



## wwPDB EM Validation Summary Report ⓘ

Apr 13, 2026 – 04:18 PM JST

PDB ID : 9UH7 / pdb\_00009uh7  
EMDB ID : EMD-64157  
Title : large lobe of human Ribonuclease MRP  
Authors : Zhou, B.; Lan, P.; Wu, J.; Lei, M.  
Deposited on : 2025-04-14  
Resolution : 2.84 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

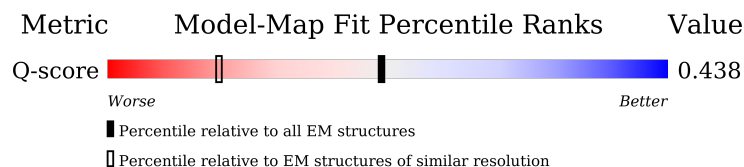
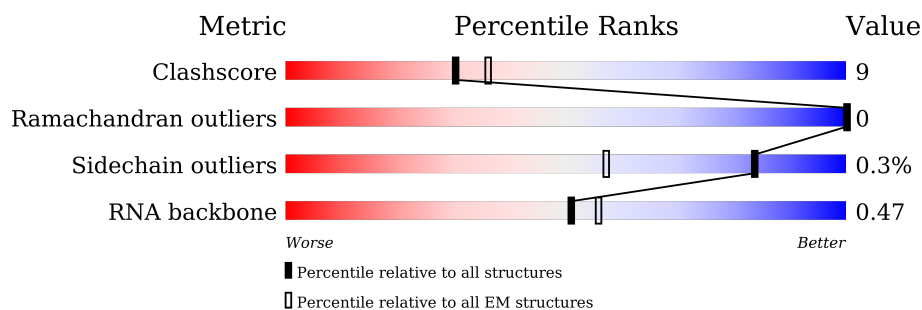
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.84 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.




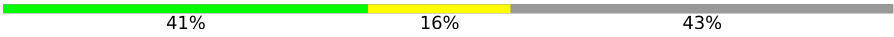







Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11884 ( 2.34 - 3.34 )

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	A	270	
2	B	1024	
3	D	220	

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Mol	Chain	Length	Quality of chain
4	E	163	 74%18%8%
5	F	199	 41%16%43%
6	G	140	 61%24%14%
7	H	124	 84%15%.
8	I	268	 76%13%12%
8	J	268	 76%16%7%
9	K	220	 10%5%85%
10	L	363	 88%12%
11	M	567	 29%12%59%

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 24267 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 RNA (270-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	204	Total	C	N	O	P	0	0
			4320	1928	752	1436	204		

- Molecule 2 is a protein called Ribonucleases P/MRP protein subunit POP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	718	Total	C	N	O	S	0	0
			5689	3628	1016	1006	39		

- Molecule 3 is a protein called Ribonuclease P protein subunit p29.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	186	Total	C	N	O	S	0	0
			1502	960	268	269	5		

- Molecule 4 is a protein called Ribonuclease P/MRP protein subunit POP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	150	Total	C	N	O	S	0	0
			1224	778	223	215	8		

- Molecule 5 is a protein called Ribonuclease P protein subunit p25.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	114	Total	C	N	O	S	0	0
			869	547	166	151	5		

- Molecule 6 is a protein called Ribonuclease P protein subunit p20.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	120	Total	C	N	O	S	0	0
			945	587	181	174	3		

- Molecule 7 is a protein called Ribonuclease P protein subunit p14.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	122	Total	C	N	O	S	0	0
			946	614	153	174	5		

- Molecule 8 is a protein called Ribonuclease P protein subunit p30.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	237	Total	C	N	O	S	0	0
			1829	1169	320	333	7		
8	J	248	Total	C	N	O	S	0	0
			1916	1227	336	346	7		

- Molecule 9 is a protein called UPF0711 protein C18orf21.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	32	Total	C	N	O	S	0	0
			260	163	51	45	1		

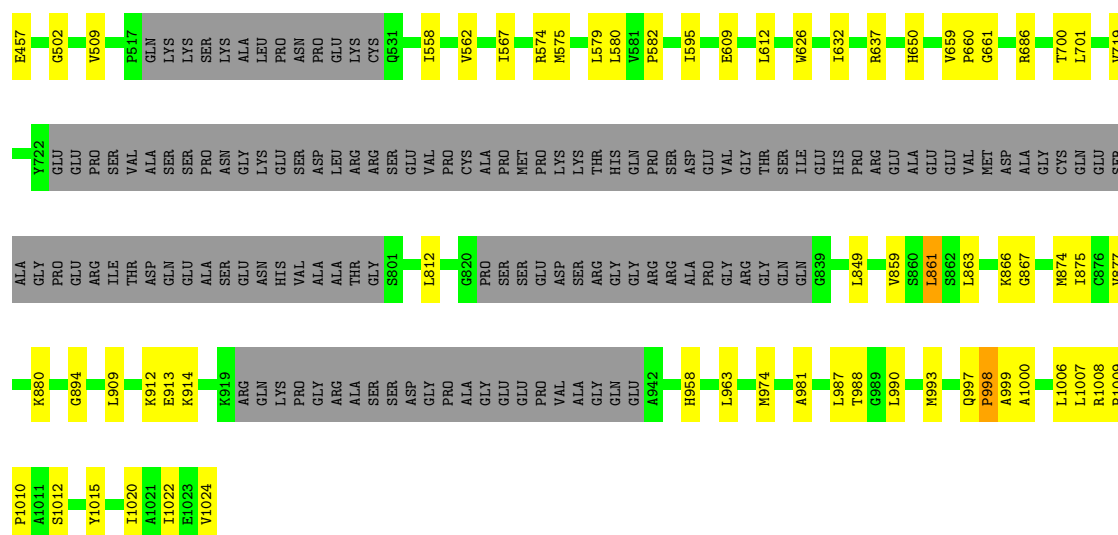
- Molecule 10 is a protein called Ribonuclease P protein subunit p40.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	362	Total	C	N	O	S	0	0
			2939	1893	489	540	17		

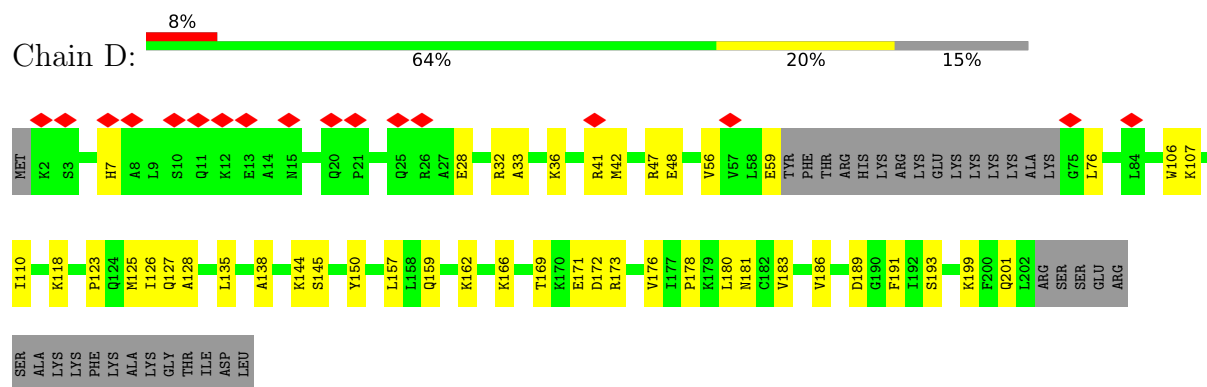
- Molecule 11 is a protein called Nucleolus and neural progenitor protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	230	Total	C	N	O	S	0	0
			1828	1190	309	315	14		

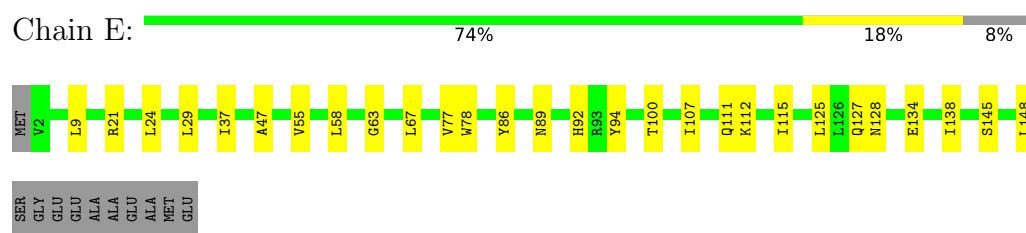




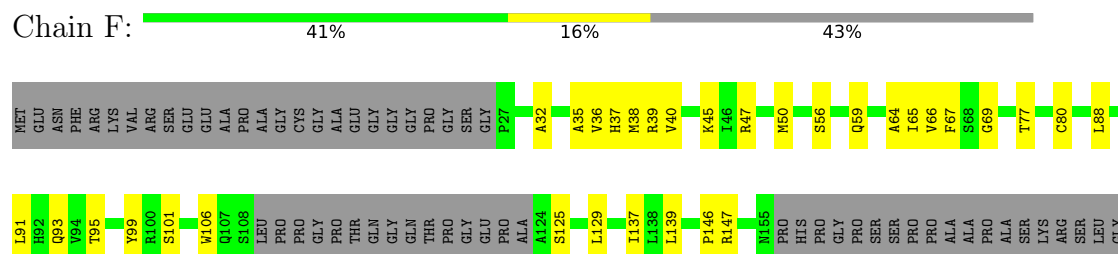
• Molecule 3: Ribonuclease P protein subunit p29



• Molecule 4: Ribonuclease P/MRP protein subunit POP5



• Molecule 5: Ribonuclease P protein subunit p25



GLU  
PRO  
ALA  
ASN  
GLY  
GLY  
SER  
ALA  
LYS  
ARG  
SER  
GLN  
PRO  
GLU  
PRO  
GLY  
PRO  
VAL  
ALA  
ASP  
GLU  
ASP  
GLN  
THR  
ALA


• Molecule 6: Ribonuclease P protein subunit p20

Chain G:  61% 24% 14%

MET  
ALA  
ASN  
GLU  
PRO  
ARG  
ALA  
VAL  
GLU  
ALA  
GLU  
ASP  
GLY  
PRO  
V18  
R23  
L30  
P31  
I37  
M41  
F45  
Q48  
K54  
L55  
L56  
D57  
G58  
G59  
A60  
Q63  
L74  
G75  
L76  
I77  
N79  
R80  
A81  
I82  
N83  
I84  
A85  
L86  
F93  
Q97  
V98

E110  
P113  
E114  
T115  
D116  
T117  
R118  
E119  
P120  
I124  
I130  
V134  
V137  
THR  
PRO  
LYS

• Molecule 7: Ribonuclease P protein subunit p14

Chain H:  84% 15%

MET  
PRO  
A3  
Q29  
N36  
A37  
A38  
L44  
V43  
K49  
D50  
V55  
L59  
P60  
D62  
R76  
T90  
K98  
L111  
L112  
A113  
L114  
N117  
S118  
R119  
D124


• Molecule 8: Ribonuclease P protein subunit p30

Chain I:  76% 13% 12%

MET  
A2  
L7  
R10  
A34  
I35  
N36  
K44  
K45  
Q46  
F58  
L61  
K67  
P70  
V102  
D123  
I127  
T130  
L133  
K138  
R139  
P140  
F152  
Y156  
M165  
I170  
L174  
K183  
I187  
S188  
S189  
A190  
R193  
E196  
L212

A217  
K216  
E233  
T237  
A238  
PHE  
GLY  
ILE  
ILE  
THR  
VAL  
LYS  
PRO  
ARG  
PRO  
SER  
GLU  
ASP  
GLU  
ASP  
CYS  
LEU  
PRO  
ALA  
SER  
LYS  
LYS  
LYS  
CYS  
GLY

• Molecule 8: Ribonuclease P protein subunit p30

Chain J:  76% 16% 7%

MET  
A2  
V3  
D6  
R10  
Y30  
N36  
F41  
K42  
P51  
F58  
Q65  
G66  
K67  
R76  
S82  
H86  
T93  
S94  
S95  
R96  
A97  
R98  
L99  
Y100  
D101  
V102  
A116  
L120  
D121  
V122  
D123  
V125  
T130  
L150  
Y156  
D162  
M165  
R166  
R167

I186  
S189  
R198  
L206  
D216  
R226  
L230  
E233  
T241  
T242  
S243  
T244  
V245  
K246  
P247  
R248  
R249  
PRO  
SER  
GLU  
GLY  
ASP  
GLU  
THR  
PHE  
GLY  
ASP  
CYS  
LEU  
PRO  
CYS  
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LEU  
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HIS  
GLY  
LYS  
SER  
SER  
ARG  
VAL  
PHE  
PHE  
VAL  
SER  
PRO  
LYS  
ALA  
LYS  
SER  
LEU  
PRO  
THR  
PRO  
LYS  
ILE  
GLN  
LYS

• Molecule 9: UPF0711 protein C18orf21

Chain K:  10% 5% 85%

MET  
R2  
Q3  
K4  
H5  
Y6  
L7  
E8  
A9  
R12  
D16  
Y24  
L25  
L26  
Y29  
T30  
H33  
ASP  
ASP  
LYS  
SER  
SER  
THR  
PHE  
GLU  
GLY  
THR  
THR  
CYS  
LYS  
PRO  
THR  
CYS  
LYS  
TYR  
CYS  
PHE  
GLN  
THR  
LEU  
LEU  
LEU  
VAL  
HIS  
HIS  
GLY  
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ALA  
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ASN  
TYR  
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PHE  
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THR  
VAL  
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HIS  
HIS  
GLY  
LYS  
SER  
SER  
ARG  
SER  
PHE  
VAL  
SER  
THR  
THR  
LEU  
LYS  
ALA  
ASN  
PRO  
THR  
ALA  
THR  
ILE  
GLN  
PRO





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	777423	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.055	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size ( $\text{\AA}$ )	281.6, 281.6, 281.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.1, 1.1, 1.1	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	A	0.08	0/4818	0.23	0/7500
2	B	0.17	1/5828 (0.0%)	0.58	9/7885 (0.1%)
3	D	0.17	0/1529	0.49	0/2056
4	E	0.15	0/1247	0.40	0/1683
5	F	0.14	0/884	0.42	0/1194
6	G	0.16	0/957	0.43	0/1293
7	H	0.14	0/963	0.40	0/1303
8	I	0.12	0/1860	0.32	0/2522
8	J	0.13	0/1949	0.32	0/2641
9	K	0.16	0/268	0.50	0/362
10	L	0.09	0/3021	0.28	0/4099
11	M	0.18	0/1864	0.47	0/2526
All	All	0.14	1/25188 (0.0%)	0.41	9/35064 (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
7	H	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	PRO	N-CD	9.70	1.61	1.47

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	999	ALA	N-CA-C	26.45	145.69	112.89
2	B	998	PRO	N-CA-C	-16.91	83.17	110.40
2	B	299	LYS	CB-CA-C	-14.51	88.70	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	999	ALA	N-CA-CB	-13.87	87.80	110.40
2	B	1000	ALA	N-CA-C	-11.38	99.21	113.55

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	H	76	ARG	Sidechain

## 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	A	4320	0	2202	72	0
2	B	5689	0	5775	101	0
3	D	1502	0	1561	45	0
4	E	1224	0	1238	23	0
5	F	869	0	912	27	0
6	G	945	0	971	29	0
7	H	946	0	977	13	0
8	I	1829	0	1914	24	0
8	J	1916	0	2015	36	0
9	K	260	0	244	9	0
10	L	2939	0	2884	33	0
11	M	1828	0	1926	57	0
All	All	24267	0	22619	424	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 9.

The worst 5 of 424 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)
4:E:58:LEU:HD13	4:E:145:SER:HB2	1.35	1.04
8:I:212:LEU:HD13	8:I:217:ALA:HA	1.44	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:10:ARG:HE	8:J:36:ASN:ND2	1.70	0.88
8:J:122:VAL:HG23	8:J:150:LEU:HD21	1.59	0.85
8:I:212:LEU:CD1	8:I:217:ALA:HA	2.06	0.85

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	704/1024 (69%)	667 (95%)	37 (5%)	0	100	100
3	D	182/220 (83%)	176 (97%)	6 (3%)	0	100	100
4	E	148/163 (91%)	143 (97%)	5 (3%)	0	100	100
5	F	110/199 (55%)	109 (99%)	1 (1%)	0	100	100
6	G	118/140 (84%)	114 (97%)	4 (3%)	0	100	100
7	H	120/124 (97%)	112 (93%)	8 (7%)	0	100	100
8	I	235/268 (88%)	229 (97%)	6 (3%)	0	100	100
8	J	246/268 (92%)	238 (97%)	8 (3%)	0	100	100
9	K	30/220 (14%)	29 (97%)	1 (3%)	0	100	100
10	L	360/363 (99%)	345 (96%)	15 (4%)	0	100	100
11	M	228/567 (40%)	223 (98%)	5 (2%)	0	100	100
All	All	2481/3556 (70%)	2385 (96%)	96 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	624/883 (71%)	623 (100%)	1 (0%)	87	95
3	D	166/196 (85%)	166 (100%)	0	100	100
4	E	134/143 (94%)	134 (100%)	0	100	100
5	F	92/150 (61%)	92 (100%)	0	100	100
6	G	102/118 (86%)	101 (99%)	1 (1%)	68	83
7	H	104/106 (98%)	104 (100%)	0	100	100
8	I	202/228 (89%)	201 (100%)	1 (0%)	81	90
8	J	212/228 (93%)	211 (100%)	1 (0%)	81	90
9	K	25/201 (12%)	25 (100%)	0	100	100
10	L	331/332 (100%)	330 (100%)	1 (0%)	86	94
11	M	208/513 (40%)	207 (100%)	1 (0%)	81	90
All	All	2200/3098 (71%)	2194 (100%)	6 (0%)	84	94

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	J	58	PHE
10	L	36	HIS
11	M	234	TYR
6	G	48	GLN
2	B	861	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
7	H	36	ASN
8	I	114	HIS
8	I	36	ASN
8	J	86	HIS
2	B	891	HIS

### 5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	202/270 (74%)	47 (23%)	1 (0%)

5 of 47 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	16	G
1	A	22	A
1	A	23	U
1	A	34	A
1	A	35	C

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	117	U

## 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.

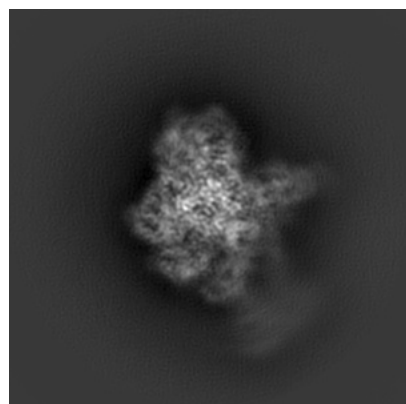
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64157. These allow visual inspection of the internal detail of the map and identification of artifacts.

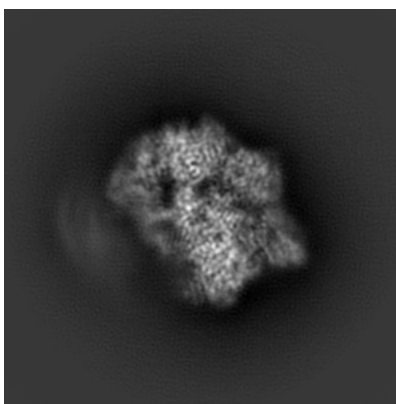
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

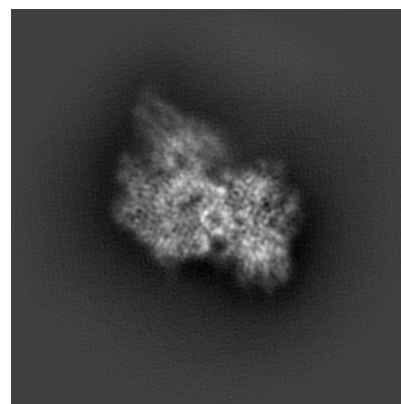
#### 6.1.1 Primary map



X

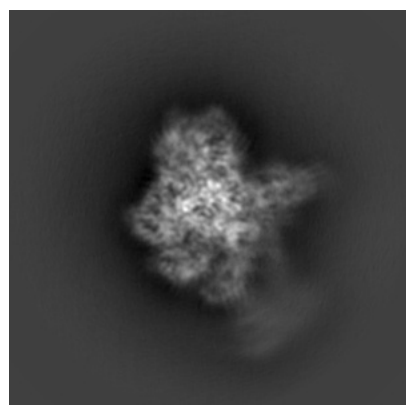


Y

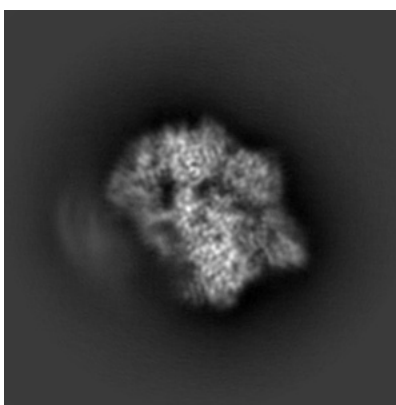


Z

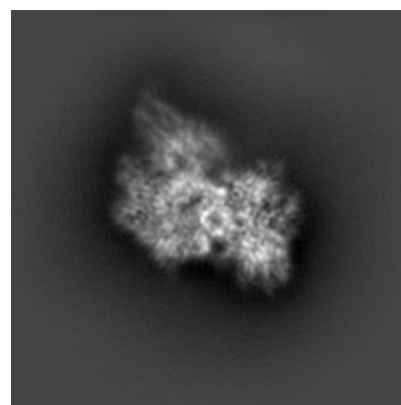
#### 6.1.2 Raw map



X



Y



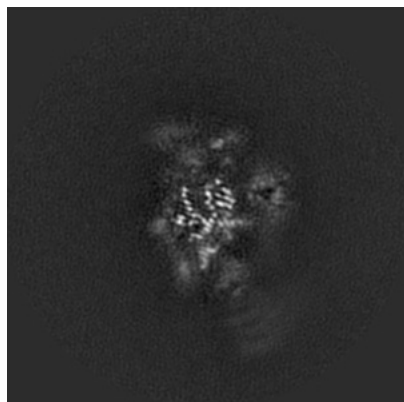
Z

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

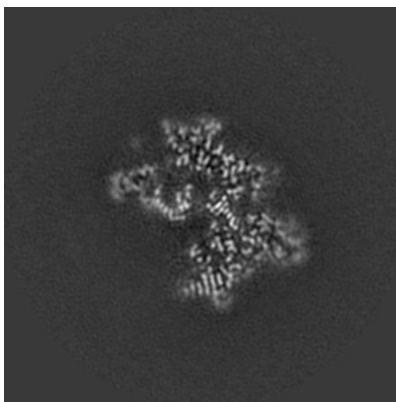


## 6.2 Central slices [i](#)

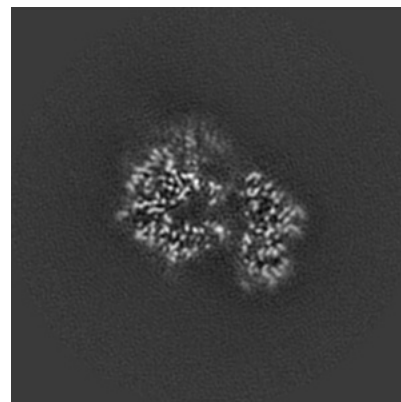
### 6.2.1 Primary map



X Index: 128

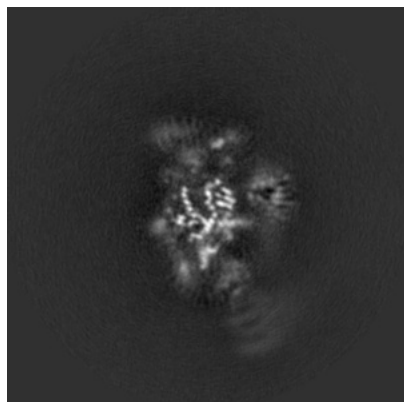


Y Index: 128

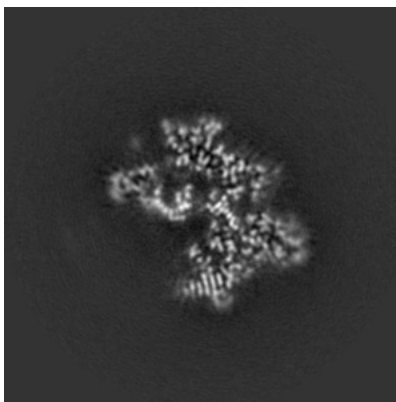


Z Index: 128

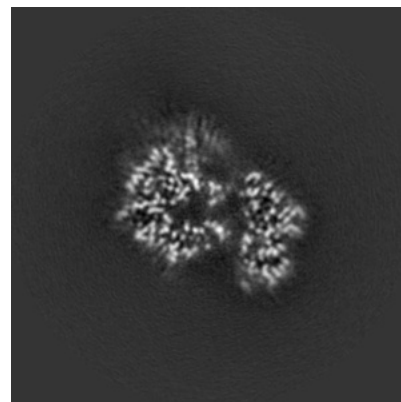
### 6.2.2 Raw map



X Index: 128



Y Index: 128

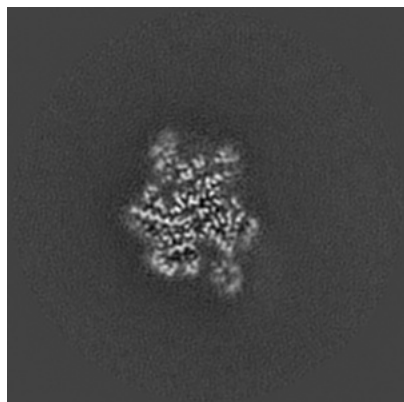


Z Index: 128

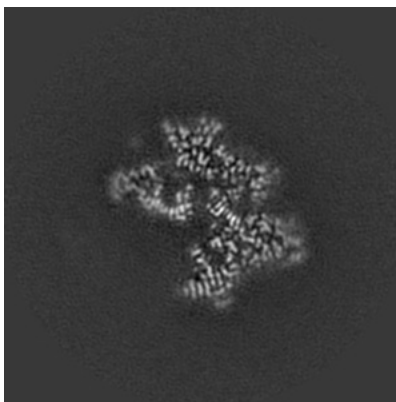
The images above show central slices of the map in three orthogonal directions.

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

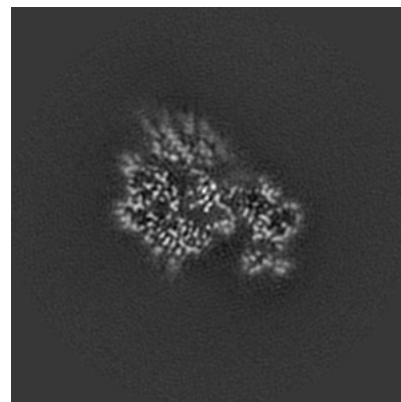
### 6.3.1 Primary map



X Index: 159

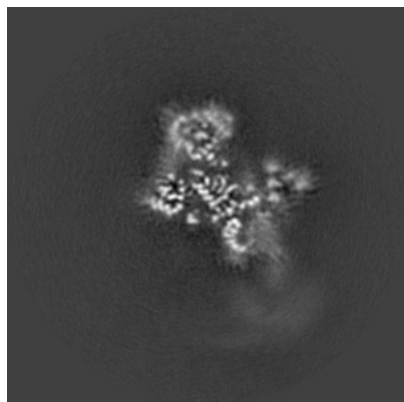


Y Index: 127

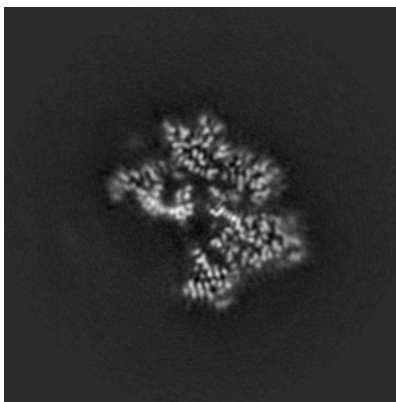


Z Index: 133

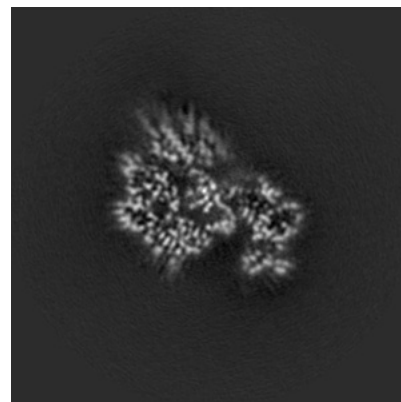
### 6.3.2 Raw map



X Index: 104



Y Index: 126

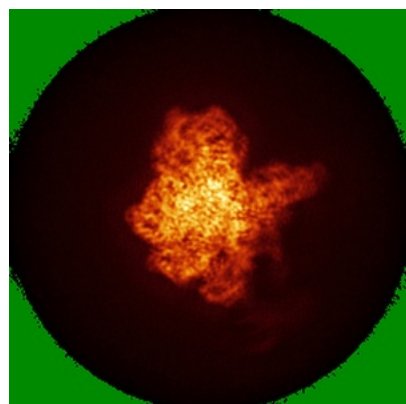


Z Index: 133

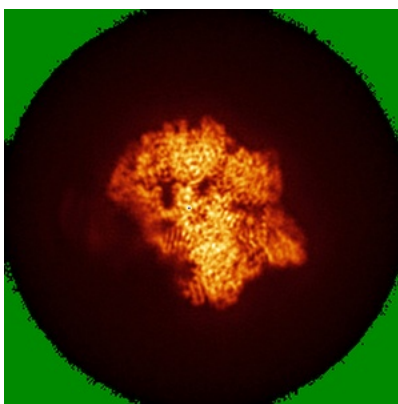
The images above show the largest variance slices of the map in three orthogonal directions.

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

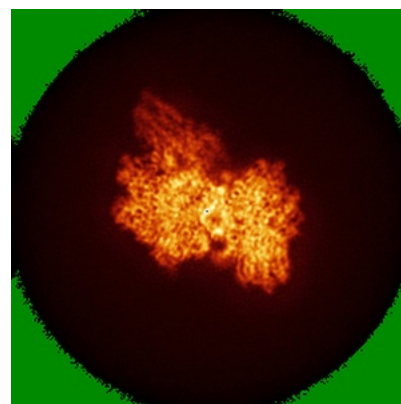
### 6.4.1 Primary map



X

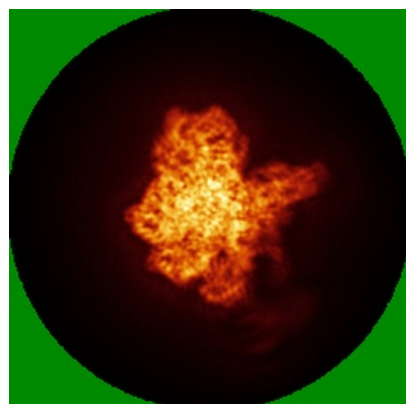


Y

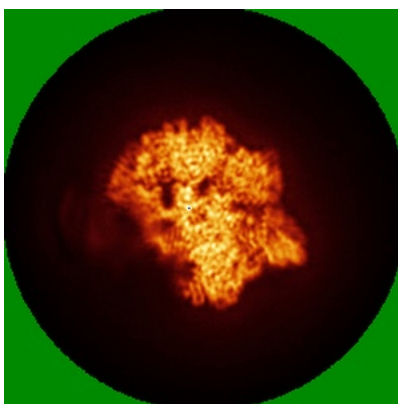


Z

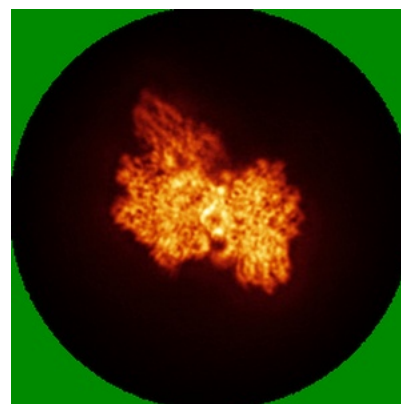
### 6.4.2 Raw map



X



Y

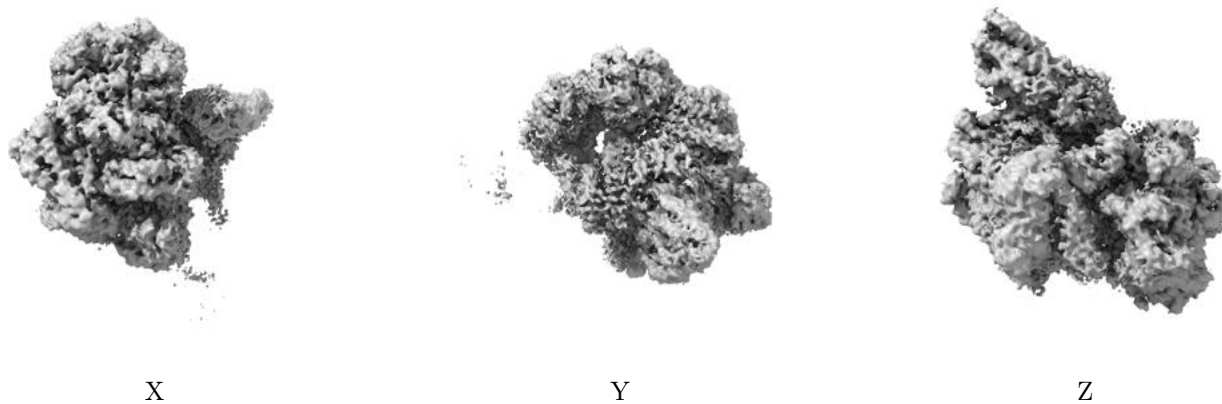


Z

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 0.005. 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.

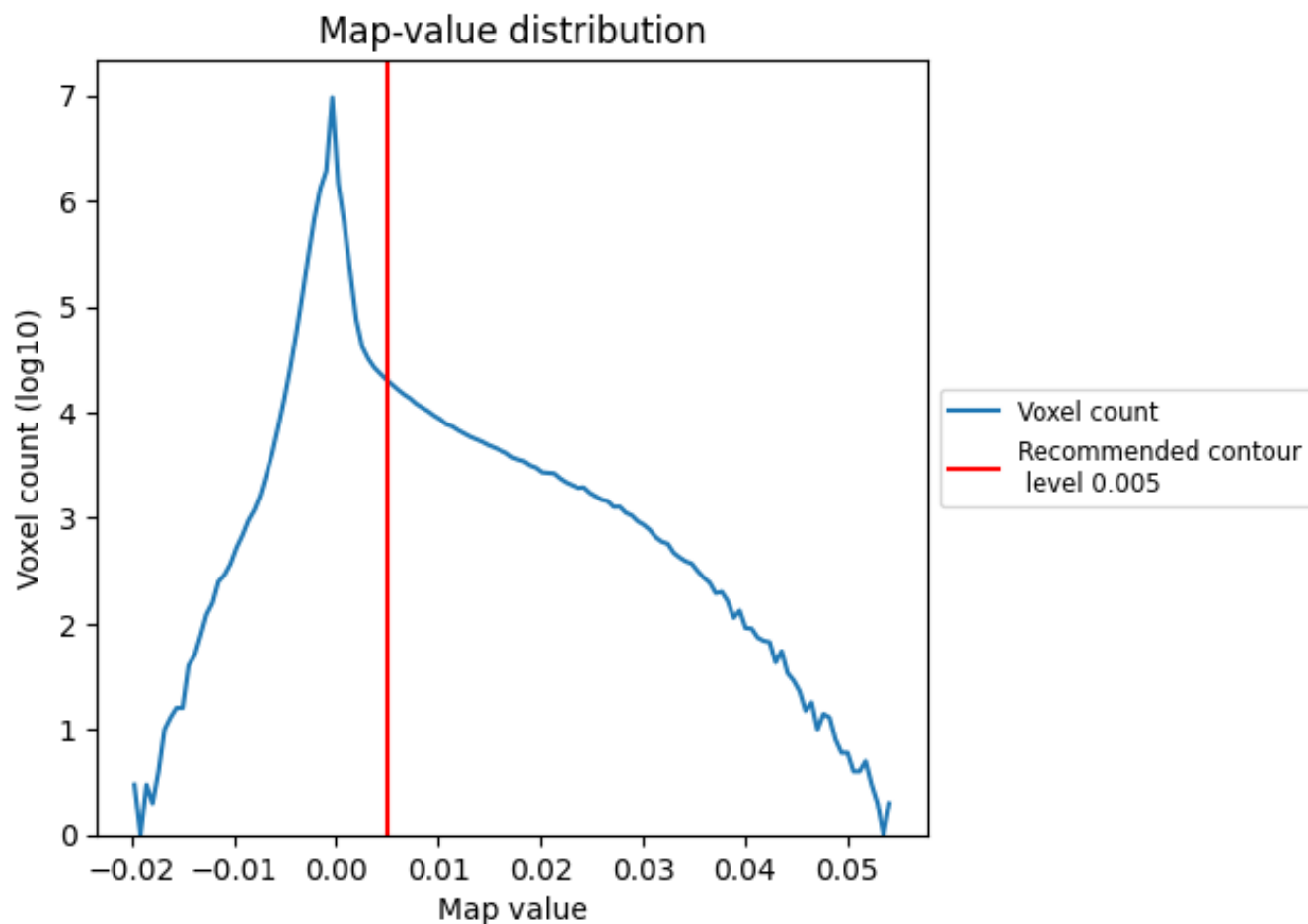
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

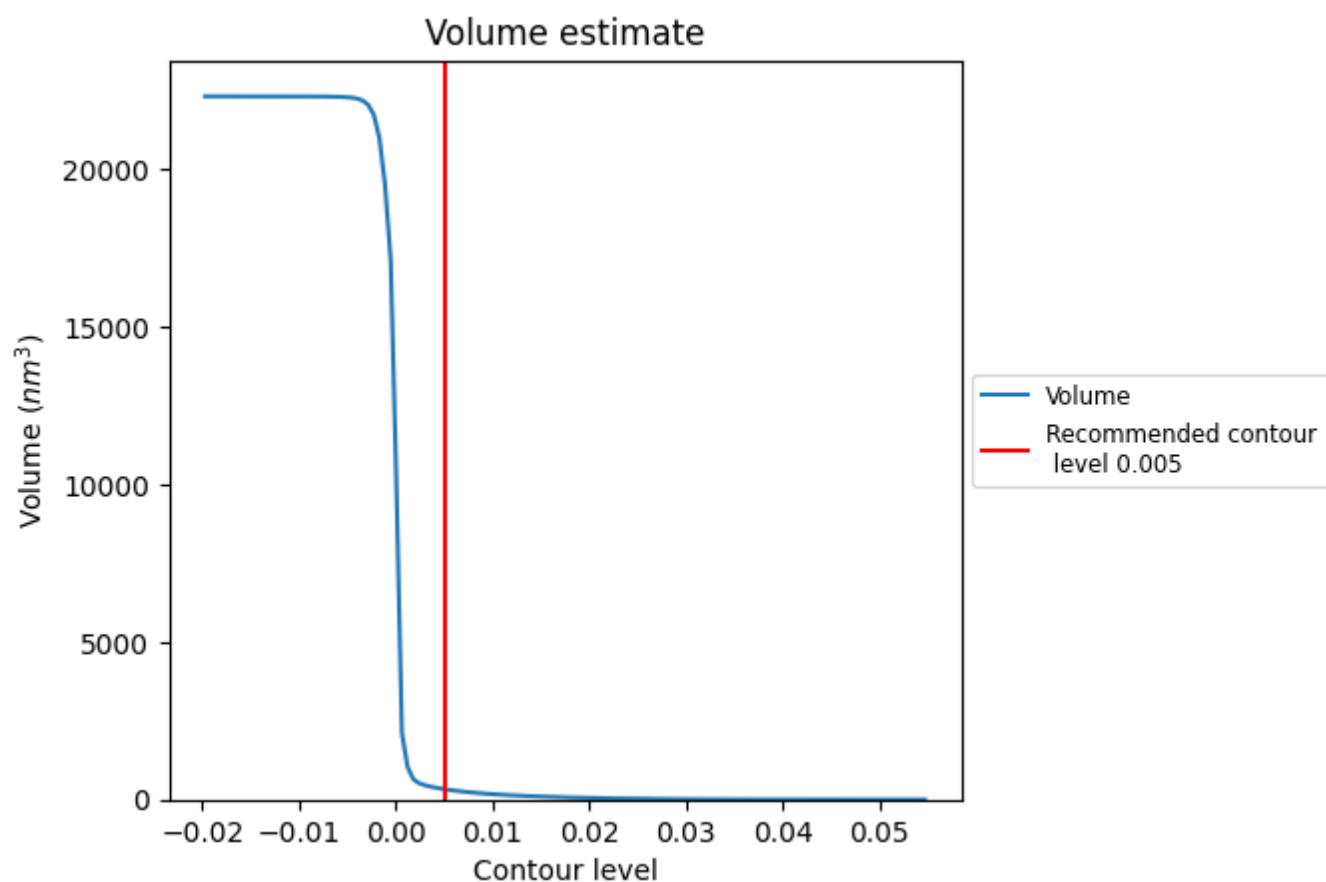
This section contains the results of statistical analysis of the map.

### 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.

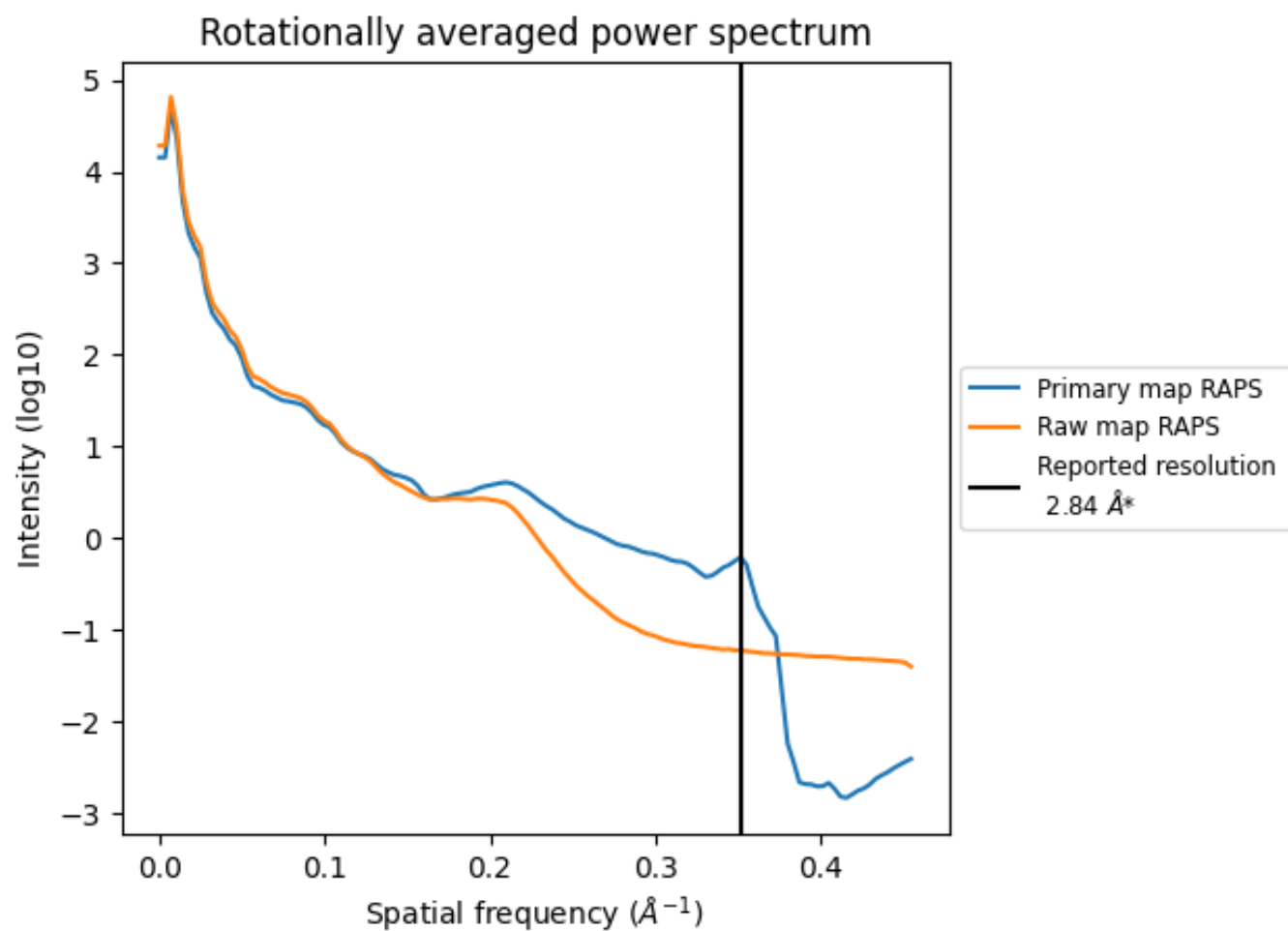
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 332  $\text{nm}^3$ ; this corresponds to an approximate mass of 300 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 ⓘ

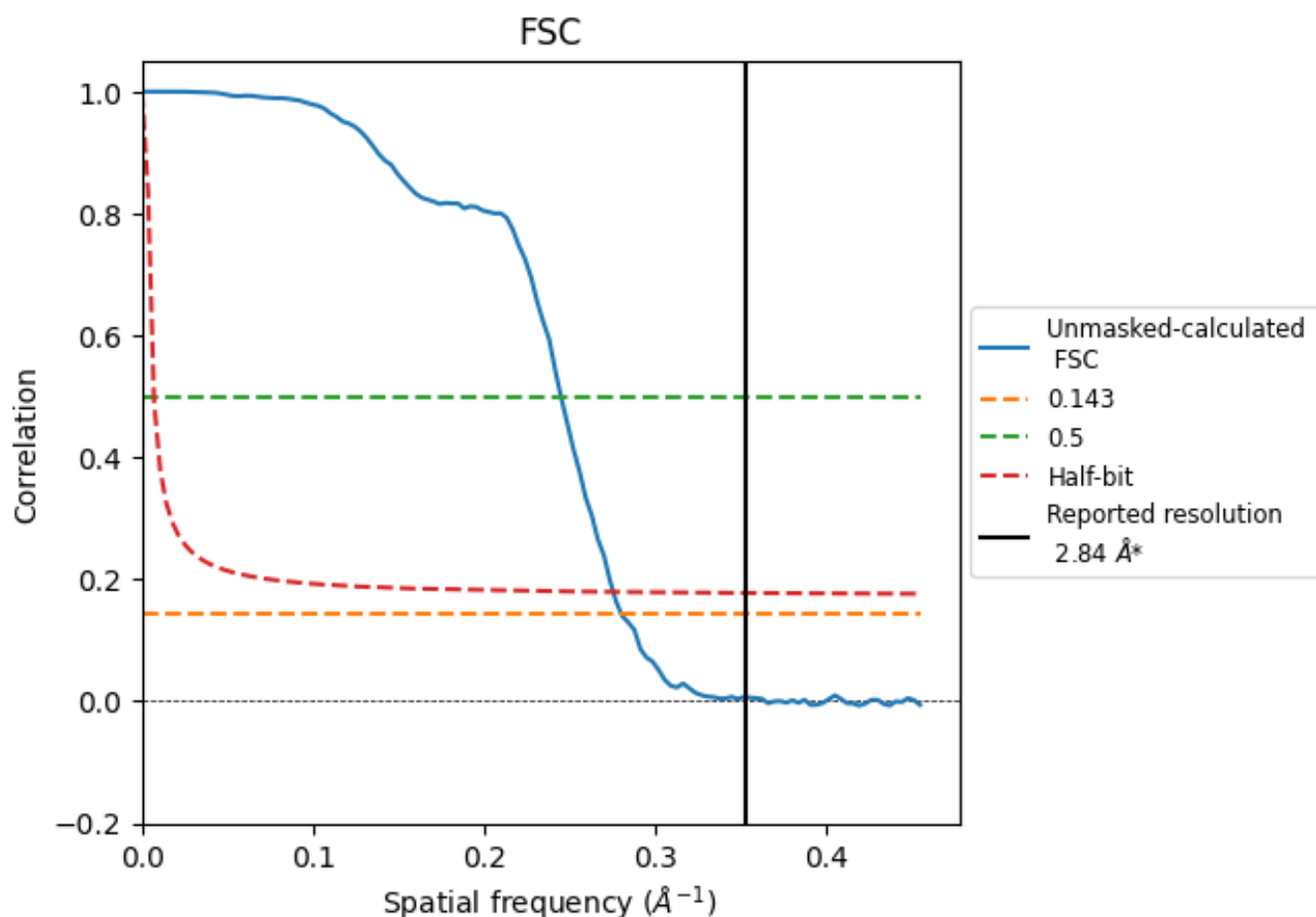


\*Reported resolution corresponds to spatial frequency of 0.352 Å<sup>-1</sup>

## 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 0.352 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

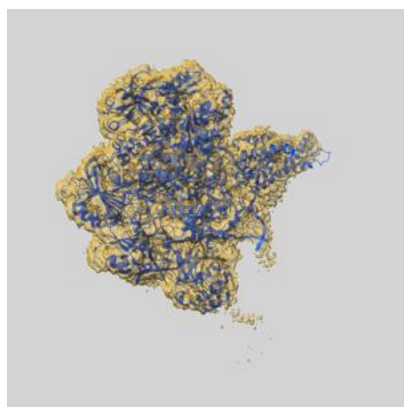
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.84	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.57	4.08	3.63

\*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 3.57 differs from the reported value 2.84 by more than 10 %

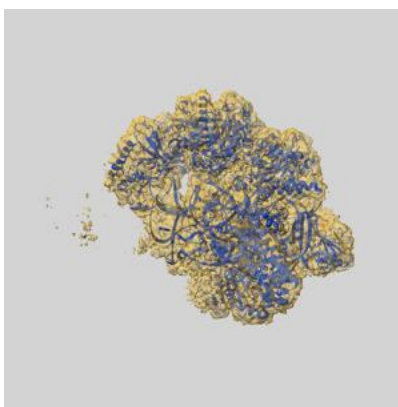
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64157 and PDB model 9UH7. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

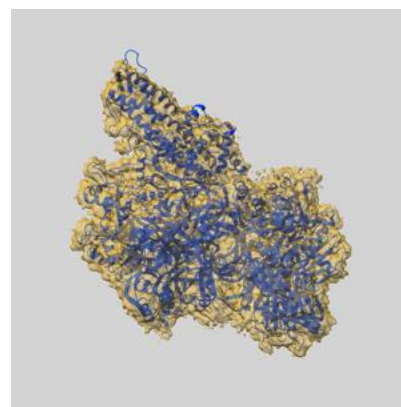
### 9.1 Map-model overlay [i](#)



X



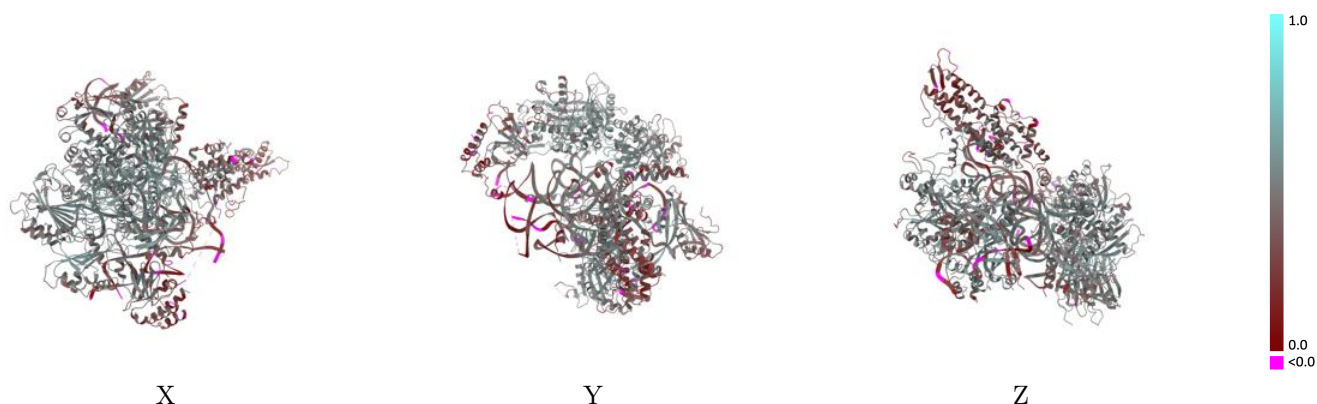
Y



Z

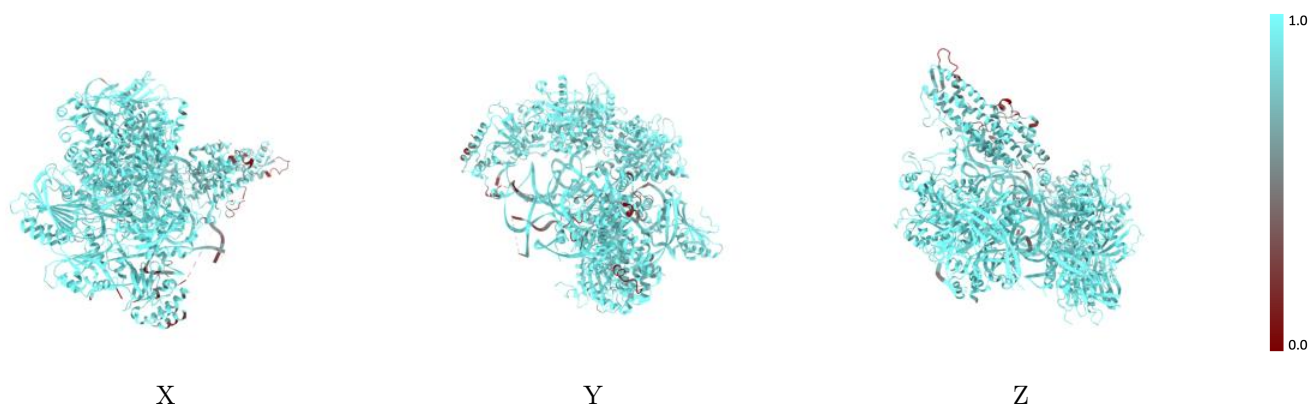
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



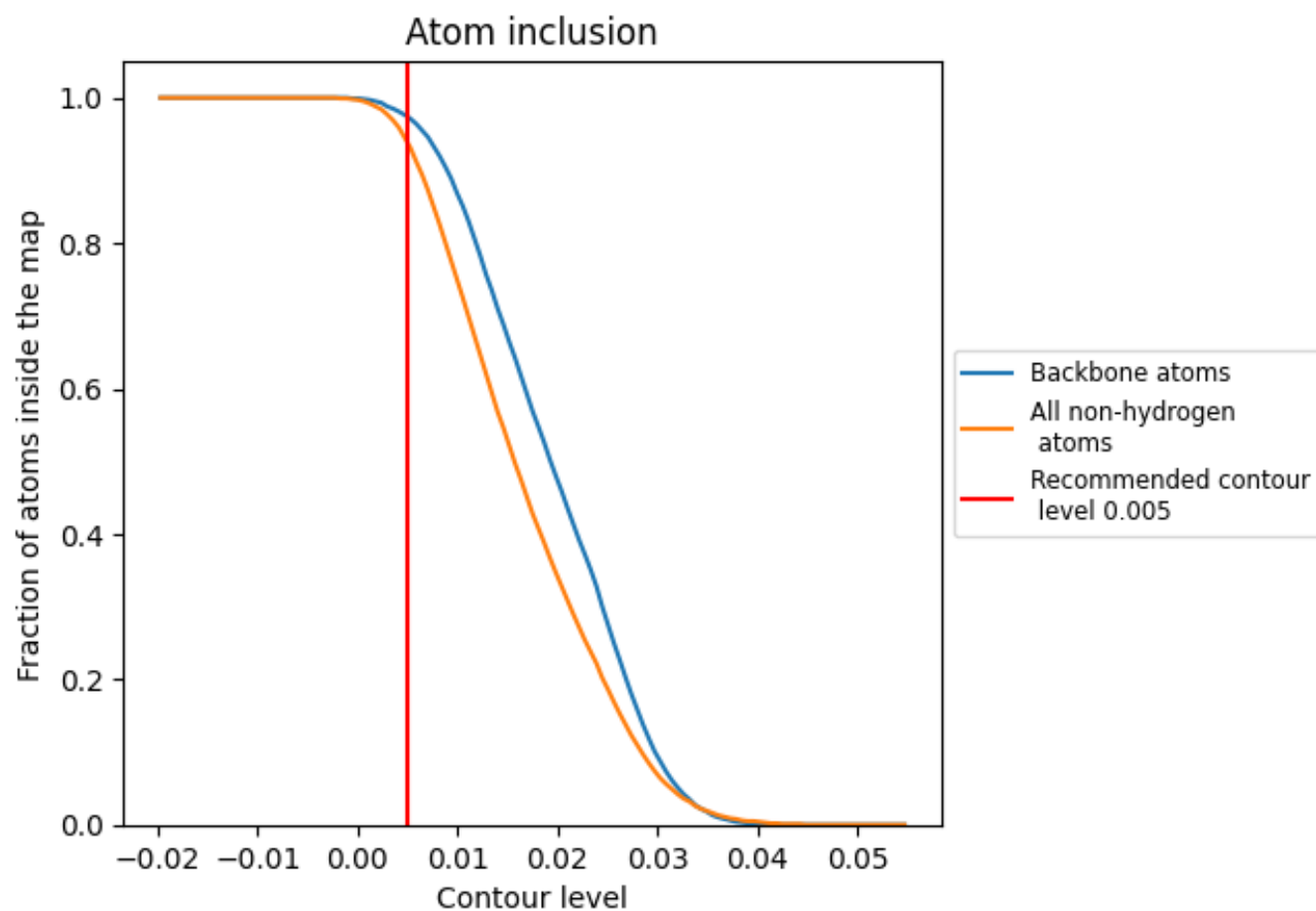
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 97% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9380	<div></div> 0.4380
A	<div></div> 0.9200	<div></div> 0.3580
B	<div></div> 0.9580	<div></div> 0.4910
D	<div></div> 0.8190	<div></div> 0.3460
E	<div></div> 0.9690	<div></div> 0.4850
F	<div></div> 0.9810	<div></div> 0.3800
G	<div></div> 0.9690	<div></div> 0.4890
H	<div></div> 0.9860	<div></div> 0.5180
I	<div></div> 0.9690	<div></div> 0.4590
J	<div></div> 0.9590	<div></div> 0.4720
K	<div></div> 0.7600	<div></div> 0.2340
L	<div></div> 0.9700	<div></div> 0.4980
M	<div></div> 0.8600	<div></div> 0.3450

