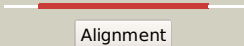

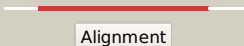

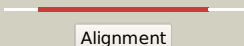







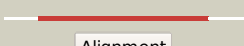









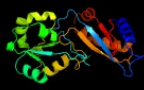


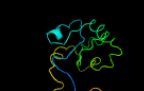
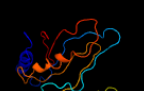






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0641_(rplA)_735520_736227
Date	Fri Jul 26 01:50:20 BST 2019
Unique Job ID	b5c422c917b894d8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3qoyA_</a>	 Alignment		100.0	51	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A; <b>PDB Molecule:</b> 50s ribosomal protein I1; <b>PDBTitle:</b> crystal structure of ribosomal protein I1 from aquifex aeolicus
2	<a href="#">c3bboD_</a>	 Alignment		100.0	46	<b>PDB header:</b> ribosome <b>Chain:</b> D; <b>PDB Molecule:</b> ribosomal protein I1; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
3	<a href="#">d1ad2a_</a>	 Alignment		100.0	49	<b>Fold:</b> Ribosomal protein L1 <b>Superfamily:</b> Ribosomal protein L1 <b>Family:</b> Ribosomal protein L1
4	<a href="#">c2gyc2_</a>	 Alignment		100.0	49	<b>PDB header:</b> ribosome <b>Chain:</b> 2; <b>PDB Molecule:</b> 50s ribosomal protein I1; <b>PDBTitle:</b> structure of the 50s subunit of a secm-stalled e. coli ribosome2 complex obtained by fitting atomic models for rna and protein3 components into cryo-em map emd-1143
5	<a href="#">c5dm70_</a>	 Alignment		100.0	57	<b>PDB header:</b> ribosome <b>Chain:</b> 0; <b>PDB Molecule:</b> 50s ribosomal protein I1; <b>PDBTitle:</b> crystal structure of the 50s ribosomal subunit from deinococcus2 radiodurans in complex with hygromycin a
6	<a href="#">d1mzpa_</a>	 Alignment		100.0	27	<b>Fold:</b> Ribosomal protein L1 <b>Superfamily:</b> Ribosomal protein L1 <b>Family:</b> Ribosomal protein L1
7	<a href="#">d1dwua_</a>	 Alignment		100.0	30	<b>Fold:</b> Ribosomal protein L1 <b>Superfamily:</b> Ribosomal protein L1 <b>Family:</b> Ribosomal protein L1
8	<a href="#">c3j21A_</a>	 Alignment		100.0	31	<b>PDB header:</b> ribosome <b>Chain:</b> A; <b>PDB Molecule:</b> 50s ribosomal protein I1p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
9	<a href="#">d1i2aa_</a>	 Alignment		100.0	28	<b>Fold:</b> Ribosomal protein L1 <b>Superfamily:</b> Ribosomal protein L1 <b>Family:</b> Ribosomal protein L1
10	<a href="#">c2zkr5_</a>	 Alignment		100.0	28	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> 5; <b>PDB Molecule:</b> 60s ribosomal protein I10a; <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
11	<a href="#">c3j39z_</a>	 Alignment		100.0	22	<b>PDB header:</b> ribosome <b>Chain:</b> Z; <b>PDB Molecule:</b> 60s ribosomal protein I27; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins

12	<a href="#">c1s1iA_</a>	Alignment		100.0	21	<b>PDB header:</b> ribosome <b>Chain:</b> A; <b>PDB Molecule:</b> 60s ribosomal protein l1; <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.
13	<a href="#">c3zf7J_</a>	Alignment		100.0	17	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> ribosomal protein; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
14	<a href="#">c3iz5A_</a>	Alignment		100.0	20	<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 a2 cryo-em map of triticum aestivum translating 80s ribosome
15	<a href="#">c2ftcA_</a>	Alignment		100.0	21	<b>PDB header:</b> ribosome <b>Chain:</b> A; <b>PDB Molecule:</b> mitochondrial ribosomal protein l1; <b>PDBTitle:</b> structural model for the large subunit of the mammalian mitochondrial2 ribosome
16	<a href="#">d2j01c1</a>	Alignment		100.0	47	<b>Fold:</b> Ribosomal protein L1 <b>Superfamily:</b> Ribosomal protein L1 <b>Family:</b> Ribosomal protein L1
17	<a href="#">c6em3K_</a>	Alignment		100.0	12	<b>PDB header:</b> ribosome <b>Chain:</b> K; <b>PDB Molecule:</b> proteasome-interacting protein cic1; <b>PDBTitle:</b> state a architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
18	<a href="#">c2ov7C_</a>	Alignment		100.0	56	<b>PDB header:</b> ribosomal protein <b>Chain:</b> C; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> the first domain of the ribosomal protein l1 from thermus thermophilus
19	<a href="#">c5yduA_</a>	Alignment		100.0	15	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A; <b>PDB Molecule:</b> ribosome biogenesis protein utp30; <b>PDBTitle:</b> crystal structure of utp30
20	<a href="#">c5jpkq_</a>	Alignment		100.0	15	<b>PDB header:</b> ribosome <b>Chain:</b> K; <b>PDB Molecule:</b> wd40 domain proteins; <b>PDBTitle:</b> cryo-em structure of the 90s pre-ribosome
21	<a href="#">c4k0qC_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> crystal structure of thermus thermophilus 70s containing trnas and2 mrna stop codon with pseudouridine
22	<a href="#">c4k0mC_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> crystal structure of thermus thermophilus 70s containing trnas and2 mrna stop codon with pseudouridine
23	<a href="#">c3j3v5_</a>	Alignment	not modelled	100.0	51	<b>PDB header:</b> ribosome <b>Chain:</b> 5; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
24	<a href="#">c4wweA_</a>	Alignment	not modelled	99.9	51	<b>PDB header:</b> ribosome <b>Chain:</b> A; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> crystal structure of bactobolin a bound to 70s ribosome-trna complex
25	<a href="#">c4wwtA_</a>	Alignment	not modelled	99.9	53	<b>PDB header:</b> ribosome <b>Chain:</b> A; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> crystal structure of bactobolin a bound to 70s ribosome-trna complex
26	<a href="#">d1piia1</a>	Alignment	not modelled	62.1	36	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
27	<a href="#">c2kzha_</a>	Alignment	not modelled	61.4	33	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> tryptophan biosynthesis protein trpcf; <b>PDBTitle:</b> three-dimensional structure of a truncated phosphoribosylanthranilate2 isomerase (residues 255-384) from escherichia coli
28	<a href="#">c4wuiA_</a>	Alignment	not modelled	56.7	33	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> n-(5'-phosphoribosyl)anthranilate isomerase; <b>PDBTitle:</b> crystal structure of trpf from jonesia denitrificans

29	<a href="#">d1v5xa_</a>	Alignment	not modelled	50.1	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
30	<a href="#">c4e1ja_</a>	Alignment	not modelled	48.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of glycerol kinase in complex with glycerol from <i>Sinorhizobium meliloti</i> 1021
31	<a href="#">c1piiA_</a>	Alignment	not modelled	47.6	35	<b>PDB header:</b> bifunctional(isomerase and synthase) <b>Chain:</b> A: <b>PDB Molecule:</b> n-(5'-phosphoribosyl)anthranilate isomerase; <b>PDBTitle:</b> three-dimensional structure of the bifunctional enzyme 2-phosphoribosylanthranilate isomerase: indoleglycerolphosphate 3-synthase from <i>Escherichia coli</i> refined at 2.0 angstroms resolution
32	<a href="#">c5vm1A_</a>	Alignment	not modelled	46.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of a xylofucose kinase from <i>Brucella ovis</i>
33	<a href="#">c3g25B_</a>	Alignment	not modelled	45.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> 1.9 angstrom crystal structure of glycerol kinase (gpk) from <i>Staphylococcus aureus</i> in complex with glycerol.
34	<a href="#">d1nsja_</a>	Alignment	not modelled	41.8	35	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
35	<a href="#">c2d4wA_</a>	Alignment	not modelled	41.7	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of glycerol kinase from <i>Cellulomonas</i> sp. 2 nt3060
36	<a href="#">c3flcX_</a>	Alignment	not modelled	41.4	8	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of the his-tagged h232r mutant of glycerol kinase 2 from <i>Enterococcus casseliflavus</i> with glycerol
37	<a href="#">c1xupO_</a>	Alignment	not modelled	41.3	8	<b>PDB header:</b> transferase <b>Chain:</b> O: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> <i>Enterococcus casseliflavus</i> glycerol kinase complexed with glycerol
38	<a href="#">c2dnpB_</a>	Alignment	not modelled	41.2	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of the glycerol kinase from <i>Thermus</i> 2 thermophilus hb8
39	<a href="#">d2i4ra1</a>	Alignment	not modelled	40.5	16	<b>Fold:</b> AtpF-like <b>Superfamily:</b> AtpF-like <b>Family:</b> AtpF-like
40	<a href="#">c2zf5O_</a>	Alignment	not modelled	39.2	12	<b>PDB header:</b> transferase <b>Chain:</b> O: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of highly thermostable glycerol kinase from a 2 hyperthermophilic archaeon
41	<a href="#">c2w40C_</a>	Alignment	not modelled	38.3	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glycerol kinase, putative; <b>PDBTitle:</b> crystal structure of <i>Plasmodium falciparum</i> glycerol kinase 2 with bound glycerol
42	<a href="#">c3ifrB_</a>	Alignment	not modelled	37.1	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carbohydrate kinase, fggy; <b>PDBTitle:</b> the crystal structure of xylulose kinase from <i>Rhodospirillum rubrum</i>
43	<a href="#">c3hz6A_</a>	Alignment	not modelled	32.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of xylulokinase from <i>Chromobacterium violaceum</i>
44	<a href="#">d2p3ra1</a>	Alignment	not modelled	30.9	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
45	<a href="#">c4aaJA_</a>	Alignment	not modelled	28.9	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> n-(5'-phosphoribosyl)anthranilate isomerase; <b>PDBTitle:</b> structure of n-(5'-phosphoribosyl)anthranilate isomerase from <i>Pyrococcus furiosus</i>
46	<a href="#">c5lhfA_</a>	Alignment	not modelled	28.3	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> n-(5'-phosphoribosyl)anthranilate isomerase; <b>PDBTitle:</b> phosphoribosyl anthranilate isomerase from <i>Thermococcus kodakaraensis</i>
47	<a href="#">c5tuuB_</a>	Alignment	not modelled	28.3	24	<b>PDB header:</b> transcription factor <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor e2f4; <b>PDBTitle:</b> crystal structure of the e2f4-dp1 coiled coil and marked-box domains
48	<a href="#">c1glbG_</a>	Alignment	not modelled	28.2	19	<b>PDB header:</b> phosphotransferase <b>Chain:</b> G: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> structure of the regulatory complex of <i>Escherichia coli</i> iiglc with 2 glycerol kinase
49	<a href="#">c3nbmA_</a>	Alignment	not modelled	27.1	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, lactose-specific iibc components; <b>PDBTitle:</b> the lactose-specific iib component domain structure of the 2-phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from <i>Streptococcus pneumoniae</i> .
50	<a href="#">c2nlxA_</a>	Alignment	not modelled	25.3	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulose kinase; <b>PDBTitle:</b> crystal structure of the apo e. coli xylulose kinase
51	<a href="#">c2nqqA_</a>	Alignment	not modelled	25.1	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis protein moea; <b>PDBTitle:</b> moea r137q
52	<a href="#">c2vhmI_</a>	Alignment	not modelled	24.9	16	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein I11; <b>PDBTitle:</b> structure of pdf binding helix in complex with the ribosome 2 (part 1 of 4)
53	<a href="#">c5o60J_</a>	Alignment	not modelled	24.8	15	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 50s ribosomal protein I11; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from

						mycobacterium2 smegmatis
54	<a href="#">c3ezwD_</a>	Alignment	not modelled	24.4	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
55	<a href="#">c3gbtA_</a>	Alignment	not modelled	21.3	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gluconate kinase; <b>PDBTitle:</b> crystal structure of gluconate kinase from lactobacillus acidophilus
56	<a href="#">d1r59o1</a>	Alignment	not modelled	21.0	8	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
57	<a href="#">c4mgeB_</a>	Alignment	not modelled	20.3	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pts system, cellobiose-specific iib component; <b>PDBTitle:</b> 1.85 angstrom resolution crystal structure of pts system cellobiose-2 specific transporter subunit iib from bacillus anthracis.
58	<a href="#">c3cjqB_</a>	Alignment	not modelled	20.0	19	<b>PDB header:</b> transferase/ribosomal protein <b>Chain:</b> B: <b>PDB Molecule:</b> 50s ribosomal protein l11; <b>PDBTitle:</b> ribosomal protein l11 methyltransferase (prma) in complex with2 dimethylated ribosomal protein l11 in space group p212121
59	<a href="#">c2ov6A_</a>	Alignment	not modelled	19.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> v-type atp synthase subunit f; <b>PDBTitle:</b> the nmr structure of subunit f of the methanogenic a1ao atp synthase2 and its interaction with the nucleotide-binding subunit b
60	<a href="#">d2azeb1</a>	Alignment	not modelled	18.6	30	<b>Fold:</b> E2F-DP heterodimerization region <b>Superfamily:</b> E2F-DP heterodimerization region <b>Family:</b> E2F dimerization segment
61	<a href="#">c5ya2A_</a>	Alignment	not modelled	18.2	7	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> autoinducer-2 kinase; <b>PDBTitle:</b> crystal structure of lsrk-hpr complex with adp
62	<a href="#">c5mq9A_</a>	Alignment	not modelled	16.2	14	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yacp; <b>PDBTitle:</b> crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
63	<a href="#">d1qapa1</a>	Alignment	not modelled	15.7	31	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
64	<a href="#">c3gg4B_</a>	Alignment	not modelled	15.6	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
65	<a href="#">d1o4ua1</a>	Alignment	not modelled	13.7	39	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
66	<a href="#">d1iiba_</a>	Alignment	not modelled	12.9	15	<b>Fold:</b> Phosphotyrosine protein phosphatases l-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Lactose/Cellobiose specific IIB subunit
67	<a href="#">d1qk1a2</a>	Alignment	not modelled	12.2	9	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Guanido kinase catalytic domain
68	<a href="#">c3wxiB_</a>	Alignment	not modelled	12.0	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
69	<a href="#">c3bboK_</a>	Alignment	not modelled	11.6	19	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> ribosomal protein l11; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
70	<a href="#">c2ftcG_</a>	Alignment	not modelled	11.3	32	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 39s ribosomal protein l11, mitochondrial; <b>PDBTitle:</b> structural model for the large subunit of the mammalian mitochondrial2 ribosome
71	<a href="#">c2mdtA_</a>	Alignment	not modelled	11.1	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfolobus solfataricus p2
72	<a href="#">c4n40A_</a>	Alignment	not modelled	11.0	19	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> protein ect2; <b>PDBTitle:</b> crystal structure of human epithelial cell-transforming sequence 22 protein
73	<a href="#">c3jvpA_</a>	Alignment	not modelled	10.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulokinase; <b>PDBTitle:</b> crystal structure of ribulokinase from bacillus halodurans
74	<a href="#">c4waaA_</a>	Alignment	not modelled	10.4	56	<b>PDB header:</b> protein binding/rna <b>Chain:</b> A: <b>PDB Molecule:</b> branchpoint-bridging protein; <b>PDBTitle:</b> crystal structure of selenomethionine msl5 protein in complex with rna2 at 2.2 a
75	<a href="#">c5tuvB_</a>	Alignment	not modelled	10.3	33	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor e2f5; <b>PDBTitle:</b> crystal structure of the e2f5-dp1-p107 ternary complex
76	<a href="#">c1jqmA_</a>	Alignment	not modelled	9.8	19	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 50s ribosomal protein l11; <b>PDBTitle:</b> fitting of l11 protein and elongation factor g (ef-g) in2 the cryo-em map of e. coli 70s ribosome bound with ef-g,3 gdp and fusidic acid
77	<a href="#">c5anbD_</a>	Alignment	not modelled	9.5	29	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> 60s ribosomal protein l12; <b>PDBTitle:</b> mechanism of eif6 release from the nascent 60s ribosomal subunit
78	<a href="#">d1k1ga_</a>	Alignment	not modelled	8.7	27	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)

79	<a href="#">c2lvsA_</a>	Alignment	not modelled	8.4	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of a crispr repeat binding protein
80	<a href="#">c2l2qA_</a>	Alignment	not modelled	8.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, cellobiose-specific iib component (cela); <b>PDBTitle:</b> solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
81	<a href="#">c4jvhA_</a>	Alignment	not modelled	7.8	67	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein quaking; <b>PDBTitle:</b> structure of the star domain of quaking protein in complex with rna
82	<a href="#">d1qpoa1</a>	Alignment	not modelled	7.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
83	<a href="#">c3ho6B_</a>	Alignment	not modelled	7.6	10	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> toxin a; <b>PDBTitle:</b> structure-function analysis of inositol hexakisphosphate-2 induced autoprocessing in clostridium difficile toxin a
84	<a href="#">c5te9A_</a>	Alignment	not modelled	7.4	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of a response regulator receiver protein from2 burkholderia phymatum
85	<a href="#">c4lp7C_</a>	Alignment	not modelled	7.3	22	<b>PDB header:</b> calcium binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> matrix protein m; <b>PDBTitle:</b> crystal structure of the human metapneumovirus matrix protein
86	<a href="#">c4w8fA_</a>	Alignment	not modelled	7.2	15	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> dynein heavy chain lysozyme chimera; <b>PDBTitle:</b> crystal structure of the dynein motor domain in the amppnp-bound state
87	<a href="#">d2ngra3</a>	Alignment	not modelled	7.0	19	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
88	<a href="#">c5colB_</a>	Alignment	not modelled	6.9	17	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> 50s ribosomal protein l11; <b>PDBTitle:</b> ribosomal protein l11 from methanococcus jannaschii
89	<a href="#">d3cjsb1</a>	Alignment	not modelled	6.8	25	<b>Fold:</b> Ribosomal L11/L12e N-terminal domain <b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain
90	<a href="#">c3iz5J_</a>	Alignment	not modelled	6.8	26	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 60s ribosomal protein l12 (l11p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
91	<a href="#">c5w78B_</a>	Alignment	not modelled	6.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acyloxyacyl hydrolase; <b>PDBTitle:</b> human acyloxyacyl hydrolase (aoah), proteolytically processed
92	<a href="#">d2d00a1</a>	Alignment	not modelled	6.7	16	<b>Fold:</b> AtpF-like <b>Superfamily:</b> AtpF-like <b>Family:</b> AtpF-like
93	<a href="#">c3cjtP_</a>	Alignment	not modelled	6.7	25	<b>PDB header:</b> transferase/ribosomal protein <b>Chain:</b> P: <b>PDB Molecule:</b> 50s ribosomal protein l11; <b>PDBTitle:</b> ribosomal protein l11 methyltransferase (prma) in complex with2 dimethylated ribosomal protein l11
94	<a href="#">d2gycg2</a>	Alignment	not modelled	6.6	25	<b>Fold:</b> Ribosomal L11/L12e N-terminal domain <b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain
95	<a href="#">c5z2hA_</a>	Alignment	not modelled	6.5	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dictyostelium discoideum mitochondrial calcium uniporter; <b>PDBTitle:</b> structure of dictyostelium discoideum mitochondrial calcium uniporter2 n-terminal domain(ddmdu-ntd)
96	<a href="#">c5el3D_</a>	Alignment	not modelled	6.4	28	<b>PDB header:</b> rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> kh domain-containing, rna-binding, signal transduction- <b>PDBTitle:</b> structure of the kh domain of t-star
97	<a href="#">d1xbpg2</a>	Alignment	not modelled	6.3	25	<b>Fold:</b> Ribosomal L11/L12e N-terminal domain <b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain
98	<a href="#">c4lzlA_</a>	Alignment	not modelled	6.2	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the inactive form of the regulatory domain from the2 repressor of iron transport regulator (ritr)
99	<a href="#">d1mmsa2</a>	Alignment	not modelled	6.2	25	<b>Fold:</b> Ribosomal L11/L12e N-terminal domain <b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain