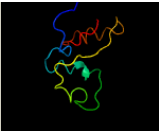
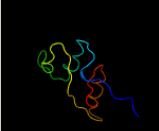

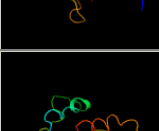
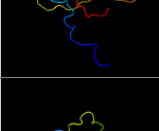

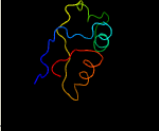

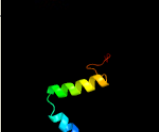


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0652_(rplL)_748852_749244
Date	Fri Jul 26 01:50:22 BST 2019
Unique Job ID	4f7971f846b93d89

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1giyl_	Alignment		100.0	58	PDB header: ribosome Chain: J; PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of the ribosome at 5.5 a resolution. this2 file, 1giy, contains the 50s ribosome subunit. the 30s3 ribosome subunit, three trna, and mrna molecules are in the4 file 1gix
2	c2gya3_	Alignment		100.0	55	PDB header: ribosome Chain: 3; PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: structure of the 50s subunit of a pre-translocational e. coli ribosome2 obtained by fitting atomic models for rna and protein components into3 cryo-em map emd-1056
3	c2ftcF_	Alignment		100.0	34	PDB header: ribosome Chain: F; PDB Molecule: 39s ribosomal protein l12, mitochondrial; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
4	d2zjq51	Alignment		99.9	58	Fold: ClpS-like Superfamily: ClpS-like Family: Ribosomal protein L7/12, C-terminal domain
5	c2zjq5_	Alignment		99.9	58	PDB header: ribosome Chain: 5; PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: interaction of l7 with l11 induced by micrococin binding to the2 deinococcus radiodurans 50s subunit
6	d1ctfa_	Alignment		99.9	62	Fold: ClpS-like Superfamily: ClpS-like Family: Ribosomal protein L7/12, C-terminal domain
7	d1dd3a2	Alignment		99.9	62	Fold: ClpS-like Superfamily: ClpS-like Family: Ribosomal protein L7/12, C-terminal domain
8	c4kdhe_	Alignment		99.9	45	PDB header: ribosome Chain: E; PDB Molecule: 50s ribosomal protein l3; PDBTitle: 70s ribosome translocation intermediate fa-4.2a containing elongation2 factor efg/fusidic acid/gdp, mrna, and trna bound in the pe*/e state.3 this entry contains the 50s ribosomal subunit a. the 30s subunit a4 can be found in 4kdg. molecule b in the same asymmetric unit is5 deposited as 4kdj (30s) and 4kdk (50s).
9	c4kd2e_	Alignment		99.9	45	PDB header: ribosome/antibiotic Chain: E; PDB Molecule: 50s ribosomal protein l3; PDBTitle: 70s ribosome translocation intermediate gdpnp-i containing elongation2 factor efg/gdpnp, mrna, and trna bound in the pe*/e state. this entry3 contains the 50s ribosomal subunit b. the 30s subunit b can be found4 in 4kd0. molecule a in the same asymmetric unit is deposited as 4kcy5 (30s) and 4kcz (50s).
10	c4kd9e_	Alignment		99.9	45	PDB header: ribosome/antibiotic Chain: E; PDB Molecule: 50s ribosomal protein l3; PDBTitle: 70s ribosome translocation intermediate fa-3.6a containing elongation2 factor efg/fusidic acid/gdp, mrna, and trna bound in the pe*/e state.3 this entry contains the 50s ribosomal subunit a. the 30s subunit a4 can be found in 4kd8. molecule b in the same asymmetric unit is5 deposited as 4kda (30s) and 4kdb (50s).
11	c4kdke_	Alignment		99.9	45	PDB header: ribosome Chain: E; PDB Molecule: 50s ribosomal protein l3; PDBTitle: 70s ribosome translocation intermediate fa-4.2a containing elongation2 factor efg/fusidic acid/gdp, mrna, and trna bound in the pe*/e state.3 this entry contains the 50s ribosomal subunit b. the 30s subunit b4 can be found in 4kdj. molecule a in the same asymmetric unit is5 deposited as 4kdg (30s) and 4kdh (50s).
						PDB header: ribosome/antibiotic

12	c4kbue	Alignment		99.9	45	Chain: E: PDB Molecule: 50s ribosomal protein I3; PDBTitle: 70s ribosome translocation intermediate gdpnp-ii containing elongation2 factor efg/gdpnp, mrna, and trna bound in the pe*/e state. this entry3 contains 50s ribosomal subunit a. the full asymmetric unit also4 contains pdb entries 4kbt (30s subunit a), 4kbv (30s subunit b), and5 4kbv (50s subunit b).
13	c4qs1e	Alignment		99.9	45	PDB header: ribosome Chain: E: PDB Molecule: 50s ribosomal protein I3; PDBTitle: 70s ribosome translocation intermediate containing elongation factor2 efg/gdp/fusidic acid, mrna, and trnas trapped in the ap/ap pe/e3 chimeric hybrid state. this entry contains the 50s ribosomal subunit4 a. the 30s subunit a can be found in 4qs0. molecule b in the same5 asymmetric unit is deposited as 4qs2 (30s) and 4qs3 (50s)
14	c4kcze	Alignment		99.9	45	PDB header: ribosome/antibiotic Chain: E: PDB Molecule: 50s ribosomal protein I3; PDBTitle: 70s ribosome translocation intermediate gdpnp-i containing elongation2 factor efg/gdpnp, mrna, and trna bound in the pe*/e state.this entry3 contains the 50s ribosomal subunit a. the 30s subunit a can be found4 in 4kcy. molecule b in the same asymmetric unit is deposited as 4kd05 (30s) and 4kd2 (50s).g1 50s ribosomal subunit i
15	c4qs3e	Alignment		99.9	45	PDB header: ribosome/antibiotic Chain: E: PDB Molecule: 50s ribosomal protein I3; PDBTitle: 70s ribosome translocation intermediate containing elongation factor2 efg/gdp/fusidic acid, mrna, and trnas trapped in the ap/ap pe/e3 chimeric hybrid state. this entry contains the 50s ribosomal subunit4 b. the 30s subunit b can be found in 4qs2. molecule a in the same5 asymmetric unit is deposited as 4qs0 (30s) and 4qs1 (50s)
16	c4kbwe	Alignment		99.9	45	PDB header: ribosome/antibiotic Chain: E: PDB Molecule: 50s ribosomal protein I3; PDBTitle: 70s ribosome translocation intermediate gdpnp-ii containing elongation2 factor efg/gdpnp, mrna, and trna bound in the pe*/e state. this entry3 contains 50s ribosomal subunit b. the full asymmetric unit also4 contains pdb entries 4kbv (30s subunit b), 4kbt (30s subunit a), and5 4kbu (50s subunit a).
17	c4kdbe	Alignment		99.9	45	PDB header: ribosome/antibiotic Chain: E: PDB Molecule: 50s ribosomal protein I3; PDBTitle: 70s ribosome translocation intermediate fa-3.6a containing elongation2 factor efg/fusidic acid/gdp, mrna, and trna bound in the pe*/e state.3 this entry contains the 50s ribosomal subunit b. the 30s subunit a4 can be found in 4kda. molecule a in the same asymmetric unit is5 deposited as 4kd8 (30s) and 4kd9 (50s).
18	d1dd3a1	Alignment		99.1	51	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
19	d1dd4d	Alignment		98.5	53	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
20	d1dd4c	Alignment		98.0	46	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
21	d2gyc31	Alignment	not modelled	97.9	34	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
22	c1dd3C	Alignment	not modelled	97.7	41	PDB header: ribosome Chain: C: PDB Molecule: 50s ribosomal protein I7/I12; PDBTitle: crystal structure of ribosomal protein I12 from thermotoga maritima
23	c1dd3D	Alignment	not modelled	97.7	41	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein I7/I12; PDBTitle: crystal structure of ribosomal protein I12 from thermotoga maritima
24	c1rqtB	Alignment	not modelled	97.5	27	PDB header: ribosome Chain: B: PDB Molecule: 50s ribosomal protein I7/I12; PDBTitle: nmr structure of dimeric n-terminal domain of ribosomal2 protein I7 from e.coli
25	d1rqtA	Alignment	not modelled	97.5	27	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
26	c1rqtA	Alignment	not modelled	97.5	27	PDB header: ribosome Chain: A: PDB Molecule: 50s ribosomal protein I7/I12; PDBTitle: nmr structure of dimeric n-terminal domain of ribosomal2 protein I7 from e.coli
27	c1zavW	Alignment	not modelled	97.3	37	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein I7/I12; PDBTitle: ribosomal protein I10-I12(ntd) complex, space group p21
28	d1zavu1	Alignment	not modelled	97.3	37	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain

						domain
29	c1zaxU_	Alignment	not modelled	97.3	37	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
30	c1zavU_	Alignment	not modelled	97.3	37	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
31	c1zaxW_	Alignment	not modelled	97.3	37	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
32	c1zaxV_	Alignment	not modelled	97.3	37	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
33	c1zavV_	Alignment	not modelled	97.3	37	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
34	c1zawW_	Alignment	not modelled	97.1	38	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
35	c1zawU_	Alignment	not modelled	97.1	38	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
36	c1zavV_	Alignment	not modelled	97.1	38	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
37	c1zaxZ_	Alignment	not modelled	97.0	38	PDB header: structural protein Chain: Z: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
38	c1zavY_	Alignment	not modelled	96.8	38	PDB header: structural protein Chain: Y: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
39	c1zaxX_	Alignment	not modelled	96.8	38	PDB header: structural protein Chain: X: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
40	c1zavX_	Alignment	not modelled	96.8	38	PDB header: structural protein Chain: X: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
41	c1zaxY_	Alignment	not modelled	96.8	38	PDB header: structural protein Chain: Y: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
42	c1zawX_	Alignment	not modelled	96.1	39	PDB header: structural protein Chain: X: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
43	c1zawY_	Alignment	not modelled	96.1	39	PDB header: structural protein Chain: Y: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
44	d1zavz1	Alignment	not modelled	94.0	37	Fold: Ribosomal protein L7/L12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/L12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/L12, oligomerisation (N-terminal) domain
45	c1zavZ_	Alignment	not modelled	94.0	37	PDB header: structural protein Chain: Z: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
46	c1zawZ_	Alignment	not modelled	93.9	37	PDB header: structural protein Chain: Z: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
47	c4uy86_	Alignment	not modelled	79.5	20	PDB header: ribosome Chain: 6: PDB Molecule: ribosomal l7 protein; PDBTitle: molecular basis for the ribosome functioning as a l-tryptophan sensor2 - cryo-em structure of a tnac stalled e.coli ribosome
48	d1aipc1	Alignment	not modelled	76.1	27	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
49	c1aipG_	Alignment	not modelled	65.1	30	PDB header: complex of two elongation factors Chain: G: PDB Molecule: elongation factor ts; PDBTitle: ef-tu ef-ts complex from thermus thermophilus
50	d1efub3	Alignment	not modelled	63.8	28	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
51	d1xb2b1	Alignment	not modelled	58.0	12	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
52	d2cp9a1	Alignment	not modelled	52.9	14	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
53	c1xb2B_	Alignment	not modelled	42.9	13	PDB header: translation Chain: B: PDB Molecule: elongation factor ts, mitochondrial; PDBTitle: crystal structure of bos taurus mitochondrial elongation2 factor tu/ts complex
54	c5xqlA_	Alignment	not modelled	40.2	17	PDB header: transcription Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of a pseudomonas aeruginosa

						transcriptional2 regulator
55	c2jmlA_	Alignment	not modelled	35.0	27	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
56	c3d6zA_	Alignment	not modelled	31.1	26	PDB header: transcription regulator/dna Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of r275e mutant of bmrr bound to dna and rhodamine
57	c1efuB_	Alignment	not modelled	31.1	29	PDB header: complex (two elongation factors) Chain: B: PDB Molecule: elongation factor ts; PDBTitle: elongation factor complex ef-tu/ef-ts from escherichia coli
58	c2m45A_	Alignment	not modelled	28.4	14	PDB header: hydrolase Chain: A: PDB Molecule: minichromosome maintenance protein mcm; PDBTitle: nmr solution structure of the c-terminus of the minichromosome2 maintenance protein mcm from sulfolobus solfataricus
59	c3i8iI_	Alignment	not modelled	26.8	22	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: elongation complex of the 70s ribosome with three trnas and mrna. this2 entry 3i8i contains 50s ribosomal subunit. 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).
60	c3m6zA_	Alignment	not modelled	24.4	26	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of an n-terminal 44 kda fragment of topoisomerase v2 in the presence of guanidium hydrochloride
61	d1q08a_	Alignment	not modelled	24.3	19	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
62	c3mmpC_	Alignment	not modelled	20.2	29	PDB header: transferase Chain: C: PDB Molecule: elongation factor tu 2, elongation factor ts; PDBTitle: structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
63	c2dt5A_	Alignment	not modelled	19.8	18	PDB header: dna binding protein Chain: A: PDB Molecule: at-rich dna-binding protein; PDBTitle: crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
64	d1mula_	Alignment	not modelled	19.2	23	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
65	d1in0a2	Alignment	not modelled	19.1	16	Fold: Ferredoxin-like Superfamily: YajQ-like Family: YajQ-like
66	c3j21L_	Alignment	not modelled	18.9	31	PDB header: ribosome Chain: L: PDB Molecule: 50s ribosomal protein l15p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
67	c2iifA_	Alignment	not modelled	18.8	18	PDB header: recombination/dna Chain: A: PDB Molecule: integration host factor; PDBTitle: single chain integration host factor mutant protein (scihf2-k45ae) in2 complex with dna
68	c4a1cK_	Alignment	not modelled	17.5	19	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein l27a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
69	c4r4eA_	Alignment	not modelled	16.4	25	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
70	c2vz4A_	Alignment	not modelled	14.3	33	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to promoter dna
71	c3j39a_	Alignment	not modelled	13.7	25	PDB header: ribosome Chain: A: PDB Molecule: 60s ribosomal protein l8; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
72	d2ogka1	Alignment	not modelled	13.6	25	Fold: RL5-like Superfamily: RL5-like Family: SSO1042-like
73	d1vqo11	Alignment	not modelled	13.5	38	Fold: Ribosomal proteins L15p and L18e Superfamily: Ribosomal proteins L15p and L18e Family: Ribosomal proteins L15p and L18e
74	d1r8da_	Alignment	not modelled	12.9	30	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
75	c4gfiA_	Alignment	not modelled	12.4	26	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topo-78, an n-terminal 78kda fragment of2 topoisomerase v
76	c5gpeB_	Alignment	not modelled	12.3	22	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, merr-family; PDBTitle: crystal structure of the transcription regulator pbrr691 from2 ralstonia metallidurans ch34 in complex with lead(ii)
77	c3gp4B_	Alignment	not modelled	12.3	22	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
78	c2ma3A_	Alignment	not modelled	12.1	25	PDB header: replication Chain: A: PDB Molecule: dna replication initiator (cdc21/cdc54); PDBTitle: nmr solution structure of the c-terminus of the minichromosome2 maintenance protein mcm from methanothermobacter thermautotrophicus

79	d1kxpd3	Alignment	not modelled	12.1	17	Fold: Serum albumin-like Superfamily: Serum albumin-like Family: Serum albumin-like
80	c3izct	Alignment	not modelled	11.8	13	PDB header: ribosome Chain: T: PDB Molecule: 60s ribosomal protein rpl19 (I19e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
81	d1r8ea1	Alignment	not modelled	11.7	23	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
82	d2axtu1	Alignment	not modelled	11.5	23	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: PsbU-like
83	d1p71a	Alignment	not modelled	11.4	21	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
84	c3qaoA	Alignment	not modelled	11.2	25	PDB header: transcription regulator Chain: A: PDB Molecule: merr-like transcriptional regulator; PDBTitle: the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
85	c5b7wB	Alignment	not modelled	10.9	24	PDB header: unknown function Chain: B: PDB Molecule: upf0234 protein xc_3703; PDBTitle: crystal structure of the yajq-family protein xc_3703 from xanthomonas2 campestris pv.campestris
86	c1in0B	Alignment	not modelled	10.8	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yajq protein; PDBTitle: yajq protein (hi1034)
87	d1nq4a	Alignment	not modelled	10.5	40	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
88	c2zkrl	Alignment	not modelled	10.3	19	PDB header: ribosomal protein/rna Chain: L: PDB Molecule: rna expansion segment es20; 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
89	c3hh0C	Alignment	not modelled	10.3	16	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
90	c4r24B	Alignment	not modelled	10.1	17	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
91	c2ndpA	Alignment	not modelled	10.0	11	PDB header: dna binding protein Chain: A: PDB Molecule: histone-like dna-binding superfamily protein; PDBTitle: structure of dna-binding hu protein from micoplasma mycoplasma2 gallisepticum
92	c2lxyA	Alignment	not modelled	9.9	38	PDB header: de novo protein Chain: A: PDB Molecule: 2-mercaptophenol-alpha3c; PDBTitle: nmr structure of 2-mercaptophenol-alpha3c
93	c4hyzA	Alignment	not modelled	9.8	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf3887 family protein (rumgna_01855) from2 ruminococcus gnavus atcc 29149 at 2.25 a resolution
94	c2l9fA	Alignment	not modelled	9.7	6	PDB header: transferase Chain: A: PDB Molecule: cale8; PDBTitle: nmr solution structure of meacp
95	d1e0ea	Alignment	not modelled	9.4	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
96	c2jw5A	Alignment	not modelled	9.3	8	PDB header: protein binding Chain: A: PDB Molecule: dna polymerase lambda; PDBTitle: polymerase lambda brct domain
97	c5j10A	Alignment	not modelled	9.1	41	PDB header: de novo protein Chain: A: PDB Molecule: peptide design 2l4hc2_24; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
98	c6c48E	Alignment	not modelled	9.1	20	PDB header: cell cycle/dna binding Chain: E: PDB Molecule: protein lin-52 homolog; PDBTitle: crystal structure of b-myb-lin9-lin52 complex
99	c3j3vL	Alignment	not modelled	9.1	50	PDB header: ribosome Chain: L: PDB Molecule: 50s ribosomal protein l15; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)