


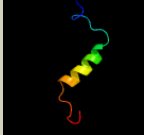
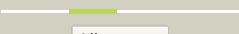
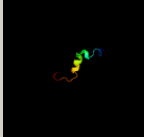

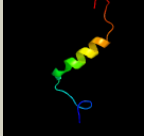

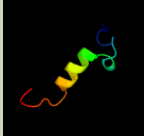
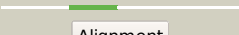
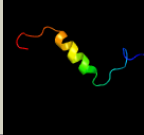

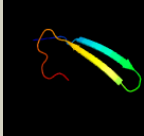


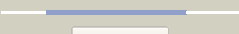




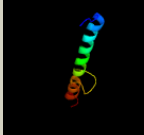


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1724c_(-)_1950639_1951058
Date	Fri Aug 2 13:30:32 BST 2019
Unique Job ID	18f7ddd6def9d01

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3j61G_</a>	 Alignment		78.3	33	<b>PDB header:</b> ribosome <b>Chain:</b> G; <b>PDB Molecule:</b> 60s ribosomal protein l8e; <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
2	<a href="#">c3j39G_</a>	 Alignment		72.3	40	<b>PDB header:</b> ribosome <b>Chain:</b> G; <b>PDB Molecule:</b> 60s ribosomal protein l7a; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
3	<a href="#">c3u5iG_</a>	 Alignment		68.1	33	<b>PDB header:</b> ribosome <b>Chain:</b> G; <b>PDB Molecule:</b> 60s ribosomal protein l8-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome b
4	<a href="#">c3zf7x_</a>	 Alignment		62.1	33	<b>PDB header:</b> ribosome <b>Chain:</b> X; <b>PDB Molecule:</b> 60s ribosomal protein l23a; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
5	<a href="#">c4a1eF_</a>	 Alignment		57.2	33	<b>PDB header:</b> ribosome <b>Chain:</b> F; <b>PDB Molecule:</b> rpl7a; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
6	<a href="#">c3j3bG_</a>	 Alignment		50.7	33	<b>PDB header:</b> ribosome <b>Chain:</b> G; <b>PDB Molecule:</b> 60s ribosomal protein l7a; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
7	<a href="#">d2je8a2</a>	 Alignment		37.2	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> beta-Galactosidase/glucuronidase domain <b>Family:</b> beta-Galactosidase/glucuronidase domain
8	<a href="#">d2dy1a3</a>	 Alignment		26.0	13	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components
9	<a href="#">d1j98a_</a>	 Alignment		24.9	17	<b>Fold:</b> LuxS/MPP-like metallohydrolase <b>Superfamily:</b> LuxS/MPP-like metallohydrolase <b>Family:</b> Autoinducer-2 production protein LuxS
10	<a href="#">c2kglA_</a>	 Alignment		20.3	31	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> mesoderm development candidate 2; <b>PDBTitle:</b> nmr solution structure of mesd
11	<a href="#">d1sknp_</a>	 Alignment		16.5	30	<b>Fold:</b> A DNA-binding domain in eukaryotic transcription factors <b>Superfamily:</b> A DNA-binding domain in eukaryotic transcription factors <b>Family:</b> A DNA-binding domain in eukaryotic transcription factors

12	<a href="#">d1jw2a_</a>	Alignment		15.2	38	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Hemolysin expression modulating protein HHA <b>Family:</b> Hemolysin expression modulating protein HHA
13	<a href="#">d1vcpa_</a>	Alignment		15.1	27	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases
14	<a href="#">d2gy9s1</a>	Alignment		13.7	46	<b>Fold:</b> Ribosomal protein S19 <b>Superfamily:</b> Ribosomal protein S19 <b>Family:</b> Ribosomal protein S19
15	<a href="#">d1vjea_</a>	Alignment		12.3	21	<b>Fold:</b> LuxS/MPP-like metallohydrolase <b>Superfamily:</b> LuxS/MPP-like metallohydrolase <b>Family:</b> Autoinducer-2 production protein LuxS
16	<a href="#">c1bb1A_</a>	Alignment		11.4	42	<b>PDB header:</b> de novo protein design <b>Chain:</b> A: <b>PDB Molecule:</b> designed, thermostable heterotrimeric coiled <b>PDBTitle:</b> crystal structure of a designed, thermostable2 heterotrimeric coiled coil
17	<a href="#">c2lxaA_</a>	Alignment		11.3	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh dehydrogenase i subunit e; <b>PDBTitle:</b> solution structure of hp1264 from helicobacter pylori
18	<a href="#">c4u5tB_</a>	Alignment		10.8	47	<b>PDB header:</b> transcription/transcription inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> vbp leucine zipper; <b>PDBTitle:</b> crystal structure of vbp leucine zipper with bound arylstibonic acid
19	<a href="#">d2gnxa2</a>	Alignment		10.7	67	<b>Fold:</b> Gelsolin-like <b>Superfamily:</b> FLJ32549 C-terminal domain-like <b>Family:</b> FLJ32549 C-terminal domain-like
20	<a href="#">c4a1bB_</a>	Alignment		10.7	67	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> rpl39; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 3.
21	<a href="#">c3okqA_</a>	Alignment	not modelled	10.1	44	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> bud site selection protein 6; <b>PDBTitle:</b> crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
22	<a href="#">c2l42A_</a>	Alignment	not modelled	10.0	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein rap1; <b>PDBTitle:</b> the solution structure of rap1 brct domain from saccharomyces2 cerevisiae
23	<a href="#">d1oeda_</a>	Alignment	not modelled	9.8	15	<b>Fold:</b> Neurotransmitter-gated ion-channel transmembrane pore <b>Superfamily:</b> Neurotransmitter-gated ion-channel transmembrane pore <b>Family:</b> Neurotransmitter-gated ion-channel transmembrane pore
24	<a href="#">c3zf7q_</a>	Alignment	not modelled	9.8	83	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> ribosomal protein l15; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
25	<a href="#">c5xxuP_</a>	Alignment	not modelled	9.7	62	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> ribosomal protein us19; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
26	<a href="#">c2mrlA_</a>	Alignment	not modelled	9.5	53	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bth i2711; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments and nmr structure2 for potential drug target from burkholderia thailandensis e264
27	<a href="#">c5e68A_</a>	Alignment	not modelled	9.4	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> s-ribosylhomocysteine lyase; <b>PDBTitle:</b> high resolution crystal structure of luxs - quorum sensor molecular2 complex from salmonella typhi at 1.58 angstroms
28	<a href="#">d1jeqa1</a>	Alignment	not modelled	9.4	67	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> SAP domain <b>Family:</b> SAP domain

29	<a href="#">d2uubs1</a>	Alignment	not modelled	9.2	62	<b>Fold:</b> Ribosomal protein S19 <b>Superfamily:</b> Ribosomal protein S19 <b>Family:</b> Ribosomal protein S19
30	<a href="#">d3eipa</a>	Alignment	not modelled	9.1	31	<b>Fold:</b> FKBP-like <b>Superfamily:</b> Colicin E3 immunity protein <b>Family:</b> Colicin E3 immunity protein
31	<a href="#">c5xyiP</a>	Alignment	not modelled	9.1	38	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> ribosomal protein s19, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
32	<a href="#">c2xzmS</a>	Alignment	not modelled	9.1	46	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> rps15e; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
33	<a href="#">c2zkr3</a>	Alignment	not modelled	9.1	44	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> 3: <b>PDB Molecule:</b> 60s ribosomal protein l39e; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
34	<a href="#">c3izso</a>	Alignment	not modelled	8.8	67	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein rpl28 (l15p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
35	<a href="#">c2vxaL</a>	Alignment	not modelled	8.6	33	<b>PDB header:</b> flavoprotein <b>Chain:</b> L: <b>PDB Molecule:</b> dodecin; <b>PDBTitle:</b> h.halophila dodecin in complex with riboflavin
36	<a href="#">c3bbsS</a>	Alignment	not modelled	8.5	31	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> ribosomal protein s19; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
37	<a href="#">c5o5jS</a>	Alignment	not modelled	8.3	23	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 30s ribosomal protein s19; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
38	<a href="#">c4xchB</a>	Alignment	not modelled	8.3	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> s-ribosylhomocysteine lyase; <b>PDBTitle:</b> s-ribosylhomocysteinase from streptococcus suis
39	<a href="#">c3j20T</a>	Alignment	not modelled	8.2	38	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 30s ribosomal protein s19p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
40	<a href="#">d2i0ka1</a>	Alignment	not modelled	8.2	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Cholesterol oxidase
41	<a href="#">d2ux9a1</a>	Alignment	not modelled	8.1	22	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> Dodecin-like <b>Family:</b> Dodecin-like
42	<a href="#">c6r1eC</a>	Alignment	not modelled	8.0	39	<b>PDB header:</b> flavoprotein <b>Chain:</b> C: <b>PDB Molecule:</b> dodecin; <b>PDBTitle:</b> structure of dodecin from streptomyces coelicolor
43	<a href="#">c3c9dB</a>	Alignment	not modelled	8.0	32	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 75; <b>PDBTitle:</b> crystal structure of vps75
44	<a href="#">c6ehtE</a>	Alignment	not modelled	7.9	56	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> pcna-associated factor; <b>PDBTitle:</b> modulation of pcna sliding surface by p15paf suggests a suppressive2 mechanism for cisplatin-induced dna lesion bypass by pol eta3 holoenzyme
45	<a href="#">c2zkqs</a>	Alignment	not modelled	7.7	46	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> S: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
46	<a href="#">c3zeyl</a>	Alignment	not modelled	7.6	46	<b>PDB header:</b> ribosome <b>Chain:</b> l: <b>PDB Molecule:</b> 40s ribosomal protein s15, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
47	<a href="#">c2rqmA</a>	Alignment	not modelled	7.5	54	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> mesoderm development candidate 2; <b>PDBTitle:</b> nmr solution structure of mesoderm development (mesd) - open2 conformation
48	<a href="#">c1s1hS</a>	Alignment	not modelled	7.5	38	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 40s ribosomal protein s15; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
49	<a href="#">c5lutK</a>	Alignment	not modelled	7.5	67	<b>PDB header:</b> transferase <b>Chain:</b> K: <b>PDB Molecule:</b> blm helicase; <b>PDBTitle:</b> structures of dhn domain of gallus gallus blm helicase
50	<a href="#">c3bxwB</a>	Alignment	not modelled	7.3	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> chitinase domain-containing protein 1; <b>PDBTitle:</b> crystal structure of stabilin-1 interacting chitinase-like protein,2 si-clp
51	<a href="#">d1wi1a</a>	Alignment	not modelled	7.3	32	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)
52	<a href="#">c6gwsE</a>	Alignment	not modelled	7.3	56	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> pcna-associated factor; <b>PDBTitle:</b> crystal structure of human pcna in complex with three p15 peptides
						<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> pcna-associated factor;

53	<a href="#">c6ehtD</a>	Alignment	not modelled	7.3	56	<b>PDBTitle:</b> modulation of pcna sliding surface by p15paf suggests a suppressive2 mechanism for cisplatin-induced dna lesion bypass by pol eta3 holoenzyme
54	<a href="#">c6gwsD</a>	Alignment	not modelled	7.2	56	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> pcna-associated factor; <b>PDBTitle:</b> crystal structure of human pcna in complex with three p15 peptides
55	<a href="#">c1sb3D</a>	Alignment	not modelled	7.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-hydroxybenzoyl-coa reductase alpha subunit; <b>PDBTitle:</b> structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
56	<a href="#">c4d2gE</a>	Alignment	not modelled	7.2	56	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> p15; <b>PDBTitle:</b> crystal structure of human pcna in complex with p15 peptide
57	<a href="#">c4d2gD</a>	Alignment	not modelled	7.2	56	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> p15; <b>PDBTitle:</b> crystal structure of human pcna in complex with p15 peptide
58	<a href="#">c2auhB</a>	Alignment	not modelled	7.2	33	<b>PDB header:</b> transferase/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> growth factor receptor-bound protein 14; <b>PDBTitle:</b> crystal structure of the grb14 bps region in complex with2 the insulin receptor tyrosine kinase
59	<a href="#">c2wj8N</a>	Alignment	not modelled	7.2	41	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> N: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> respiratory syncytial virus ribonucleoprotein
60	<a href="#">c3izbR</a>	Alignment	not modelled	7.0	38	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 40s ribosomal protein rps15 (s19p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
61	<a href="#">c3oqtP</a>	Alignment	not modelled	6.7	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> P: <b>PDB Molecule:</b> rv1498a protein; <b>PDBTitle:</b> crystal structure of rv1498a protein from mycobacterium tuberculosis
62	<a href="#">c3onrl</a>	Alignment	not modelled	6.7	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> protein transport protein sece2; <b>PDBTitle:</b> crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
63	<a href="#">d1t3qb2</a>	Alignment	not modelled	6.6	22	<b>Fold:</b> Molybdenum cofactor-binding domain <b>Superfamily:</b> Molybdenum cofactor-binding domain <b>Family:</b> Molybdenum cofactor-binding domain
64	<a href="#">c3j38P</a>	Alignment	not modelled	6.6	54	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 40s ribosomal protein s15, isoform a; <b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins
65	<a href="#">c4gh9A</a>	Alignment	not modelled	6.5	50	<b>PDB header:</b> viral protein,rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> crystal structure of marburg virus vp35 rna binding domain
66	<a href="#">c4uebF</a>	Alignment	not modelled	6.4	60	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> designed 4e-bp; <b>PDBTitle:</b> complex of d. melanogaster eif4e with a designed 4e-binding protein2 (form ii)
67	<a href="#">c1ueoA</a>	Alignment	not modelled	6.1	86	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> penaeidin-3a; <b>PDBTitle:</b> solution structure of the [t8a]-penaeidin-3
68	<a href="#">c3gyvA</a>	Alignment	not modelled	6.1	31	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> nucleosome assembly protein 1, putative; <b>PDBTitle:</b> crystal structure of nucleosome assembly protein from plasmodium2 falciparum
69	<a href="#">d1g2qa</a>	Alignment	not modelled	5.9	26	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
70	<a href="#">c1jirA</a>	Alignment	not modelled	5.8	67	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> thyroid autoantigen; <b>PDBTitle:</b> the three-dimensional structure of the c-terminal dna2 binding domain of human ku70
71	<a href="#">c2ww9O</a>	Alignment	not modelled	5.8	44	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein l39; <b>PDBTitle:</b> cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
72	<a href="#">d1euvb</a>	Alignment	not modelled	5.8	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
73	<a href="#">c3j21f</a>	Alignment	not modelled	5.7	67	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 50s ribosomal protein l6p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
74	<a href="#">d2gr8a1</a>	Alignment	not modelled	5.7	17	<b>Fold:</b> Pili subunits <b>Superfamily:</b> Pili subunits <b>Family:</b> YadA C-terminal domain-like
75	<a href="#">d2d8xa1</a>	Alignment	not modelled	5.6	54	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
76	<a href="#">c3ks8D</a>	Alignment	not modelled	5.3	70	<b>PDB header:</b> viral protein/rna <b>Chain:</b> D: <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> crystal structure of reston ebolavirus vp35 rna binding domain in2 complex with 18bp dsrna
77	<a href="#">c4axgC</a>	Alignment	not modelled	5.3	60	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> protein cup; <b>PDBTitle:</b> structure of eif4e-cup complex
78	<a href="#">c2yewG</a>	Alignment	not modelled	5.2	19	<b>PDB header:</b> virus <b>Chain:</b> G: <b>PDB Molecule:</b> capsid protein;

