



## wwPDB EM Validation Summary Report ⓘ

Apr 13, 2026 – 04:34 PM JST

PDB ID : 9UHA / pdb\_00009uha  
EMDB ID : EMD-64160  
Title : human Ribonuclease MRP state 2  
Authors : Zhou, B.; Lan, P.; Wu, J.; Lei, M.  
Deposited on : 2025-04-14  
Resolution : 3.93 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

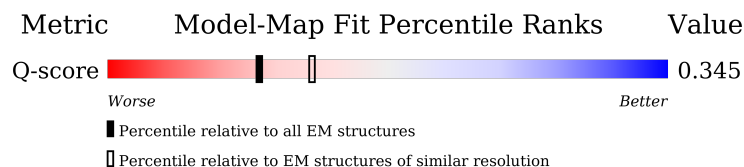
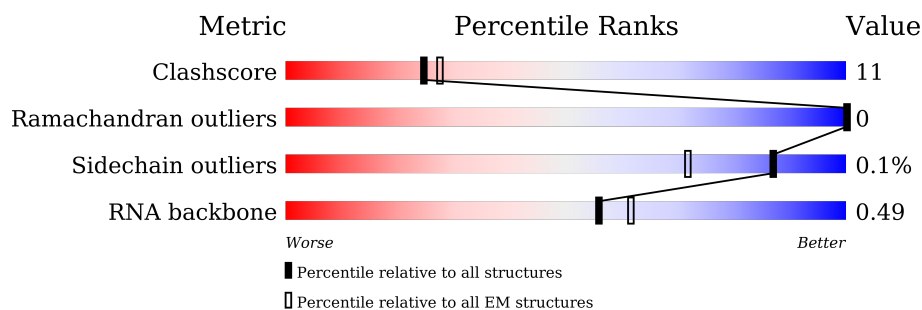
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.93 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.





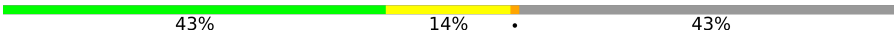




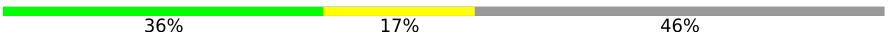


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7811 ( 3.43 - 4.43 )

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	C	283	

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Mol	Chain	Length	Quality of chain
4	D	220	
5	E	163	
6	F	199	
7	G	140	
8	H	124	
9	I	268	
9	J	268	
10	K	220	
11	L	363	
12	M	567	

## 2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 27442 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	270	Total	C	N	O	P	0	0
			5722	2553	1002	1897	270		

- 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 p38.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	137	Total	C	N	O	S	0	0
			1078	692	193	188	5		

- Molecule 4 is a protein called Ribonuclease P protein subunit p29.

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

- Molecule 5 is a protein called Ribonuclease P/MRP protein subunit POP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	149	Total	C	N	O	S	0	0
			1215	773	222	212	8		

- Molecule 6 is a protein called Ribonuclease P protein subunit p25.

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

- Molecule 7 is a protein called Ribonuclease P protein subunit p20.

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

- Molecule 8 is a protein called Ribonuclease P protein subunit p14.

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

- Molecule 9 is a protein called Ribonuclease P protein subunit p30.

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

- Molecule 10 is a protein called UPF0711 protein C18orf21.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	118	Total	C	N	O	S	0	0
			963	606	182	169	6		

- Molecule 11 is a protein called Ribonuclease P protein subunit p40.

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

- Molecule 12 is a protein called Nucleolus and neural progenitor protein.

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

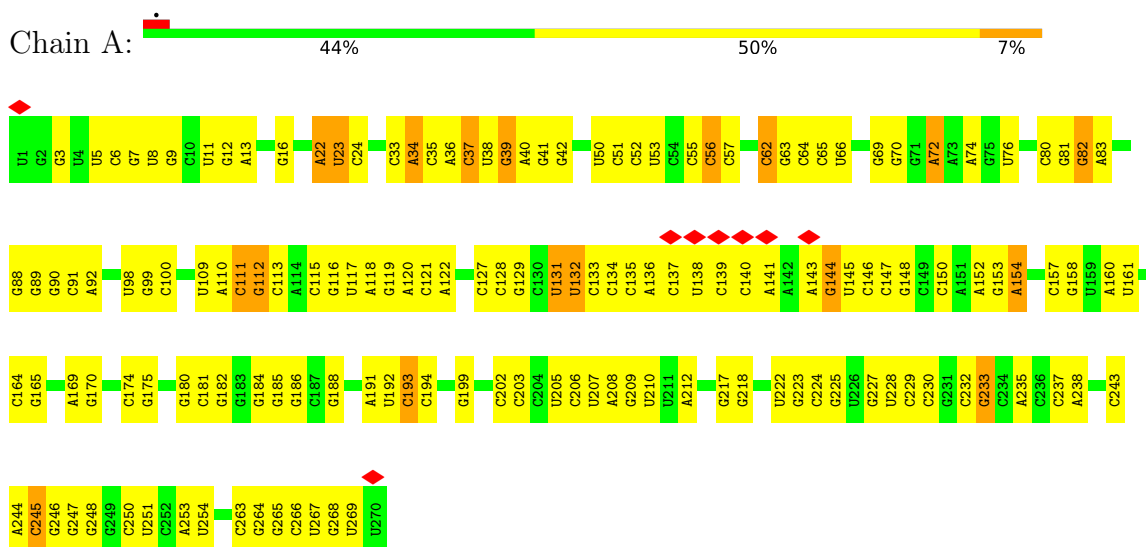
- Molecule 13 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
13	K	1	Total	Zn	0
			1	1	

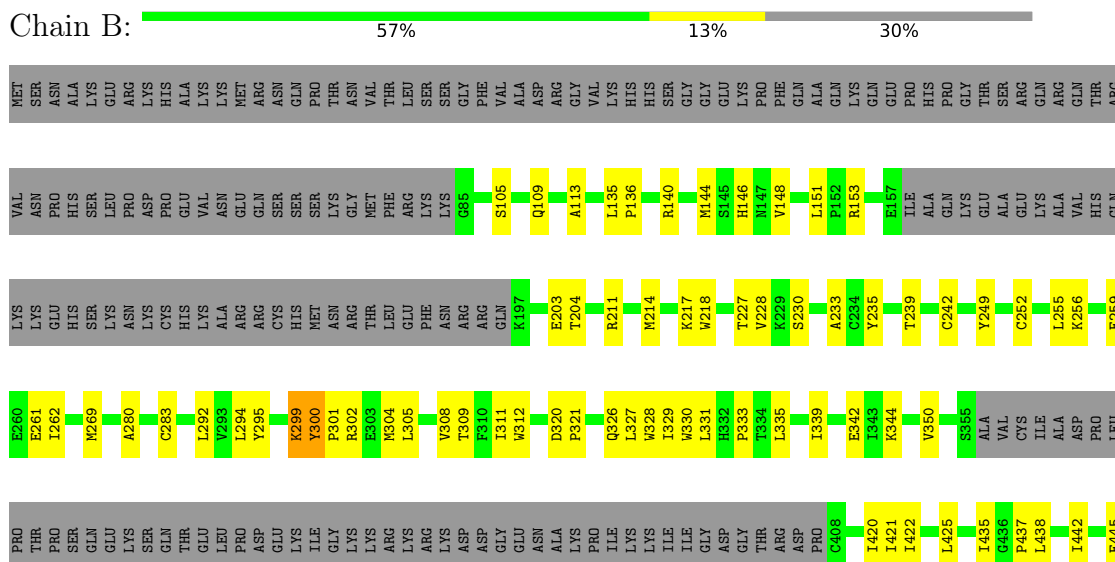
### 3 Residue-property plots

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: RNA (270-MER)



#### • Molecule 2: Ribonucleases P/MRP protein subunit POP1

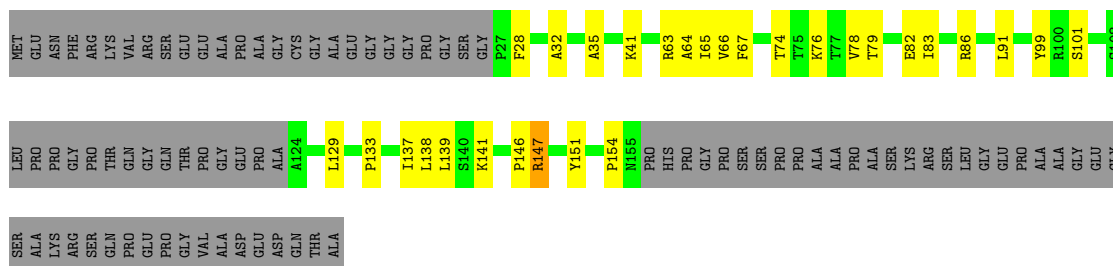






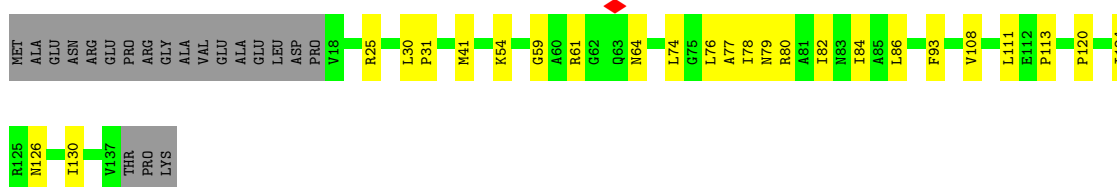
• Molecule 6: Ribonuclease P protein subunit p25

Chain F: 43% 14% 43%



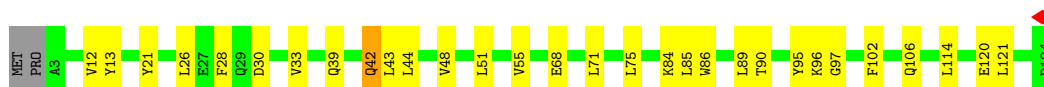
• Molecule 7: Ribonuclease P protein subunit p20

Chain G: 68% 18% 14%



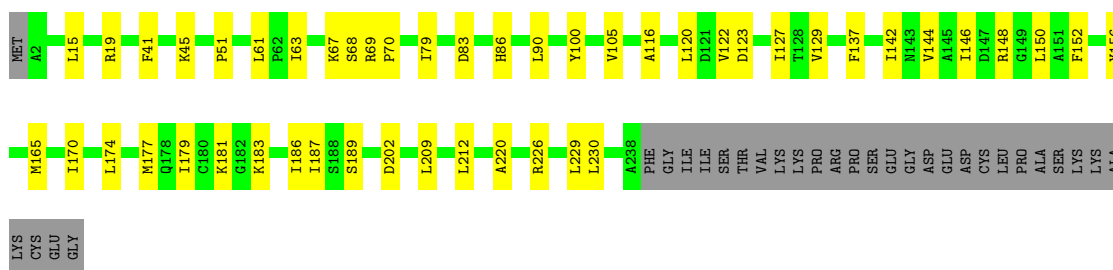
• Molecule 8: Ribonuclease P protein subunit p14

Chain H: 74% 23% 3%



• Molecule 9: Ribonuclease P protein subunit p30

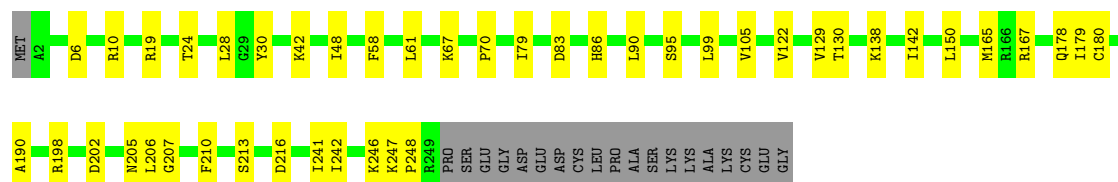
Chain I: 71% 18% 12%



• Molecule 9: Ribonuclease P protein subunit p30

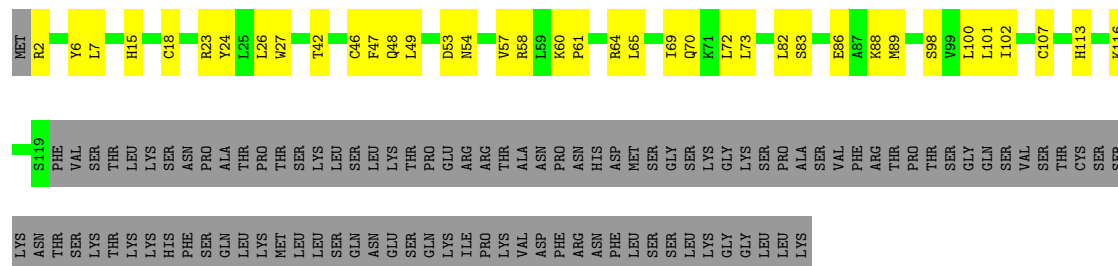
Chain J: 76% 16% 8%





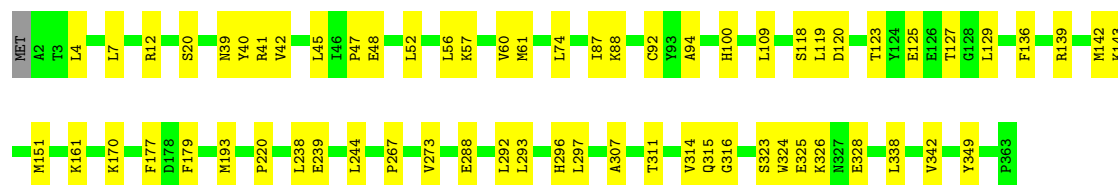
• Molecule 10: UPF0711 protein C18orf21

Chain K: 36% 17% 46%



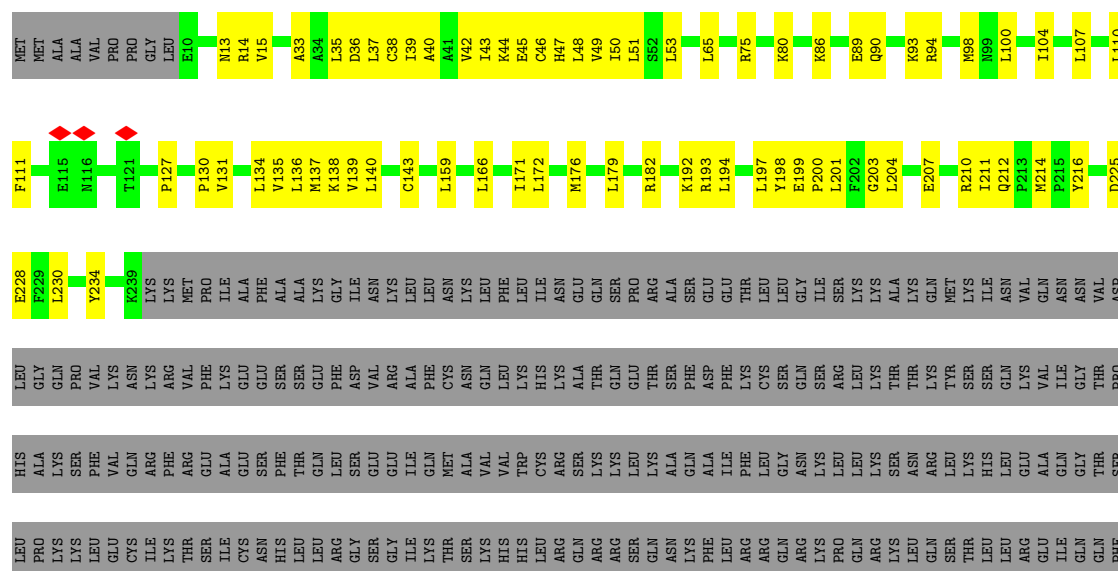
• Molecule 11: Ribonuclease P protein subunit p40

Chain L: 82% 18%



• Molecule 12: Nucleolus and neural progenitor protein

Chain M: 28% 13% 59%



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

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	294518	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	0.034	Depositor
Minimum map value	-0.015	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.003	Depositor
Map size ( $\text{\AA}$ )	334.4, 334.4, 334.4	wwPDB
Map dimensions	304, 304, 304	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

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0/6384	0.23	0/9943
2	B	0.13	0/5828	0.57	9/7885 (0.1%)
3	C	0.12	0/1095	0.41	1/1482 (0.1%)
4	D	0.13	0/1529	0.35	0/2056
5	E	0.16	0/1238	0.42	0/1671
6	F	0.15	0/884	0.43	1/1194 (0.1%)
7	G	0.11	0/957	0.35	0/1293
8	H	0.15	0/963	0.45	1/1303 (0.1%)
9	I	0.11	0/1860	0.32	0/2522
9	J	0.12	0/1949	0.35	1/2641 (0.0%)
10	K	0.15	0/982	0.48	0/1316
11	L	0.13	0/3021	0.36	0/4099
12	M	0.18	0/1864	0.54	0/2526
All	All	0.13	0/28554	0.41	13/39931 (0.0%)

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	999	ALA	N-CA-C	28.70	148.39	112.23
2	B	999	ALA	N-CA-CB	-15.85	85.89	110.30
2	B	998	PRO	N-CA-C	-13.69	84.28	112.47
2	B	1000	ALA	N-CA-C	-10.93	99.46	113.12
2	B	299	LYS	CB-CA-C	-8.89	96.30	111.23

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	A	5722	0	2917	104	0
2	B	5689	0	5775	99	0
3	C	1078	0	1156	28	0
4	D	1502	0	1561	50	0
5	E	1215	0	1232	40	0
6	F	869	0	912	25	0
7	G	945	0	971	23	0
8	H	946	0	977	24	0
9	I	1829	0	1914	40	0
9	J	1916	0	2015	29	0
10	K	963	0	990	40	0
11	L	2939	0	2884	53	0
12	M	1828	0	1926	56	0
13	K	1	0	0	0	0
All	All	27442	0	25230	556	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 11.

The worst 5 of 556 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)
5:E:118:ASN:OD1	5:E:142:VAL:HG13	1.69	0.93
11:L:92:CYS:SG	11:L:109:LEU:HD21	2.11	0.89
11:L:311:THR:HG22	11:L:342:VAL:HG22	1.55	0.89
1:A:235:A:H5''	11:L:12:ARG:HH12	1.40	0.85
8:H:55:VAL:HG11	9:I:209:LEU:HD21	1.60	0.83

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	
2	B	704/1024 (69%)	662 (94%)	42 (6%)	0	100	100
3	C	133/283 (47%)	130 (98%)	3 (2%)	0	100	100
4	D	182/220 (83%)	172 (94%)	10 (6%)	0	100	100
5	E	147/163 (90%)	139 (95%)	8 (5%)	0	100	100
6	F	110/199 (55%)	110 (100%)	0	0	100	100
7	G	118/140 (84%)	115 (98%)	3 (2%)	0	100	100
8	H	120/124 (97%)	115 (96%)	5 (4%)	0	100	100
9	I	235/268 (88%)	227 (97%)	8 (3%)	0	100	100
9	J	246/268 (92%)	240 (98%)	6 (2%)	0	100	100
10	K	116/220 (53%)	106 (91%)	10 (9%)	0	100	100
11	L	360/363 (99%)	353 (98%)	7 (2%)	0	100	100
12	M	228/567 (40%)	221 (97%)	7 (3%)	0	100	100
All	All	2699/3839 (70%)	2590 (96%)	109 (4%)	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	
2	B	624/883 (71%)	623 (100%)	1 (0%)	87	88
3	C	122/255 (48%)	122 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	166/196 (85%)	165 (99%)	1 (1%)	78	81
5	E	133/143 (93%)	132 (99%)	1 (1%)	73	77
6	F	92/150 (61%)	92 (100%)	0	100	100
7	G	102/118 (86%)	102 (100%)	0	100	100
8	H	104/106 (98%)	104 (100%)	0	100	100
9	I	202/228 (89%)	202 (100%)	0	100	100
9	J	212/228 (93%)	212 (100%)	0	100	100
10	K	107/201 (53%)	107 (100%)	0	100	100
11	L	331/332 (100%)	331 (100%)	0	100	100
12	M	208/513 (40%)	208 (100%)	0	100	100
All	All	2403/3353 (72%)	2400 (100%)	3 (0%)	87	90

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	891	HIS
4	D	165	PHE
5	E	73	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
11	L	135	GLN
12	M	13	ASN
12	M	212	GLN
11	L	347	GLN
7	G	126	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	269/270 (99%)	61 (22%)	2 (0%)

5 of 61 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 (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	117	U
1	A	174	C

## 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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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.



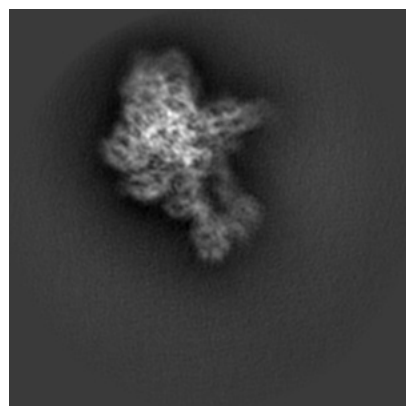
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64160. These allow visual inspection of the internal detail of the map and identification of artifacts.

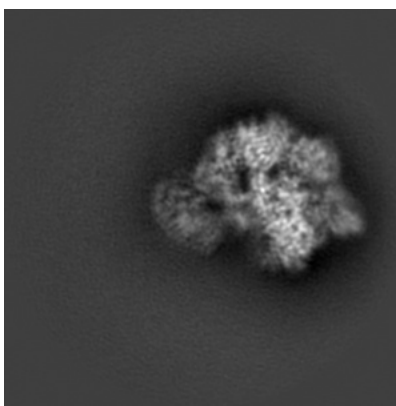
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

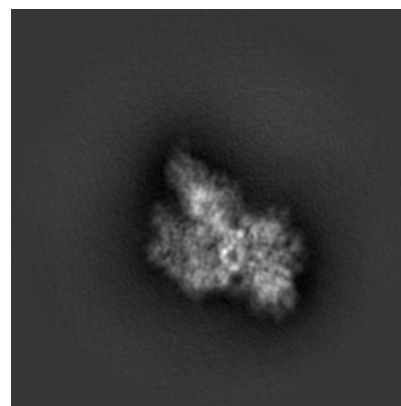
#### 6.1.1 Primary map



X

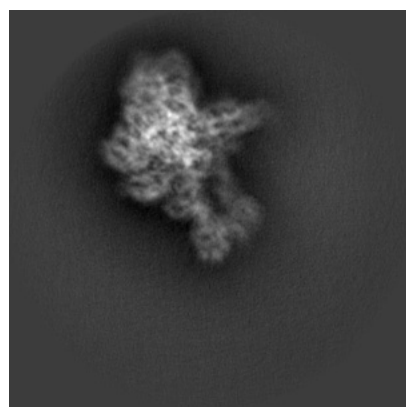


Y

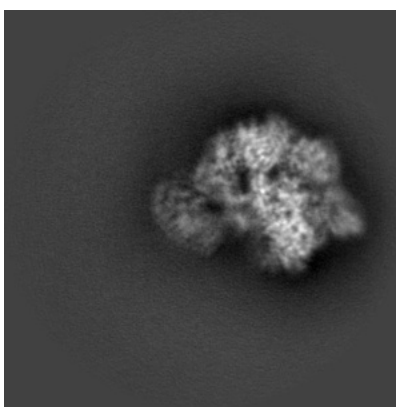


Z

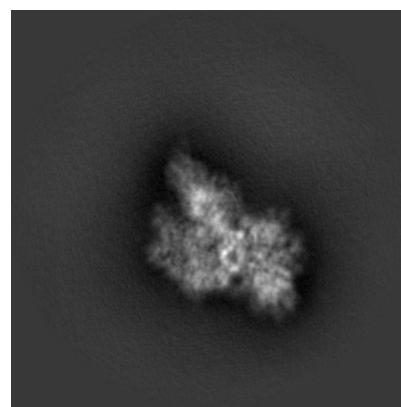
#### 6.1.2 Raw map



X



Y

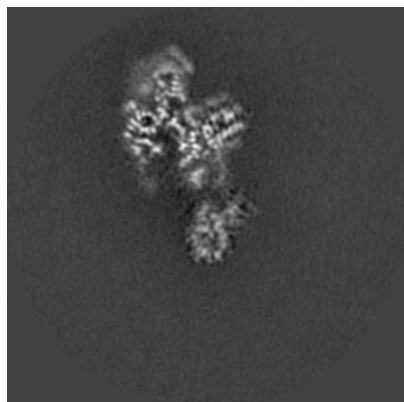


Z

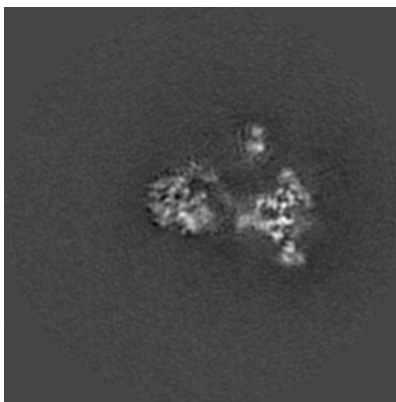
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

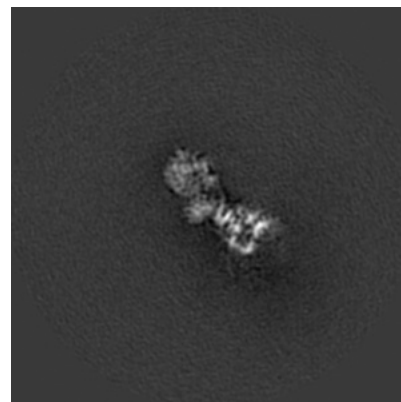
### 6.2.1 Primary map



X Index: 152

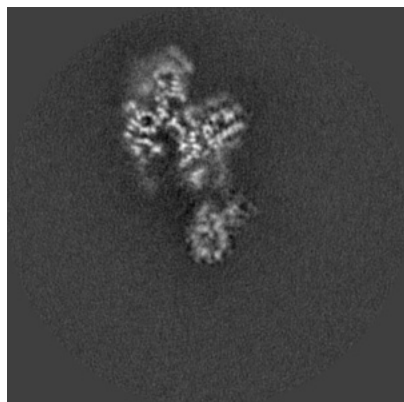


Y Index: 152

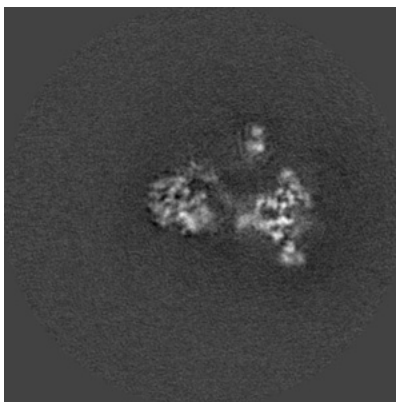


Z Index: 152

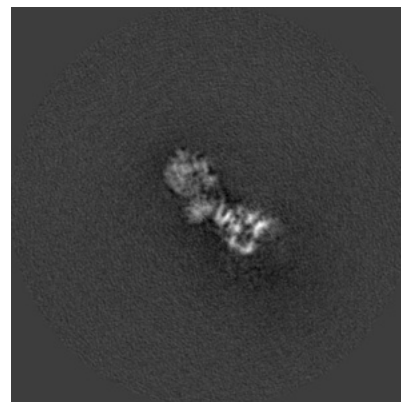
### 6.2.2 Raw map



X Index: 152



Y Index: 152

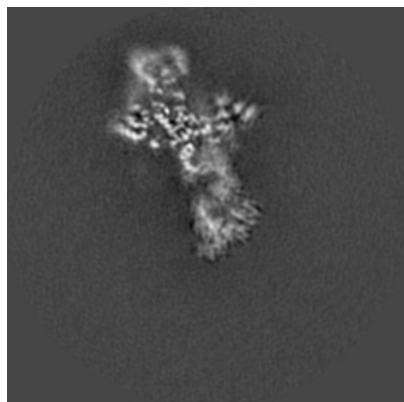


Z Index: 152

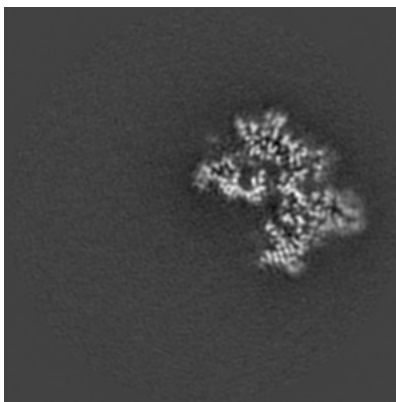
The images above show central slices of the map in three orthogonal directions.

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

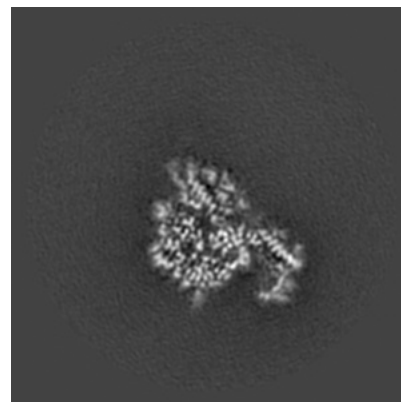
### 6.3.1 Primary map



X Index: 142

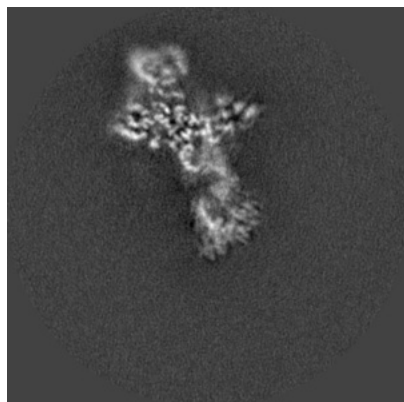


Y Index: 121

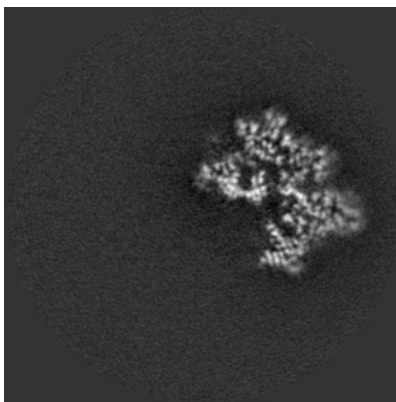


Z Index: 213

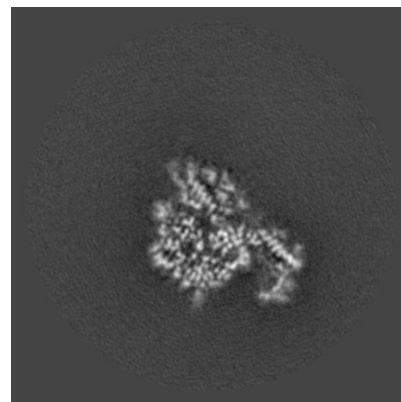
### 6.3.2 Raw map



X Index: 141



Y Index: 120

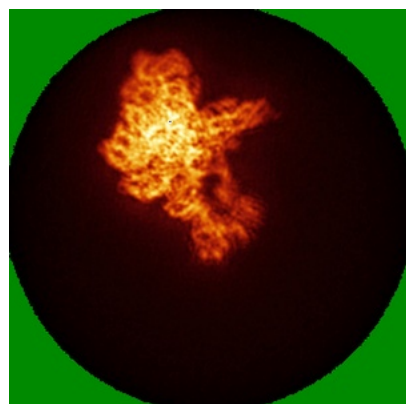


Z Index: 213

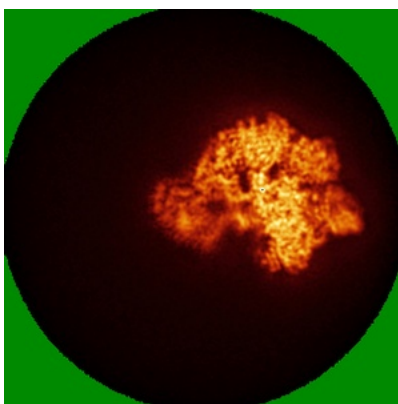
The images above show the largest variance slices of the map in three orthogonal directions.

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

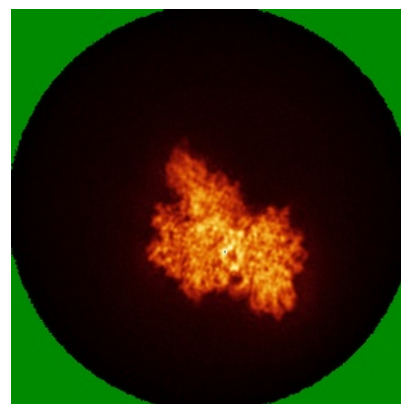
### 6.4.1 Primary map



X

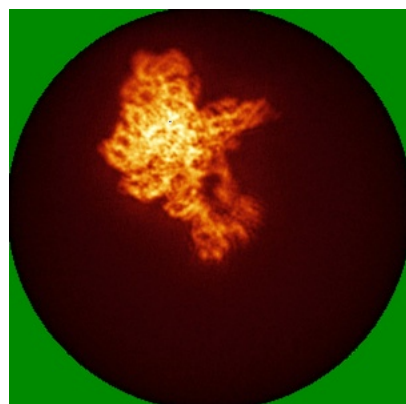


Y

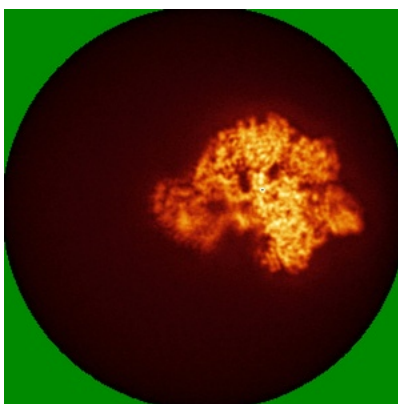


Z

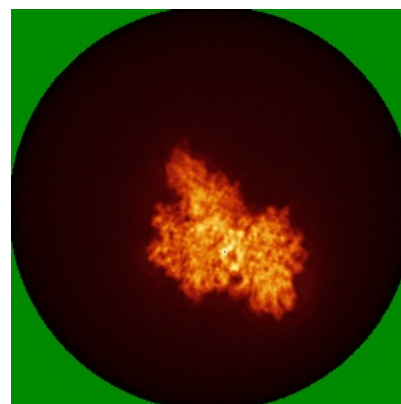
### 6.4.2 Raw map



X



Y

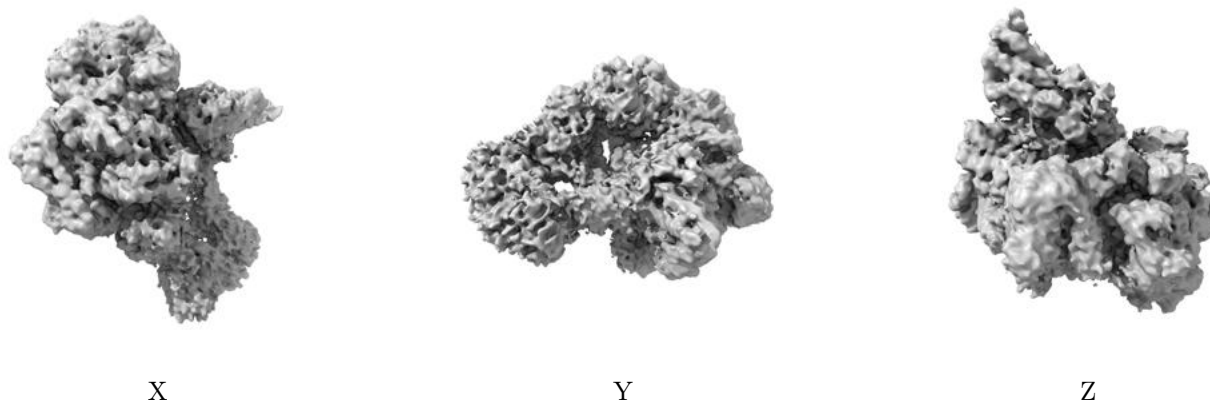


Z

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.

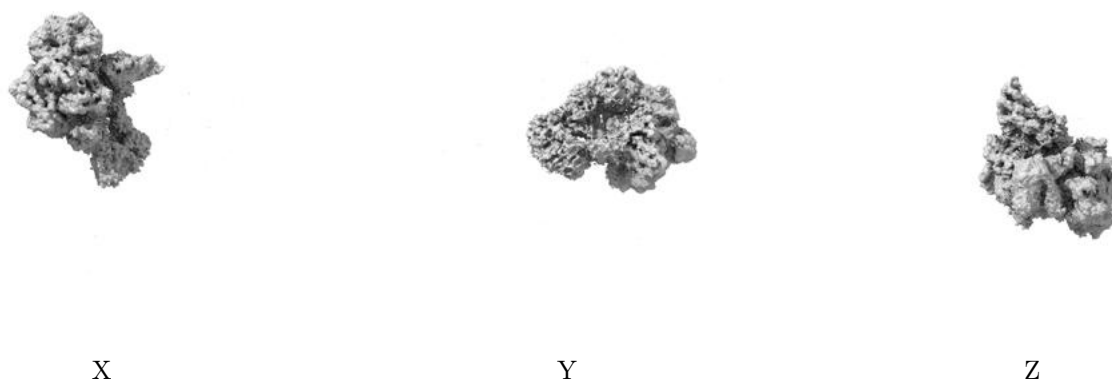
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.003. 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.

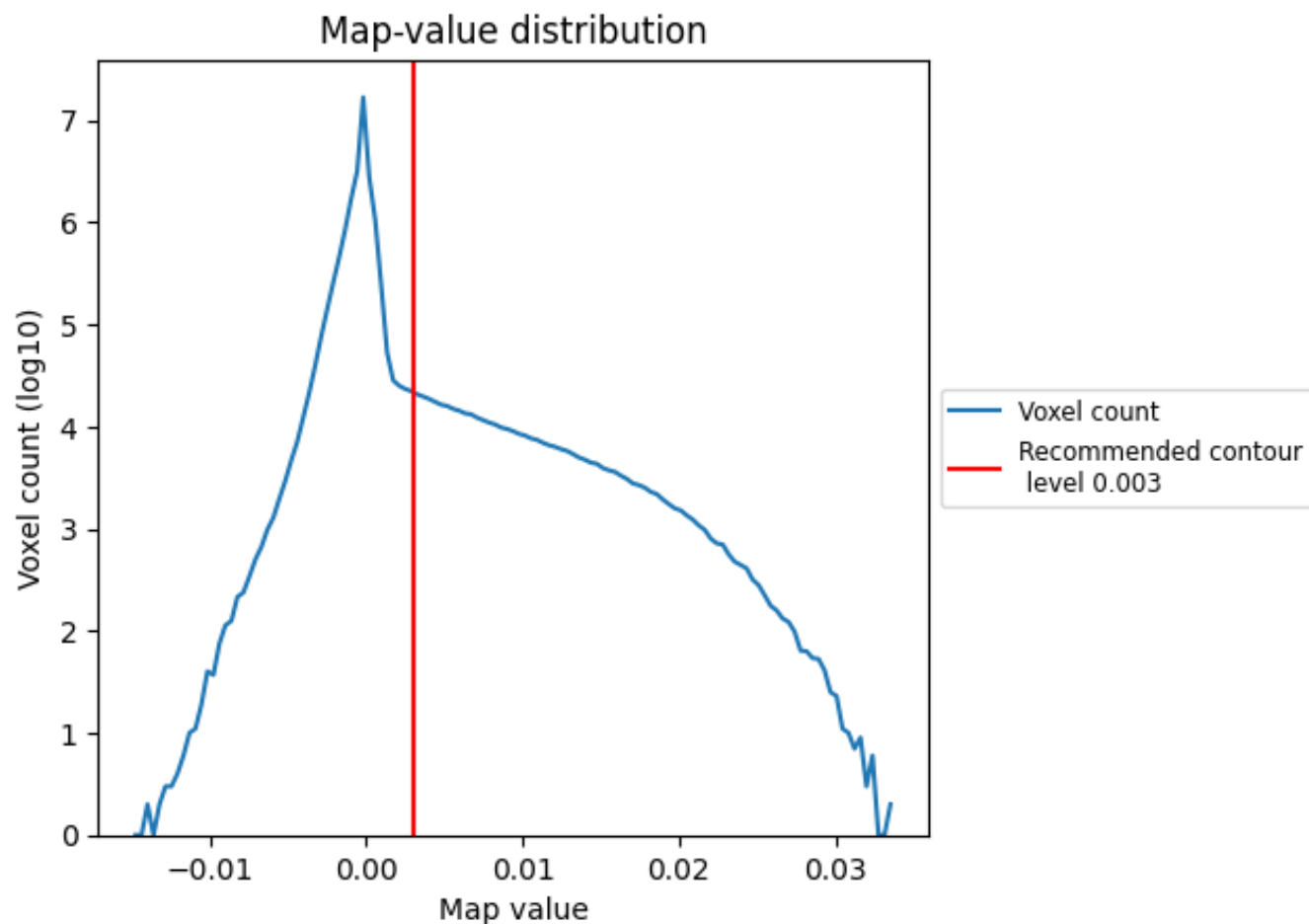
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

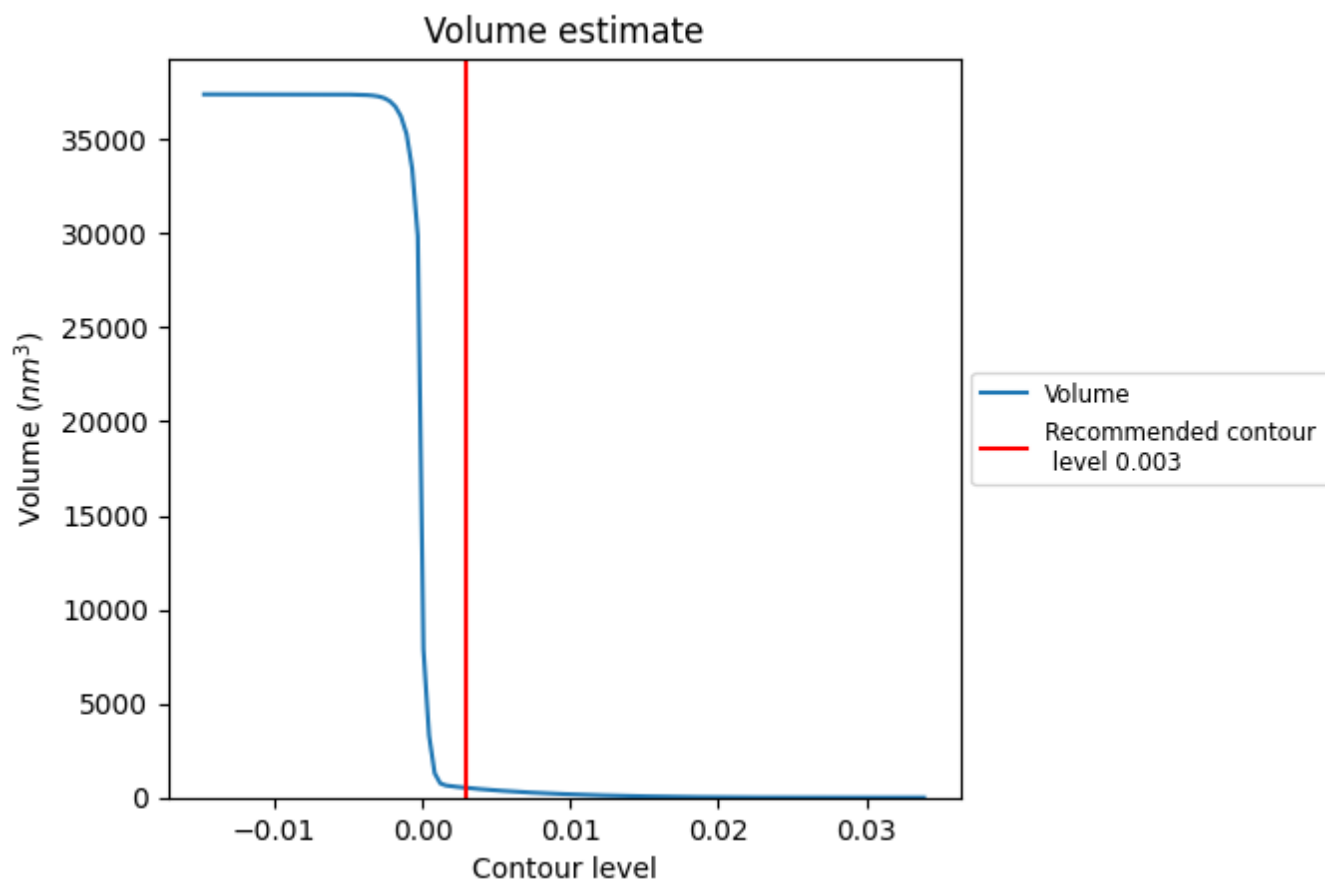
This section contains the results of statistical analysis of the map.

### 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.

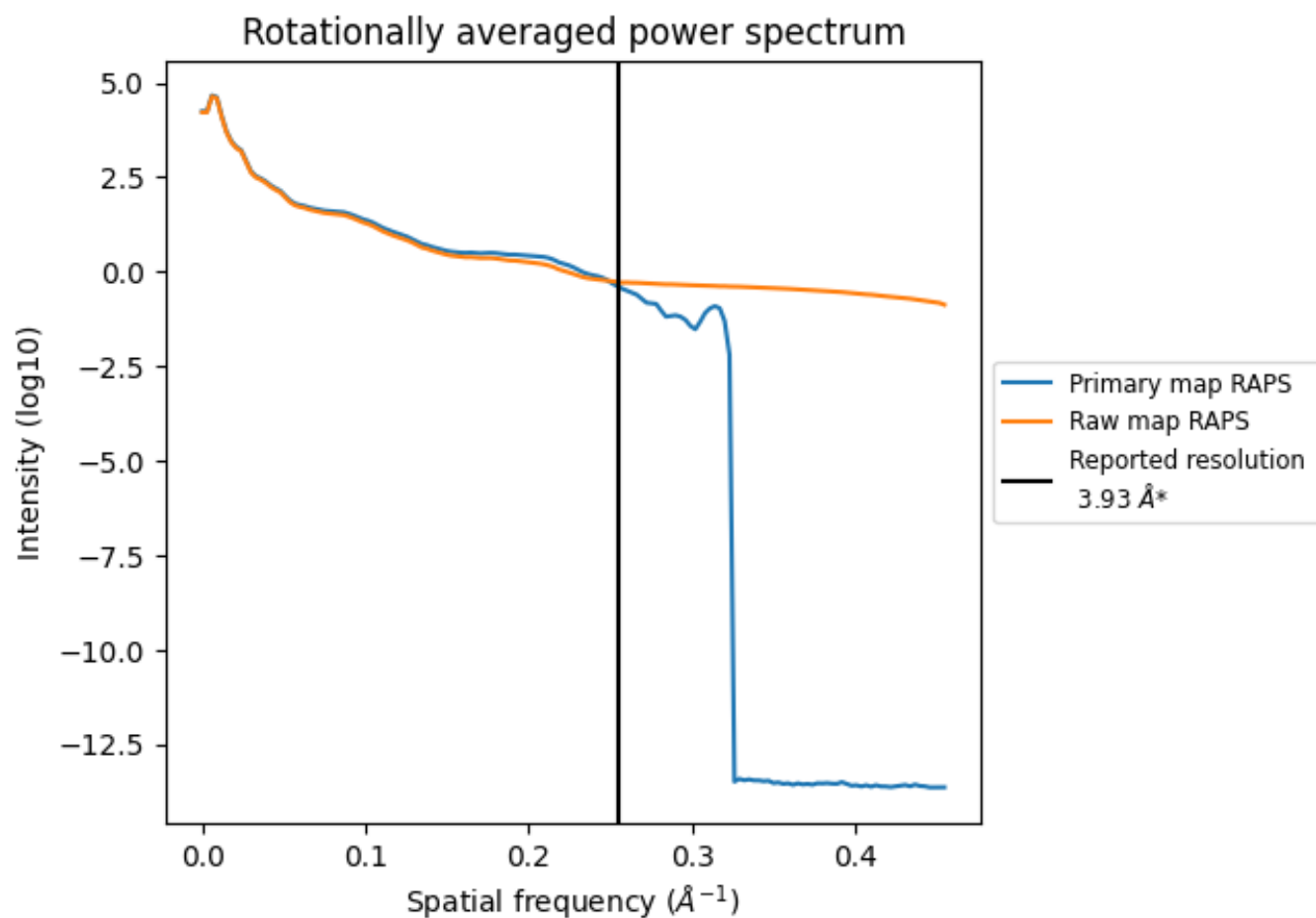
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 515 nm<sup>3</sup>; this corresponds to an approximate mass of 465 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 ⓘ



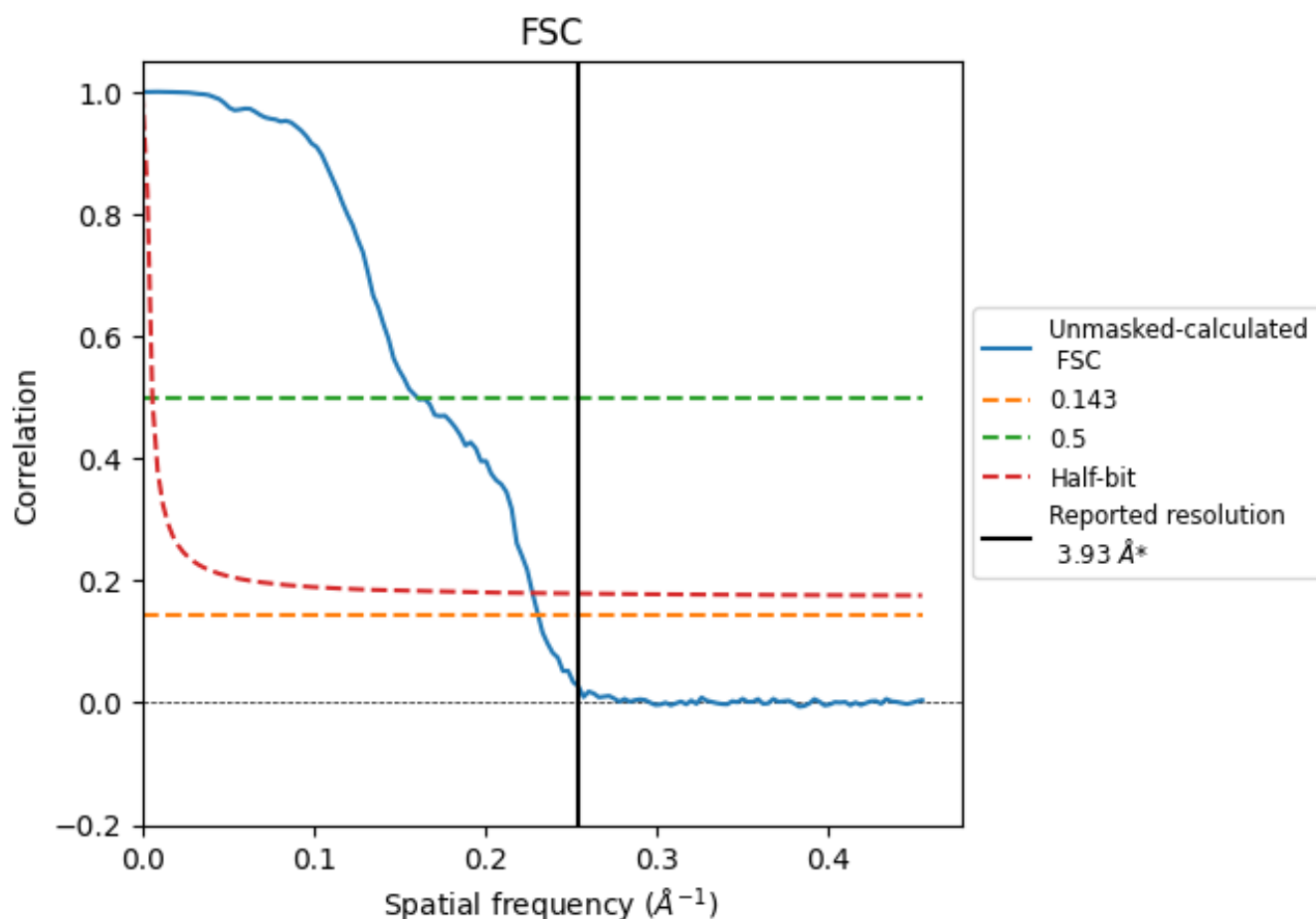
\*Reported resolution corresponds to spatial frequency of 0.254 Å<sup>-1</sup>



## 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 0.254 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

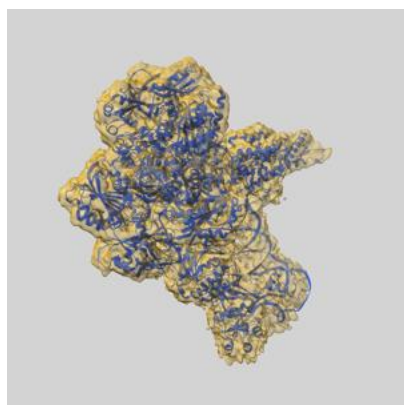
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.93	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.33	6.24	4.40

\*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 4.33 differs from the reported value 3.93 by more than 10 %

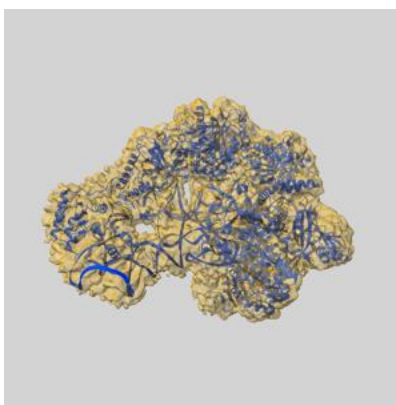
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64160 and PDB model 9UHA. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

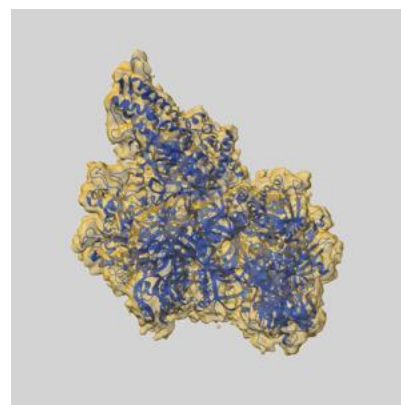
### 9.1 Map-model overlay [i](#)



X



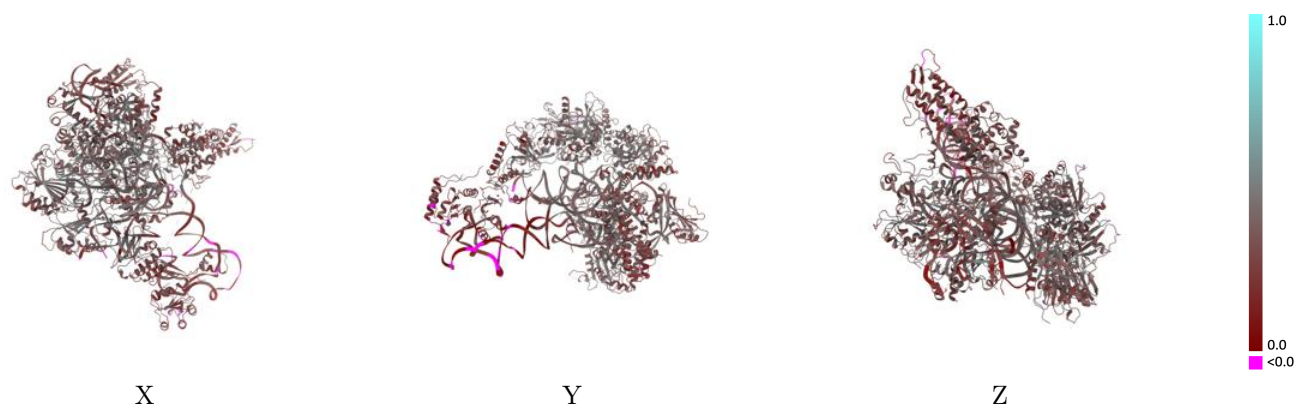
Y



Z

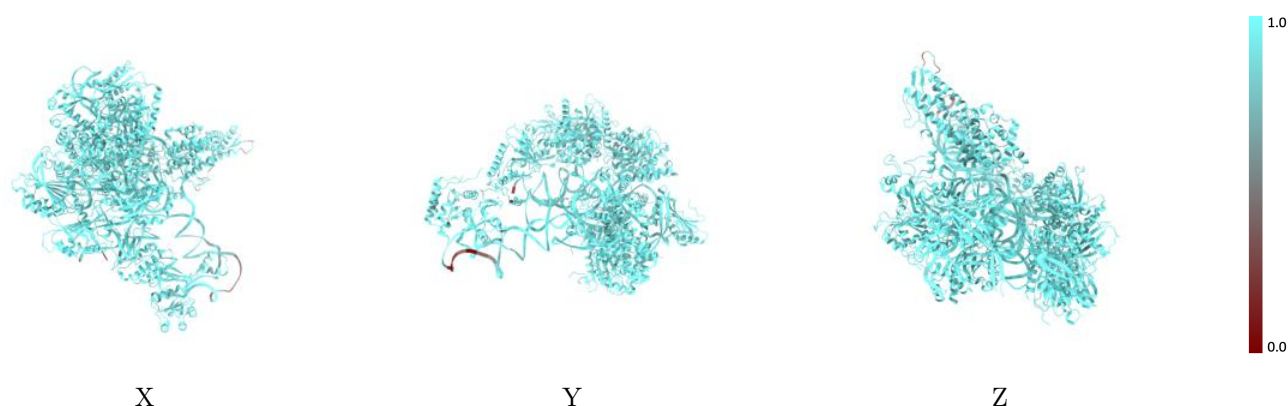
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



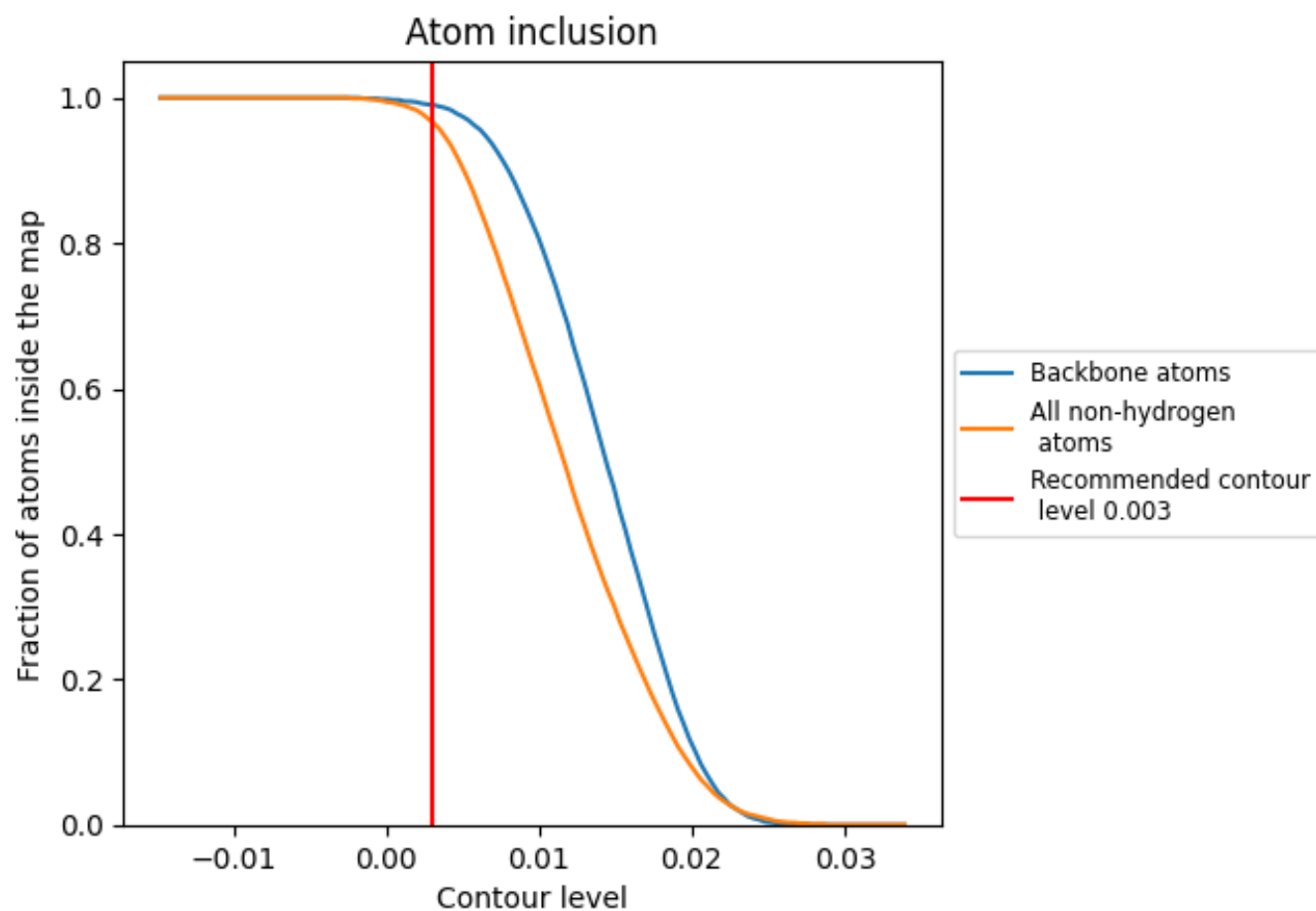
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.003).





























## 9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 97% 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 (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9670	 0.3450
A	 0.9510	 0.2890
B	 0.9800	 0.3880
C	 0.9490	 0.2610
D	 0.9630	 0.3430
E	 0.9740	 0.3730
F	 0.9930	 0.2600
G	 0.9850	 0.3680
H	 0.9800	 0.4080
I	 0.9810	 0.3580
J	 0.9720	 0.3880
K	 0.9440	 0.2790
L	 0.9800	 0.3980
M	 0.9360	 0.3060

