



wwPDB EM Validation Summary Report ⓘ

Oct 1, 2025 – 02:33 PM JST

PDB ID : 9V1I / pdb_00009v1i
EMDB ID : EMD-64694
Title : Cryo- EM structure of ribosomal large subunit (LSU) from Entamoeba histolytica at 2.8 angstrom resolution
Authors : Sharma, S.; Mishra, S.; Gourinath, S.; Kaushal, P.S.
Deposited on : 2025-05-19
Resolution : 2.80 Å (reported)
Based on initial models : 4UG0, 5XXB

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 ⓘ 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 ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

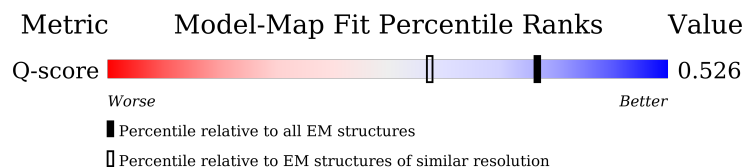
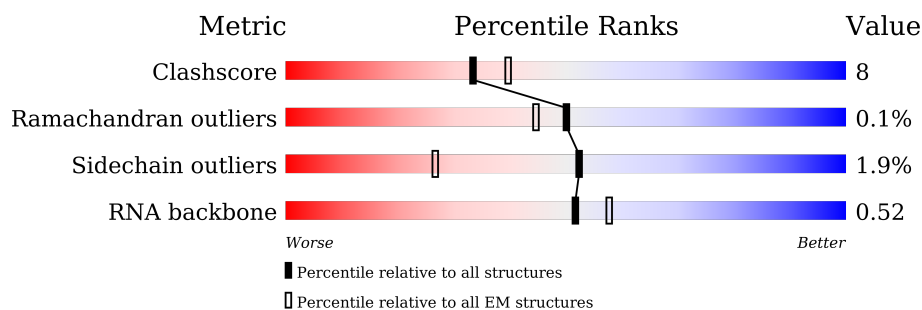
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.















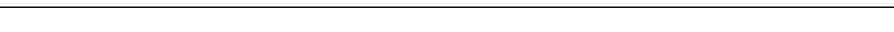

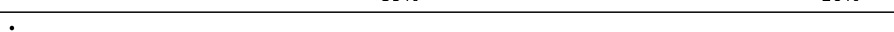

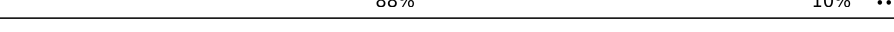



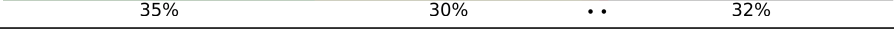




Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	11806 (2.30 - 3.30)

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 $\leq 5\%$. 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	1A	3503	
2	1B	155	
3	1C	117	











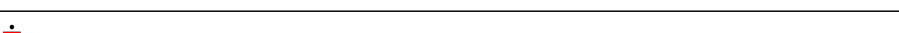

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Mol	Chain	Length	Quality of chain
4	ID	257	
5	IE	402	
6	IF	431	
7	IG	286	
8	IH	204	
9	II	230	
10	IJ	286	
11	IK	197	
12	IL	210	
13	IM	174	
14	IN	291	
15	IO	205	
16	IP	135	
17	IQ	205	
18	IR	179	
19	IS	168	
20	IT	173	
21	IU	198	
22	IV	166	
23	IW	137	
24	IX	140	
25	IY	121	
26	IZ	163	
27	la	213	
28	lb	139	

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Mol	Chain	Length	Quality of chain
29	lc	149	 86% 13% ..
30	ld	64	 88% 6% 6%
31	le	109	 15% 72% 22% 6%
32	lf	150	 13% 79% 17% ..
33	lg	134	 81% 16% .
34	lh	137	 64% 12% 23%
35	li	122	 87% 13%
36	lj	108	 86% 12% .
37	lk	104	 70% 15% 14%
38	ll	77	 71% 21% . 6%
39	lm	93	 78% 18% .
40	ln	84	 10% 63% 23% . 13%
41	lo	51	 86% 10% ..
42	lp	56	 59% 32% . 5%
43	lq	98	 81% 13% 6%
44	lr	13	 100%

2 Entry composition

There are 44 unique types of molecules in this entry. The entry contains 121291 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 25S rRNA (3068-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	3067	Total	C	N	O	P	0	0
			65572	29397	11934	21174	3067		

- Molecule 2 is a RNA chain called 5.8S rRNA (145-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1B	145	Total	C	N	O	P	0	0
			3097	1390	560	1002	145		

- Molecule 3 is a RNA chain called 5S rRNA (117-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1C	117	Total	C	N	O	P	0	0
			2477	1108	425	827	117		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1D	246	Total	C	N	O	S	0	0
			1881	1165	382	326	8		

- Molecule 5 is a protein called 60S ribosomal protein L3, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1E	387	Total	C	N	O	S	0	0
			3076	1956	578	527	15		

- Molecule 6 is a protein called 60S ribosomal protein L4, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1F	424	Total	C	N	O	S	0	0
			3272	2085	622	551	14		

- Molecule 7 is a protein called 60S ribosomal protein L5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	lG	279	Total	C	N	O	S	0	0
			2222	1421	400	393	8		

- Molecule 8 is a protein called 60S ribosomal protein L6, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	lH	203	Total	C	N	O	S	0	0
			1607	1053	272	278	4		

- Molecule 9 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	lI	210	Total	C	N	O	S	0	0
			1658	1067	301	282	8		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	lJ	213	Total	C	N	O	S	0	0
			1727	1114	317	291	5		

- Molecule 11 is a protein called 60S ribosomal protein L9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	lK	193	Total	C	N	O	S	0	0
			1538	974	279	279	6		

- Molecule 12 is a protein called Ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	lL	200	Total	C	N	O	S	0	0
			1597	1017	302	264	14		

- Molecule 13 is a protein called 60S ribosomal protein L11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	lM	170	Total	C	N	O	S	0	0
			1350	857	243	245	5		

- Molecule 14 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	lN	232	Total	C	N	O	S	0	0
			1872	1186	369	309	8		

- Molecule 15 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	lO	204	Total	C	N	O	S	0	0
			1616	1030	302	275	9		

- Molecule 16 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	lP	132	Total	C	N	O	S	0	0
			1039	666	192	177	4		

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	lQ	204	Total	C	N	O	S	0	0
			1676	1051	356	264	5		

- Molecule 18 is a protein called 60S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	lR	158	Total	C	N	O	S	0	0
			1232	779	238	210	5		

- Molecule 19 is a protein called 60S ribosomal protein L18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	lS	167	Total	C	N	O	S	0	0
			1321	835	258	219	9		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	lT	173	Total	C	N	O	S	0	0
			1413	910	259	235	9		

- Molecule 21 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	IU	150	Total	C	N	O	S	0	0
			1235	787	246	197	5		

- Molecule 22 is a protein called 60S ribosomal protein L21, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	IV	165	Total	C	N	O	S	0	0
			1320	846	254	217	3		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	IW	93	Total	C	N	O	S	0	0
			763	493	132	133	5		

- Molecule 24 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	IX	133	Total	C	N	O	S	0	0
			1015	629	196	182	8		

- Molecule 25 is a protein called Ribosomal protein L23A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	IY	116	Total	C	N	O	S	0	0
			926	597	166	159	4		

- Molecule 26 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	IZ	57	Total	C	N	O	S	0	0
			481	318	88	73	2		

- Molecule 27 is a protein called 60S ribosomal protein L26, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	la	210	Total	C	N	O	S	0	0
			1651	1055	304	285	7		

- Molecule 28 is a protein called 60S ribosomal protein L27, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	lb	137	Total	C	N	O	S	0	0
			1094	707	196	187	4		

- Molecule 29 is a protein called Large ribosomal subunit protein uL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	lc	148	Total	C	N	O	S	0	0
			1192	757	236	194	5		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	ld	60	Total	C	N	O	S	0	0
			478	297	97	82	2		

- Molecule 31 is a protein called 60S ribosomal protein L30, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	le	103	Total	C	N	O	S	0	0
			768	486	131	149	2		

- Molecule 32 is a protein called 60S ribosomal protein L31, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	lf	146	Total	C	N	O	S	0	0
			1184	759	219	200	6		

- Molecule 33 is a protein called 60S ribosomal protein L32, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	lg	129	Total	C	N	O	S	0	0
			1058	672	209	172	5		

- Molecule 34 is a protein called 60S ribosomal protein L34, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	lh	105	Total	C	N	O	S	0	0
			820	512	169	133	6		

- Molecule 35 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	li	122	Total	C	N	O	S	0	0
			974	620	188	162	4		

- Molecule 36 is a protein called 60S ribosomal protein L35a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	lj	106	Total	C	N	O	S	0	0
			841	545	158	135	3		

- Molecule 37 is a protein called 60S ribosomal protein L36, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	lk	89	Total	C	N	O	S	0	0
			712	447	144	116	5		

- Molecule 38 is a protein called 60S ribosomal protein L37-A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	ll	72	Total	C	N	O	S	0	0
			591	361	132	91	7		

- Molecule 39 is a protein called 60S ribosomal protein L37A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	lm	90	Total	C	N	O	S	0	0
			688	428	135	119	6		

- Molecule 40 is a protein called 60S ribosomal protein L38, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	ln	73	Total	C	N	O	S	0	0
			584	378	104	100	2		

- Molecule 41 is a protein called Ribosomal protein L39, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	lo	50	Total	C	N	O	S	0	0
			432	275	91	63	3		

- Molecule 42 is a protein called 60S ribosomal protein L40, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	lp	53	Total	C	N	O	S	0	0
			420	259	86	69	6		

- Molecule 43 is a protein called 60S ribosomal protein L44, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	lq	92	Total	C	N	O	S	0	0
			756	480	148	122	6		

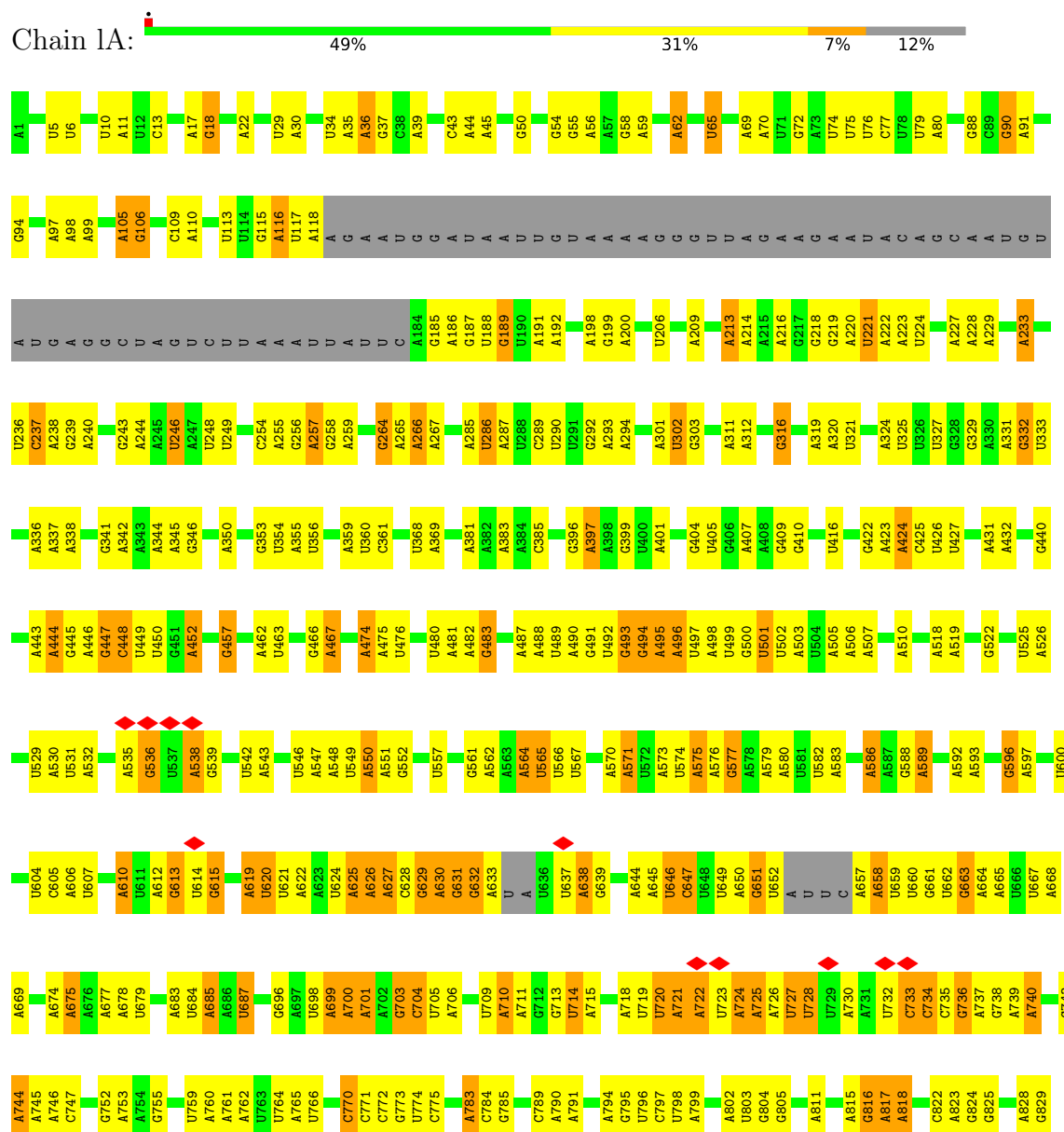
- Molecule 44 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	lr	13	Total	C	N	O	0	0
			65	39	13	13		

3 Residue-property plots

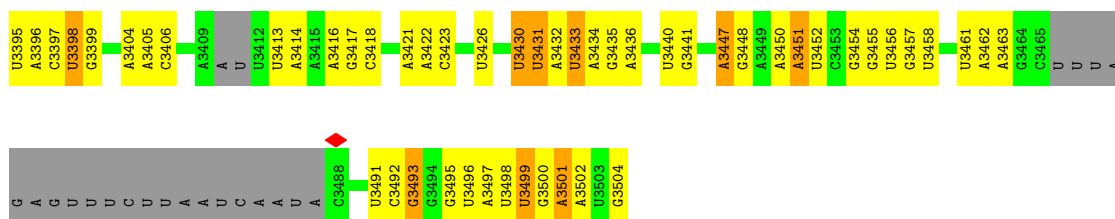
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 25S rRNA (3068-MER)



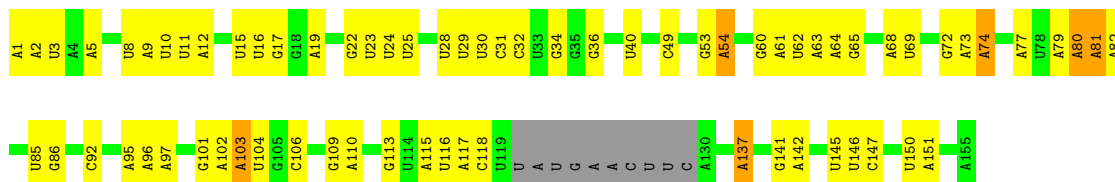






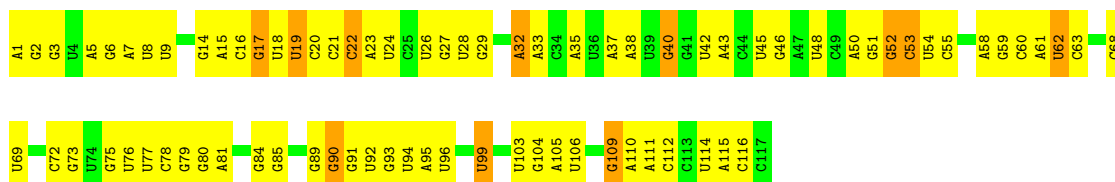
• Molecule 2: 5.8S rRNA (145-MER)

Chain IB: 48% 41% 6%



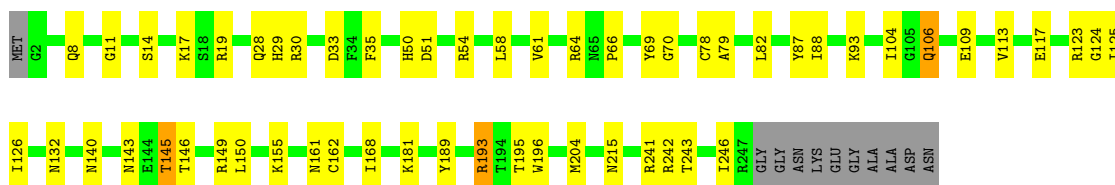
• Molecule 3: 5S rRNA (117-MER)

Chain IC: 32% 58% 9%



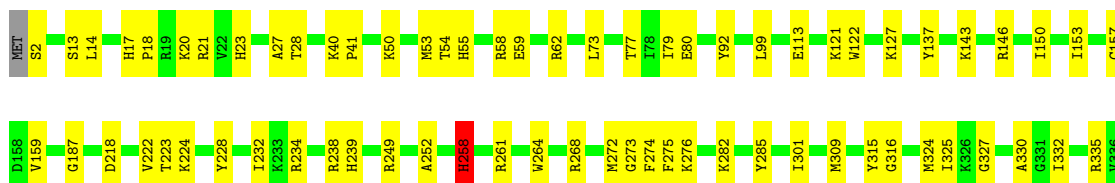
• Molecule 4: Large ribosomal subunit protein uL2

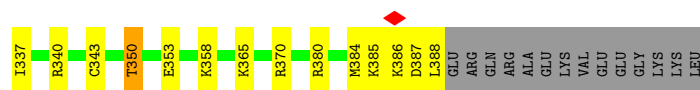
Chain ID: 74% 21% . .



• Molecule 5: 60S ribosomal protein L3, putative

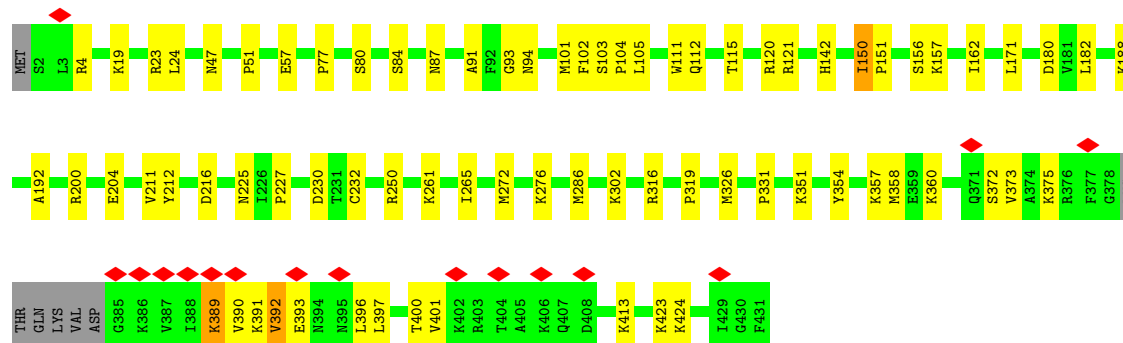
Chain IE: 76% 20% .





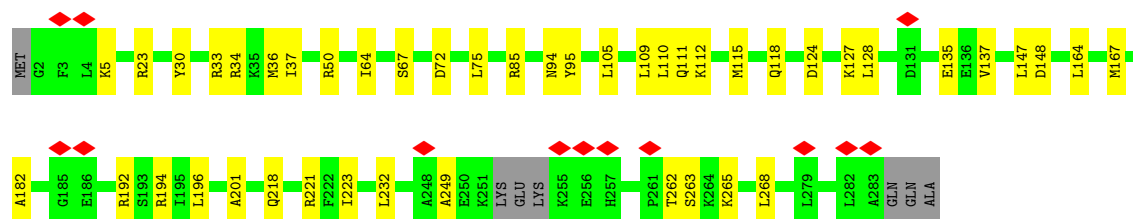
- Molecule 6: 60S ribosomal protein L4, putative

Chain IF: 81% 17% ..



- Molecule 7: 60S ribosomal protein L5, putative

Chain IG: 5% 82% 16% .



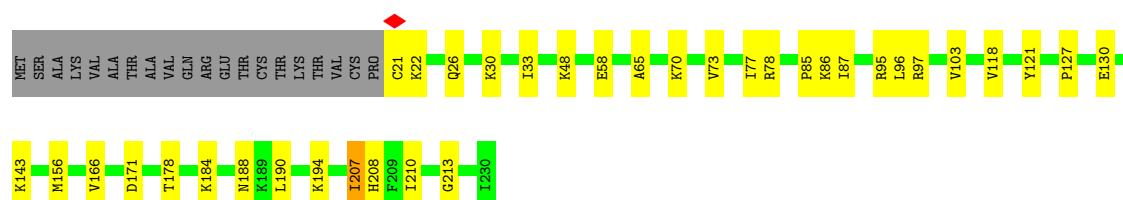
- Molecule 8: 60S ribosomal protein L6, putative


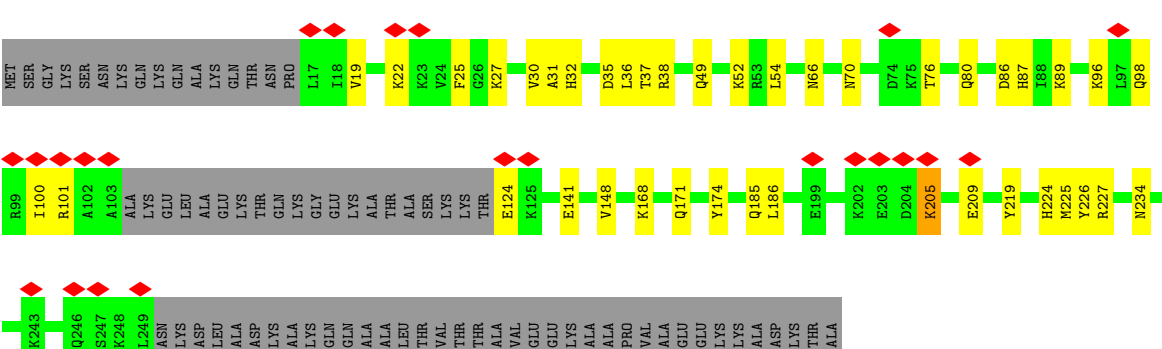
Chain IH: 78% 21%







- Molecule 9: 60S ribosomal protein L7, putative


Chain II: 76% 15% 9%



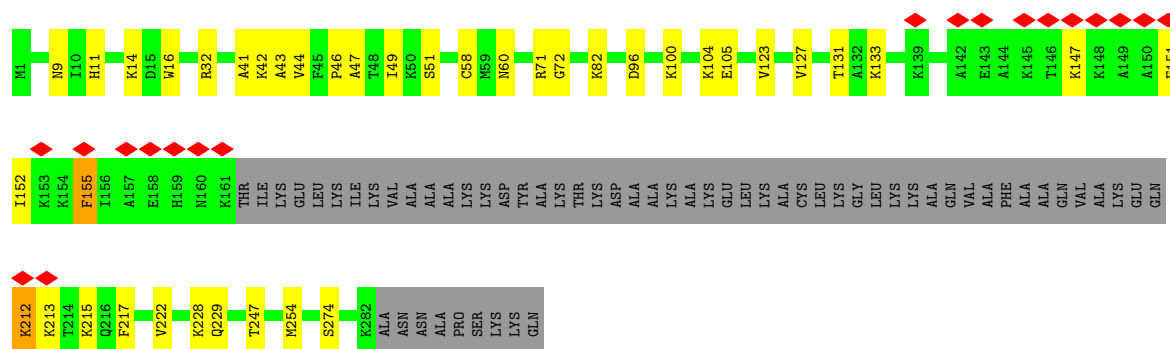
- Chain 1J: 
- 
- | Position | Amino Acid | Frequency (bits) |
|----------|------------|------------------|
| 1 | Met | 0.00 |
| 2 | Ser | 0.00 |
| 3 | Gly | 0.00 |
| 4 | Lys | 0.00 |
| 5 | Ser | 0.00 |
| 6 | Asn | 0.00 |
| 7 | Gln | 0.00 |
| 8 | Lys | 0.00 |
| 9 | Gln | 0.00 |
| 10 | Ala | 0.00 |
| 11 | Lys | 0.00 |
| 12 | Gln | 0.00 |
| 13 | Thr | 0.00 |
| 14 | Asn | 0.00 |
| 15 | Pro | 0.00 |
| 16 | Lys | 0.00 |
| 17 | Lys | 0.00 |
| 18 | Lys | 0.00 |
| 19 | Lys | 0.00 |
| 20 | Lys | 0.00 |
| 21 | Ala | 0.00 |
| 22 | Thr | 0.00 |
| 23 | Ala | 0.00 |
| 24 | Ser | 0.00 |
| 25 | Lys | 0.00 |
| 26 | Lys | 0.00 |
| 27 | Thr | 0.00 |
| 28 | Ala | 0.00 |
| 29 | Ala | 0.00 |
| 30 | Thr | 0.00 |
| 31 | Lys | 0.00 |
| 32 | Lys | 0.00 |
| 33 | Lys | 0.00 |
| 34 | Thr | 0.00 |
| 35 | Ala | 0.00 |
| 36 | Ala | 0.00 |
| 37 | Ala | 0.00 |
| 38 | Ala | 0.00 |
| 39 | Ala | 0.00 |
| 40 | Ala | 0.00 |
| 41 | Ala | 0.00 |
| 42 | Ala | 0.00 |
| 43 | Ala | 0.00 |
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| 48 | Ala | 0.00 |
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| 100 | Ala | 0.00 |
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| 137 | Ala | 0.00 |
| 138 | Ala | 0.00 |
| 139 | Ala | 0. |

- Chain 1K: 

- Chain 1L: 
- 
- 

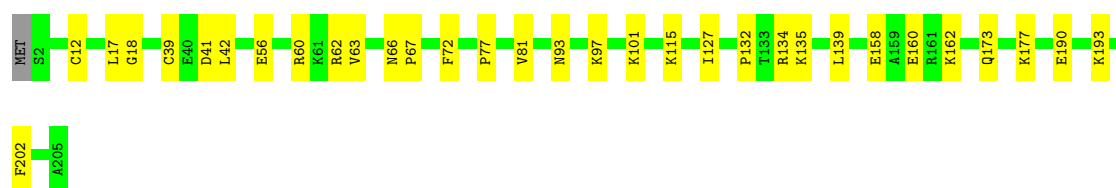
- Chain IM: 

- Chain IN: 



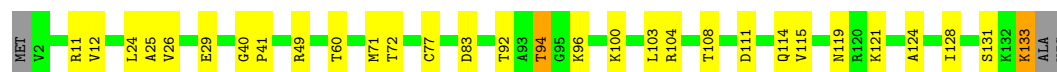
- Molecule 15: 60S ribosomal protein L13, putative

Chain IO: 84% 16%



- Molecule 16: 60S ribosomal protein L14, putative

Chain IP: 76% 21% ..



- Molecule 17: Ribosomal protein L15

Chain IQ: 89% 10%



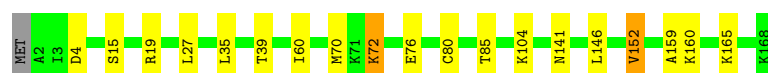
- Molecule 18: 60S ribosomal protein L17, putative

Chain IR: 79% 8% 12%



- Molecule 19: 60S ribosomal protein L18, putative

Chain IS: 88% 10% ..



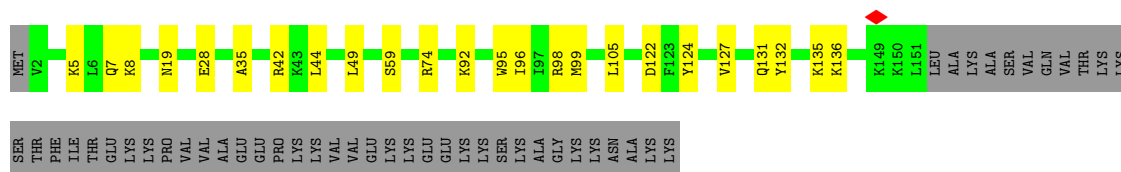
- Molecule 20: 60S ribosomal protein L18a

Chain IT:  86% 13% .



- Molecule 21: Ribosomal protein L19

Chain IU:  64% 12% 24%



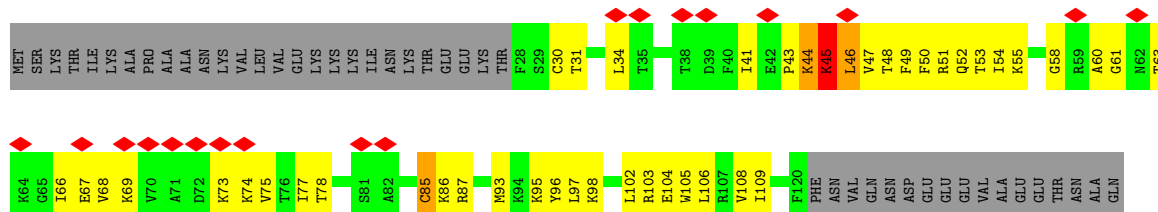
- Molecule 22: 60S ribosomal protein L21, putative

Chain IV:  86% 13% ..



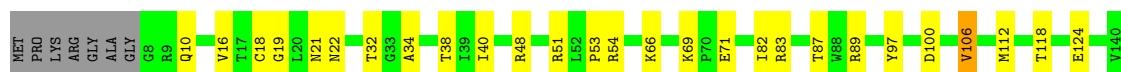
- Molecule 23: Large ribosomal subunit protein eL22

Chain IW:  13% 35% 30% .. 32%




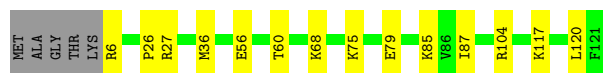
- Molecule 24: 60S ribosomal protein L23, putative

Chain IX:  76% 19% . 5%

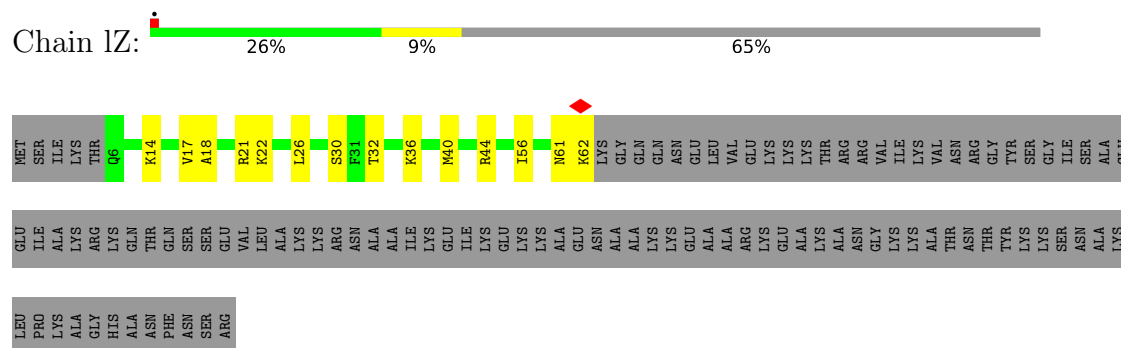


- Molecule 25: Ribosomal protein L23A, putative

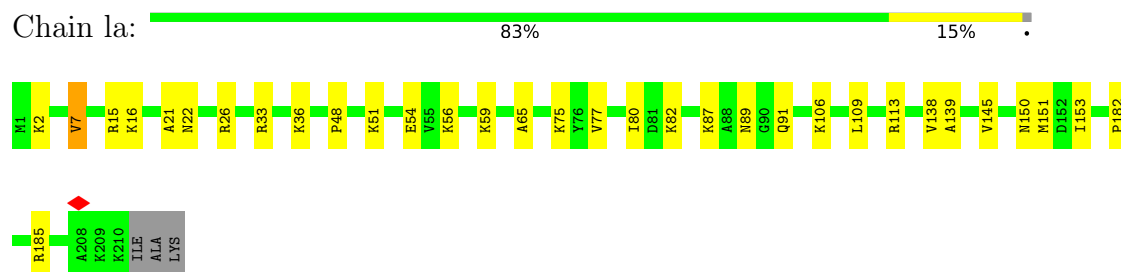
Chain IY:  84% 12% .



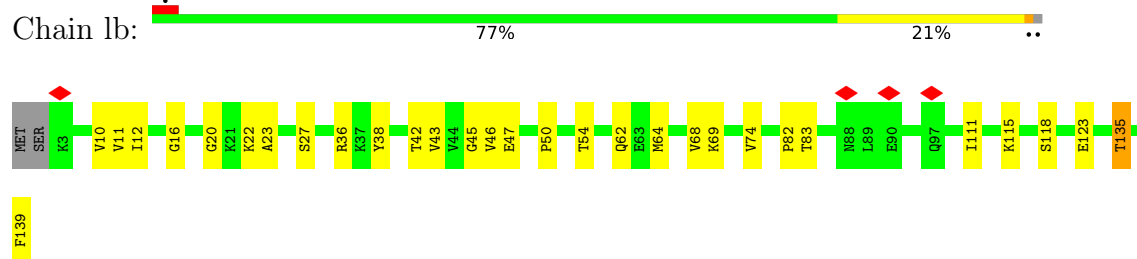
- Molecule 26: 60S ribosomal protein L24, putative



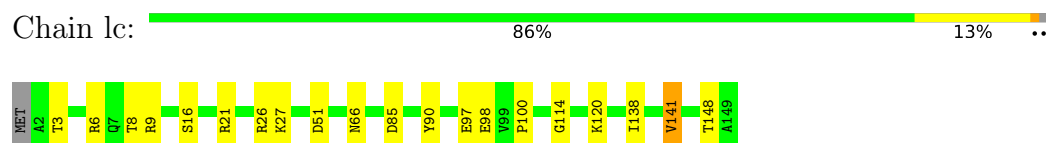
- Molecule 27: 60S ribosomal protein L26, putative



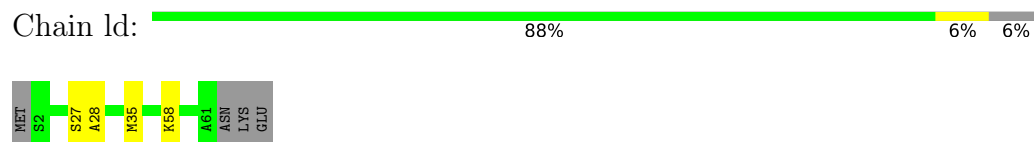
- Molecule 28: 60S ribosomal protein L27, putative



- Molecule 29: Large ribosomal subunit protein uL15A



- Molecule 30: 60S ribosomal protein L29

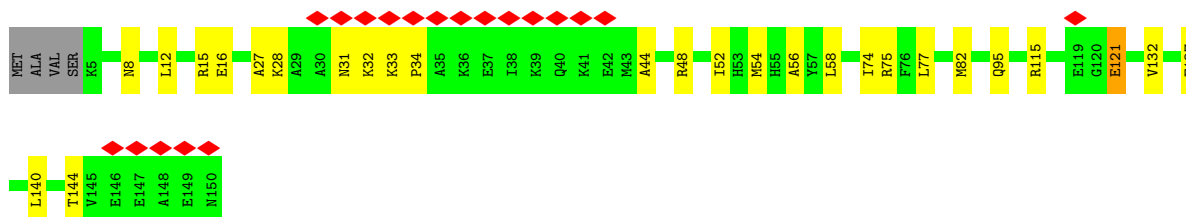
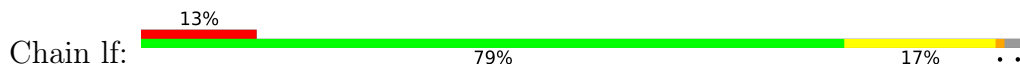


- Molecule 31: 60S ribosomal protein L30, putative

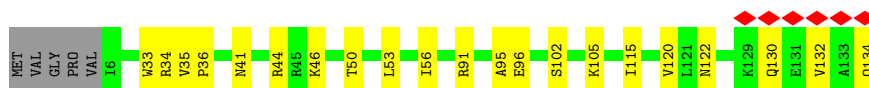
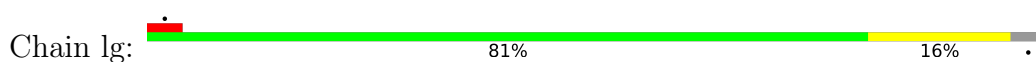




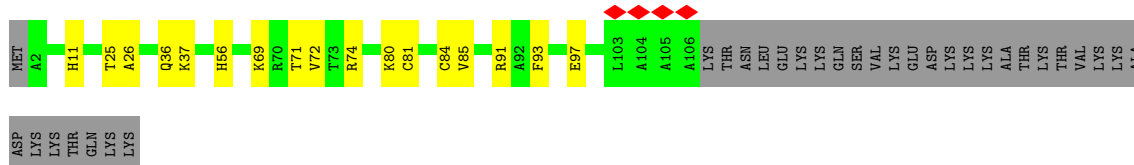
- Molecule 32: 60S ribosomal protein L31, putative



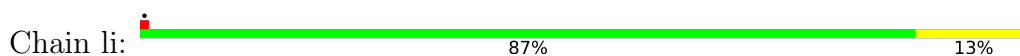
- Molecule 33: 60S ribosomal protein L32, putative



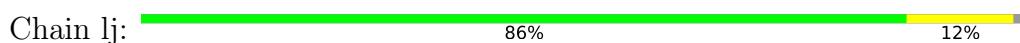
- Molecule 34: 60S ribosomal protein L34, putative



- Molecule 35: uL29



- Molecule 36: 60S ribosomal protein L35a, putative



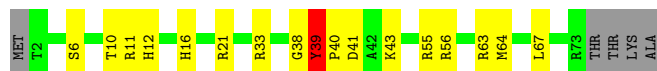
- Molecule 37: 60S ribosomal protein L36, putative





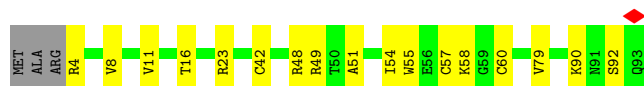
- Molecule 38: 60S ribosomal protein L37-A, putative

Chain ll: 71% 21% 6%



- Molecule 39: 60S ribosomal protein L37A, putative

Chain lm: 78% 18% 4%



- Molecule 40: 60S ribosomal protein L38, putative

Chain ln: 10% 63% 23% 4%



- Molecule 41: Ribosomal protein L39, putative

Chain lo: 86% 10% 4%



- Molecule 42: 60S ribosomal protein L40, putative

Chain lp: 59% 32% 5%



- Molecule 43: 60S ribosomal protein L44, putative

Chain lq: 81% 13% 6%



- Molecule 44: Unknown peptide

Chain lr:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	378061	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 ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	18.211	Depositor
Minimum map value	-6.837	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (Å)	321.00003, 321.00003, 321.00003	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	1A	0.19	0/73480	0.30	0/114456
2	1B	0.19	0/3470	0.30	0/5401
3	1C	0.20	0/2765	0.37	2/4303 (0.0%)
4	1D	0.18	0/1920	0.29	0/2582
5	1E	0.18	0/3140	0.33	0/4216
6	1F	0.19	0/3330	0.30	1/4468 (0.0%)
7	1G	0.14	0/2261	0.29	0/3028
8	1H	0.14	0/1639	0.31	0/2203
9	1I	0.16	0/1680	0.29	0/2252
10	1J	0.12	0/1757	0.28	0/2360
11	1K	0.13	0/1562	0.23	0/2103
12	1L	0.16	0/1633	0.31	0/2184
13	1M	0.11	0/1369	0.26	0/1834
14	1N	0.16	0/1900	0.29	0/2534
15	1O	0.17	0/1646	0.28	0/2209
16	1P	0.23	0/1051	0.34	1/1411 (0.1%)
17	1Q	0.18	0/1707	0.24	0/2276
18	1R	0.18	0/1251	0.26	0/1675
19	1S	0.16	0/1342	0.25	0/1796
20	1T	0.16	0/1445	0.26	0/1946
21	1U	0.14	0/1253	0.24	0/1666
22	1V	0.17	0/1351	0.27	0/1819
23	1W	0.27	0/774	0.67	1/1031 (0.1%)
24	1X	0.17	0/1030	0.29	0/1384
25	1Y	0.14	0/941	0.22	0/1262
26	1Z	0.12	0/492	0.24	0/656
27	1a	0.14	0/1673	0.23	0/2236
28	1b	0.13	0/1112	0.26	0/1489
29	1c	0.19	0/1223	0.27	0/1636
30	1d	0.18	0/485	0.31	0/639
31	1e	0.13	0/776	0.29	0/1044
32	1f	0.15	0/1205	0.28	0/1609
33	1g	0.18	0/1075	0.26	0/1434
34	1h	0.16	0/833	0.23	0/1115

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	li	0.14	0/984	0.23	0/1310
36	lj	0.19	0/862	0.29	0/1163
37	lk	0.11	0/721	0.22	0/955
38	ll	0.20	0/602	0.33	0/797
39	lm	0.16	0/696	0.33	0/928
40	ln	0.15	0/592	0.29	0/789
41	lo	0.19	0/444	0.23	0/587
42	lp	0.17	0/425	0.54	2/563 (0.4%)
43	lq	0.16	0/770	0.24	0/1019
All	All	0.18	0/130667	0.30	7/192368 (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
5	lE	0	1
20	lT	0	1
23	lW	0	1
38	lI	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	lC	62	U	OP2-P-O3'	-8.80	81.60	108.00
3	lC	62	U	OP1-P-O3'	-8.53	82.40	108.00
42	lp	24	CYS	CA-CB-SG	6.31	128.92	114.40
42	lp	35	CYS	CA-CB-SG	5.99	128.18	114.40
6	lF	389	LYS	CA-CB-CG	5.92	125.94	114.10

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	lE	258	HIS	Peptide
20	lT	172	LEU	Peptide
23	lW	44	LYS	Peptide
38	lI	39	TYR	Peptide

5.2 Too-close contacts ⓘ

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	lA	65572	0	32902	942	0
2	lB	3097	0	1552	41	0
3	lC	2477	0	1252	95	0
4	lD	1881	0	1928	40	0
5	lE	3076	0	3209	62	0
6	lF	3272	0	3500	63	0
7	lG	2222	0	2304	35	0
8	lH	1607	0	1726	31	0
9	lI	1658	0	1802	29	0
10	lJ	1727	0	1849	25	0
11	lK	1538	0	1598	28	0
12	lL	1597	0	1654	23	0
13	lM	1350	0	1390	28	0
14	lN	1872	0	2034	37	0
15	lO	1616	0	1700	21	0
16	lP	1039	0	1133	23	0
17	lQ	1676	0	1777	16	0
18	lR	1232	0	1307	12	0
19	lS	1321	0	1427	14	0
20	lT	1413	0	1479	17	0
21	lU	1235	0	1369	21	0
22	lV	1320	0	1406	18	0
23	lW	763	0	818	38	0
24	lX	1015	0	1054	24	0
25	lY	926	0	997	11	0
26	lZ	481	0	518	10	0
27	la	1651	0	1822	23	0
28	lb	1094	0	1174	22	0
29	lc	1192	0	1205	18	0
30	ld	478	0	507	3	0
31	le	768	0	810	15	0
32	lf	1184	0	1270	18	0
33	lg	1058	0	1140	15	0
34	lh	820	0	864	13	0
35	li	974	0	1093	14	0
36	lj	841	0	878	9	0
37	lk	712	0	755	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	ll	591	0	617	13	0
39	lm	688	0	728	14	0
40	ln	584	0	643	13	0
41	lo	432	0	444	6	0
42	lp	420	0	450	15	0
43	lq	756	0	821	10	0
44	lr	65	0	16	0	0
All	All	121291	0	88922	1660	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 8.

The worst 5 of 1660 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)
3:1C:79:G:N1	3:1C:95:A:C2	2.13	1.17
3:1C:79:G:N1	3:1C:95:A:H2	1.41	1.15
3:1C:81:A:H2	3:1C:93:G:N1	1.44	1.13
1:1A:3454:G:N1	1:1A:3502:A:H2	1.50	1.09
1:1A:3454:G:N1	1:1A:3502:A:C2	2.20	1.05

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	
4	1D	244/257 (95%)	229 (94%)	15 (6%)	0	100	100
5	1E	385/402 (96%)	373 (97%)	12 (3%)	0	100	100
6	1F	420/431 (97%)	404 (96%)	16 (4%)	0	100	100
7	1G	275/286 (96%)	259 (94%)	16 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	IH	201/204 (98%)	183 (91%)	18 (9%)	0	100	100
9	II	208/230 (90%)	200 (96%)	8 (4%)	0	100	100
10	IJ	209/286 (73%)	200 (96%)	9 (4%)	0	100	100
11	IK	191/197 (97%)	185 (97%)	6 (3%)	0	100	100
12	IL	196/210 (93%)	187 (95%)	9 (5%)	0	100	100
13	IM	166/174 (95%)	158 (95%)	7 (4%)	1 (1%)	22	51
14	IN	228/291 (78%)	212 (93%)	16 (7%)	0	100	100
15	IO	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
16	IP	130/135 (96%)	128 (98%)	2 (2%)	0	100	100
17	IQ	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
18	IR	156/179 (87%)	153 (98%)	3 (2%)	0	100	100
19	IS	165/168 (98%)	153 (93%)	12 (7%)	0	100	100
20	IT	171/173 (99%)	165 (96%)	6 (4%)	0	100	100
21	IU	148/198 (75%)	145 (98%)	3 (2%)	0	100	100
22	IV	163/166 (98%)	158 (97%)	5 (3%)	0	100	100
23	IW	91/137 (66%)	82 (90%)	8 (9%)	1 (1%)	12	37
24	IX	131/140 (94%)	128 (98%)	3 (2%)	0	100	100
25	IY	114/121 (94%)	112 (98%)	2 (2%)	0	100	100
26	IZ	55/163 (34%)	54 (98%)	1 (2%)	0	100	100
27	la	208/213 (98%)	200 (96%)	8 (4%)	0	100	100
28	lb	135/139 (97%)	133 (98%)	2 (2%)	0	100	100
29	lc	146/149 (98%)	140 (96%)	6 (4%)	0	100	100
30	ld	58/64 (91%)	55 (95%)	3 (5%)	0	100	100
31	le	101/109 (93%)	92 (91%)	9 (9%)	0	100	100
32	lf	144/150 (96%)	135 (94%)	9 (6%)	0	100	100
33	lg	127/134 (95%)	123 (97%)	4 (3%)	0	100	100
34	lh	103/137 (75%)	99 (96%)	4 (4%)	0	100	100
35	li	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
36	lj	104/108 (96%)	100 (96%)	4 (4%)	0	100	100
37	lk	83/104 (80%)	82 (99%)	1 (1%)	0	100	100
38	ll	70/77 (91%)	63 (90%)	5 (7%)	2 (3%)	3	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	lm	88/93 (95%)	82 (93%)	6 (7%)	0	100	100
40	ln	71/84 (84%)	69 (97%)	2 (3%)	0	100	100
41	lo	48/51 (94%)	48 (100%)	0	0	100	100
42	lp	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
43	lq	90/98 (92%)	88 (98%)	2 (2%)	0	100	100
All	All	6198/6846 (90%)	5938 (96%)	256 (4%)	4 (0%)	50	77

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	lW	45	LYS
38	ll	39	TYR
38	ll	40	PRO
13	lM	28	ASP

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	lD	195/201 (97%)	189 (97%)	6 (3%)	35	69
5	lE	330/343 (96%)	326 (99%)	4 (1%)	67	89
6	lF	338/345 (98%)	329 (97%)	9 (3%)	40	74
7	lG	225/231 (97%)	224 (100%)	1 (0%)	89	96
8	lH	172/173 (99%)	170 (99%)	2 (1%)	67	89
9	lI	178/195 (91%)	175 (98%)	3 (2%)	56	84
10	lJ	186/242 (77%)	179 (96%)	7 (4%)	28	62
11	lK	171/174 (98%)	170 (99%)	1 (1%)	84	95
12	lL	169/176 (96%)	167 (99%)	2 (1%)	67	89
13	lM	144/147 (98%)	142 (99%)	2 (1%)	62	87
14	lN	200/243 (82%)	196 (98%)	4 (2%)	50	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	IO	167/168 (99%)	163 (98%)	4 (2%)	44	77
16	IP	116/118 (98%)	113 (97%)	3 (3%)	41	75
17	IQ	171/172 (99%)	170 (99%)	1 (1%)	84	95
18	IR	129/147 (88%)	125 (97%)	4 (3%)	35	69
19	IS	142/143 (99%)	138 (97%)	4 (3%)	38	72
20	IT	156/156 (100%)	154 (99%)	2 (1%)	65	88
21	IU	132/174 (76%)	132 (100%)	0	100	100
22	IV	144/145 (99%)	141 (98%)	3 (2%)	48	80
23	IW	86/125 (69%)	77 (90%)	9 (10%)	5	18
24	IX	109/113 (96%)	108 (99%)	1 (1%)	75	92
25	IY	99/102 (97%)	98 (99%)	1 (1%)	73	91
26	IZ	52/137 (38%)	49 (94%)	3 (6%)	17	45
27	la	177/179 (99%)	175 (99%)	2 (1%)	70	90
28	lb	121/123 (98%)	118 (98%)	3 (2%)	42	75
29	lc	120/121 (99%)	117 (98%)	3 (2%)	42	75
30	ld	50/54 (93%)	49 (98%)	1 (2%)	50	81
31	le	86/92 (94%)	83 (96%)	3 (4%)	31	65
32	lf	125/128 (98%)	122 (98%)	3 (2%)	44	77
33	lg	112/116 (97%)	108 (96%)	4 (4%)	30	64
34	lh	86/116 (74%)	84 (98%)	2 (2%)	45	78
35	li	103/103 (100%)	103 (100%)	0	100	100
36	lj	89/91 (98%)	89 (100%)	0	100	100
37	lk	71/82 (87%)	69 (97%)	2 (3%)	38	72
38	ll	60/64 (94%)	59 (98%)	1 (2%)	56	84
39	lm	72/74 (97%)	72 (100%)	0	100	100
40	ln	63/73 (86%)	62 (98%)	1 (2%)	58	85
41	lo	44/45 (98%)	43 (98%)	1 (2%)	45	78
42	lp	45/48 (94%)	45 (100%)	0	100	100
43	lq	85/91 (93%)	84 (99%)	1 (1%)	67	89
All	All	5320/5770 (92%)	5217 (98%)	103 (2%)	52	82

5 of 103 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	IT	58	GLN
24	IX	106	VAL
38	II	10	THR
22	IV	27	THR
23	IW	45	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
20	IT	101	GLN
25	IY	58	HIS
22	IV	5	ASN
24	IX	22	ASN
29	Ic	28	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	IA	3047/3503 (86%)	553 (18%)	0
2	IB	143/155 (92%)	32 (22%)	0
3	IC	116/117 (99%)	15 (12%)	0
All	All	3306/3775 (87%)	600 (18%)	0

5 of 600 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	IA	18	G
1	IA	22	A
1	IA	29	U
1	IA	30	A
1	IA	36	A

There are no RNA pucker outliers to report.

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

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.

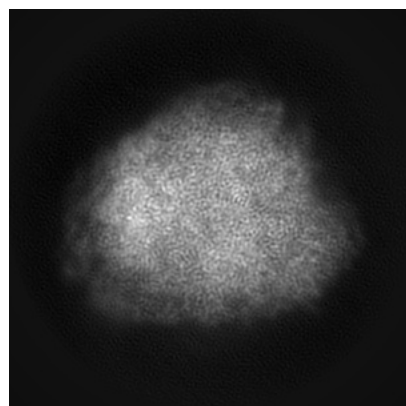
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64694. These allow visual inspection of the internal detail of the map and identification of artifacts.

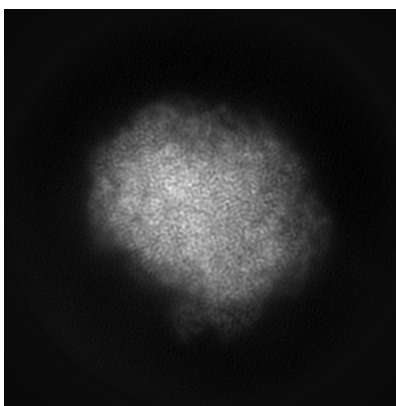
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

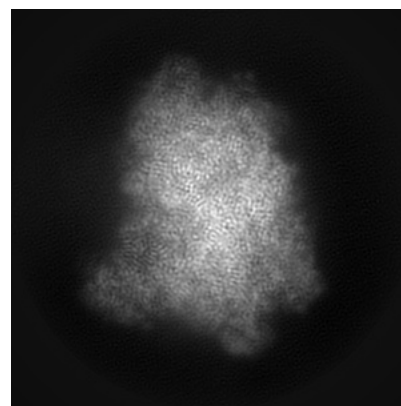
6.1.1 Primary map



X

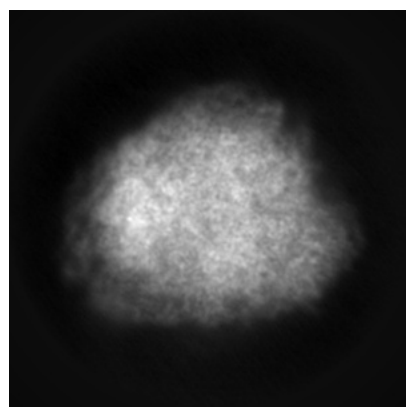


Y

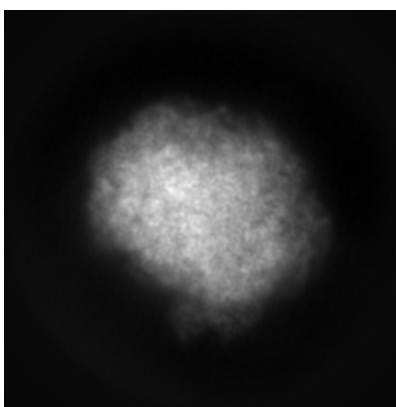


Z

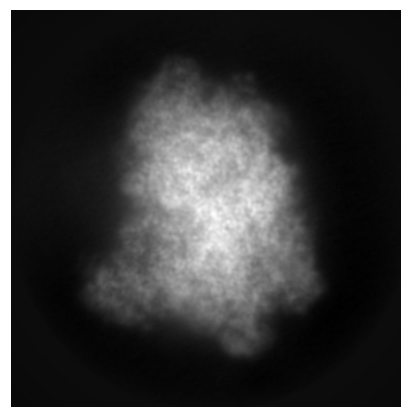
6.1.2 Raw map



X



Y

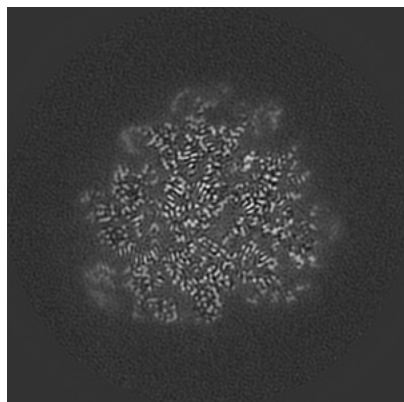


Z

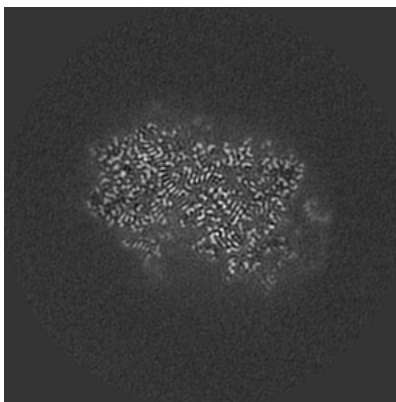
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

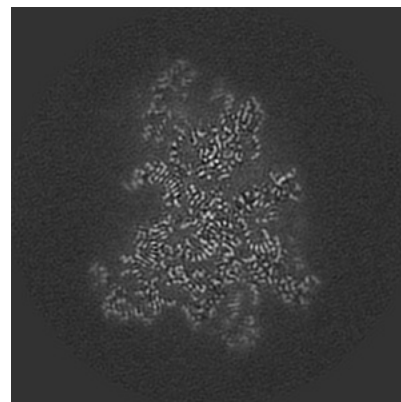
6.2.1 Primary map



X Index: 150

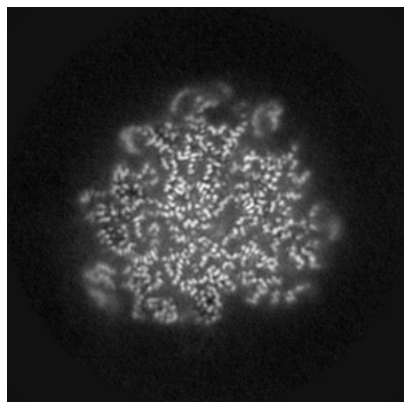


Y Index: 150

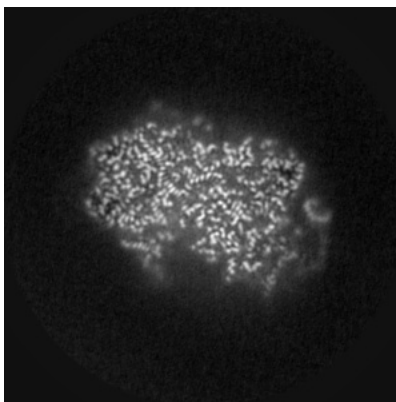


Z Index: 150

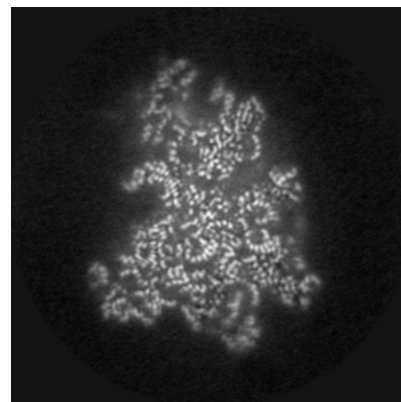
6.2.2 Raw map



X Index: 150



Y Index: 150

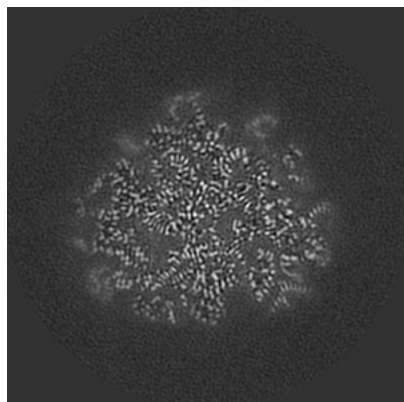


Z Index: 150

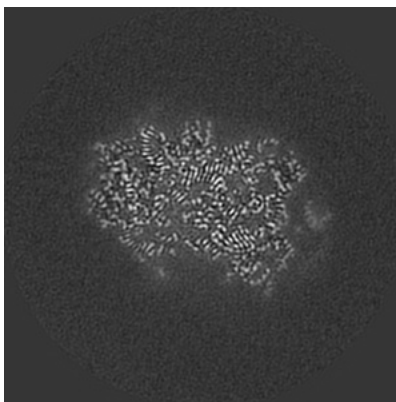
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

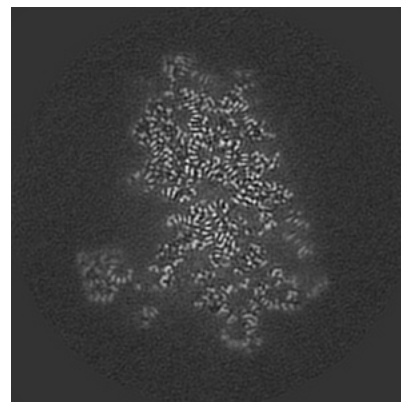
6.3.1 Primary map



X Index: 156

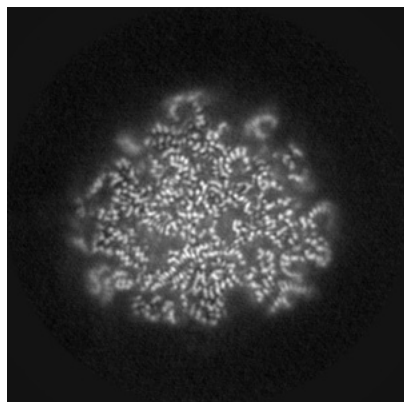


Y Index: 153

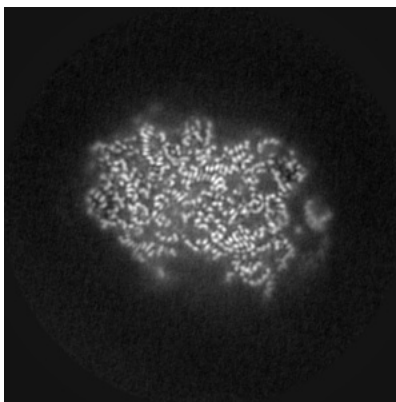


Z Index: 134

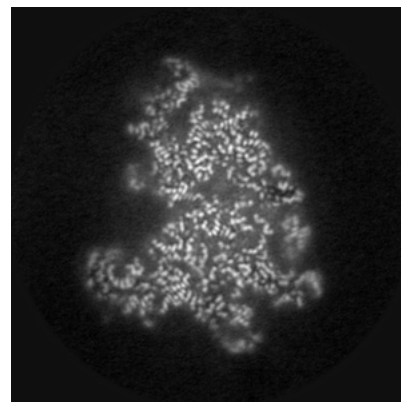
6.3.2 Raw map



X Index: 156



Y Index: 153

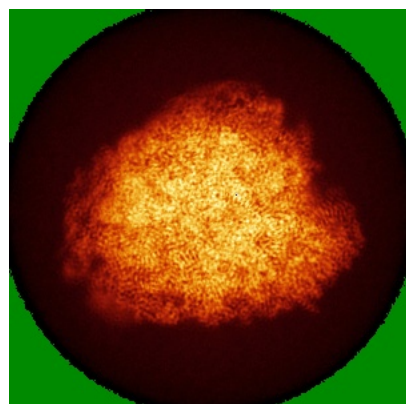


Z Index: 141

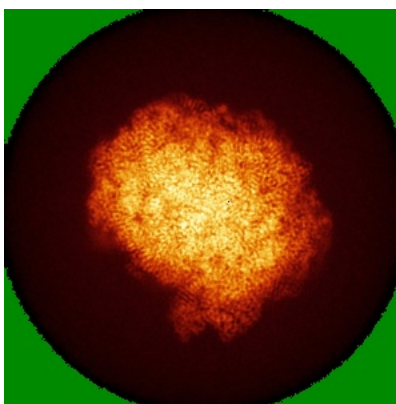
The images above show the largest variance slices of the map in three orthogonal directions.

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

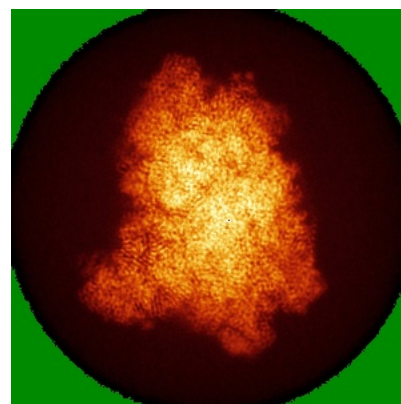
6.4.1 Primary map



X

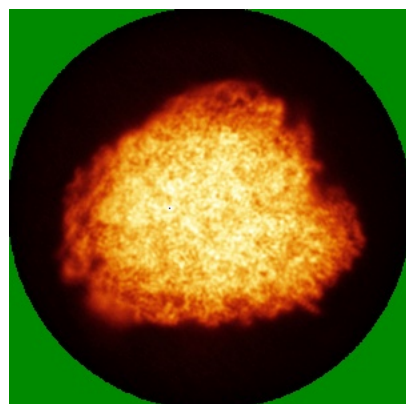


Y

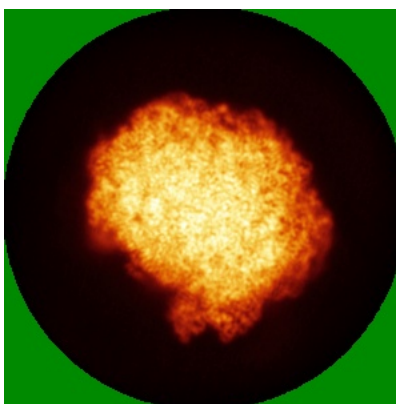


Z

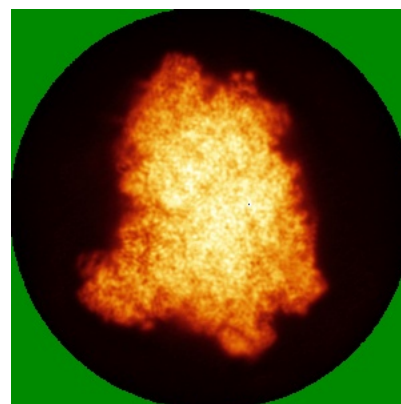
6.4.2 Raw map



X



Y

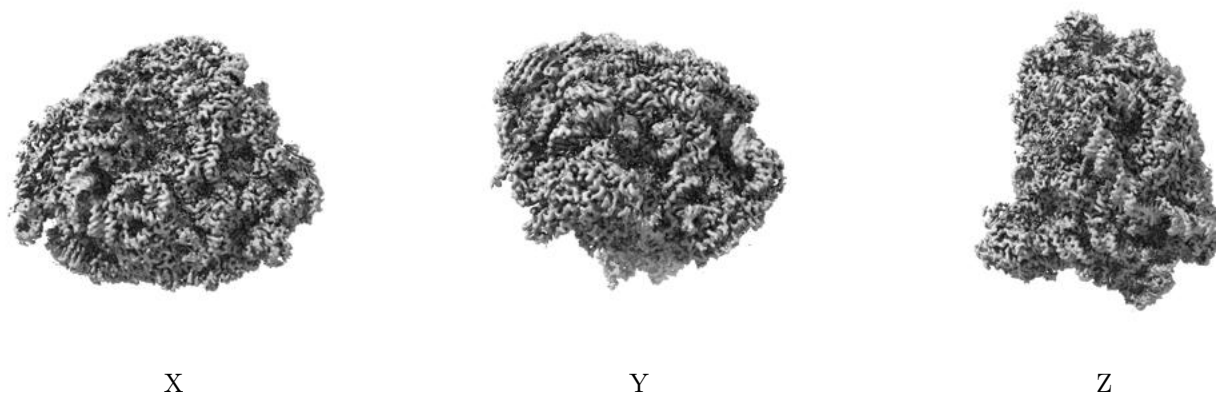


Z

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.

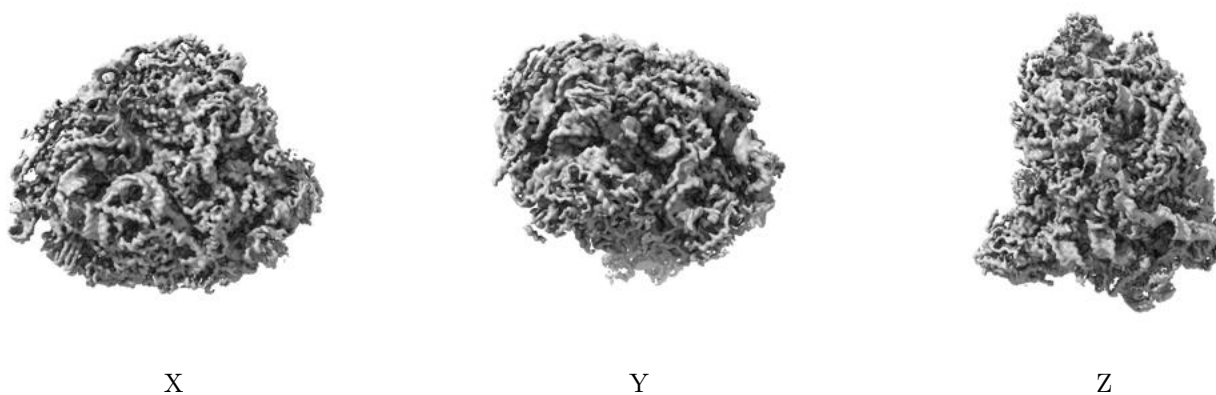
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.0. 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



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.

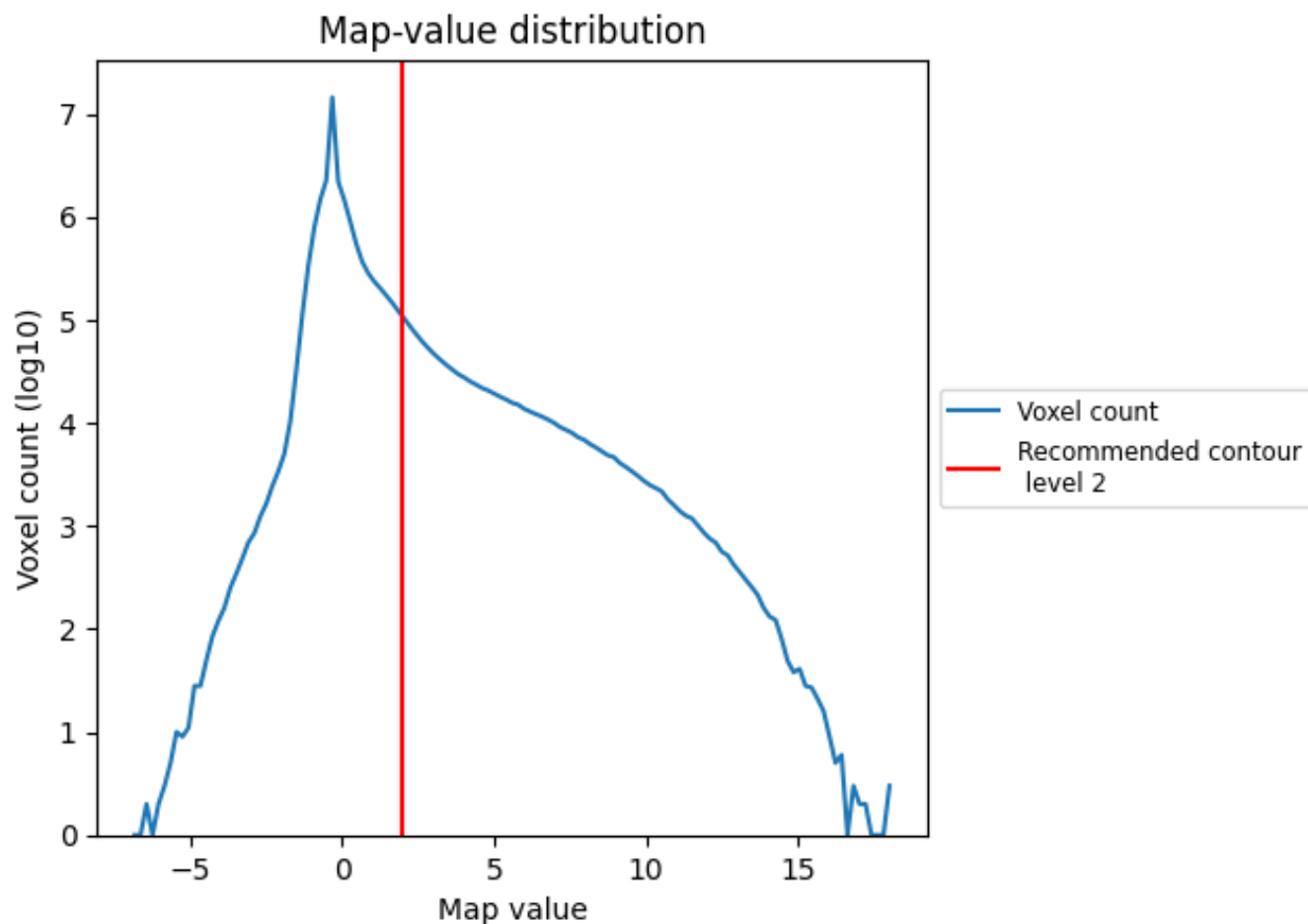
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

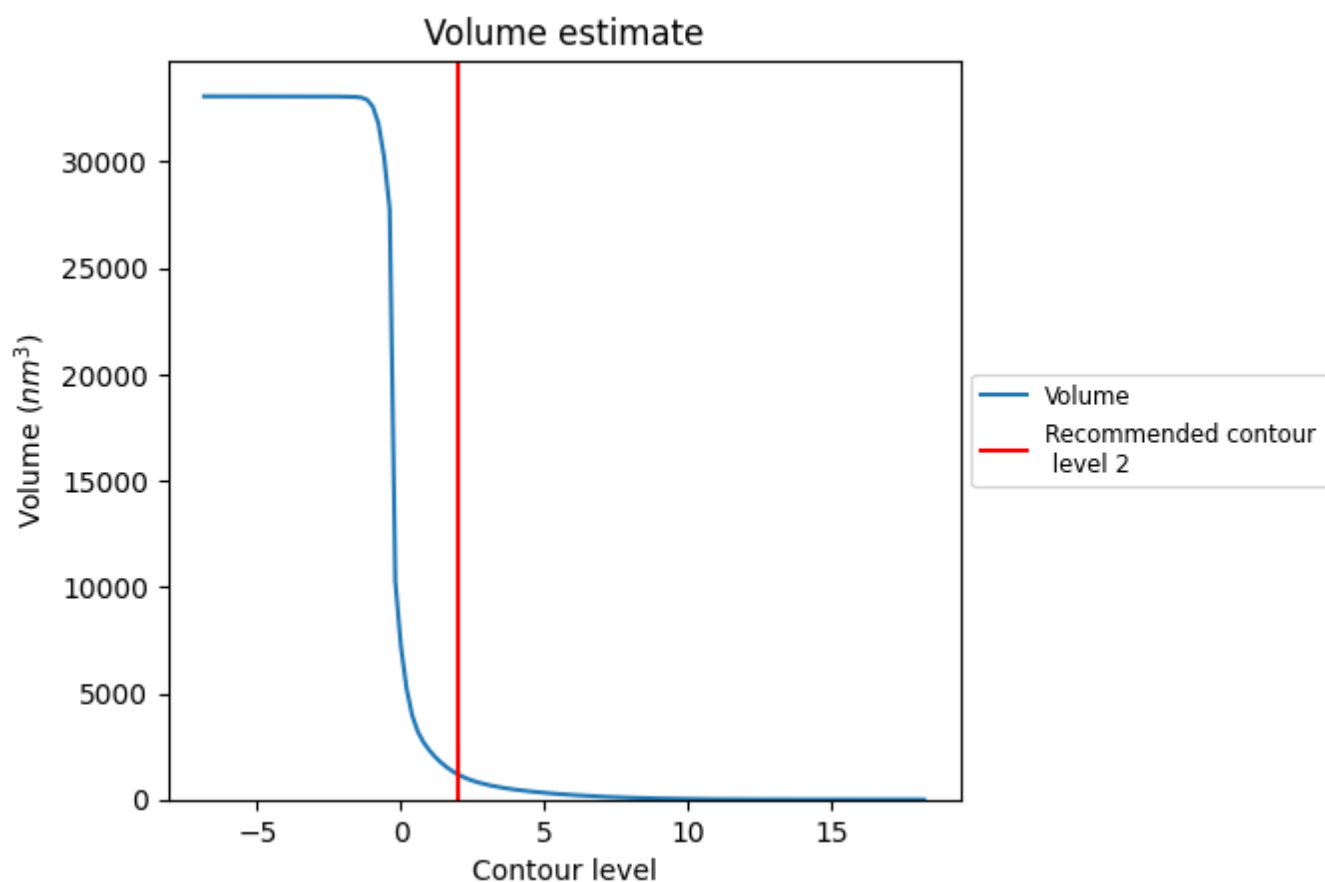
This section contains the results of statistical analysis of the map.

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.

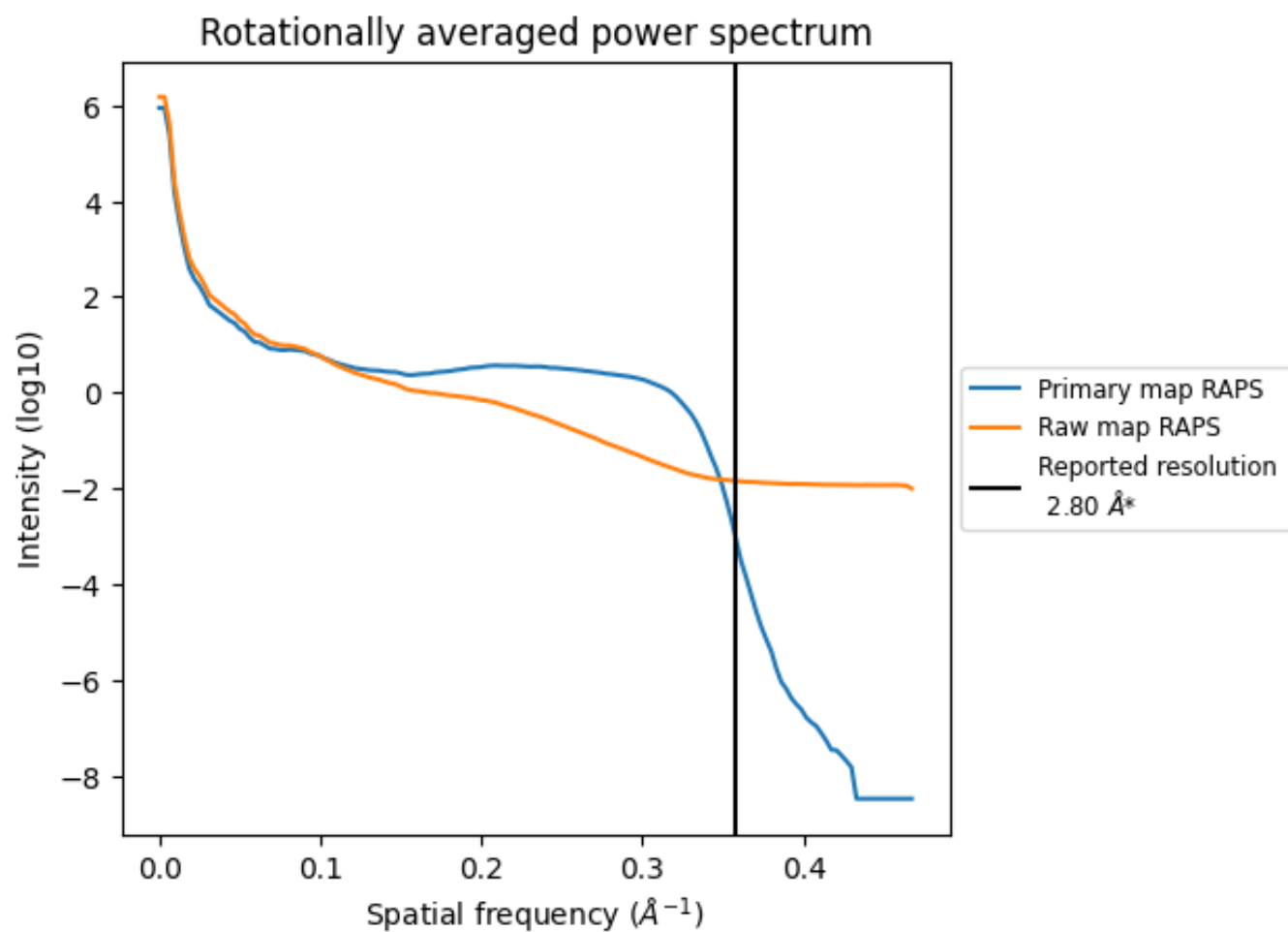
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1183 nm³; this corresponds to an approximate mass of 1069 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 ⓘ

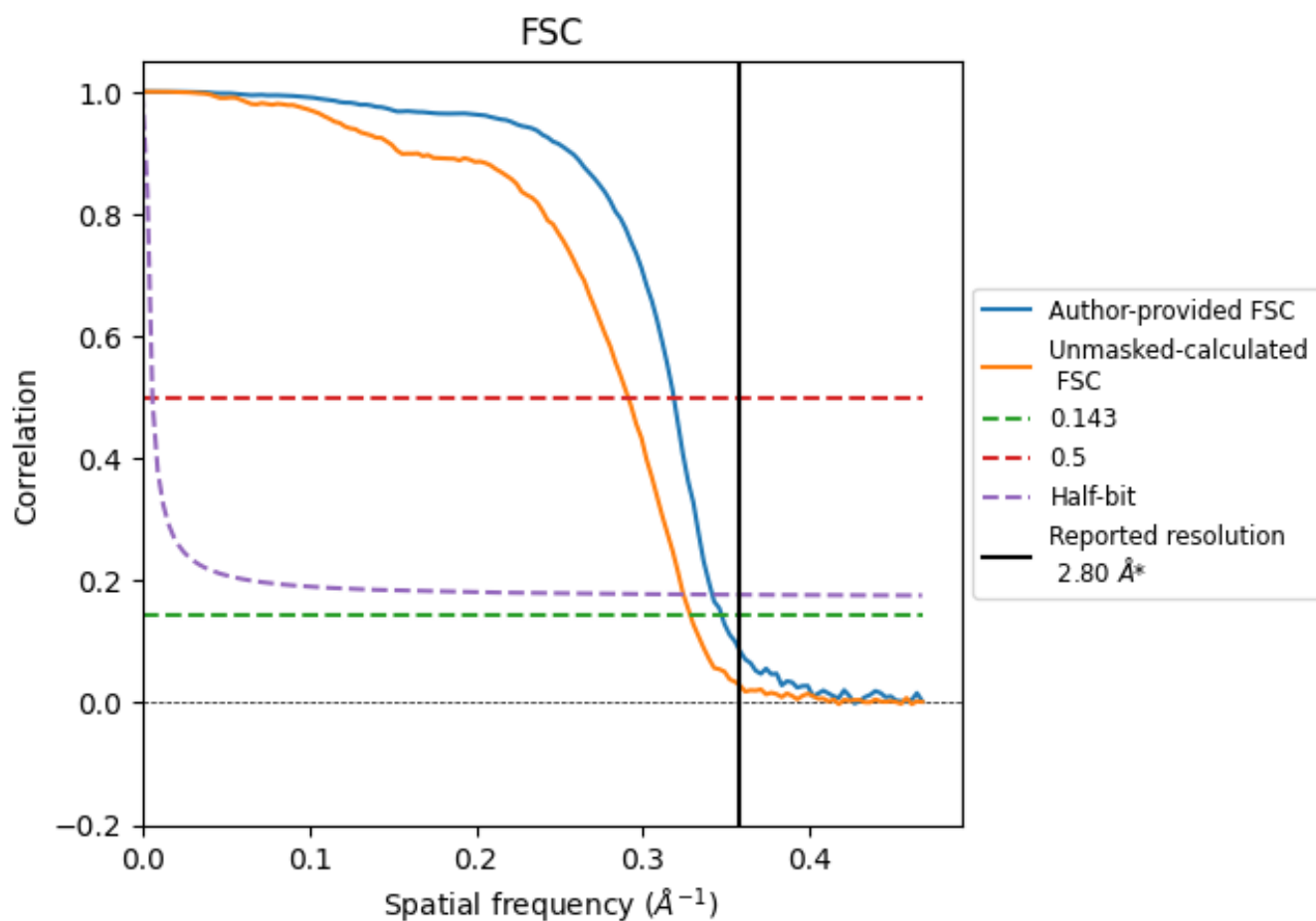


*Reported resolution corresponds to spatial frequency of 0.357 \AA^{-1}

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

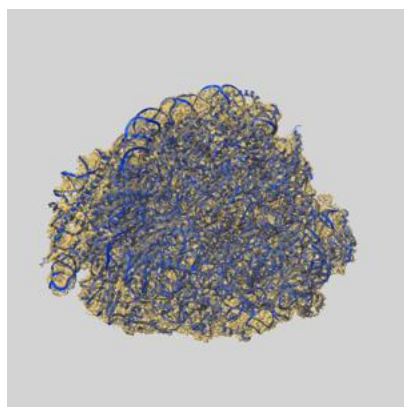
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.88	3.14	2.93
Unmasked-calculated*	3.05	3.44	3.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

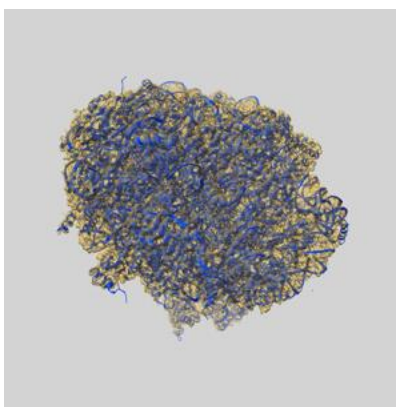
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64694 and PDB model 9V1I. Per-residue inclusion information can be found in section 3 on page 12.

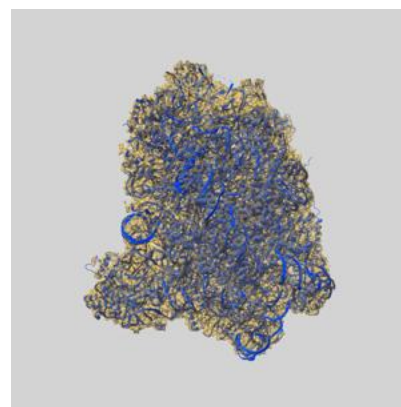
9.1 Map-model overlay [i](#)



X



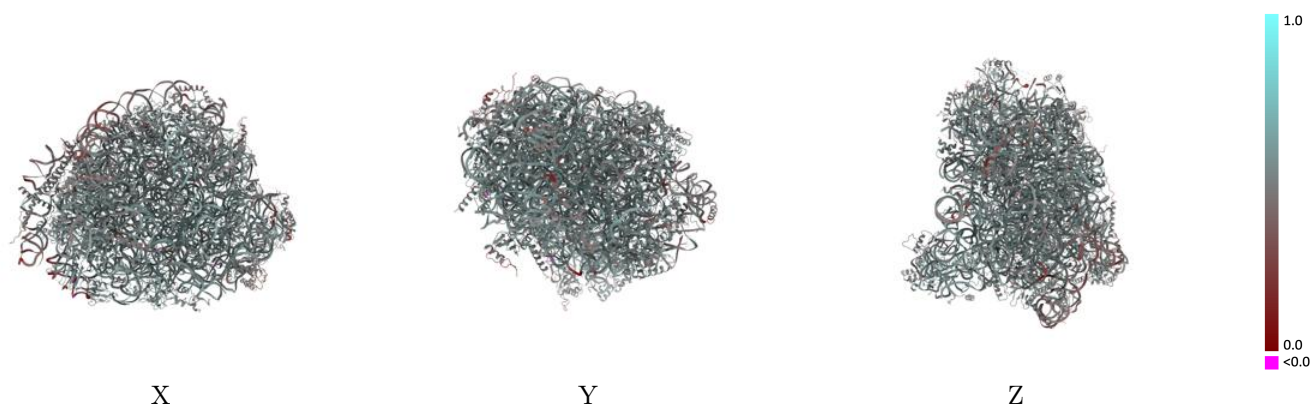
Y



Z

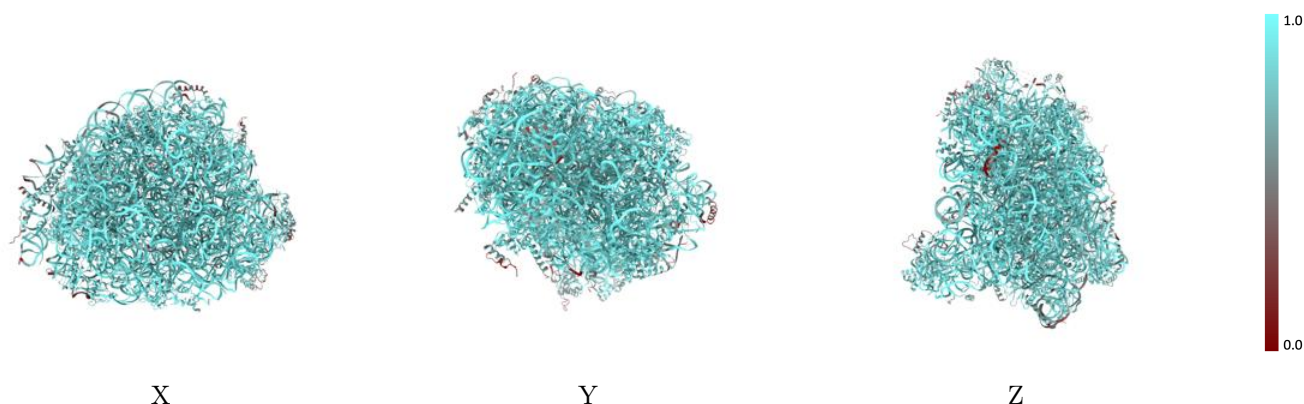
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



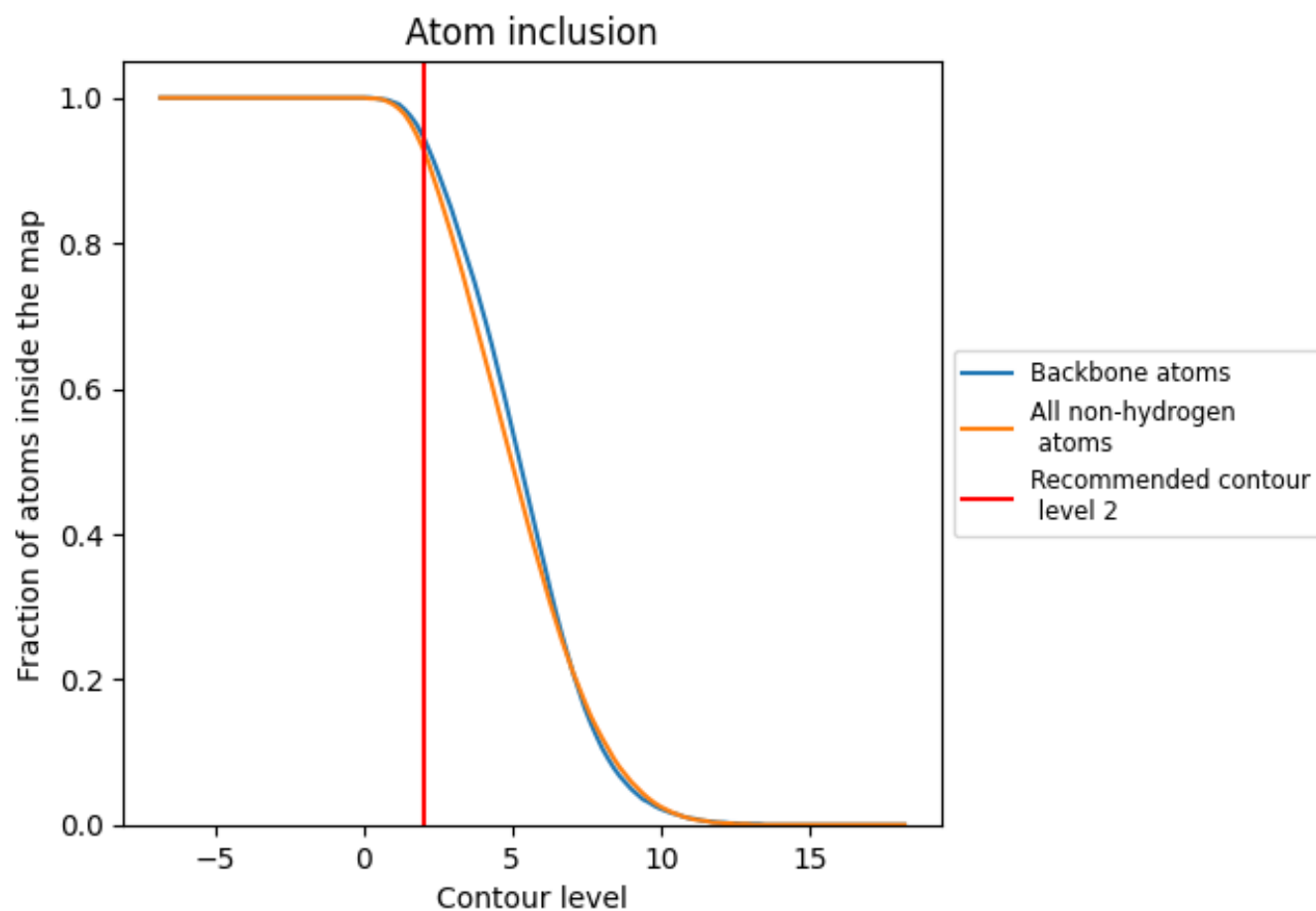
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9300	 0.5260
1A	 0.9560	 0.5250
1B	 0.9860	 0.5280
1C	 0.9780	 0.5440
1D	 0.9510	 0.5560
1E	 0.9400	 0.5500
1F	 0.8800	 0.5260
1G	 0.8320	 0.5270
1H	 0.8100	 0.4890
1I	 0.9320	 0.5320
1J	 0.7750	 0.4870
1K	 0.8960	 0.5420
1L	 0.9260	 0.5460
1M	 0.6820	 0.4760
1N	 0.8290	 0.5040
1O	 0.9300	 0.5480
1P	 0.9200	 0.5450
1Q	 0.9770	 0.5550
1R	 0.9400	 0.5380
1S	 0.9610	 0.5370
1T	 0.9600	 0.5540
1U	 0.9070	 0.5310
1V	 0.9320	 0.5550
1W	 0.6540	 0.3900
1X	 0.9460	 0.5520
1Y	 0.9080	 0.5220
1Z	 0.8870	 0.5390
1a	 0.8830	 0.5060
1b	 0.7920	 0.5080
1c	 0.9590	 0.5530
1d	 0.9470	 0.5490
1e	 0.7280	 0.4770
1f	 0.7940	 0.4830
1g	 0.9210	 0.5230
1h	 0.9280	 0.5330



Continued on next page...

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Chain	Atom inclusion	Q-score
li	 0.8940	 0.5120
lj	 0.9770	 0.5530
lk	 0.9190	 0.5270
ll	 0.9840	 0.5480
lm	 0.8920	 0.5380
ln	 0.7550	 0.4650
lo	 0.9830	 0.5380
lp	 0.9060	 0.5340
lq	 0.9610	 0.5560
lr	 0.9540	 0.5150