



wwPDB EM Validation Summary Report ⓘ

Nov 25, 2024 – 12:20 am GMT

PDB ID : 9H5J
EMDB ID : EMD-51886
Title : PAD12 0N3R tau PHF seeded by AD
Authors : Lovestam, S.; Scheres, S.H.W.; Goedert, M.
Deposited on : 2024-10-22
Resolution : 2.72 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

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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

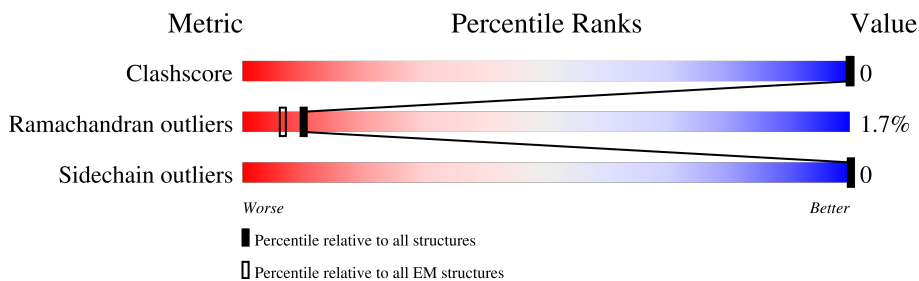
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.72 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	352	
1	B	352	
1	C	352	
1	D	352	
1	E	352	
1	F	352	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3300 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 Isoform Fetal-tau of Microtubule-associated protein tau.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	72	550	346	100	103	1	0	0
1	B	72	550	346	100	103	1	0	0
1	C	72	550	346	100	103	1	0	0
1	D	72	550	346	100	103	1	0	0
1	E	72	550	346	100	103	1	0	0
1	F	72	550	346	100	103	1	0	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	212	ASP	THR	conflict	UNP P10636
A	233	ASP	SER	conflict	UNP P10636
A	236	ASP	THR	conflict	UNP P10636
A	243	ASP	THR	conflict	UNP P10636
A	245	ASP	SER	conflict	UNP P10636
A	248	ASP	THR	conflict	UNP P10636
A	262	ASP	THR	conflict	UNP P10636
A	266	ASP	SER	conflict	UNP P10636
A	396	ASP	SER	conflict	UNP P10636
A	400	ASP	SER	conflict	UNP P10636
A	403	ASP	THR	conflict	UNP P10636
A	404	ASP	SER	conflict	UNP P10636
B	212	ASP	THR	conflict	UNP P10636
B	233	ASP	SER	conflict	UNP P10636
B	236	ASP	THR	conflict	UNP P10636
B	243	ASP	THR	conflict	UNP P10636
B	245	ASP	SER	conflict	UNP P10636
B	248	ASP	THR	conflict	UNP P10636

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Chain	Residue	Modelled	Actual	Comment	Reference
B	262	ASP	THR	conflict	UNP P10636
B	266	ASP	SER	conflict	UNP P10636
B	396	ASP	SER	conflict	UNP P10636
B	400	ASP	SER	conflict	UNP P10636
B	403	ASP	THR	conflict	UNP P10636
B	404	ASP	SER	conflict	UNP P10636
C	212	ASP	THR	conflict	UNP P10636
C	233	ASP	SER	conflict	UNP P10636
C	236	ASP	THR	conflict	UNP P10636
C	243	ASP	THR	conflict	UNP P10636
C	245	ASP	SER	conflict	UNP P10636
C	248	ASP	THR	conflict	UNP P10636
C	262	ASP	THR	conflict	UNP P10636
C	266	ASP	SER	conflict	UNP P10636
C	396	ASP	SER	conflict	UNP P10636
C	400	ASP	SER	conflict	UNP P10636
C	403	ASP	THR	conflict	UNP P10636
C	404	ASP	SER	conflict	UNP P10636
D	212	ASP	THR	conflict	UNP P10636
D	233	ASP	SER	conflict	UNP P10636
D	236	ASP	THR	conflict	UNP P10636
D	243	ASP	THR	conflict	UNP P10636
D	245	ASP	SER	conflict	UNP P10636
D	248	ASP	THR	conflict	UNP P10636
D	262	ASP	THR	conflict	UNP P10636
D	266	ASP	SER	conflict	UNP P10636
D	396	ASP	SER	conflict	UNP P10636
D	400	ASP	SER	conflict	UNP P10636
D	403	ASP	THR	conflict	UNP P10636
D	404	ASP	SER	conflict	UNP P10636
E	212	ASP	THR	conflict	UNP P10636
E	233	ASP	SER	conflict	UNP P10636
E	236	ASP	THR	conflict	UNP P10636
E	243	ASP	THR	conflict	UNP P10636
E	245	ASP	SER	conflict	UNP P10636
E	248	ASP	THR	conflict	UNP P10636
E	262	ASP	THR	conflict	UNP P10636
E	266	ASP	SER	conflict	UNP P10636
E	396	ASP	SER	conflict	UNP P10636
E	400	ASP	SER	conflict	UNP P10636
E	403	ASP	THR	conflict	UNP P10636
E	404	ASP	SER	conflict	UNP P10636

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Chain	Residue	Modelled	Actual	Comment	Reference
F	212	ASP	THR	conflict	UNP P10636
F	233	ASP	SER	conflict	UNP P10636
F	236	ASP	THR	conflict	UNP P10636
F	243	ASP	THR	conflict	UNP P10636
F	245	ASP	SER	conflict	UNP P10636
F	248	ASP	THR	conflict	UNP P10636
F	262	ASP	THR	conflict	UNP P10636
F	266	ASP	SER	conflict	UNP P10636
F	396	ASP	SER	conflict	UNP P10636
F	400	ASP	SER	conflict	UNP P10636
F	403	ASP	THR	conflict	UNP P10636
F	404	ASP	SER	conflict	UNP P10636

● Molecule 1: Isoform Fetal-tau of Microtubule-associated protein tau

Chain F:  20% . 80%

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

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

PRO LYS
LYS ASP
PRO PRO
VAL VAL
SER SER
GLY GLY
PRO PRO
PRO PRO
LYS LYS
SER SER
GLY GLY
ASP ASP
ARG ARG
SER SER
TYR TYR
SER SER
SER SER
PRO PRO
GLY GLY
ASP ASP
PRO PRO
GLY GLY
SER SER
ARG ARG
SER SER
ARG ARG
SER SER
LYS LYS
LYS LYS
PRO PRO
THR THR
LYS LYS
ASP ASP
PRO PRO
SER SER
PRO PRO
SER SER

ALA LYS
SER SER
ARG ARG
LEU LEU
GLN GLN
THR THR
ALA ALA
PRO PRO
VAL VAL
ASP ASP
MET MET
PRO PRO
PRO PRO
ASP ASP
LYS LYS
LEU LEU
LYS LYS
ASN ASN
SER SER
VAL VAL
LYS LYS
SER SER
SER SER
LYS LYS
ILE ILE
GLY GLY
SER SER
THR THR
GLU GLU
ASN ASN
LEU LEU
LYS LYS
HIS HIS
SER SER
GLN GLN
PRO PRO
GLY GLY
GLY GLY
LYS LYS
VAL VAL
G367
Y310
E342
G355
F378
ARG ARG
GLU GLU
ASN ASN
ALA ALA
LYS LYS
ALA ALA
LYS LYS
THR THR
THR THR
ASP ASP
HIS HIS
GLY GLY
ALA ALA
GLU GLU
ILE ILE

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

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=179.393°, rise=2.42 Å, axial sym=C1	Depositor
Number of segments used	125334	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 ($e^-/\text{Å}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.051	Depositor
Minimum map value	-0.029	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.00968	Depositor
Map size (Å)	285.696, 285.696, 285.696	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.744, 0.744, 0.744	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	0.55	0/559	0.91	0/748
1	B	0.55	0/559	0.91	0/748
1	C	0.54	0/559	0.91	0/748
1	D	0.56	0/559	0.93	1/748 (0.1%)
1	E	0.55	0/559	0.95	1/748 (0.1%)
1	F	0.55	0/559	0.88	0/748
All	All	0.55	0/3354	0.92	2/4488 (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
1	D	0	1
1	E	0	1
1	F	0	1
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	349	ARG	NE-CZ-NH1	5.79	123.20	120.30
1	D	349	ARG	NE-CZ-NH1	5.49	123.04	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	349	ARG	Sidechain
1	E	349	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	F	310	TYR	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	550	0	570	0	0
1	B	550	0	570	0	0
1	C	550	0	570	0	0
1	D	550	0	570	0	0
1	E	550	0	570	0	0
1	F	550	0	570	0	0
All	All	3300	0	3420	0	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 0.

There are no clashes within the asymmetric unit.

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	70/352 (20%)	65 (93%)	4 (6%)	1 (1%)	9 22
1	B	70/352 (20%)	65 (93%)	4 (6%)	1 (1%)	9 22
1	C	70/352 (20%)	65 (93%)	3 (4%)	2 (3%)	3 8
1	D	70/352 (20%)	64 (91%)	5 (7%)	1 (1%)	9 22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	70/352 (20%)	64 (91%)	5 (7%)	1 (1%)	9	22
1	F	70/352 (20%)	64 (91%)	5 (7%)	1 (1%)	9	22
All	All	420/2112 (20%)	387 (92%)	26 (6%)	7 (2%)	10	18

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	348	ASP
1	C	348	ASP
1	C	355	GLY
1	F	355	GLY
1	B	355	GLY

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	
1	A	63/285 (22%)	63 (100%)	0	100	100
1	B	63/285 (22%)	63 (100%)	0	100	100
1	C	63/285 (22%)	63 (100%)	0	100	100
1	D	63/285 (22%)	63 (100%)	0	100	100
1	E	63/285 (22%)	63 (100%)	0	100	100
1	F	63/285 (22%)	63 (100%)	0	100	100
All	All	378/1710 (22%)	378 (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. There are no such sidechains identified.

5.3.3 RNA [i](#)

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.

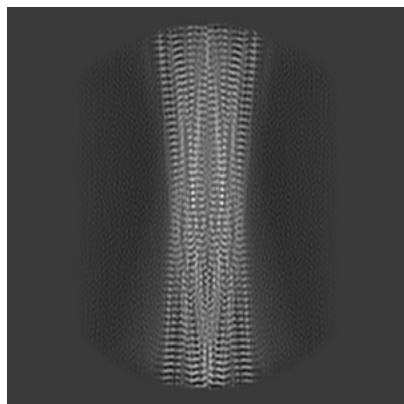
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51886. These allow visual inspection of the internal detail of the map and identification of artifacts.

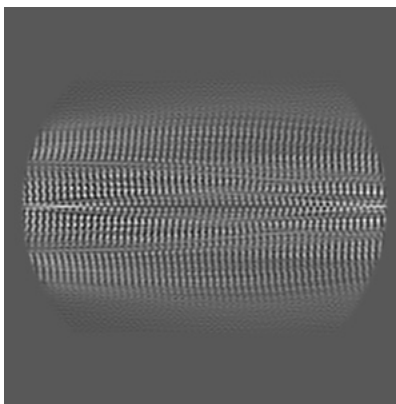
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

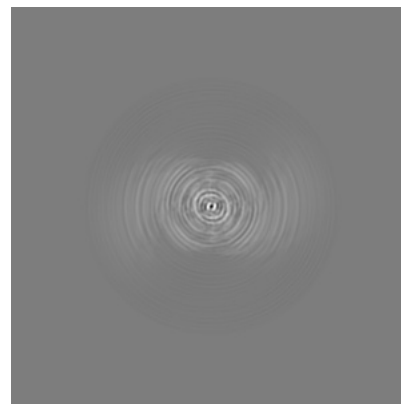
6.1.1 Primary map



X

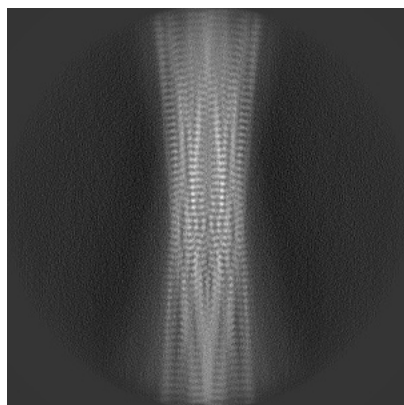


Y

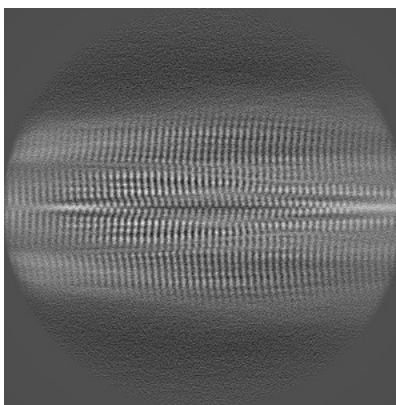


Z

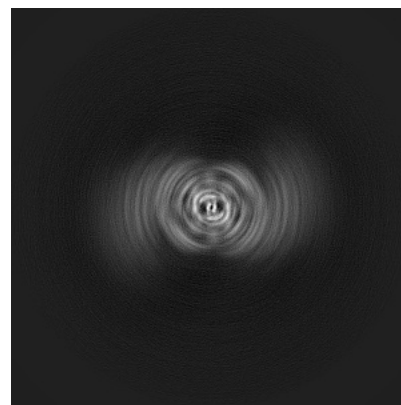
6.1.2 Raw map



X



Y

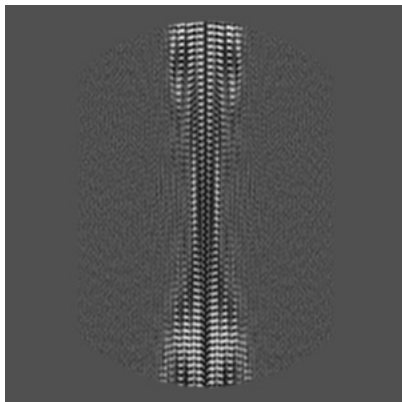


Z

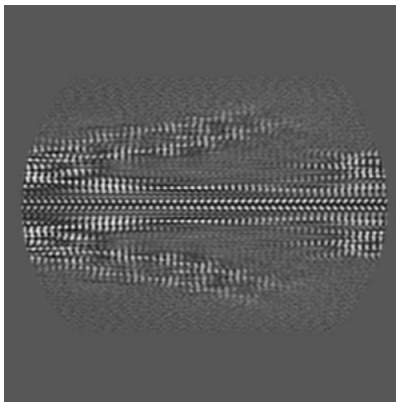
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

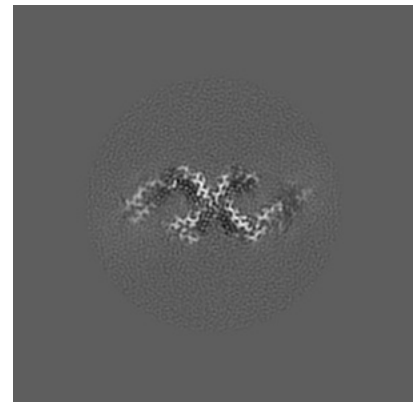
6.2.1 Primary map



X Index: 192

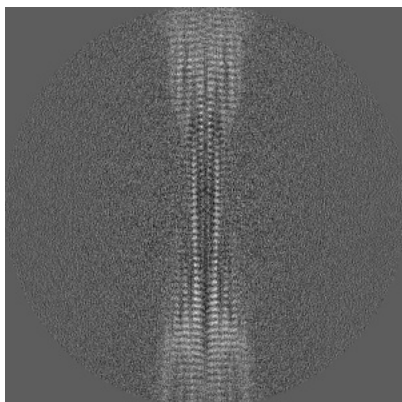


Y Index: 192

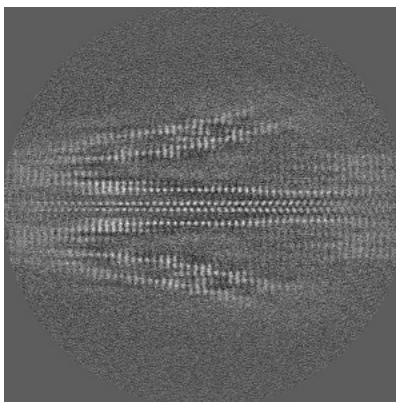


Z Index: 192

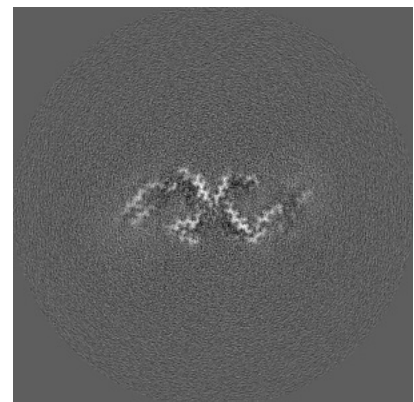
6.2.2 Raw map



X Index: 192



Y Index: 192

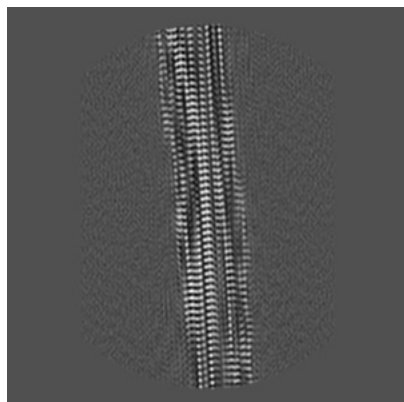


Z Index: 192

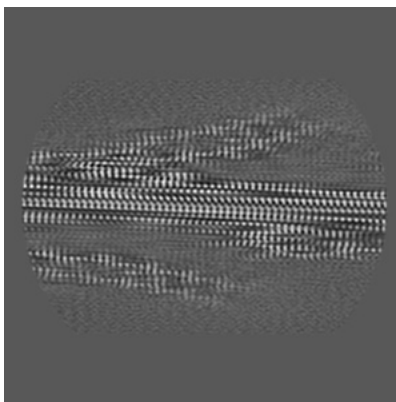
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

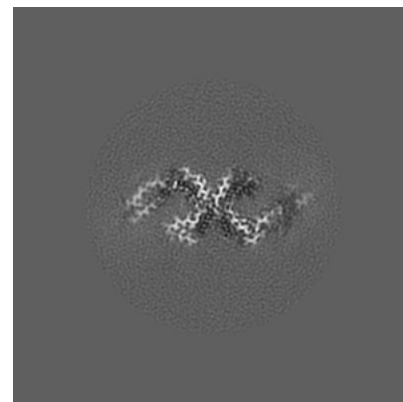
6.3.1 Primary map



X Index: 208

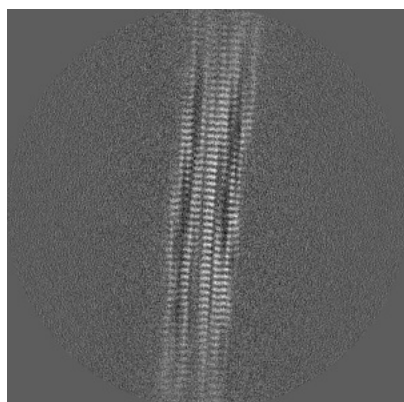


Y Index: 182

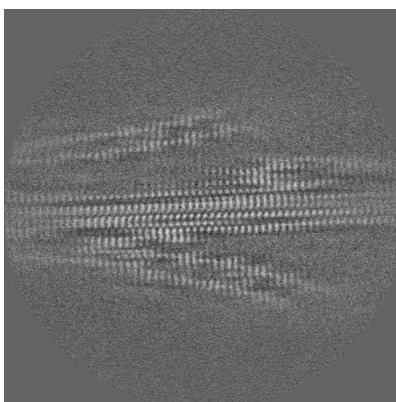


Z Index: 198

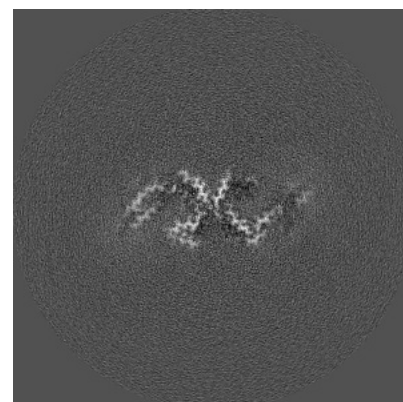
6.3.2 Raw map



X Index: 176



Y Index: 202

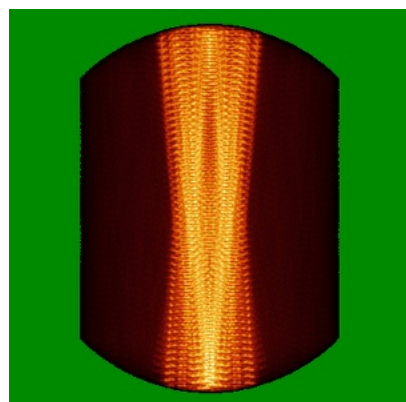


Z Index: 185

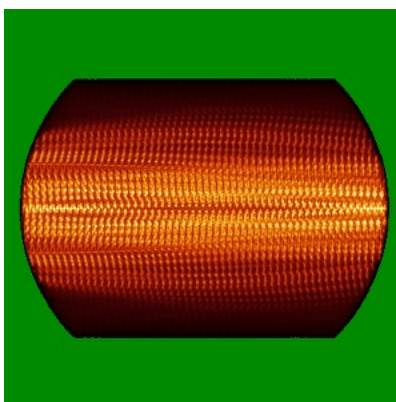
The images above show the largest variance slices of the map in three orthogonal directions.

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

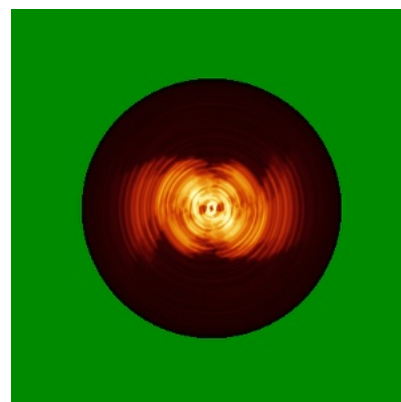
6.4.1 Primary map



X

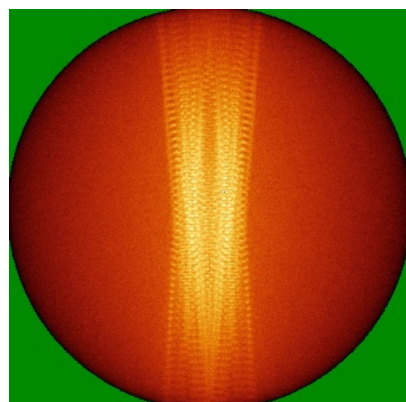


Y

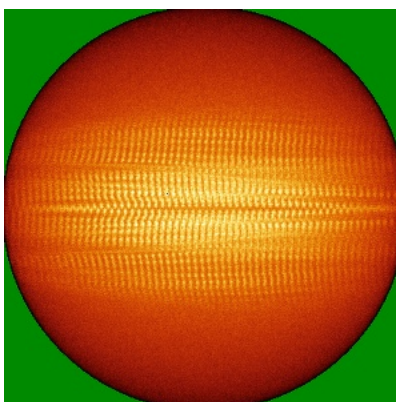


Z

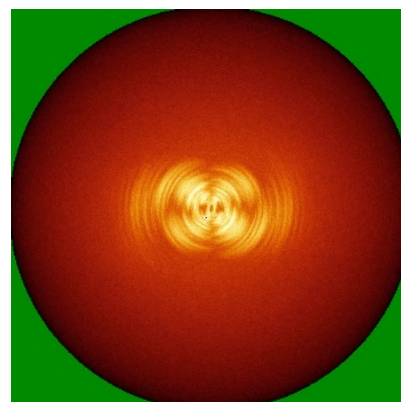
6.4.2 Raw map



X



Y

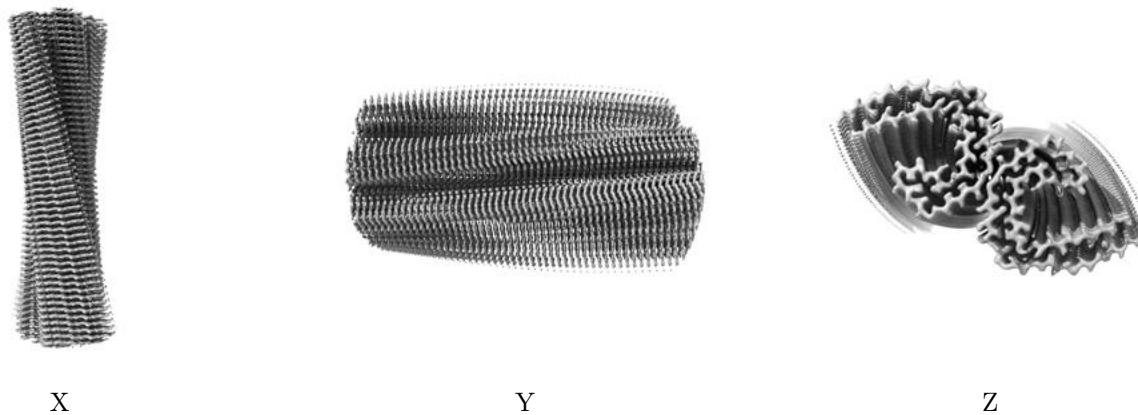


Z

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.

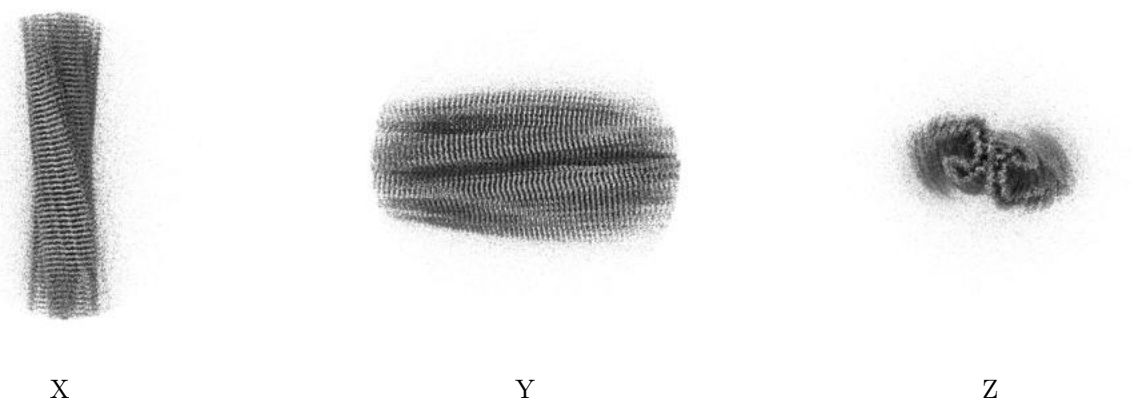
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00968. 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.

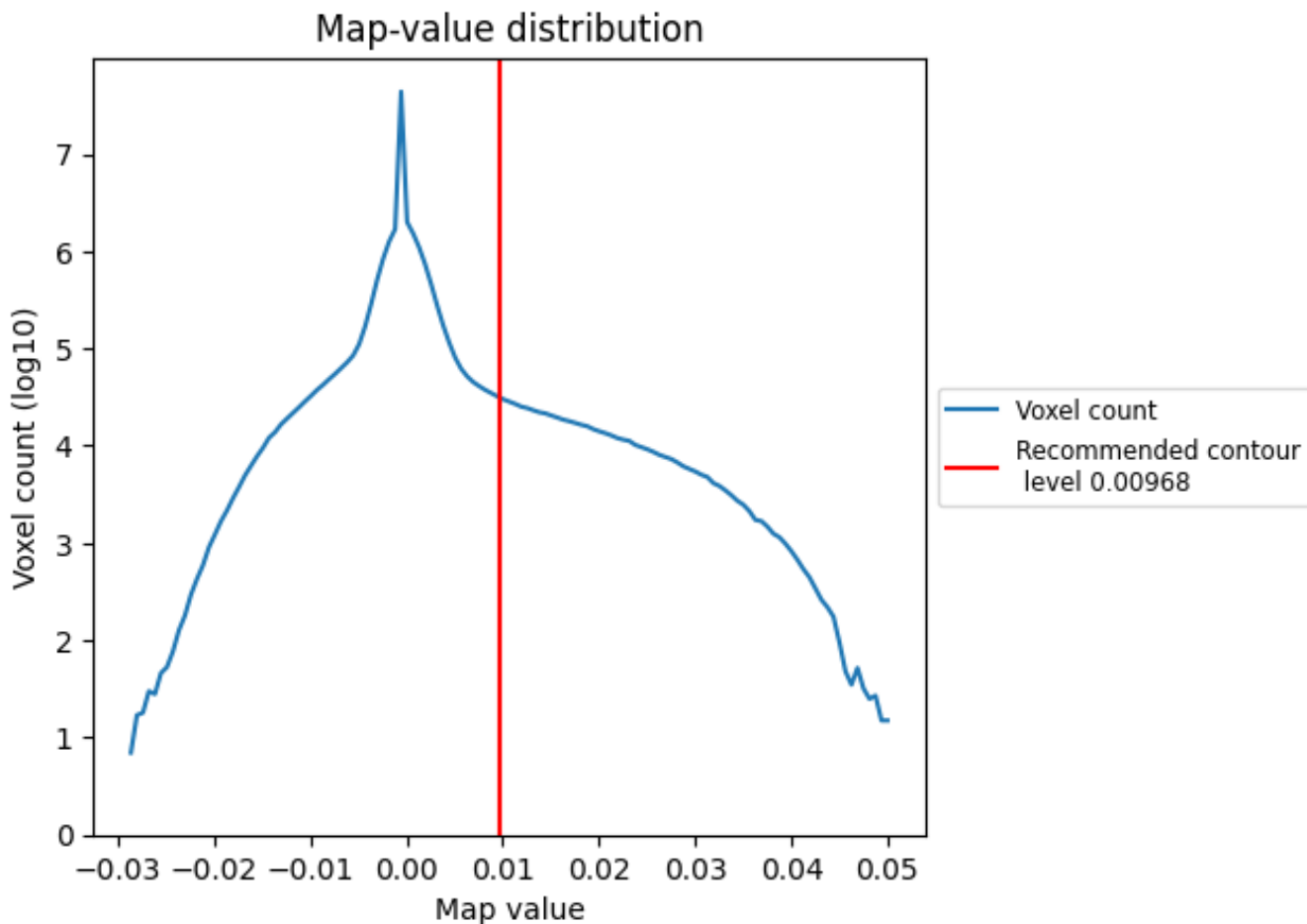
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

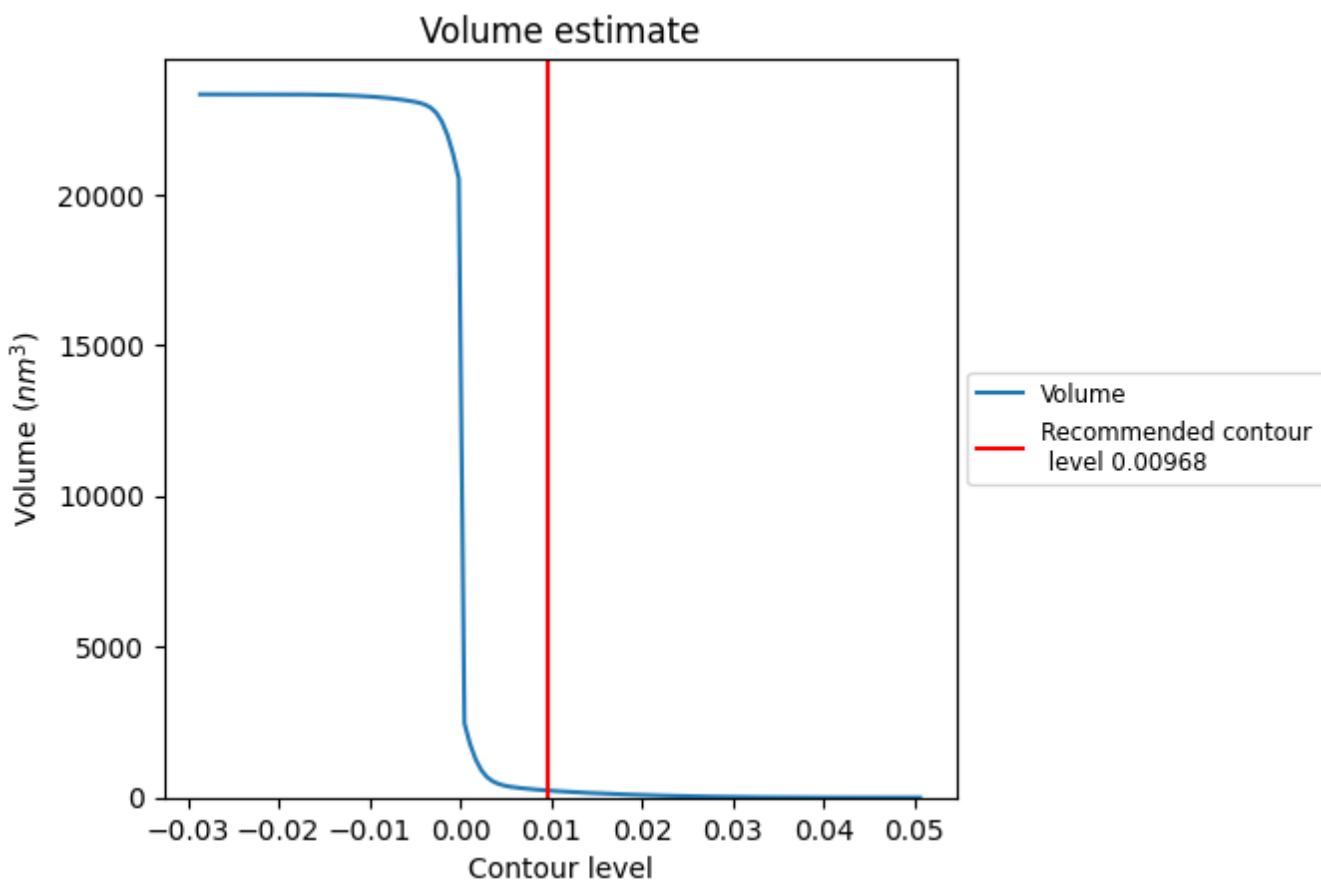
This section contains the results of statistical analysis of the map.

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.

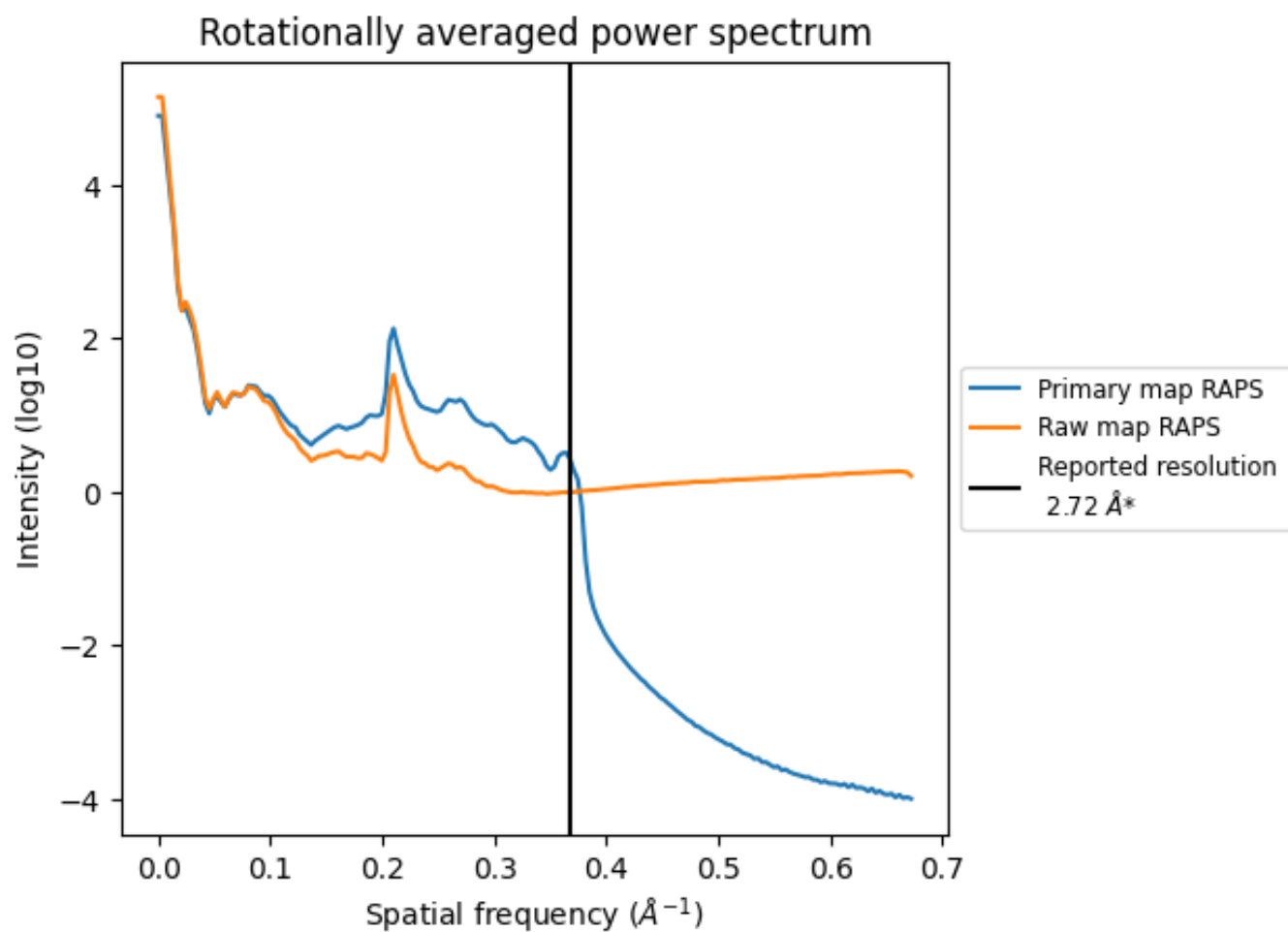
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 233 nm³; this corresponds to an approximate mass of 211 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 [i](#)

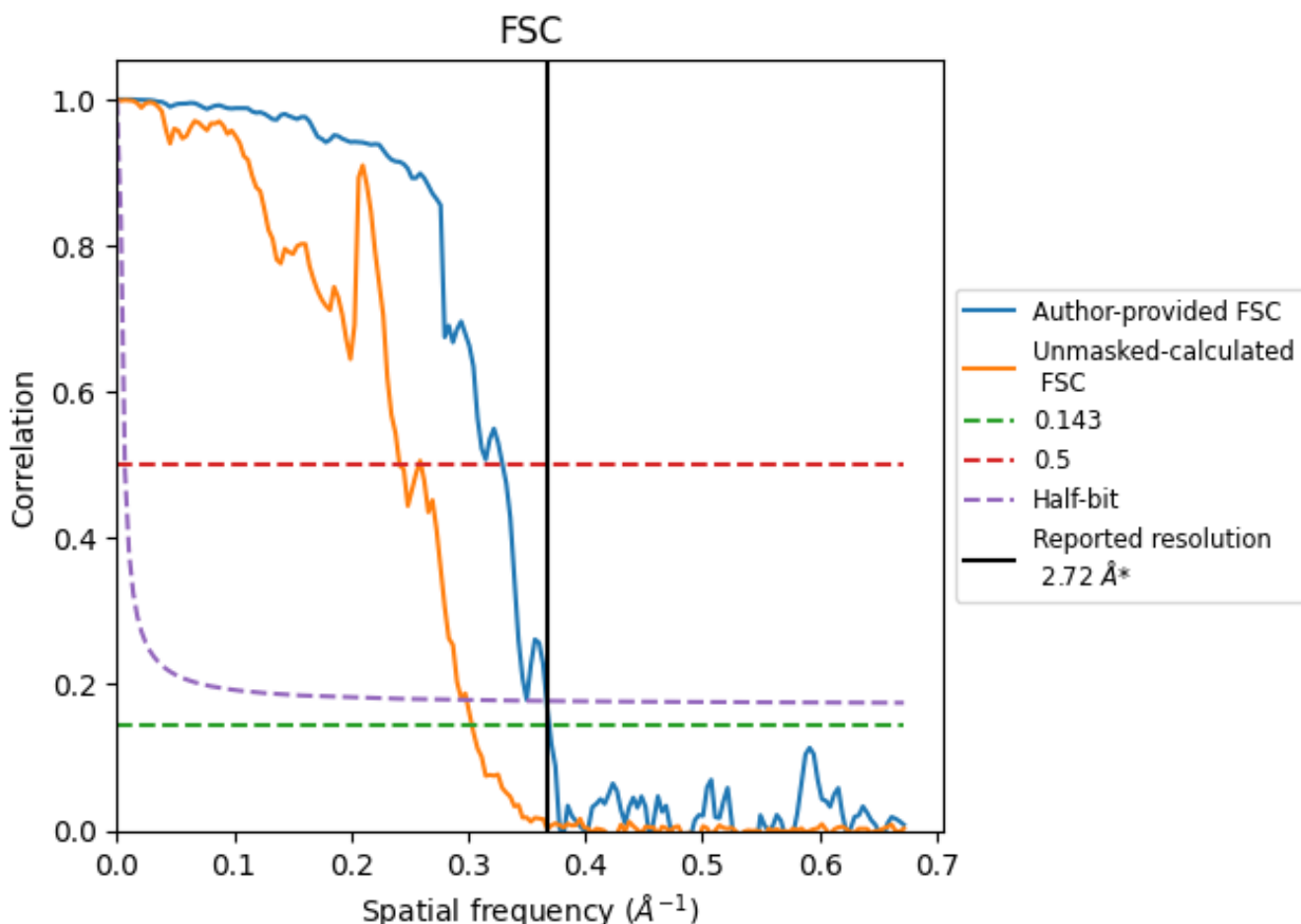


*Reported resolution corresponds to spatial frequency of 0.368 Å⁻¹

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 0.368 Å⁻¹

8.2 Resolution estimates [i](#)

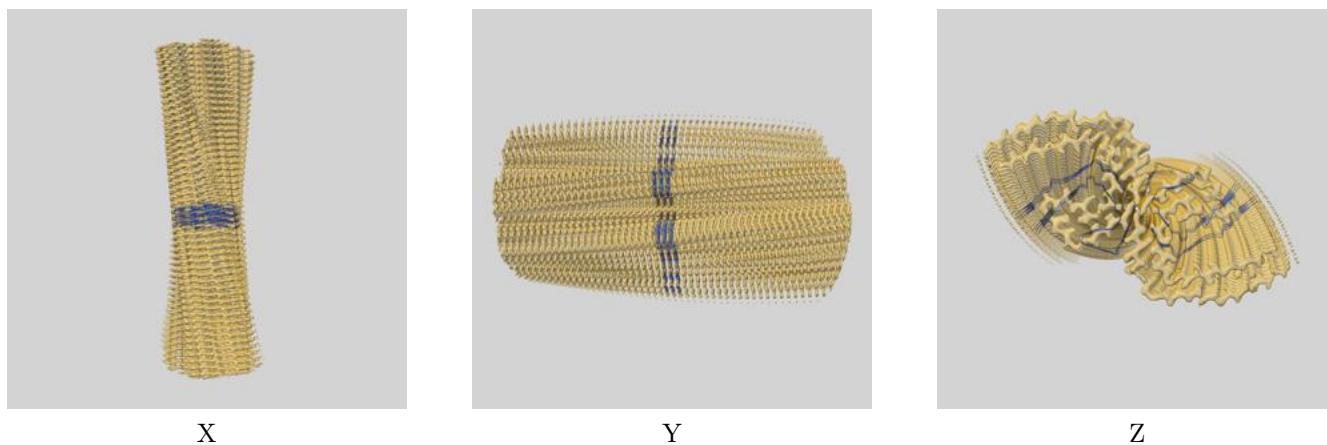
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.72	-	-
Author-provided FSC curve	2.71	3.04	2.72
Unmasked-calculated*	3.30	4.14	3.35

*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 3.30 differs from the reported value 2.72 by more than 10 %

9 Map-model fit [i](#)

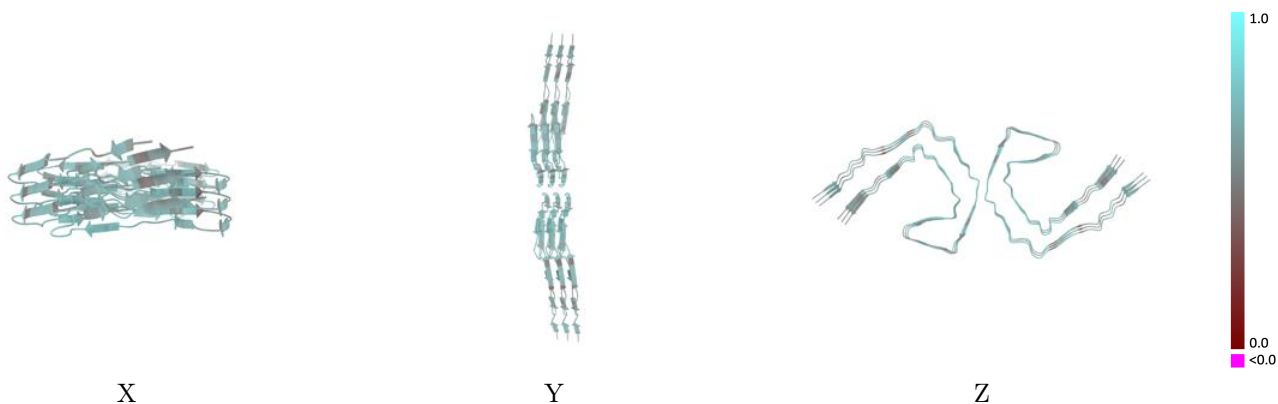
This section contains information regarding the fit between EMDB map EMD-51886 and PDB model 9H5J. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



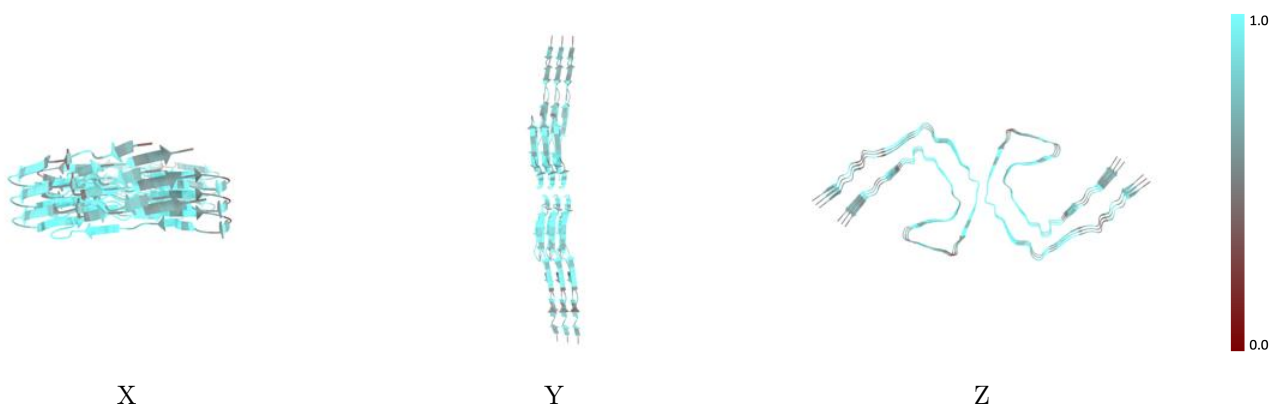
The images above show the 3D surface view of the map at the recommended contour level 0.00968 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



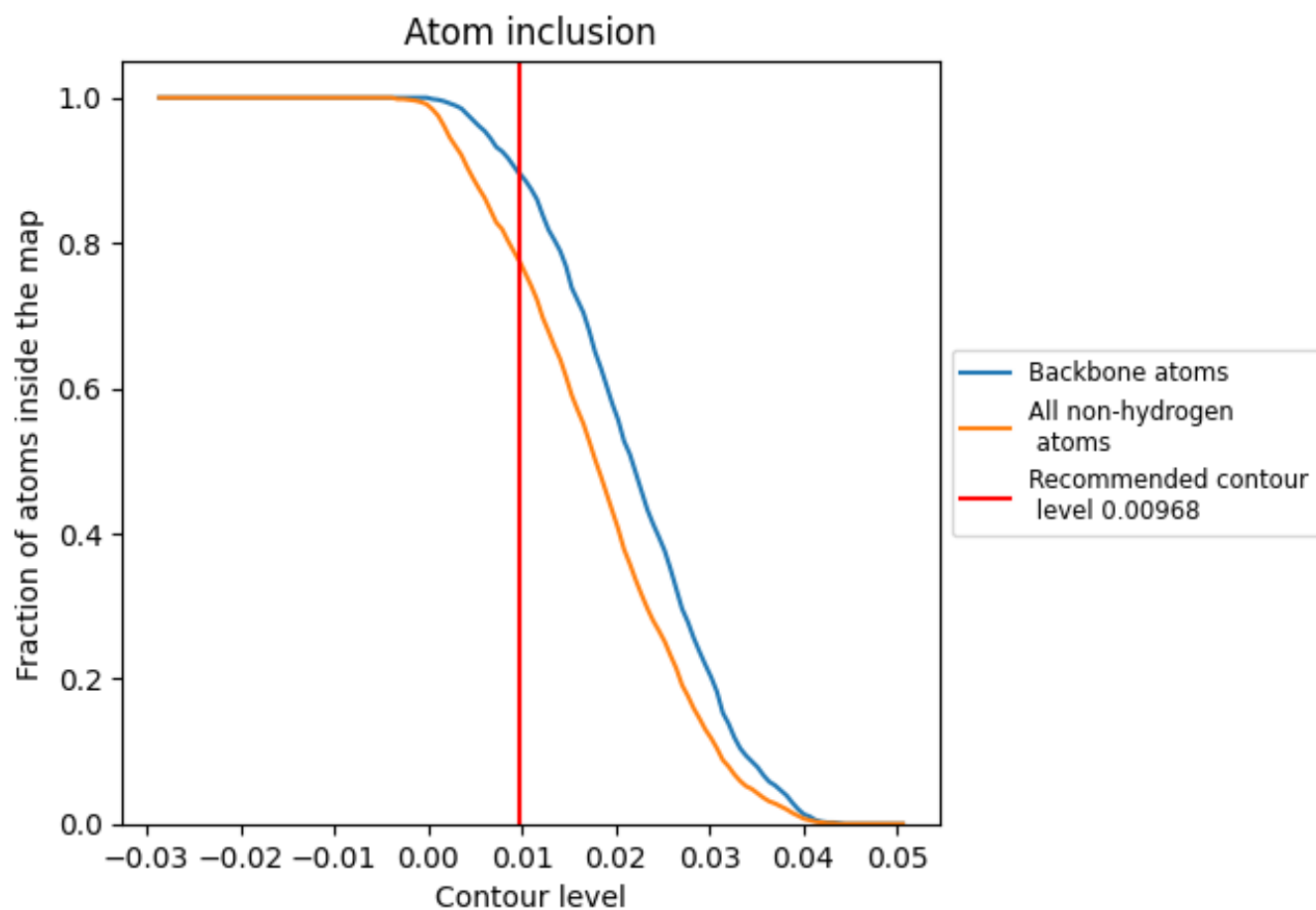
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00968).















9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 78% 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 (0.00968) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7760	 0.6010
A	 0.7680	 0.5990
B	 0.7770	 0.6000
C	 0.7770	 0.6010
D	 0.7770	 0.6050
E	 0.7840	 0.6040
F	 0.7750	 0.6000

