



## wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 01:25 AM UTC

PDB ID : 9OZ9 / pdb\_00009oz9  
EMDB ID : EMD-71052  
Title : Flavobacterium johnsoniae 70S initiation complex with Shine-Dalgarno-less mRNA.  
Authors : Ortega, J.; Arpin, D.  
Deposited on : 2025-06-05  
Resolution : 2.60 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

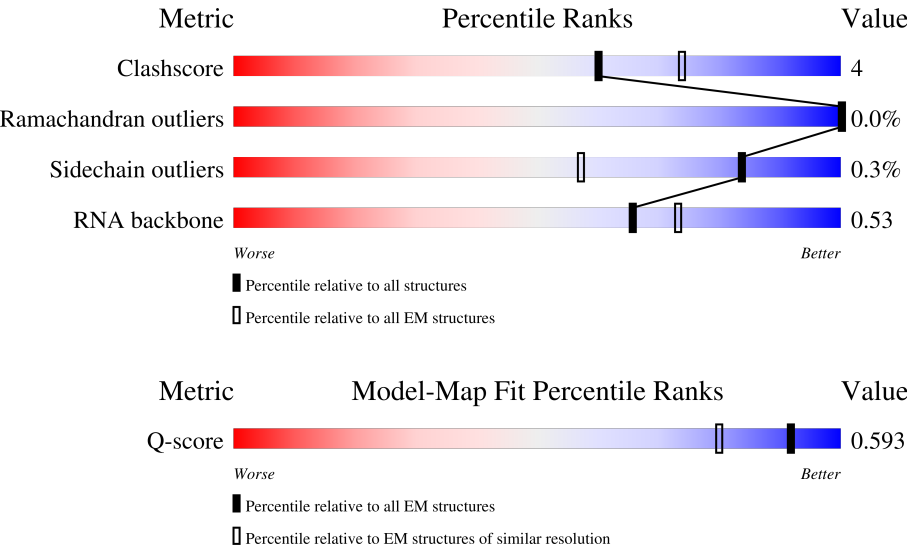
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance ⓘ

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

The reported resolution of this entry is 2.60 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	8728 ( 2.10 - 3.10 )

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  $\geq 3$ , 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  $\leq 5\%$ . 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	1	2862	72% 21% . .
2	2	1520	66% 27% 5% .
3	3	111	77% 21% ..







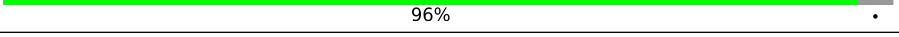

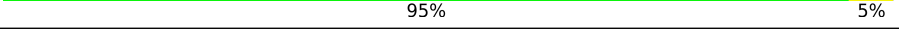

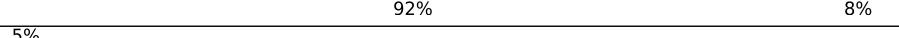
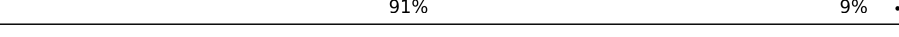

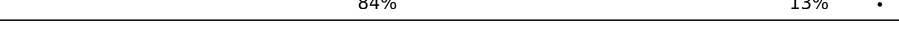


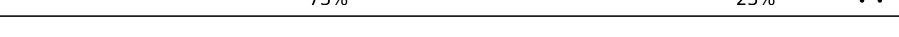

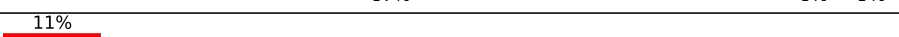






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Mol	Chain	Length	Quality of chain
4	4	50	
5	5	30	
6	6	6	
7	A	77	
8	B	274	
9	C	205	
10	D	209	
11	E	183	
12	F	180	
13	G	146	
14	H	254	
15	J	151	
16	K	122	
17	L	150	
18	M	141	
19	N	163	
20	O	116	
21	P	116	
22	Q	114	
23	R	147	
24	S	137	
25	T	96	
26	U	104	
27	V	203	
28	W	86	




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Mol	Chain	Length	Quality of chain
29	X	78	
30	Y	63	
31	Z	60	
32	a	84	
33	b	64	
34	c	60	
35	d	53	
36	e	65	
37	f	38	
38	h	252	
39	i	201	
40	j	173	
41	k	113	
42	l	158	
43	m	132	
44	n	128	
45	o	101	
46	p	127	
47	q	127	
48	r	124	
49	s	89	
50	t	88	
51	u	188	
52	v	86	
53	w	98	

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Mol	Chain	Length	Quality of chain
54	x	92	
55	y	83	
56	z	64	

## 2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 137848 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2754	Total	C	N	O	P	0	0
			59085	26384	10861	19086	2754		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	342	A	U	conflict	GB 1735479352
1	406	A	G	conflict	GB 1735479352
1	429	C	U	conflict	GB 1735479352
1	645	C	U	conflict	GB 1735479352
1	925	C	U	conflict	GB 1735479352
1	1510	A	U	conflict	GB 1735479352
1	1687	U	G	conflict	GB 1735479352
1	1745	U	C	conflict	GB 1735479352
1	1746	G	C	conflict	GB 1735479352
1	1753	C	G	conflict	GB 1735479352
1	1754	A	G	conflict	GB 1735479352
1	1815	U	C	conflict	GB 1735479352
1	2098	C	U	conflict	GB 1735479352
1	2209	U	C	conflict	GB 1735479352
1	2471	U	C	conflict	GB 1735479352
1	2569	U	C	conflict	GB 1735479352

- Molecule 2 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1481	Total	C	N	O	P	0	0
			31728	14167	5801	10279	1481		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	110	Total	C	N	O	P	0	0
			2339	1043	406	780	110		

- Molecule 4 is a protein called 50S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	36	Total	C	N	O	S	0	0
			278	183	44	49	2		

- Molecule 5 is a protein called 50S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	5	27	Total	C	N	O	0	0
			231	140	61	30		

- Molecule 6 is a RNA chain called mFjoh\_4413 mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	6	Total	C	N	O	P	0	0
			128	57	21	44	6		

- Molecule 7 is a RNA chain called fMet-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	73	Total	C	N	O	P	0	0
			1562	696	286	507	73		

- Molecule 8 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	271	Total	C	N	O	S	0	0
			2053	1277	403	365	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	35	SER	ALA	conflict	UNP A0A1B2U0Q0
B	194	GLU	ALA	conflict	UNP A0A1B2U0Q0

- Molecule 9 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	204	Total	C	N	O	S	0	0
			1515	956	280	272	7		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	87	ALA	THR	conflict	UNP A0A1M5L9Q4
C	88	ALA	GLU	conflict	UNP A0A1M5L9Q4
C	90	ALA	LYS	conflict	UNP A0A1M5L9Q4
C	138	GLN	ASN	conflict	UNP A0A1M5L9Q4

- Molecule 10 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	D	206	Total	C	N	O	0	0
			1509	964	281	264		

- Molecule 11 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	E	179	Total	C	N	O	S	0
			1300	836	229	230	5	0

- Molecule 12 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	F	177	Total	C	N	O	S	0
			1249	802	227	219	1	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	96	ALA	SER	conflict	UNP A0A1M5L807
F	100	ASN	GLN	conflict	UNP A0A1M5L807
F	128	ALA	LYS	conflict	UNP A0A1M5L807
F	130	ALA	LYS	conflict	UNP A0A1M5L807

- Molecule 13 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	G	56	Total	C	N	O	S	0
			405	265	70	69	1	0

- Molecule 14 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	H	219	Total	C	N	O	S	0
			1658	1058	291	301	8	0



- Molecule 15 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	150	Total	C	N	O	S	0	0
			1112	705	207	195	5		

- Molecule 16 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	121	Total	C	N	O	S	0	0
			889	559	173	153	4		

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	150	Total	C	N	O	S	0	0
			1048	654	209	183	2		

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	139	Total	C	N	O	S	0	0
			1056	683	199	167	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	96	TRP	ALA	conflict	UNP A0A1B2U0I0

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	125	Total	C	N	O	S	0	0
			980	615	189	170	6		

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	O	115	Total	C	N	O	0	0
			846	532	164	150		

- Molecule 21 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	P	112	Total	C	N	O	0	0
			848	554	154	140		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	115	LEU	ARG	conflict	UNP A0A1M5PX52

- Molecule 22 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	113	Total	C	N	O	S	0	0
			904	571	185	143	5		

- Molecule 23 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	R	104	Total	C	N	O	0	0
			768	499	145	124		

- Molecule 24 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	128	Total	C	N	O	S	0	0
			964	600	198	163	3		

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	85	Total	C	N	O	S	0	0
			647	416	116	114	1		

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	U	94	Total	C	N	O	0	0
			679	433	134	112		

- Molecule 27 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	124	Total	C	N	O	S	0	0
			867	567	147	151	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	66	ALA	LYS	conflict	UNP A0A1M5HDD0
V	137	ILE	LEU	conflict	UNP A0A1M5HDD0
V	139	GLU	ASP	conflict	UNP A0A1M5HDD0
V	175	ALA	CYS	conflict	UNP A0A1M5HDD0

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	78	Total	C	N	O		0	0
			586	365	119	102			

- Molecule 29 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	76	Total	C	N	O	S	0	0
			586	370	114	99	3		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	52	GLN	ALA	conflict	UNP A0A1B2U1R1
X	53	ARG	ALA	conflict	UNP A0A1B2U1R1
X	74	ALA	GLU	conflict	UNP A0A1B2U1R1

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	59	Total	C	N	O		0	0
			409	257	80	72			

- Molecule 31 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	56	Total	C	N	O	S	0	0
			400	254	77	67	2		

- Molecule 32 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	58	Total	C	N	O	S	0	0
			421	271	71	77	2		

- Molecule 33 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	59	Total	C	N	O	S	0	0
			475	300	99	75	1		

- Molecule 34 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	54	Total	C	N	O	S	0	0
			415	263	81	70	1		

- Molecule 35 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	51	Total	C	N	O	S	0	0
			416	252	101	61	2		

- Molecule 36 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	64	Total	C	N	O	S	0	0
			506	322	103	80	1		

- Molecule 37 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	38	Total	C	N	O	S	0	0
			305	190	68	45	2		

- Molecule 38 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	215	Total	C	N	O	S	0	0
			1600	1015	290	289	6		

- Molecule 39 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	200	Total	C	N	O	S	0	0
			1576	998	291	284	3		

- Molecule 40 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	172	Total	C	N	O	S	0	0
			1179	744	229	205	1		

- Molecule 41 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	107	Total	C	N	O	S	0	0
			815	534	149	130	2		

- Molecule 42 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	153	Total	C	N	O	S	0	0
			1179	744	230	200	5		

- Molecule 43 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	131	Total	C	N	O	S	0	0
			961	623	167	169	2		

- Molecule 44 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	125	Total	C	N	O	S	0	0
			972	612	188	168	4		

- Molecule 45 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	98	Total	C	N	O	S	0	0
			701	450	123	126	2		

- Molecule 46 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	117	Total	C	N	O	S	0	0
			819	512	159	143	5		

- Molecule 47 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	121	Total	C	N	O	S	0	0
			922	567	195	157	3		

- Molecule 48 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	117	Total	C	N	O	S	0	0
			883	544	181	155	3		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	115	THR	-	expression tag	UNP P0A7T1
r	116	VAL	-	expression tag	UNP P0A7T1
r	117	ALA	-	expression tag	UNP P0A7T1
r	118	ASN	-	expression tag	UNP P0A7T1
r	119	LYS	-	expression tag	UNP P0A7T1
r	120	LYS	-	expression tag	UNP P0A7T1
r	121	LYS	-	expression tag	UNP P0A7T1
r	122	ALA	-	expression tag	UNP P0A7T1
r	123	THR	-	expression tag	UNP P0A7T1
r	124	LYS	-	expression tag	UNP P0A7T1

- Molecule 49 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	88	Total	C	N	O	S	0	0
			665	416	136	110	3		

- Molecule 50 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	t	88	Total	C	N	O	0	0
			694	443	136	115		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	71	ARG	LYS	conflict	UNP A0A1M6QTP8

- Molecule 51 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	u	109	Total	C	N	O	0	0
			783	492	151	140		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	56	ILE	ALA	conflict	UNP A0A1M6QGN9
u	62	GLN	ASN	conflict	UNP A0A1M6QGN9

- Molecule 52 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	80	Total	C	N	O	S	0	0
			638	404	124	107	3		

- Molecule 53 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	65	Total	C	N	O	S	0	0
			521	342	96	81	2		

- Molecule 54 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	83	Total	C	N	O	S	0	0
			636	406	118	110	2		

- Molecule 55 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	79	Total	C	N	O	S	0	0
			615	381	129	104	1		

- Molecule 56 is a protein called 30S ribosomal protein S21.

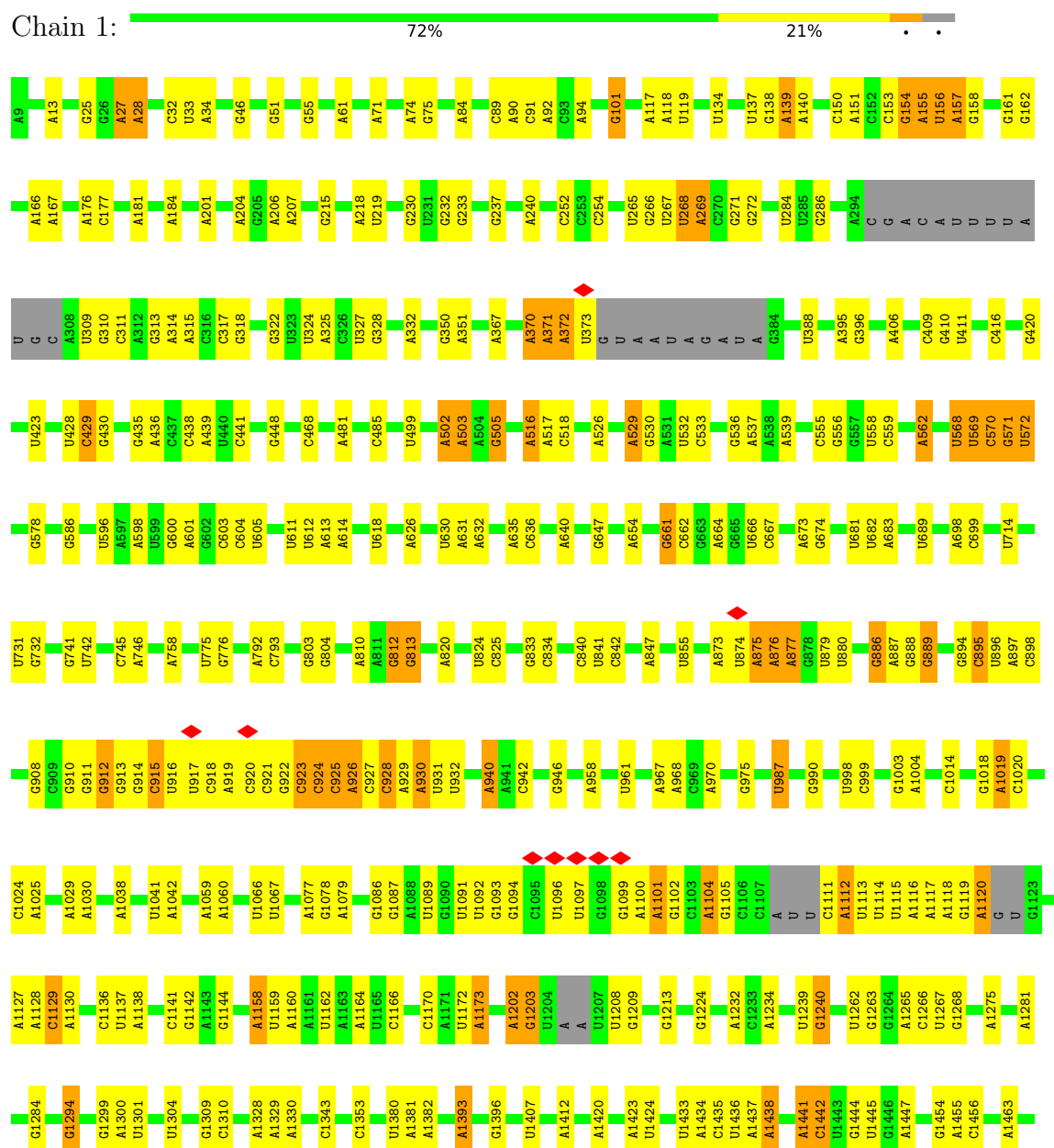
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	z	64	522	331	99	91	1	0	0

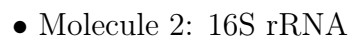


### 3 Residue-property plots

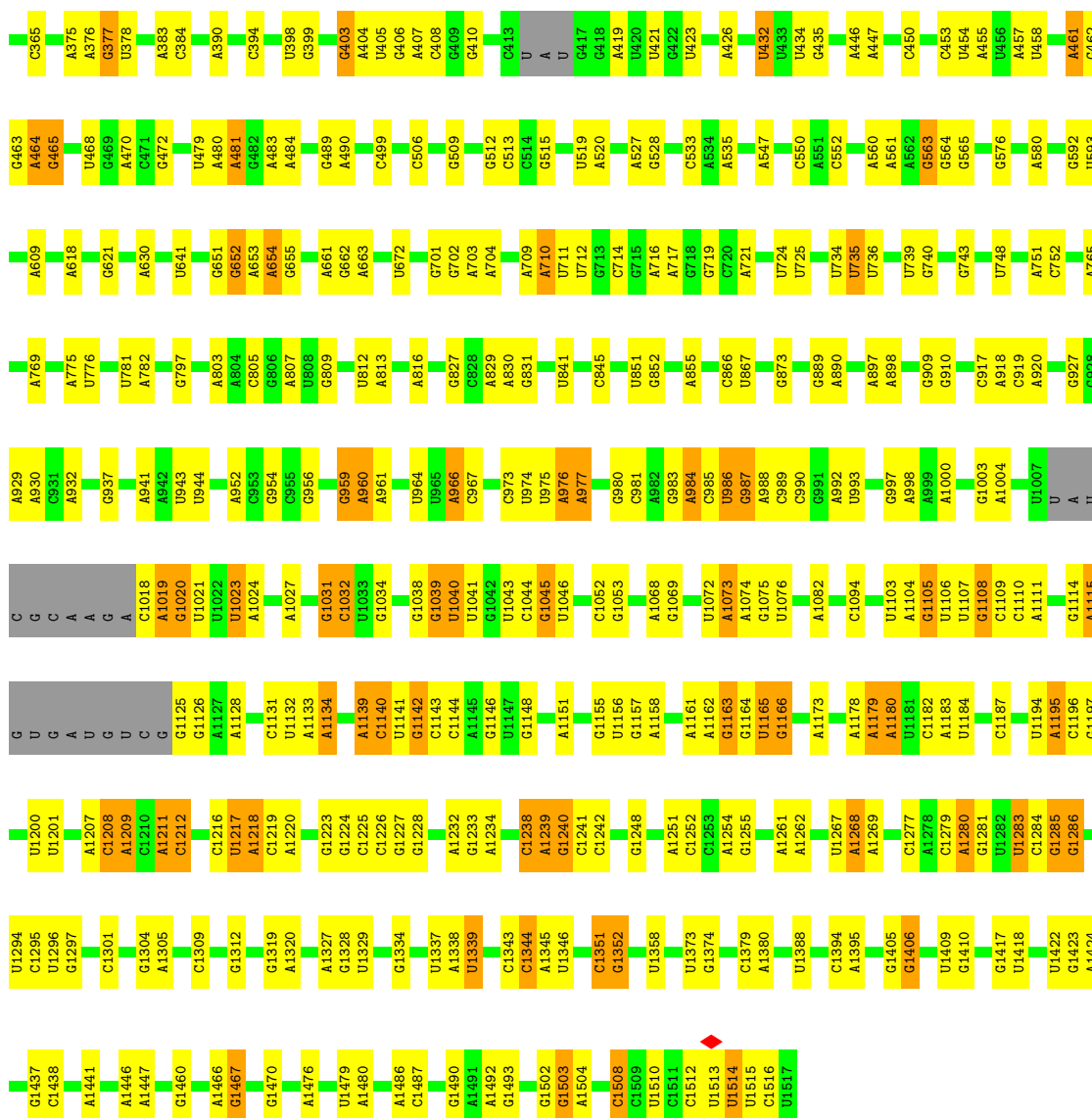
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 23S rRNA



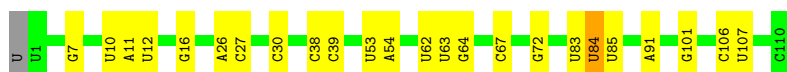


G220	A110	U
A221	C111	A-1
U222		U0
		A1
A236	G125	C2
U237	C126	G3
U238	C127	G3
A239	U128	A4
G240	U129	A4
		A8
		G9
G244	G133	U17
	A134	C18
A251	G135	
	G137	G21
U254	G138	G22
	G139	
		A29
G259	A147	A32
G260	G148	
A272	U154	G35
G274		C36
A275	G158	
	A159	G39
G282	U160	C40
		G41
G282	C167	G42
A293	U168	
	C169	C47
A314	A170	U48
C315		
U316	A175	A51
G317		G61
A320	G181	
C321	A182	
A322	G183	G64
	C184	
		G69
G325	A188	
	U189	G72
C328	C190	A
A329	A191	G
G330	C192	G
A331	U193	U
	U194	C
G340	U195	U
G344	A196	U
C345	U197	C
G346	A198	C
A346	A199	G
G347	U200	G
	U201	C
G355	A202	
	A203	U
U358	A204	U
		G
U360	C207	A89
U361		
G362	A211	C98



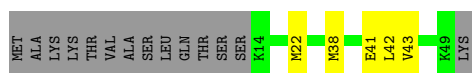
- Molecule 3: 5S rRNA

Chain 3: 77% 21% ::



- Molecule 4: 50S ribosomal protein L38

Chain 4: 62% 10% 28%

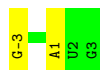


- Molecule 5: 50S ribosomal protein L38

Chain 5: 83% 7% 10%



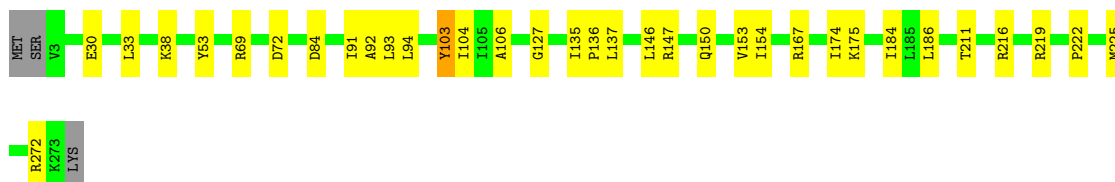
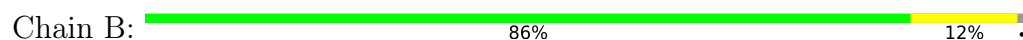
- Molecule 6: mFjoh\_4413 mRNA



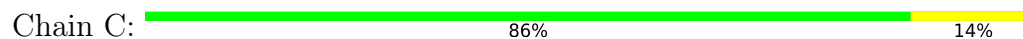
- Molecule 7: fMet-tRNA



- Molecule 8: 50S ribosomal protein L2



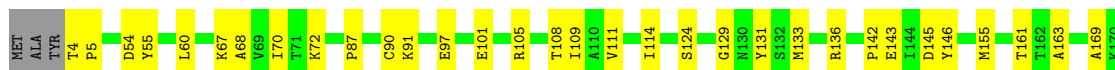
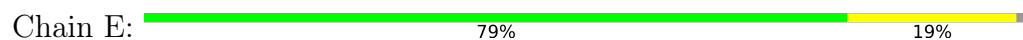
- Molecule 9: 50S ribosomal protein L3

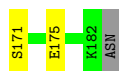


- Molecule 10: 50S ribosomal protein L4

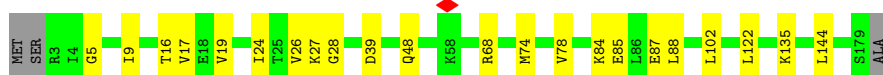
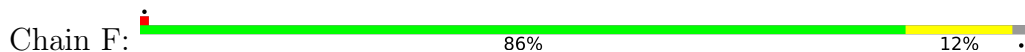


- Molecule 11: 50S ribosomal protein L5

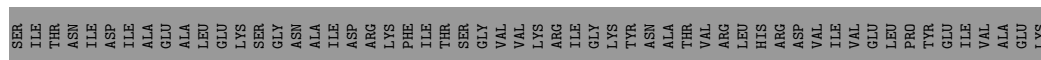
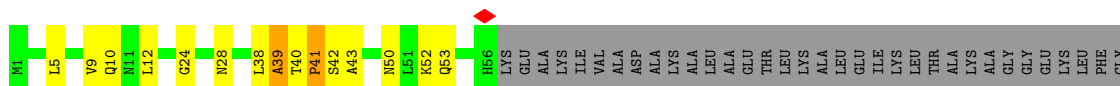




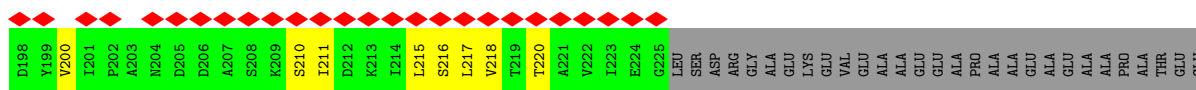
- Molecule 12: 50S ribosomal protein L6



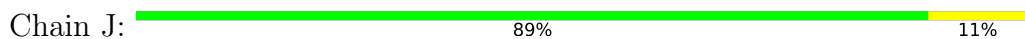
- Molecule 13: 50S ribosomal protein L9



- Molecule 14: 30S ribosomal protein S2



- Molecule 15: 50S ribosomal protein L13



- Molecule 16: 50S ribosomal protein L14





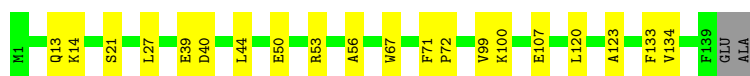
- Molecule 17: 50S ribosomal protein L15

Chain L: 93% 7%



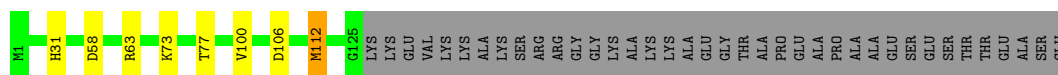
- Molecule 18: 50S ribosomal protein L16

Chain M: 84% 14%



- Molecule 19: 50S ribosomal protein L17

Chain N: 72% 23%



- Molecule 20: 50S ribosomal protein L18

Chain O: 89% 10%



- Molecule 21: 50S ribosomal protein L19

Chain P: 90% 7%



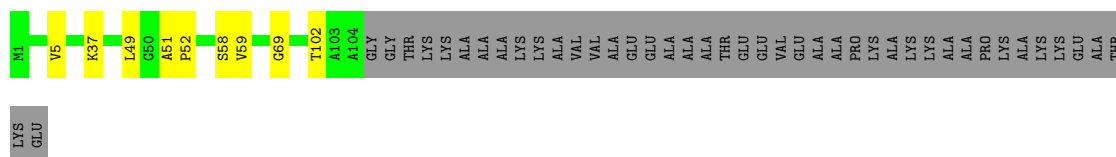
- Molecule 22: 50S ribosomal protein L20

Chain Q: 89% 10%

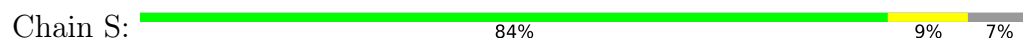


- Molecule 23: 50S ribosomal protein L21

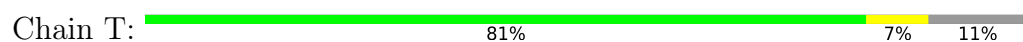
Chain R: 65% 6% 29%



- Molecule 24: 50S ribosomal protein L22



- Molecule 25: 50S ribosomal protein L23



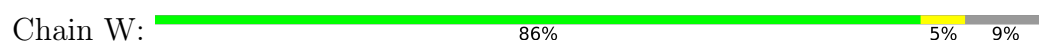
- Molecule 26: 50S ribosomal protein L24



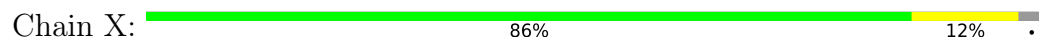
- Molecule 27: 50S ribosomal protein L25




- Molecule 28: 50S ribosomal protein L27



- Molecule 29: 50S ribosomal protein L28




- Molecule 30: 50S ribosomal protein L29

Chain Y:  79% 14% 6%



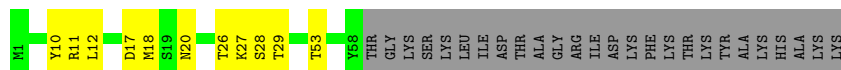
- Molecule 31: 50S ribosomal protein L30

Chain Z:  82% 12% 7%




- Molecule 32: 50S ribosomal protein L31

Chain a:  56% 13% 31%




- Molecule 33: 50S ribosomal protein L32

Chain b:  84% 8% 8%



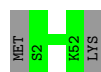
- Molecule 34: 50S ribosomal protein L33

Chain c:  78% 12% 10%



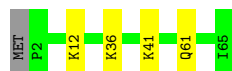
- Molecule 35: 50S ribosomal protein L34

Chain d:  96% .



- Molecule 36: 50S ribosomal protein L35

Chain e:  92% 6% .



- Molecule 37: 50S ribosomal protein L36

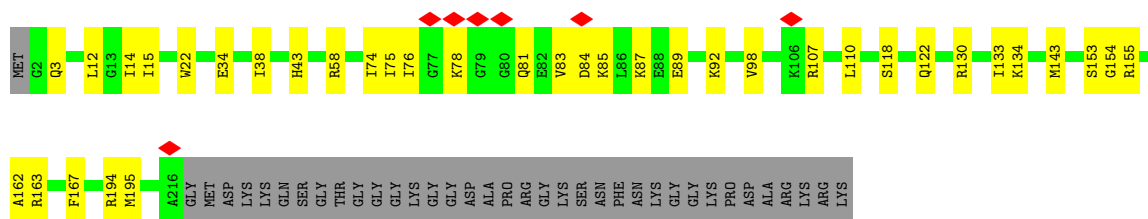


Chain f:  95% 5%




- Molecule 38: 30S ribosomal protein S3

Chain h:  71% 15% 15%

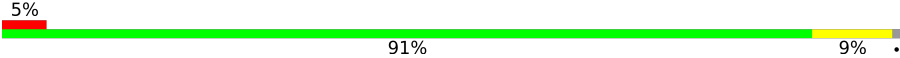


- Molecule 39: 30S ribosomal protein S4

Chain i:  92% 8%




- Molecule 40: 30S ribosomal protein S5

Chain j:  5% 91% 9%




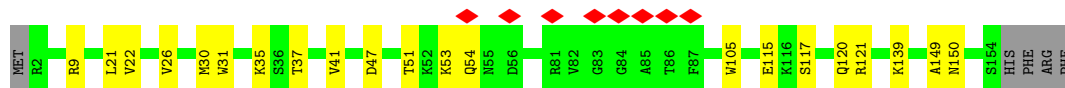
- Molecule 41: 30S ribosomal protein S6

Chain k:  88% 7% 5%




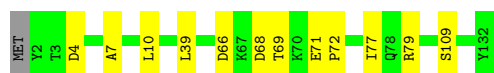
- Molecule 42: 30S ribosomal protein S7

Chain l:  5% 84% 13%



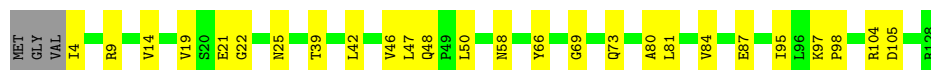
- Molecule 43: 30S ribosomal protein S8

Chain m:  90% 9%



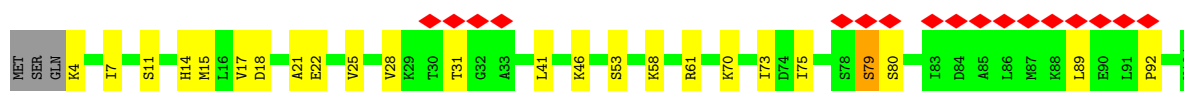
- Molecule 44: 30S ribosomal protein S9

Chain n: 77% 20%



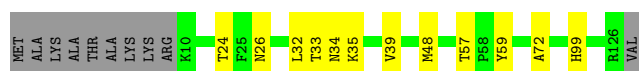
- Molecule 45: 30S ribosomal protein S10

Chain o: 17% 73% 23%



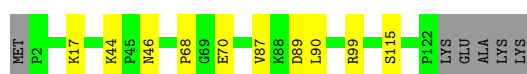
- Molecule 46: 30S ribosomal protein S11

Chain p: 83% 9% 8%



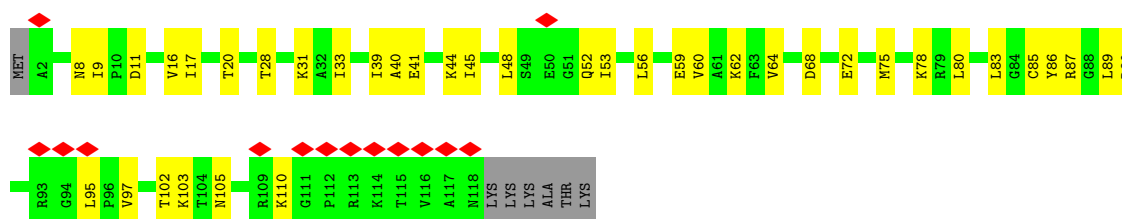
- Molecule 47: 30S ribosomal protein S12

Chain q: 87% 8% 5%



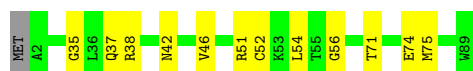
- Molecule 48: 30S ribosomal protein S13

Chain r: 11% 63% 31% 6%




- Molecule 49: 30S ribosomal protein S14

Chain s: 85% 13%



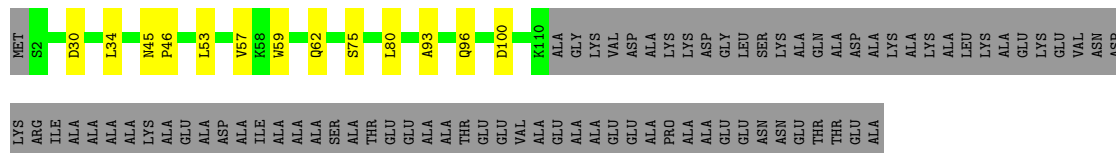
- Molecule 50: 30S ribosomal protein S15

Chain t:  86% 14%




- Molecule 51: 30S ribosomal protein S16

Chain u:  51% 7% 42%



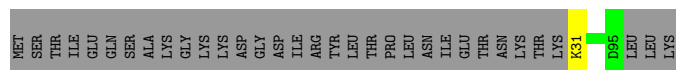
- Molecule 52: 30S ribosomal protein S17

Chain v:  76% 17% 7%



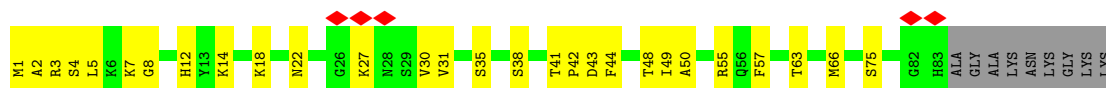
- Molecule 53: 30S ribosomal protein S18

Chain w:  65% 34%



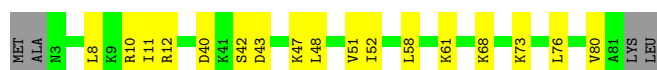
- Molecule 54: 30S ribosomal protein S19

Chain x:  5% 60% 30% 10%




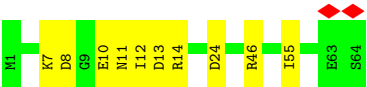
- Molecule 55: 30S ribosomal protein S20

Chain y:  75% 20% 5%



- Molecule 56: 30S ribosomal protein S21

Chain z:  84% 16%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	189894	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.497	Depositor
Minimum map value	-0.113	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	410.40002, 410.40002, 410.40002	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8550001, 0.8550001, 0.8550001	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	1	0.25	0/66183	0.32	0/103212
2	2	0.19	0/35523	0.30	0/55388
3	3	0.18	0/2611	0.24	0/4067
4	4	0.19	0/282	0.47	0/377
5	5	0.17	0/234	0.27	0/301
6	6	0.15	0/142	0.32	0/219
7	A	0.13	0/1745	0.25	0/2717
8	B	0.23	0/2090	0.34	0/2815
9	C	0.23	0/1538	0.36	0/2061
10	D	0.20	0/1530	0.32	0/2065
11	E	0.19	0/1321	0.38	0/1789
12	F	0.16	0/1266	0.31	0/1713
13	G	0.30	0/411	0.66	2/556 (0.4%)
14	H	0.18	0/1684	0.44	0/2278
15	J	0.24	0/1130	0.40	0/1529
16	K	0.19	0/896	0.30	0/1204
17	L	0.22	0/1060	0.36	0/1422
18	M	0.21	0/1077	0.34	0/1442
19	N	0.22	0/994	0.36	1/1331 (0.1%)
20	O	0.17	0/854	0.35	0/1144
21	P	0.21	0/863	0.35	0/1163
22	Q	0.23	0/918	0.35	0/1220
23	R	0.20	0/778	0.37	0/1045
24	S	0.21	0/974	0.35	0/1305
25	T	0.19	0/652	0.31	0/877
26	U	0.15	0/682	0.28	0/911
27	V	0.16	0/884	0.34	0/1212
28	W	0.22	0/594	0.36	0/794
29	X	0.19	0/593	0.31	0/794
30	Y	0.15	0/412	0.39	0/561
31	Z	0.20	0/403	0.36	0/545
32	a	0.16	0/431	0.38	0/586
33	b	0.23	0/488	0.30	0/657
34	c	0.19	0/421	0.36	0/569

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	d	0.22	0/422	0.30	0/553
36	e	0.23	0/512	0.42	0/672
37	f	0.20	0/307	0.33	0/405
38	h	0.14	0/1623	0.32	0/2190
39	i	0.14	0/1606	0.28	0/2157
40	j	0.16	0/1194	0.31	0/1615
41	k	0.16	0/834	0.26	0/1129
42	l	0.16	0/1200	0.37	0/1615
43	m	0.17	0/976	0.28	0/1324
44	n	0.16	0/986	0.42	0/1322
45	o	0.14	0/712	0.39	1/973 (0.1%)
46	p	0.17	0/833	0.33	0/1130
47	q	0.20	0/935	0.34	0/1258
48	r	0.20	0/891	0.54	0/1192
49	s	0.16	0/676	0.34	0/906
50	t	0.19	0/704	0.31	0/946
51	u	0.16	0/799	0.32	0/1086
52	v	0.17	0/646	0.35	0/866
53	w	0.20	0/531	0.33	0/710
54	x	0.16	0/652	0.37	0/881
55	y	0.17	0/619	0.31	0/825
56	z	0.16	0/527	0.29	0/701
All	All	0.22	0/149849	0.32	4/224325 (0.0%)

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
13	G	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	G	41	PRO	CA-N-CD	-6.20	103.32	112.00
45	o	79	SER	CB-CA-C	-5.66	110.06	116.63
19	N	112	MET	CB-CG-SD	5.38	128.86	112.70
13	G	50	ASN	N-CA-C	-5.03	105.80	111.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	G	39	ALA	Peptide

## 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	1	59085	0	29705	287	0
2	2	31728	0	15978	207	0
3	3	2339	0	1181	9	0
4	4	278	0	295	6	0
5	5	231	0	268	1	0
6	6	128	0	64	1	0
7	A	1562	0	794	9	0
8	B	2053	0	2127	27	0
9	C	1515	0	1548	21	0
10	D	1509	0	1532	10	0
11	E	1300	0	1267	27	0
12	F	1249	0	1264	15	0
13	G	405	0	417	13	0
14	H	1658	0	1695	43	0
15	J	1112	0	1149	13	0
16	K	889	0	946	0	0
17	L	1048	0	1048	9	0
18	M	1056	0	1109	16	0
19	N	980	0	1017	5	0
20	O	846	0	873	7	0
21	P	848	0	846	5	0
22	Q	904	0	956	10	0
23	R	768	0	810	6	0
24	S	964	0	992	14	0
25	T	647	0	696	4	0
26	U	679	0	733	7	0
27	V	867	0	828	12	0
28	W	586	0	607	4	0
29	X	586	0	618	7	0
30	Y	409	0	405	7	0
31	Z	400	0	416	7	0

*Continued on next page...*



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	a	421	0	384	7	0
33	b	475	0	468	4	0
34	c	415	0	432	5	0
35	d	416	0	449	0	0
36	e	506	0	574	3	0
37	f	305	0	337	1	0
38	h	1600	0	1604	24	0
39	i	1576	0	1592	11	0
40	j	1179	0	1185	11	0
41	k	815	0	780	4	0
42	l	1179	0	1181	14	0
43	m	961	0	978	10	0
44	n	972	0	1005	25	0
45	o	701	0	694	21	0
46	p	819	0	809	10	0
47	q	922	0	973	8	0
48	r	883	0	921	42	0
49	s	665	0	669	9	0
50	t	694	0	703	13	0
51	u	783	0	739	12	0
52	v	638	0	684	9	0
53	w	521	0	553	1	0
54	x	636	0	628	26	0
55	y	615	0	672	12	0
56	z	522	0	573	12	0
All	All	137848	0	91771	1018	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 4.

The worst 5 of 1018 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)
18:M:44:LEU:CD1	18:M:99:VAL:HG21	1.63	1.28
50:t:81:ILE:HD11	50:t:86:ILE:O	1.38	1.21
44:n:4:ILE:HD13	44:n:87:GLU:OE2	1.40	1.21
44:n:4:ILE:CD1	44:n:87:GLU:OE2	2.01	1.08
18:M:44:LEU:HD12	18:M:99:VAL:HG21	1.33	1.05

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	
4	4	34/50 (68%)	33 (97%)	1 (3%)	0	100	100
5	5	25/30 (83%)	25 (100%)	0	0	100	100
8	B	269/274 (98%)	256 (95%)	12 (4%)	1 (0%)	30	51
9	C	202/205 (98%)	189 (94%)	13 (6%)	0	100	100
10	D	204/209 (98%)	192 (94%)	12 (6%)	0	100	100
11	E	177/183 (97%)	166 (94%)	11 (6%)	0	100	100
12	F	175/180 (97%)	170 (97%)	5 (3%)	0	100	100
13	G	54/146 (37%)	49 (91%)	5 (9%)	0	100	100
14	H	217/254 (85%)	207 (95%)	10 (5%)	0	100	100
15	J	148/151 (98%)	129 (87%)	19 (13%)	0	100	100
16	K	119/122 (98%)	112 (94%)	7 (6%)	0	100	100
17	L	148/150 (99%)	134 (90%)	14 (10%)	0	100	100
18	M	137/141 (97%)	130 (95%)	7 (5%)	0	100	100
19	N	123/163 (76%)	117 (95%)	6 (5%)	0	100	100
20	O	113/116 (97%)	106 (94%)	7 (6%)	0	100	100
21	P	110/116 (95%)	104 (94%)	6 (6%)	0	100	100
22	Q	111/114 (97%)	105 (95%)	6 (5%)	0	100	100
23	R	102/147 (69%)	93 (91%)	9 (9%)	0	100	100
24	S	126/137 (92%)	125 (99%)	1 (1%)	0	100	100
25	T	81/96 (84%)	76 (94%)	5 (6%)	0	100	100
26	U	88/104 (85%)	80 (91%)	8 (9%)	0	100	100
27	V	120/203 (59%)	115 (96%)	5 (4%)	0	100	100
28	W	76/86 (88%)	74 (97%)	2 (3%)	0	100	100
29	X	74/78 (95%)	72 (97%)	2 (3%)	0	100	100
30	Y	57/63 (90%)	53 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	Z	54/60 (90%)	49 (91%)	5 (9%)	0	100	100
32	a	56/84 (67%)	52 (93%)	4 (7%)	0	100	100
33	b	57/64 (89%)	50 (88%)	7 (12%)	0	100	100
34	c	52/60 (87%)	51 (98%)	1 (2%)	0	100	100
35	d	49/53 (92%)	49 (100%)	0	0	100	100
36	e	62/65 (95%)	54 (87%)	8 (13%)	0	100	100
37	f	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
38	h	213/252 (84%)	195 (92%)	18 (8%)	0	100	100
39	i	198/201 (98%)	190 (96%)	8 (4%)	0	100	100
40	j	170/173 (98%)	162 (95%)	8 (5%)	0	100	100
41	k	105/113 (93%)	102 (97%)	3 (3%)	0	100	100
42	l	151/158 (96%)	145 (96%)	6 (4%)	0	100	100
43	m	129/132 (98%)	123 (95%)	6 (5%)	0	100	100
44	n	123/128 (96%)	118 (96%)	5 (4%)	0	100	100
45	o	96/101 (95%)	89 (93%)	7 (7%)	0	100	100
46	p	115/127 (91%)	112 (97%)	3 (3%)	0	100	100
47	q	119/127 (94%)	112 (94%)	7 (6%)	0	100	100
48	r	115/124 (93%)	107 (93%)	8 (7%)	0	100	100
49	s	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
50	t	86/88 (98%)	85 (99%)	1 (1%)	0	100	100
51	u	107/188 (57%)	102 (95%)	5 (5%)	0	100	100
52	v	78/86 (91%)	75 (96%)	3 (4%)	0	100	100
53	w	63/98 (64%)	61 (97%)	2 (3%)	0	100	100
54	x	81/92 (88%)	74 (91%)	7 (9%)	0	100	100
55	y	77/83 (93%)	75 (97%)	2 (3%)	0	100	100
56	z	62/64 (97%)	62 (100%)	0	0	100	100
All	All	5630/6366 (88%)	5322 (94%)	307 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	B	136	PRO

### 5.3.2 Protein sidechains ⓘ

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	
4	4	30/44 (68%)	30 (100%)	0	100	100
5	5	23/26 (88%)	23 (100%)	0	100	100
8	B	215/225 (96%)	214 (100%)	1 (0%)	81	92
9	C	156/162 (96%)	156 (100%)	0	100	100
10	D	150/181 (83%)	150 (100%)	0	100	100
11	E	121/156 (78%)	121 (100%)	0	100	100
12	F	120/148 (81%)	120 (100%)	0	100	100
13	G	39/118 (33%)	38 (97%)	1 (3%)	40	68
14	H	170/207 (82%)	170 (100%)	0	100	100
15	J	115/128 (90%)	115 (100%)	0	100	100
16	K	89/100 (89%)	88 (99%)	1 (1%)	65	84
17	L	93/115 (81%)	93 (100%)	0	100	100
18	M	102/116 (88%)	102 (100%)	0	100	100
19	N	101/131 (77%)	100 (99%)	1 (1%)	68	86
20	O	79/90 (88%)	78 (99%)	1 (1%)	61	82
21	P	78/98 (80%)	78 (100%)	0	100	100
22	Q	89/94 (95%)	89 (100%)	0	100	100
23	R	72/112 (64%)	72 (100%)	0	100	100
24	S	93/116 (80%)	93 (100%)	0	100	100
25	T	70/85 (82%)	70 (100%)	0	100	100
26	U	68/89 (76%)	68 (100%)	0	100	100
27	V	80/163 (49%)	80 (100%)	0	100	100
28	W	60/69 (87%)	60 (100%)	0	100	100
29	X	62/69 (90%)	62 (100%)	0	100	100
30	Y	36/55 (66%)	36 (100%)	0	100	100
31	Z	41/52 (79%)	41 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	a	40/75 (53%)	39 (98%)	1 (2%)	42	69
33	b	44/53 (83%)	44 (100%)	0	100	100
34	c	45/56 (80%)	44 (98%)	1 (2%)	45	72
35	d	42/46 (91%)	42 (100%)	0	100	100
36	e	55/59 (93%)	55 (100%)	0	100	100
37	f	31/34 (91%)	31 (100%)	0	100	100
38	h	153/201 (76%)	152 (99%)	1 (1%)	76	89
39	i	163/173 (94%)	163 (100%)	0	100	100
40	j	111/138 (80%)	111 (100%)	0	100	100
41	k	74/101 (73%)	73 (99%)	1 (1%)	59	81
42	l	113/136 (83%)	112 (99%)	1 (1%)	70	87
43	m	93/111 (84%)	93 (100%)	0	100	100
44	n	99/107 (92%)	99 (100%)	0	100	100
45	o	72/94 (77%)	72 (100%)	0	100	100
46	p	79/102 (78%)	79 (100%)	0	100	100
47	q	97/107 (91%)	97 (100%)	0	100	100
48	r	87/100 (87%)	87 (100%)	0	100	100
49	s	61/73 (84%)	60 (98%)	1 (2%)	55	79
50	t	66/79 (84%)	66 (100%)	0	100	100
51	u	68/136 (50%)	68 (100%)	0	100	100
52	v	71/81 (88%)	71 (100%)	0	100	100
53	w	52/87 (60%)	52 (100%)	0	100	100
54	x	67/78 (86%)	67 (100%)	0	100	100
55	y	65/72 (90%)	65 (100%)	0	100	100
56	z	56/56 (100%)	56 (100%)	0	100	100
All	All	4256/5304 (80%)	4245 (100%)	11 (0%)	84	94

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	h	43	HIS
41	k	79	PHE
49	s	42	ASN

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Mol	Chain	Res	Type
42	l	31	TRP
20	O	41	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
42	l	150	ASN
51	u	62	GLN
44	n	58	ASN
46	p	89	ASN
20	O	35	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2746/2862 (95%)	414 (15%)	25 (0%)
2	2	1476/1520 (97%)	268 (18%)	27 (1%)
3	3	109/111 (98%)	12 (11%)	0
6	6	5/6 (83%)	1 (20%)	0
7	A	71/77 (92%)	8 (11%)	0
All	All	4407/4576 (96%)	703 (15%)	52 (1%)

5 of 703 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	13	A
1	1	28	A
1	1	34	A
1	1	46	G
1	1	51	G

5 of 52 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	236	A
2	2	1109	C
2	2	1351	C
2	2	321	C
2	2	1031	G

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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.

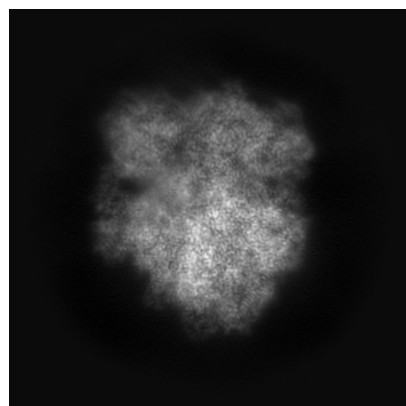
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71052. These allow visual inspection of the internal detail of the map and identification of artifacts.

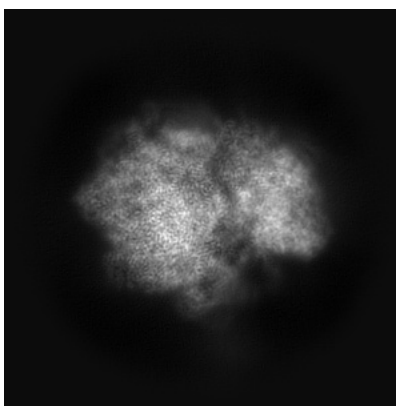
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

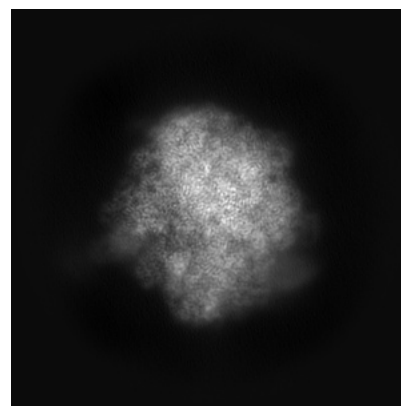
#### 6.1.1 Primary map



X

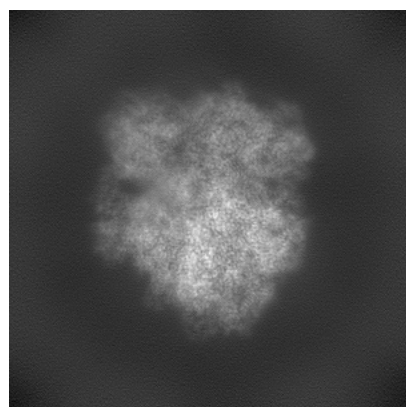


Y

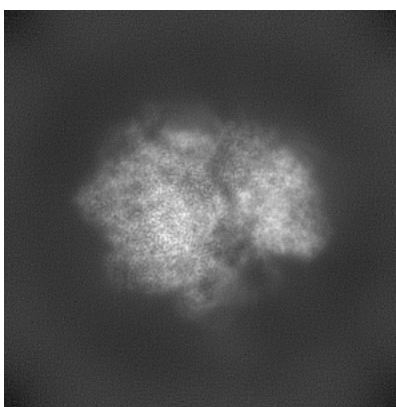


Z

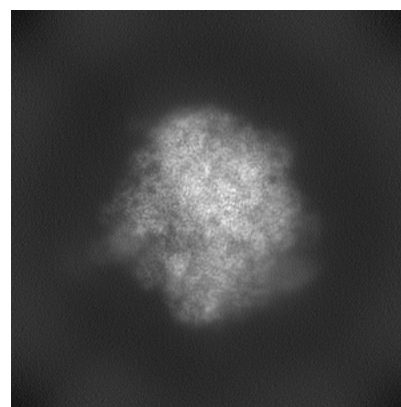
#### 6.1.2 Raw map



X



Y



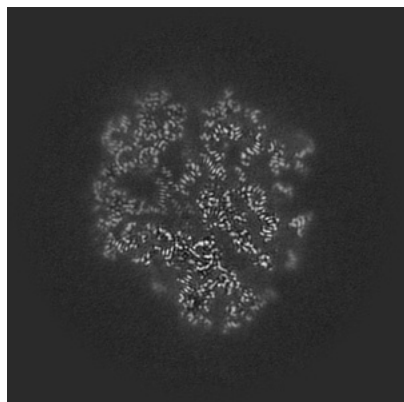
Z

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

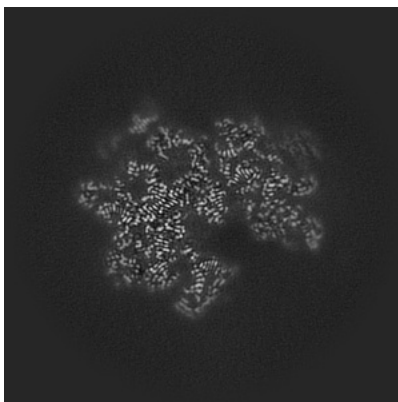


## 6.2 Central slices [i](#)

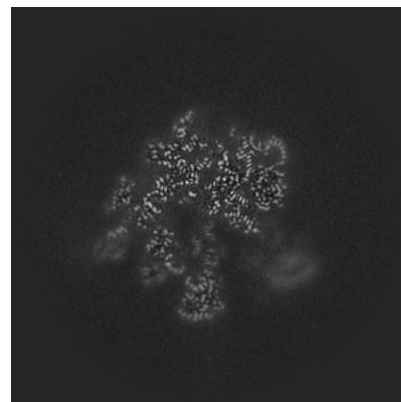
### 6.2.1 Primary map



X Index: 240

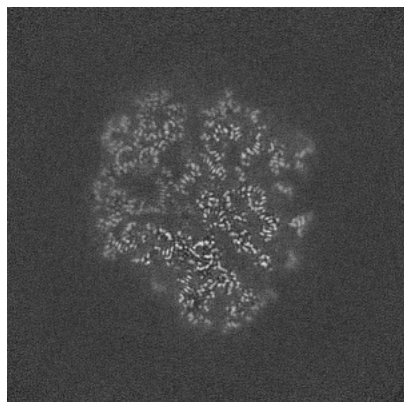


Y Index: 240

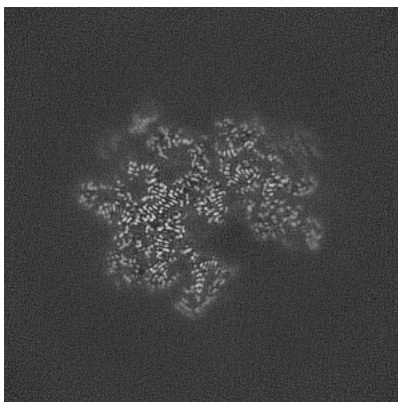


Z Index: 240

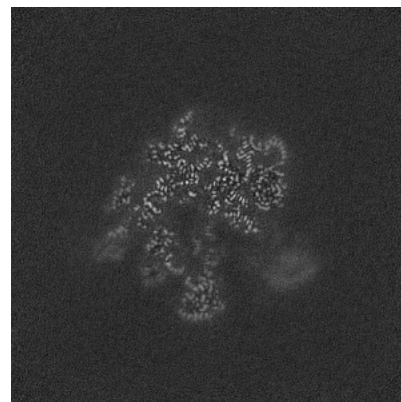
### 6.2.2 Raw map



X Index: 240



Y Index: 240

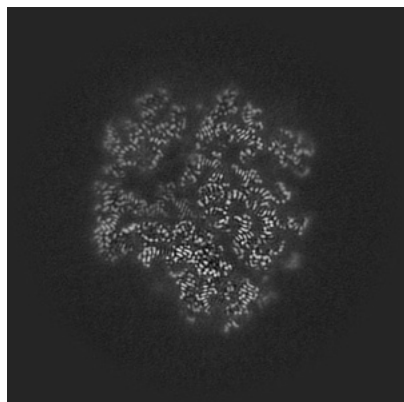


Z Index: 240

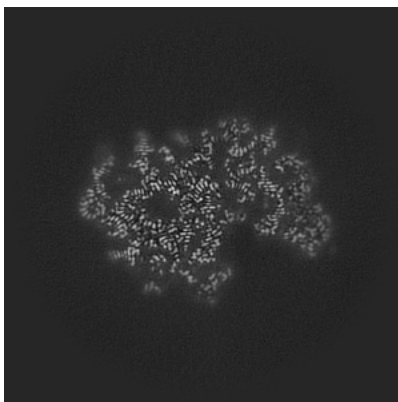
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

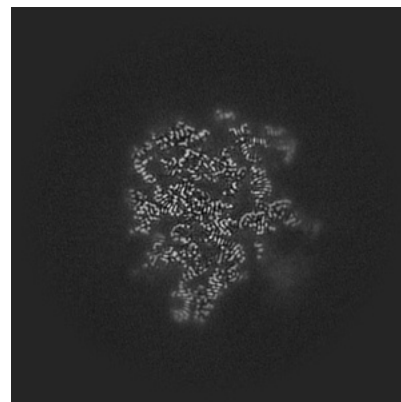
### 6.3.1 Primary map



X Index: 235

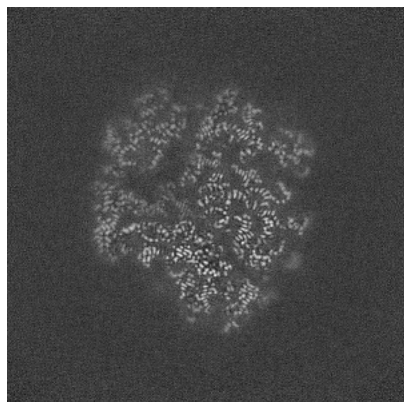


Y Index: 264

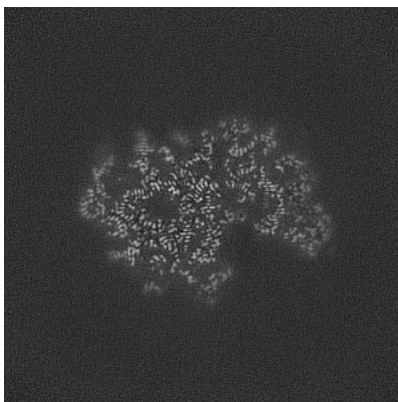


Z Index: 193

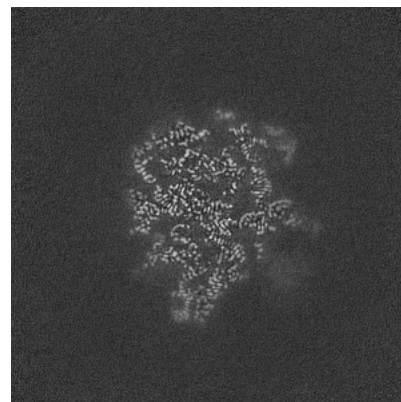
### 6.3.2 Raw map



X Index: 235



Y Index: 264



Z Index: 193

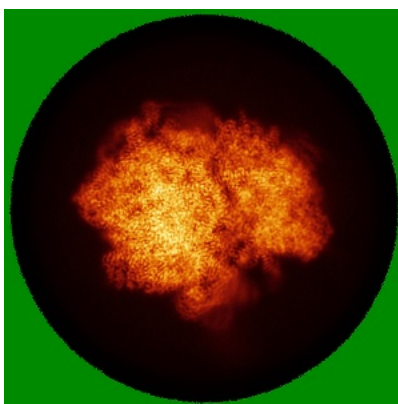
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

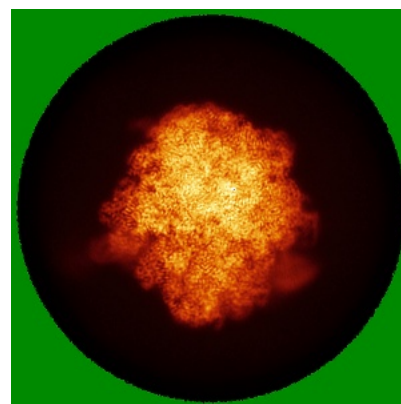
### 6.4.1 Primary map



X

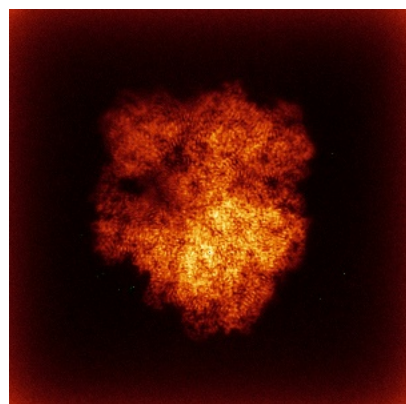


Y

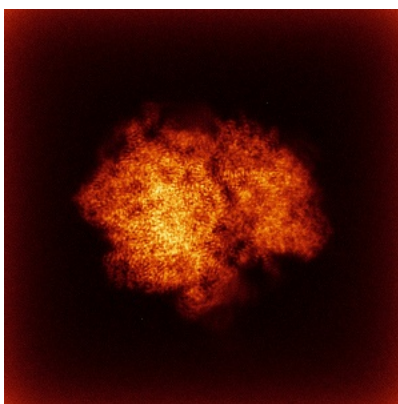


Z

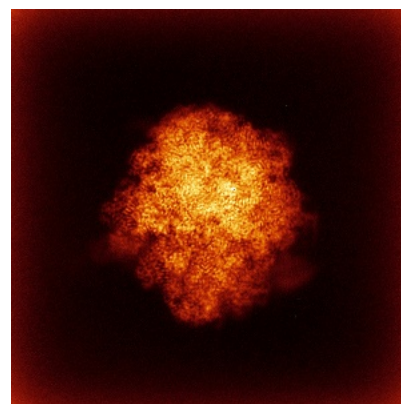
### 6.4.2 Raw map



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](#)

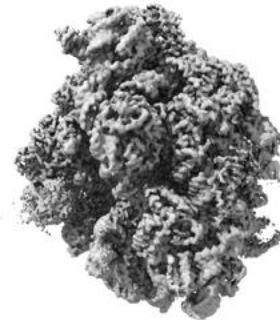
### 6.5.1 Primary map



X



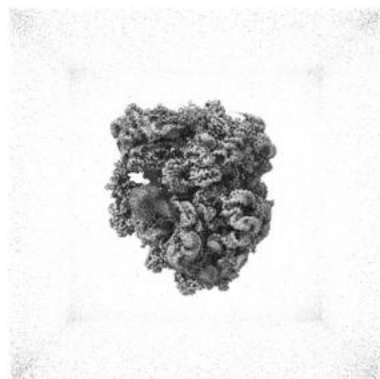
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.07. 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](#)

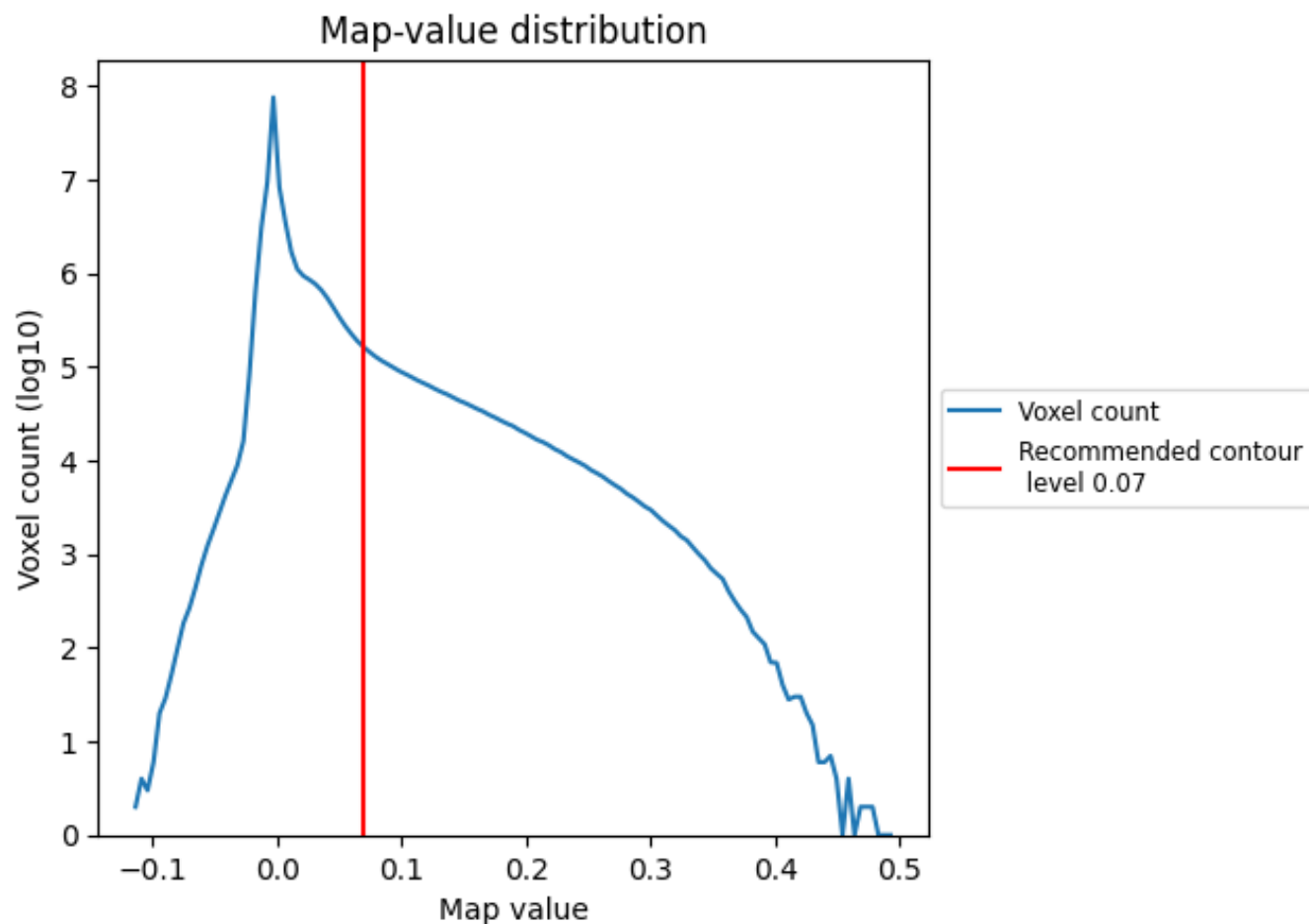
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

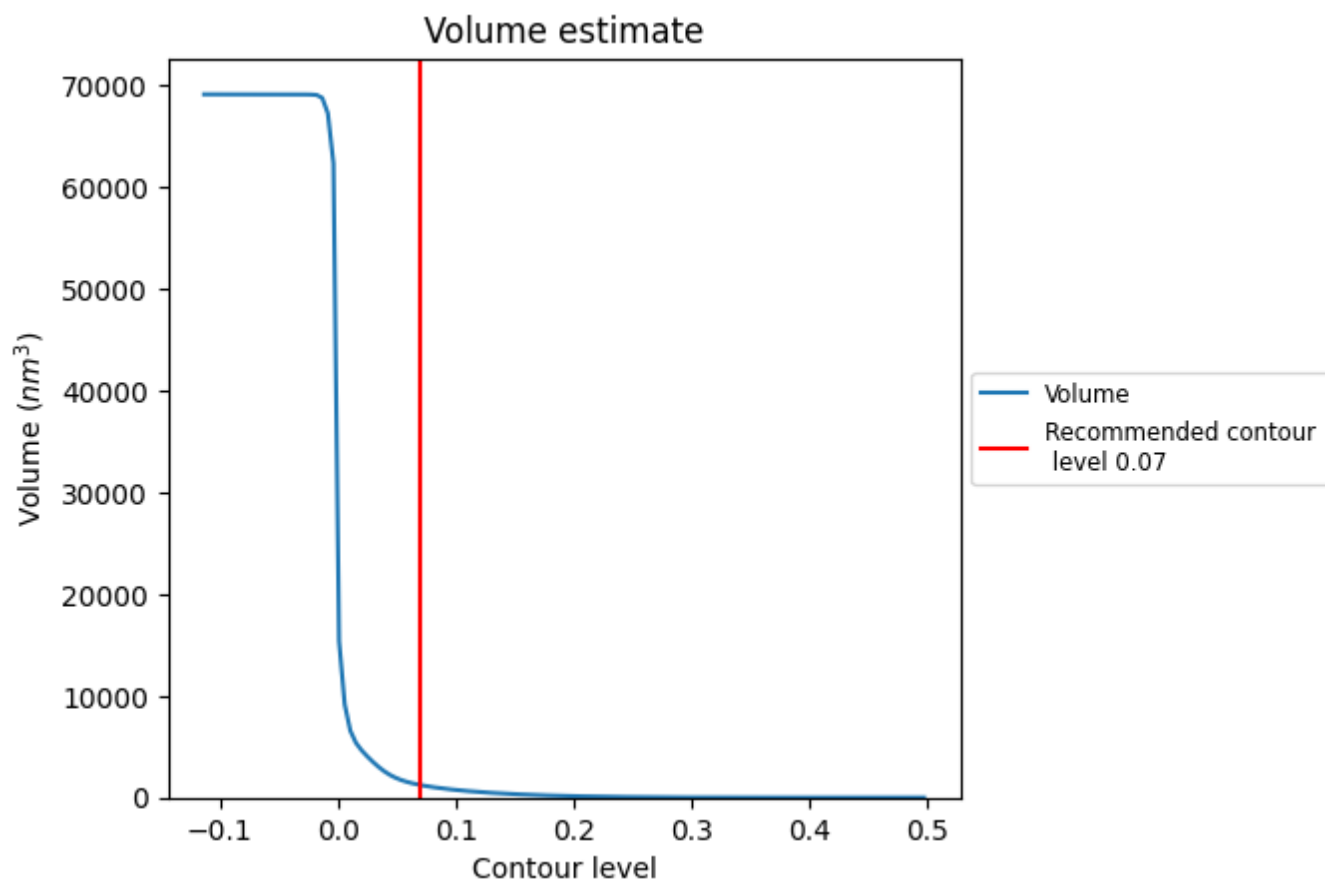
This section contains the results of statistical analysis of the map.

### 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.

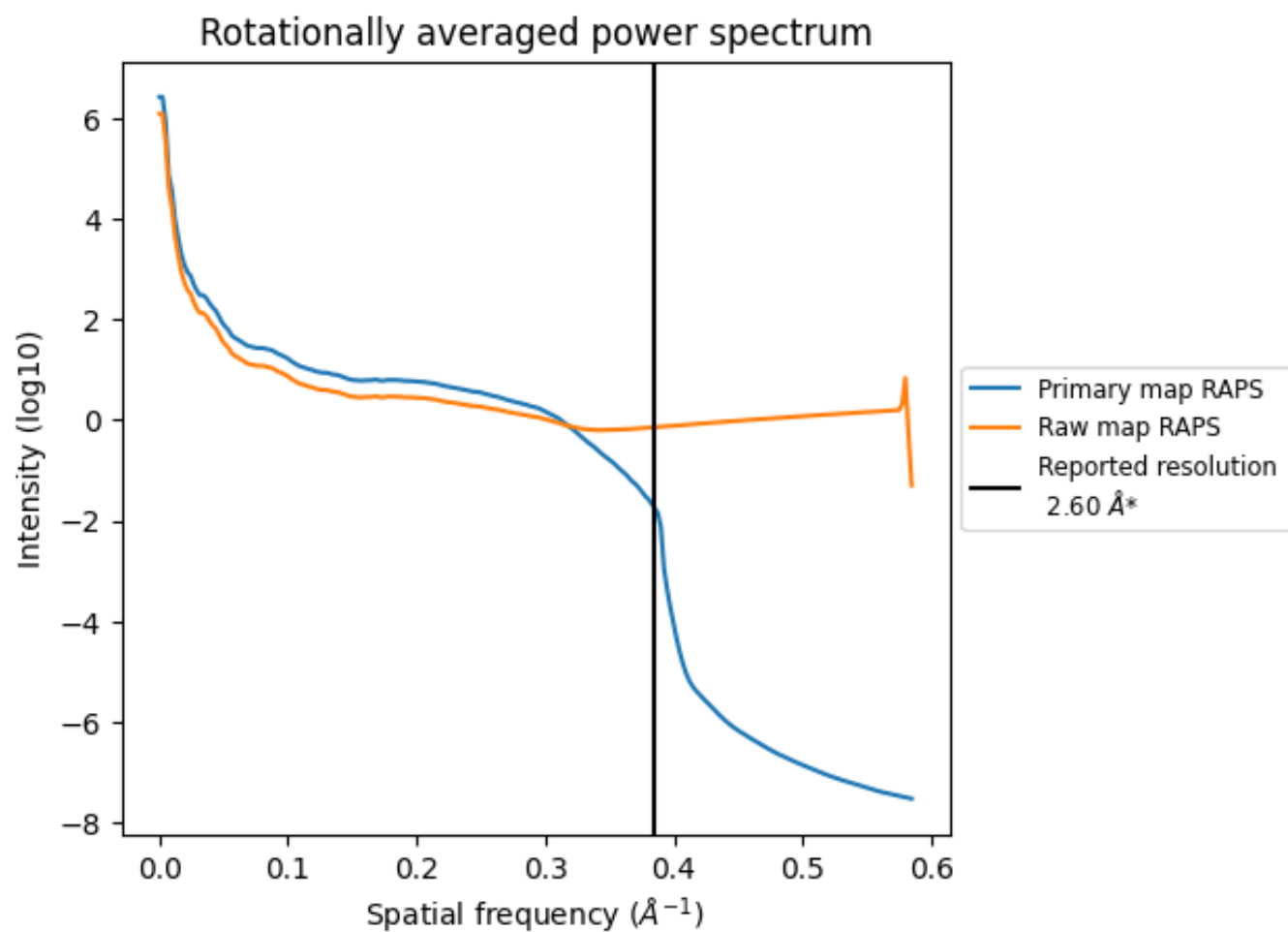
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1239 nm<sup>3</sup>; this corresponds to an approximate mass of 1119 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 ⓘ

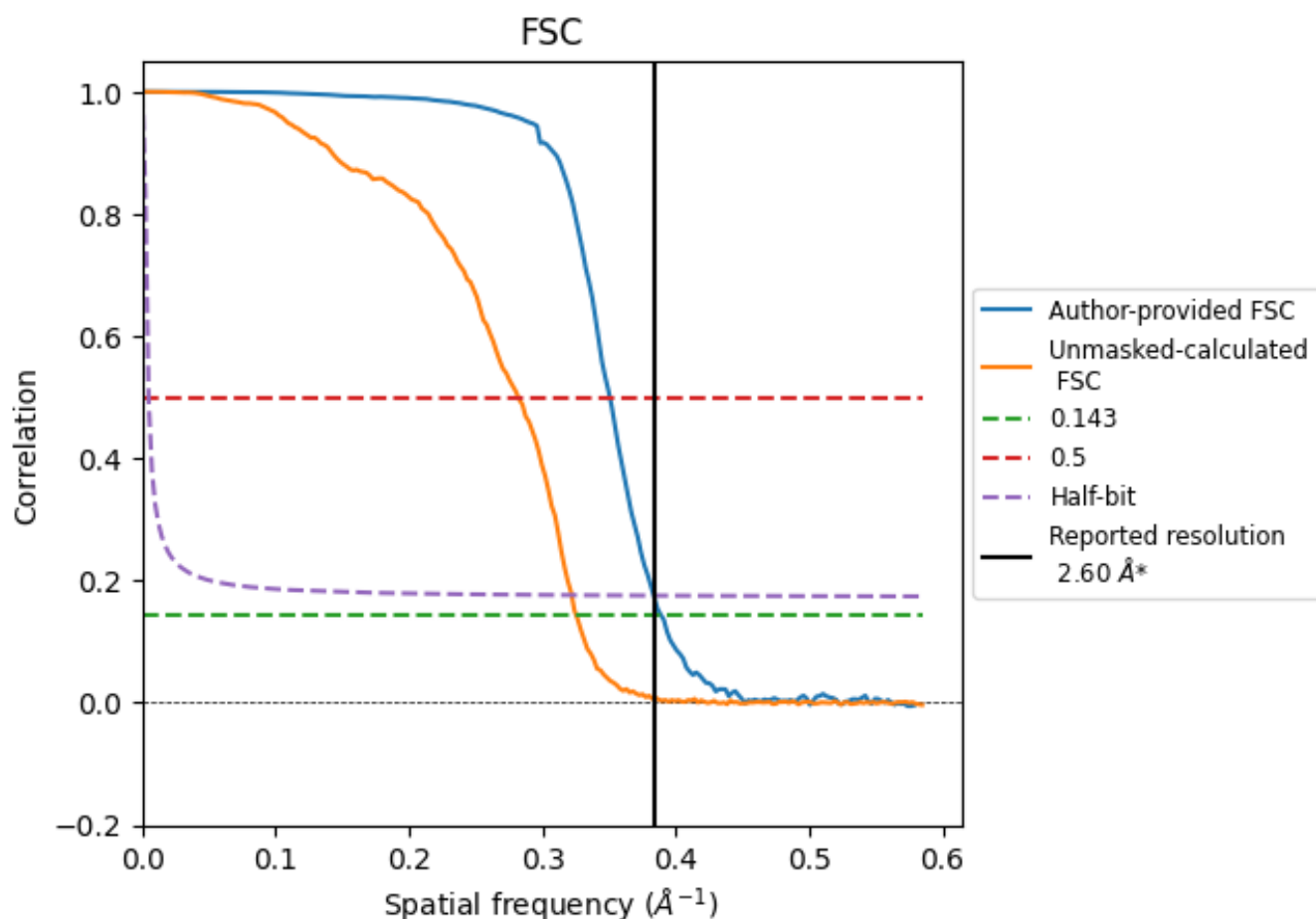


\*Reported resolution corresponds to spatial frequency of 0.385 Å<sup>-1</sup>

## 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 0.385 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

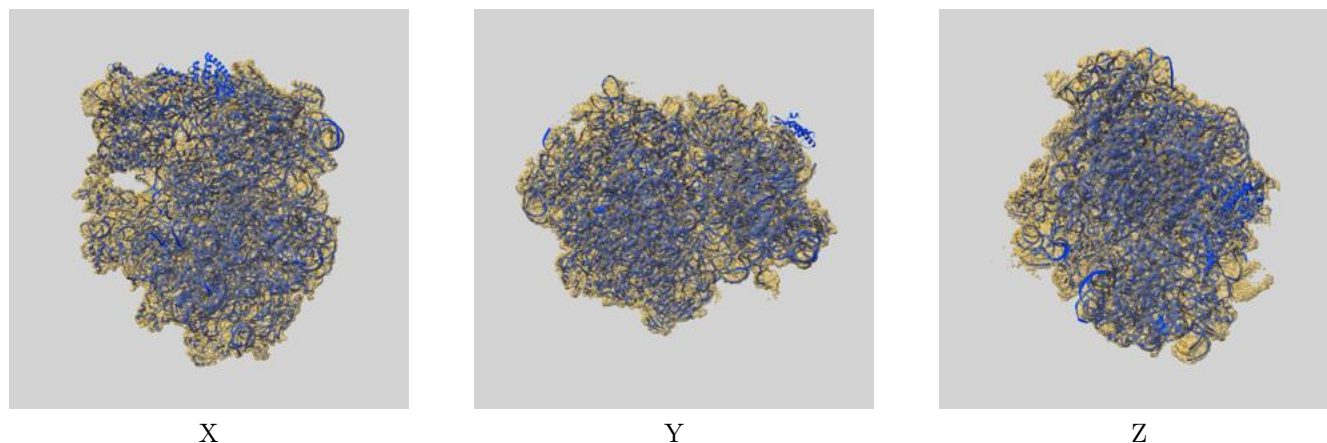
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.57	2.85	2.61
Unmasked-calculated*	3.07	3.55	3.11

\*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 3.07 differs from the reported value 2.6 by more than 10 %

## 9 Map-model fit [i](#)

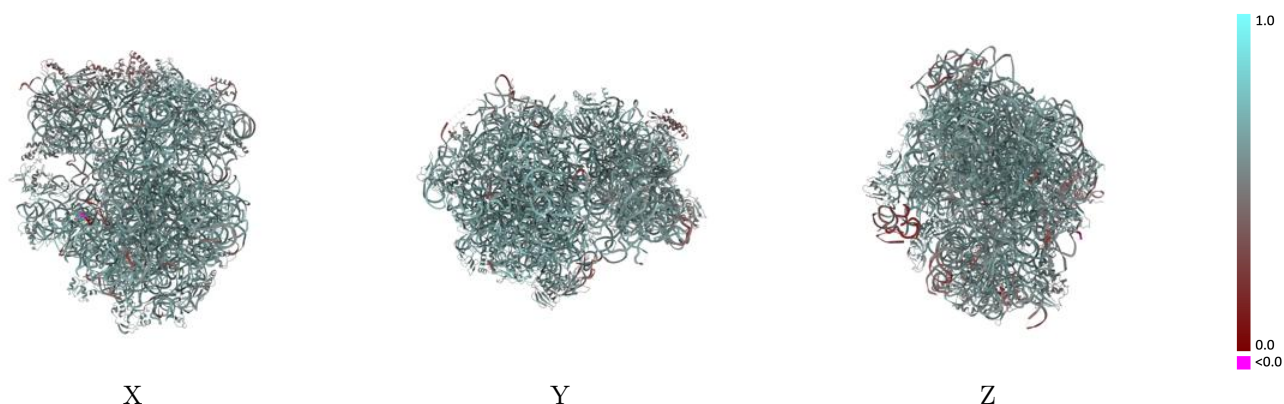
This section contains information regarding the fit between EMDB map EMD-71052 and PDB model 9OZ9. Per-residue inclusion information can be found in section [3](#) on page [17](#).

### 9.1 Map-model overlay [i](#)



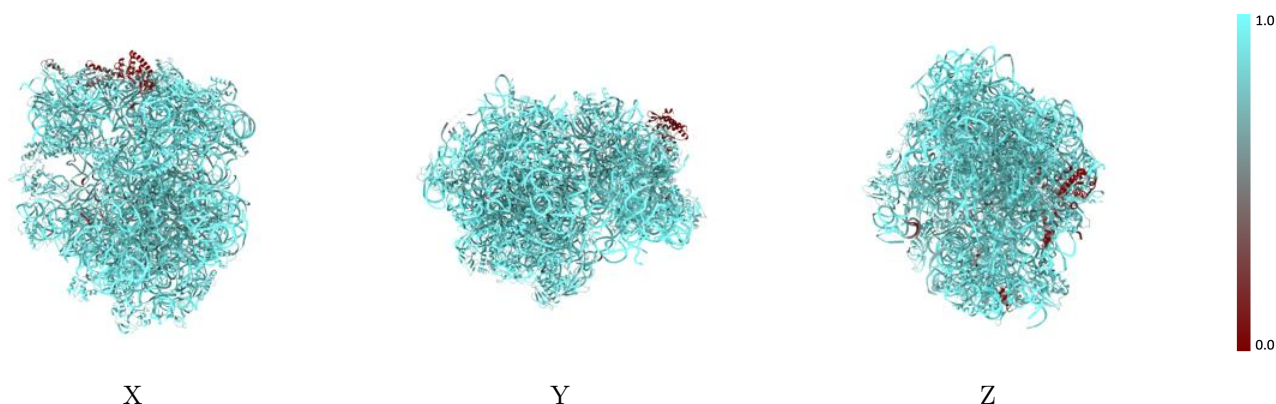
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



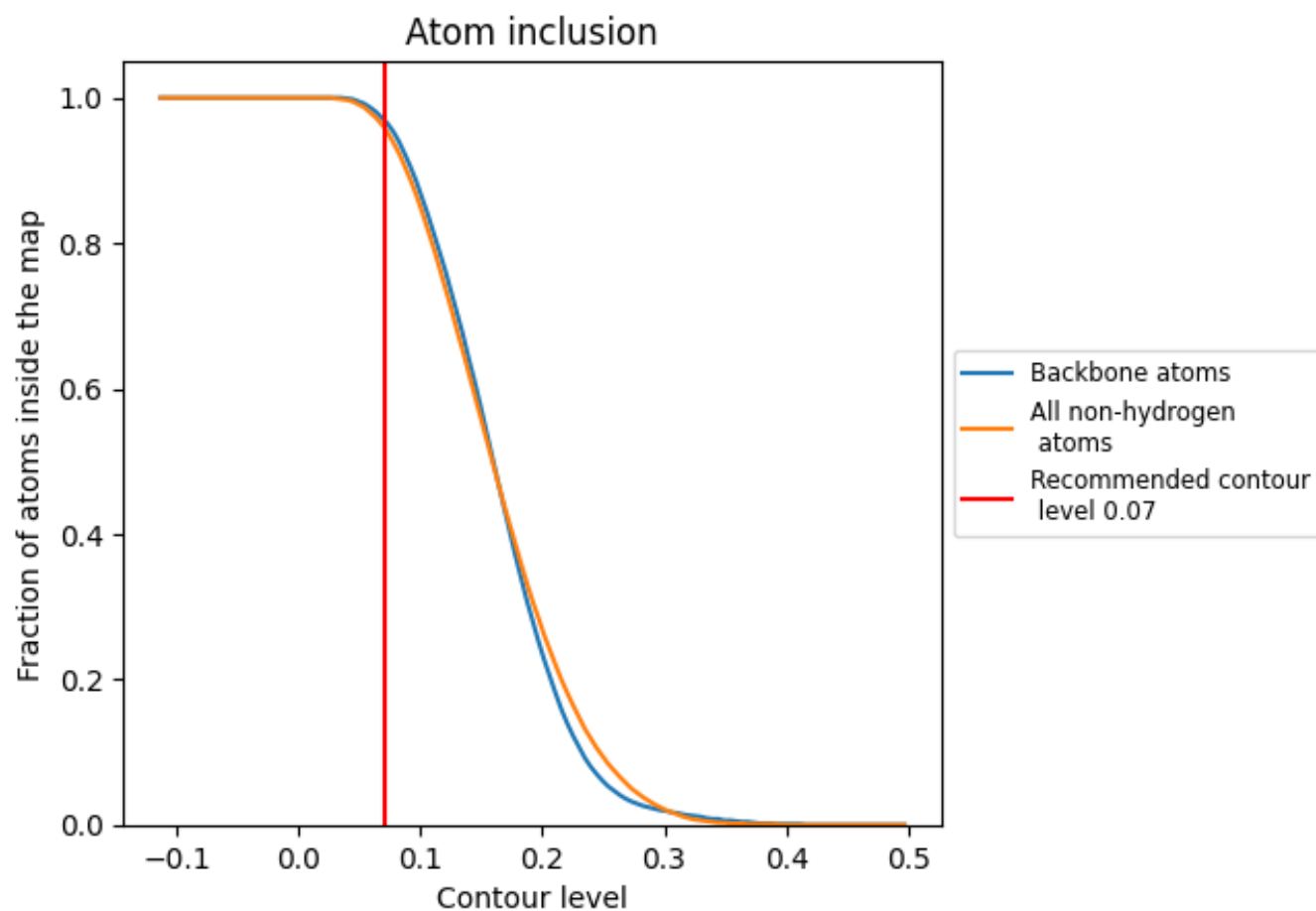
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



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 (0.07).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 97% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ













































The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9600	 0.5930
1	 0.9850	 0.6070
2	 0.9860	 0.5870
3	 0.9870	 0.5870
4	 0.9090	 0.5570
5	 0.9590	 0.6200
6	 0.7660	 0.5830
A	 0.8160	 0.5730
B	 0.9760	 0.6280
C	 0.9710	 0.6220
D	 0.9780	 0.5990
E	 0.8990	 0.5520
F	 0.9220	 0.5550
G	 0.8830	 0.5280
H	 0.2400	 0.4400
J	 0.9710	 0.6050
K	 0.9660	 0.6270
L	 0.9730	 0.6110
M	 0.9710	 0.6180
N	 0.9810	 0.6250
O	 0.9560	 0.5820
P	 0.9750	 0.6240
Q	 0.9840	 0.6190
R	 0.9840	 0.6130
S	 0.9800	 0.6080
T	 0.9500	 0.5840
U	 0.9040	 0.5640
V	 0.9410	 0.5650
W	 0.9790	 0.6280
X	 0.9770	 0.6090
Y	 0.9150	 0.5330
Z	 0.9800	 0.6060
a	 0.9010	 0.5520
b	 0.9960	 0.6370
c	 0.9630	 0.6090



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Chain	Atom inclusion	Q-score
d	 0.9980	 0.6470
e	 0.9840	 0.6250
f	 0.9760	 0.6250
h	 0.8360	 0.5260
i	 0.8920	 0.5490
j	 0.9360	 0.5800
k	 0.9820	 0.5970
l	 0.8440	 0.5350
m	 0.9710	 0.5990
n	 0.9110	 0.5400
o	 0.7450	 0.4920
p	 0.9660	 0.5960
q	 0.9450	 0.6040
r	 0.7360	 0.5160
s	 0.9420	 0.5610
t	 0.9630	 0.5860
u	 0.9520	 0.5530
v	 0.9470	 0.5910
w	 0.9840	 0.6050
x	 0.8180	 0.5280
y	 0.9400	 0.5690
z	 0.8400	 0.5770