



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 07:06 PM UTC

PDB ID : 7R5H / pdb_00007r5h
EMDB ID : EMD-14320
Title : In vitro assembled 266/297 - 391 tau filaments with KCl (10b)
Authors : Lovestam, S.; Scheres, S.H.W.
Deposited on : 2022-02-10
Resolution : 2.59 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
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

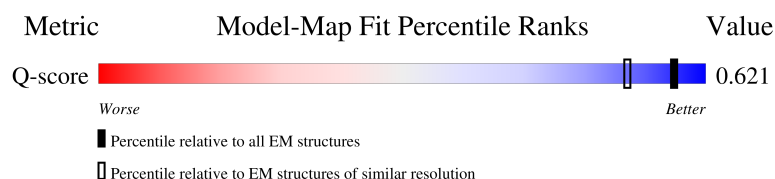
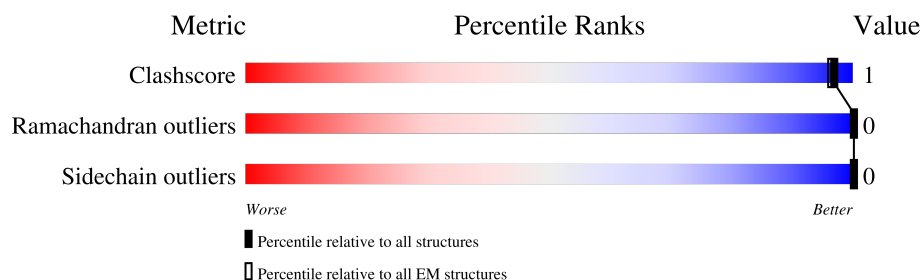
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.59 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	-
Q-score	-	25397	7741 (2.09 - 3.09)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	441	
1	B	441	
1	C	441	
1	D	441	

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Mol	Chain	Length	Quality of chain
1	E	441	 17%83%
1	F	441	 17%83%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7440 atoms, of which 3786 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.

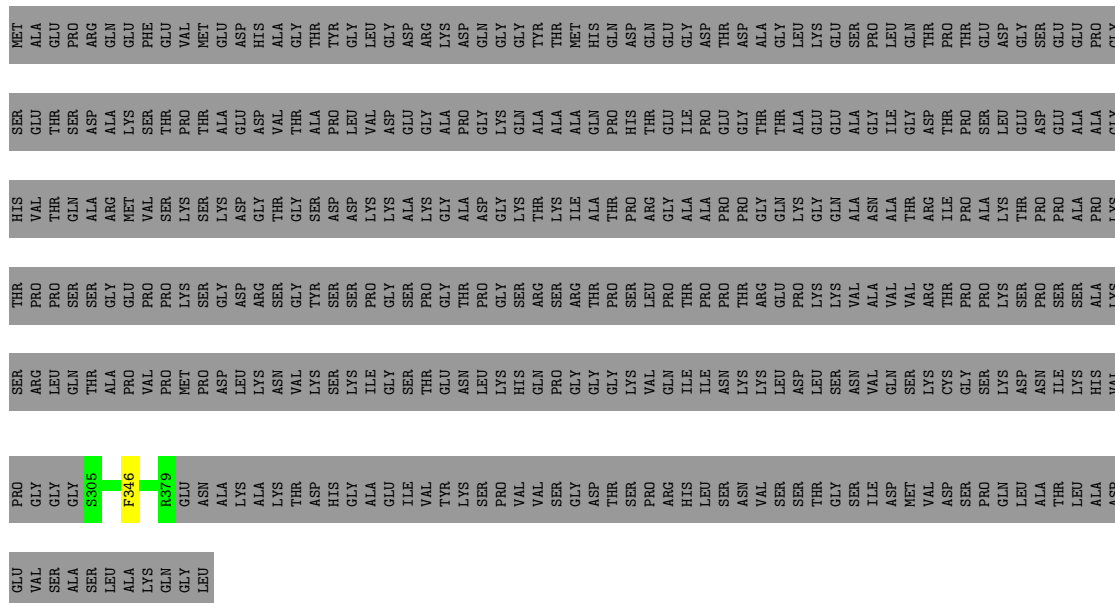
- Molecule 1 is a protein called Microtubule-associated protein tau.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	84	Total	C	H	N	O	S	0	0
			1308	401	664	120	122	1		
1	B	84	Total	C	H	N	O	S	0	0
			1308	401	664	120	122	1		
1	C	84	Total	C	H	N	O	S	0	0
			1308	401	664	120	122	1		
1	D	75	Total	C	H	N	O	S	0	0
			1172	360	598	106	107	1		
1	E	75	Total	C	H	N	O	S	0	0
			1172	360	598	106	107	1		
1	F	75	Total	C	H	N	O	S	0	0
			1172	360	598	106	107	1		

- Molecule 1: Microtubule-associated protein tau



- Molecule 1: Microtubule-associated protein tau



- Molecule 1: Microtubule-associated protein tau

[illegible]

Chain F: 17% 83%

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

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-0.88°, rise=4.77 Å, axial sym=C1	Depositor
Number of segments used	111483	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.029	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00579	Depositor
Map size (Å)	316.41602, 316.41602, 316.41602	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82400006, 0.82400006, 0.82400006	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.70	0/654	1.27	1/875 (0.1%)
1	B	0.68	0/654	1.26	1/875 (0.1%)
1	C	0.69	0/654	1.25	2/875 (0.2%)
1	D	0.70	0/583	1.20	1/780 (0.1%)
1	E	0.70	0/583	1.20	0/780
1	F	0.68	0/583	1.21	1/780 (0.1%)
All	All	0.69	0/3711	1.23	6/4965 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	346	PHE	CA-CB-CG	5.47	119.27	113.80
1	A	346	PHE	CA-CB-CG	5.40	119.20	113.80
1	C	346	PHE	CA-CB-CG	5.29	119.09	113.80
1	B	388	HIS	CB-CG-CD2	-5.09	124.59	131.20
1	C	362	HIS	CB-CG-CD2	-5.07	124.61	131.20
1	F	346	PHE	CA-CB-CG	5.04	118.83	113.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	644	664	663	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	644	664	663	1	0
1	C	644	664	663	2	0
1	D	574	598	597	0	0
1	E	574	598	597	0	0
1	F	574	598	597	0	0
All	All	3654	3786	3780	5	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 1.

All (5) 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)
1:A:326:GLY:CA	1:A:361:THR:HG21	2.41	0.50
1:C:326:GLY:HA2	1:C:361:THR:HG21	1.98	0.45
1:A:326:GLY:HA2	1:A:361:THR:HG21	1.98	0.45
1:B:326:GLY:HA3	1:B:361:THR:HG21	1.99	0.44
1:C:326:GLY:CA	1:C:361:THR:HG21	2.50	0.42

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	
1	A	82/441 (19%)	77 (94%)	5 (6%)	0	100	100
1	B	82/441 (19%)	79 (96%)	3 (4%)	0	100	100
1	C	82/441 (19%)	78 (95%)	4 (5%)	0	100	100
1	D	73/441 (17%)	72 (99%)	1 (1%)	0	100	100
1	E	73/441 (17%)	72 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	73/441 (17%)	72 (99%)	1 (1%)	0	100	100
All	All	465/2646 (18%)	450 (97%)	15 (3%)	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	
1	A	73/358 (20%)	73 (100%)	0	100	100
1	B	73/358 (20%)	73 (100%)	0	100	100
1	C	73/358 (20%)	73 (100%)	0	100	100
1	D	66/358 (18%)	66 (100%)	0	100	100
1	E	66/358 (18%)	66 (100%)	0	100	100
1	F	66/358 (18%)	66 (100%)	0	100	100
All	All	417/2148 (19%)	417 (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. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	362	HIS
1	C	381	ASN
1	F	359	ASN
1	F	368	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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.

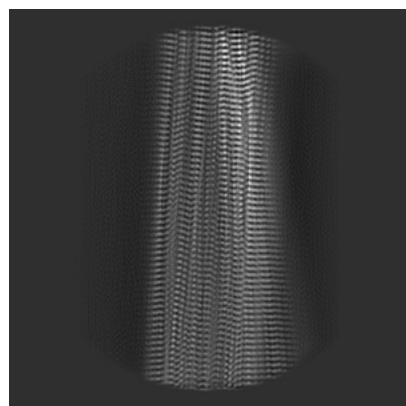
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14320. These allow visual inspection of the internal detail of the map and identification of artifacts.

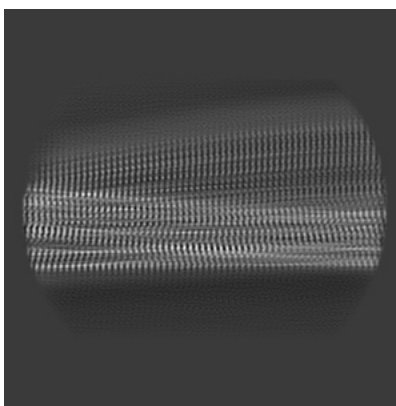
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

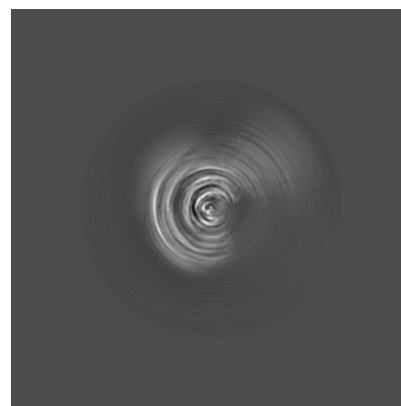
6.1.1 Primary map



X

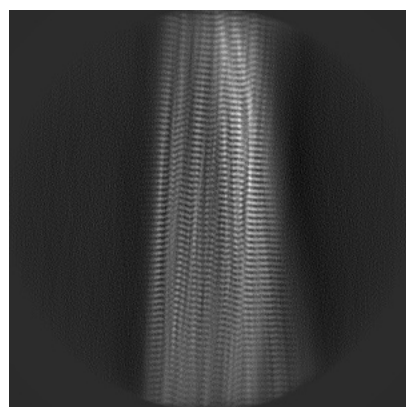


Y

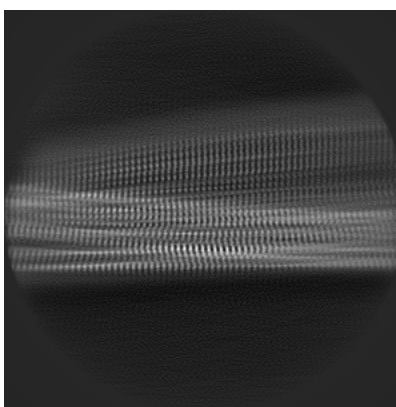


Z

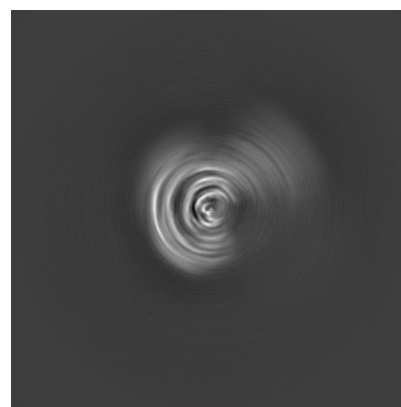
6.1.2 Raw map



X



Y

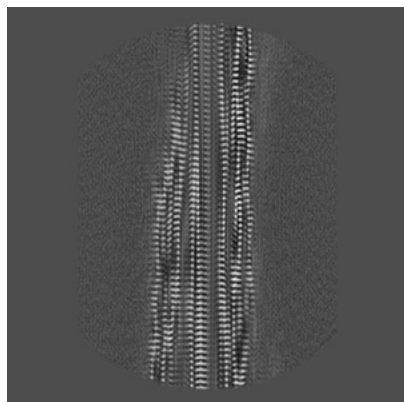


Z

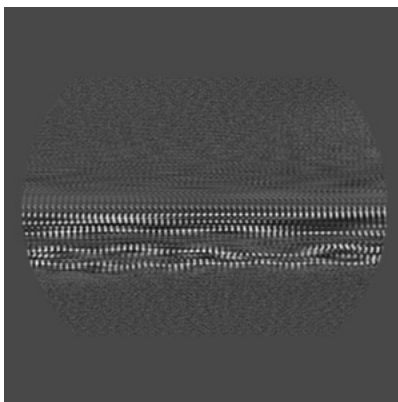
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

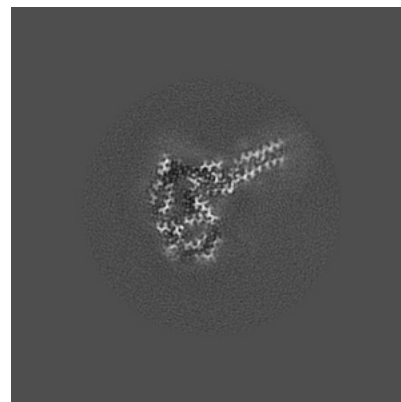
6.2.1 Primary map



X Index: 192

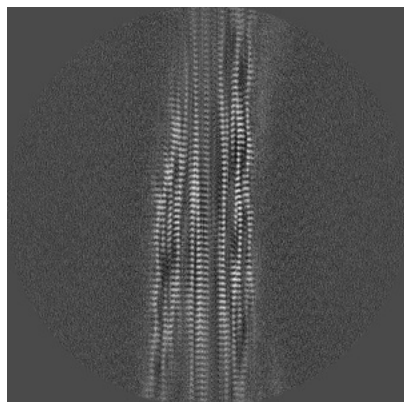


Y Index: 192

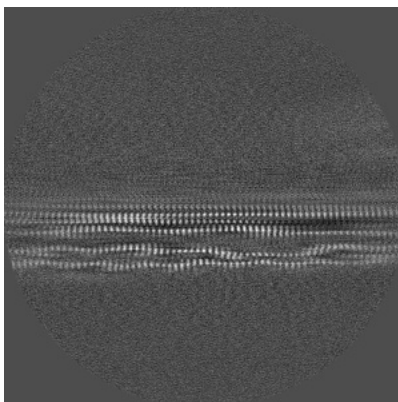


Z Index: 192

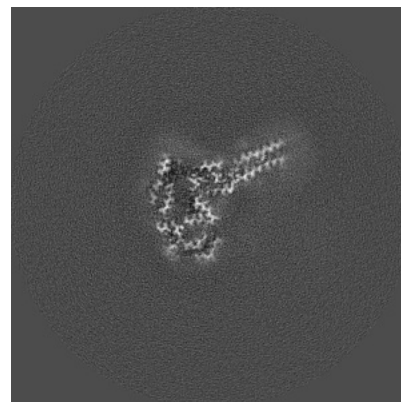
6.2.2 Raw map



X Index: 192



Y Index: 192

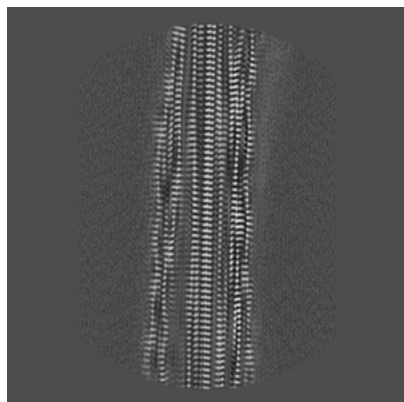


Z Index: 192

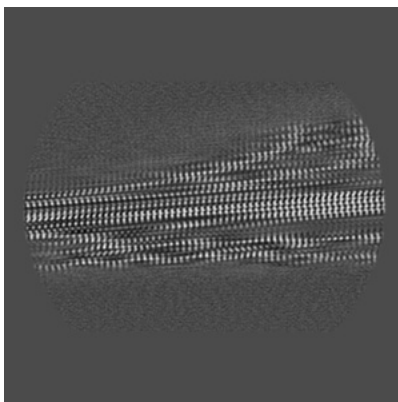
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

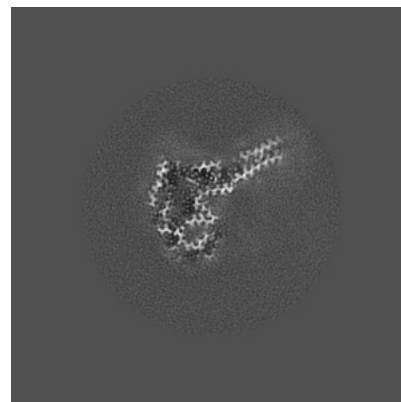
6.3.1 Primary map



X Index: 184

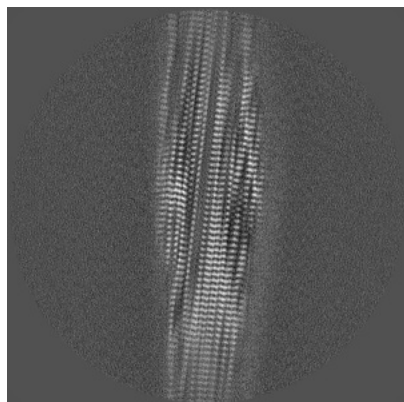


Y Index: 221

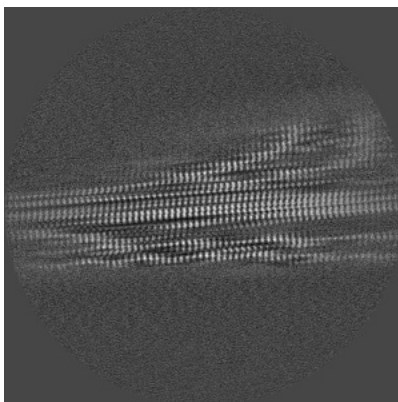


Z Index: 181

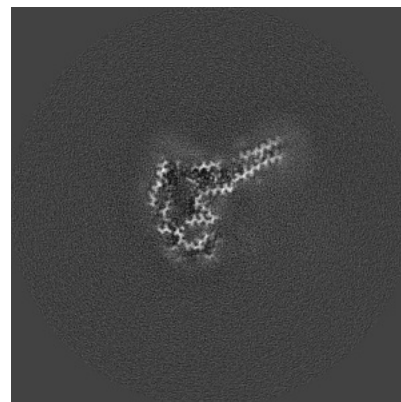
6.3.2 Raw map



X Index: 151



Y Index: 221

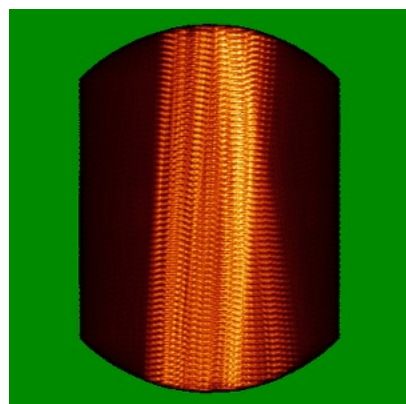


Z Index: 181

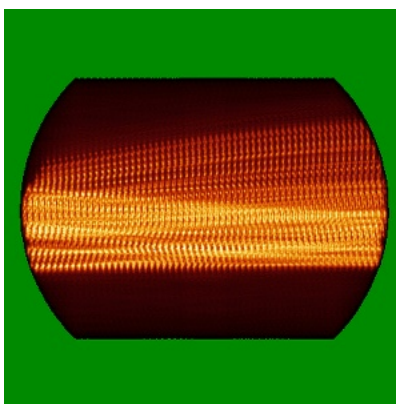
The images above show the largest variance slices of the map in three orthogonal directions.

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

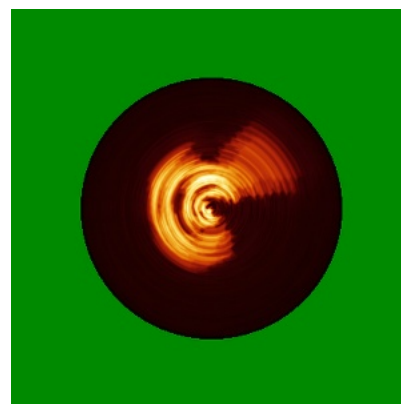
6.4.1 Primary map



X

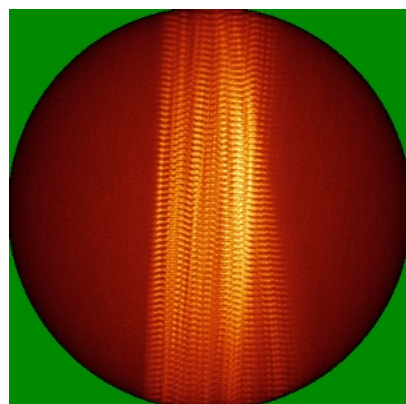


Y

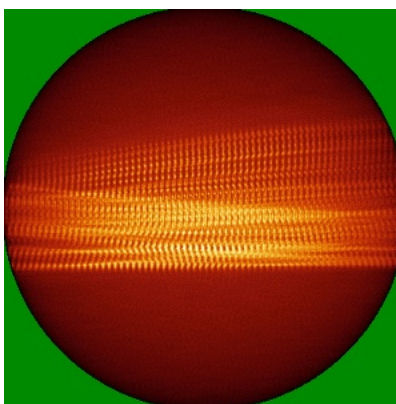


Z

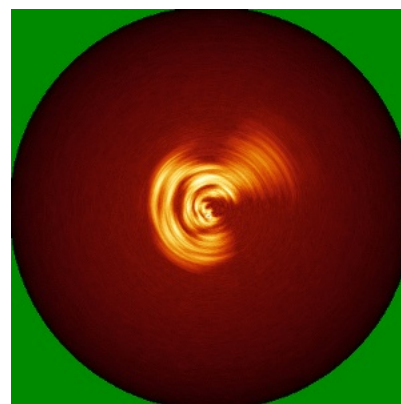
6.4.2 Raw map



X



Y

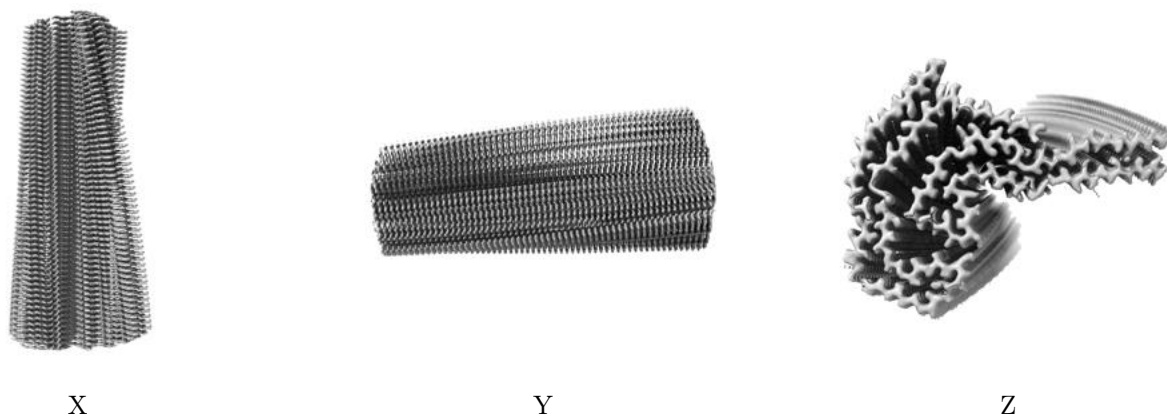


Z

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.

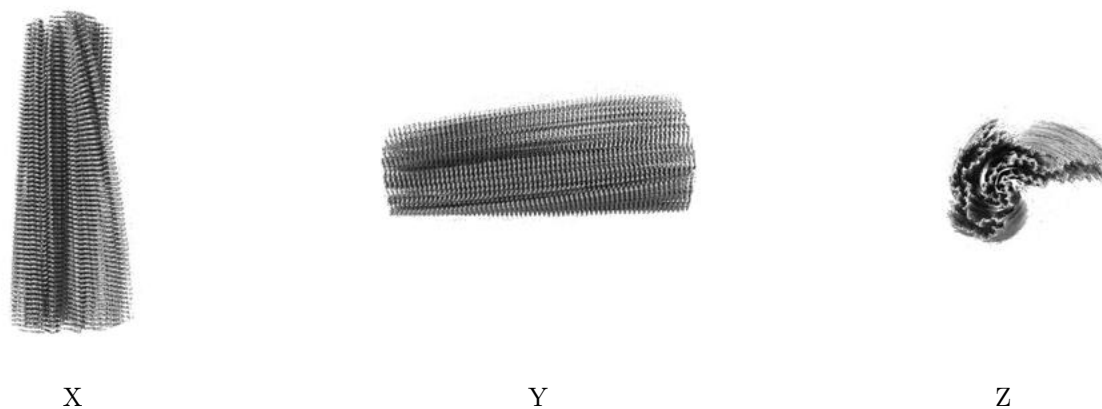
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00579. 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.

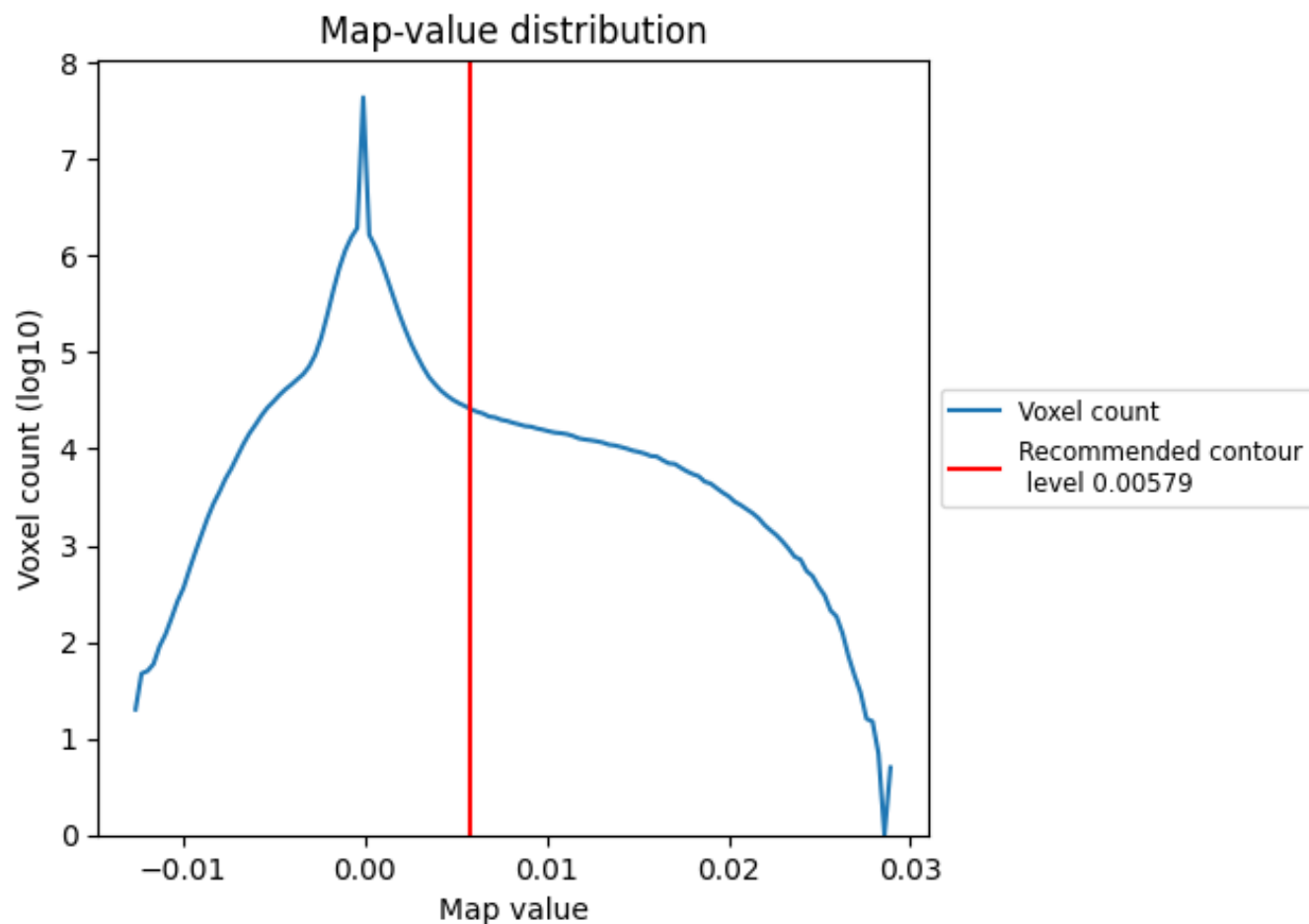
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

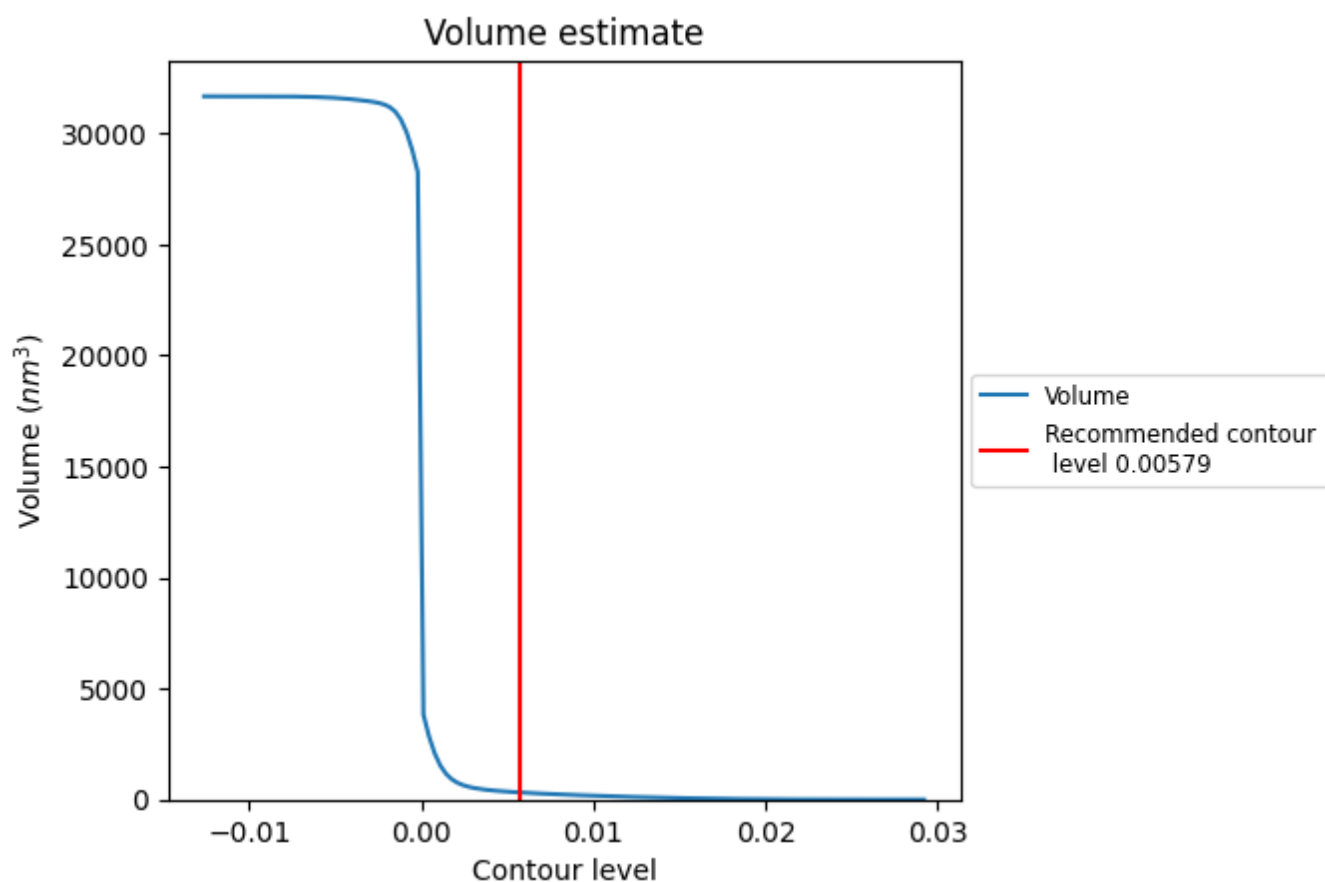
This section contains the results of statistical analysis of the map.

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.

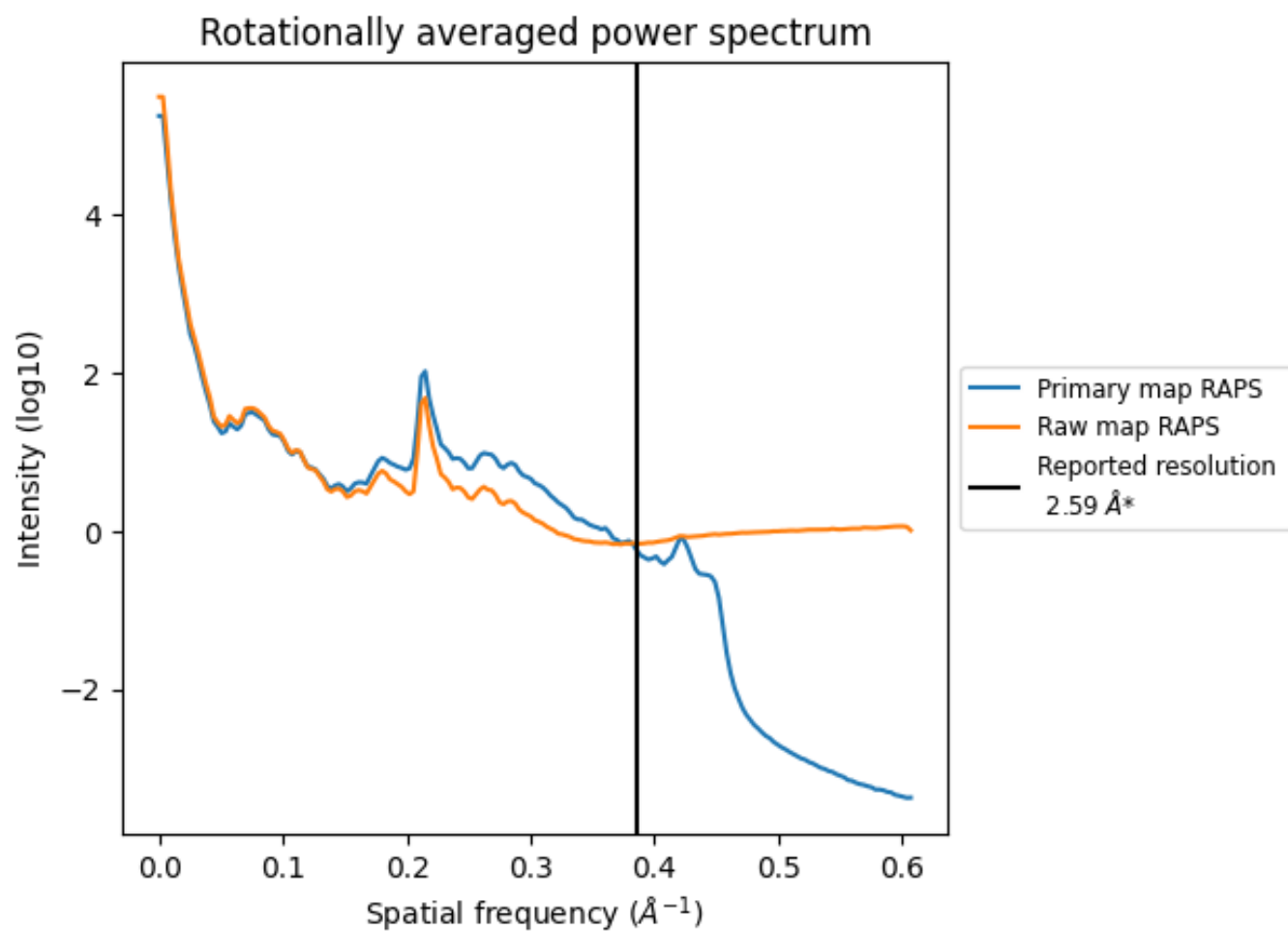
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 318 nm³; this corresponds to an approximate mass of 287 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 ⓘ

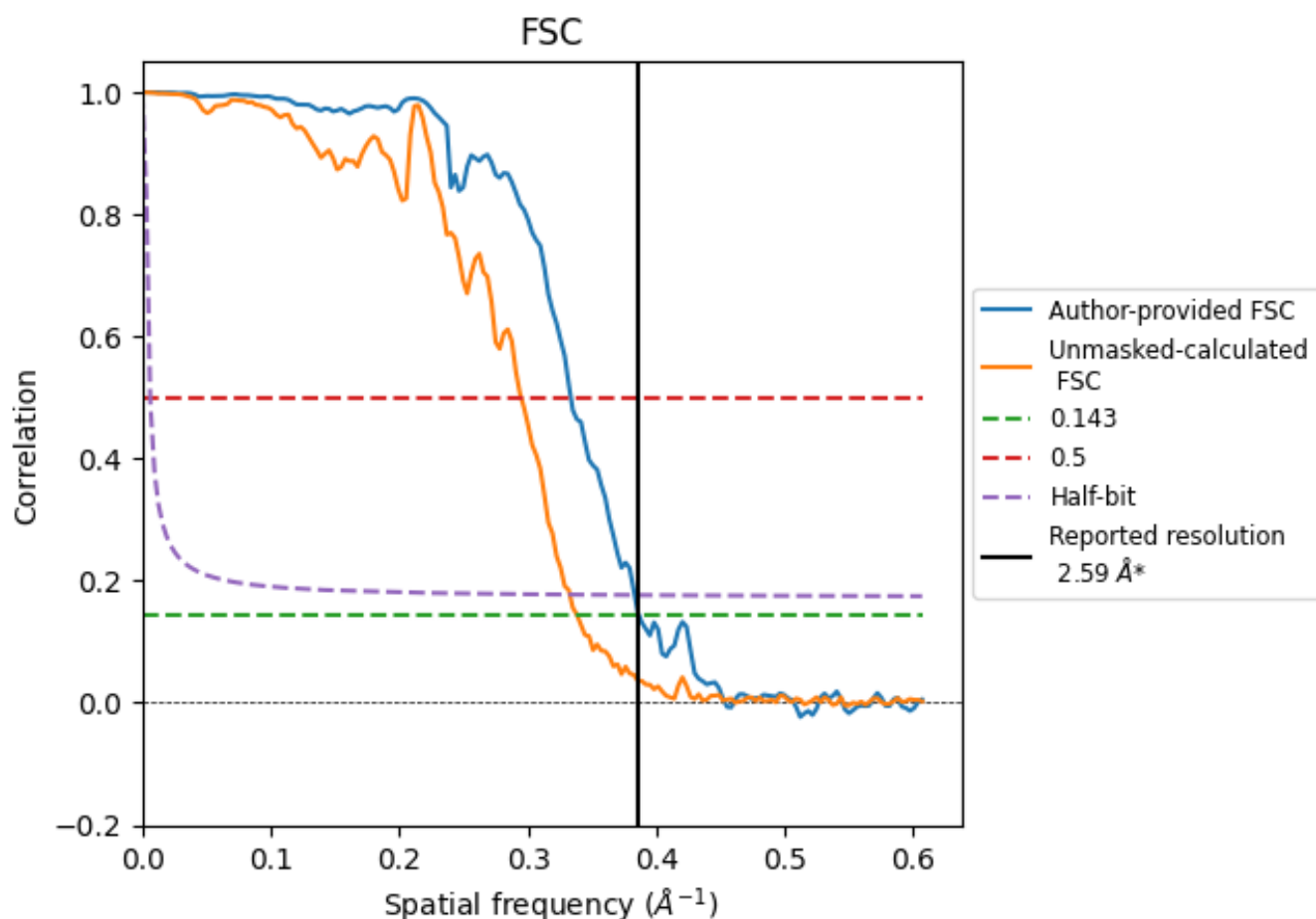


*Reported resolution corresponds to spatial frequency of 0.386 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.386 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.59	-	-
Author-provided FSC curve	2.59	3.00	2.61
Unmasked-calculated*	2.96	3.39	3.01

*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 2.96 differs from the reported value 2.59 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14320 and PDB model 7R5H. Per-residue inclusion information can be found in section [3](#) on page [5](#).

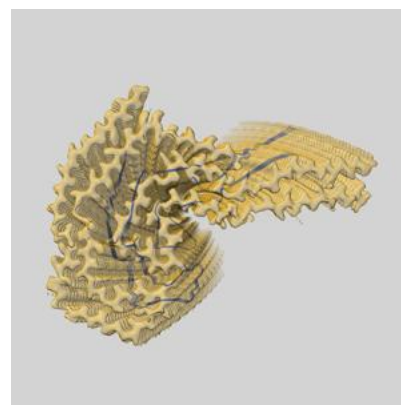
9.1 Map-model overlay [i](#)



X



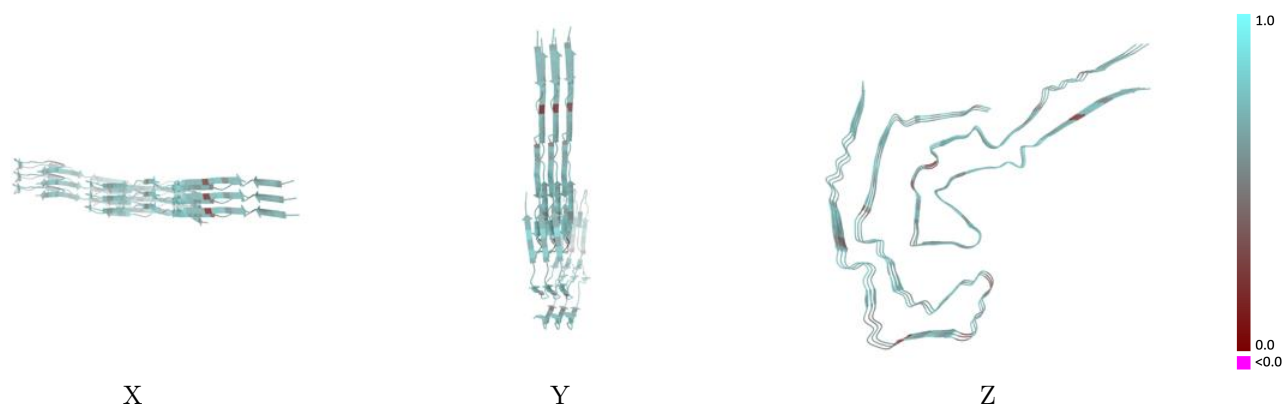
Y



Z

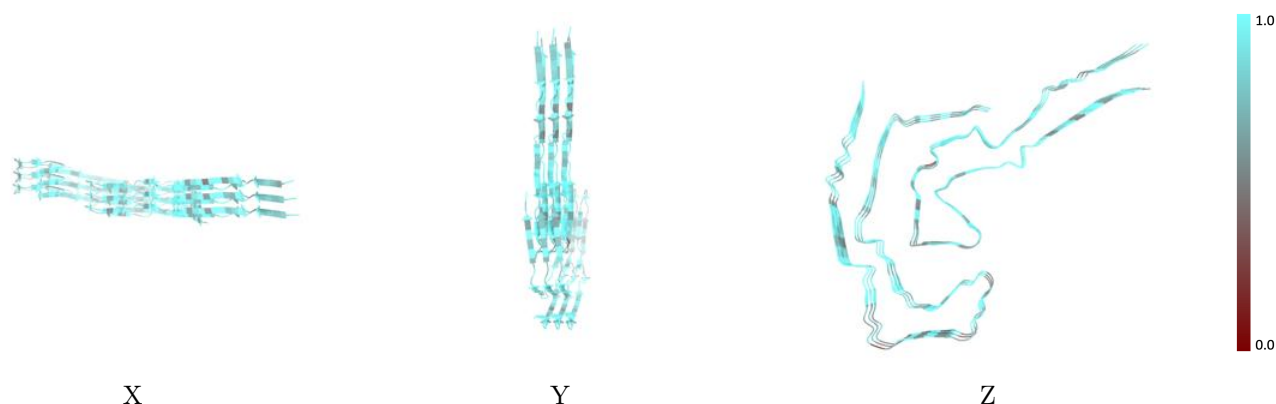
The images above show the 3D surface view of the map at the recommended contour level 0.00579 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



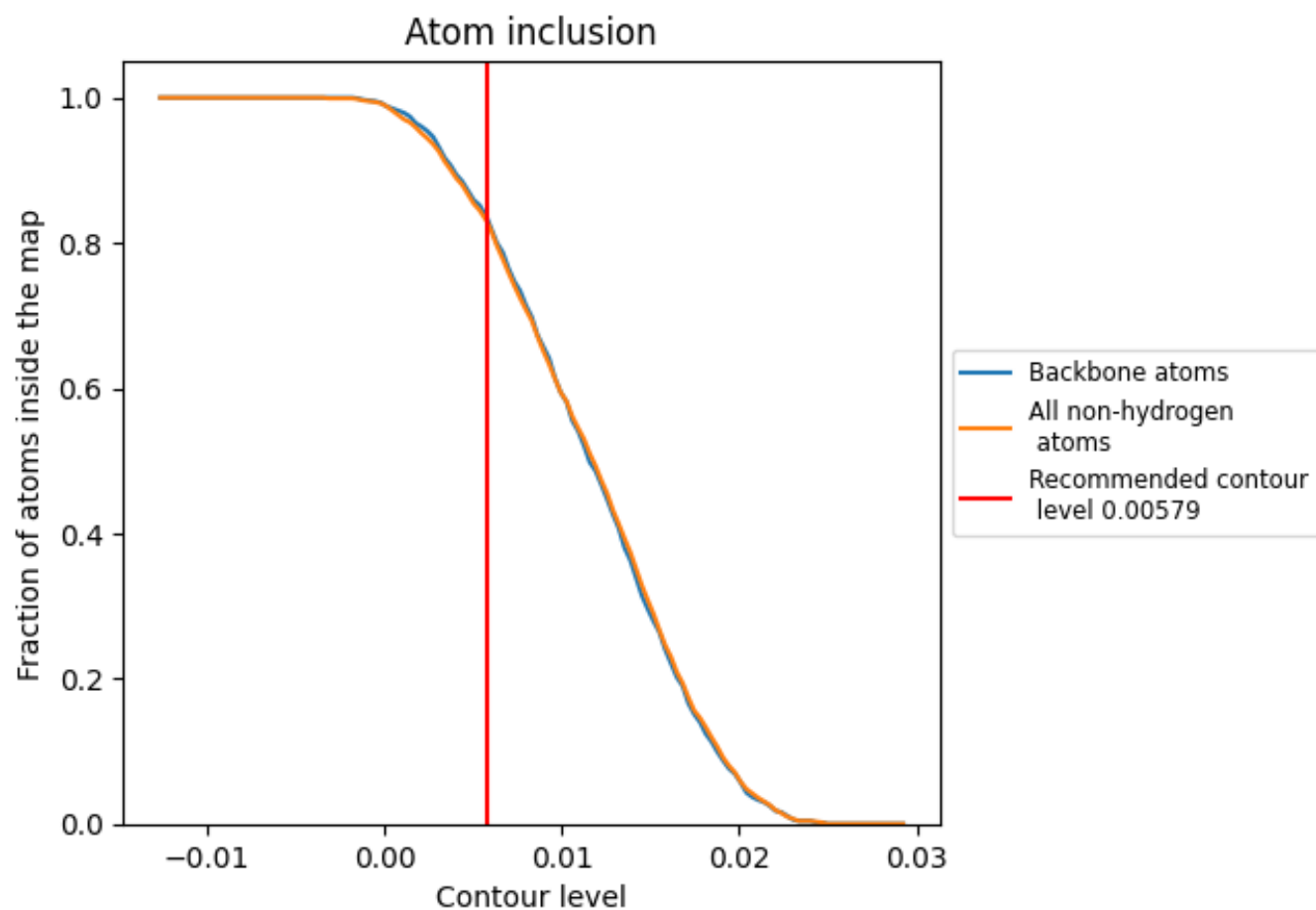
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00579).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 83% 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 (0.00579) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8290	0.6210
A	0.8230	0.6210
B	0.8250	0.6190
C	0.8280	0.6160
D	0.8280	0.6260
E	0.8260	0.6220
F	0.8240	0.6230

