a href="#">c5lj5Q_</a>	Alignment	not modelled	21.8	23	<b>PDB header:</b> splicing <b>Chain:</b> Q: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna helicase prp16; <b>PDBTitle:</b> overall structure of the yeast spliceosome immediately after2 branching.
31	<a href="#">c4ljyA_</a>	Alignment	not modelled	21.0	19	<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
32	<a href="#">d1jr6a_</a>	Alignment	not modelled	20.6	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
33	<a href="#">c4b6eB_</a>	Alignment	not modelled	20.1	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> non-structural protein 4a, serine protease ns3; <b>PDBTitle:</b> discovery of an allosteric mechanism for the regulation of2 hcv ns3 protein function
34	<a href="#">c4d0uD_</a>	Alignment	not modelled	19.7	50	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> fiber protein; <b>PDBTitle:</b> crystal structure of the fiber head domain of the adenovirus snake2 adenovirus 1, selenomethionine-derivative
35	<a href="#">c1c4oA_</a>	Alignment	not modelled	19.2	22	<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
36	<a href="#">c5aorA_</a>	Alignment	not modelled	19.0	31	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> dosage compensation regulator; <b>PDBTitle:</b> structure of mle rna adp alf4 complex
37	<a href="#">c6icZ_</a>	Alignment	not modelled	18.3	24	<b>PDB header:</b> splicing <b>Chain:</b> Y: <b>PDB Molecule:</b> atp-dependent rna helicase dhx8; <b>PDBTitle:</b> cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
38	<a href="#">d2fwr1</a>	Alignment	not modelled	17.3	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
39	<a href="#">c5z58x_</a>	Alignment	not modelled	16.7	29	<b>PDB header:</b> splicing <b>Chain:</b> X: <b>PDB Molecule:</b> smad nuclear-interacting protein 1; <b>PDBTitle:</b> cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
40	<a href="#">c3kz4A_</a>	Alignment	not modelled	16.4	40	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> inner capsid protein vp2; <b>PDBTitle:</b> crystal structure of the rotavirus double layered particle
41	<a href="#">c5ivwV_</a>	Alignment	not modelled	16.3	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
42	<a href="#">c6cd2B_</a>	Alignment	not modelled	15.7	32	<b>PDB header:</b> membrane protein/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> papgii adhesin protein; <b>PDBTitle:</b> crystal structure of the papc usher bound to the chaperone-adhesin2 papd-papg
43	<a href="#">c5jb2A_</a>	Alignment	not modelled	15.3	17	<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.
44	<a href="#">d1wfxa_</a>	Alignment	not modelled	14.5	18	<b>Fold:</b> ADP-ribosylation <b>Superfamily:</b> ADP-ribosylation <b>Family:</b> Tpt1/KptA
45	<a href="#">c2k9iB_</a>	Alignment	not modelled	14.0	42	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein orf56; <b>PDBTitle:</b> nmr structure of plasmid copy control protein orf56 from sulfobolus2 islandicus
46	<a href="#">d1e0ta1</a>	Alignment	not modelled	13.7	24	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> Pyruvate kinase beta-barrel domain
47	<a href="#">c6h57A_</a>	Alignment	not modelled	13.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase dhr1; <b>PDBTitle:</b> crystal structure of s. cerevisiae deah-box rna helicase dhr1,2 essential for small ribosomal subunit biogenesis
48	<a href="#">c3crnA_</a>	Alignment	not modelled	12.8	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver domain protein, chey-like; <b>PDBTitle:</b> crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
49	<a href="#">c2i4iA_</a>	Alignment	not modelled	12.6	14	<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
50	<a href="#">c6ogyK_</a>	Alignment	not modelled	12.3	35	<b>PDB header:</b> viral protein/transferase/rna <b>Chain:</b> K: <b>PDB Molecule:</b> inner capsid protein vp2; <b>PDBTitle:</b> in situ structure of rotavirus rna-dependent rna polymerase at duplex-2 open state
51	<a href="#">d1qbea_</a>	Alignment	not modelled	12.1	33	<b>Fold:</b> RNA bacteriophage capsid protein <b>Superfamily:</b> RNA bacteriophage capsid protein <b>Family:</b> RNA bacteriophage capsid protein
52	<a href="#">c5xdrA_</a>	Alignment	not modelled	12.1	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna helicase dhx15; <b>PDBTitle:</b> crystal structure of human deah-box rna helicase dhx15 in complex with2 adp
53	<a href="#">d1t0fa2</a>	Alignment	not modelled	11.9	44	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> TnsA endonuclease, N-terminal domain

54	<a href="#">c5wsge</a>	Alignment	not modelled	11.9	29	<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
55	<a href="#">c1xvr3</a>	Alignment	not modelled	11.7	23	<b>PDB header:</b> virus <b>Chain:</b> 3: <b>PDB Molecule:</b> genome polyprotein, coat protein vp3; <b>PDB Fragment:</b> residues 620-630 <b>PDBTitle:</b> poliovirus 135s cell entry intermediate
56	<a href="#">c2d7dA</a>	Alignment	not modelled	11.7	28	<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
57	<a href="#">c2hjb</a>	Alignment	not modelled	11.3	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
58	<a href="#">c5mq0V</a>	Alignment	not modelled	11.3	29	<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
59	<a href="#">c6fa5A</a>	Alignment	not modelled	11.2	29	<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
60	<a href="#">d1hjra</a>	Alignment	not modelled	11.1	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> RuvC resolvase
61	<a href="#">d1c4oa2</a>	Alignment	not modelled	10.8	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
62	<a href="#">c3zueB</a>	Alignment	not modelled	10.7	40	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> capsid structural protein vp60; <b>PDBTitle:</b> rabbit hemorrhagic disease virus (rhdv)capsid protein
63	<a href="#">d2g50a1</a>	Alignment	not modelled	10.5	24	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> Pyruvate kinase beta-barrel domain
64	<a href="#">c4db4A</a>	Alignment	not modelled	10.3	33	<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
65	<a href="#">c4cbhD</a>	Alignment	not modelled	10.3	4	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> serine protease ns3; <b>PDBTitle:</b> pestivirus ns3 helicase
66	<a href="#">d2a1ia1</a>	Alignment	not modelled	10.2	16	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> XPF/Rad1/Mus81 nuclease
67	<a href="#">c3ltgA</a>	Alignment	not modelled	10.1	17	<b>PDB header:</b> transferase/transferase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> epidermal growth factor receptor; <b>PDBTitle:</b> crystal structure of the drosophila epidermal growth factor receptor2 ectodomain complexed with a low affinity spitz mutant
68	<a href="#">c3kx2A</a>	Alignment	not modelled	10.1	35	<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
69	<a href="#">c5jcfB</a>	Alignment	not modelled	10.1	23	<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).
70	<a href="#">d1pkma1</a>	Alignment	not modelled	10.0	24	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> Pyruvate kinase beta-barrel domain
71	<a href="#">d1r1a3</a>	Alignment	not modelled	10.0	26	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
72	<a href="#">c3fcgB</a>	Alignment	not modelled	10.0	19	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> f1 capsule-anchoring protein; <b>PDBTitle:</b> crystal structure analysis of the middle domain of the2 caf1a usher
73	<a href="#">c6i3oA</a>	Alignment	not modelled	9.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative pre-mrna splicing factor; <b>PDBTitle:</b> crystal structure of deah-box atpase prp22
74	<a href="#">c6hegA</a>	Alignment	not modelled	9.7	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase hrpb; <b>PDBTitle:</b> crystal structure of escherichia coli deah/rha helicase hrpb
75	<a href="#">c2k4zA</a>	Alignment	not modelled	9.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dsrr; <b>PDBTitle:</b> solution nmr structure of allochromatium vinosum dsrr:2 northeast structural genomics consortium target op5
76	<a href="#">c6dlhA</a>	Alignment	not modelled	9.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,4-endofucoidanase; <b>PDBTitle:</b> endo-fucoidan hydrolase mffcna4 from glycoside hydrolase family 107
77	<a href="#">d1ei5a1</a>	Alignment	not modelled	9.3	39	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> D-aminopeptidase, middle and C-terminal domains <b>Family:</b> D-aminopeptidase, middle and C-terminal domains
78	<a href="#">c1s2mA</a>	Alignment	not modelled	9.2	14	<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
79	<a href="#">d1nwba</a>	Alignment	not modelled	9.1	17	<b>Fold:</b> HesB-like domain <b>Superfamily:</b> HesB-like domain

						<b>Family:</b> HesB-like domain
80	<a href="#">c5ylzW_</a>	Alignment	not modelled	9.0	29	<b>PDB header:</b> splicing <b>Chain:</b> W: <b>PDB Molecule:</b> pre-mrna-splicing factor atp-dependent rna helicase prp22; <b>PDBTitle:</b> cryo-em structure of the post-catalytic spliceosome from saccharomyces2 cerevisiae at 3.6 angstrom
81	<a href="#">c4kr7A_</a>	Alignment	not modelled	9.0	23	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna sulfurtransferase; <b>PDBTitle:</b> crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
82	<a href="#">c5x7fA_</a>	Alignment	not modelled	8.9	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative o-methyltransferase rv1220c; <b>PDBTitle:</b> structure of a o-methyltransferase from mycobacterium tuberculosis at2 2.0 resolution
83	<a href="#">c5supB_</a>	Alignment	not modelled	8.9	24	<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
84	<a href="#">d1d4m3_</a>	Alignment	not modelled	8.8	23	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
85	<a href="#">c2b7fD_</a>	Alignment	not modelled	8.7	47	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> htlv protease; <b>PDBTitle:</b> crystal structure of human t-cell leukemia virus protease, a novel2 target for anti-cancer design
86	<a href="#">d2j0sa2</a>	Alignment	not modelled	8.7	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
87	<a href="#">c5gi4A_</a>	Alignment	not modelled	8.7	33	<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
88	<a href="#">c2apnA_</a>	Alignment	not modelled	8.7	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein hi1723; <b>PDBTitle:</b> hi1723 solution structure
89	<a href="#">c2p64B_</a>	Alignment	not modelled	8.4	8	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> f-box/wd repeat protein 1a; <b>PDBTitle:</b> d domain of b-trcp
90	<a href="#">c1f1zB_</a>	Alignment	not modelled	8.4	44	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> tnsa endonuclease; <b>PDBTitle:</b> tnsa, a catalytic component of the tn7 transposition system
91	<a href="#">c2db3D_</a>	Alignment	not modelled	8.2	20	<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
92	<a href="#">d1b8qa_</a>	Alignment	not modelled	8.2	13	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
93	<a href="#">c3js3C_</a>	Alignment	not modelled	8.1	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
94	<a href="#">c4pxaA_</a>	Alignment	not modelled	8.0	12	<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
95	<a href="#">c3c0fB_</a>	Alignment	not modelled	7.9	24	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein af_1514; <b>PDBTitle:</b> crystal structure of a novel non-pfam protein af1514 from archeoglobus2 fulgidus dsm 4304 solved by s-sad using a cr x-ray source
96	<a href="#">c4ct4B_</a>	Alignment	not modelled	7.9	19	<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
97	<a href="#">c3rxyA_</a>	Alignment	not modelled	7.8	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nif3 protein; <b>PDBTitle:</b> crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
98	<a href="#">c4nhoA_</a>	Alignment	not modelled	7.8	23	<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
99	<a href="#">d1gqna_</a>	Alignment	not modelled	7.8	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase