



wwPDB EM Validation Summary Report ⓘ

Apr 5, 2026 – 11:24 PM UTC

PDB ID : 9T1H / pdb_00009t1h
EMDB ID : EMD-55435
Title : E. coli 70S ribosome from delta-RlmE strain, PTC class 7
Authors : Larsson, D.S.D.; Selmer, M.
Deposited on : 2025-10-21
Resolution : 2.33 Å (reported)
Based on initial model : 9SYH

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:

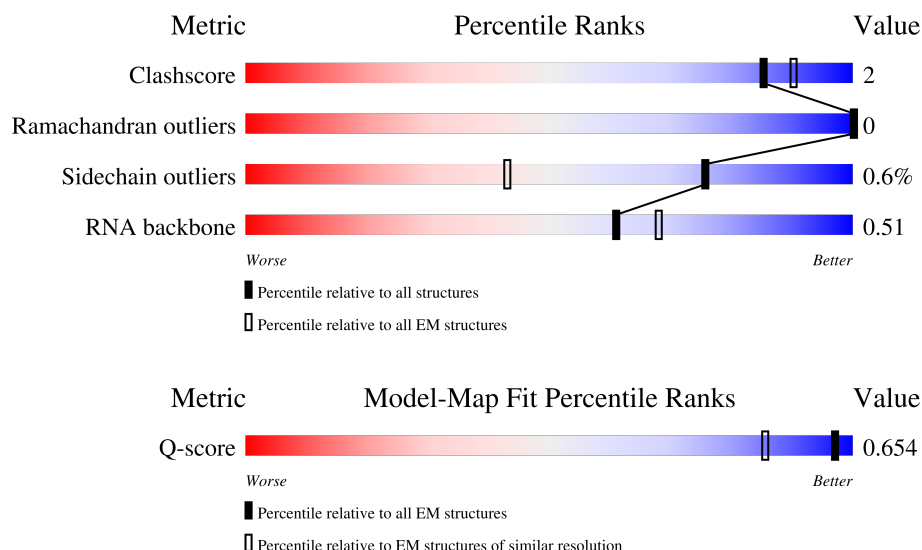
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 2.33 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.



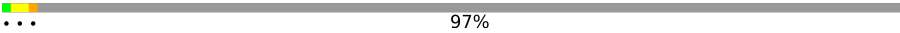
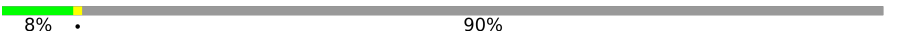


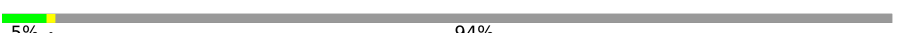






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4434 (1.83 - 2.83)

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	Y	76	
2	Z	77	
3	a	2904	

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Mol	Chain	Length	Quality of chain
4	b	120	 97%
5	c	273	 90%
6	d	209	 79%
7	e	201	 89%
8	i	142	 94%
9	k	144	 82%
10	l	136	 65%
11	q	103	 93%
12	r	110	 94%
13	v	85	 88%
14	z	57	 86%

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 15256 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 tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Y	12	Total	C	N	O	P	0	0
			257	114	48	83	12		

- Molecule 2 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Z	18	Total	C	N	O	P	0	0
			384	171	72	123	18		

- Molecule 3 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	a	596	Total	C	N	O	P	0	0
			12772	5710	2332	4134	596		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	b	4	Total	C	N	O	P	0	0
			80	36	10	30	4		

- Molecule 5 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	26	Total	C	N	O	S	0	0
			191	116	41	33	1		

- Molecule 6 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	d	43	Total	C	N	O	S	0	0
			333	206	68	58	1		

- Molecule 7 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	e	23	Total	C	N	O	0	0
			182	115	39	28		

- Molecule 8 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	i	8	Total	C	N	O	0	0
			55	34	12	9		

- Molecule 9 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	k	26	Total	C	N	O	S	0	0
			182	106	42	33	1		

- Molecule 10 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	l	48	Total	C	N	O	S	0	0
			386	242	81	60	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	82	MS6	MET	conflict	UNP A7ZSK2

- Molecule 11 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	q	7	Total	C	N	O	0	0
			75	48	19	8		

- Molecule 12 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	r	7	Total	C	N	O	0	0
			53	30	14	9		

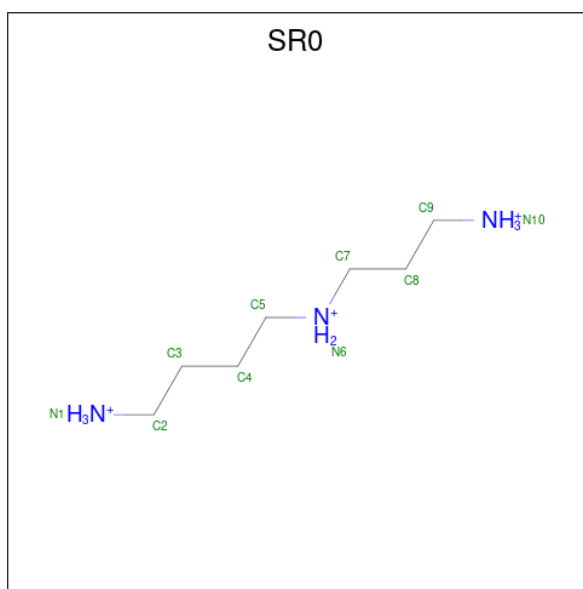
- Molecule 13 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	v	10	Total	C	N	O	0	0
			74	39	17	18		

- Molecule 14 is a protein called Large ribosomal subunit protein bL32.

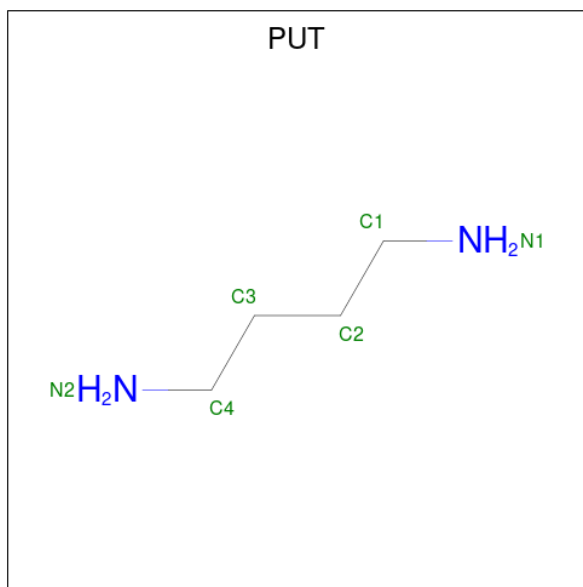
Mol	Chain	Residues	Atoms				AltConf	Trace
14	z	8	Total	C	N	O	0	0
			61	37	12	12		

- Molecule 15 is N 1 -(3-azaniumylpropyl)butane-1,4-diaminium (CCD ID: SR0) (formula: $C_7H_{22}N_3$).



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

- Molecule 16 is 1,4-DIAMINOBTUTANE (CCD ID: PUT) (formula: $C_4H_{12}N_2$).



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

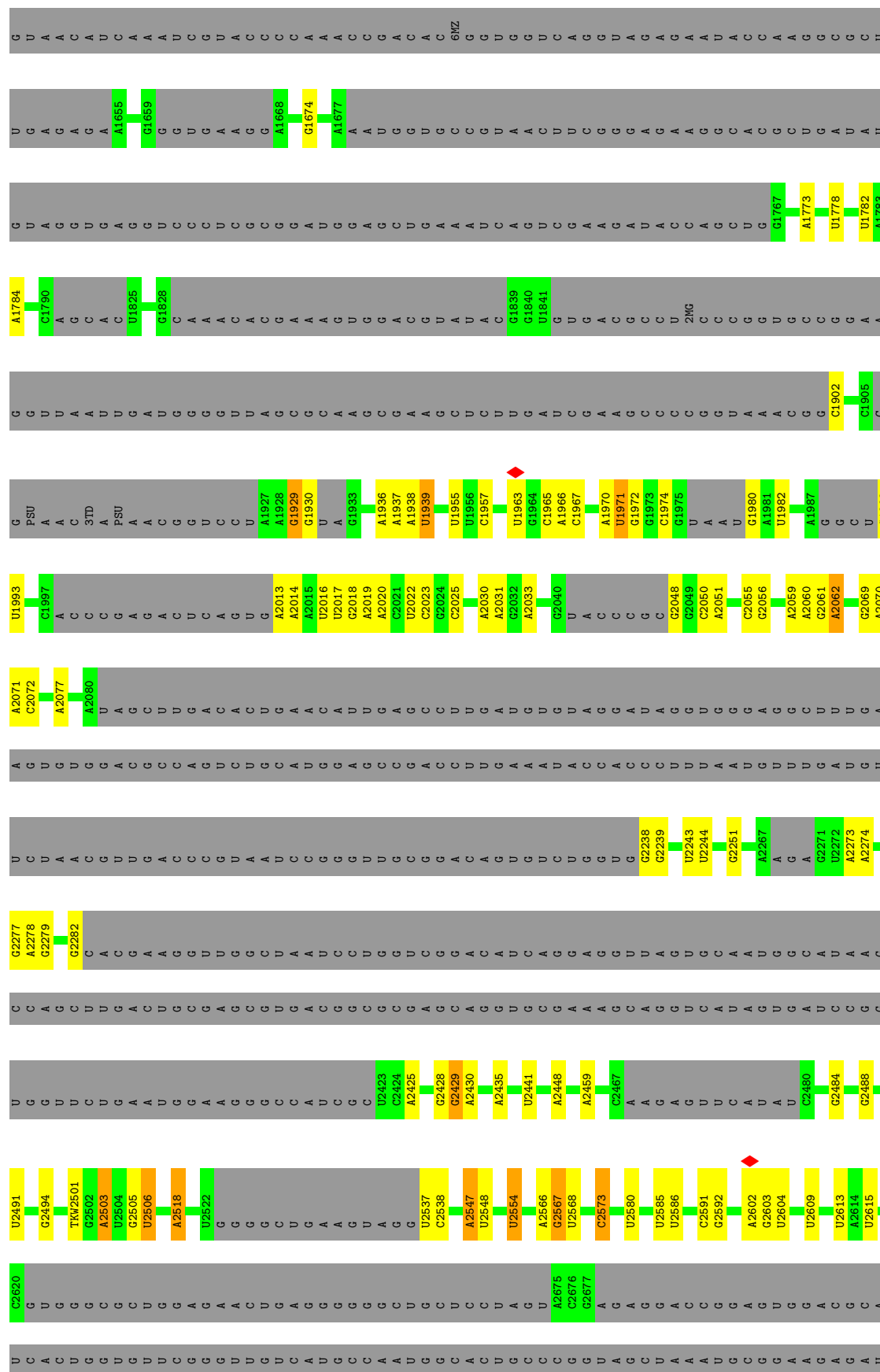
- Molecule 17 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
17	a	100	Total	Mg	0
			100	100	
17	d	1	Total	Mg	0
			1	1	
17	v	1	Total	Mg	0
			1	1	

- Molecule 18 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
18	a	42	Total	K	0
			42	42	
18	e	1	Total	K	0
			1	1	

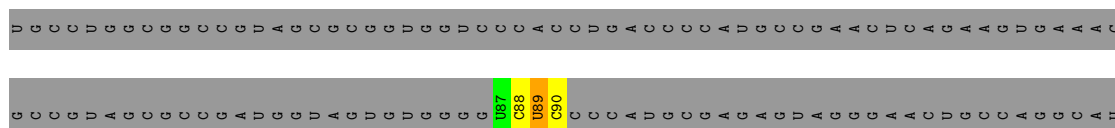






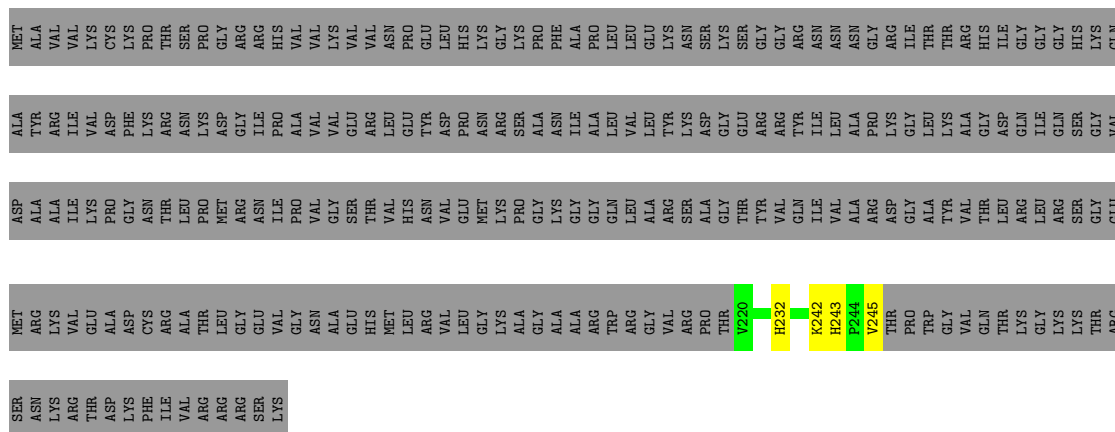
- Molecule 4: 5S rRNA

Chain b: ... 97%



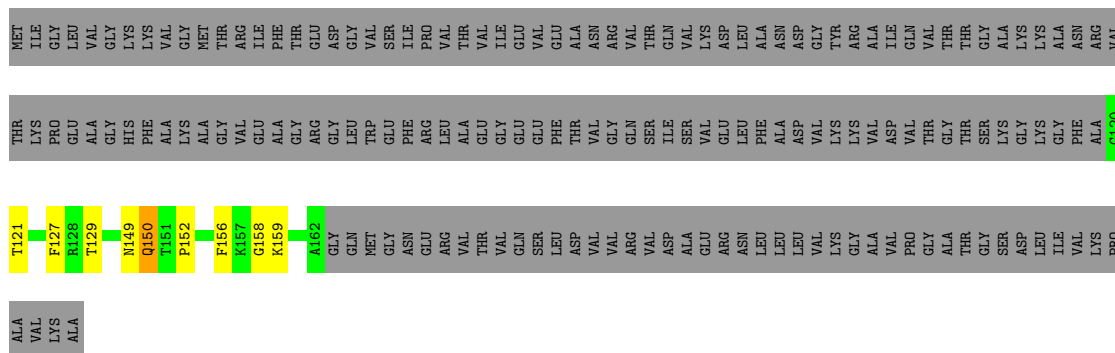
- Molecule 5: Large ribosomal subunit protein uL2

Chain c:  8% 90%



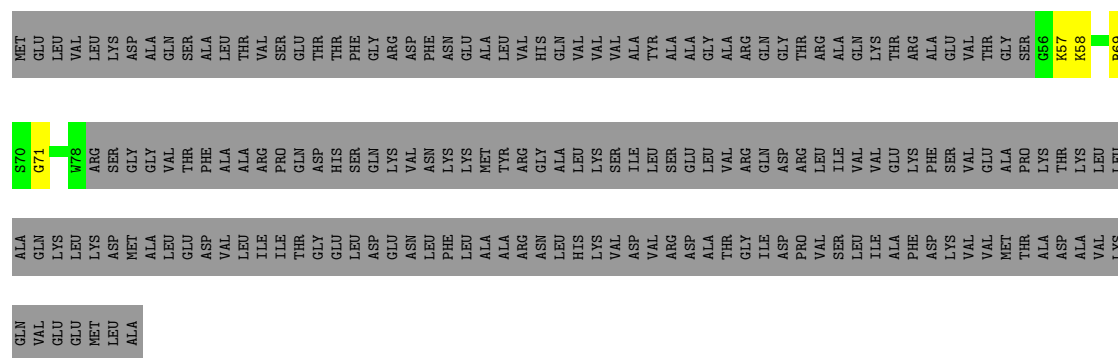
- Molecule 6: Large ribosomal subunit protein uL3

Chain d: 16% 79%

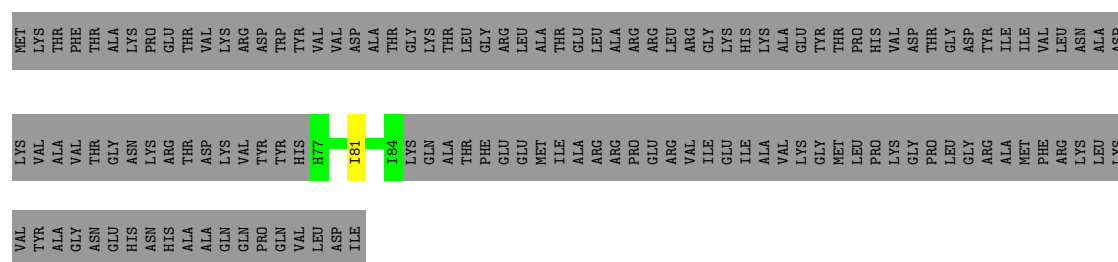


- Molecule 7: Large ribosomal subunit protein uL4

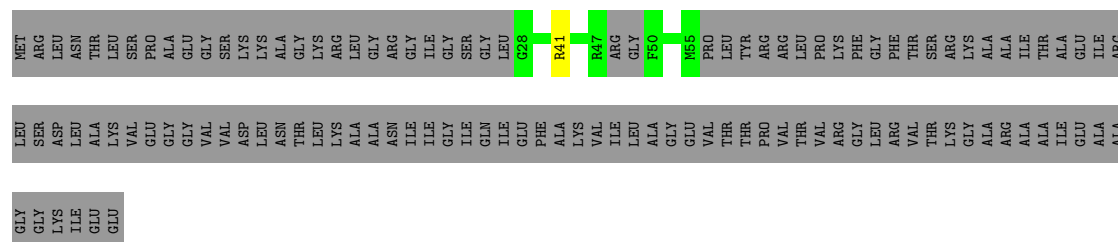
Chain e:  9% . 89%



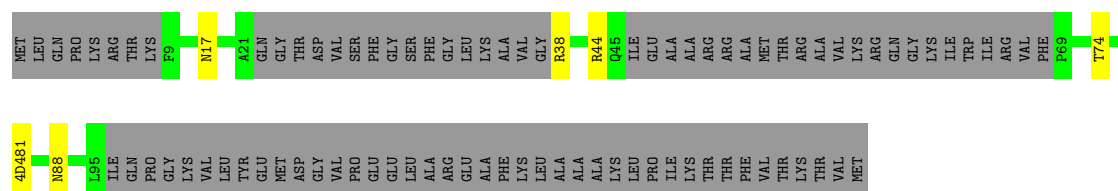
- Molecule 8: Large ribosomal subunit protein uL13



- Molecule 9: Large ribosomal subunit protein uL15



- Molecule 10: Large ribosomal subunit protein uL16



- Molecule 11: Large ribosomal subunit protein bL21



MET TYR ALA VAL PHE GLN SER GLY LYS LYS HIS ARG VAL SER GLU GLY GLN THR VAL ARG LYS LEU GLU LYS LEU ASP ILE THR GLY THR VAL GLU PHE THR ALA GLY VAL LEU MET ILE ALA ASN GLY GLU VAL LYS ILE GLY VAL PRO PHE VAL ASP GLY GLY VAL ILE LYS

ALA GLU VAL VAL ALA HIS GLY ARG GLY LYS LYS VAL VAL ILE VAL SER LYS F77 Y43 ARG LYS LYS GLN GLU GLY HIS ARG GLN TRP PHE THR ASP VAL LYS ILE THR PHE GLY ILE SER ALA

- Molecule 12: Large ribosomal subunit protein uL22

Chain r: 6% 94%

MET GLU THR ILE ALA LYS HIS ARG LYS LYS THR SER SER ALA GLN LYS VAL ARG LEU VAL VAL ASP MET LYS LEU ILE ARG ILE GLY LYS VAL SER GLN ALA LEU LYS THR TYR THR ASN LYS LYS ALA VAL LEU VAL LYS VAL LYS VAL LEU SER SER ILE ALA ASN ALA GLU HIS

ASN ASP GLY ALA ASP ASP ASP LEU LYS LYS THR THR ILE PHE VAL VAL ASP GLU GLY PRO ARG MET LYS ARG ILE MET PRO R88 D94 ARG ILE LEU LYS ARG THR SER HIS ILE THR VAL VAL VAL SER ASP ARG

- Molecule 13: Large ribosomal subunit protein bL27

Chain v: 12% 88%

MET ALA HIS LYS LYS ALA GLY G8 S9 E7 ALA LYS ARG ARG LEU GLY VAL LYS ARG ARG PHE GLY GLY GLU THR VAL LEU ALA GLY SER ILE VAL ARG GLN ARG GLY THR LYS PHE HIS ALA GLY ALA ASN VAL GLY CYS ARG ASP HIS THR LEU PHE ALA LYS ALA ASP GLY LYS

VAL LYS PHE GLU VAL LYS GLY PRO ASN ARG LYS PHE ILE SER ILE LEU GLU ALA GLU

- Molecule 14: Large ribosomal subunit protein bL32

Chain z: 9% 5% 86%

MET A2 V3 Q5 T9 ARG SER LYS LYS GLY MET ARG ARG SER HIS ASP ALA LEU THR THR VAL THR SER LEU SER VAL ASP LYS THR SER GLY GLU LYS HIS LEU ARG HIS HIS ILE THR ALA ASP GLY TYR TYR ARG GLY ARG LYS VAL ILE ALA LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51232	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 ($e^-/\text{\AA}^2$)	42.1	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.503	Depositor
Minimum map value	-0.135	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	421.2736, 421.2736, 421.2736	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8228, 0.8228, 0.8228	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, PUT, K, OMC, 4D4, TKW, 1MG, H2U, G7M, 6MZ, MEQ, 2MA, 2MG, PSU, OMG, MS6, MG, 5MC, SR0

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	Y	0.61	0/285	0.93	0/438
2	Z	0.57	0/427	0.84	0/661
3	a	0.55	0/13812	1.05	44/21450 (0.2%)
4	b	0.55	0/87	1.11	0/132
5	c	0.73	0/197	1.02	0/265
6	d	0.70	0/329	1.11	1/438 (0.2%)
7	e	0.67	0/187	0.96	0/248
8	i	0.70	0/56	1.07	0/74
9	k	0.72	0/182	1.13	0/232
10	l	0.66	0/370	0.99	0/487
11	q	0.79	0/77	1.13	0/99
12	r	0.75	0/52	0.95	0/66
13	v	0.70	0/73	1.06	0/95
14	z	0.70	0/61	1.10	1/82 (1.2%)
All	All	0.56	0/16195	1.05	46/24767 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	k	0	1
10	l	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	a	1132	U	O3'-P-O5'	-19.43	74.85	104.00
3	a	980	A	O3'-P-O5'	-12.70	84.95	104.00
3	a	1971	U	O3'-P-O5'	-10.67	87.99	104.00
3	a	980	A	C4'-C3'-O3'	8.80	126.20	113.00
3	a	781	A	O3'-P-O5'	-8.24	91.63	104.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	k	41	ARG	Sidechain
10	l	44	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Y	257	0	134	7	0
2	Z	384	0	200	2	0
3	a	12772	0	6468	34	0
4	b	80	0	43	1	0
5	c	191	0	177	2	0
6	d	333	0	336	5	0
7	e	182	0	193	2	0
8	i	55	0	51	1	0
9	k	182	0	179	0	0
10	l	386	0	399	2	0
11	q	75	0	76	0	0
12	r	53	0	55	0	0
13	v	74	0	64	0	0
14	z	61	0	62	3	0
15	a	20	0	0	0	0
16	a	6	0	12	0	0
17	a	100	0	0	0	0
17	d	1	0	0	0	0
17	v	1	0	0	0	0
18	a	42	0	0	0	0
18	e	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	15256	0	8449	50	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 2.

The worst 5 of 50 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:a:568:U:H1'	3:a:2030:6MZ:H9C1	1.62	0.80
7:e:58:LYS:HG3	7:e:71:GLY:HA2	1.77	0.65
10:l:17:ASN:O	10:l:38:ARG:HD3	1.96	0.65
1:Y:74:C:H5	3:a:2554:U:H3	1.47	0.62
3:a:1027:A:C2	3:a:2488:G:H5'	2.35	0.62

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	
5	c	24/273 (9%)	23 (96%)	1 (4%)	0	100	100
6	d	40/209 (19%)	36 (90%)	4 (10%)	0	100	100
7	e	21/201 (10%)	20 (95%)	1 (5%)	0	100	100
8	i	6/142 (4%)	6 (100%)	0	0	100	100
9	k	22/144 (15%)	19 (86%)	3 (14%)	0	100	100
10	l	40/136 (29%)	39 (98%)	1 (2%)	0	100	100
11	q	5/103 (5%)	5 (100%)	0	0	100	100
12	r	5/110 (4%)	5 (100%)	0	0	100	100
13	v	8/85 (9%)	6 (75%)	2 (25%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	z	6/57 (10%)	6 (100%)	0	0	100	100
All	All	177/1460 (12%)	165 (93%)	12 (7%)	0	100	100

There are no Ramachandran outliers to report.

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	
5	c	19/218 (9%)	19 (100%)	0	100	100
6	d	34/163 (21%)	34 (100%)	0	100	100
7	e	18/165 (11%)	17 (94%)	1 (6%)	19	23
8	i	5/116 (4%)	5 (100%)	0	100	100
9	k	16/103 (16%)	16 (100%)	0	100	100
10	l	36/107 (34%)	36 (100%)	0	100	100
11	q	7/84 (8%)	7 (100%)	0	100	100
12	r	4/93 (4%)	4 (100%)	0	100	100
13	v	8/63 (13%)	8 (100%)	0	100	100
14	z	7/48 (15%)	7 (100%)	0	100	100
All	All	154/1160 (13%)	153 (99%)	1 (1%)	76	86

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	e	57	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
9	k	54	GLN
14	z	6	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Y	10/76 (13%)	6 (60%)	1 (10%)
2	Z	16/77 (20%)	5 (31%)	0
3	a	559/2904 (19%)	83 (14%)	0
4	b	3/120 (2%)	3 (100%)	0
All	All	588/3177 (18%)	97 (16%)	1 (0%)

5 of 97 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Y	70	G
1	Y	71	G
1	Y	72	C
1	Y	73	A
1	Y	74	C

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	Y	71	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	5MU	a	747	3	19,22,23	0.30	0	27,32,35	0.50	0
3	PSU	a	2604	3	18,21,22	0.38	0	21,30,33	0.46	0
3	PSU	a	2580	3	18,21,22	0.41	0	21,30,33	0.75	1 (4%)
3	PSU	a	2504	3,18	18,21,22	0.24	0	21,30,33	0.39	0
3	H2U	a	2449	3	18,21,22	0.43	0	19,30,33	0.33	0
3	1MG	a	745	3	23,26,27	0.62	0	33,39,42	0.57	1 (3%)
6	MEQ	d	150	6	8,9,10	0.68	0	5,10,12	1.25	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	6MZ	a	2030	3	22,25,26	0.28	0	29,36,39	0.39	0
3	5MU	a	1939	3,18	19,22,23	0.53	0	27,32,35	0.78	1 (3%)
3	OMC	a	2498	3,17	19,22,23	0.27	0	25,31,34	0.36	0
3	TKW	a	2501	3,18	19,22,23	0.43	0	26,32,35	0.71	1 (3%)
3	PSU	a	955	3	18,21,22	0.40	0	21,30,33	0.37	0
3	PSU	a	2605	3	18,21,22	0.30	0	21,30,33	0.51	0
3	5MC	a	1962	3,18	19,22,23	0.31	0	26,32,35	0.34	0
3	G7M	a	2069	3,18	23,26,27	0.41	0	34,39,42	0.53	0
3	PSU	a	2457	3	18,21,22	0.33	0	21,30,33	0.37	0
3	2MG	a	2445	3	23,26,27	0.42	0	33,38,41	0.32	0
3	PSU	a	746	3,17	18,21,22	0.35	0	21,30,33	0.40	0
3	2MA	a	2503	3,17,18	22,25,26	1.02	1 (4%)	32,37,40	1.25	3 (9%)
3	OMG	a	2251	3,2,18	23,26,27	0.38	0	32,38,41	0.25	0
10	MS6	l	82	10	5,7,8	0.28	0	2,7,9	0.03	0
10	4D4	l	81	10	9,11,12	0.89	0	7,13,15	1.22	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	5MU	a	747	3	-	0/7/25/26	0/2/2/2
3	PSU	a	2604	3	-	0/7/25/26	0/2/2/2
3	PSU	a	2580	3	-	0/7/25/26	0/2/2/2
3	PSU	a	2504	3,18	-	1/7/25/26	0/2/2/2
3	H2U	a	2449	3	-	0/7/38/39	0/2/2/2
3	1MG	a	745	3	-	0/7/25/26	0/3/3/3
6	MEQ	d	150	6	-	3/8/9/11	-
3	6MZ	a	2030	3	-	2/9/27/28	0/3/3/3
3	5MU	a	1939	3,18	-	0/7/25/26	0/2/2/2
3	OMC	a	2498	3,17	-	0/9/27/28	0/2/2/2
3	TKW	a	2501	3,18	-	4/7/25/26	0/2/2/2
3	PSU	a	955	3	-	0/7/25/26	0/2/2/2
3	PSU	a	2605	3	-	0/7/25/26	0/2/2/2
3	5MC	a	1962	3,18	-	0/7/25/26	0/2/2/2
3	G7M	a	2069	3,18	-	2/7/25/26	0/3/3/3
3	PSU	a	2457	3	-	0/7/25/26	0/2/2/2
3	2MG	a	2445	3	-	0/9/27/28	0/3/3/3
3	PSU	a	746	3,17	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	2MA	a	2503	3,17,18	-	3/7/25/26	0/3/3/3
3	OMG	a	2251	3,2,18	-	1/9/27/28	0/3/3/3
10	MS6	l	82	10	-	1/4/6/8	-
10	4D4	l	81	10	-	1/11/12/14	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	a	2503	2MA	C6-N6	-3.66	1.24	1.34

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	a	2503	2MA	N6-C6-N1	4.54	123.16	117.03
3	a	2503	2MA	C2-N1-C6	3.44	123.39	118.10
3	a	2503	2MA	C5-C6-N1	-3.38	113.64	118.90
3	a	1939	5MU	O3'-C3'-C2'	-3.11	101.86	111.82
3	a	2501	TKW	OAC-C5-C4	2.66	120.36	114.82

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	d	150	MEQ	C-CA-CB-CG
3	a	2251	OMG	C1'-C2'-O2'-CM2
6	d	150	MEQ	OE1-CD-CG-CB
6	d	150	MEQ	NE2-CD-CG-CB
3	a	2030	6MZ	O4'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	a	747	5MU	1	0
3	a	2604	PSU	1	0
6	d	150	MEQ	1	0
3	a	2030	6MZ	2	0
3	a	1939	5MU	1	0
3	a	2503	2MA	1	0
3	a	2251	OMG	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 148 ligands modelled in this entry, 145 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
15	SR0	a	3002	-	9,9,9	0.53	0	8,8,8	0.49	0
16	PUT	a	3003	-	5,5,5	0.28	0	4,4,4	0.29	0
15	SR0	a	3001	-	9,9,9	0.50	0	8,8,8	0.50	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	SR0	a	3002	-	-	3/7/7/7	-
16	PUT	a	3003	-	-	0/3/3/3	-
15	SR0	a	3001	-	-	2/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	a	3002	SR0	N6-C7-C8-C9
15	a	3002	SR0	C8-C7-N6-C5
15	a	3002	SR0	C2-C3-C4-C5
15	a	3001	SR0	C2-C3-C4-C5
15	a	3001	SR0	N1-C2-C3-C4

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

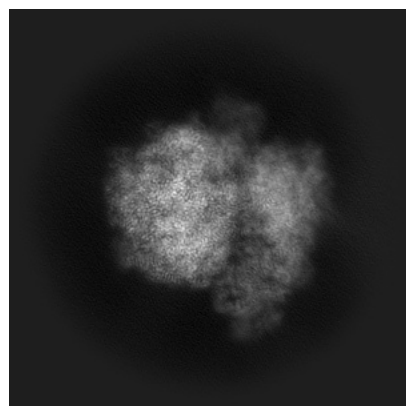
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55435. These allow visual inspection of the internal detail of the map and identification of artifacts.

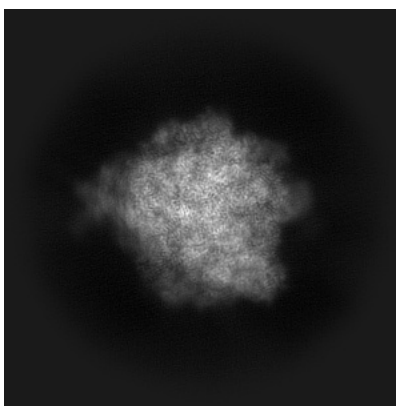
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

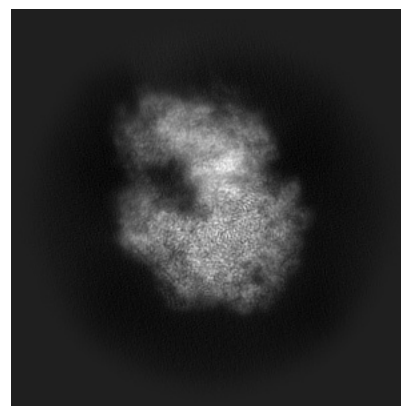
6.1.1 Primary map



X

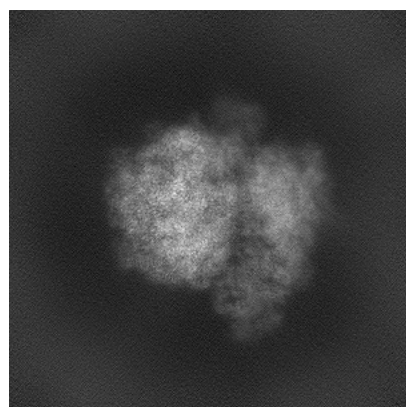


Y

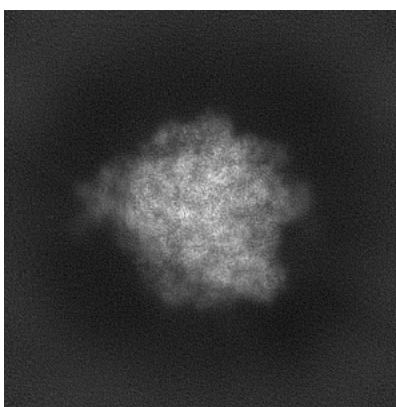


Z

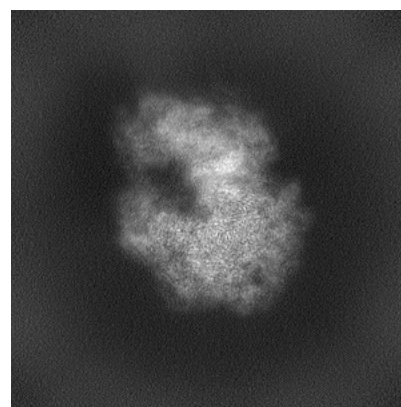
6.1.2 Raw map



X



Y

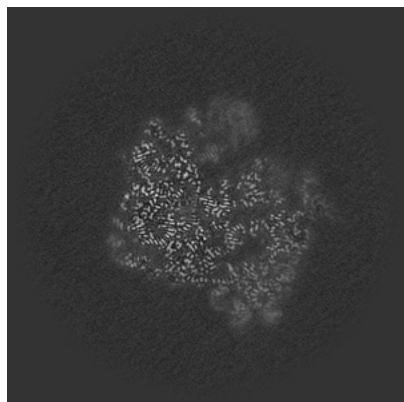


Z

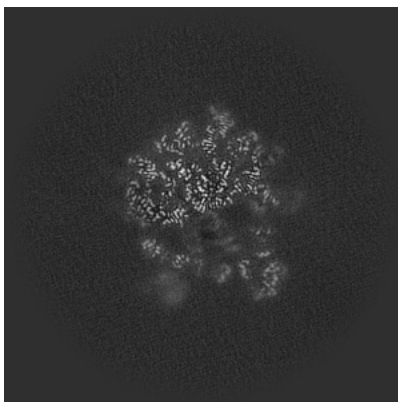
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

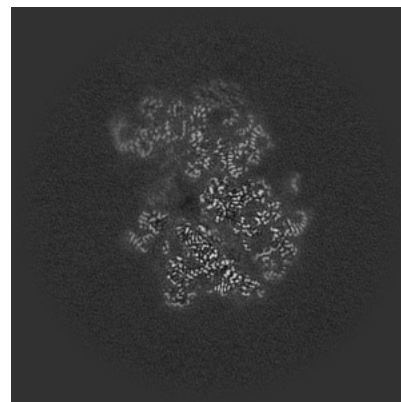
6.2.1 Primary map



X Index: 256

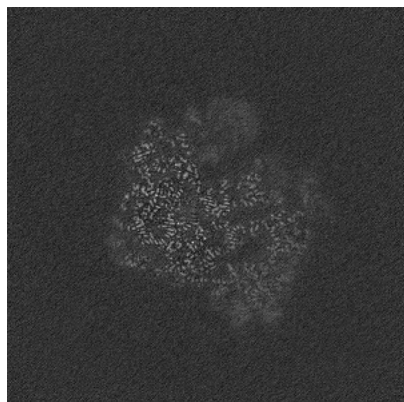


Y Index: 256

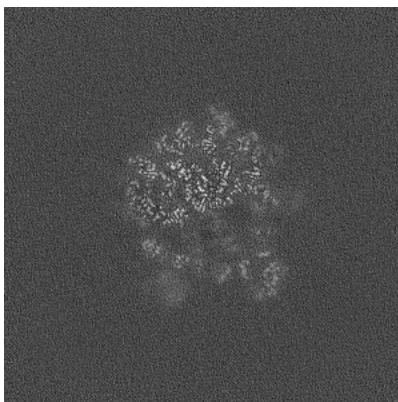


Z Index: 256

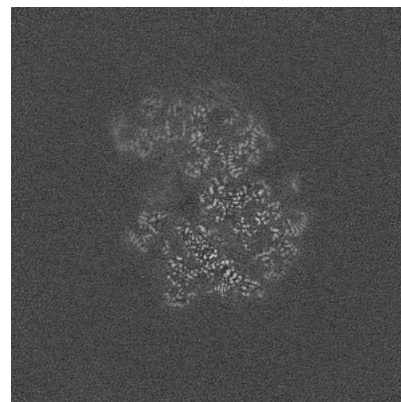
6.2.2 Raw map



X Index: 256



Y Index: 256

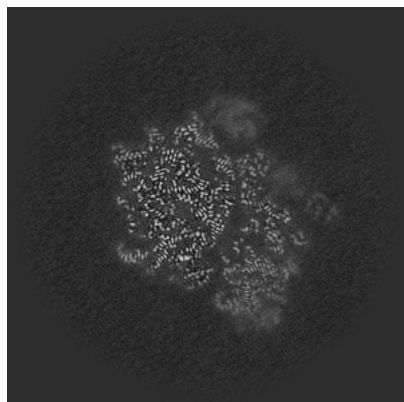


Z Index: 256

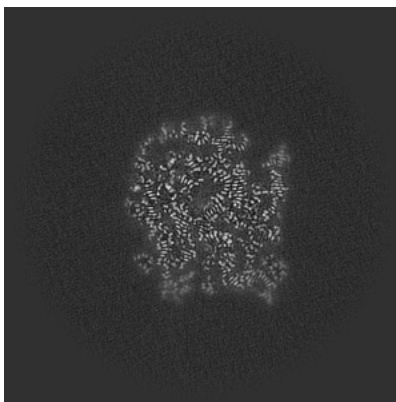
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

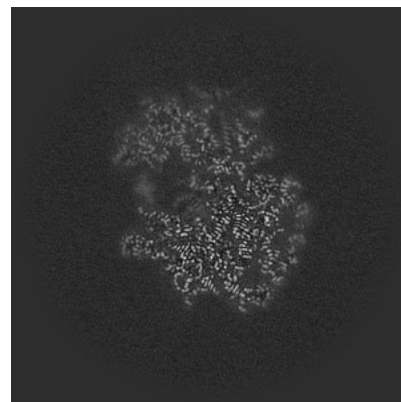
6.3.1 Primary map



X Index: 267

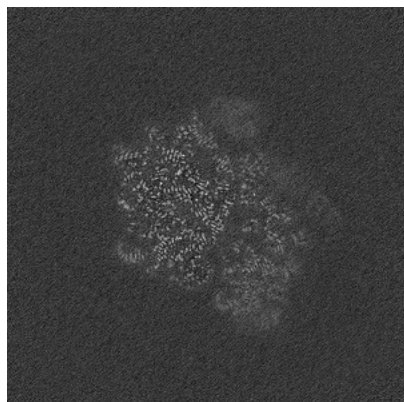


Y Index: 221

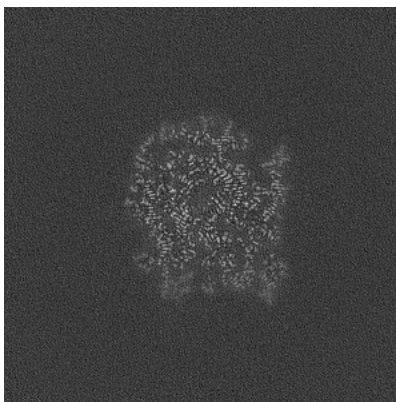


Z Index: 270

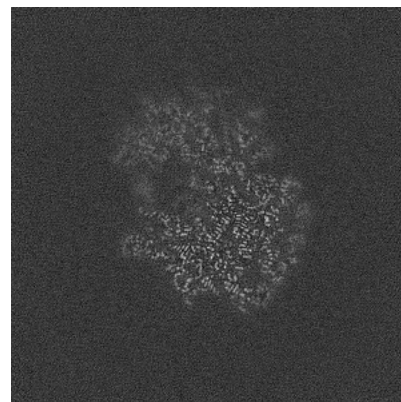
6.3.2 Raw map



X Index: 266



Y Index: 222

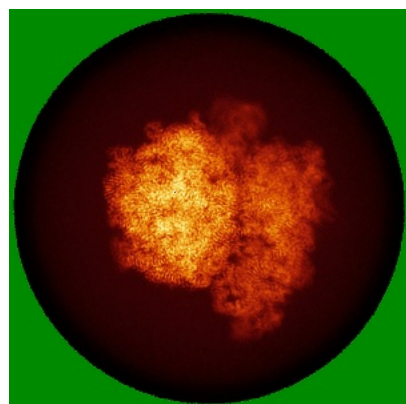


Z Index: 270

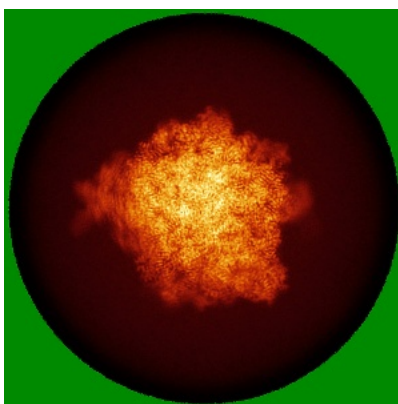
The images above show the largest variance slices of the map in three orthogonal directions.

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

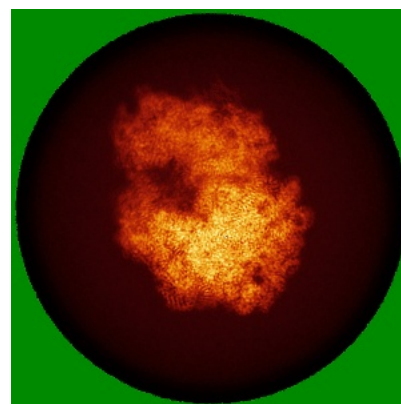
6.4.1 Primary map



X

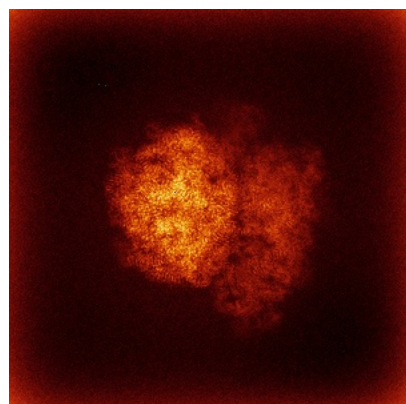


Y

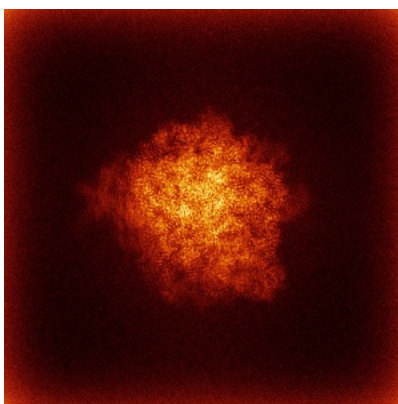


Z

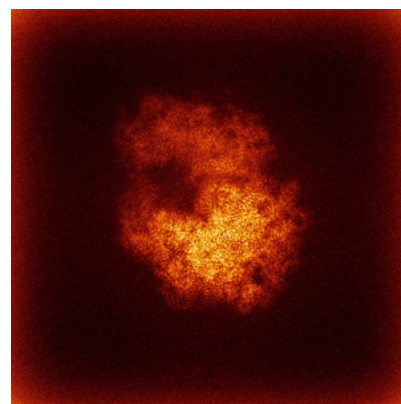
6.4.2 Raw map



X



Y

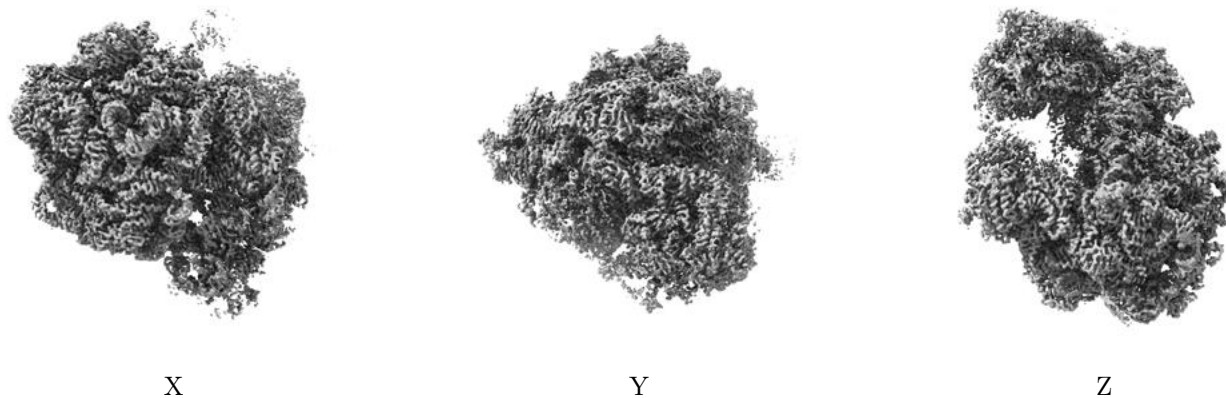


Z

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.

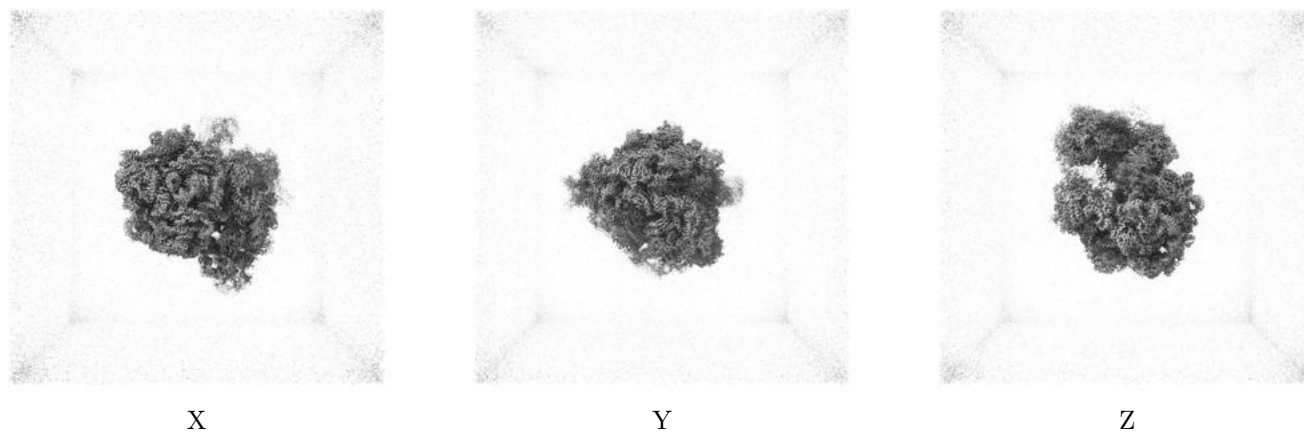
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.09. 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.

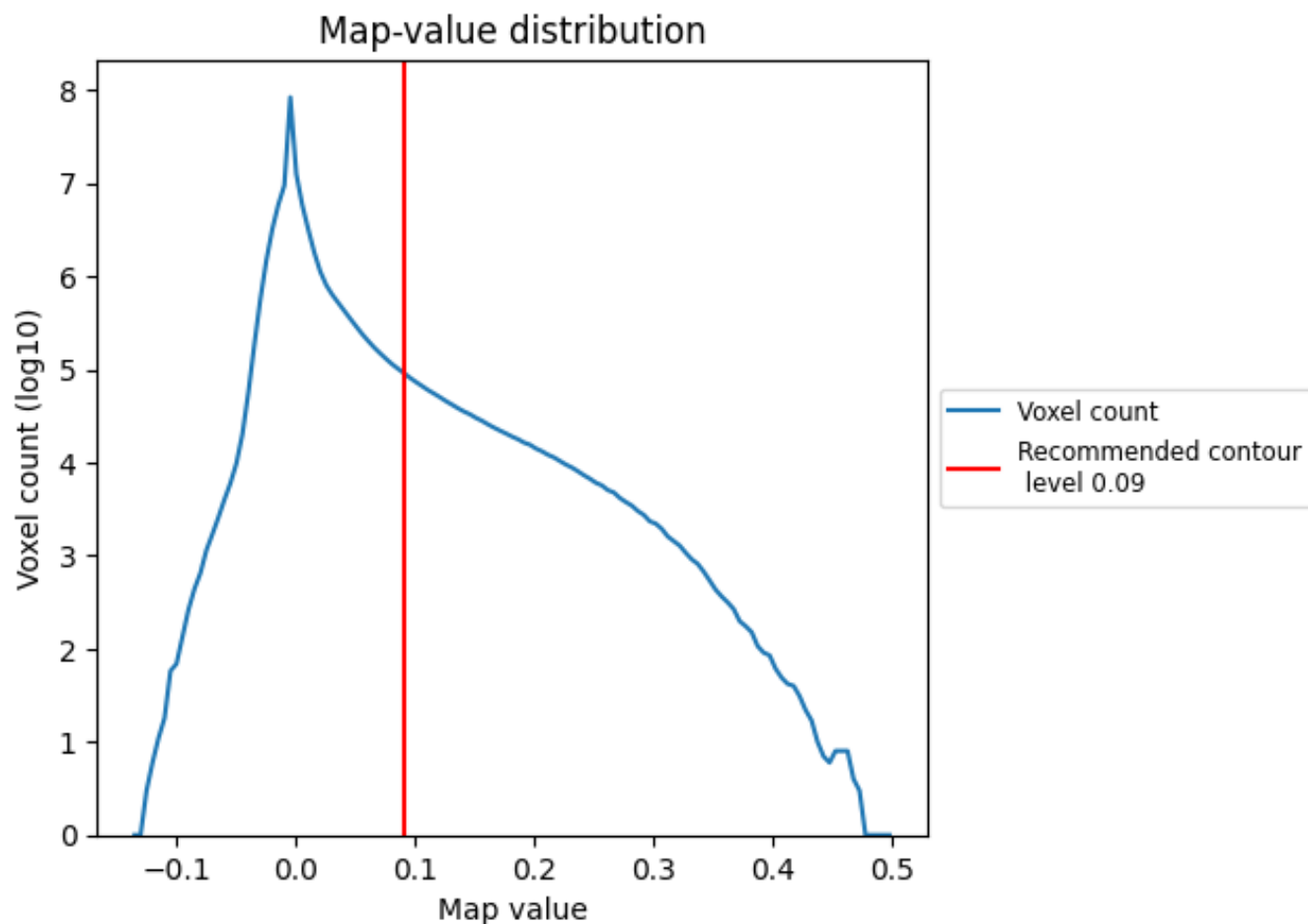
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

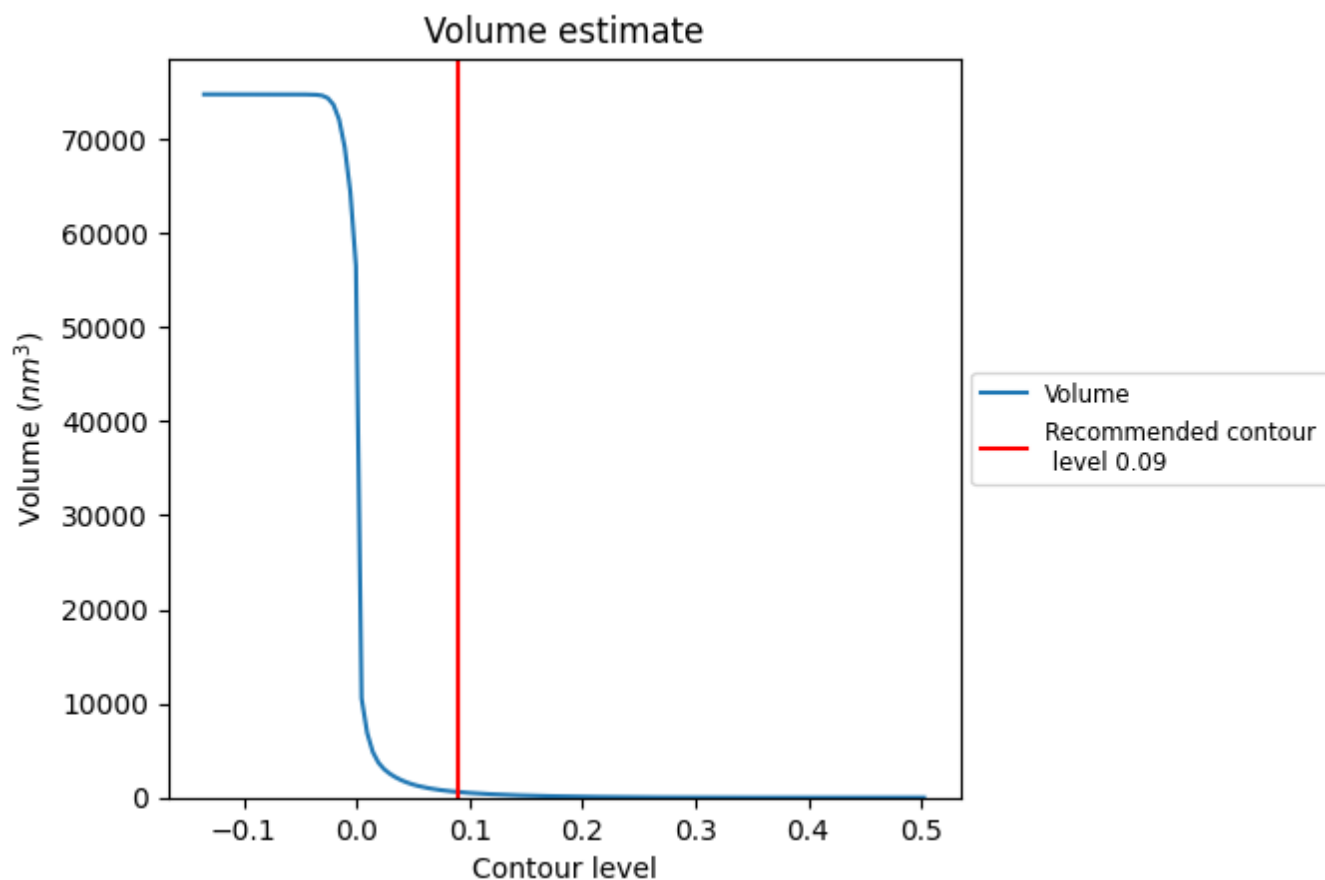
This section contains the results of statistical analysis of the map.

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.

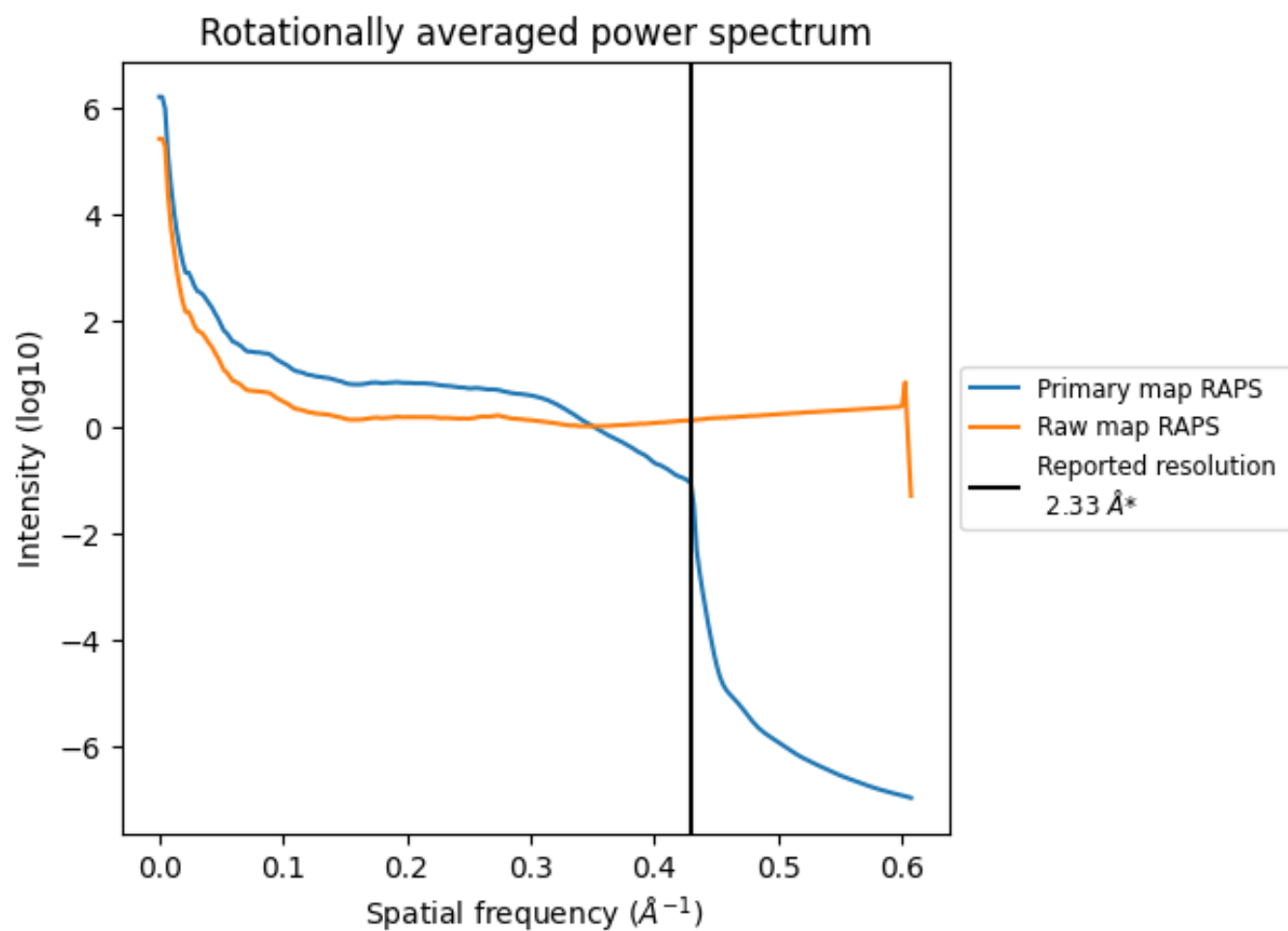
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 591 nm³; this corresponds to an approximate mass of 533 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 ⓘ

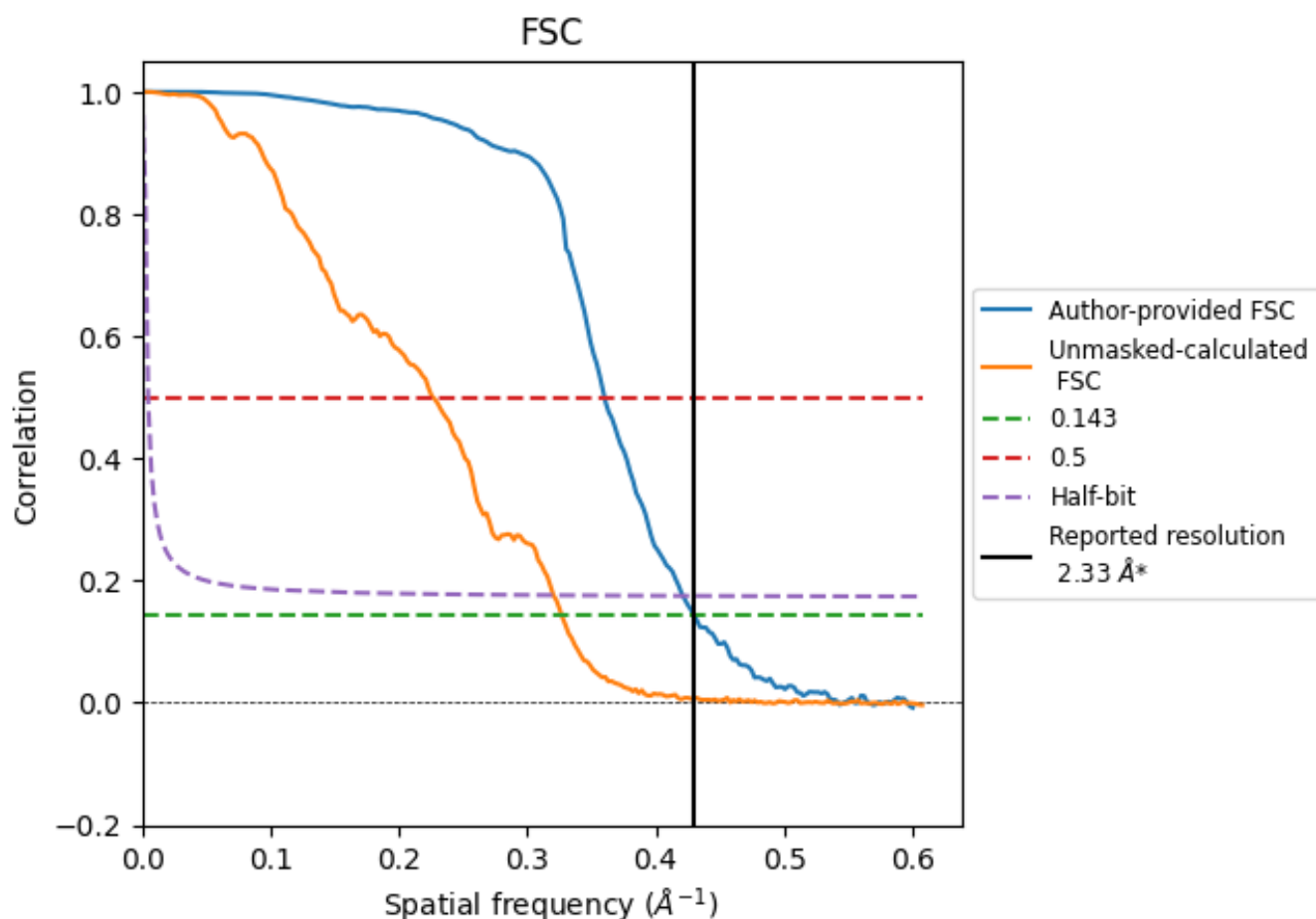


*Reported resolution corresponds to spatial frequency of 0.429 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.429 \AA^{-1}

8.2 Resolution estimates [i](#)

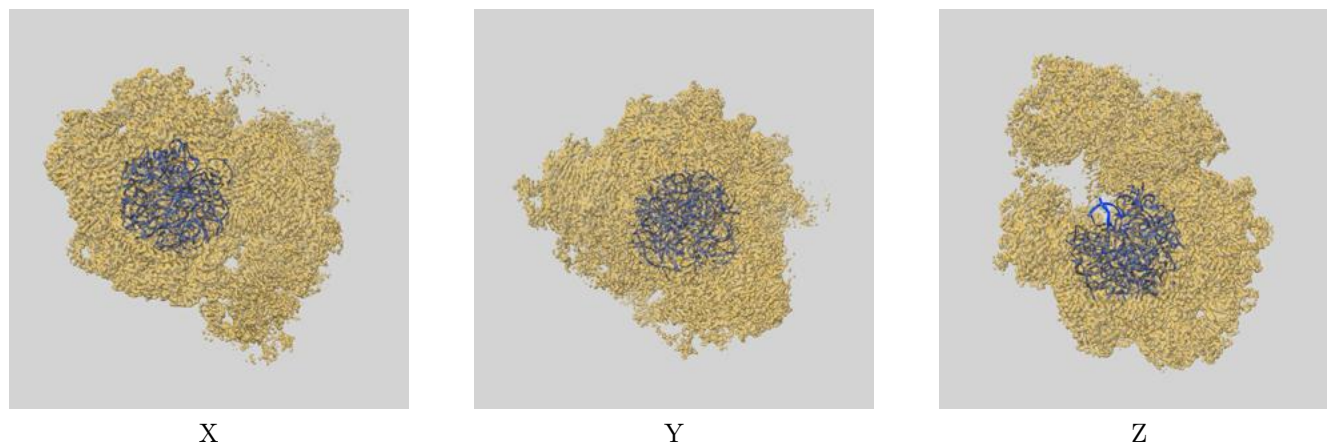
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.33	-	-
Author-provided FSC curve	2.33	2.78	2.37
Unmasked-calculated*	3.06	4.42	3.12

*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 3.06 differs from the reported value 2.33 by more than 10 %

9 Map-model fit [i](#)

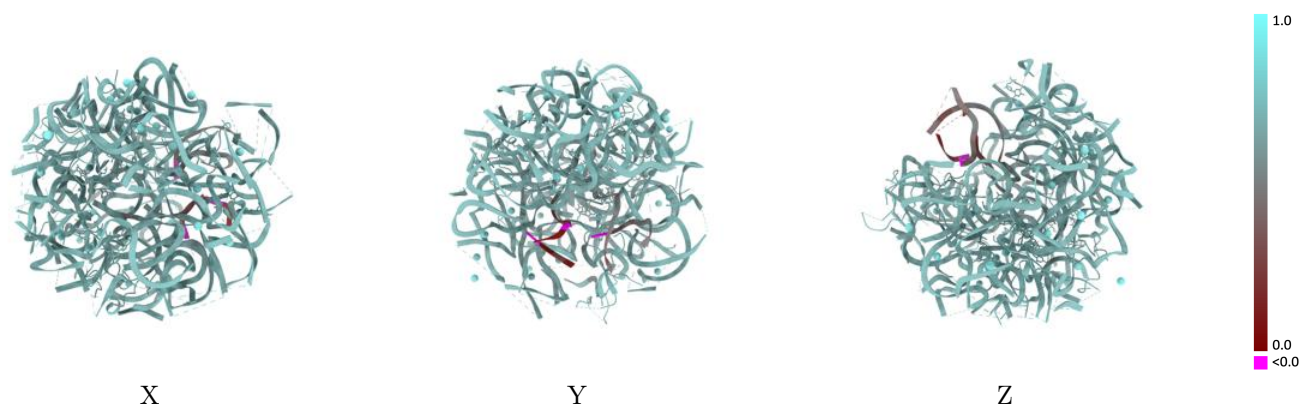
This section contains information regarding the fit between EMDB map EMD-55435 and PDB model 9T1H. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



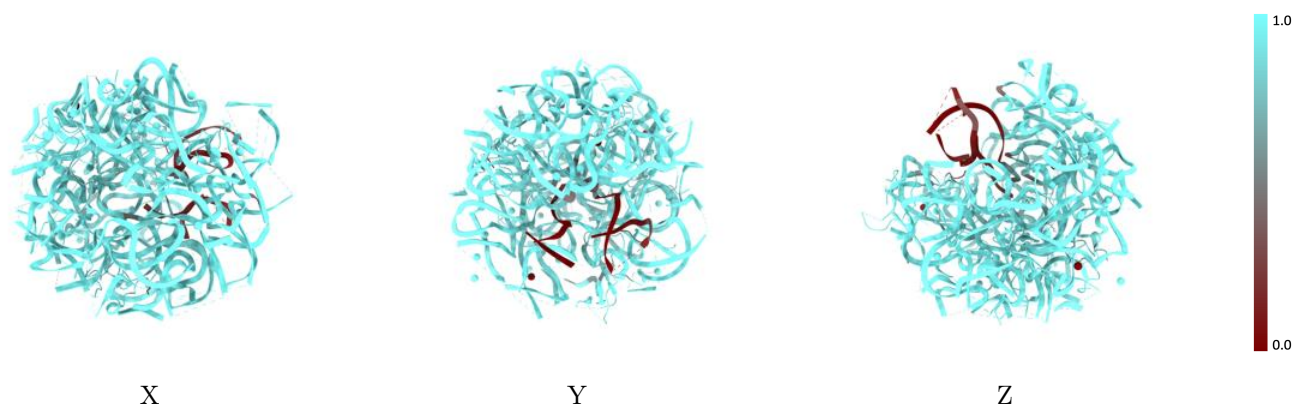
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



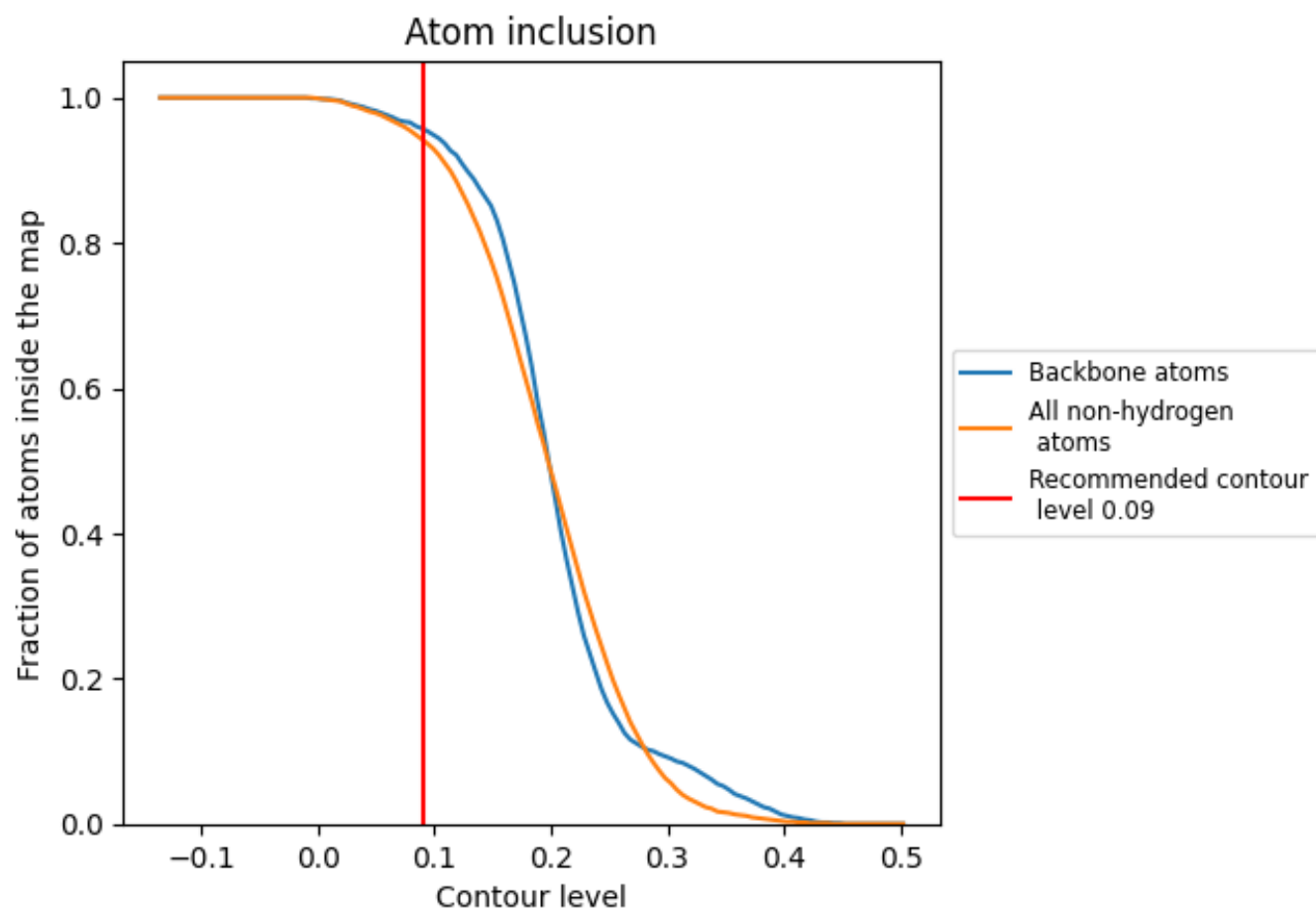
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.09).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 94% 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 (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9420	<div></div> 0.6540
Y	<div></div> 0.0390	<div></div> 0.1980
Z	<div></div> 0.1770	<div></div> 0.4360
a	<div></div> 0.9850	<div></div> 0.6680
b	<div></div> 0.7750	<div></div> 0.5730
c	<div></div> 0.9730	<div></div> 0.6820
d	<div></div> 0.9690	<div></div> 0.6770
e	<div></div> 0.8630	<div></div> 0.6600
i	<div></div> 0.9820	<div></div> 0.6850
k	<div></div> 0.9770	<div></div> 0.6830
l	<div></div> 0.9220	<div></div> 0.6640
q	<div></div> 1.0000	<div></div> 0.6840
r	<div></div> 0.8570	<div></div> 0.6640
v	<div></div> 0.7180	<div></div> 0.6130
z	<div></div> 1.0000	<div></div> 0.6840

