



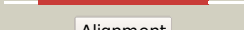

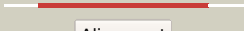









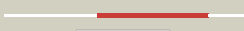







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3579c_(-)_4021604_4022572
Date	Fri Aug 9 18:20:26 BST 2019
Unique Job ID	ea97a962df9d7cf5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gz0H_	 Alignment		100.0	33	PDB header: transferase Chain: H: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase rImb
2	c3gyqB_	 Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: rrna (adenosine-2'-o-)-methyltransferase; PDBTitle: structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
3	c1ipaA_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: rna 2'-o-ribose methyltransferase; PDBTitle: crystal structure of rna 2'-o ribose methyltransferase
4	c4x3mB_	 Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: rna 2'-o ribose methyltransferase; PDBTitle: crystal structure of ttha0275 from thermus thermophilus (hb8) in2 complex with adenosine in space group p212121
5	c5kzkA_	 Alignment		100.0	24	PDB header: rna binding protein Chain: A: PDB Molecule: probable rna methyltransferase, trmh family; PDBTitle: crystal structure of rrna methyltransferase from sinorhizobium2 meliloti
6	c1x7pB_	 Alignment		100.0	27	PDB header: transferase Chain: B: PDB Molecule: rrna methyltransferase; PDBTitle: crystal structure of the spoU methyltransferase avirb from2 streptomyces viridochromogenes in complex with the cofactor adomet
7	c2i6dA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: rrna methyltransferase, trmh family; PDBTitle: the structure of a putative rna methyltransferase of the trmh family2 from porphyromonas gingivalis.
8	d1gz0a1	 Alignment		100.0	41	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
9	c1gz0G_	 Alignment		100.0	41	PDB header: transferase Chain: G: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase rImb
10	c1zjrA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: trna (guanosine-2'-o-)-methyltransferase; PDBTitle: crystal structure of a. aeolicus trmh/spoU trna modifying enzyme
11	c5co4A_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: putative trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: structural insights into the 2-oh methylation of c/u34 on trna

12	d1v2xa_	Alignment		100.0	27	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
13	d1ipaa1	Alignment		100.0	27	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
14	c2ha8A_	Alignment		100.0	21	PDB header: rna binding protein Chain: A: PDB Molecule: tar (hiv-1) rna loop binding protein; PDBTitle: methyltransferase domain of human tar (hiv-1) rna binding2 protein 1
15	c4pzka_	Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: crystal structure of putative rna methyltransferase from bacillus2 anthracis.
16	d1mxia_	Alignment		100.0	20	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
17	c3onpA_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: trna(rrna) methyltransferase (spou); PDBTitle: crystal structure of trna/rrna methyltransferase spou from rhodobacter2 sphaeroides
18	c3ic6A_	Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methylase family protein; PDBTitle: crystal structure of putative methylase family protein from neisseria2 gonorrhoeae
19	c5gm8A_	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: methylation at position 32 of trna catalyzed by trmj alters oxidative2 stress response in pseudomonas aeruginosa
20	c3e5yB_	Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: trmh family rna methyltransferase; PDBTitle: crystal structure of trmh family rna methyltransferase from2 burkholderia pseudomallei
21	c3l8uA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: putative rrna methylase; PDBTitle: crystal structure of smu.1707c, a putative rrna methyltransferase from2 streptococcus mutans ua159
22	c4cngB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: spou rrna methylase; PDBTitle: crystal structure of sulfolobus acidocaldarius trmj in2 complex with s-adenosyl-l-homocysteine
23	c5graA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: crystal structure of trmj from z. mobilis zm4
24	c4cndB_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: crystal structure of e.coli trmj
25	c3ktyA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: probable methyltransferase; PDBTitle: crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
26	c4xboA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: crystal structure of full length e.coli trmj in complex with sah
27	c3ilkB_	Alignment	not modelled	100.0	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized trna/rrna methyltransferase hi0380; PDBTitle: the structure of a probable methylase family protein from haemophilus2 influenzae rd kw20
						PDB header: transferase Chain: X: PDB Molecule: uncharacterized protein tm_1570;

28	c3dcmX_	Alignment	not modelled	99.9	17	PDBTitle: crystal structure of the thermotoga maritima spout family rna-2 methyltransferase protein tm1570 in complex with s-adenosyl-3 methionine
29	c6ahwB_	Alignment	not modelled	99.8	25	PDB header: transferase Chain: B; PDB Molecule: circular-permuted trna (cytidine(34)-2'-o)- PDBTitle: crystal structure of circular-permuted yibk methyltransferase from2 haemophilus influenzae
30	d1gz0f2	Alignment	not modelled	99.7	23	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
31	d1gz0a2	Alignment	not modelled	99.6	25	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
32	d1ipaa2	Alignment	not modelled	99.1	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
33	c2yy8B_	Alignment	not modelled	97.6	21	PDB header: transferase Chain: B; PDB Molecule: upf0106 protein ph0461; PDBTitle: crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
34	c1vhkA_	Alignment	not modelled	97.1	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein yqeu; PDBTitle: crystal structure of an hypothetical protein
35	d1vhka2	Alignment	not modelled	96.8	14	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
36	d2o3aa1	Alignment	not modelled	96.7	26	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF0751-like
37	c5o96F_	Alignment	not modelled	96.3	16	PDB header: transferase Chain: F; PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: structure of the putative methyltransferase lpg2936 from legionella2 pneumophila in complex with the bound cofactor sam
38	c3ai9X_	Alignment	not modelled	95.7	15	PDB header: transferase Chain: X; PDB Molecule: upf0217 protein mj1640; PDBTitle: crystal structure of duf358 protein reveals a putative spout-class2 rna methyltransferase
39	c4a1dG_	Alignment	not modelled	95.7	15	PDB header: ribosome Chain: G; PDB Molecule: rpl30; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rna and proteins of3 molecule 4.
40	d2bo1a1	Alignment	not modelled	95.3	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
41	c4j3cB_	Alignment	not modelled	95.2	20	PDB header: transferase Chain: B; PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s ribosomal rna methyltransferase rsme
42	c1vhyB_	Alignment	not modelled	95.1	16	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: hypothetical protein hi0303; PDBTitle: crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558
43	d1vqof1	Alignment	not modelled	95.1	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
44	c3zf7g_	Alignment	not modelled	95.0	20	PDB header: ribosome Chain: G; PDB Molecule: PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
45	d1nxza2	Alignment	not modelled	94.9	12	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
46	d1w41a1	Alignment	not modelled	94.8	20	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
47	d1rlga_	Alignment	not modelled	94.7	15	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
48	c3cpqB_	Alignment	not modelled	94.6	12	PDB header: ribosomal protein Chain: B; PDB Molecule: 50s ribosomal protein l30e; PDBTitle: crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
49	d1ij2f_	Alignment	not modelled	94.3	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
50	d2fc3a1	Alignment	not modelled	94.2	14	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
51	c2zkr6_	Alignment	not modelled	94.2	18	PDB header: ribosomal protein/rna Chain: 6; PDB Molecule: 60s ribosomal protein l30e; PDBTitle: 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
52	c2lbwA_	Alignment	not modelled	94.2	17	PDB header: rna binding protein Chain: A; PDB Molecule: h/aca ribonucleoprotein complex subunit 2; PDBTitle: solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant PDB header: ribosome

53	c3j21Z_	Alignment	not modelled	94.1	20	Chain: Z; PDB Molecule: 50s ribosomal protein l30e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by 2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
54	d1xbia1	Alignment	not modelled	94.0	14	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
55	c5vm8A_	Alignment	not modelled	94.0	11	PDB header: transferase Chain: A; PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of a ribosomal rna small subunit methyltransferase e2 from neisseria gonorrhoeae bound to s-adenosyl methionine
56	c3kw2A_	Alignment	not modelled	94.0	10	PDB header: transferase Chain: A; PDB Molecule: probable r-rna methyltransferase; PDBTitle: crystal structure of probable rrna-methyltransferase from 2 porphyromonas gingivalis
57	d1t0kb_	Alignment	not modelled	93.9	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
58	d2czwa1	Alignment	not modelled	93.4	13	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
59	c3o85A_	Alignment	not modelled	93.3	18	PDB header: ribosomal protein Chain: A; PDB Molecule: ribosomal protein l7ae; PDBTitle: giardia lamblia 15.5kd rna binding protein
60	c4l69A_	Alignment	not modelled	93.2	16	PDB header: transferase Chain: A; PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: rv2372c of mycobacterium tuberculosis is rsmc like methyltransferase
61	d2aifa1	Alignment	not modelled	93.0	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
62	c5ewrA_	Alignment	not modelled	92.9	20	PDB header: rna binding protein Chain: A; PDB Molecule: box c/d snornc and u4 snrnc component snu13p; PDBTitle: c merolae u4 snrnc protein snu13
63	c3v7qB_	Alignment	not modelled	92.6	14	PDB header: rna binding protein Chain: B; PDB Molecule: probable ribosomal protein ylxq; PDBTitle: crystal structure of b. subtilis ylxq at 1.55 a resolution
64	d2qi2a3	Alignment	not modelled	92.2	20	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
65	d2qwva1	Alignment	not modelled	92.2	16	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF1056-like
66	c3zeyF_	Alignment	not modelled	92.1	22	PDB header: ribosome Chain: F; PDB Molecule: 40s ribosomal protein s12; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
67	c5xyiM_	Alignment	not modelled	91.6	11	PDB header: ribosome Chain: M; PDB Molecule: ribosomal protein l7ae, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
68	d2ozba1	Alignment	not modelled	91.3	13	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
69	c2xznU_	Alignment	not modelled	89.2	24	PDB header: ribosome Chain: U; PDB Molecule: ribosomal protein l7ae containing protein; PDBTitle: 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 2
70	c2ktvA_	Alignment	not modelled	89.2	21	PDB header: translation Chain: A; PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: human erf1 c-domain, "open" conformer
71	c2cx8A_	Alignment	not modelled	88.1	17	PDB header: transferase Chain: A; PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
72	c3on1A_	Alignment	not modelled	88.0	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: bh2414 protein; PDBTitle: the structure of a protein with unknown function from bacillus2 halodurans c
73	c2qi2A_	Alignment	not modelled	87.9	17	PDB header: cell cycle Chain: A; PDB Molecule: cell division protein pelota related protein; PDBTitle: crystal structure of the thermoplasma acidophilum pelota2 protein
74	d1dt9a2	Alignment	not modelled	87.7	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
75	c3j3aM_	Alignment	not modelled	87.6	14	PDB header: ribosome Chain: M; PDB Molecule: 40s ribosomal protein s12; PDBTitle: structure of the human 40s ribosomal proteins
76	d1x52a1	Alignment	not modelled	87.3	12	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
77	c2egwB_	Alignment	not modelled	87.1	17	PDB header: rna methyltransferase Chain: B; PDB Molecule: upf0088 protein aq_165; PDBTitle: crystal structure of rrna methyltransferase with sah ligand
78	c4af1A_	Alignment	not modelled	86.9	19	PDB header: hydrolase Chain: A; PDB Molecule: peptide chain release factor subunit 1; PDBTitle: archeal release factor arf1

79	d2vgna3	Alignment	not modelled	86.9	21	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
80	d2alea1	Alignment	not modelled	86.6	19	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
81	d1v6za2	Alignment	not modelled	86.3	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
82	c1dt9A_	Alignment	not modelled	85.6	17	PDB header: translation Chain: A: PDB Molecule: protein (eukaryotic peptide chain release factor PDBTitle: the crystal structure of human eukaryotic release factor2 erf1-mechanism of stop codon recognition and peptidyl-trna3 hydrolysis
83	c2cx8B_	Alignment	not modelled	85.0	18	PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
84	c3agiD_	Alignment	not modelled	85.0	14	PDB header: translation/hydrolase Chain: D: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
85	c3agkA_	Alignment	not modelled	84.9	26	PDB header: translation Chain: A: PDB Molecule: peptide chain release factor subunit 1; PDBTitle: crystal structure of archaeal translation termination factor, arf1
86	c3agiB_	Alignment	not modelled	84.7	14	PDB header: translation/hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
87	c2vgmA_	Alignment	not modelled	83.7	21	PDB header: cell cycle Chain: A: PDB Molecule: dom34; PDBTitle: structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
88	c1z85B_	Alignment	not modelled	83.7	23	PDB header: transferase Chain: B: PDB Molecule: hypothetical protein tm1380; PDBTitle: crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution
89	c3obwA_	Alignment	not modelled	83.1	14	PDB header: hydrolase Chain: A: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of two archaeal pelotas reveal inter-domain2 structural plasticity
90	c2zkrf_	Alignment	not modelled	81.9	17	PDB header: ribosomal protein/rna Chain: F: PDB Molecule: rna expansion segment es7 part iii; PDBTitle: 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
91	c4a1eF_	Alignment	not modelled	77.5	16	PDB header: ribosome Chain: F: PDB Molecule: rpl7a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
92	c5xxuM_	Alignment	not modelled	77.3	16	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein es12; PDBTitle: small subunit of toxoplasma gondii ribosome
93	c2ekcA_	Alignment	not modelled	76.7	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
94	c3j15A_	Alignment	not modelled	76.4	22	PDB header: translation/transport protein Chain: A: PDB Molecule: protein pelota; PDBTitle: model of ribosome-bound archaeal pelota and abce1
95	c3mcaB_	Alignment	not modelled	75.2	14	PDB header: translation regulation/hydrolase Chain: B: PDB Molecule: protein dom34; PDBTitle: structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
96	c3j38M_	Alignment	not modelled	74.8	14	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s12; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
97	c3obyB_	Alignment	not modelled	73.0	21	PDB header: hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
98	d2qmma1	Alignment	not modelled	72.5	20	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF1056-like
99	c3j61G_	Alignment	not modelled	70.8	19	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l8e; PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
100	c3v7eB_	Alignment	not modelled	67.1	17	PDB header: ribosomal protein/rna Chain: B: PDB Molecule: ribosome-associated protein l7ae-like; PDBTitle: crystal structure of ybxf bound to the sam-i riboswitch aptamer
101	c3e20C_	Alignment	not modelled	66.0	16	PDB header: translation Chain: C: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of s.pombe erf1/erf3 complex
102	c3iz5H_	Alignment	not modelled	65.2	14	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l7a (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
103	c3j3bG_	Alignment	not modelled	64.4	19	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l7a; PDBTitle: structure of the human 60s ribosomal proteins
						PDB header: lyase

104	c3gndC_	Alignment	not modelled	62.8	17	Chain: C; PDB Molecule: aldolase lsrt; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
105	c2csuB_	Alignment	not modelled	61.6	17	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
106	c3izcH_	Alignment	not modelled	60.6	18	PDB header: ribosome Chain: H; PDB Molecule: 60s ribosomal protein rpl8 (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
107	c3ir9A_	Alignment	not modelled	60.2	22	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: peptide chain release factor subunit 1; PDBTitle: c-terminal domain of peptide chain release factor from methanosarcina2 mazel.
108	c3e20H_	Alignment	not modelled	59.5	12	PDB header: translation Chain: H; PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of s.pombe erf1/erf3 complex
109	c3l07B_	Alignment	not modelled	56.5	17	PDB header: oxidoreductase,hydrolase Chain: B; PDB Molecule: bifunctional protein fold; PDBTitle: methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
110	c3cg6A_	Alignment	not modelled	56.2	20	PDB header: cell cycle Chain: A; PDB Molecule: growth arrest and dna-damage-inducible 45 gamma; PDBTitle: crystal structure of gadd45 gamma
111	c3ib6B_	Alignment	not modelled	55.1	11	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
112	c2gqnB_	Alignment	not modelled	53.3	12	PDB header: lyase Chain: B; PDB Molecule: cystathionine beta-lyase; PDBTitle: cystathionine beta-lyase (cbl) from escherichia coli in complex with2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
113	c3u5cM_	Alignment	not modelled	52.0	10	PDB header: ribosome Chain: M; PDB Molecule: 40s ribosomal protein s12; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
114	d1jvna2	Alignment	not modelled	43.7	9	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
115	d1cs1a_	Alignment	not modelled	43.7	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
116	c2c3zA_	Alignment	not modelled	42.8	14	PDB header: lyase Chain: A; PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
117	c4e8bA_	Alignment	not modelled	42.8	9	PDB header: transferase Chain: A; PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s rrna methyltransferase rsme from e.coli
118	d1xcfa_	Alignment	not modelled	41.5	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
119	d1cl1a_	Alignment	not modelled	41.5	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
120	c1s1iG_	Alignment	not modelled	40.6	12	PDB header: ribosome Chain: G; PDB Molecule: 60s ribosomal protein l8-a; PDBTitle: 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.