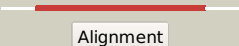
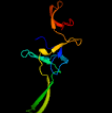

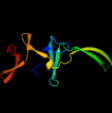
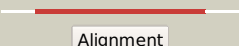
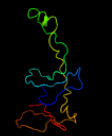

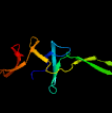


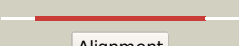
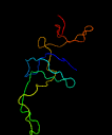

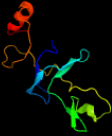

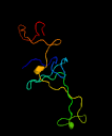






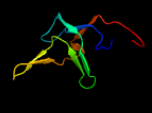


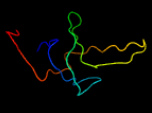
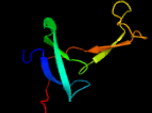






# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0715\_(rplX)\_811745\_812062  
 Date Fri Jul 26 01:50:28 BST 2019  
 Unique Job ID e1fd50a5af5bd73f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5mmiV_</a>	 Alignment		100.0	35	<b>PDB header:</b> ribosome <b>Chain:</b> V; <b>PDB Molecule:</b> plastid ribosomal protein ul24c; <b>PDBTitle:</b> structure of the large subunit of the chloroplast ribosome
2	<a href="#">c5o60V_</a>	 Alignment		100.0	92	<b>PDB header:</b> ribosome <b>Chain:</b> V; <b>PDB Molecule:</b> 50s ribosomal protein l24; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
3	<a href="#">c3j3vU_</a>	 Alignment		100.0	57	<b>PDB header:</b> ribosome <b>Chain:</b> U; <b>PDB Molecule:</b> 50s ribosomal protein l24; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
4	<a href="#">c4v19Y_</a>	 Alignment		100.0	39	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> mitoribosomal protein ul24m, mrpl24; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
5	<a href="#">d2zjrr1</a>	 Alignment		100.0	45	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e
6	<a href="#">c3bboW_</a>	 Alignment		100.0	33	<b>PDB header:</b> ribosome <b>Chain:</b> W; <b>PDB Molecule:</b> ribosomal protein l24; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
7	<a href="#">d2gycs1</a>	 Alignment		100.0	44	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e
8	<a href="#">d2j01y1</a>	 Alignment		100.0	46	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e
9	<a href="#">c2ftcN_</a>	 Alignment		100.0	42	<b>PDB header:</b> ribosome <b>Chain:</b> N; <b>PDB Molecule:</b> mitochondrial ribosomal protein l24; <b>PDBTitle:</b> structural model for the large subunit of the mammalian mitochondrial2 ribosome
10	<a href="#">c3iz5Y_</a>	 Alignment		99.9	33	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> 60s ribosomal protein l26 (l24p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
11	<a href="#">d1vqot1</a>	 Alignment		99.9	31	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e

12	<a href="#">c3j21U</a>	Alignment		99.9	35	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 50s ribosomal protein l24p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
13	<a href="#">c4a1cS</a>	Alignment		99.8	35	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> rpl26; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna,3 5.8s rna and proteins of molecule 4.
14	<a href="#">c3zf7Z</a>	Alignment		99.8	34	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 60s ribosomal protein l26, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
15	<a href="#">c1s1iU</a>	Alignment		99.8	29	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 60s ribosomal protein l26-a; <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, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
16	<a href="#">c1vw4Q</a>	Alignment		99.6	18	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 54s ribosomal protein l40, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
17	<a href="#">c2zkrT</a>	Alignment		99.4	41	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> T: <b>PDB Molecule:</b> rna expansion segment es39 part iii; <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
18	<a href="#">c3p8bB</a>	Alignment		96.8	34	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
19	<a href="#">c2kvqG</a>	Alignment		96.8	22	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> solution structure of nuse:nusg-ctd complex
20	<a href="#">c2jvvA</a>	Alignment		96.8	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> solution structure of e. coli nusg carboxyterminal domain
21	<a href="#">c2mi6A</a>	Alignment	not modelled	96.8	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription termination/antitermination protein nusg; <b>PDBTitle:</b> solution structure of the carboxy terminal domain of nusg from2 mycobacterium tuberculosis
22	<a href="#">d1nppa2</a>	Alignment	not modelled	96.8	31	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> N-utilization substance G protein NusG, C-terminal domain
23	<a href="#">d1nz9a</a>	Alignment	not modelled	96.5	33	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> N-utilization substance G protein NusG, C-terminal domain
24	<a href="#">c4ytiB</a>	Alignment	not modelled	96.2	34	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> structure of the kow2-kow3 domain of transcription elongation factor2 spt5.
25	<a href="#">c2lq8A</a>	Alignment	not modelled	96.0	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> domain interaction in thermotoga maritima nusg
26	<a href="#">d2do3a1</a>	Alignment	not modelled	96.0	31	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> SPT5 KOW domain-like
27	<a href="#">c5ohoB</a>	Alignment	not modelled	95.9	31	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> crystal structure of the kowx-kow4 domain of human dsif
28	<a href="#">c5tbzK</a>	Alignment	not modelled	95.9	22	<b>PDB header:</b> transcription/rna <b>Chain:</b> K: <b>PDB Molecule:</b> transcription termination/antitermination protein nusg; <b>PDBTitle:</b> e. coli rna polymerase complexed with nusg
29	<a href="#">c4zn3A</a>	Alignment	not modelled	95.9	35	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5;

						<b>PDBTitle:</b> crystal structure of mjspt4:spt5 complex conformation b
30	<a href="#">c2ckkA</a>	Alignment	not modelled	95.7	18	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> kin17; <b>PDBTitle:</b> high resolution crystal structure of the human kin17 c-terminal domain2 containing a kow motif
31	<a href="#">c2xhcA</a>	Alignment	not modelled	95.1	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
32	<a href="#">c5oikZ</a>	Alignment	not modelled	95.0	18	<b>PDB header:</b> transcription <b>Chain:</b> Z: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> structure of an rna polymerase ii-disf transcription elongation2 complex
33	<a href="#">c5xonW</a>	Alignment	not modelled	95.0	26	<b>PDB header:</b> transcription/rna <b>Chain:</b> W: <b>PDB Molecule:</b> protein that forms a complex with spt4p; <b>PDBTitle:</b> rna polymerase ii elongation complex bound with spt4/5 and tffis
34	<a href="#">c1m1gB</a>	Alignment	not modelled	94.4	31	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
35	<a href="#">c5ohqA</a>	Alignment	not modelled	94.4	30	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> crystal structure of the kow6-kow7 domain of human dsif
36	<a href="#">c6ir9W</a>	Alignment	not modelled	94.3	26	<b>PDB header:</b> transcription/rna/dna <b>Chain:</b> W: <b>PDB Molecule:</b> spt5; <b>PDBTitle:</b> rna polymerase ii elongation complex bound with elf1 and spt4/5,2 stalled at shl(-1) of the nucleosome
37	<a href="#">c3zf7v</a>	Alignment	not modelled	93.8	17	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 60s ribosomal protein l22, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
38	<a href="#">c2lcIA</a>	Alignment	not modelled	93.4	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional activator rfah; <b>PDBTitle:</b> solution structure of rfah carboxyterminal domain
39	<a href="#">c3j3bM</a>	Alignment	not modelled	93.1	30	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l14; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
40	<a href="#">c3j39M</a>	Alignment	not modelled	91.8	35	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l14; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
41	<a href="#">d2joya1</a>	Alignment	not modelled	91.6	29	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal protein L14e
42	<a href="#">c3izcN</a>	Alignment	not modelled	91.3	28	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 60s ribosomal protein rpl14 (l14e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
43	<a href="#">c2e6zA</a>	Alignment	not modelled	90.9	30	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> solution structure of the second kow motif of human2 transcription elongation factor spt5
44	<a href="#">c3zf7P</a>	Alignment	not modelled	89.9	32	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> probable 60s ribosomal protein l14; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
45	<a href="#">c3j215</a>	Alignment	not modelled	89.8	39	<b>PDB header:</b> ribosome <b>Chain:</b> 5: <b>PDB Molecule:</b> 50s ribosomal protein l14e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
46	<a href="#">c4a19F</a>	Alignment	not modelled	89.3	28	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> rpl14; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
47	<a href="#">c3iz5N</a>	Alignment	not modelled	88.8	39	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 60s ribosomal protein l14 (l14e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
48	<a href="#">c3izcG</a>	Alignment	not modelled	85.9	21	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein rpl6 (l6e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
49	<a href="#">c3j3bZ</a>	Alignment	not modelled	85.7	33	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 60s ribosomal protein l27; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
50	<a href="#">c4a18N</a>	Alignment	not modelled	85.5	34	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> rpl27; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
51	<a href="#">c3zf7a</a>	Alignment	not modelled	85.2	30	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
52	<a href="#">c3j39E</a>	Alignment	not modelled	84.7	21	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 60s ribosomal protein l6, isoform a; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
53	<a href="#">c3j39Z</a>	Alignment	not modelled	84.4	30	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 60s ribosomal protein l27; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
54	<a href="#">c4a1dE</a>	Alignment	not modelled	82.1	21	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> rpl6; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with

						initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
55	<a href="#">c2e70A_</a>	Alignment	not modelled	82.1	38	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> solution structure of the fifth kow motif of human2 transcription elongation factor spt5
56	<a href="#">c3u5eZ_</a>	Alignment	not modelled	80.0	24	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 60s ribosomal protein l27-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a
57	<a href="#">c4ytkA_</a>	Alignment	not modelled	79.6	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> structure of the kow1-linker1 domain of transcription elongation2 factor spt5
58	<a href="#">c3j3bE_</a>	Alignment	not modelled	79.5	21	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 60s ribosomal protein l6; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
59	<a href="#">c3zey1_</a>	Alignment	not modelled	77.2	18	<b>PDB header:</b> ribosome <b>Chain:</b> 1: <b>PDB Molecule:</b> 40s ribosomal protein s4, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
60	<a href="#">c3j20E_</a>	Alignment	not modelled	73.7	26	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 30s ribosomal protein s4e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
61	<a href="#">c3iz5G_</a>	Alignment	not modelled	70.0	18	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l6 (l6e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
62	<a href="#">c2xzmW_</a>	Alignment	not modelled	68.6	13	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 40s ribosomal protein s4; <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
63	<a href="#">c5xxuE_</a>	Alignment	not modelled	66.4	15	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> ribosomal protein es4; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
64	<a href="#">c3kbgA_</a>	Alignment	not modelled	64.1	17	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s4e; <b>PDBTitle:</b> crystal structure of the 30s ribosomal protein s4e from thermoplasma2 acidophilum. northeast structural genomics consortium target tar28.
65	<a href="#">c3iz6D_</a>	Alignment	not modelled	62.6	22	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 40s ribosomal protein s4 (s4e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
66	<a href="#">c4xi7A_</a>	Alignment	not modelled	62.4	38	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase mib1; <b>PDBTitle:</b> crystal structure of the mzm-rep domains of mind bomb 1 in complex2 with jagged1 n-box peptide
67	<a href="#">c3zf7U_</a>	Alignment	not modelled	60.5	29	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 60s ribosomal protein l21e, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
68	<a href="#">d1vhka1</a>	Alignment	not modelled	60.3	23	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Yggj N-terminal domain-like
69	<a href="#">c4a1aP_</a>	Alignment	not modelled	59.3	26	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l21; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
70	<a href="#">d1nxza1</a>	Alignment	not modelled	58.3	11	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Yggj N-terminal domain-like
71	<a href="#">c3j3bT_</a>	Alignment	not modelled	57.6	28	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 60s ribosomal protein l21; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
72	<a href="#">c4tseA_</a>	Alignment	not modelled	54.8	39	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase mib1; <b>PDBTitle:</b> crystal structure of the mib repeat domain of mind bomb 1
73	<a href="#">c3iz5U_</a>	Alignment	not modelled	54.5	26	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 60s ribosomal protein l21 (l21e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
74	<a href="#">c4ca9B_</a>	Alignment	not modelled	53.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 39 kda fk506-binding nuclear protein; <b>PDBTitle:</b> structure of the nucleoplasmin-like n-terminal domain of drosophila2 fkbp39
75	<a href="#">c5xyiE_</a>	Alignment	not modelled	52.6	21	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 40s ribosomal protein s4; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
76	<a href="#">c3izcU_</a>	Alignment	not modelled	49.7	30	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 60s ribosomal protein rpl21 (l21e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
77	<a href="#">c3u5cE_</a>	Alignment	not modelled	45.4	21	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 40s ribosomal protein s4-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
78	<a href="#">c2zkrq_</a>	Alignment	not modelled	44.3	30	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> Q: <b>PDB Molecule:</b> rna expansion segment es31 part ii; <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 an 3.87 Å cryo-em map
79	<a href="#">c3iz5a_</a>	Alignment	not modelled	41.7	27	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 60s ribosomal protein l1 (l1p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 Å cryo-em map of triticum aestivum translating 80s ribosome
80	<a href="#">c5k26A_</a>	Alignment	not modelled	41.1	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase kinase 11, chimera <b>PDBTitle:</b> structure of the sh3 domain of mlk3 bound to peptide generated from 2 phage display
81	<a href="#">d1wlpb2</a>	Alignment	not modelled	36.4	39	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
82	<a href="#">d1ng2a2</a>	Alignment	not modelled	34.9	22	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
83	<a href="#">c4j3cB_</a>	Alignment	not modelled	33.7	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase e; <b>PDBTitle:</b> crystal structure of 16s ribosomal rna methyltransferase rsme
84	<a href="#">d1k4us_</a>	Alignment	not modelled	33.5	39	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
85	<a href="#">c4u1eG_</a>	Alignment	not modelled	32.5	24	<b>PDB header:</b> translation <b>Chain:</b> G: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit g; <b>PDBTitle:</b> crystal structure of the eif3b-ctd/eif3i/eif3g-ntd translation2 initiation complex
86	<a href="#">c2k6dA_</a>	Alignment	not modelled	30.6	30	<b>PDB header:</b> sh3 domain/ubiquitin <b>Chain:</b> A: <b>PDB Molecule:</b> sh3 domain-containing kinase-binding protein 1; <b>PDBTitle:</b> cin85 sh3-c domain in complex with ubiquitin
87	<a href="#">c1z85B_</a>	Alignment	not modelled	29.0	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein tm1380; <b>PDBTitle:</b> crystal structure of a predicted rna methyltransferase (tm1380) from thermotoga maritima msb8 at 2.12 Å resolution
88	<a href="#">c3izbD_</a>	Alignment	not modelled	28.8	22	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 40s ribosomal protein rps4 (s4e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 Å cryo-em map of saccharomyces cerevisiae translating 80s ribosome
89	<a href="#">c4rugA_</a>	Alignment	not modelled	28.7	30	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> slit-robo rho gtpase-activating protein 2; <b>PDBTitle:</b> crystal structure of slit-robo rho gtpase-activating protein 22 fragment
90	<a href="#">c2drmB_</a>	Alignment	not modelled	28.2	35	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> acanthamoeba myosin ib; <b>PDBTitle:</b> acanthamoeba myosin i sh3 domain bound to acan125
91	<a href="#">c4glmD_</a>	Alignment	not modelled	27.9	17	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> dynamamin-binding protein; <b>PDBTitle:</b> crystal structure of the sh3 domain of dnmbp protein [homo sapiens]
92	<a href="#">d1jb0e_</a>	Alignment	not modelled	27.8	21	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Photosystem I accessory protein E (PsaE)
93	<a href="#">c2eyxA_</a>	Alignment	not modelled	27.2	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> v-crk sarcoma virus ct10 oncogene homolog <b>PDBTitle:</b> c-terminal sh3 domain of ct10-regulated kinase
94	<a href="#">c2ed0A_</a>	Alignment	not modelled	27.0	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> abl interactor 2; <b>PDBTitle:</b> solution structure of the sh3 domain of abl interactor 22 (abelson interactor 2)
95	<a href="#">c2i0aA_</a>	Alignment	not modelled	26.3	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducing adapter molecule 1; <b>PDBTitle:</b> solution nmr structure of signal transducing adapter molecule 1 stam-12 from homo sapiens, northeast structural genomics consortium target3 hr4479e
96	<a href="#">c3izca_</a>	Alignment	not modelled	26.2	17	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 60s ribosomal protein rpl1 (l1p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 Å cryo-em map of saccharomyces cerevisiae translating 80s ribosome
97	<a href="#">d2c78a1</a>	Alignment	not modelled	26.2	23	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
98	<a href="#">d1psea_</a>	Alignment	not modelled	25.3	18	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Photosystem I accessory protein E (PsaE)
99	<a href="#">c3gqhB_</a>	Alignment	not modelled	24.9	28	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> preneck appendage protein; <b>PDBTitle:</b> crystal structure of the bacteriophage phi29 gene product 12 c-2 terminal fragment
100	<a href="#">d1gria2</a>	Alignment	not modelled	24.4	30	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
101	<a href="#">c3j21R_</a>	Alignment	not modelled	24.3	20	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 50s ribosomal protein l21e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by 2 cryo-em: implications for evolution of eukaryotic ribosomes (50s ribosomal proteins)
102	<a href="#">c1wxBA_</a>	Alignment	not modelled	23.7	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> epidermal growth factor receptor pathway <b>PDBTitle:</b> solution structure of the sh3 domain from human epidermal2 growth factor receptor pathway substrate 8-like protein <b>PDB header:</b> signaling protein

103	<a href="#">c1x2qA</a>	Alignment	not modelled	23.4	22	<b>Chain:</b> A: <b>PDB Molecule:</b> signal transducing adapter molecule 2; <b>PDBTitle:</b> solution structure of the sh3 domain of the signal2 transducing adaptor molecule 2
104	<a href="#">c2csqA</a>	Alignment	not modelled	23.1	17	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> rim binding protein 2; <b>PDBTitle:</b> solution structure of the second sh3 domain of human rim-2 binding protein 2
105	<a href="#">c6h5tB</a>	Alignment	not modelled	22.9	39	<b>PDB header:</b> endocytosis <b>Chain:</b> B: <b>PDB Molecule:</b> intersectin-1; <b>PDBTitle:</b> intersectin sh3a short isoform
106	<a href="#">d1qp3a</a>	Alignment	not modelled	22.6	18	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Photosystem I accessory protein E (PsaE)
107	<a href="#">c1s1iQ</a>	Alignment	not modelled	22.6	28	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein l21-a; <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, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
108	<a href="#">c2bz8B</a>	Alignment	not modelled	22.2	22	<b>PDB header:</b> sh3 domain <b>Chain:</b> B: <b>PDB Molecule:</b> sh3-domain kinase binding protein 1; <b>PDBTitle:</b> n-terminal sh3 domain of cin85 bound to cbl-b peptide
109	<a href="#">d1tova</a>	Alignment	not modelled	22.1	20	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
110	<a href="#">d1uhfa</a>	Alignment	not modelled	21.7	22	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
111	<a href="#">c2dbkA</a>	Alignment	not modelled	21.4	28	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> crk-like protein; <b>PDBTitle:</b> solution structures of the sh3 domain of human crk-like2 protein
112	<a href="#">c4e8bA</a>	Alignment	not modelled	21.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase e; <b>PDBTitle:</b> crystal structure of 16s rrna methyltransferase rsme from e.coli
113	<a href="#">c2dxcG</a>	Alignment	not modelled	20.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> thiocyanate hydrolase subunit alpha; <b>PDBTitle:</b> recombinant thiocyanate hydrolase, fully-matured form
114	<a href="#">c2dnuA</a>	Alignment	not modelled	20.7	35	<b>PDB header:</b> structural genomics, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> sh3 multiple domains 1; <b>PDBTitle:</b> solution structure of rsgi ruh-061, a sh3 domain from human
115	<a href="#">d1vqoq1</a>	Alignment	not modelled	20.5	20	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> Ribosomal proteins L24p and L21e
116	<a href="#">c1wi7A</a>	Alignment	not modelled	20.4	26	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> sh3-domain kinase binding protein 1; <b>PDBTitle:</b> solution structure of the sh3 domain of sh3-domain kinase2 binding protein 1
117	<a href="#">d2exda1</a>	Alignment	not modelled	20.2	45	<b>Fold:</b> OB-fold <b>Superfamily:</b> NfeD domain-like <b>Family:</b> NfeD domain-like