wwPDB EM Validation Summary Report (i)

Aug 17, 2026 – 08:24 pm BST

PDB ID	:	9T6M / pdb_00009t6m
EMDB ID	:	EMD-55618
Title	:	E. coli 70S ribosome from delta-10 strain
Authors	:	Larsson, D.S.D.; Selmer, M.
Deposited on	:	2025-11-07
Resolution	:	1.87 Å(reported)
Based on initial model	:	9T0Y

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

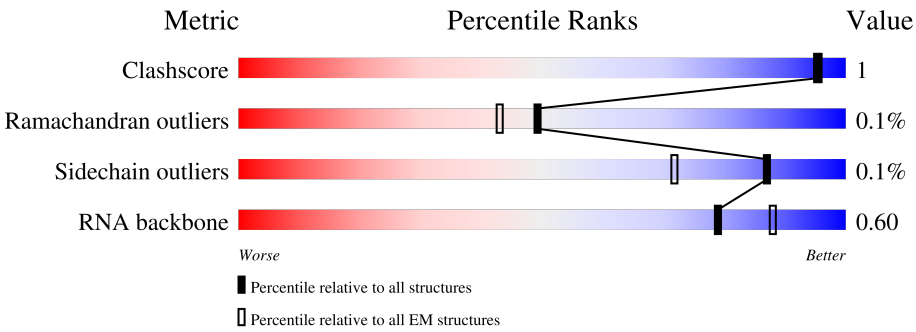
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

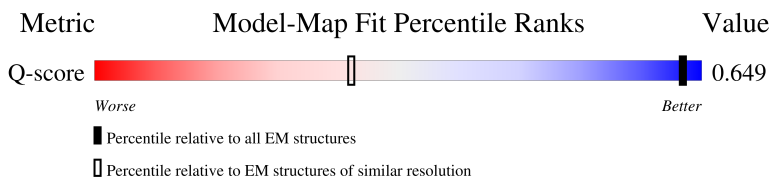
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 1.87 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	985 (1.37 - 2.37)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1542	8% 80% 18% • •
2	B	241	68% 88% • 11%
3	C	233	23% 87% • 12%

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Mol	Chain	Length	Quality of chain
4	D	206	46% 83% 16%
5	E	167	81% 11% 8%
6	F	135	19% 75% 25%
7	G	179	47% 82% 14%
8	H	130	8% 95%
9	I	130	29% 95%
10	J	103	50% 88% 5% 7%
11	K	129	11% 89% 9%
12	L	124	14% 85% 11%
13	M	118	44% 93%
14	N	101	17% 96%
15	O	89	11% 98%
16	P	82	21% 87% 6%
17	Q	84	25% 93% 6%
18	R	75	13% 85% 15%
19	S	92	53% 90% 9%
20	T	87	18% 99%
21	U	71	48% 97%
22	X	120	15% 10% 8% 82%
23	Y	76	91% 74% 14% 9%
24	5	77	83% 75% 16% 8%
24	Z	77	68% 75% 19% 5%
25	a	2904	5% 76% 20%
26	b	120	81% 14% 5%
27	c	273	92% 7%

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Mol	Chain	Length	Quality of chain
28	d	209	95%
29	e	201	9% 93% 6%
30	f	179	21% 97%
31	g	177	5% 91% 5%
32	h	149	9% 26% 72%
33	i	142	92% 8%
34	j	123	92% 7%
35	k	144	98%
36	l	136	93% 7%
37	m	127	85% 8% 7%
38	n	117	97%
39	o	115	96%
40	p	118	92% 7%
41	q	103	95%
42	r	110	99%
43	s	100	85% 8% 7%
44	t	104	5% 97%
45	u	94	98%
46	v	85	11% 93% 5%
47	w	78	95%
48	x	63	89% 5% 5%
49	y	59	93% 5%
50	z	57	84% 11% 5%
51	0	55	87% 9%
52	1	46	93%

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Mol	Chain	Length	Quality of chain
53	2	65	91% 8%
54	3	38	89% 11%
55	4	70	49% 83% 13%

2 Entry composition (i)

There are 61 unique types of molecules in this entry. The entry contains 150408 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1518	32582	14540	5977	10547	1518	0	0

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	215	1693	1071	305	309	8	0	0

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	206	1624	1028	305	288	3	0	0

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	205	1643	1026	315	298	4	0	0

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	154	1135	706	215	208	6	0	0

- Molecule 6 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	101	824	520	149	149	6	0	0

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	154	1214	756	235	219	4	0	0

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	129	979	616	173	184	6	0	0

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	127	1022	634	206	179	3	0	0

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	96	775	487	148	139	1	0	0

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	117	877	540	173	161	3	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	modified residue	UNP P0A7R9

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	121	942	582	193	162	5	0	0

- Molecule 13 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	115	891	552	179	157	3	0	0

- Molecule 14 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	N	100	805	499	164	139	3	0	0

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	O	88	714	439	144	130	1	0	0

- Molecule 16 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	P	79	629	394	124	110	1	0	0

- Molecule 17 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	Q	79	641	406	120	112	3	0	0

- Molecule 18 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	R	64	524	330	99	94	1	0	0

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	S	84	668	427	127	112	2	0	0

- Molecule 20 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	T	86	670	414	138	115	3	0	0

- Molecule 21 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	U	70	589	366	125	97	1	0	0

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
22	X	22	474	212	88	152	22	0	0

- Molecule 23 is a RNA chain called tRNA(Phe).

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	N	O	P	S		
23	Y	69	1488	666	267	484	69	2	0	0

- Molecule 24 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	N	O	P	S		
24	Z	73	1565	698	288	505	73	1	0	0
24	5	71	1583	708	294	507	73	1	3	0

- Molecule 25 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
25	a	2851	61328	27366	11280	19827	2855	6	0

- Molecule 26 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
26	b	120	2569	1144	468	837	120	0	0

- Molecule 27 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	c	271	2082	1288	423	364	7	0	0

- Molecule 28 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	d	207	1552	972	286	291	3	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	e	201	1552	974	283	290	5	0	0

- Molecule 30 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	f	177	1410	899	249	256	6	0	0

- Molecule 31 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	g	168	1255	791	228	234	2	0	0

- Molecule 32 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	h	41	303	194	54	54	1	0	0

- Molecule 33 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	i	141	1121	709	211	198	3	0	0

- Molecule 34 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	j	123	946	593	181	166	6	0	0

- Molecule 35 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	k	144	1053	654	207	190	2	0	0

- Molecule 36 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	l	136	1075	686	205	177	7	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
l	82	MS6	MET	modified residue	UNP A7ZSK2

- Molecule 37 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	m	118	945	585	194	161	5	0	0

- Molecule 38 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
38	n	116	892	552	178	162	0	0

- Molecule 39 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	o	114	917	574	179	163	1	0	0

- Molecule 40 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	p	117	947	604	192	151	0	0

- Molecule 41 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	q	103	816	516	153	145	2	0	0

- Molecule 42 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	r	109	845	526	162	154	3	0	0

- Molecule 43 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	s	93	738	466	139	131	2	0	0

- Molecule 44 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
44	t	102	779	492	146	141	0	0

- Molecule 45 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	u	93	745	474	136	133	2	0	0

- Molecule 46 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	v	84	634	391	129	113	1	0	0

- Molecule 47 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	w	77	625	388	129	106	2	0	0

- Molecule 48 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	x	60	491	303	96	91	1	0	0

- Molecule 49 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	y	58	449	281	87	79	2	0	0

- Molecule 50 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	z	54	429	260	91	77	1	0	0

- Molecule 51 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
51	0	50	413	267	75	71	0	0

- Molecule 52 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	1	45	367	222	88	55	2	0	0

- Molecule 53 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	2	64	504	323	105	74	2	0	0

- Molecule 54 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	3	38	302	185	65	48	4	0	0

- Molecule 55 is a protein called Large ribosomal subunit protein bL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	4	61	487	304	91	86	6	0	0

- Molecule 56 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
			Total	K	
56	A	20	20	20	0
56	F	1	1	1	0
56	M	1	1	1	0
56	a	104	104	104	0
56	b	1	1	1	0
56	c	3	3	3	0
56	e	1	1	1	0
56	v	1	1	1	0

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
57	A	63	63	63	0
57	a	241	241	241	0
57	b	5	5	5	0
57	c	3	3	3	0
57	d	1	1	1	0

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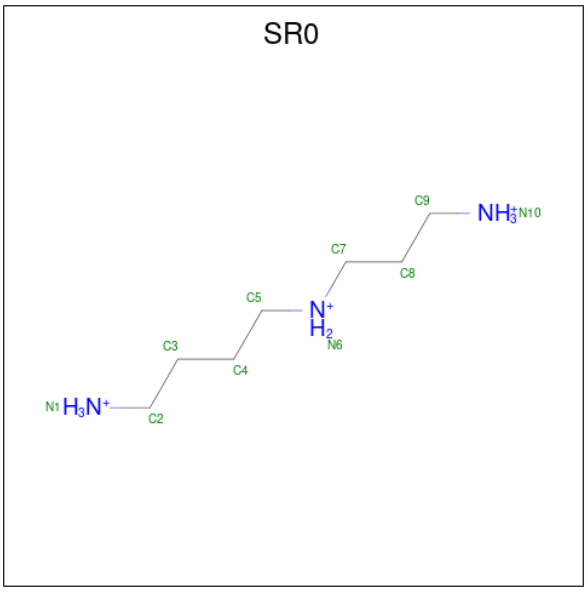
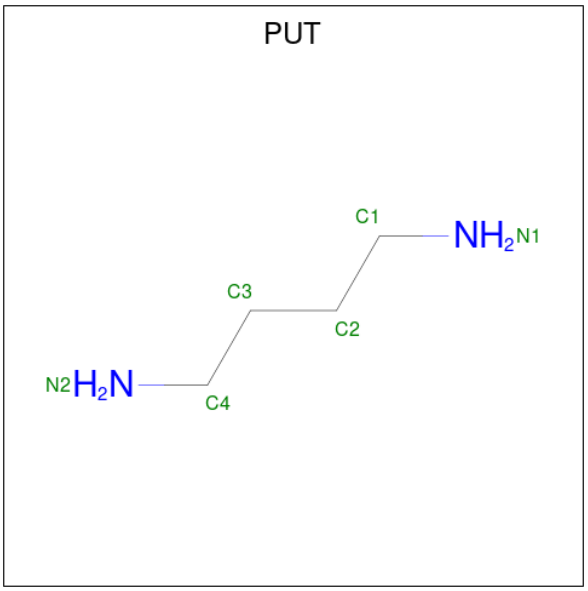
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
57	p	1	1	1	0
			Total	Mg	
57	z	2	2	2	0

- Molecule 58 is N 1 -(3-azaniumylpropyl)butane-1,4-diaminium (CCD ID: SR0) (formula: $C_7H_{22}N_3$).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	N	
58	a	1	10	7	3	0
			Total	C	N	
58	a	1	10	7	3	0
			Total	C	N	
58	a	1	10	7	3	0
			Total	C	N	
58	a	1	10	7	3	0
			Total	C	N	
58	a	1	10	7	3	0

- Molecule 59 is 1,4-DIAMINOBUTANE (CCD ID: PUT) (formula: $C_4H_{12}N_2$).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	N	
59	a	1	6	4	2	0
59	a	1	6	4	2	0
59	a	1	6	4	2	0
59	a	1	6	4	2	0
59	a	1	6	4	2	0
59	a	1	6	4	2	0
59	a	1	6	4	2	0
59	a	1	6	4	2	0

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
60	3	1	1	1	0
60	4	1	1	1	0

- Molecule 61 is water.

Mol	Chain	Residues	Atoms	AltConf
61	A	234	Total O 234 234	0
61	E	1	Total O 1 1	0
61	H	2	Total O 2 2	0
61	K	1	Total O 1 1	0
61	N	1	Total O 1 1	0
61	O	1	Total O 1 1	0
61	R	1	Total O 1 1	0
61	a	3680	Total O 3680 3680	0
61	c	112	Total O 112 112	0
61	d	73	Total O 73 73	0
61	e	45	Total O 45 45	0
61	g	1	Total O 1 1	0
61	i	42	Total O 42 42	0
61	j	29	Total O 29 29	0
61	k	52	Total O 52 52	0
61	l	41	Total O 41 41	0
61	m	45	Total O 45 45	0
61	o	27	Total O 27 27	0
61	p	54	Total O 54 54	0
61	q	26	Total O 26 26	0
61	r	49	Total O 49 49	0
61	s	21	Total O 21 21	0

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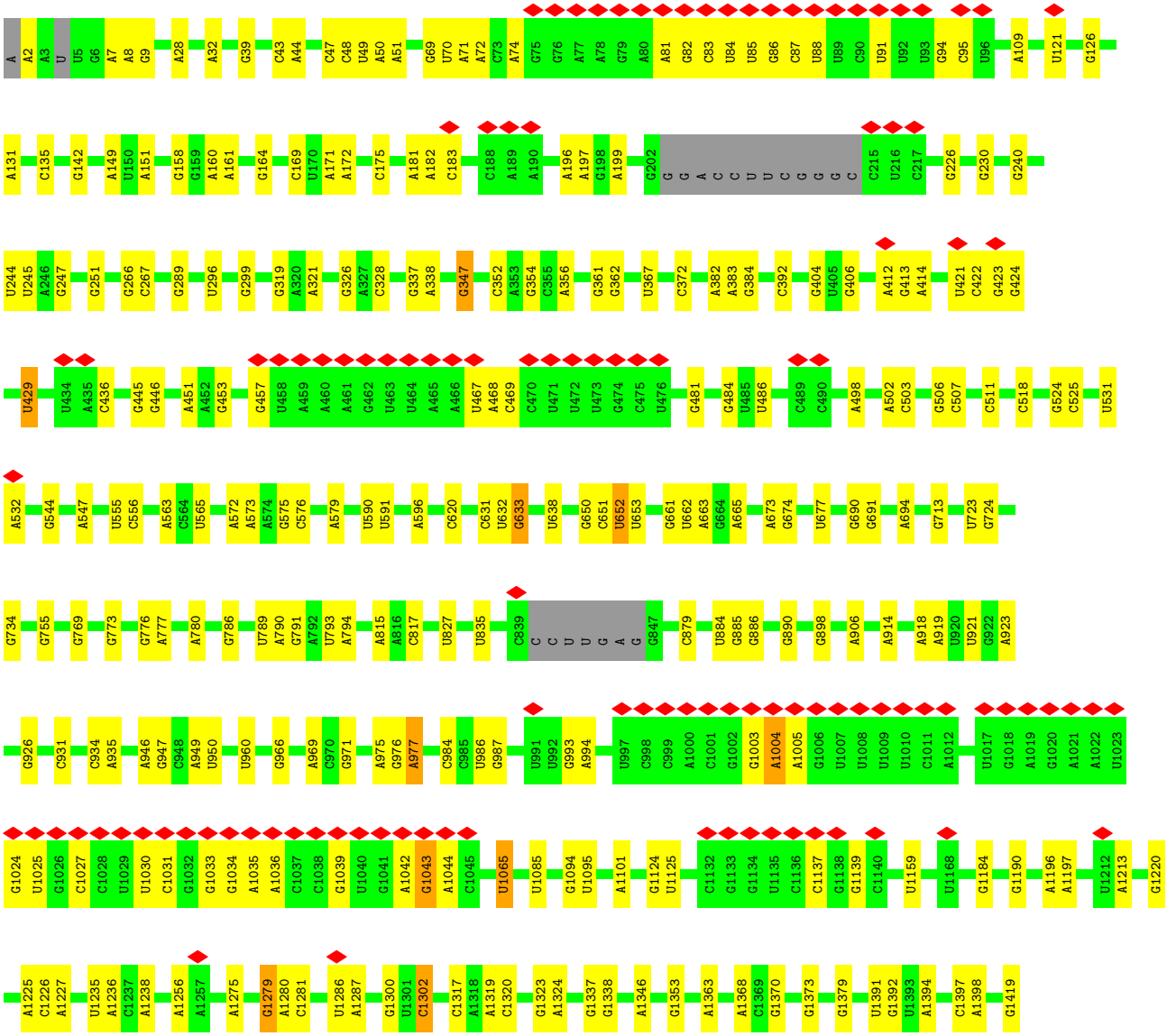
Mol	Chain	Residues	Atoms		AltConf
			Total	O	
61	t	10	10	10	0
			Total	O	
61	u	14	14	14	0
			Total	O	
61	v	18	18	18	0
			Total	O	
61	w	25	25	25	0
			Total	O	
61	x	6	6	6	0
			Total	O	
61	y	16	16	16	0
			Total	O	
61	z	37	37	37	0
			Total	O	
61	0	5	5	5	0
			Total	O	
61	1	33	33	33	0
			Total	O	
61	2	29	29	29	0
			Total	O	
61	3	7	7	7	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

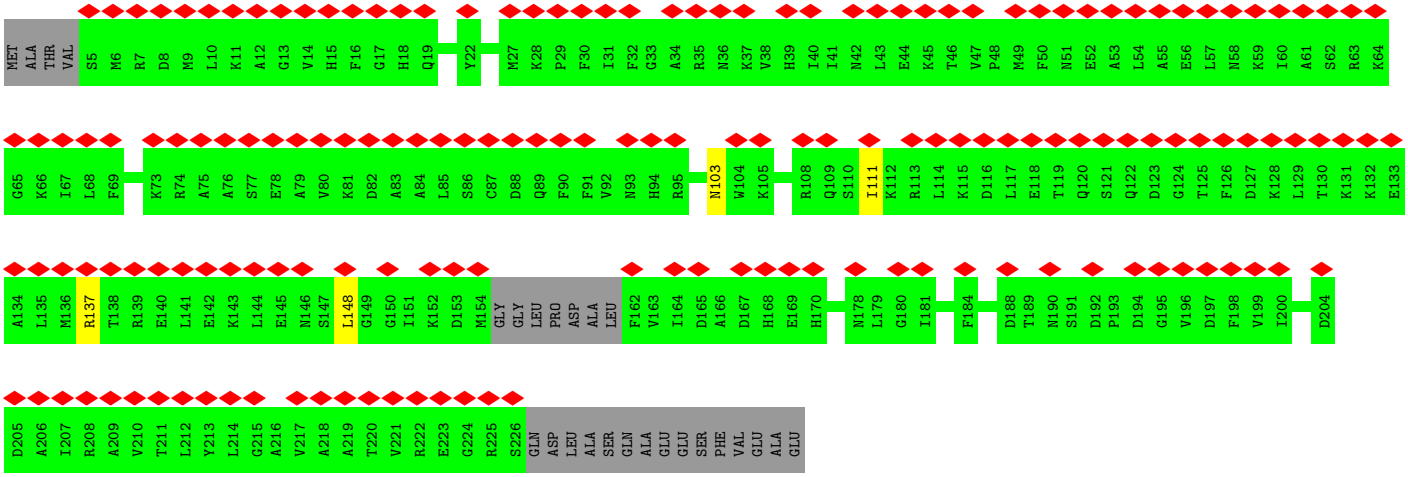
- Molecule 1: 16S rRNA

Chain A: 8% 80% 18%



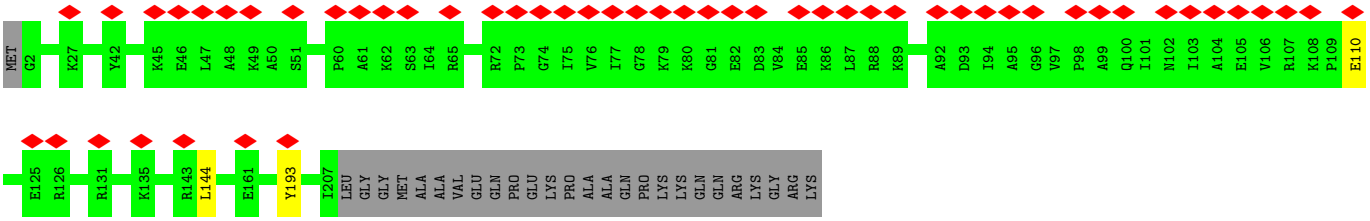
• Molecule 2: Small ribosomal subunit protein uS2

Chain B:



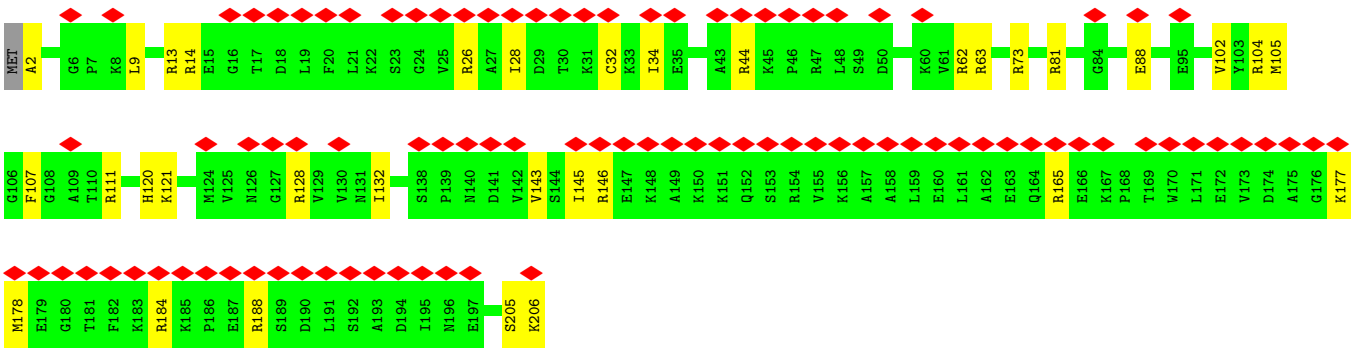
• Molecule 3: Small ribosomal subunit protein uS3

Chain C:



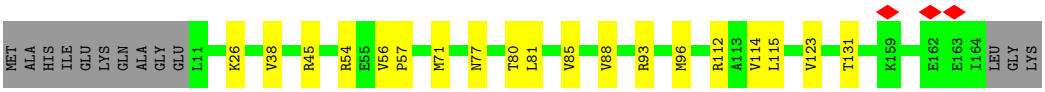
• Molecule 4: Small ribosomal subunit protein uS4

Chain D:



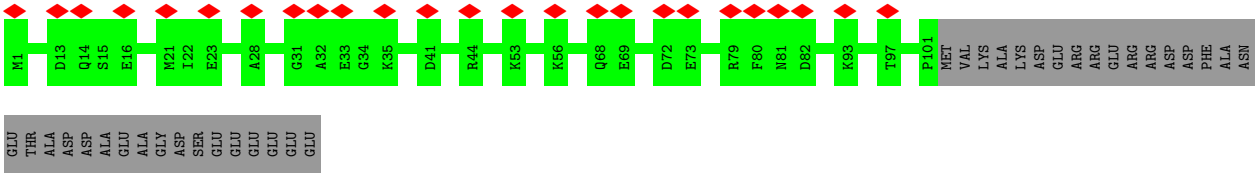
• Molecule 5: Small ribosomal subunit protein uS5

Chain E:



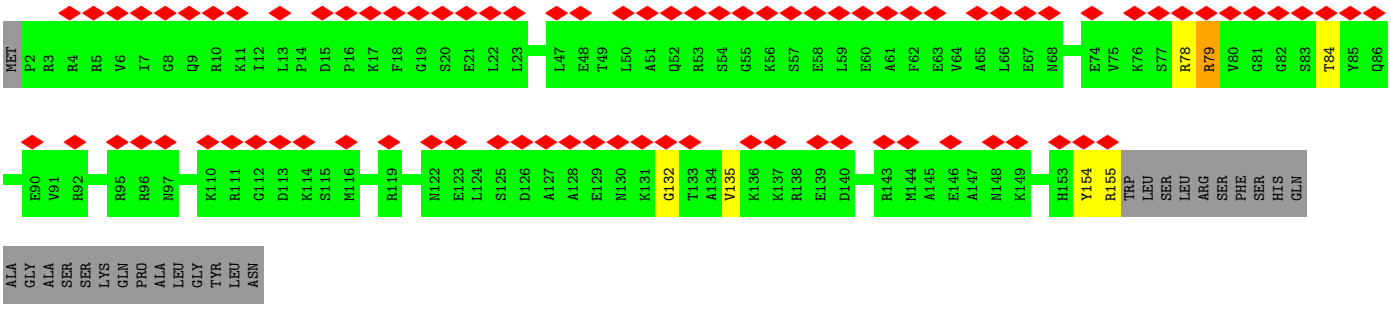
• Molecule 6: Small ribosomal subunit protein bS6, fully modified isoform

Chain F:



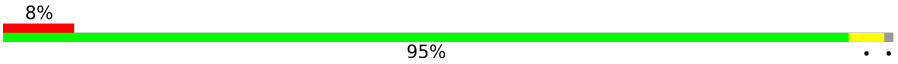
• Molecule 7: Small ribosomal subunit protein uS7

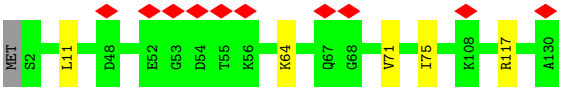
Chain G:



• Molecule 8: Small ribosomal subunit protein uS8

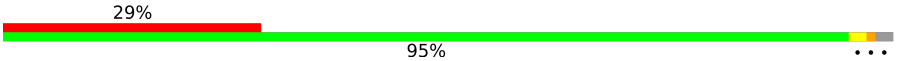
Chain H:

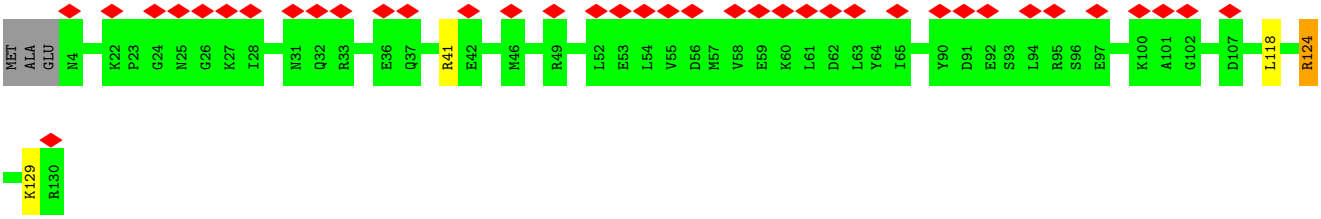




• Molecule 9: Small ribosomal subunit protein uS9

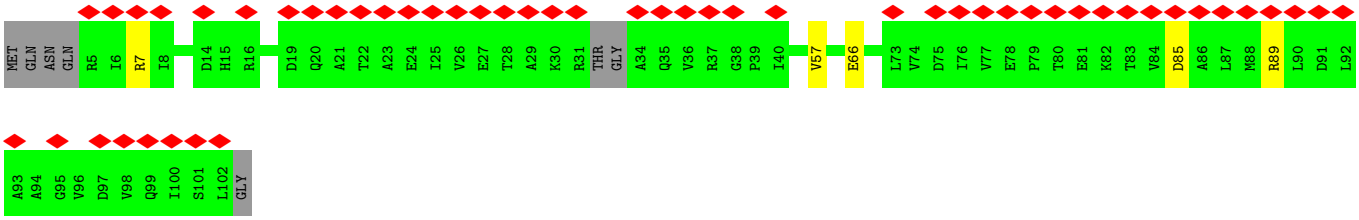
Chain I:





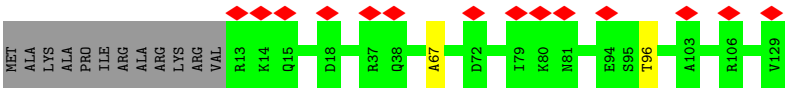
• Molecule 10: Small ribosomal subunit protein uS10

Chain J: 50% 88% 5% 7%



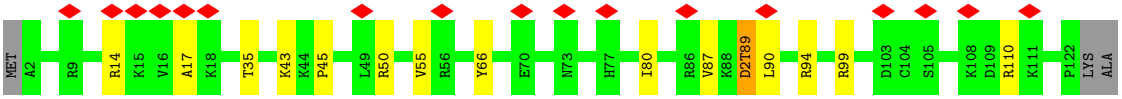
- Molecule 11: Small ribosomal subunit protein uS11

Chain K: 11% 89% 9%



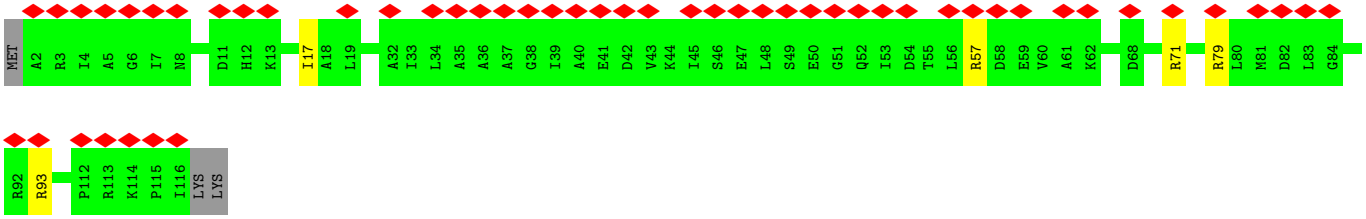
- Molecule 12: Small ribosomal subunit protein uS12

Chain L: 14% 85% 11%



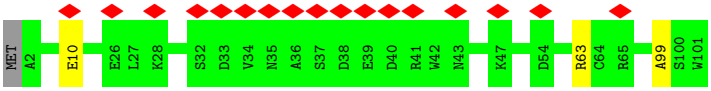
- Molecule 13: Small ribosomal subunit protein uS13

Chain M: 44% 93%



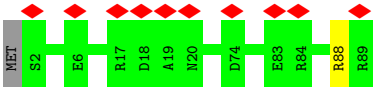
- Molecule 14: Small ribosomal subunit protein uS14

Chain N: 17% 96%



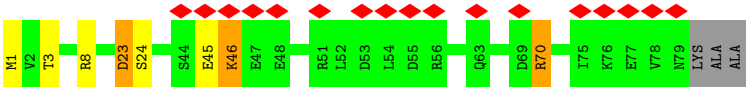
- Molecule 15: Small ribosomal subunit protein uS15

Chain O: 11% 98%



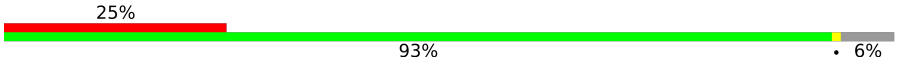
- Molecule 16: Small ribosomal subunit protein bS16

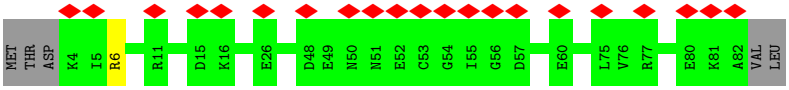
Chain P:



- Molecule 17: Small ribosomal subunit protein uS17

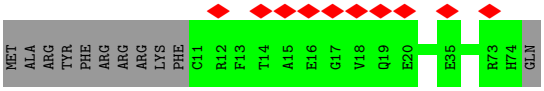
Chain Q:





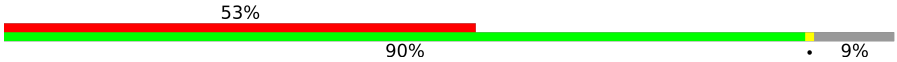
- Molecule 18: Small ribosomal subunit protein bS18

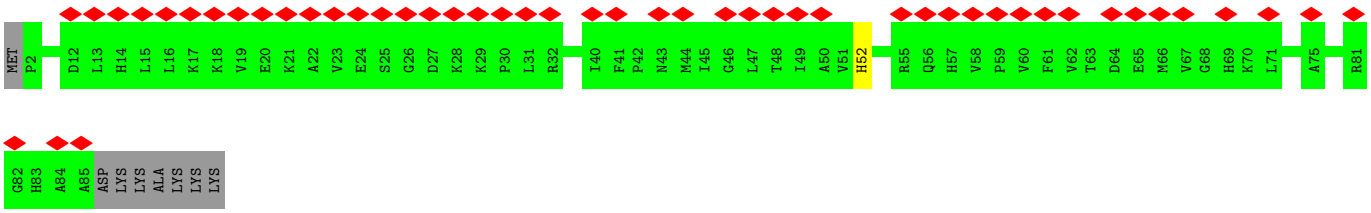
Chain R:



- Molecule 19: Small ribosomal subunit protein uS19

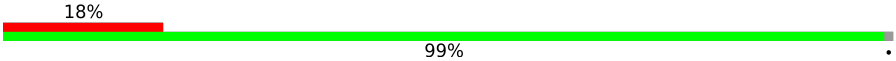
Chain S:

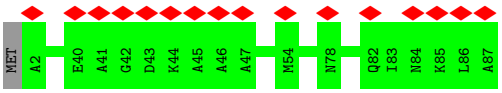




- Molecule 20: Small ribosomal subunit protein bS20

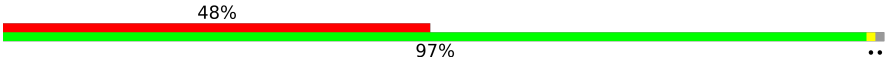
Chain T:

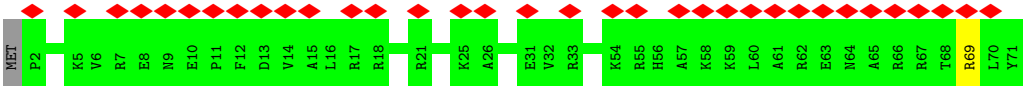




- Molecule 21: Small ribosomal subunit protein bS21

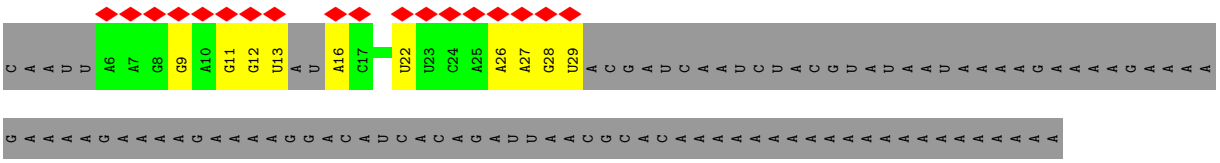
Chain U:





- Molecule 22: mRNA

Chain X: 15% 10% 8% 82%

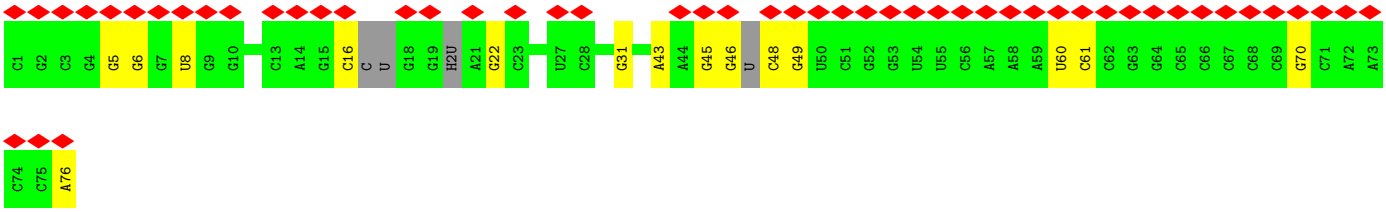


- Molecule 23: tRNA(Phe)

Chain Y: 91% 74% 14% • 9%

- Molecule 24: tRNA(fMet)

Chain Z: 68% 75% 19% 5%

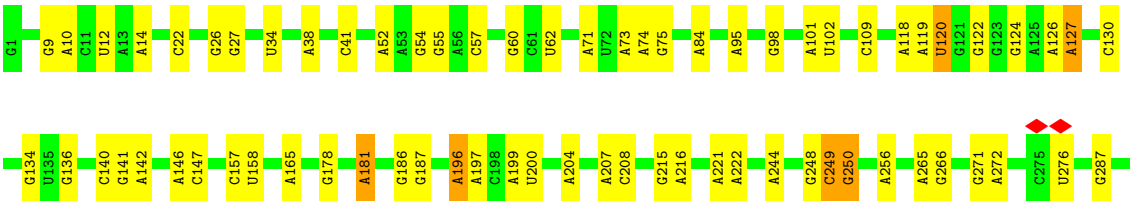


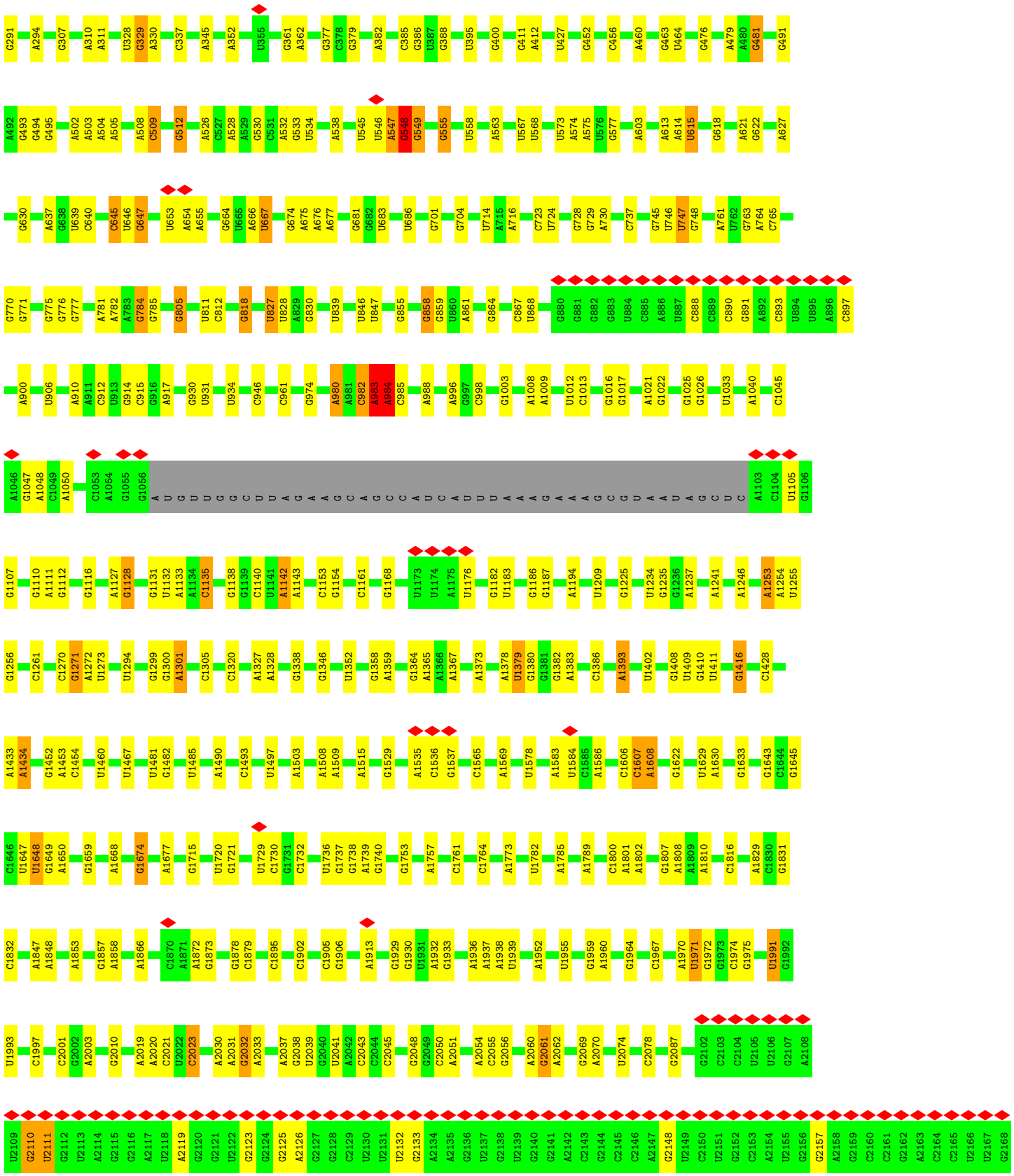
- Molecule 24: tRNA(fMet)

Chain 5: 83% 75% 16% • 8%

- Molecule 25: 23S rRNA

Chain a: 5% 76% 20% • •

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A492 G493 G494 G495 A502 A503 A504 A505 A508 C509 G512 A526 C527 A528 A529 G530 C531 A532 G533 U534 A538 U545 U546 A547 G548 G549 G555 U558 A563 U567 U568 U573 A574 A575 U576 G577 A603 A613 A614 U615 G618 A621 G622 A627
G630 A637 G638 U639 C640 C645 U646 G647 U653 A654 A655 G664 U665 A666 U667 G674 A675 A676 A677 G681 G682 U683 U686 G701 G704 U714 A715 A716 C723 U724 G728 G729 A730 C737 G745 U746 U747 G748 A761 U762 G763 A764 C765
G770 G771 G775 G776 G777 A781 A782 A783 G784 G785 G805 U811 C812 G818 U827 U828 A829 G830 U839 U846 U847 G855 G858 G859 U860 A861 G864 C867 U868 G880 G881 G882 G883 U884 C885 A886 U887 C888 C889 C890 G891 A892 C893 U894 U895 A896 C897
A900 U906 A910 A911 C912 U913 G914 C915 G916 A917 G930 U931 U934 C946 C961 G974 A980 A981 C982 A983 A984 C985 A988 A996 G997 C998 G1003 A1008 A1009 U1012 C1013 G1016 G1017 A1021 G1022 G1025 G1026 U1033 A1040 C1045
A1046 G1047 A1048 C1049 A1050 C1053 A1054 G1055 G1056 A U G U U G G C U U A G A A G C A G C C A U C A U U U A A A G A A A G C G U A A U A G C U C A1103 C1104 U1105 G1106
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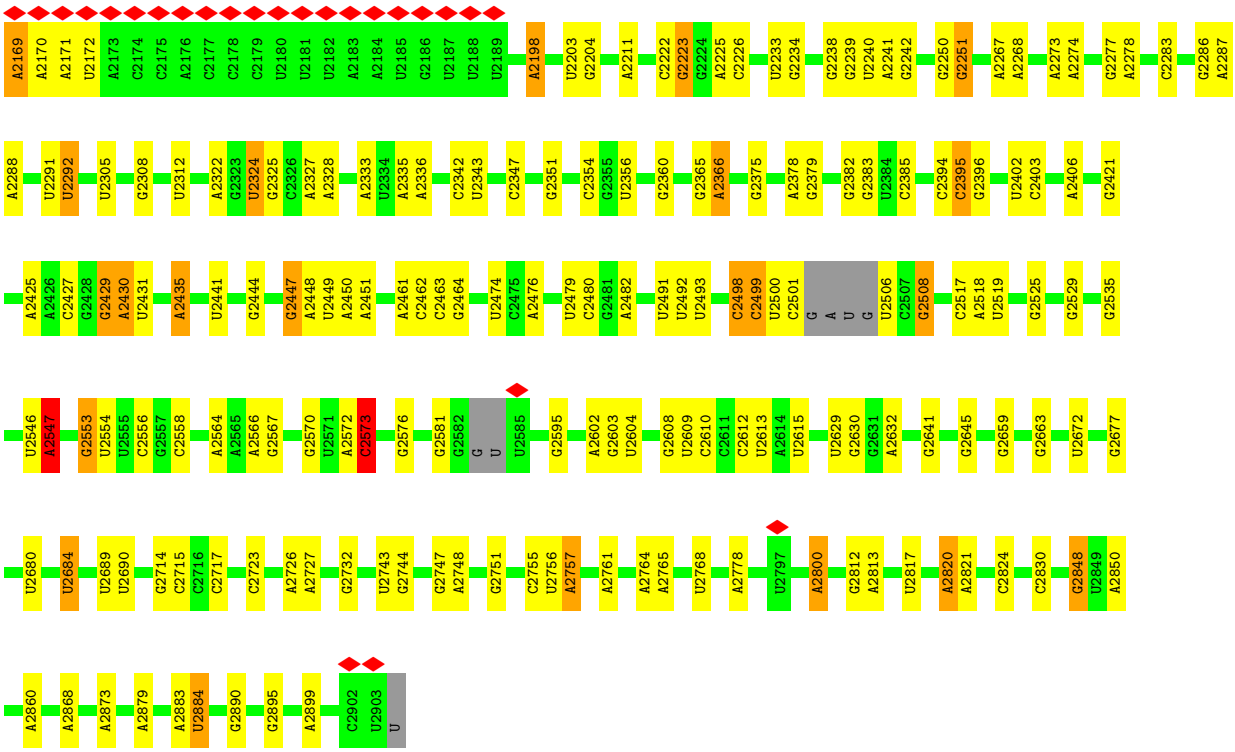
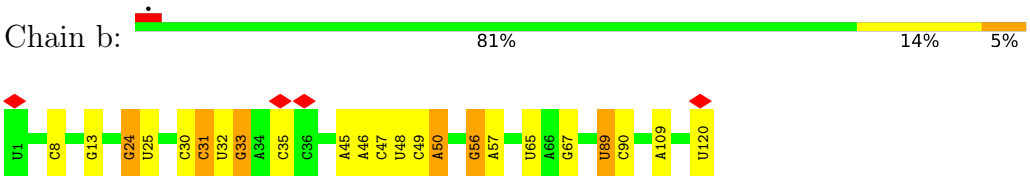
G1256 C1261 C1270 G1271 A1272 U1273 U1294 G1299 G1300 A1301 C1305 C1320 A1327 A1328 G1338 G1346 U1352 G1358 A1359 G1364 A1365 A1366 A1367 A1373 A1378 U1379 G1380 G1381 G1382 A1383 C1386 A1393 U1402 G1408 U1409 G1410 U1411 G1416 C1428
A1433 A1434 G1452 A1453 C1454 U1460 U1467 U1481 G1482 U1485 A1490 C1493 U1497 A1503 A1508 A1509 A1515 G1529 A1535 C1536 G1537 C1565 A1569 U1578 A1583 U1584 C1585 A1586 C1606 C1607 A1608 G1622 U1629 A1630 G1633 G1643 C1644 G1645
C1646 U1647 U1648 G1649 A1650 G1659 A1668 G1674 A1677 G1715 U1720 G1721 U1729 C1730 G1731 C1732 U1736 G1737 G1738 A1739 G1740 G1753 A1757 C1761 C1764 A1773 U1782 A1785 A1789 C1800 A1801 A1802 G1807 A1808 A1809 A1810 C1816 A1829 C1830 G1831
C1832 A1847 A1848 A1853 G1857 A1858 A1866 C1870 A1871 A1872 G1873 G1878 C1879 C1895 C1902 C1905 G1906 A1913 G1929 G1930 U1931 A1932 G1933 A1936 A1937 A1938 U1939 A1952 U1955 G1959 A1960 G1964 C1967 A1970 U1971 G1972 G1973 C1974 G1975 U1991 G1992
U1993 C1997 C2001 G2002 A2003 G2010 A2019 A2020 C2021 U2022 C2023 A2030 A2031 G2032 A2033 A2037 G2038 U2039 G2040 U2041 A2042 C2043 C2044 C2045 G2048 G2049 C2050 A2051 A2054 C2055 G2056 A2060 G2061 A2062 G2069 A2070 U2074 C2078 G2087 G2102 C2103 C2104 U2105 U2106 G2107 A2108
U2109 G2110 U2111 G2112 U2113 A2114 G2115 G2116 A2117 U2118 A2119 G2120 G2121 U2122 G2123 G2124 G2125 A2126 G2127 G2128 C2129 U2130 U2131 U2132 G2133 A2134 A2135 C2136 U2137 G2138 U2139 G2140 G2141 A2142 C2143 G2144 C2145 C2146 A2147 G2148 U2149 C2150 U2151 G2152 C2153 A2154 U2155 G2156 G2157 A2158 G2159 C2160 C2161 G2162 A2163 C2164 C2165 U2166 U2167 G2168



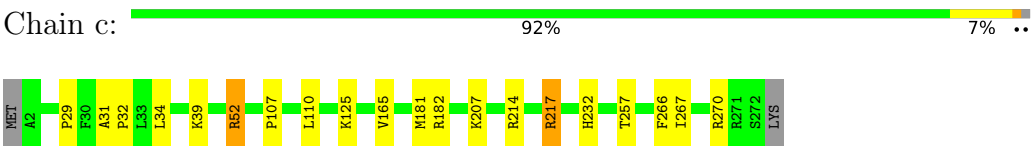
- Molecule 26: 5S rRNA

Chain b:



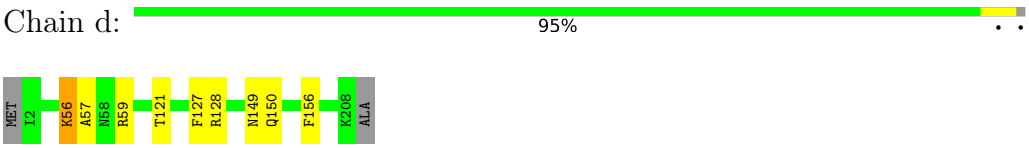
- Molecule 27: Large ribosomal subunit protein uL2

Chain c:



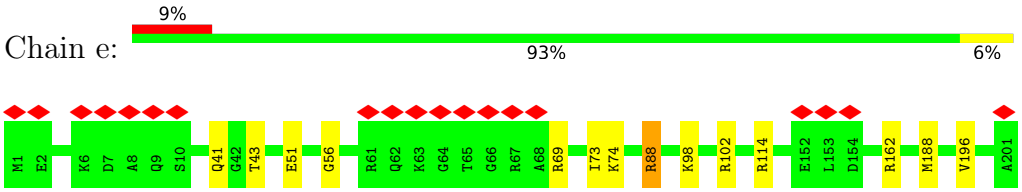
- Molecule 28: Large ribosomal subunit protein uL3

Chain d:



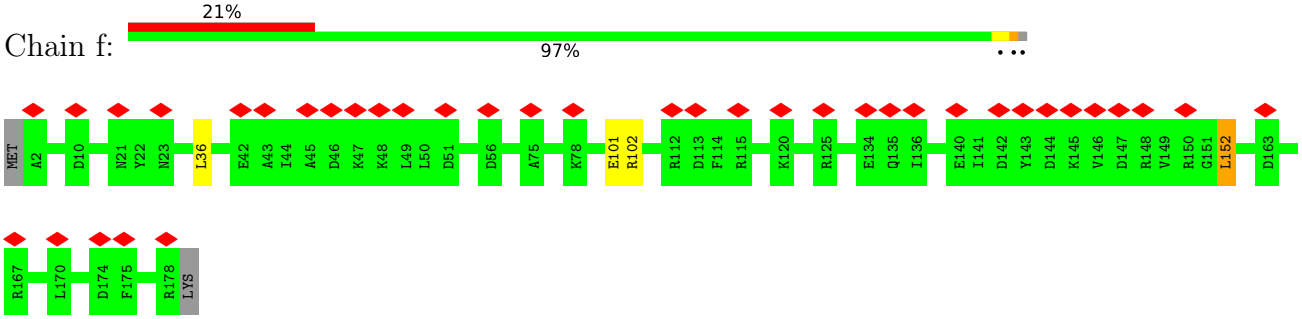
- Molecule 29: Large ribosomal subunit protein uL4

Chain e:



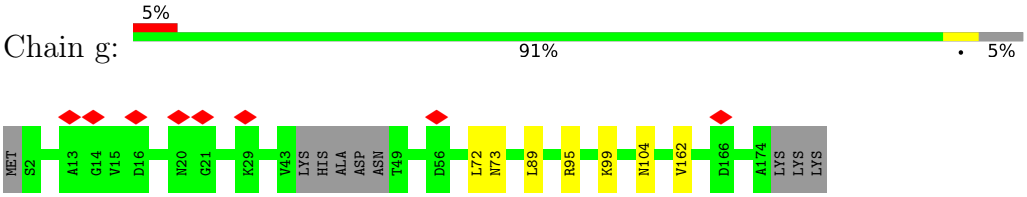
• Molecule 30: Large ribosomal subunit protein uL5

Chain f:



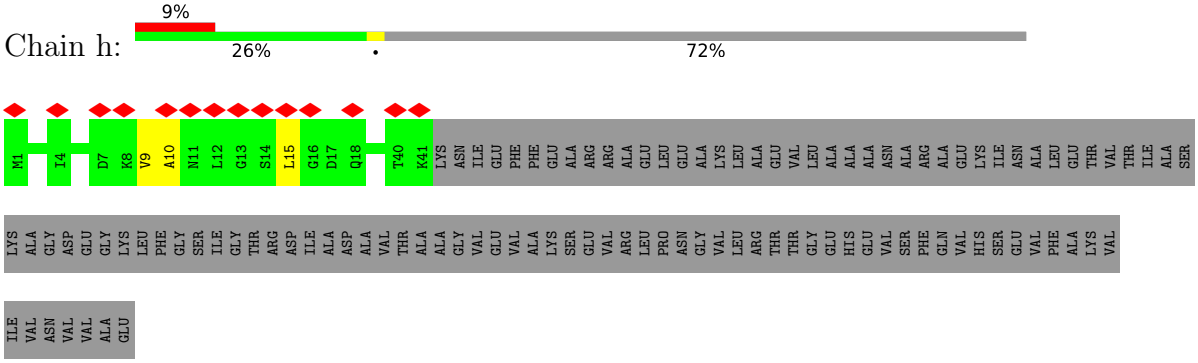
• Molecule 31: Large ribosomal subunit protein uL6

Chain g:



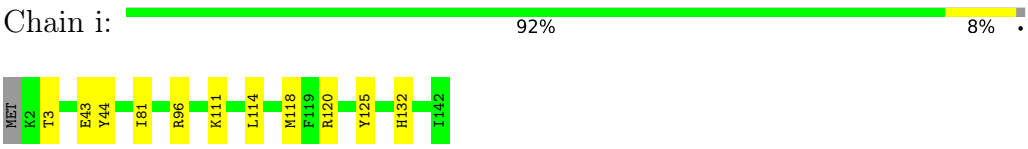
• Molecule 32: Large ribosomal subunit protein bL9

Chain h:



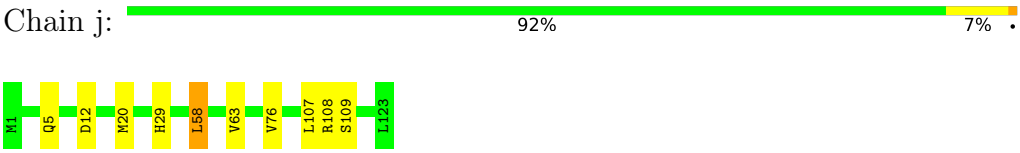
• Molecule 33: Large ribosomal subunit protein uL13

Chain i:



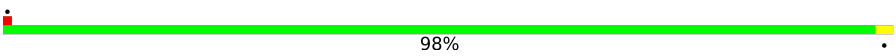
• Molecule 34: Large ribosomal subunit protein uL14

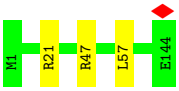
Chain j:



• Molecule 35: Large ribosomal subunit protein uL15

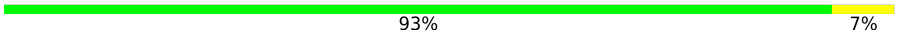
Chain k:

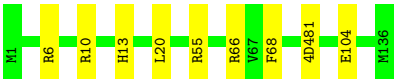




• Molecule 36: Large ribosomal subunit protein uL16

Chain l:



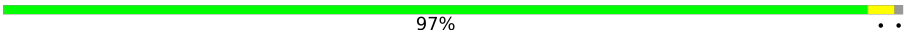


• Molecule 37: Large ribosomal subunit protein bL17

Chain m:

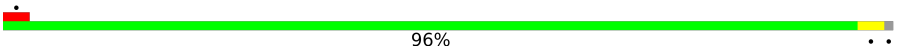
• Molecule 38: Large ribosomal subunit protein uL18

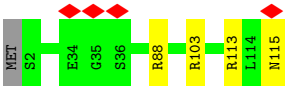
Chain n:



• Molecule 39: Large ribosomal subunit protein bL19

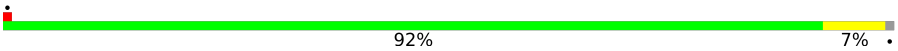
Chain o:

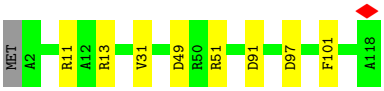




• Molecule 40: Large ribosomal subunit protein bL20

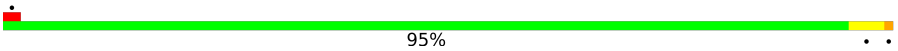
Chain p:

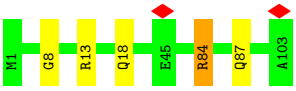




• Molecule 41: Large ribosomal subunit protein bL21

Chain q:



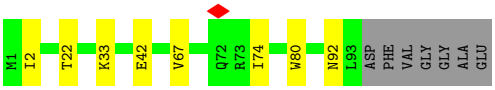


• Molecule 42: Large ribosomal subunit protein uL22

Chain r: 99%

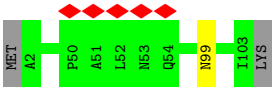
• Molecule 43: Large ribosomal subunit protein uL23

Chain s: 85% 8% 7%



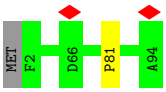
• Molecule 44: Large ribosomal subunit protein uL24

Chain t: 5% 97%



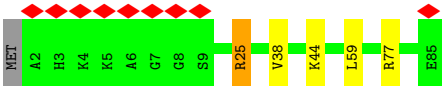
• Molecule 45: Large ribosomal subunit protein bL25

Chain u: 98%



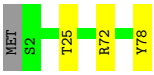
• Molecule 46: Large ribosomal subunit protein bL27

Chain v: 11% 93% 5%



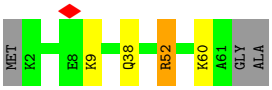
• Molecule 47: Large ribosomal subunit protein bL28

Chain w: 95%



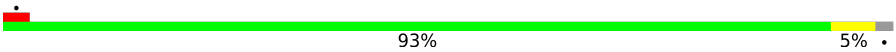
• Molecule 48: Large ribosomal subunit protein uL29

Chain x: 89% 5% 5%



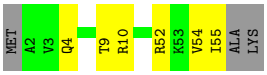
• Molecule 49: Large ribosomal subunit protein uL30

Chain y:



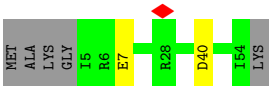
• Molecule 50: Large ribosomal subunit protein bL32

Chain z:



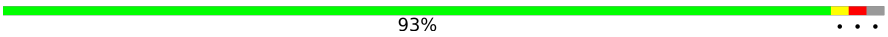
• Molecule 51: Large ribosomal subunit protein bL33

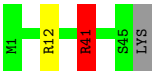
Chain 0:



• Molecule 52: Large ribosomal subunit protein bL34

Chain 1:





• Molecule 53: Large ribosomal subunit protein bL35

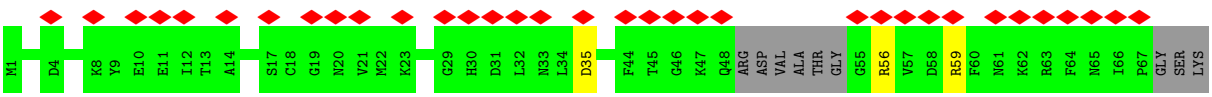
Chain 2:

• Molecule 54: Large ribosomal subunit protein bL36A

Chain 3:

• Molecule 55: Large ribosomal subunit protein bL31A

Chain 4:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	582240	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	30	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.116	Depositor
Minimum map value	-0.017	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.013	Depositor
Map size (Å)	420.608, 420.608, 420.608	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8215, 0.8215, 0.8215	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MIA, 4SU, PSU, 5MC, PUT, K, 5MU, IAS, MG, 6MZ, G7M, 1MG, MEQ, D2T, 2MG, OMC, MS6, SR0, ZN, 3TD, MA6, H2U, 4D4, UR3, 4OC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.54	0/36200	0.91	29/56459 (0.1%)
2	B	0.49	0/1722	1.00	1/2316 (0.0%)
3	C	0.49	0/1651	0.90	0/2225
4	D	0.52	0/1665	1.02	0/2227
5	E	0.51	0/1148	0.92	1/1545 (0.1%)
6	F	0.49	0/843	0.87	0/1140
7	G	0.51	0/1230	1.02	1/1649 (0.1%)
8	H	0.50	0/989	0.94	0/1326
9	I	0.48	0/1034	0.96	0/1375
10	J	0.50	0/784	0.96	0/1059
11	K	0.53	0/884	0.90	0/1191
12	L	0.56	0/945	0.98	1/1268 (0.1%)
13	M	0.51	0/900	0.99	0/1204
14	N	0.49	0/817	0.95	0/1088
15	O	0.49	0/722	1.00	0/964
16	P	0.54	0/639	1.02	2/859 (0.2%)
17	Q	0.51	0/650	0.92	0/871
18	R	0.51	0/532	0.96	0/715
19	S	0.52	0/685	0.92	0/922
20	T	0.51	0/676	1.05	0/895
21	U	0.52	0/597	1.05	0/792
22	X	0.60	0/530	0.88	0/822
23	Y	0.61	1/1466 (0.1%)	0.84	0/2275
24	5	0.60	1/1675 (0.1%)	0.79	0/2601
24	Z	0.59	1/1656 (0.1%)	0.91	2/2575 (0.1%)
25	a	0.66	4/68350 (0.0%)	1.12	274/106621 (0.3%)
26	b	0.58	0/2872	1.07	12/4478 (0.3%)
27	c	0.88	2/2121 (0.1%)	1.17	6/2852 (0.2%)
28	d	0.86	0/1562	1.12	1/2102 (0.0%)
29	e	0.72	1/1571 (0.1%)	1.06	1/2113 (0.0%)
30	f	0.48	0/1434	1.02	1/1926 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
31	g	0.53	0/1273	0.97	0/1725
32	h	0.53	0/306	0.95	0/413
33	i	0.81	0/1144	1.13	3/1541 (0.2%)
34	j	0.75	0/955	1.13	2/1279 (0.2%)
35	k	0.82	1/1062 (0.1%)	1.16	0/1413
36	l	0.76	1/1073 (0.1%)	1.12	1/1433 (0.1%)
37	m	0.91	1/958 (0.1%)	1.26	8/1281 (0.6%)
38	n	0.60	0/902	1.00	2/1209 (0.2%)
39	o	0.73	0/929	1.09	1/1242 (0.1%)
40	p	0.92	0/960	1.21	4/1278 (0.3%)
41	q	0.75	0/829	1.13	3/1107 (0.3%)
42	r	0.87	0/852	1.09	0/1142
43	s	0.69	0/744	1.06	1/994 (0.1%)
44	t	0.62	0/787	0.98	0/1051
45	u	0.65	0/758	1.04	0/1015
46	v	0.81	0/642	1.15	3/848 (0.4%)
47	w	0.81	0/635	1.12	1/848 (0.1%)
48	x	0.54	0/492	1.00	1/655 (0.2%)
49	y	0.76	0/453	1.05	0/605
50	z	0.89	0/435	1.27	2/581 (0.3%)
51	0	0.69	0/420	1.04	1/560 (0.2%)
52	1	1.04	0/370	1.36	2/487 (0.4%)
53	2	0.97	0/513	1.17	2/676 (0.3%)
54	3	0.84	0/303	1.19	3/397 (0.8%)
55	4	0.49	0/496	0.95	0/661
All	All	0.63	13/156841 (0.0%)	1.05	372/234896 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	1
4	D	0	15
5	E	0	2
7	G	0	1
8	H	0	1
9	I	0	2
10	J	0	1
12	L	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	M	0	2
16	P	0	1
17	Q	0	1
21	U	0	1
25	a	0	53
27	c	0	3
28	d	0	2
29	e	0	5
31	g	0	1
33	i	0	2
36	l	0	3
39	o	0	1
40	p	0	2
41	q	0	1
46	v	0	1
48	x	0	1
52	1	0	1
53	2	0	1
54	3	0	1
55	4	0	1
All	All	0	113

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	a	574	A	O5'-C5'	-7.43	1.31	1.42
25	a	1187	G	O5'-C5'	-6.61	1.32	1.42
25	a	196	A	O5'-C5'	-6.12	1.33	1.42
35	k	47	ARG	NE-CZ	-5.51	1.26	1.33
24	Z	8	4SU	O3'-P	5.29	1.61	1.56

The worst 5 of 372 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
25	a	1971	U	O3'-P-O5'	-14.51	82.23	104.00
25	a	1974	C	O3'-P-O5'	-12.05	85.92	104.00
25	a	2222	C	O3'-P-O5'	-11.71	86.44	104.00
25	a	2553	G	O3'-P-O5'	-11.22	87.17	104.00
25	a	1246	A	O3'-P-O5'	-10.93	87.60	104.00

There are no chirality outliers.

5 of 113 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	898	G	Sidechain
2	B	137	ARG	Sidechain
4	D	13	ARG	Sidechain
4	D	14	ARG	Sidechain
4	D	26	ARG	Sidechain

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32582	0	16415	53	0
2	B	1693	0	1718	1	0
3	C	1624	0	1696	2	0
4	D	1643	0	1707	11	0
5	E	1135	0	1179	9	0
6	F	824	0	815	0	0
7	G	1214	0	1267	3	0
8	H	979	0	1031	2	0
9	I	1022	0	1070	2	0
10	J	775	0	817	2	0
11	K	877	0	884	1	0
12	L	942	0	999	4	0
13	M	891	0	952	3	0
14	N	805	0	844	2	0
15	O	714	0	734	1	0
16	P	629	0	643	6	0
17	Q	641	0	682	0	0
18	R	524	0	543	0	0
19	S	668	0	693	1	0
20	T	670	0	719	0	0
21	U	589	0	629	0	0
22	X	474	0	238	3	0
23	Y	1488	0	767	1	0
24	5	1583	0	814	3	0
24	Z	1565	0	802	3	0
25	a	61328	0	30834	91	0
26	b	2569	0	1301	3	0
27	c	2082	0	2153	7	0
28	d	1552	0	1601	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	e	1552	0	1619	5	0
30	f	1410	0	1444	2	0
31	g	1255	0	1296	3	0
32	h	303	0	327	2	0
33	i	1121	0	1150	4	0
34	j	946	0	1023	6	0
35	k	1053	0	1129	2	0
36	l	1075	0	1145	2	0
37	m	945	0	989	1	0
38	n	892	0	923	1	0
39	o	917	0	962	1	0
40	p	947	0	1019	3	0
41	q	816	0	839	2	0
42	r	845	0	909	0	0
43	s	738	0	807	3	0
44	t	779	0	830	1	0
45	u	745	0	768	1	0
46	v	634	0	653	1	0
47	w	625	0	652	1	0
48	x	491	0	523	2	0
49	y	449	0	488	3	0
50	z	429	0	440	5	0
51	0	413	0	448	1	0
52	1	367	0	404	1	0
53	2	504	0	572	2	0
54	3	302	0	340	1	0
55	4	487	0	485	2	0
56	A	20	0	0	0	0
56	F	1	0	0	0	0
56	M	1	0	0	0	0
56	a	104	0	0	0	0
56	b	1	0	0	0	0
56	c	3	0	0	0	0
56	e	1	0	0	0	0
56	v	1	0	0	0	0
57	A	63	0	0	0	0
57	a	241	0	0	0	0
57	b	5	0	0	0	0
57	c	3	0	0	0	0
57	d	1	0	0	0	0
57	p	1	0	0	0	0
57	z	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	a	50	0	0	0	0
59	a	48	0	96	4	0
60	3	1	0	0	0	0
60	4	1	0	0	0	0
61	0	5	0	0	0	0
61	1	33	0	0	0	0
61	2	29	0	0	0	0
61	3	7	0	0	0	0
61	A	234	0	0	0	0
61	E	1	0	0	0	0
61	H	2	0	0	0	0
61	K	1	0	0	0	0
61	N	1	0	0	0	0
61	O	1	0	0	0	0
61	R	1	0	0	0	0
61	a	3680	0	0	1	0
61	c	112	0	0	0	0
61	d	73	0	0	0	0
61	e	45	0	0	0	0
61	g	1	0	0	0	0
61	i	42	0	0	0	0
61	j	29	0	0	0	0
61	k	52	0	0	0	0
61	l	41	0	0	0	0
61	m	45	0	0	0	0
61	o	27	0	0	0	0
61	p	54	0	0	0	0
61	q	26	0	0	0	0
61	r	49	0	0	0	0
61	s	21	0	0	0	0
61	t	10	0	0	0	0
61	u	14	0	0	0	0
61	v	18	0	0	0	0
61	w	25	0	0	0	0
61	x	6	0	0	0	0
61	y	16	0	0	0	0
61	z	37	0	0	0	0
All	All	150408	0	96827	235	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

The worst 5 of 235 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:a:2500[A]:U:H4'	25:a:2501[A]:C:OP2	1.92	0.70
1:A:769:G:H4'	1:A:1513:A:H4'	1.76	0.66
27:c:29:PRO:HG2	27:c:34:LEU:HD11	1.81	0.61
24:Z:76:A:N6	25:a:2450[A]:A:H1'	2.18	0.59
25:a:1182:G:H2'	25:a:1183:U:O4'	2.05	0.55

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	211/241 (88%)	199 (94%)	12 (6%)	0	100	100
3	C	204/233 (88%)	199 (98%)	5 (2%)	0	100	100
4	D	203/206 (98%)	197 (97%)	6 (3%)	0	100	100
5	E	152/167 (91%)	148 (97%)	4 (3%)	0	100	100
6	F	99/135 (73%)	95 (96%)	4 (4%)	0	100	100
7	G	152/179 (85%)	150 (99%)	2 (1%)	0	100	100
8	H	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
9	I	125/130 (96%)	118 (94%)	7 (6%)	0	100	100
10	J	92/103 (89%)	90 (98%)	1 (1%)	1 (1%)	11	3
11	K	113/129 (88%)	110 (97%)	3 (3%)	0	100	100
12	L	118/124 (95%)	110 (93%)	7 (6%)	1 (1%)	16	5
13	M	113/118 (96%)	112 (99%)	1 (1%)	0	100	100
14	N	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
15	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
16	P	77/82 (94%)	74 (96%)	2 (3%)	1 (1%)	9	2
17	Q	77/84 (92%)	75 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	R	62/75 (83%)	59 (95%)	3 (5%)	0	100	100
19	S	82/92 (89%)	81 (99%)	1 (1%)	0	100	100
20	T	84/87 (97%)	84 (100%)	0	0	100	100
21	U	68/71 (96%)	68 (100%)	0	0	100	100
27	c	269/273 (98%)	259 (96%)	10 (4%)	0	100	100
28	d	204/209 (98%)	198 (97%)	6 (3%)	0	100	100
29	e	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
30	f	175/179 (98%)	161 (92%)	14 (8%)	0	100	100
31	g	164/177 (93%)	159 (97%)	5 (3%)	0	100	100
32	h	39/149 (26%)	33 (85%)	6 (15%)	0	100	100
33	i	139/142 (98%)	138 (99%)	1 (1%)	0	100	100
34	j	121/123 (98%)	117 (97%)	3 (2%)	1 (1%)	16	5
35	k	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
36	l	132/136 (97%)	129 (98%)	3 (2%)	0	100	100
37	m	116/127 (91%)	113 (97%)	3 (3%)	0	100	100
38	n	114/117 (97%)	111 (97%)	3 (3%)	0	100	100
39	o	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
40	p	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
41	q	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
42	r	107/110 (97%)	105 (98%)	2 (2%)	0	100	100
43	s	91/100 (91%)	88 (97%)	2 (2%)	1 (1%)	11	3
44	t	100/104 (96%)	96 (96%)	4 (4%)	0	100	100
45	u	91/94 (97%)	89 (98%)	2 (2%)	0	100	100
46	v	82/85 (96%)	81 (99%)	1 (1%)	0	100	100
47	w	75/78 (96%)	75 (100%)	0	0	100	100
48	x	58/63 (92%)	57 (98%)	1 (2%)	0	100	100
49	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
50	z	52/57 (91%)	52 (100%)	0	0	100	100
51	0	48/55 (87%)	48 (100%)	0	0	100	100
52	1	43/46 (94%)	43 (100%)	0	0	100	100
53	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	3	36/38 (95%)	36 (100%)	0	0	100	100
55	4	57/70 (81%)	56 (98%)	1 (2%)	0	100	100
All	All	5443/5913 (92%)	5285 (97%)	153 (3%)	5 (0%)	49	37

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	J	57	VAL
16	P	46	LYS
34	j	108	ARG
12	L	17	ALA
43	s	92	ASN

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	180/199 (90%)	180 (100%)	0	100	100
3	C	170/190 (90%)	170 (100%)	0	100	100
4	D	172/173 (99%)	171 (99%)	1 (1%)	78	72
5	E	117/126 (93%)	117 (100%)	0	100	100
6	F	88/116 (76%)	88 (100%)	0	100	100
7	G	127/147 (86%)	127 (100%)	0	100	100
8	H	104/105 (99%)	104 (100%)	0	100	100
9	I	105/107 (98%)	105 (100%)	0	100	100
10	J	85/90 (94%)	85 (100%)	0	100	100
11	K	89/98 (91%)	89 (100%)	0	100	100
12	L	101/103 (98%)	100 (99%)	1 (1%)	68	60
13	M	93/96 (97%)	93 (100%)	0	100	100
14	N	83/84 (99%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	O	76/77 (99%)	76 (100%)	0	100	100
16	P	64/65 (98%)	64 (100%)	0	100	100
17	Q	73/78 (94%)	73 (100%)	0	100	100
18	R	55/65 (85%)	55 (100%)	0	100	100
19	S	72/79 (91%)	72 (100%)	0	100	100
20	T	65/66 (98%)	65 (100%)	0	100	100
21	U	60/61 (98%)	60 (100%)	0	100	100
27	c	216/218 (99%)	216 (100%)	0	100	100
28	d	162/163 (99%)	162 (100%)	0	100	100
29	e	165/165 (100%)	165 (100%)	0	100	100
30	f	148/150 (99%)	148 (100%)	0	100	100
31	g	130/138 (94%)	130 (100%)	0	100	100
32	h	32/114 (28%)	32 (100%)	0	100	100
33	i	115/116 (99%)	115 (100%)	0	100	100
34	j	104/104 (100%)	103 (99%)	1 (1%)	68	60
35	k	103/103 (100%)	103 (100%)	0	100	100
36	l	107/107 (100%)	107 (100%)	0	100	100
37	m	98/103 (95%)	98 (100%)	0	100	100
38	n	86/87 (99%)	86 (100%)	0	100	100
39	o	99/100 (99%)	99 (100%)	0	100	100
40	p	89/90 (99%)	89 (100%)	0	100	100
41	q	84/84 (100%)	84 (100%)	0	100	100
42	r	92/93 (99%)	92 (100%)	0	100	100
43	s	80/84 (95%)	80 (100%)	0	100	100
44	t	83/85 (98%)	83 (100%)	0	100	100
45	u	77/78 (99%)	77 (100%)	0	100	100
46	v	62/63 (98%)	62 (100%)	0	100	100
47	w	67/68 (98%)	67 (100%)	0	100	100
48	x	54/55 (98%)	54 (100%)	0	100	100
49	y	48/49 (98%)	48 (100%)	0	100	100
50	z	46/48 (96%)	46 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	0	46/49 (94%)	46 (100%)	0	100	100
52	1	37/38 (97%)	37 (100%)	0	100	100
53	2	51/52 (98%)	51 (100%)	0	100	100
54	3	34/34 (100%)	34 (100%)	0	100	100
55	4	56/62 (90%)	56 (100%)	0	100	100
All	All	4550/4825 (94%)	4547 (100%)	3 (0%)	87	85

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	88	GLU
12	L	45	PRO
34	j	58	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
46	v	57	HIS
48	x	27	ASN
11	K	118	HIS
10	J	58	ASN
48	x	45	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1513/1542 (98%)	176 (11%)	23 (1%)
22	X	20/120 (16%)	6 (30%)	0
23	Y	65/76 (85%)	9 (13%)	2 (3%)
24	5	63/77 (81%)	9 (14%)	0
24	Z	70/77 (90%)	10 (14%)	2 (2%)
25	a	2841/2904 (97%)	289 (10%)	0
26	b	119/120 (99%)	11 (9%)	0
All	All	4691/4916 (95%)	510 (10%)	27 (0%)

5 of 510 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	A
1	A	8	A
1	A	9	G
1	A	32	A
1	A	39	G

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1024	G
1	A	1124	G
23	Y	68	C
1	A	1042	A
1	A	1225	A

5.4 Non-standard residues in protein, DNA, RNA chains (i)

46 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
24	OMC	Z	32	24	19,22,23	0.19	0	26,31,34	0.35	0
1	4OC	A	1402	1,57	20,23,24	0.37	0	26,32,35	0.58	0
25	5MU	a	1939	25,56	19,22,23	0.78	0	28,32,35	0.53	0
25	PSU	a	955	25	18,21,22	0.82	0	22,30,33	0.69	0
25	6MZ	a	1618	25	22,25,26	0.57	0	30,36,39	0.58	0
23	PSU	Y	32	23	18,21,22	0.22	0	22,30,33	0.31	0
23	PSU	Y	55	23	18,21,22	0.25	0	22,30,33	0.29	0
25	1MG	a	745	25	22,26,27	0.77	0	33,39,42	0.79	1 (3%)
25	5MU	a	747	25	19,22,23	0.70	1 (5%)	28,32,35	0.85	2 (7%)
25	H2U	a	2449[B]	25	18,21,22	0.38	0	21,30,33	1.32	2 (9%)
24	4SU	5	8	24	18,21,22	0.20	0	26,30,33	0.31	0
36	4D4	l	81	36	9,11,12	1.93	2 (22%)	8,13,15	0.97	1 (12%)
25	PSU	a	1911	25	18,21,22	0.26	0	22,30,33	0.34	0
23	4SU	Y	8	23	18,21,22	0.18	0	26,30,33	0.23	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
23	MIA	Y	37	23	28,31,32	0.33	0	40,44,47	0.44	0
1	MA6	A	1518	1	23,26,27	0.22	0	34,38,41	0.72	1 (2%)
1	5MC	A	967	1	18,22,23	0.19	0	26,32,35	0.43	0
28	MEQ	d	150	28	8,9,10	0.62	0	5,10,12	0.93	0
24	PSU	5	55	24	18,21,22	0.26	0	22,30,33	0.36	0
12	D2T	L	89	12	7,9,10	0.95	0	6,11,13	1.41	1 (16%)
1	5MC	A	1407	1	18,22,23	0.34	0	26,32,35	0.56	0
25	H2U	a	2449[A]	25	18,21,22	0.51	0	21,30,33	1.37	2 (9%)
1	G7M	A	527	1	23,26,27	0.23	0	35,39,42	0.49	0
24	4SU	Z	8	24	18,21,22	0.19	0	26,30,33	0.29	0
23	H2U	Y	16	23	18,21,22	0.22	0	21,30,33	0.94	1 (4%)
24	OMC	5	32	24	19,22,23	0.20	0	26,31,34	0.56	0
23	G7M	Y	46	23	23,26,27	1.43	2 (8%)	35,39,42	1.45	4 (11%)
23	PSU	Y	39	23	18,21,22	0.24	0	22,30,33	0.40	0
36	MS6	l	82	36	5,7,8	0.50	0	2,7,9	0.40	0
24	5MU	Z	54	24	19,22,23	0.20	0	28,32,35	0.29	0
25	5MC	a	1962	25,56	18,22,23	0.47	0	26,32,35	0.44	0
1	PSU	A	516	1	18,21,22	0.17	0	22,30,33	0.41	0
1	2MG	A	1207	1,56	23,26,27	0.29	0	32,38,41	0.40	0
25	PSU	a	1917	25	18,21,22	0.23	0	22,30,33	0.38	0
1	2MG	A	1516	1	23,26,27	0.46	0	32,38,41	0.36	0
24	5MU	5	54	24	19,22,23	0.18	0	28,32,35	0.26	0
11	IAS	K	119	11	6,7,8	0.85	0	6,8,10	0.92	0
1	MA6	A	1519	1	23,26,27	0.46	0	34,38,41	0.69	1 (2%)
24	PSU	Z	55	24	18,21,22	0.26	0	22,30,33	0.45	0
1	UR3	A	1498	1	19,22,23	0.31	0	26,32,35	0.31	0
23	5MU	Y	54	23	19,22,23	0.26	0	28,32,35	0.38	0
25	6MZ	a	2030	25	22,25,26	0.58	0	30,36,39	0.62	0
1	2MG	A	966	1	23,26,27	0.37	0	32,38,41	0.33	0
25	3TD	a	1915	25	18,22,23	0.21	0	22,32,35	0.33	0
25	PSU	a	746	25,57	18,21,22	1.15	1 (5%)	22,30,33	0.83	0
25	2MG	a	1835	25	23,26,27	0.61	0	32,38,41	0.40	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	OMC	Z	32	24	-	0/9/27/28	0/2/2/2
1	4OC	A	1402	1,57	-	0/9/29/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	5MU	a	1939	25,56	-	0/7/25/26	0/2/2/2
25	PSU	a	955	25	-	0/7/25/26	0/2/2/2
25	6MZ	a	1618	25	-	0/9/27/28	0/3/3/3
23	PSU	Y	32	23	-	0/7/25/26	0/2/2/2
23	PSU	Y	55	23	-	0/7/25/26	0/2/2/2
25	1MG	a	745	25	-	0/7/25/26	0/3/3/3
25	5MU	a	747	25	-	0/7/25/26	0/2/2/2
25	H2U	a	2449[B]	25	-	3/7/38/39	0/2/2/2
24	4SU	5	8	24	-	0/7/25/26	0/2/2/2
36	4D4	l	81	36	-	1/11/12/14	-
25	PSU	a	1911	25	-	0/7/25/26	0/2/2/2
23	4SU	Y	8	23	-	0/7/25/26	0/2/2/2
23	MIA	Y	37	23	-	0/15/33/34	0/3/3/3
1	MA6	A	1518	1	-	0/11/29/30	0/3/3/3
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
28	MEQ	d	150	28	-	6/8/9/11	-
24	PSU	5	55	24	-	0/7/25/26	0/2/2/2
12	D2T	L	89	12	-	2/7/12/14	-
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
25	H2U	a	2449[A]	25	-	3/7/38/39	0/2/2/2
1	G7M	A	527	1	-	0/7/25/26	0/3/3/3
24	4SU	Z	8	24	-	0/7/25/26	0/2/2/2
23	H2U	Y	16	23	-	1/7/38/39	0/2/2/2
24	OMC	5	32	24	-	0/9/27/28	0/2/2/2
23	G7M	Y	46	23	-	2/7/25/26	0/3/3/3
23	PSU	Y	39	23	-	0/7/25/26	0/2/2/2
36	MS6	l	82	36	-	1/4/6/8	-
24	5MU	Z	54	24	-	0/7/25/26	0/2/2/2
25	5MC	a	1962	25,56	-	2/7/25/26	0/2/2/2
1	PSU	A	516	1	-	0/7/25/26	0/2/2/2
1	2MG	A	1207	1,56	-	0/9/27/28	0/3/3/3
25	PSU	a	1917	25	-	1/7/25/26	0/2/2/2
1	2MG	A	1516	1	-	0/9/27/28	0/3/3/3
24	5MU	5	54	24	-	0/7/25/26	0/2/2/2
11	IAS	K	119	11	-	0/7/7/8	-
1	MA6	A	1519	1	-	2/11/29/30	0/3/3/3
24	PSU	Z	55	24	-	0/7/25/26	0/2/2/2
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
23	5MU	Y	54	23	-	0/7/25/26	0/2/2/2
25	6MZ	a	2030	25	-	1/9/27/28	0/3/3/3
1	2MG	A	966	1	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	3TD	a	1915	25	-	0/7/25/26	0/2/2/2
25	PSU	a	746	25,57	-	1/7/25/26	0/2/2/2
25	2MG	a	1835	25	-	0/9/27/28	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	Y	46	G7M	C8-N7	5.42	1.42	1.33
36	l	81	4D4	CZ-NE	4.14	1.41	1.33
36	l	81	4D4	CZ-NH1	3.82	1.50	1.34
23	Y	46	G7M	C8-N9	3.57	1.45	1.35
25	a	746	PSU	C4-N3	-3.04	1.33	1.38

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
25	a	2449[A]	H2U	O4'-C1'-N1	4.99	116.10	109.30
23	Y	46	G7M	C8-N7-C5	4.55	113.47	107.78
23	Y	46	G7M	N9-C8-N7	-4.55	100.96	112.21
25	a	2449[B]	H2U	C4-N3-C2	-4.46	122.09	125.79
23	Y	16	H2U	C4-N3-C2	-3.92	122.54	125.79

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
28	d	150	MEQ	C-CA-CB-CG
28	d	150	MEQ	OE1-CD-CG-CB
28	d	150	MEQ	NE2-CD-CG-CB
1	A	1519	MA6	O4'-C4'-C5'-O5'
25	a	2449[B]	H2U	C2'-C1'-N1-C6

There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	a	1939	5MU	1	0
1	A	1518	MA6	1	0
28	d	150	MEQ	1	0
12	L	89	D2T	1	0
1	A	1519	MA6	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	a	2030	6MZ	2	0
1	A	966	2MG	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 463 ligands modelled in this entry, 450 are monoatomic - leaving 13 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
58	SR0	a	3002	-	9,9,9	0.65	0	8,8,8	0.93	0
59	PUT	a	3007	-	5,5,5	0.44	0	4,4,4	0.56	0
59	PUT	a	3006	-	5,5,5	0.35	0	4,4,4	0.15	0
59	PUT	a	3010	-	5,5,5	0.59	0	4,4,4	0.74	0
58	SR0	a	3004	-	9,9,9	0.60	0	8,8,8	0.34	0
59	PUT	a	3009	-	5,5,5	0.57	0	4,4,4	0.15	0
59	PUT	a	3011	-	5,5,5	0.41	0	4,4,4	0.26	0
59	PUT	a	3012	-	5,5,5	0.34	0	4,4,4	0.48	0
59	PUT	a	3013	-	5,5,5	0.57	0	4,4,4	0.44	0
58	SR0	a	3005	-	9,9,9	0.68	0	8,8,8	0.63	0
59	PUT	a	3008	-	5,5,5	0.31	0	4,4,4	0.28	0
58	SR0	a	3001	-	9,9,9	0.31	0	8,8,8	0.48	0
58	SR0	a	3003	-	9,9,9	0.55	0	8,8,8	0.48	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	SR0	a	3002	-	-	5/7/7/7	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	PUT	a	3007	-	-	0/3/3/3	-
59	PUT	a	3006	-	-	0/3/3/3	-
59	PUT	a	3010	-	-	0/3/3/3	-
58	SR0	a	3004	-	-	3/7/7/7	-
59	PUT	a	3009	-	-	1/3/3/3	-
59	PUT	a	3011	-	-	1/3/3/3	-
59	PUT	a	3012	-	-	1/3/3/3	-
59	PUT	a	3013	-	-	2/3/3/3	-
58	SR0	a	3005	-	-	3/7/7/7	-
59	PUT	a	3008	-	-	1/3/3/3	-
58	SR0	a	3001	-	-	3/7/7/7	-
58	SR0	a	3003	-	-	1/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	a	3005	SR0	N6-C7-C8-C9
58	a	3002	SR0	N6-C7-C8-C9
58	a	3005	SR0	C8-C7-N6-C5
58	a	3004	SR0	C3-C4-C5-N6
58	a	3001	SR0	C3-C4-C5-N6

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	a	3007	PUT	1	0
59	a	3010	PUT	2	0
59	a	3013	PUT	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

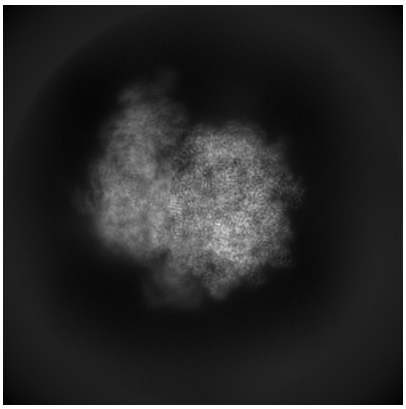
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-55618. These allow visual inspection of the internal detail of the map and identification of artifacts.

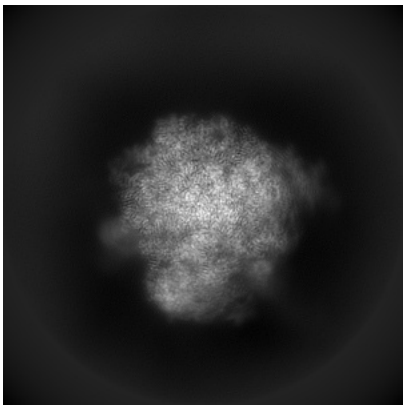
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

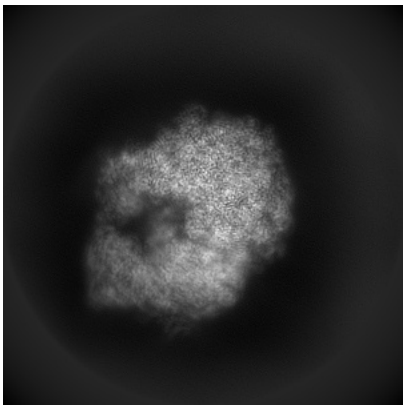
6.1.1 Primary map



X

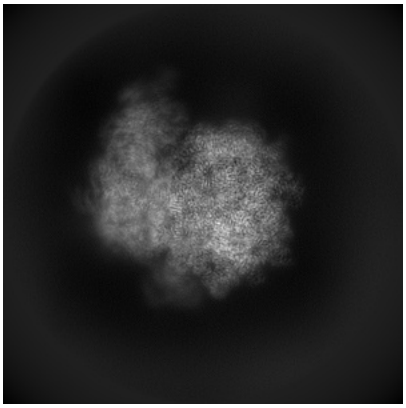


Y

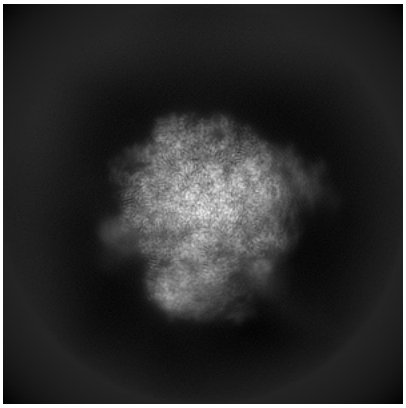


Z

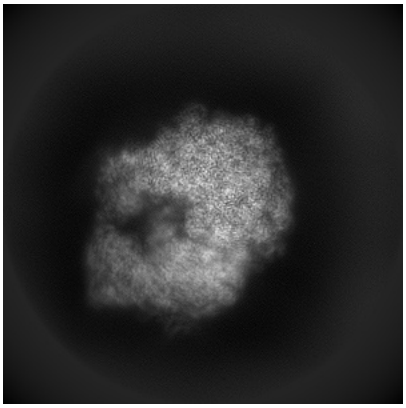
6.1.2 Raw map



X



Y

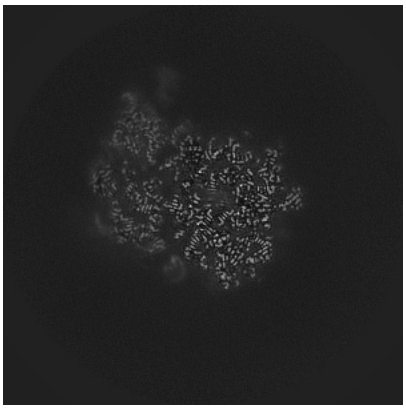


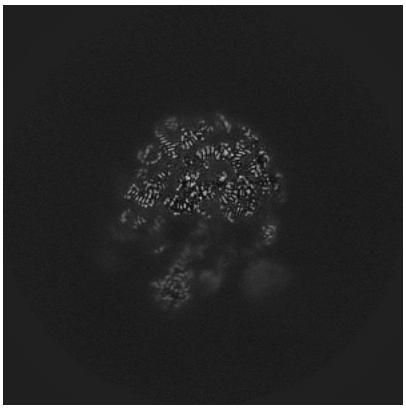
Z

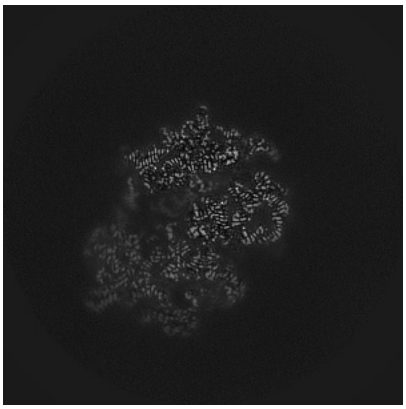
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

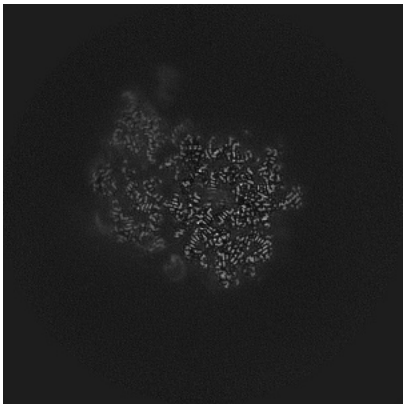
6.2.1 Primary map

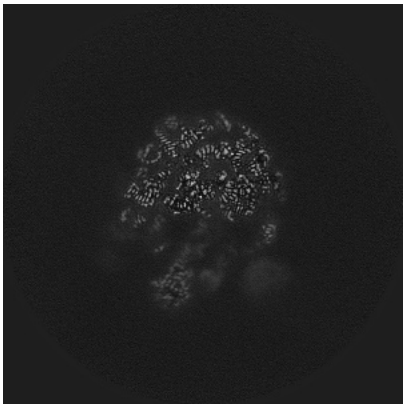

X Index: 256

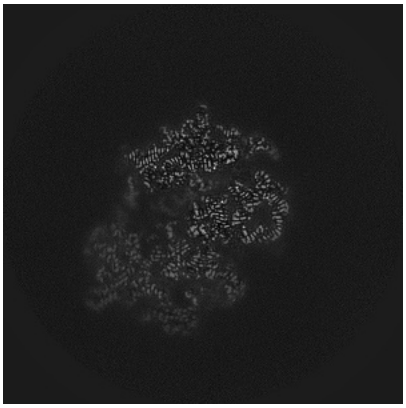

Y Index: 256


Z Index: 256

6.2.2 Raw map


X Index: 256

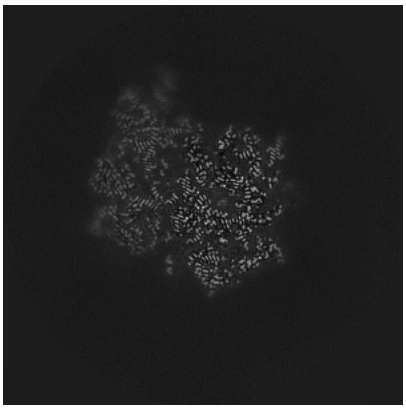

Y Index: 256


Z Index: 256

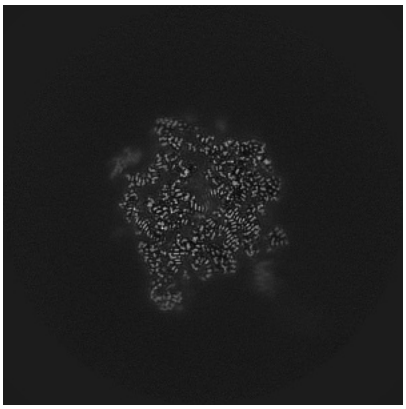
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

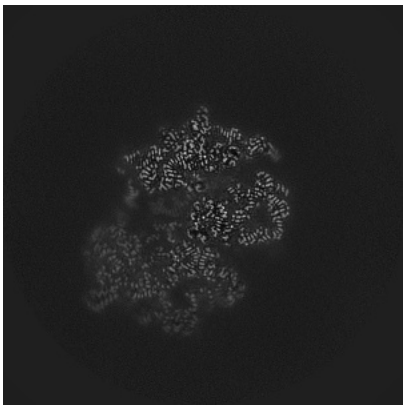
6.3.1 Primary map



X Index: 265

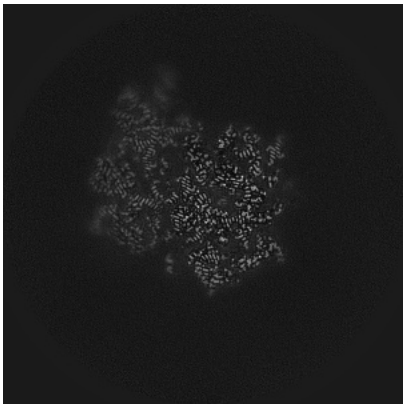


Y Index: 286

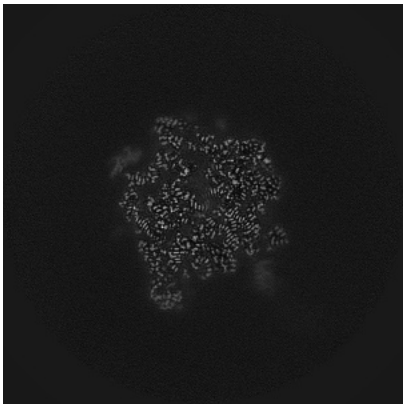


Z Index: 254

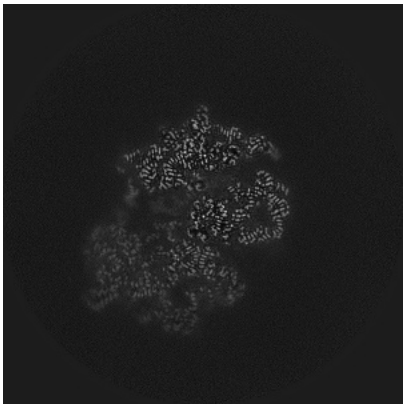
6.3.2 Raw map



X Index: 265



Y Index: 286

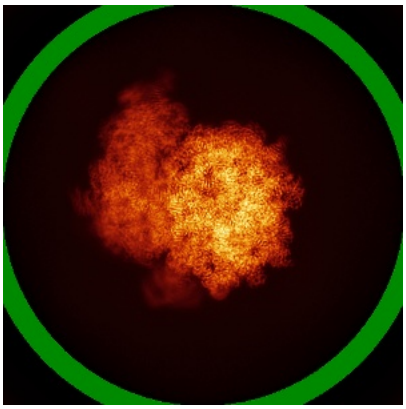


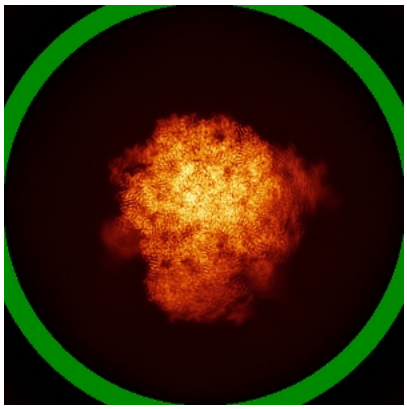
Z Index: 254

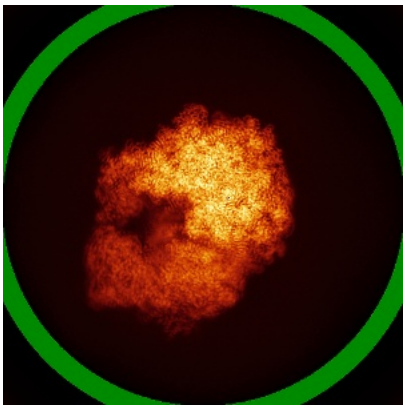
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

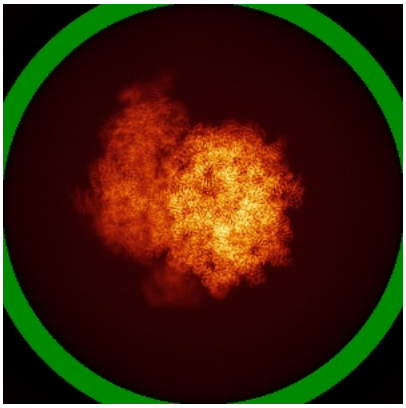
6.4.1 Primary map

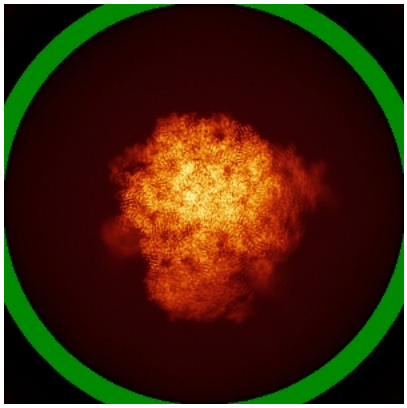

X

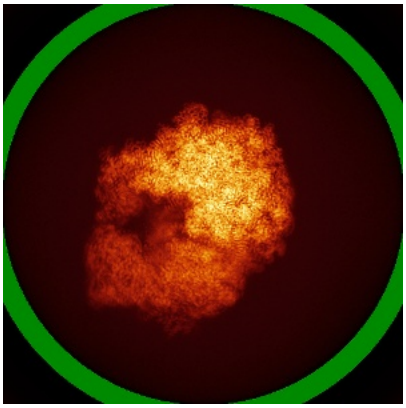

Y


Z

6.4.2 Raw map


X


Y


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.013. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

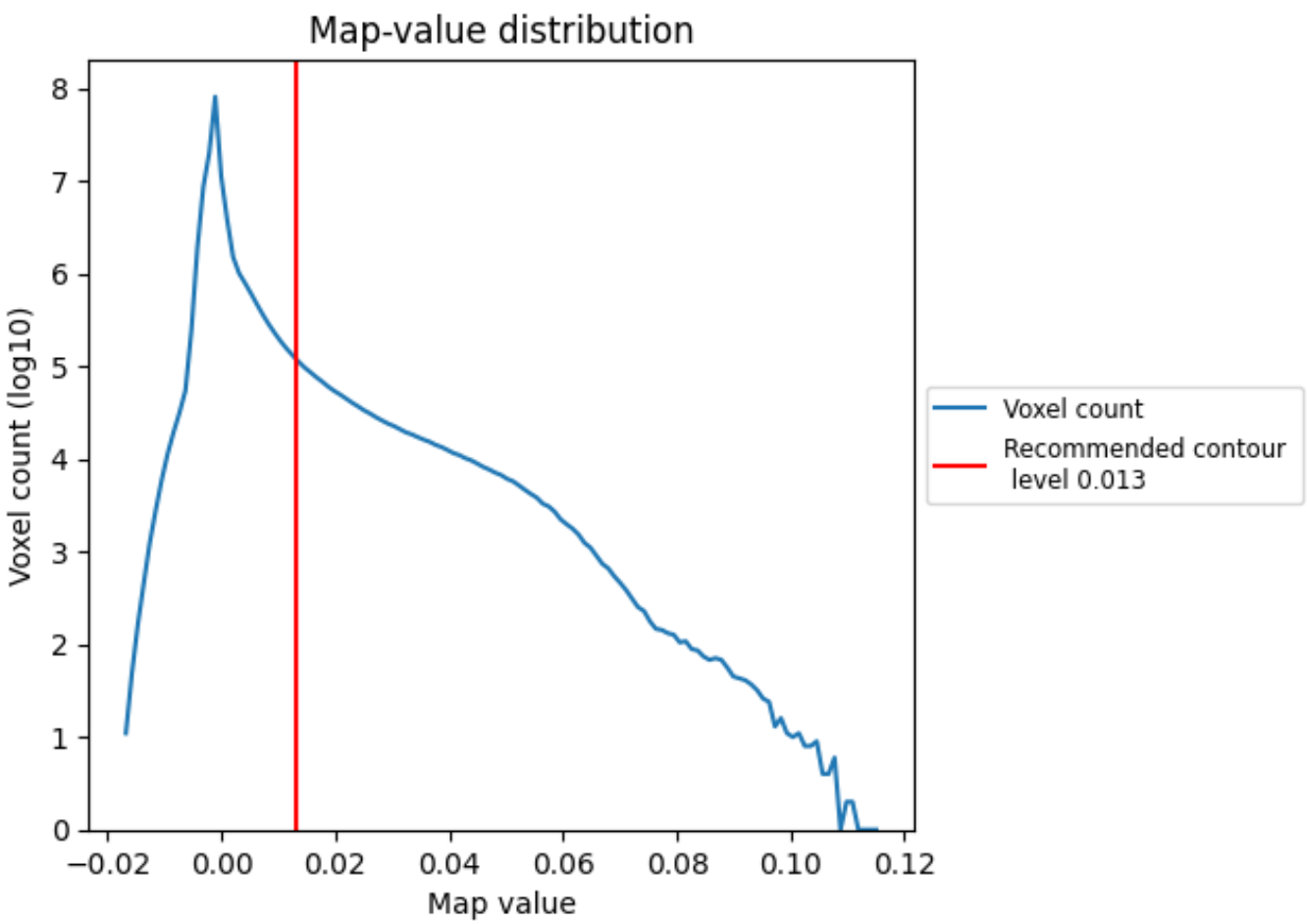
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis (i)

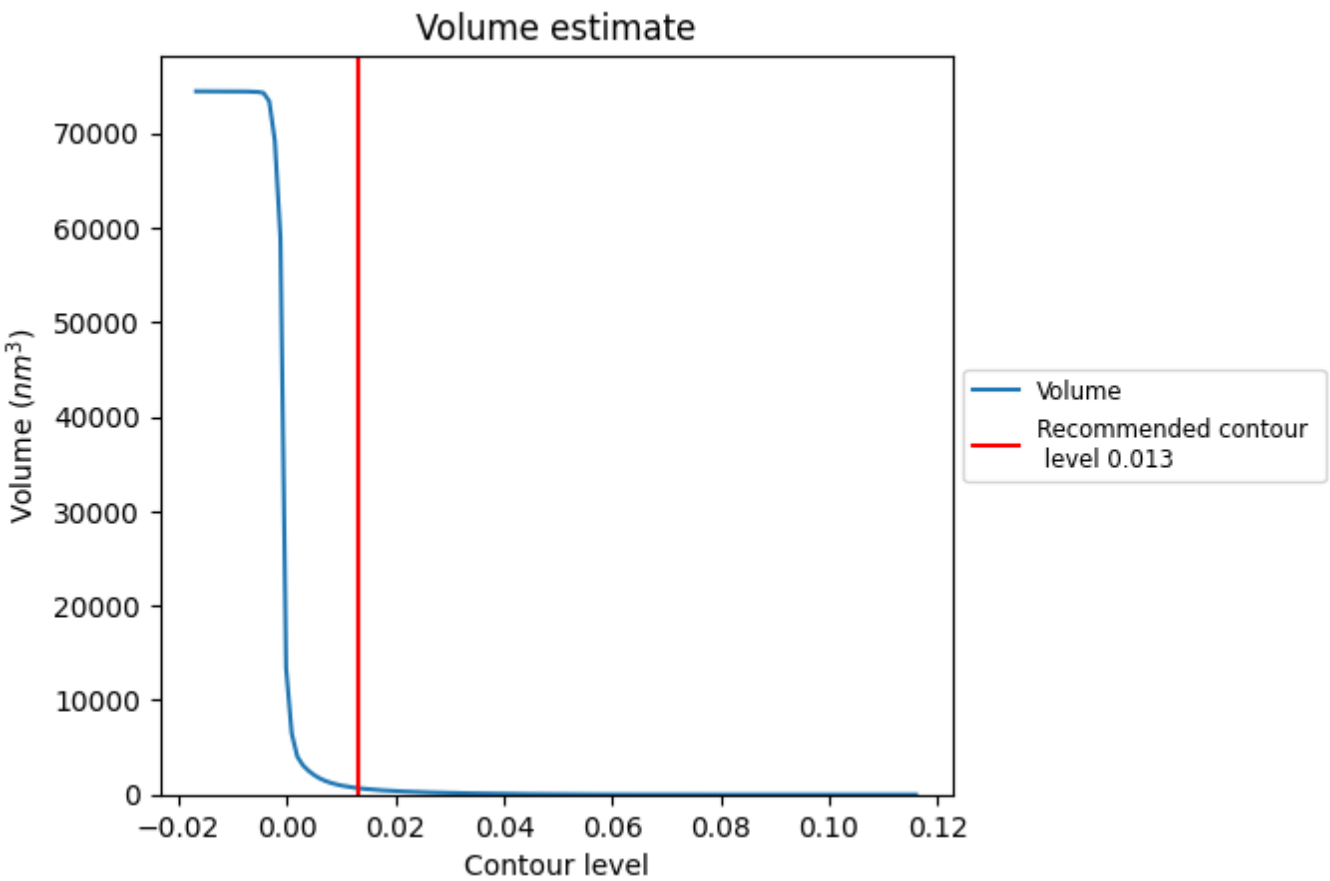
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

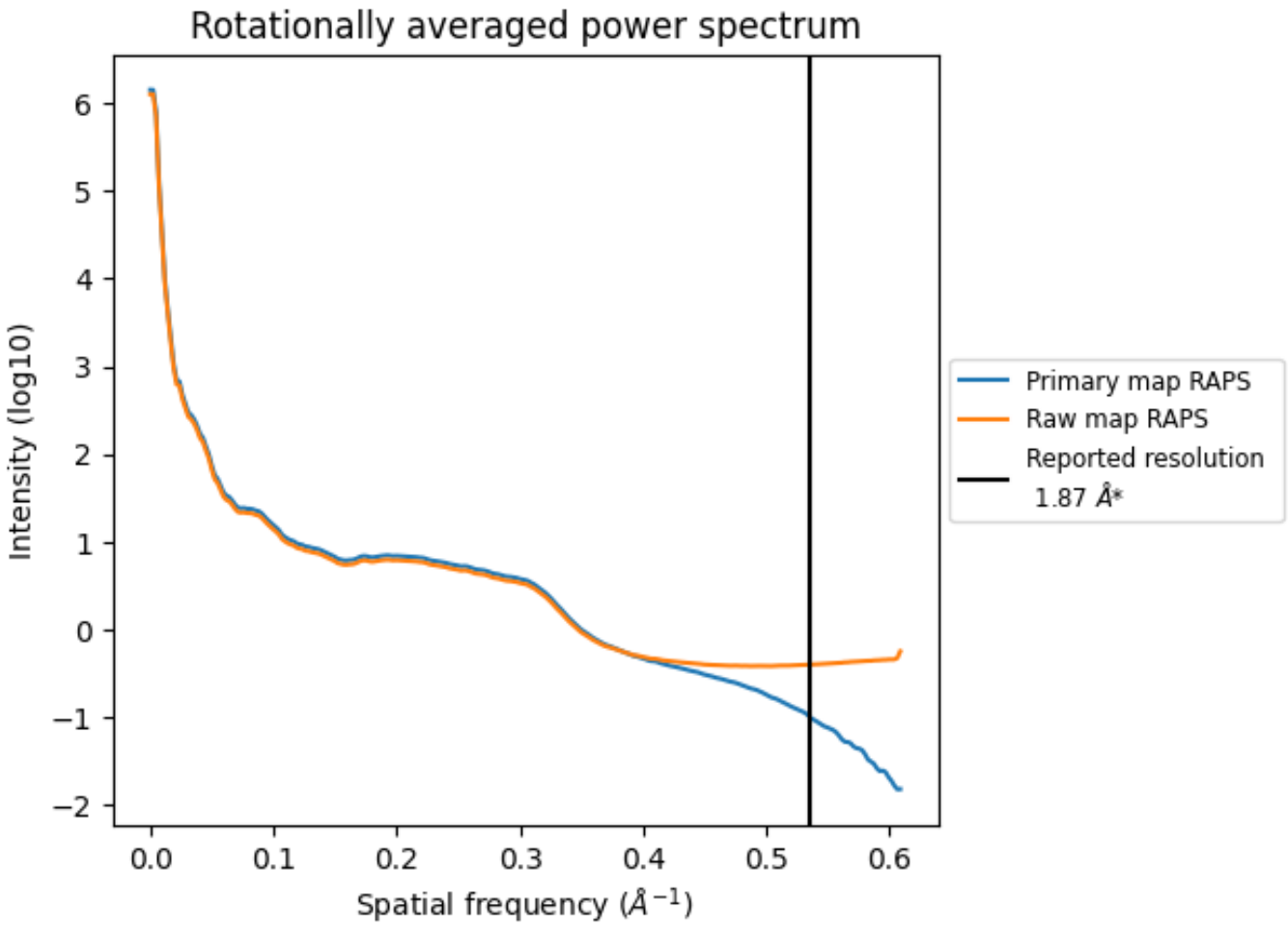
7.2 Volume estimate (i)



The volume at the recommended contour level is 690 nm^3; this corresponds to an approximate mass of 623 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

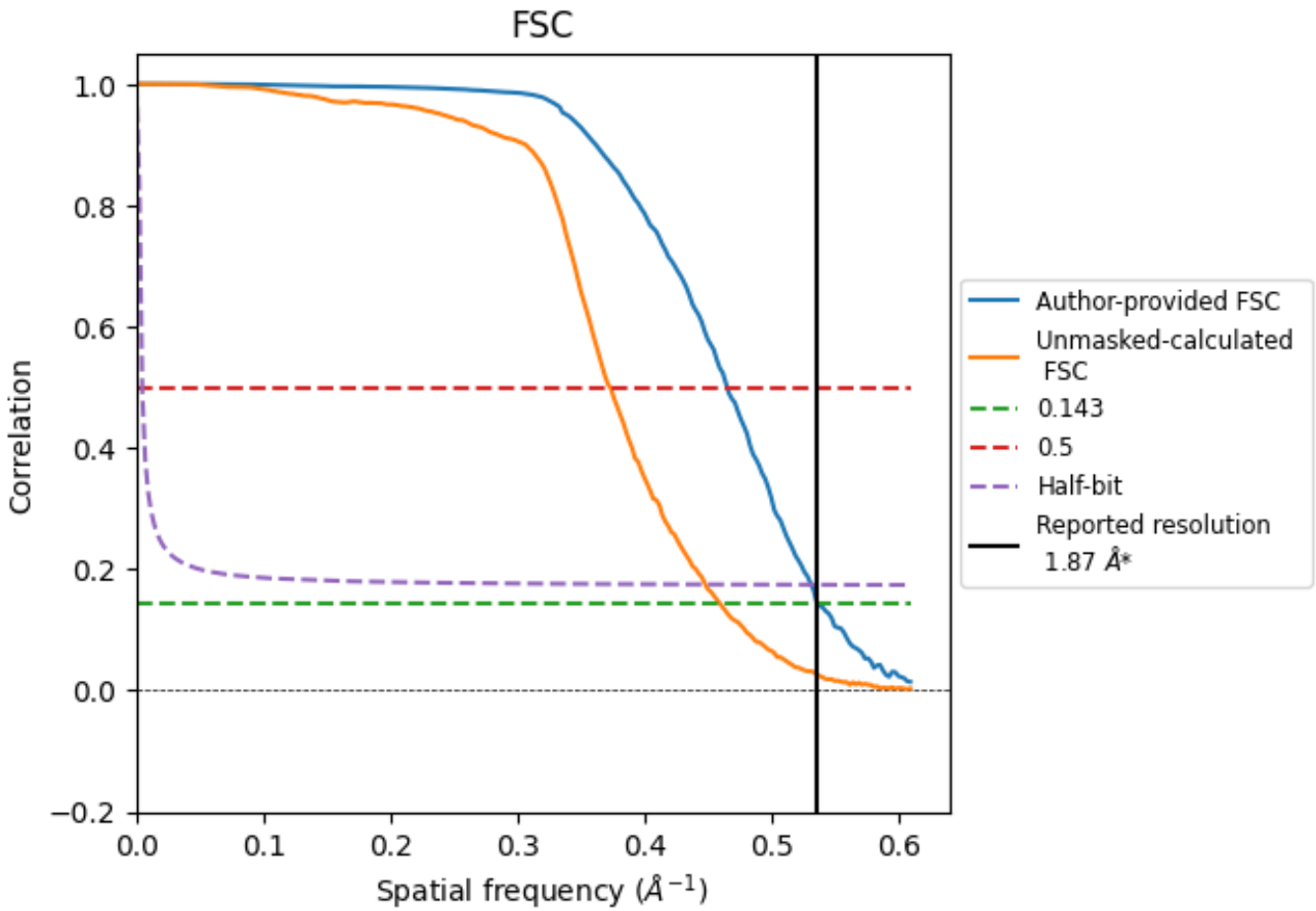


*Reported resolution corresponds to spatial frequency of 0.535 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.535 Å^{-1}

8.2 Resolution estimates (i)

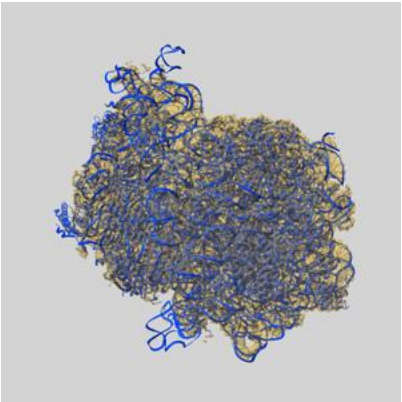
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.87	-	-
Author-provided FSC curve	1.87	2.15	1.88
Unmasked-calculated*	2.18	2.68	2.23

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.18 differs from the reported value 1.87 by more than 10 %

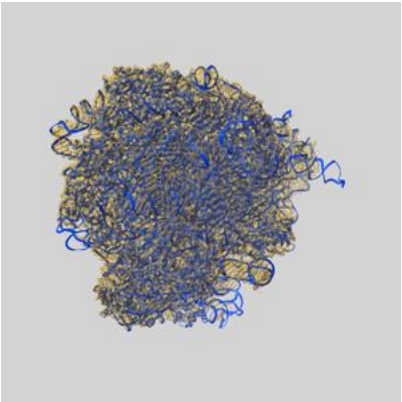
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-55618 and PDB model 9T6M. Per-residue inclusion information can be found in section 3 on page 19.

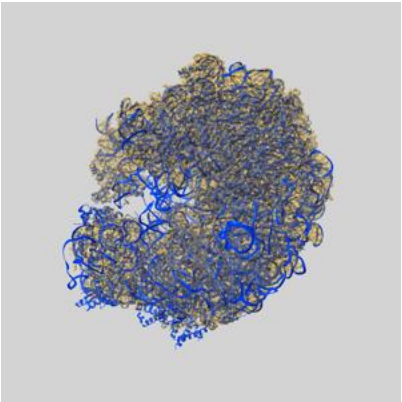
9.1 Map-model overlay (i)



X



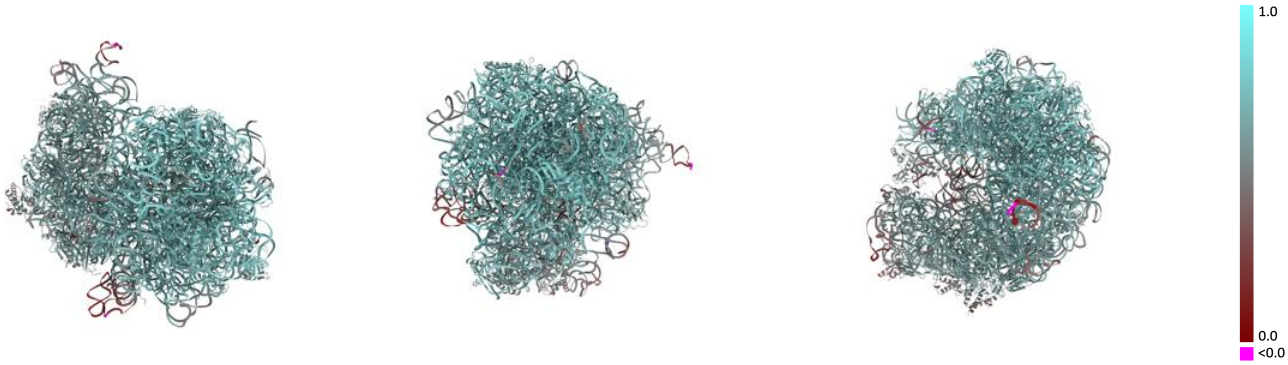
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

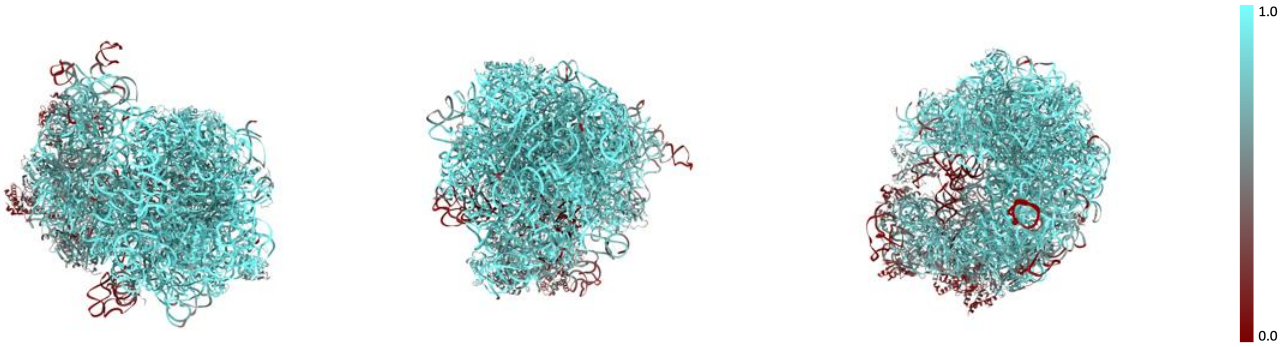
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

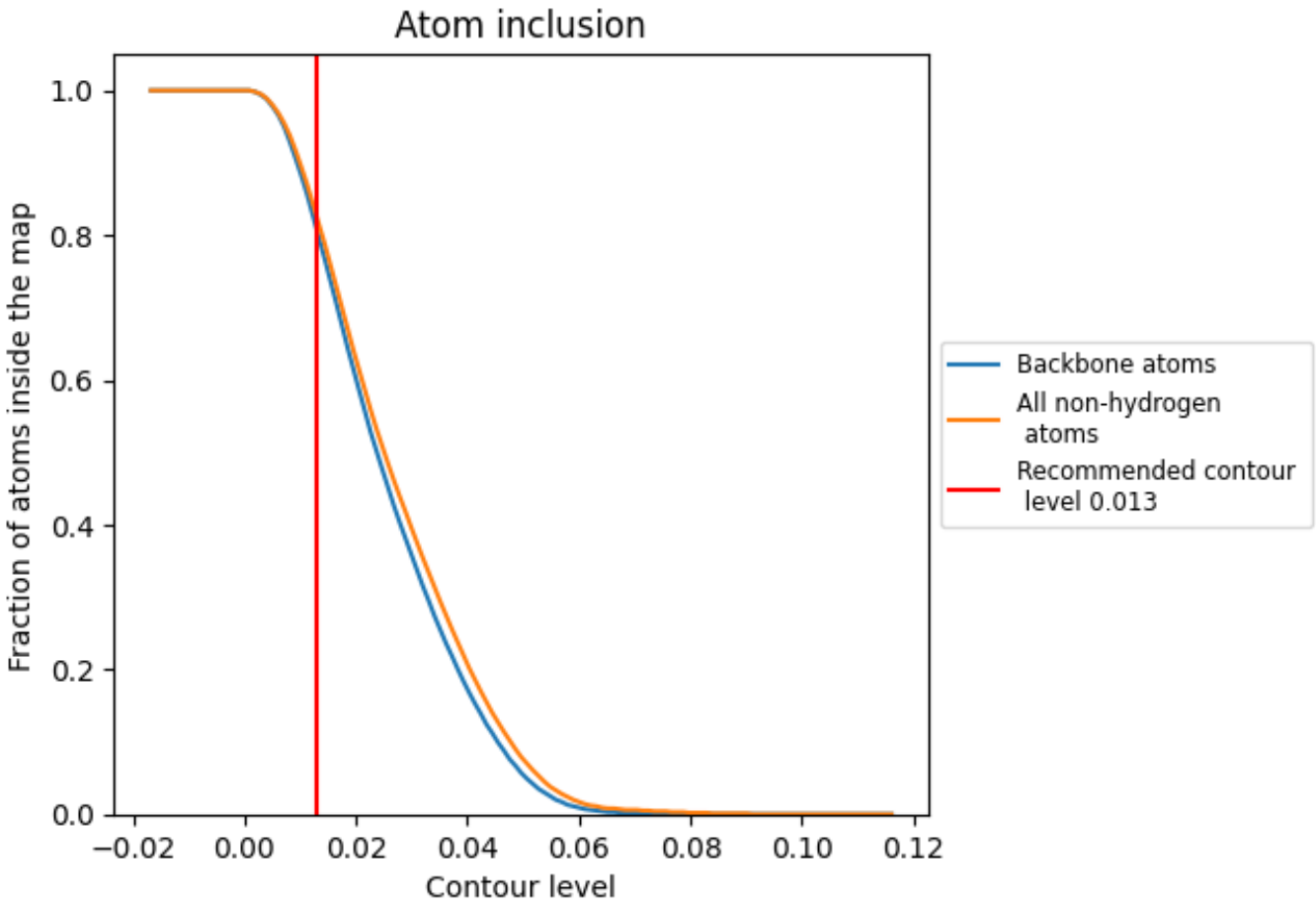
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.013).

9.4 Atom inclusion (i)



At the recommended contour level, 81% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8250	0.6490
0	0.8810	0.7070
1	0.9910	0.7670
2	0.9760	0.7610
3	0.9390	0.6950
4	0.3950	0.4900
5	0.1240	0.2920
A	0.8370	0.6160
B	0.2330	0.4900
C	0.5800	0.5770
D	0.3970	0.5590
E	0.7960	0.6320
F	0.5820	0.5710
G	0.3530	0.5070
H	0.7340	0.6280
I	0.5680	0.5560
J	0.4070	0.5100
K	0.7010	0.6190
L	0.6640	0.5890
M	0.4880	0.5500
N	0.6000	0.5750
O	0.7130	0.6100
P	0.6360	0.6090
Q	0.5840	0.5630
R	0.7180	0.6000
S	0.3820	0.5210
T	0.6440	0.5880
U	0.4170	0.5110
X	0.2170	0.3730
Y	0.0080	0.3980
Z	0.3090	0.5500
a	0.9360	0.6920
b	0.9450	0.6600
c	0.9590	0.7420
d	0.9480	0.7340

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Chain	Atom inclusion	Q-score
e	0.8110	0.6850
f	0.6080	0.5430
g	0.7460	0.6170
h	0.5900	0.6120
i	0.9500	0.7350
j	0.9300	0.7210
k	0.9350	0.7290
l	0.9310	0.7180
m	0.9810	0.7570
n	0.8770	0.6670
o	0.9000	0.7130
p	0.9750	0.7550
q	0.9020	0.7090
r	0.9310	0.7330
s	0.8930	0.6930
t	0.8580	0.6740
u	0.8560	0.6750
v	0.8470	0.7020
w	0.9420	0.7210
x	0.8230	0.6580
y	0.9130	0.7160
z	0.9570	0.7420