



## wwPDB EM Validation Summary Report ⓘ

Jun 9, 2026 – 04:46 pm BST

PDB ID : 9SS0 / pdb\_00009ss0  
EMDB ID : EMD-55171  
Title : 30S ribosomal subunit RimM-KO with IF1 and IF3 (State I)  
Authors : Hassan, A.H.; Demo, G.  
Deposited on : 2025-09-25  
Resolution : 3.00 Å(reported)  
Based on initial model : 6WDE

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:

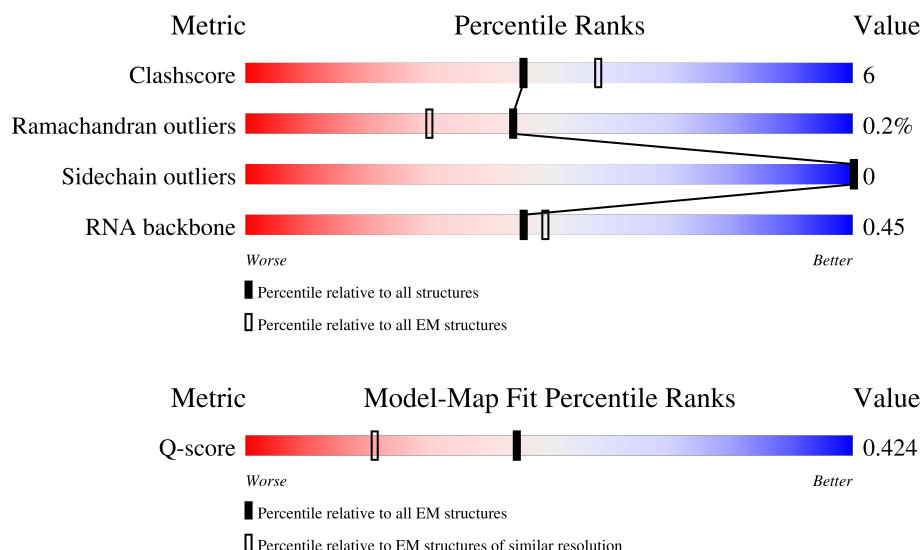
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : 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 3.00 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	14081 ( 2.50 - 3.50 )

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	AA	241	
2	AC	206	
3	AD	167	

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Mol	Chain	Length	Quality of chain
4	AE	135	
5	AF	179	
6	AG	130	
7	AH	130	
8	AJ	129	
9	AK	124	
10	AN	89	
11	AO	82	
12	AP	84	
13	AQ	75	
14	AS	87	
15	AT	71	
16	D1	1540	
17	F1	72	
18	F3	180	

## 2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 47149 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 protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	225	Total	C	N	O	S	0	0
			1756	1111	315	322	8		

- Molecule 2 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 3 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AD	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 4 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AE	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 5 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AF	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 6 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 7 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AH	119	Total	C	N	O	S	0	0
			946	588	187	168	3		

- Molecule 8 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AJ	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 9 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AK	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 10 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 11 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AO	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 12 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AP	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 13 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AQ	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 14 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AS	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 15 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AT	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 16 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	D1	1475	Total	C	N	O	P	0	0
			31650	14117	5812	10247	1474		

- Molecule 17 is a protein called Translation initiation factor IF-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	F1	70	Total	C	N	O	S	0	0
			557	350	99	105	3		

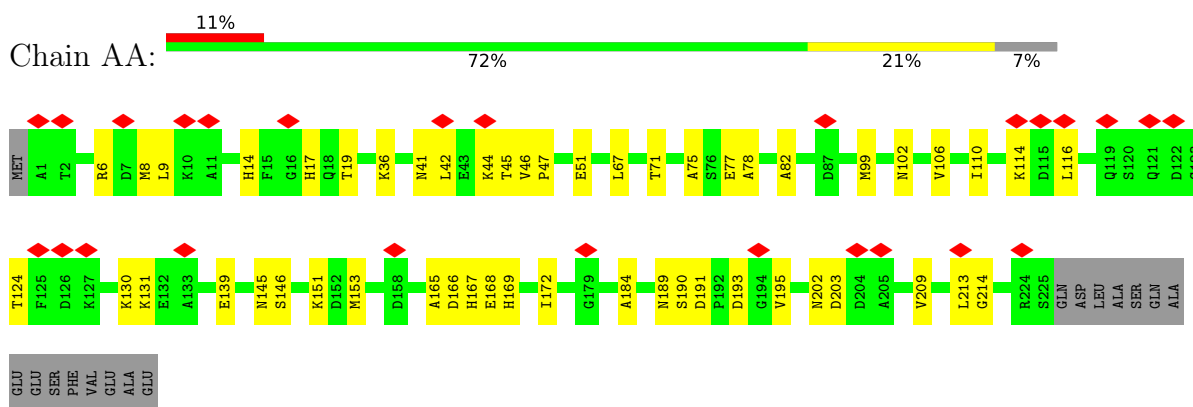
- Molecule 18 is a protein called Translation initiation factor IF-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	F3	108	Total	C	N	O	S	0	0
			885	562	160	159	4		

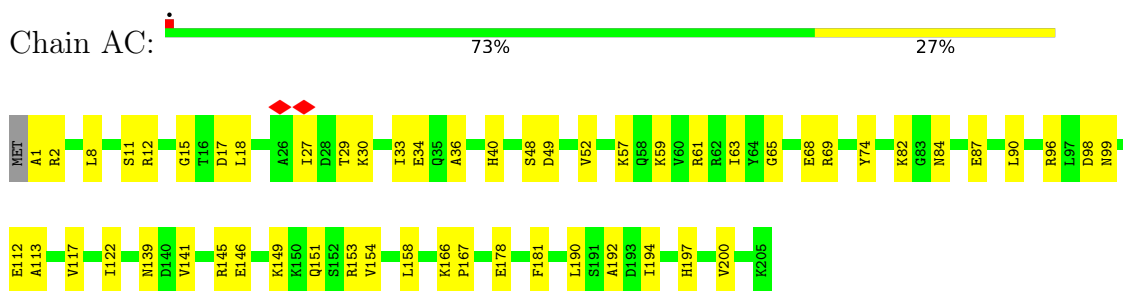
### 3 Residue-property plots

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.

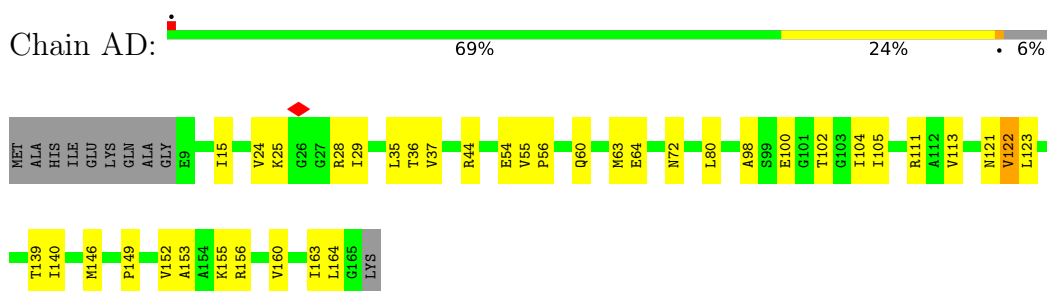
- Molecule 1: Small ribosomal subunit protein uS2



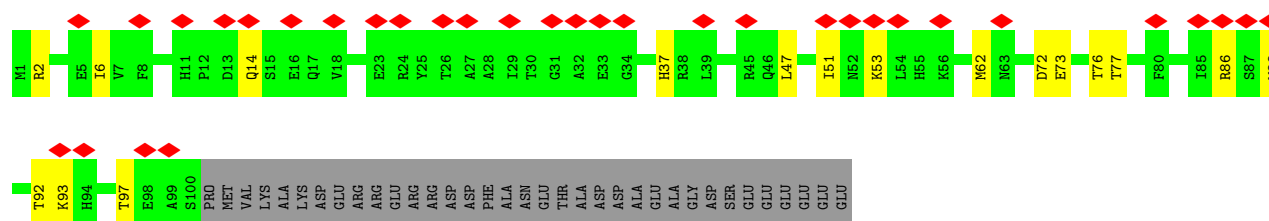
- Molecule 2: Small ribosomal subunit protein uS4



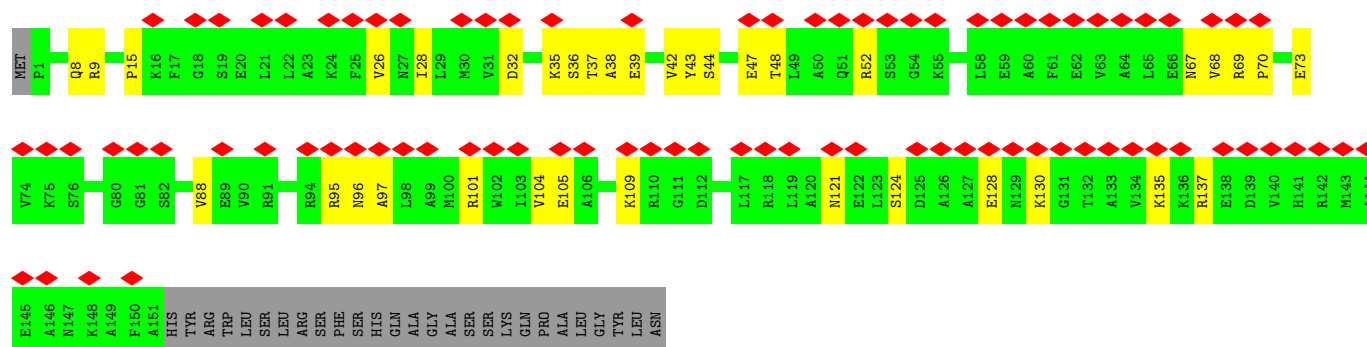
- Molecule 3: Small ribosomal subunit protein uS5



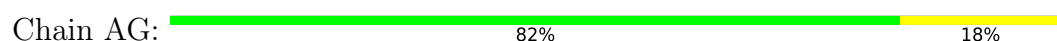
- Molecule 4: Small ribosomal subunit protein bS6, fully modified isoform



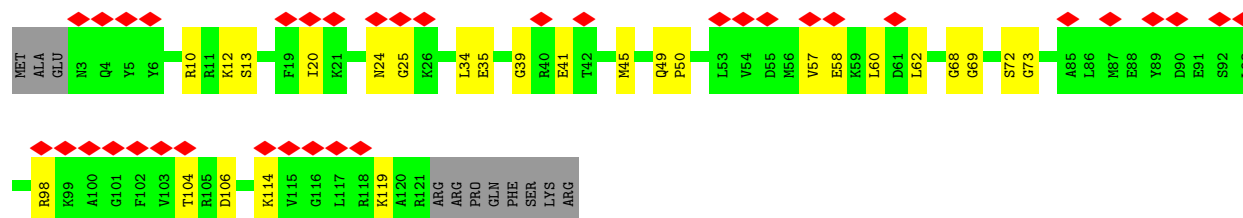
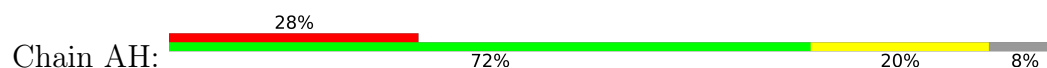
• Molecule 5: Small ribosomal subunit protein uS7



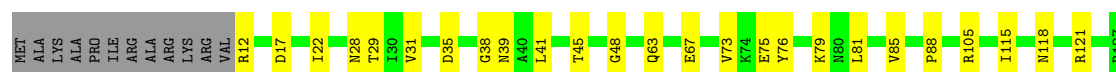
• Molecule 6: Small ribosomal subunit protein uS8



• Molecule 7: Small ribosomal subunit protein uS9




• Molecule 8: Small ribosomal subunit protein uS11






VAL

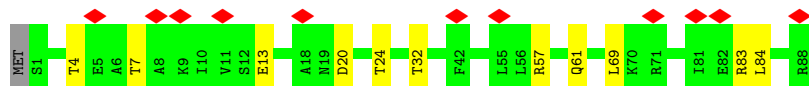
- Molecule 9: Small ribosomal subunit protein uS12

Chain AK:  78% 21% .




- Molecule 10: Small ribosomal subunit protein uS15

Chain AN:  12% 87% 12% .




- Molecule 11: Small ribosomal subunit protein bS16

Chain AO:  88% 12% .




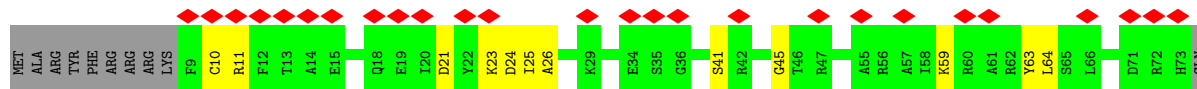
- Molecule 12: Small ribosomal subunit protein uS17

Chain AP:  80% 15% 5% .




- Molecule 13: Small ribosomal subunit protein bS18

Chain AQ:  35% 71% 16% 13% .




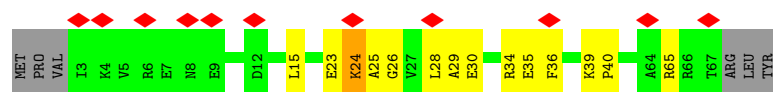
- Molecule 14: Small ribosomal subunit protein bS20

Chain AS:  82% 16% .

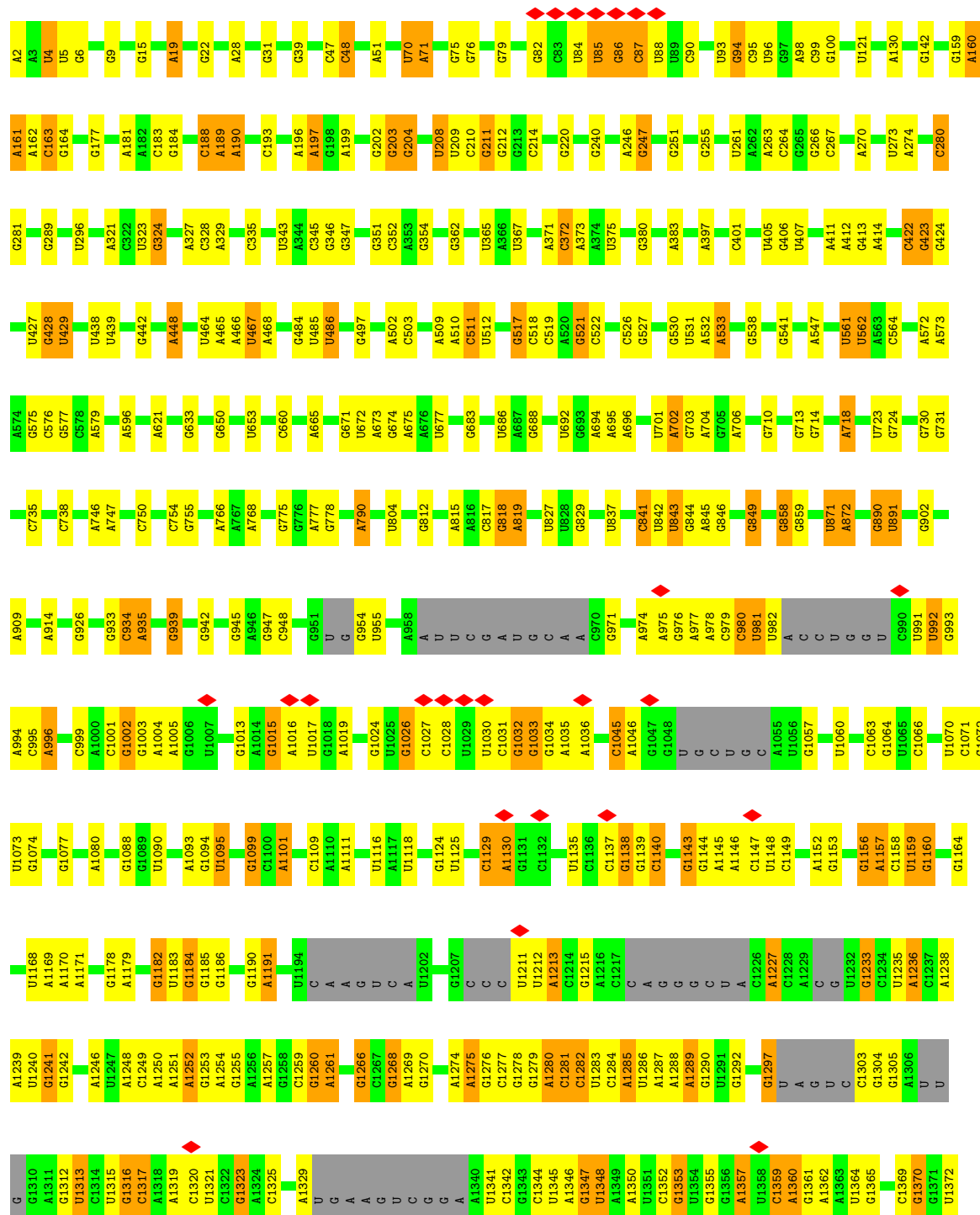


- Molecule 15: Small ribosomal subunit protein bS21

Chain AT:  15% 72% 18% 8% .

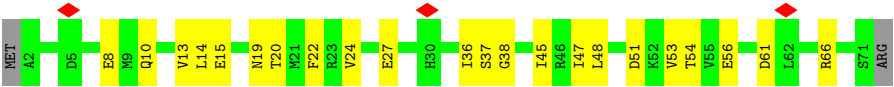


• Molecule 16: 16S Ribosomal RNA

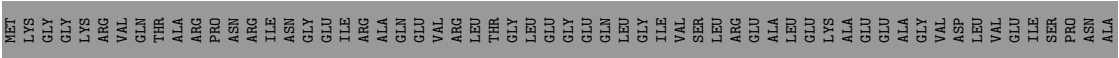




• Molecule 17: Translation initiation factor IF-1



• Molecule 18: Translation initiation factor IF-3



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	12314	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 ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	19.717	Depositor
Minimum map value	-6.304	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.815	Depositor
Recommended contour level	3	Depositor
Map size (Å)	400.32, 400.32, 400.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.834, 0.834, 0.834	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	AA	0.19	0/1787	0.43	0/2408
2	AC	0.21	0/1665	0.39	0/2227
3	AD	0.23	0/1169	0.47	0/1573
4	AE	0.18	0/835	0.43	0/1128
5	AF	0.16	0/1195	0.40	0/1602
6	AG	0.23	0/989	0.34	0/1326
7	AH	0.16	0/956	0.40	0/1274
8	AJ	0.19	0/885	0.44	0/1195
9	AK	0.23	0/969	0.39	0/1300
10	AN	0.16	0/722	0.36	0/964
11	AO	0.24	0/659	0.32	0/884
12	AP	0.23	0/657	0.38	0/881
13	AQ	0.18	0/544	0.43	0/731
14	AS	0.23	0/671	0.41	0/888
15	AT	0.23	0/550	0.61	0/728
16	D1	0.23	0/35430	0.31	0/55246
17	F1	0.16	0/564	0.34	0/759
18	F3	0.19	0/895	0.44	0/1186
All	All	0.22	0/51142	0.34	0/76300

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	AA	1756	0	1787	37	0
2	AC	1643	0	1710	39	0
3	AD	1156	0	1199	27	0
4	AE	817	0	808	13	0
5	AF	1181	0	1240	28	0
6	AG	979	0	1034	15	0
7	AH	946	0	989	22	0
8	AJ	869	0	878	19	0
9	AK	955	0	1019	22	0
10	AN	714	0	737	6	0
11	AO	649	0	666	7	0
12	AP	648	0	691	9	0
13	AQ	535	0	552	12	0
14	AS	665	0	714	15	0
15	AT	544	0	579	11	0
16	D1	31650	0	15941	235	0
17	F1	557	0	573	15	0
18	F3	885	0	942	15	0
All	All	47149	0	32059	472	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 6.

The worst 5 of 472 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)
16:D1:1157:A:N6	16:D1:1178:G:C2	2.37	0.92
16:D1:1026:G:N1	16:D1:1035:A:C2	2.38	0.91
1:AA:82:ALA:HB2	1:AA:213:LEU:HD13	1.52	0.90
6:AG:46:GLU:O	6:AG:61:THR:OG1	1.93	0.85
16:D1:1323:G:O2'	16:D1:1362:A:O2'	1.95	0.84

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	
1	AA	223/241 (92%)	205 (92%)	18 (8%)	0	100	100
2	AC	203/206 (98%)	179 (88%)	24 (12%)	0	100	100
3	AD	155/167 (93%)	135 (87%)	19 (12%)	1 (1%)	21	56
4	AE	98/135 (73%)	84 (86%)	14 (14%)	0	100	100
5	AF	149/179 (83%)	132 (89%)	17 (11%)	0	100	100
6	AG	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
7	AH	117/130 (90%)	94 (80%)	23 (20%)	0	100	100
8	AJ	114/129 (88%)	99 (87%)	15 (13%)	0	100	100
9	AK	121/124 (98%)	99 (82%)	22 (18%)	0	100	100
10	AN	86/89 (97%)	76 (88%)	10 (12%)	0	100	100
11	AO	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
12	AP	78/84 (93%)	68 (87%)	10 (13%)	0	100	100
13	AQ	63/75 (84%)	55 (87%)	8 (13%)	0	100	100
14	AS	83/87 (95%)	76 (92%)	7 (8%)	0	100	100
15	AT	63/71 (89%)	45 (71%)	16 (25%)	2 (3%)	3	18
17	F1	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
18	F3	106/180 (59%)	99 (93%)	7 (7%)	0	100	100
All	All	1934/2181 (89%)	1706 (88%)	225 (12%)	3 (0%)	44	76

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AD	122	VAL
15	AT	24	LYS
15	AT	36	PHE

### 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	
1	AA	186/199 (94%)	186 (100%)	0	100	100
2	AC	172/173 (99%)	172 (100%)	0	100	100
3	AD	119/126 (94%)	119 (100%)	0	100	100
4	AE	87/116 (75%)	87 (100%)	0	100	100
5	AF	124/147 (84%)	124 (100%)	0	100	100
6	AG	104/105 (99%)	104 (100%)	0	100	100
7	AH	97/107 (91%)	97 (100%)	0	100	100
8	AJ	89/99 (90%)	89 (100%)	0	100	100
9	AK	103/104 (99%)	103 (100%)	0	100	100
10	AN	76/77 (99%)	76 (100%)	0	100	100
11	AO	65/65 (100%)	65 (100%)	0	100	100
12	AP	74/78 (95%)	74 (100%)	0	100	100
13	AQ	56/65 (86%)	56 (100%)	0	100	100
14	AS	65/66 (98%)	65 (100%)	0	100	100
15	AT	55/61 (90%)	55 (100%)	0	100	100
17	F1	63/65 (97%)	63 (100%)	0	100	100
18	F3	97/156 (62%)	97 (100%)	0	100	100
All	All	1632/1809 (90%)	1632 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
18	F3	108	GLN
15	AT	55	HIS
11	AO	59	HIS
8	AJ	21	HIS
14	AS	47	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	D1	1463/1540 (95%)	293 (20%)	17 (1%)

5 of 293 RNA backbone outliers are listed below:



Mol	Chain	Res	Type
16	D1	4	U
16	D1	5	U
16	D1	9	G
16	D1	19	A
16	D1	22	G

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	D1	1190	G
16	D1	1534	A
16	D1	438	U
16	D1	561	U
16	D1	703	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.

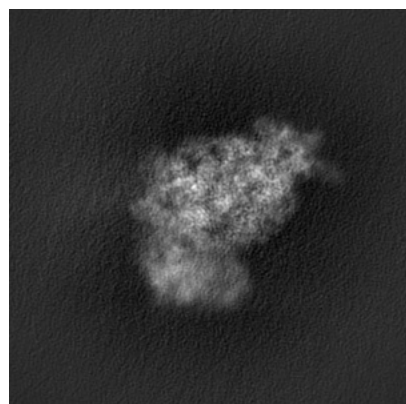
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55171. These allow visual inspection of the internal detail of the map and identification of artifacts.

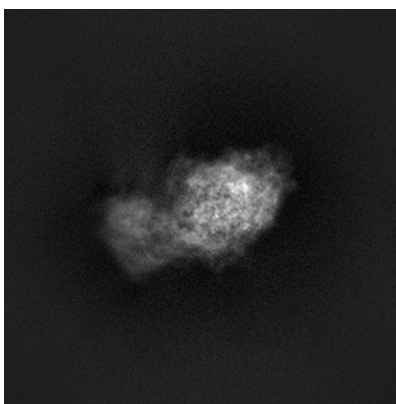
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

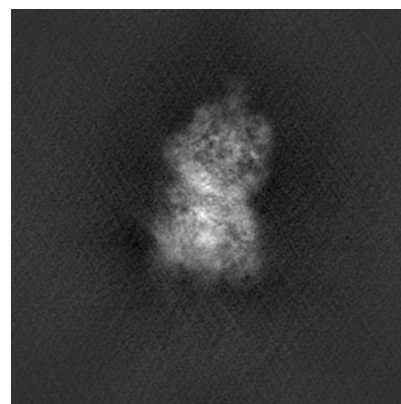
#### 6.1.1 Primary map



X

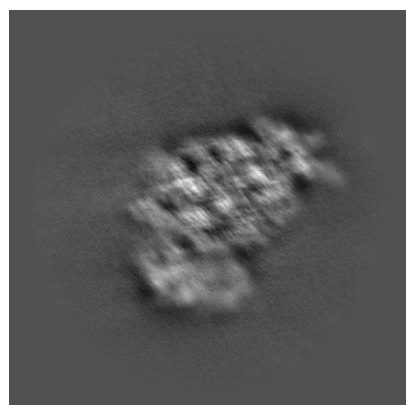


Y

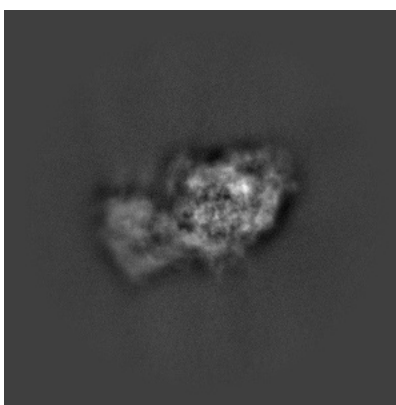


Z

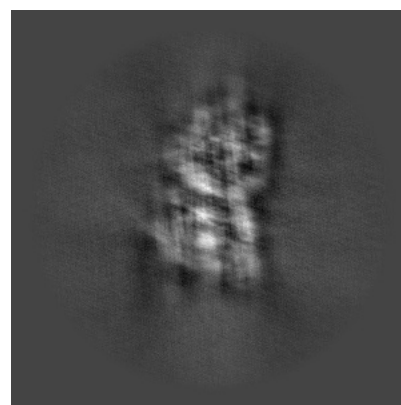
#### 6.1.2 Raw map



X



Y

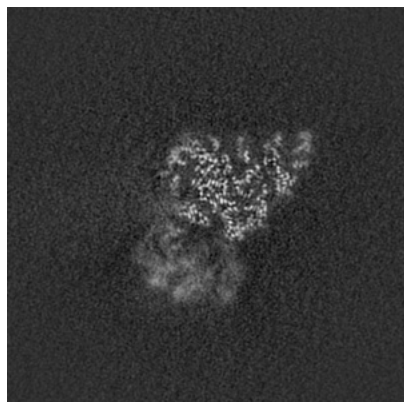


Z

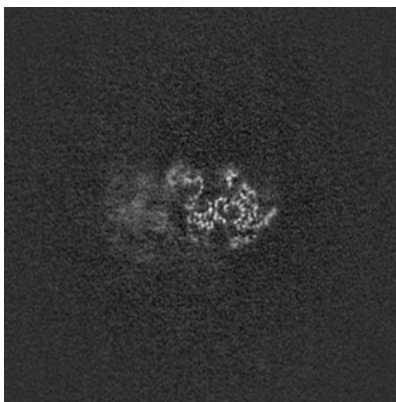
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

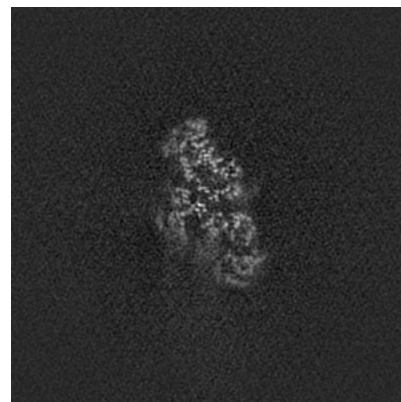
### 6.2.1 Primary map



X Index: 240

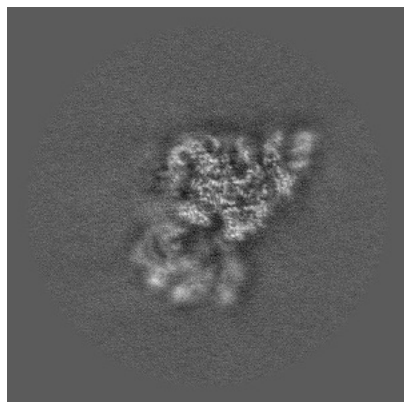


Y Index: 240

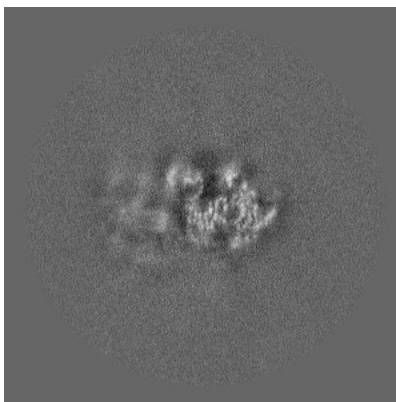


Z Index: 240

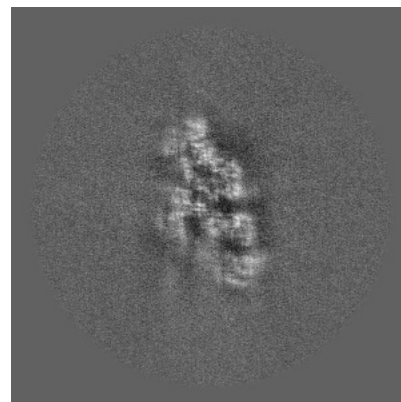
### 6.2.2 Raw map



X Index: 240



Y Index: 240

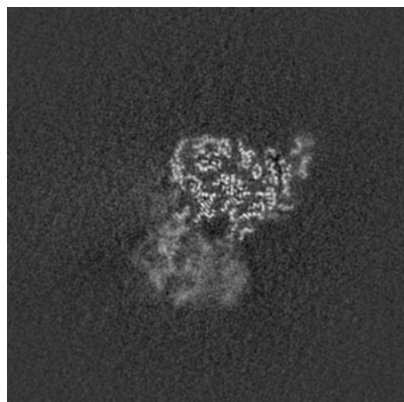


Z Index: 240

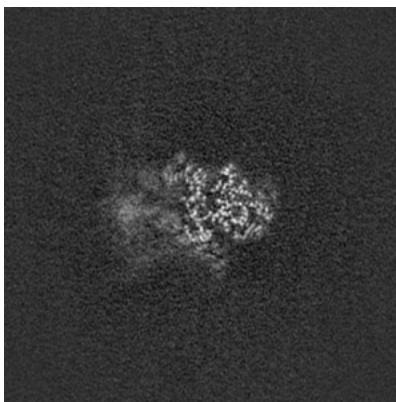
The images above show central slices of the map in three orthogonal directions.

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

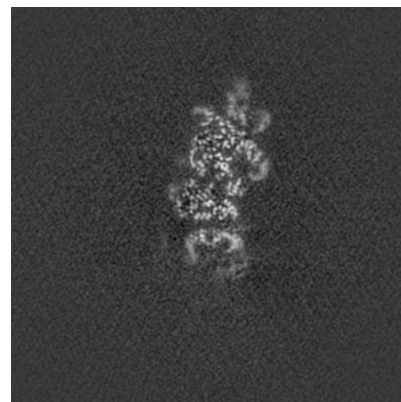
### 6.3.1 Primary map



X Index: 231

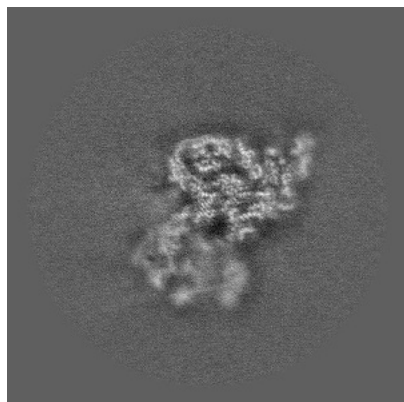


Y Index: 230

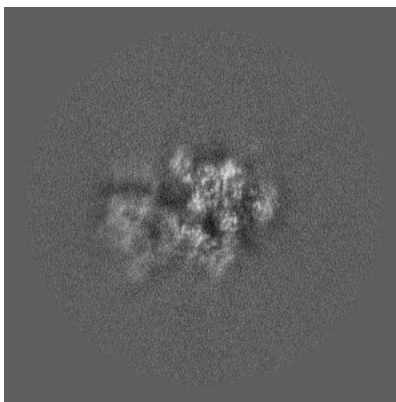


Z Index: 289

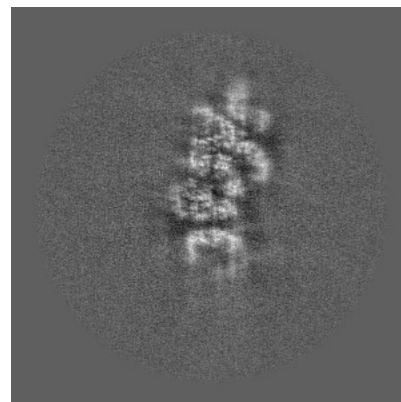
### 6.3.2 Raw map



X Index: 231



Y Index: 221

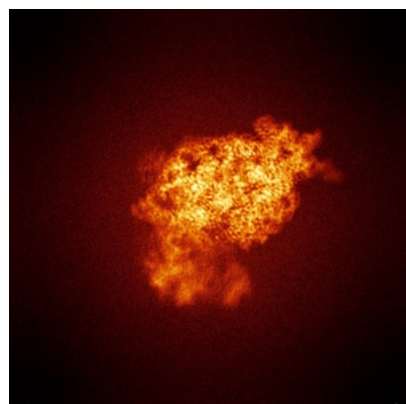


Z Index: 290

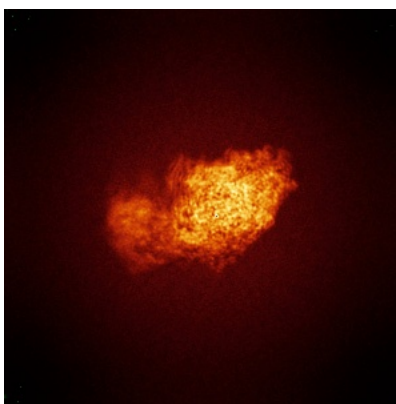
The images above show the largest variance slices of the map in three orthogonal directions.

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

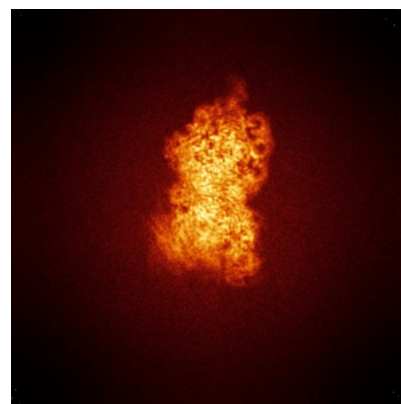
### 6.4.1 Primary map



X

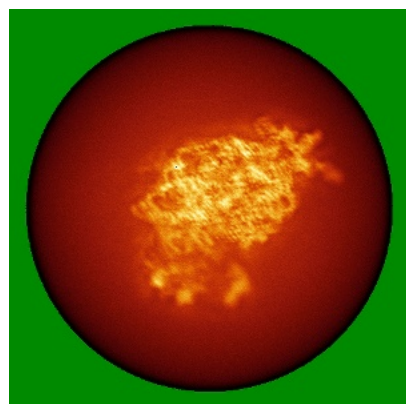


Y

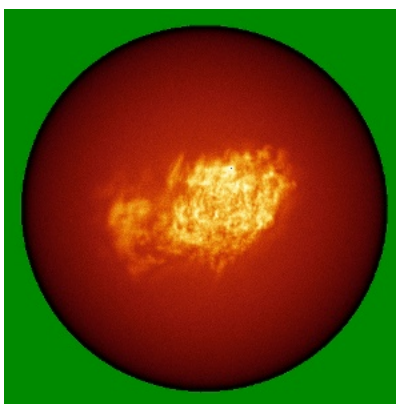


Z

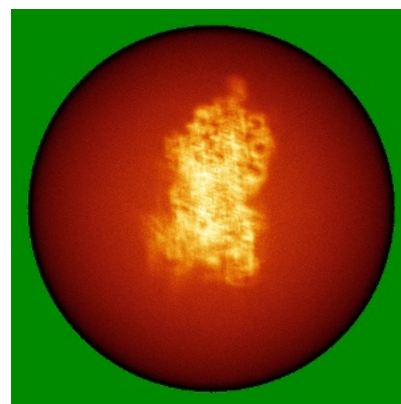
### 6.4.2 Raw map



X



Y



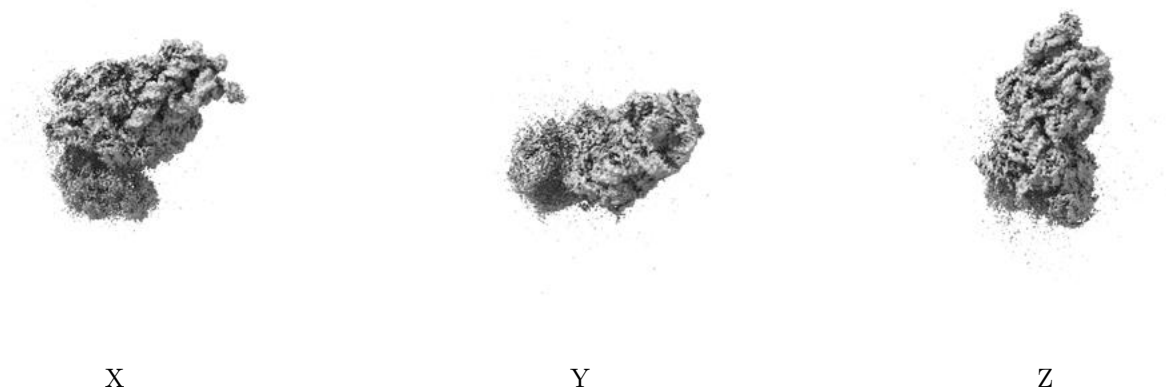
Z

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.



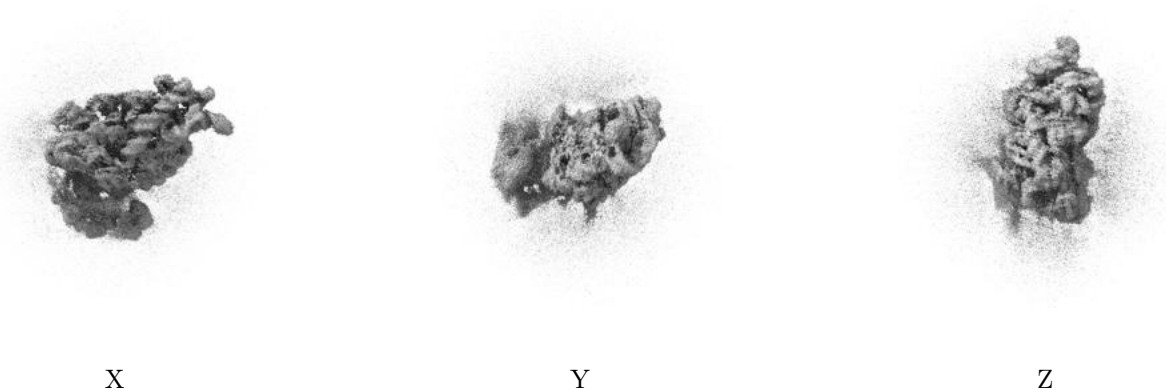
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. 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.

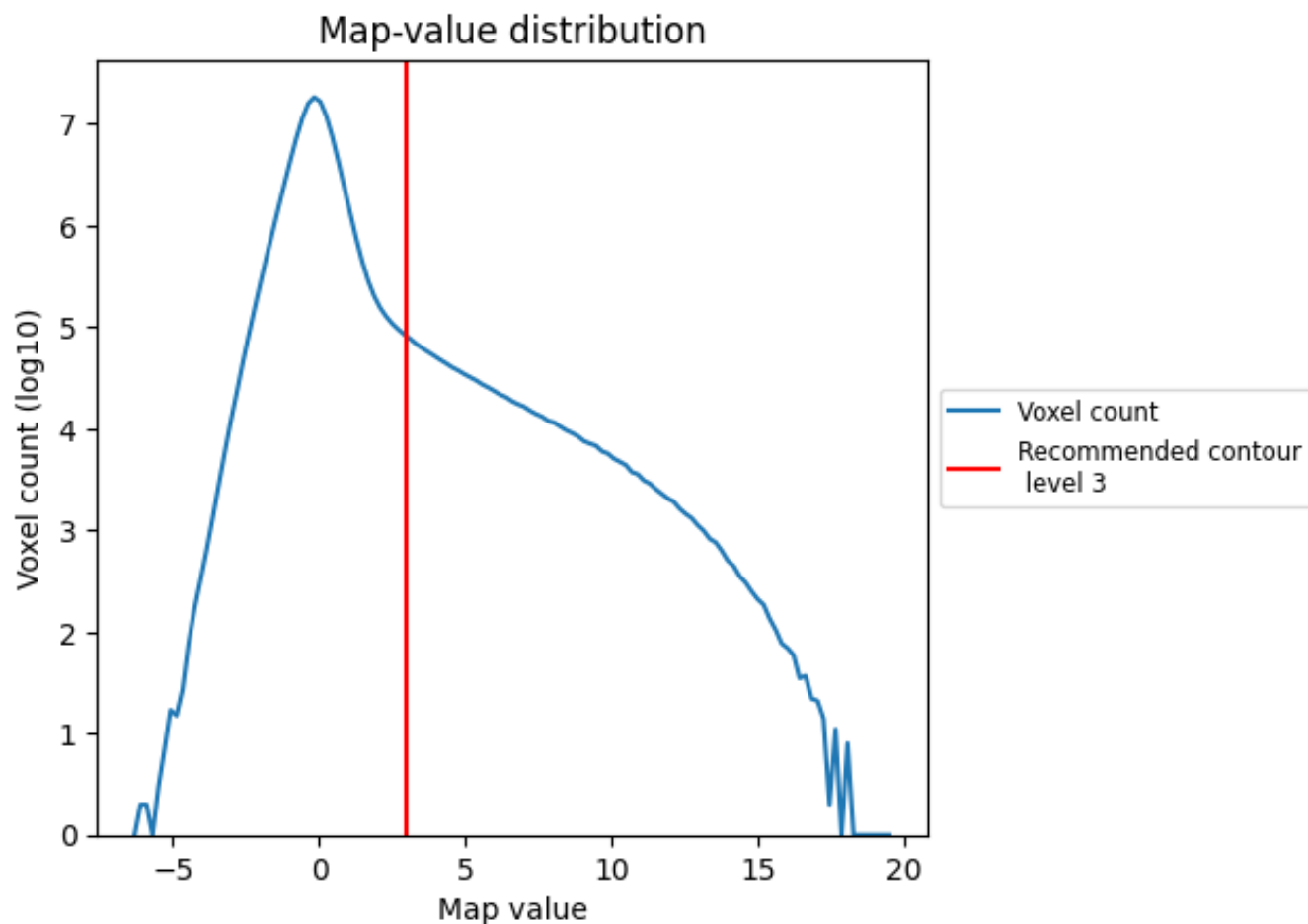
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

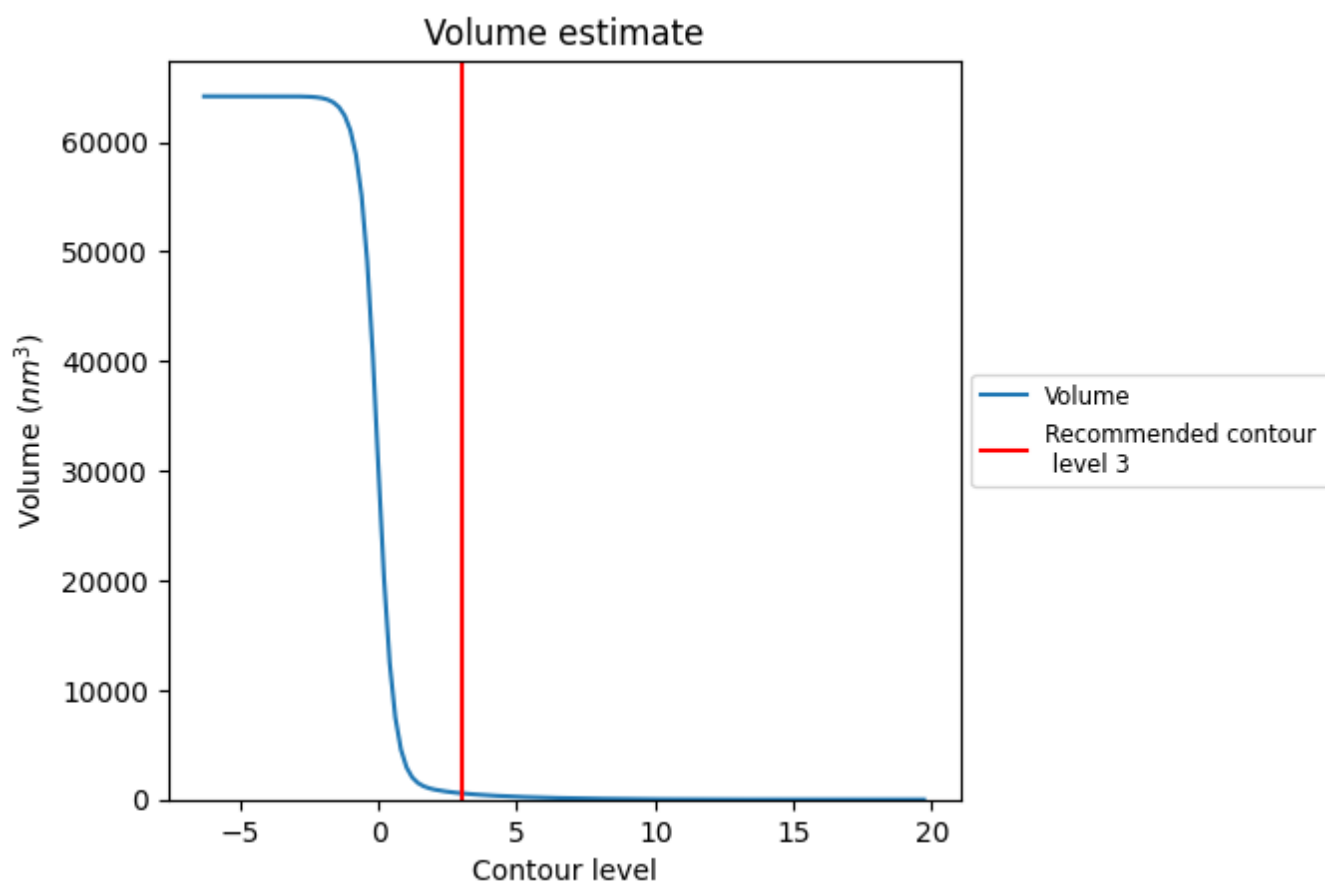
This section contains the results of statistical analysis of the map.

### 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](#)

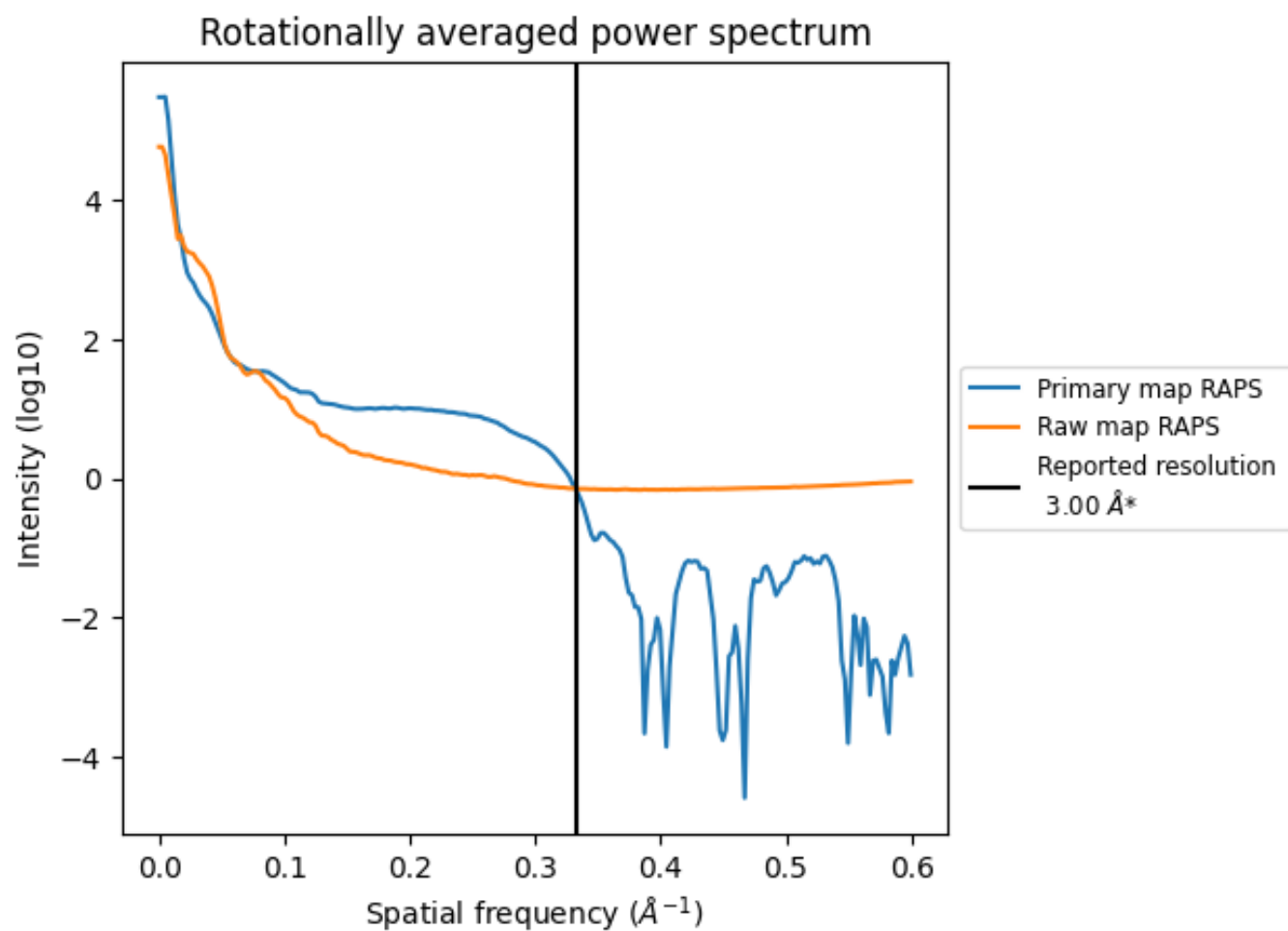


The volume at the recommended contour level is 573 nm<sup>3</sup>; this corresponds to an approximate mass of 518 kDa.

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 ⓘ

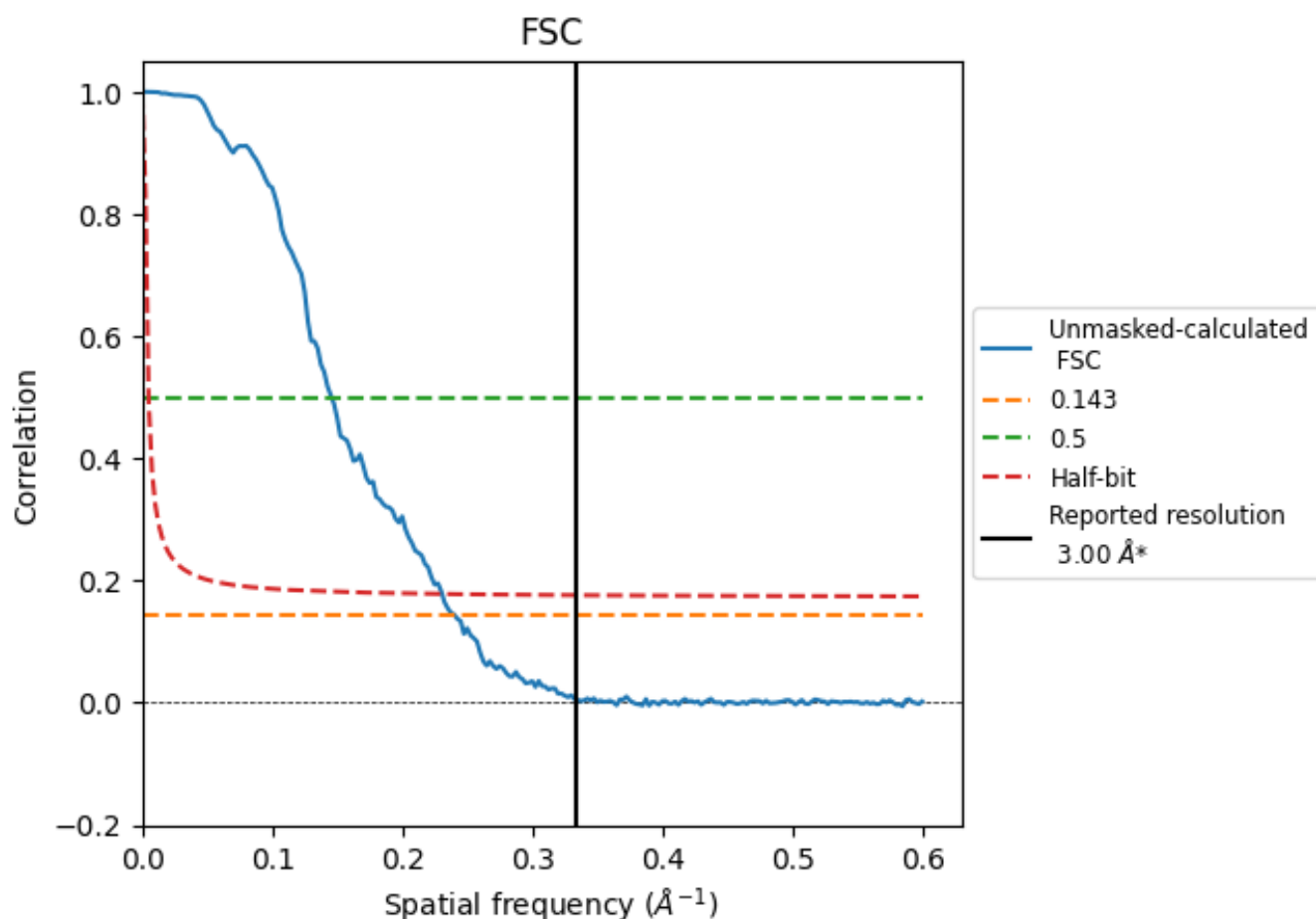


\*Reported resolution corresponds to spatial frequency of 0.333 Å<sup>-1</sup>

## 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 0.333 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

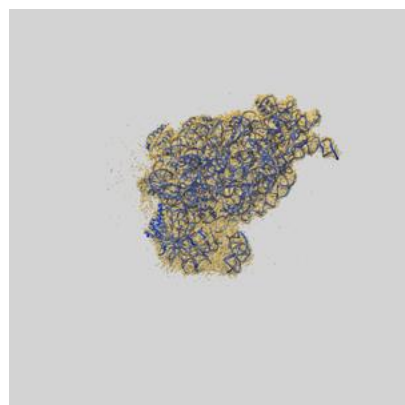
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.16	6.87	4.34

\*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 4.16 differs from the reported value 3.0 by more than 10 %

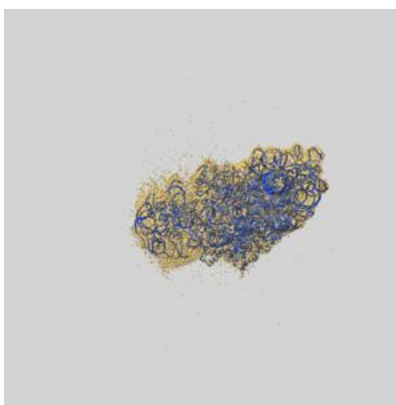
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55171 and PDB model 9SS0. Per-residue inclusion information can be found in section [3](#) on page [7](#).

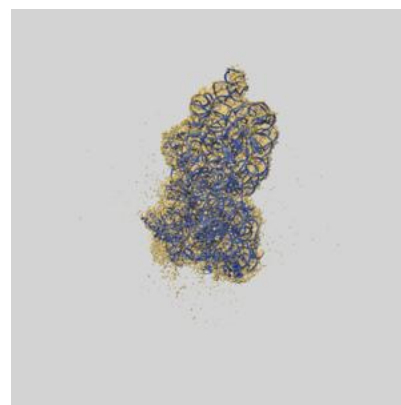
### 9.1 Map-model overlay [i](#)



X



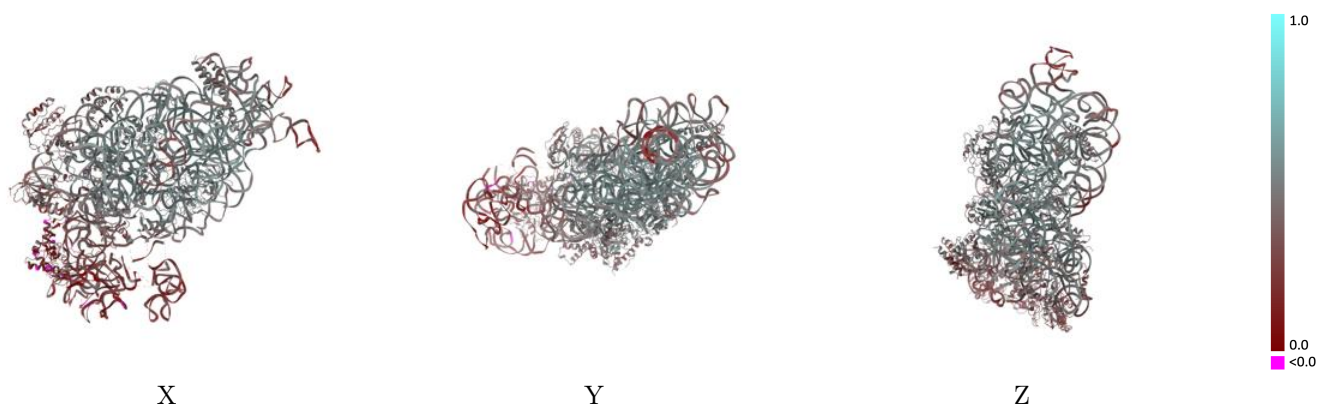
Y



Z

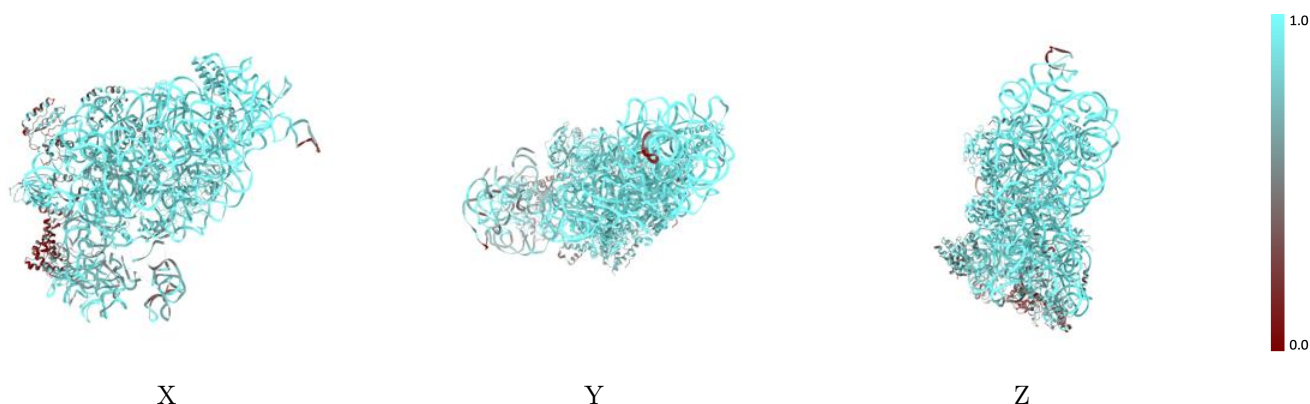
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



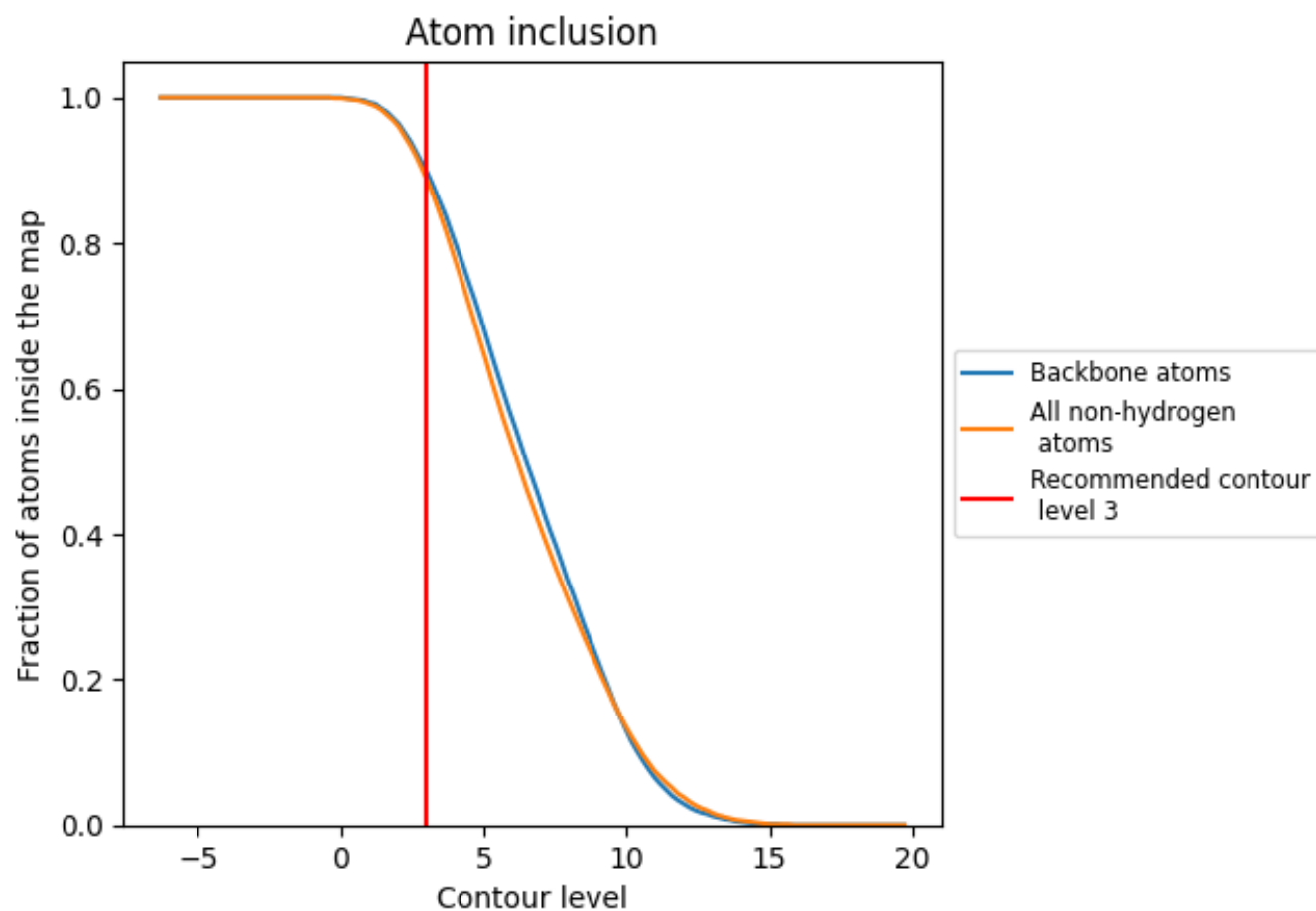
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).







































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 89% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8880	 0.4240
AA	 0.7210	 0.3980
AC	 0.9240	 0.4550
AD	 0.9500	 0.4910
AE	 0.5330	 0.3360
AF	 0.3600	 0.2320
AG	 0.9410	 0.5220
AH	 0.6160	 0.2420
AJ	 0.9030	 0.4160
AK	 0.9510	 0.5150
AN	 0.7550	 0.4320
AO	 0.9350	 0.5220
AP	 0.9600	 0.5090
AQ	 0.5060	 0.3770
AS	 0.9250	 0.4700
AT	 0.6440	 0.3320
D1	 0.9390	 0.4290
F1	 0.7980	 0.4490
F3	 0.8170	 0.3800

