
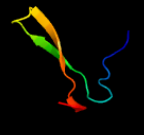









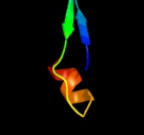

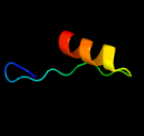





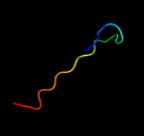

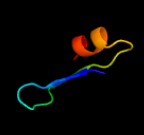


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1813c (-) _2055688_2056119
Date	Fri Aug 2 13:30:42 BST 2019
Unique Job ID	1182017a7b41df9d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6j69A_</a>	 Alignment		66.4	23	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> protein kibra; <b>PDBTitle:</b> structure of kibra and dendrin complex
2	<a href="#">d1x49a1</a>	 Alignment		53.3	15	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
3	<a href="#">c2kxhA_</a>	 Alignment		45.6	29	<b>PDB header:</b> gene regulation,nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease 3; <b>PDBTitle:</b> drosha double-stranded rna binding motif
4	<a href="#">d1qu6a2</a>	 Alignment		43.9	27	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
5	<a href="#">d1o0wa2</a>	 Alignment		42.5	31	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
6	<a href="#">c3adjA_</a>	 Alignment		41.0	35	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> f21m12.9 protein; <b>PDBTitle:</b> structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
7	<a href="#">c2n3hA_</a>	 Alignment		40.7	27	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> double-stranded rna-binding protein 4; <b>PDBTitle:</b> solution structure of drb4 dsrbd2 (viz. drb4(81-151))
8	<a href="#">d1t4na_</a>	 Alignment		40.0	19	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
9	<a href="#">d1x47a1</a>	 Alignment		39.7	30	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
10	<a href="#">c2aivA_</a>	 Alignment		36.9	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> fragment of nucleoporin nup116/nsp116; <b>PDBTitle:</b> multiple conformations in the ligand-binding site of the yeast nuclear2 pore targeting domain of nup116p
11	<a href="#">d1x48a1</a>	 Alignment		35.8	23	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)

12	<a href="#">d1t4lb_</a>	Alignment		35.3	19	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
13	<a href="#">c2n3gA_</a>	Alignment		35.3	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> double-stranded rna-binding protein 4; <b>PDBTitle:</b> solution structure of drb4 dsrbd1 (viz. drb4(1-72))
14	<a href="#">c1t4oA_</a>	Alignment		33.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease iii; <b>PDBTitle:</b> crystal structure of rnt1p dsrbd
15	<a href="#">d1t4oa_</a>	Alignment		33.5	19	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
16	<a href="#">d1qu6a1</a>	Alignment		32.7	23	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
17	<a href="#">c2mdrA_</a>	Alignment		28.0	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> double-stranded rna-specific adenosine deaminase; <b>PDBTitle:</b> solution structure of the third double-stranded rna-binding domain2 (dsrbd3) of human adenosine-deaminase adar1
18	<a href="#">c2q5xA_</a>	Alignment		27.7	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear pore complex protein nup98; <b>PDBTitle:</b> crystal structure of the c-terminal domain of hnup98
19	<a href="#">c3adiC_</a>	Alignment		26.5	15	<b>PDB header:</b> gene regulation/rna <b>Chain:</b> C: <b>PDB Molecule:</b> f21m12.9 protein; <b>PDBTitle:</b> structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
20	<a href="#">d2nuga2</a>	Alignment		25.7	23	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
21	<a href="#">c3kepA_</a>	Alignment	not modelled	24.0	24	<b>PDB header:</b> protein transport, rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoporin nup145; <b>PDBTitle:</b> crystal structure of the autoproteolytic domain from the nuclear pore2 complex component nup145 from saccharomyces cerevisiae
22	<a href="#">c1h2iG_</a>	Alignment	not modelled	23.3	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair protein rad52 homolog; <b>PDBTitle:</b> human rad52 protein, n-terminal domain
23	<a href="#">d1z1ba1</a>	Alignment	not modelled	22.8	23	<b>Fold:</b> DNA-binding domain <b>Superfamily:</b> DNA-binding domain <b>Family:</b> lambda integrase N-terminal domain
24	<a href="#">c1kjkA_</a>	Alignment	not modelled	22.8	23	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> solution structure of the lambda integrase amino-terminal2 domain
25	<a href="#">c5yq7H_</a>	Alignment	not modelled	22.4	27	<b>PDB header:</b> photosynthesis <b>Chain:</b> H: <b>PDB Molecule:</b> alpha subunit of light-harvesting 1; <b>PDBTitle:</b> cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
26	<a href="#">c5n1tM_</a>	Alignment	not modelled	19.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> copc; <b>PDBTitle:</b> crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
27	<a href="#">c3adiA_</a>	Alignment	not modelled	19.1	14	<b>PDB header:</b> gene regulation/rna <b>Chain:</b> A: <b>PDB Molecule:</b> risc-loading complex subunit tarbp2; <b>PDBTitle:</b> structure of trbp2 and its molecule implications for mirna processing
28	<a href="#">c4ce4h_</a>	Alignment	not modelled	18.8	21	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome

29	<a href="#">c1vw45_</a>	Alignment	not modelled	17.7	18	<b>PDB header:</b> ribosome <b>Chain:</b> 5; <b>PDB Molecule:</b> 54s ribosomal protein l3, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
30	<a href="#">c4pv3D_</a>	Alignment	not modelled	17.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> l-asparaginase beta subunit; <b>PDBTitle:</b> crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with na+ cations
31	<a href="#">d1whna_</a>	Alignment	not modelled	16.7	23	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
32	<a href="#">d1kn0a_</a>	Alignment	not modelled	15.7	19	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> The homologous-pairing domain of Rad52 recombinase
33	<a href="#">c2l2nA_</a>	Alignment	not modelled	15.6	19	<b>PDB header:</b> rna binding protein, plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> hyponastic leave 1; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for the first2 dsrbd of protein hyl1
34	<a href="#">c2lrsA_</a>	Alignment	not modelled	15.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endoribonuclease dicer homolog 1; <b>PDBTitle:</b> the second dsrbd domain from a. thaliana dicer-like 1
35	<a href="#">d2cpna1</a>	Alignment	not modelled	15.0	14	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
36	<a href="#">c2zalD_</a>	Alignment	not modelled	14.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
37	<a href="#">c1ymzA_</a>	Alignment	not modelled	13.9	24	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> cc45; <b>PDBTitle:</b> cc45, an artificial ww domain designed using statistical2 coupling analysis
38	<a href="#">c2n3fA_</a>	Alignment	not modelled	13.2	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> double-stranded rna-binding protein 4; <b>PDBTitle:</b> solution structure of both dsrbds of drb4 along with linker (viz.2 drb4(1-153))
39	<a href="#">d1uila_</a>	Alignment	not modelled	13.1	13	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
40	<a href="#">c2bzvA_</a>	Alignment	not modelled	12.7	18	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> fiber protein 2; <b>PDBTitle:</b> human enteric adenovirus serotype 41 short fiber head (ph8)
41	<a href="#">d1stua_</a>	Alignment	not modelled	12.3	19	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
42	<a href="#">c4v1ah_</a>	Alignment	not modelled	11.8	21	<b>PDB header:</b> ribosome <b>Chain:</b> H; <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
43	<a href="#">d1kaca_</a>	Alignment	not modelled	11.8	18	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Adenovirus fiber protein "knob" domain
44	<a href="#">c3nf5A_</a>	Alignment	not modelled	11.8	25	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> nucleoporin nup116; <b>PDBTitle:</b> crystal structure of the c-terminal domain of nuclear pore complex2 component nup116 from candida glabrata
45	<a href="#">c4oogC_</a>	Alignment	not modelled	11.7	17	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> C; <b>PDB Molecule:</b> ribonuclease 3; <b>PDBTitle:</b> crystal structure of yeast rnase iii (rnt1p) complexed with the2 product of dsrna processing
46	<a href="#">c2gezF_</a>	Alignment	not modelled	11.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> l-asparaginase beta subunit; <b>PDBTitle:</b> crystal structure of potassium-independent plant asparaginase
47	<a href="#">c6fjqA_</a>	Alignment	not modelled	11.1	32	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> fiber; <b>PDBTitle:</b> adenovirus species 48, fiber knob protein
48	<a href="#">c2zalB_</a>	Alignment	not modelled	11.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
49	<a href="#">d1qhva_</a>	Alignment	not modelled	11.0	32	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Adenovirus fiber protein "knob" domain
50	<a href="#">d1knba_</a>	Alignment	not modelled	10.9	27	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Adenovirus fiber protein "knob" domain
51	<a href="#">d1dj2a_</a>	Alignment	not modelled	10.9	15	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
52	<a href="#">c4xl8B_</a>	Alignment	not modelled	10.9	23	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> fiber-1; <b>PDBTitle:</b> crystal structure of human adenovirus 52 short fiber knob in complex2 with 2-o-methyl-5-n-acetylneuraminic acid
53	<a href="#">c6fjoA_</a>	Alignment	not modelled	10.7	27	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> fiber; <b>PDBTitle:</b> adenovirus species 26 knob protein, very high resolution
54	<a href="#">c1t3mD_</a>	Alignment	not modelled	10.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
55	<a href="#">c1jn9B_</a>	Alignment	not modelled	10.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> structure of putative asparaginase encoded by

						escherichia coli ybik2 gene
56	<a href="#">c1t3mB_</a>	Alignment	not modelled	10.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
57	<a href="#">c5zz9E_</a>	Alignment	not modelled	10.5	44	<b>PDB header:</b> protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> peptide from drebrin; <b>PDBTitle:</b> crystal structure of homer2 evh1/drebrin ppxxf complex
58	<a href="#">d2j12a1</a>	Alignment	not modelled	10.0	32	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Adenovirus fiber protein "knob" domain
59	<a href="#">d2q8oa1</a>	Alignment	not modelled	9.8	13	<b>Fold:</b> TNF-like <b>Superfamily:</b> TNF-like <b>Family:</b> TNF-like
60	<a href="#">c2ltsA_</a>	Alignment	not modelled	9.7	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein rde-4; <b>PDBTitle:</b> solution structure of rde-4(150-235)
61	<a href="#">c1jn9D_</a>	Alignment	not modelled	9.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> structure of putative asparaginase encoded by escherichia coli ybik2 gene
62	<a href="#">c1k2xB_</a>	Alignment	not modelled	9.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
63	<a href="#">c1k2xD_</a>	Alignment	not modelled	9.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
64	<a href="#">d1de3a_</a>	Alignment	not modelled	9.1	17	<b>Fold:</b> Microbial ribonucleases <b>Superfamily:</b> Microbial ribonucleases <b>Family:</b> Ribotoxin
65	<a href="#">c4kt3B_</a>	Alignment	not modelled	9.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> structure of a type vi secretion system effector-immunity complex from2 pseudomonas protegens
66	<a href="#">d1uhza_</a>	Alignment	not modelled	8.8	25	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
67	<a href="#">c3llhB_</a>	Alignment	not modelled	8.6	27	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> risc-loading complex subunit tarbp2; <b>PDBTitle:</b> crystal structure of the first dsrbd of tar rna-binding protein 2
68	<a href="#">c6htuA_</a>	Alignment	not modelled	8.5	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> double-stranded rna-binding protein staufen homolog 1; <b>PDBTitle:</b> structure of hstau1 dsrbd3-4 in complex with arf1 rna
69	<a href="#">c1qiuC_</a>	Alignment	not modelled	8.2	32	<b>PDB header:</b> fibre protein <b>Chain:</b> C: <b>PDB Molecule:</b> adenovirus fibre; <b>PDBTitle:</b> a triple beta-spiral in the adenovirus fibre shaft reveals a new2 structural motif for biological fibres
70	<a href="#">d1bf5a3</a>	Alignment	not modelled	8.2	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
71	<a href="#">c5icuA_</a>	Alignment	not modelled	7.9	4	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> copc; <b>PDBTitle:</b> the crystal structure of copc from methylosinus trichosporium ob3b
72	<a href="#">c1p4vA_</a>	Alignment	not modelled	7.8	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n(4)-(beta-n-acetylglucosaminy)l-l-asparaginase <b>PDBTitle:</b> crystal structure of the glycosylasparaginase precursor2 d151n mutant with glycine
73	<a href="#">c2o7pA_</a>	Alignment	not modelled	7.7	28	<b>PDB header:</b> hydrolase, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribd; <b>PDBTitle:</b> the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
74	<a href="#">c3zpgA_</a>	Alignment	not modelled	7.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribd; <b>PDBTitle:</b> acinetobacter baumannii ribd, form 2
75	<a href="#">c3rv0B_</a>	Alignment	not modelled	7.3	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> k. polysporus dcr1; <b>PDBTitle:</b> crystal structure of k. polysporus dcr1 without the c-terminal dsrbd
76	<a href="#">d2dixa1</a>	Alignment	not modelled	7.3	21	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
77	<a href="#">c5bpwA_</a>	Alignment	not modelled	7.3	12	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> anaphase-promoting complex subunit 4; <b>PDBTitle:</b> atomic-resolution structures of the apc/c subunits apc4 and the apc52 n-terminal domain
78	<a href="#">d2b7ta1</a>	Alignment	not modelled	7.2	31	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
79	<a href="#">c2xr4A_</a>	Alignment	not modelled	7.1	26	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lectin; <b>PDBTitle:</b> c-terminal domain of bc2l-c lectin from burkholderia cenocepacia
80	<a href="#">d2o39a1</a>	Alignment	not modelled	7.0	20	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Adenovirus fiber protein "knob" domain
81	<a href="#">d1ixta_</a>	Alignment	not modelled	6.9	39	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Conotoxin

82	<a href="#">c1xtA_</a>	Alignment	not modelled	6.9	39	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> spasmodic protein tx9a-like protein; <b>PDBTitle:</b> structure of a novel p-superfamily spasmodic conotoxin2 reveals an inhibitory cystine knot motif
83	<a href="#">c4g4fA_</a>	Alignment	not modelled	6.8	10	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor ligand superfamily member 18; <b>PDBTitle:</b> crystal structure of gitrl from bushbaby
84	<a href="#">d1ekza_</a>	Alignment	not modelled	6.8	19	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
85	<a href="#">d2b3za2</a>	Alignment	not modelled	6.8	22	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
86	<a href="#">c2ysbA_</a>	Alignment	not modelled	6.7	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> salvador homolog 1 protein; <b>PDBTitle:</b> solution structure of the first ww domain from the mouse2 salvador homolog 1 protein (sav1)
87	<a href="#">c5npaA_</a>	Alignment	not modelled	6.6	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> loquacious; <b>PDBTitle:</b> solution structure of drosophila melanogaster loquacious dsrbd2
88	<a href="#">c5cwwA_</a>	Alignment	not modelled	6.6	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoporin nup145n; <b>PDBTitle:</b> crystal structure of the chaetomium thermophilum heterotrimeric nup822 ntd-nup159 tail-nup145n apd complex
89	<a href="#">c1vw4d_</a>	Alignment	not modelled	6.6	14	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
90	<a href="#">c2zakB_</a>	Alignment	not modelled	6.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-asparaginase precursor; <b>PDBTitle:</b> orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
91	<a href="#">c3gb8B_</a>	Alignment	not modelled	6.6	31	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> snurportin-1; <b>PDBTitle:</b> crystal structure of crm1/snurportin-1 complex
92	<a href="#">c4gduB_</a>	Alignment	not modelled	6.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> crystal structure of sulfate-bound human l-asparaginase protein
93	<a href="#">c5hoyA_</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> amyloid beta a4 protein; <b>PDBTitle:</b> x-ray crystallographic structure of an a-beta 17_36 beta-hairpin. x-2 ray diffractometer data set. (lvffaedcgsnkcaii(sar)lmv).
94	<a href="#">c5hoxC_</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> amyloid beta a4 protein; <b>PDBTitle:</b> x-ray crystallographic structure of an a-beta 17_36 beta-hairpin.2 synchrotron data set. (lvffaedcgsnkcaii(sar)lmv).
95	<a href="#">c5hoyE_</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> amyloid beta a4 protein; <b>PDBTitle:</b> x-ray crystallographic structure of an a-beta 17_36 beta-hairpin. x-2 ray diffractometer data set. (lvffaedcgsnkcaii(sar)lmv).
96	<a href="#">c5hoxA_</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> amyloid beta a4 protein; <b>PDBTitle:</b> x-ray crystallographic structure of an a-beta 17_36 beta-hairpin.2 synchrotron data set. (lvffaedcgsnkcaii(sar)lmv).
97	<a href="#">c5hoyB_</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> amyloid beta a4 protein; <b>PDBTitle:</b> x-ray crystallographic structure of an a-beta 17_36 beta-hairpin. x-2 ray diffractometer data set. (lvffaedcgsnkcaii(sar)lmv).
98	<a href="#">c5hoyC_</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> amyloid beta a4 protein; <b>PDBTitle:</b> x-ray crystallographic structure of an a-beta 17_36 beta-hairpin. x-2 ray diffractometer data set. (lvffaedcgsnkcaii(sar)lmv).
99	<a href="#">c5hoyD_</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> amyloid beta a4 protein; <b>PDBTitle:</b> x-ray crystallographic structure of an a-beta 17_36 beta-hairpin. x-2 ray diffractometer data set. (lvffaedcgsnkcaii(sar)lmv).