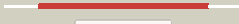
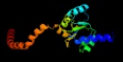

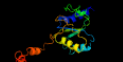
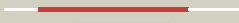


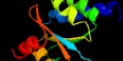



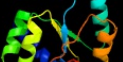
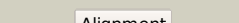
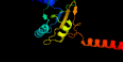





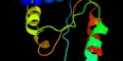

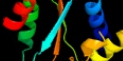
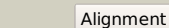











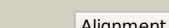

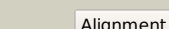

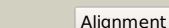





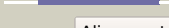




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0651_(rplj)_748279_748815
Date	Fri Jul 26 01:50:21 BST 2019
Unique Job ID	ab3f35d1bc41361d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1zava1	 Alignment		100.0	38	Fold: Ferredoxin-like Superfamily: Ribosomal protein L10-like Family: Ribosomal protein L10-like
2	c3uosH	 Alignment		100.0	34	PDB header: ribosome Chain: H; PDB Molecule: 50s ribosomal protein l10; PDBTitle: crystal structure of release factor rf3 trapped in the gtp state on a2 rotated conformation of the ribosome (without viomycin)
3	c5mmil	 Alignment		100.0	26	PDB header: ribosome Chain: I; PDB Molecule: plastid ribosomal protein ul10c; PDBTitle: structure of the large subunit of the chloroplast ribosome
4	c5o60L	 Alignment		100.0	83	PDB header: ribosome Chain: I; PDB Molecule: 50s ribosomal protein l10; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
5	c3i8iY	 Alignment		100.0	32	PDB header: ribosome Chain: Y; PDB Molecule: 50s ribosomal protein l10; PDBTitle: elongation complex of the 70s ribosome with three trnas and mrna. this2 entry 3i8i contains 50s ribosomal subnit. the 30s ribosomal subunit3 can be found in pdb entry 3i8h. molecule a in the same asymmetric4 unit is deposited as 3i8f (50s) and 3i8g (30s).
6	c4v19J	 Alignment		100.0	21	PDB header: ribosome Chain: J; PDB Molecule: mitoribosomal protein ul10m, mrpl10; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
7	c3a1yG	 Alignment		99.9	21	PDB header: ribosomal protein Chain: G; PDB Molecule: acidic ribosomal protein p0; PDBTitle: the structure of archaeal ribosomal stalk p1/p0 complex
8	c4byuq	 Alignment		99.9	19	PDB header: ribosome Chain: Q; PDB Molecule: 60s ribosomal protein l18-a; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnramet2 eukaryotic translation initiation complex
9	c2qa4G	 Alignment		99.8	20	PDB header: ribosome Chain: G; PDB Molecule: acidic ribosomal protein p0 homo; PDBTitle: a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
10	c3jyw8	 Alignment		99.8	20	PDB header: ribosome Chain: 8; PDB Molecule: 60s ribosomal protein lp0; PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
11	c3u5iq	 Alignment		99.8	21	PDB header: ribosome Chain: Q; PDB Molecule: 60s ribosomal protein l18-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome b

12	c4b6aq_	 Alignment		99.8	21	PDB header: ribosome Chain: Q; PDB Molecule: 60s ribosomal protein l18-b; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
13	c3jsyA_	 Alignment		99.8	22	PDB header: ribosomal protein Chain: A; PDB Molecule: acidic ribosomal protein p0 homolog; PDBTitle: n-terminal fragment of ribosomal protein l10 from methanococcus2 jannaschii
14	c3j3bq_	 Alignment		99.8	17	PDB header: ribosome Chain: Q; PDB Molecule: 60s ribosomal protein l18; PDBTitle: structure of the human 60s ribosomal proteins
15	c3iz5s_	 Alignment		99.8	24	PDB header: ribosome Chain: S; PDB Molecule: 60s ribosomal protein l18a (l18ae); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
16	c3izcs_	 Alignment		99.8	21	PDB header: ribosome Chain: S; PDB Molecule: 60s ribosomal protein rpl20 (l18ae); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
17	c4hubG_	 Alignment		99.8	22	PDB header: ribosome Chain: G; PDB Molecule: 50s ribosomal protein l10e; PDBTitle: the re-refined crystal structure of the haloarcula marismortui large2 ribosomal subunit at 2.4 angstrom resolution: more complete structure3 of the l7/l12 and l1 stalk, l5 and lx proteins
18	c3j21k_	 Alignment		99.7	23	PDB header: ribosome Chain: K; PDB Molecule: 50s ribosomal protein l14e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
19	c3j65n_	 Alignment		99.7	16	PDB header: ribosome Chain: N; PDB Molecule: 60s ribosomal protein l28; PDBTitle: arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
20	c4nwbA_	 Alignment		99.7	15	PDB header: unknown function Chain: A; PDB Molecule: mrna turnover protein 4; PDBTitle: crystal structure of mrt4
21	c5ancC_	 Alignment	not modelled	99.6	17	PDB header: translation Chain: C; PDB Molecule: 60s acidic ribosomal protein p0; PDBTitle: mechanism of eif6 release from the nascent 60s ribosomal subunit
22	c6humN_	 Alignment	not modelled	41.2	27	PDB header: proton transport Chain: N; PDB Molecule: nad(p)h-quinone oxidoreductase subunit n; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
23	c3rhtB_	 Alignment	not modelled	32.7	8	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: (gatase1)-like protein; PDBTitle: crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
24	c4jqsc_	 Alignment	not modelled	20.0	11	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative thua-like protein (bacunij_01602) from2 bacteroides uniformis atcc 8492 at 2.30 a resolution
25	d1a9xb2	 Alignment	not modelled	19.7	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
26	c1keeH_	 Alignment	not modelled	17.4	21	PDB header: ligase Chain: H; PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
27	c4h3za_	 Alignment	not modelled	17.4	15	PDB header: transferase Chain: A; PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of a symmetric dimer of a trna (guanine-(n(1)-)-2 methyltransferase from burkholderia phymatum bound to s-adenosyl3 homocystein in both half-sites

28	d1luza_	Alignment	not modelled	17.0	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
29	c5uazB_	Alignment	not modelled	16.3	16	PDB header: protein transport Chain: B: PDB Molecule: nucleoporin nup53; PDBTitle: crystal structure of the yeast nucleoporin
30	c5e8bB_	Alignment	not modelled	15.9	31	PDB header: transcription Chain: B: PDB Molecule: rna polymerase-associated protein rtf1; PDBTitle: crystal structure of the s. cerevisiae rtf1 histone modification2 domain mutant r126a
31	c3brcA_	Alignment	not modelled	15.5	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein of unknown function; PDBTitle: crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
32	c2lndA_	Alignment	not modelled	14.8	20	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein, pfk fold; PDBTitle: solution nmr structure of de novo designed protein, pfk fold,2 northeast structural genomics consortium target or134
33	c4qkoA_	Alignment	not modelled	14.6	21	PDB header: antimicrobial protein Chain: A: PDB Molecule: pyocin-s2 immunity protein; PDBTitle: the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms
34	c5wylB_	Alignment	not modelled	13.2	13	PDB header: ribosomal protein/nuclear protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of chaetomium thermophilum utp10 n-terminal domain2 in complex with utp17 c-terminal helices
35	c5wylD_	Alignment	not modelled	13.1	13	PDB header: ribosomal protein/nuclear protein Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of chaetomium thermophilum utp10 n-terminal domain2 in complex with utp17 c-terminal helices
36	c5emxA_	Alignment	not modelled	12.5	31	PDB header: transcription Chain: A: PDB Molecule: rna polymerase-associated protein rtf1; PDBTitle: crystal structure of the s. cerevisiae rtf1 histone modification2 domain mutant r124a r126a r128a
37	c3j7jA_	Alignment	not modelled	12.4	9	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit a; PDBTitle: model of the human eif3 pci-mpn octamer docked into the 43s-hcv ires2 em map
38	c3j7kA_	Alignment	not modelled	12.4	9	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit a; PDBTitle: model of the human eif3 pci-mpn octamer docked into the 43s em map
39	c3j8cA_	Alignment	not modelled	12.4	9	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit a; PDBTitle: model of the human eif3 pci-mpn octamer docked into the 43s em map
40	c3j8bA_	Alignment	not modelled	12.4	9	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit a; PDBTitle: model of the human eif3 pci-mpn octamer docked into the 43s-hcv ires2 em map
41	c3m20A_	Alignment	not modelled	11.5	16	PDB header: isomerase Chain: A: PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
42	c5d5pC_	Alignment	not modelled	11.4	10	PDB header: transferase Chain: C: PDB Molecule: hcgB; PDBTitle: hcgB from methanococcus maripaludis
43	c2qv6D_	Alignment	not modelled	11.1	17	PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase iii; PDBTitle: gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
44	d1jo0a_	Alignment	not modelled	10.9	18	Fold: IF3-like Superfamily: YhbY-like Family: YhbY-like
45	d1gyxa_	Alignment	not modelled	10.6	26	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
46	c3d5dJ_	Alignment	not modelled	10.5	58	PDB header: ribosome Chain: J: PDB Molecule: 50s ribosomal protein l10; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of the second 70s ribosome. the entire3 crystal structure contains two 70s ribosomes as described in remark4 400.
47	c3d5bJ_	Alignment	not modelled	10.5	58	PDB header: ribosome Chain: J: PDB Molecule: 50s ribosomal protein l10; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
48	d2gk3a1	Alignment	not modelled	10.3	8	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: STM3548-like
49	c5oiyC_	Alignment	not modelled	9.9	41	PDB header: viral protein Chain: C: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
50	c5oixE_	Alignment	not modelled	9.9	41	PDB header: viral protein Chain: E: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
51	c5oiyG_	Alignment	not modelled	9.9	41	PDB header: viral protein Chain: G: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
52	c5oiyE_	Alignment	not modelled	9.9	41	PDB header: viral protein Chain: E: PDB Molecule: phosphoprotein;

						PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
53	c5oixA_	Alignment	not modelled	9.9	41	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
54	c4bxtD_	Alignment	not modelled	9.9	41	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
55	c5oixF_	Alignment	not modelled	9.9	41	PDB header: viral protein Chain: F: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
56	c5oixB_	Alignment	not modelled	9.7	41	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
57	c4bxtE_	Alignment	not modelled	9.7	41	PDB header: viral protein Chain: E: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
58	c4bxtF_	Alignment	not modelled	9.7	41	PDB header: viral protein Chain: F: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
59	c4bxtB_	Alignment	not modelled	9.7	41	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
60	c5oiyH_	Alignment	not modelled	9.7	41	PDB header: viral protein Chain: H: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
61	c5oixC_	Alignment	not modelled	9.6	41	PDB header: viral protein Chain: C: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
62	c5oiyB_	Alignment	not modelled	9.6	41	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
63	c4bxtG_	Alignment	not modelled	9.6	41	PDB header: viral protein Chain: G: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
64	c5oiyA_	Alignment	not modelled	9.6	41	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
65	c5oixG_	Alignment	not modelled	9.6	41	PDB header: viral protein Chain: G: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
66	c4bxtH_	Alignment	not modelled	9.5	41	PDB header: viral protein Chain: H: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
67	c3mrzI_	Alignment	not modelled	9.5	58	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: recognition of the amber stop codon by release factor rf1. this entry2 3mrz contains 50s ribosomal subunit. the 30s ribosomal subunit can be3 found in pdb entry 3ms0. molecule a in the same asymmetric unit is4 deposited as 3mr8 (50s) and 3ms1 (30s).
68	c3ms1I_	Alignment	not modelled	9.5	58	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: recognition of the amber stop codon by release factor rf1. this entry2 3ms1 contains 50s ribosomal subunit. the 30s ribosomal subunit can be3 found in pdb entry 3mr8. molecule b in the same asymmetric unit is4 deposited as 3mrz (50s) and 3ms0 (30s).
69	c5oiyF_	Alignment	not modelled	9.4	41	PDB header: viral protein Chain: F: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
70	c3oepA_	Alignment	not modelled	9.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha0988; PDBTitle: crystal structure of ttha0988 in space group p43212
71	c5oixH_	Alignment	not modelled	9.3	41	PDB header: viral protein Chain: H: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
72	c5oiyD_	Alignment	not modelled	9.3	41	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
73	c4bxtA_	Alignment	not modelled	9.3	41	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
74	c5oixD_	Alignment	not modelled	9.3	41	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
75	d1iioa_	Alignment	not modelled	9.1	19	Fold: EF Hand-like Superfamily: Hypothetical protein MTH865 Family: Hypothetical protein MTH865
76	c4bxtC_	Alignment	not modelled	9.1	41	PDB header: viral protein Chain: C: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
77	c6fj3A_	Alignment	not modelled	8.5	23	PDB header: membrane protein Chain: A: PDB Molecule: parathyroid hormone/parathyroid hormone-related peptide PDBTitle: high resolution crystal structure of parathyroid hormone 1

						receptor in2 complex with a peptide agonist.
78	d2qkwa1	Alignment	not modelled	8.1	29	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Avirulence protein AvrPto Family: Avirulence protein AvrPto
79	c2qkwa	Alignment	not modelled	8.1	29	PDB header: transferase Chain: A: PDB Molecule: avirulence protein; PDBTitle: structural basis for activation of plant immunity by2 bacterial effector protein avrpto
80	c1e0tD	Alignment	not modelled	8.0	11	PDB header: phosphotransferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: r292d mutant of e. coli pyruvate kinase
81	d1yc5a1	Alignment	not modelled	8.0	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
82	c2p3wB	Alignment	not modelled	8.0	16	PDB header: protein binding Chain: B: PDB Molecule: probable serine protease htra3; PDBTitle: crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgrwv)
83	c2m4mA	Alignment	not modelled	7.9	16	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: solution structure of the rrm domain of the hypothetical protein2 cagl0m09691g from candida glabrata
84	c4hylB	Alignment	not modelled	7.7	12	PDB header: transcription regulator Chain: B: PDB Molecule: stage ii sporulation protein; PDBTitle: the crystal structure of an anti-sigma-factor antagonist from2 haliangium ochraceum dsm 14365
85	c4ij0B	Alignment	not modelled	7.7	16	PDB header: electron transport Chain: B: PDB Molecule: mamp; PDBTitle: crystal structure of mamp
86	c5mquA	Alignment	not modelled	7.5	16	PDB header: virus Chain: A: PDB Molecule: vp1; PDBTitle: crystal structure of bovine enterovirus 2 determined with serial2 femtosecond x-ray crystallography
87	c3ku7B	Alignment	not modelled	7.4	11	PDB header: cell cycle Chain: B: PDB Molecule: cell division topological specificity factor; PDBTitle: crystal structure of helicobacter pylori mine, a cell division2 topological specificity factor
88	c3j9tQ	Alignment	not modelled	7.3	15	PDB header: hydrolase Chain: Q: PDB Molecule: v-type proton atpase subunit d; PDBTitle: yeast v-atpase state 1
89	c6emvA	Alignment	not modelled	7.0	9	PDB header: rna binding protein Chain: A: PDB Molecule: trna (guanine(9)-/adenine(9)-n1)-methyltransferase; PDBTitle: crystal structure of dual specific trm10 construct from thermococcus2 kodakaraensis.
90	d1ni5a1	Alignment	not modelled	6.8	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
91	d1rq8a	Alignment	not modelled	6.4	11	Fold: IF3-like Superfamily: YhbY-like Family: YhbY-like
92	c3oirA	Alignment	not modelled	6.3	16	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter sulfate transporter family protein; PDBTitle: crystal structure of sulfate transporter family protein from wolinella2 succinogenes
93	c5vymB	Alignment	not modelled	6.2	11	PDB header: hydrolase Chain: B: PDB Molecule: beta-galactosidase bgab; PDBTitle: crystal structure of beta-galactosidase from bifidobacterium2 adolescentis
94	d1jjga	Alignment	not modelled	6.2	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
95	c3ccjG	Alignment	not modelled	6.1	45	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l10e; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u
96	c1s72G	Alignment	not modelled	6.1	45	PDB header: ribosome Chain: G: PDB Molecule: acidic ribosomal protein p0 homolog; PDBTitle: refined crystal structure of the haloarcula marismortui large2 ribosomal subunit at 2.4 angstrom resolution
97	c3cmaG	Alignment	not modelled	6.1	45	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l10e; PDBTitle: the structure of cca and cca-phe-cap-bio bound to the large ribosomal2 subunit of haloarcula marismortui
98	c1w2bG	Alignment	not modelled	6.1	45	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l10e; PDBTitle: trigger factor ribosome binding domain in complex with 50s
99	c3g6eG	Alignment	not modelled	6.1	45	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l10e; PDBTitle: co-crystal structure of homoharringtonine bound to the large ribosomal2 subunit