



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:15 AM UTC

PDB ID : 7QL0 / pdb_00007ql0
EMDB ID : EMD-14059
Title : In vitro assembled 266/297 - 391 tau filaments with MgSO4 and NaCl (15c)
Authors : Lovestam, S.; Scheres, S.H.W.
Deposited on : 2021-12-19
Resolution : 3.13 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.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

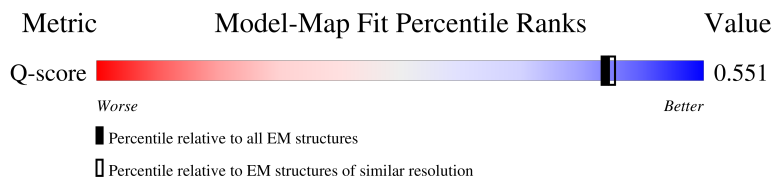
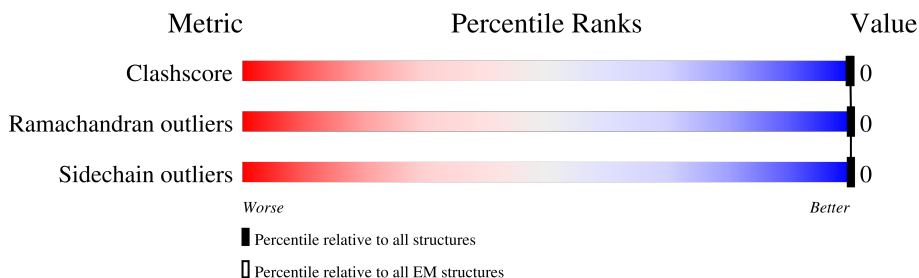
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.13 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	14478 (2.63 - 3.63)

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	16% 84%
1	B	441	16% 84%
1	C	441	15% 84%
1	D	441	16% 84%

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Mol	Chain	Length	Quality of chain
1	E	441	 15%84%
1	c	441	 15%84%

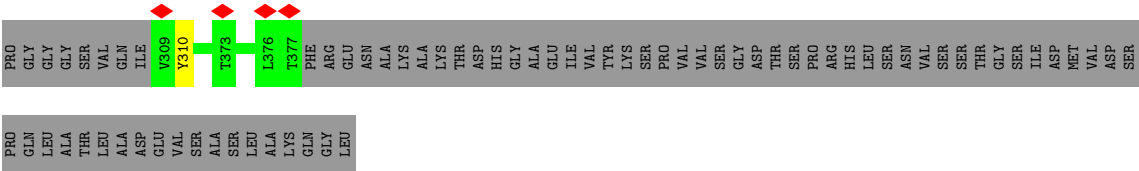
2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6390 atoms, of which 3258 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.

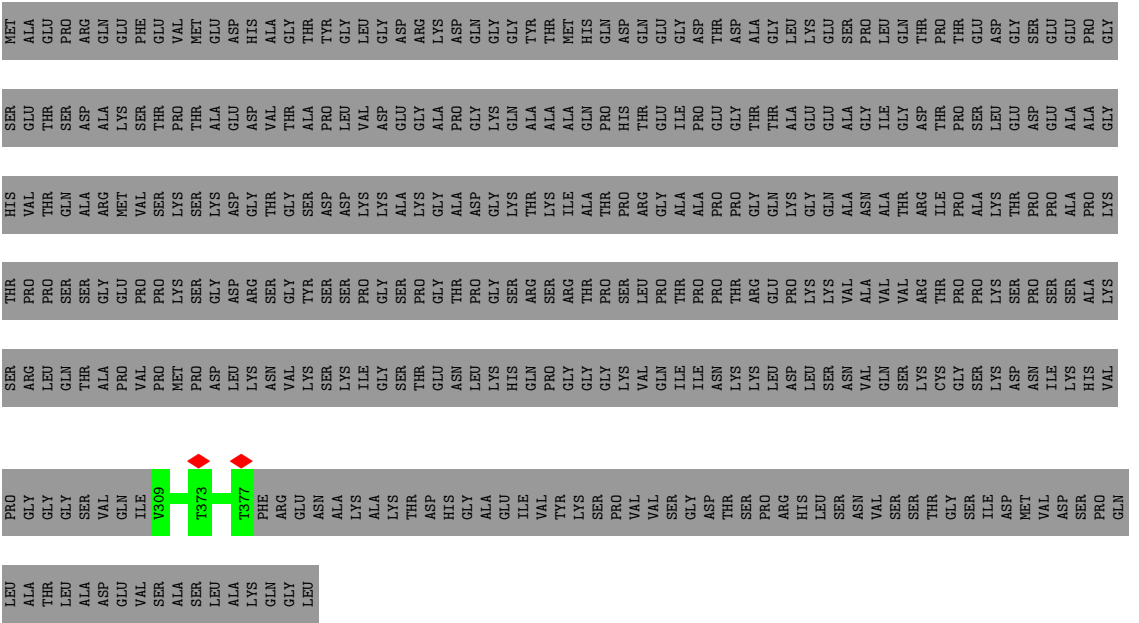
- Molecule 1 is a protein called Microtubule-associated protein tau.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	B	69	Total	C	H	N	O	S	0	0
			1065	326	543	96	99	1		
1	c	69	Total	C	H	N	O	S	0	0
			1065	326	543	96	99	1		
1	A	69	Total	C	H	N	O	S	0	0
			1065	326	543	96	99	1		
1	C	69	Total	C	H	N	O	S	0	0
			1065	326	543	96	99	1		
1	D	69	Total	C	H	N	O	S	0	0
			1065	326	543	96	99	1		
1	E	69	Total	C	H	N	O	S	0	0
			1065	326	543	96	99	1		



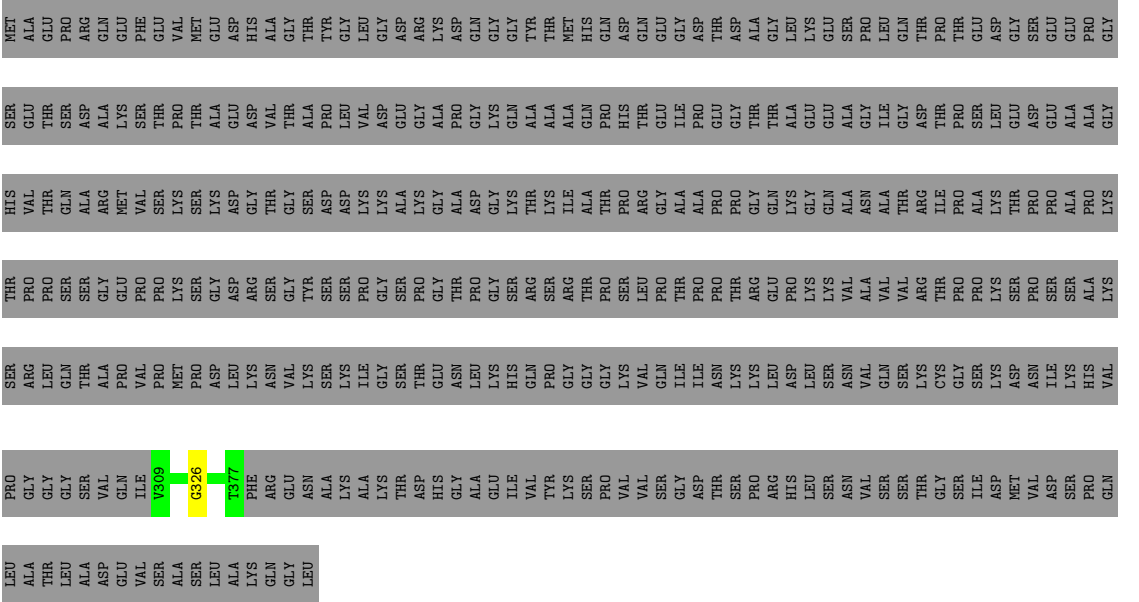
● Molecule 1: Microtubule-associated protein tau

Chain A: 16% 84%



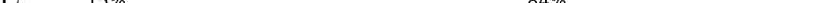
● Molecule 1: Microtubule-associated protein tau

Chain C: 15% 84%



Chain D: 16% 84%

- Molecule 1: Microtubule-associated protein tau

Chain E:  15% 84%

ALA	THR	PRO	SER	THR	SER	THR	ALA	THR	HIS	SER	MET
THR	LEU	GLY	ARG	PRO	PRO	PRO	GLN	VAL	VAL	GLU	ALA
LEU	LEU	GLY	LEU	SER	SER	SER	GLN	THR	THR	THR	THR
ALA	ASP	SER	THR	THR	THR	THR	ALA	ALA	ALA	ASP	PRO
GLU	GLU	VAL	ALA	GLY	GLY	GLY	ARG	MET	ARG	ALA	GLN
VAL	VAL	GLN	PRO	GLU	GLU	GLU	MET	VAL	VAL	LYS	GLU
SER	SER	ILE	VAL	PRO	PRO	PRO	VAL	VAL	VAL	PHE	GLU
ALA	ALA	V309	PRO	PRO	PRO	PRO	VAL	THR	THR	THR	VAL
LEU	LEU	Y310	MET	LYS	LYS	LYS	VAL	LYS	LYS	VAL	GLU
ALA	LEU		PRO	SER	SER	SER	THR	SER	SER	THR	MET
LEU	LEU		ASP	GLY	GLY	GLY	ALA	LYS	LYS	ALA	GLU
LYS	LYS	PHE	LEU	ASP	ASP	ASP	ASP	ASP	ASP	GLU	ASP
GLN	GLU	ARG	LYS	LYS	LYS	LYS	GLY	GLY	GLY	ASP	HIS
GLY	GLY	ASN	VAL	ARG	ARG	ARG	VAL	VAL	VAL	VAL	ALA
LEU	LEU	ALA	VAL	LYS	LYS	TYR	ALA	SER	SER	THR	THR
			LYS	SER	SER	SER	ALA	ASP	ASP	LEU	TYR
			ALA	LYS	ILE	ILE	GLY	LYS	LYS	VAL	GLY
			THR	GLY	GLY	GLY	GLY	GLY	GLY	ASP	GLY
			ASP	SER	SER	SER	ALA	ALA	LYS	GLY	ARG
			HIS	THR	THR	THR	GLY	GLY	GLY	ALA	LYS
			GLY	GLU	GLY	GLY	THR	ALA	ALA	PRO	ASP
			ALA	ASN	LEU	LEU	PRO	GLY	GLY	GLY	ASN
			GLU	LEU	LEU	LEU	PRO	GLY	GLY	GLY	GLN
			ILE	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLN
			VAL	HIS	HIS	HIS	SER	LYS	LYS	GLN	GLY
			THR	VAL	VAL	VAL	GLN	ARG	THR	ALA	TYR
			LYS	PRO	PRO	PRO	SER	LYS	LYS	ALA	THR
			SER	GLY	GLY	GLY	ARG	ILE	ALA	ALA	MET
			PRO	THR	THR	THR	THR	ALA	GLN	HIS	GLN
			VAL	GLY	GLY	GLY	PRO	THR	THR	GLN	GLN
			VAL	VAL	VAL	VAL	LYS	PRO	HIS	PRO	GLN
			SER	VAL	VAL	VAL	GLN	ARG	THR	THR	GLN
			GLY	ILE	ILE	ILE	GLN	GLY	GLY	GLU	GLY
			ASP	THR	THR	THR	THR	ALA	ILE	PRO	GLY
			THR	THR	THR	THR	ILE	ALA	ALA	ASP	THR
			PRO	ASN	ASN	ASN	PRO	PRO	PRO	GLU	THR
			PRO	LYS	LYS	LYS	THR	PRO	GLY	ASP	THR
			ARG	LYS	LYS	LYS	ARG	GLY	THR	ALA	ALA
			HIS	LEU	LEU	LEU	GLU	GLN	GLY	THR	GLY
			LEU	ASP	ASP	ASP	PRO	LYS	ALA	ALA	LYS
			LEU	LEU	LEU	LEU	LYS	GLY	GLY	GLU	LYS
			SER	VAL	VAL	VAL	GLN	ASN	ASN	GLY	PRO
			SER	SER	SER	SER	VAL	ALA	ALA	ALA	LEU
			THR	THR	THR	THR	VAL	ALA	ALA	ILE	GLN
			GLY	GLY	GLY	GLY	ARG	THR	GLY	GLY	THR
			SER	CYS	SER	SER	ILE	THR	THR	ASP	THR
			ILE	GLY	GLY	GLY	PRO	PRO	PRO	PRO	THR
			ASP	SER	SER	SER	ALA	ALA	SER	LEU	GLU
			MET	LYS	LYS	LYS	LYS	LYS	LYS	LEU	ASP
			VAL	ASP	ASP	ASP	SER	THR	THR	GLU	GLY
			ASP	ASN	ASN	ASN	PRO	PRO	PRO	ASP	SER
			SER	ILE	ILE	ILE	SER	PRO	PRO	GLU	GLU
			PRO	LYS	LYS	LYS	SER	ALA	ALA	ALA	ALA
			GLN	VAL	VAL	VAL	PRO	PRO	PRO	ALA	ALA
			HIS	THR	THR</						

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-1.33°, rise=4.75 Å, axial sym=C1	Depositor
Number of segments used	14590	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k 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	0.002	Depositor
Recommended contour level	0.00802	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	0.71	0/530	1.27	0/709
1	B	0.73	0/530	1.29	0/709
1	C	0.69	0/530	1.24	1/709 (0.1%)
1	D	0.69	0/530	1.26	0/709
1	E	0.68	0/530	1.24	0/709
1	c	0.71	0/530	1.28	0/709
All	All	0.70	0/3180	1.26	1/4254 (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	E	0	1
1	c	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	326	GLY	N-CA-C	5.67	118.23	110.69

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	310	TYR	Sidechain
1	c	310	TYR	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	522	543	542	0	0
1	B	522	543	542	0	0
1	C	522	543	542	0	0
1	D	522	543	542	0	0
1	E	522	543	542	0	0
1	c	522	543	542	0	0
All	All	3132	3258	3252	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

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	67/441 (15%)	65 (97%)	2 (3%)	0	100	100
1	B	67/441 (15%)	64 (96%)	3 (4%)	0	100	100
1	C	67/441 (15%)	64 (96%)	3 (4%)	0	100	100
1	D	67/441 (15%)	64 (96%)	3 (4%)	0	100	100
1	E	67/441 (15%)	65 (97%)	2 (3%)	0	100	100
1	c	67/441 (15%)	64 (96%)	3 (4%)	0	100	100
All	All	402/2646 (15%)	386 (96%)	16 (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	
1	A	60/358 (17%)	60 (100%)	0	100	100
1	B	60/358 (17%)	60 (100%)	0	100	100
1	C	60/358 (17%)	60 (100%)	0	100	100
1	D	60/358 (17%)	60 (100%)	0	100	100
1	E	60/358 (17%)	60 (100%)	0	100	100
1	c	60/358 (17%)	60 (100%)	0	100	100
All	All	360/2148 (17%)	360 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	336	GLN
1	D	362	HIS
1	E	351	GLN
1	E	336	GLN
1	C	336	GLN

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.

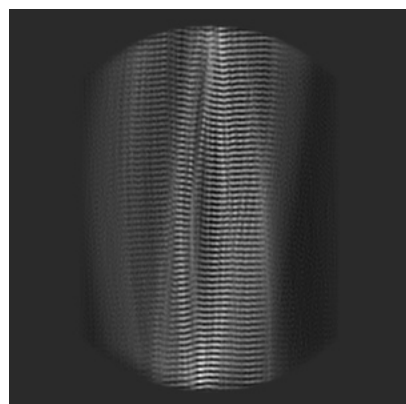
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14059. These allow visual inspection of the internal detail of the map and identification of artifacts.

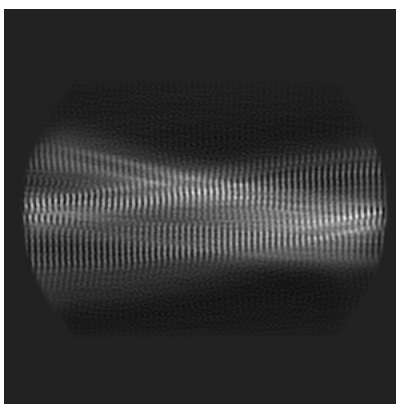
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

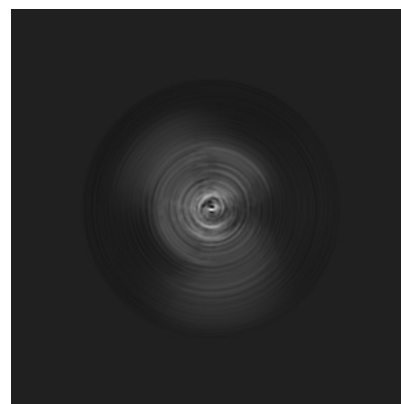
6.1.1 Primary map



X

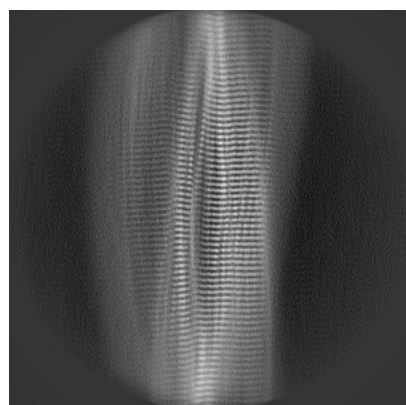


Y

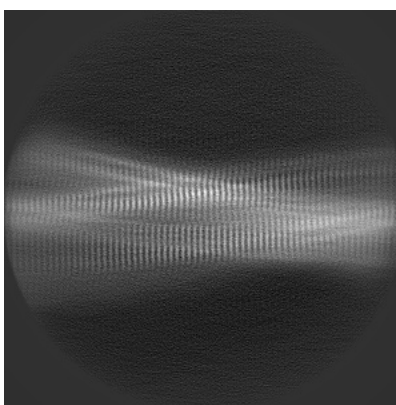


Z

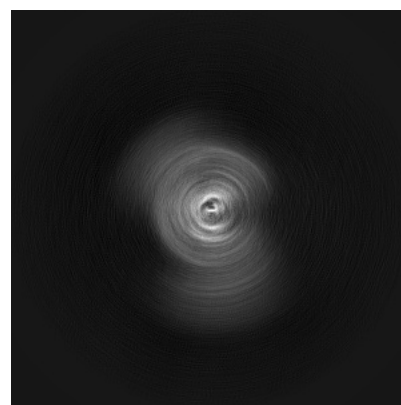
6.1.2 Raw map



X



Y

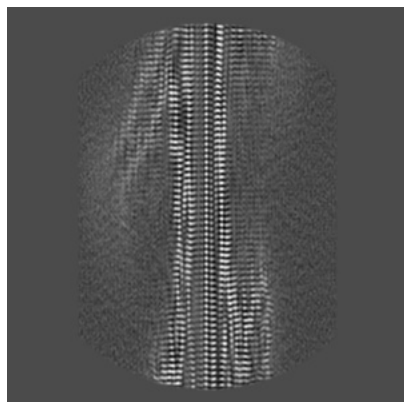


Z

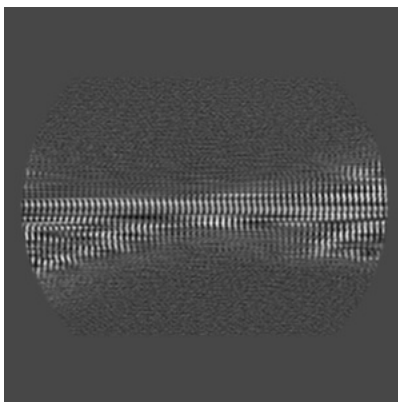
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

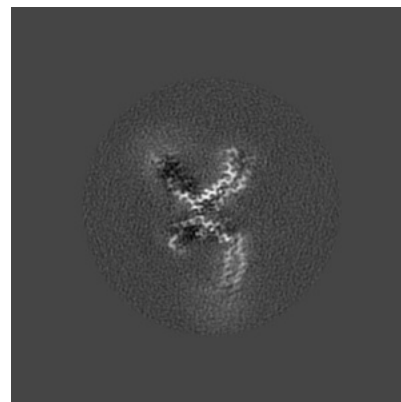
6.2.1 Primary map



X Index: 192

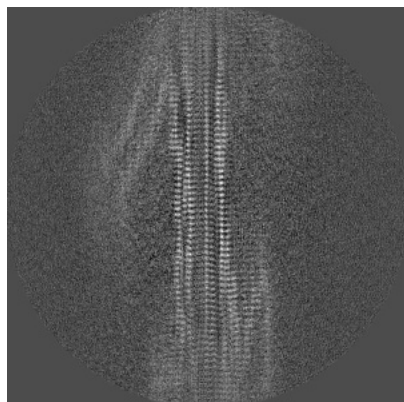


Y Index: 192

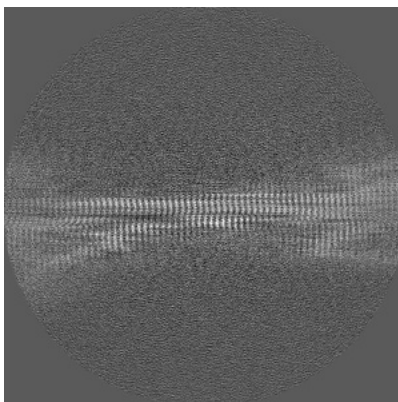


Z Index: 192

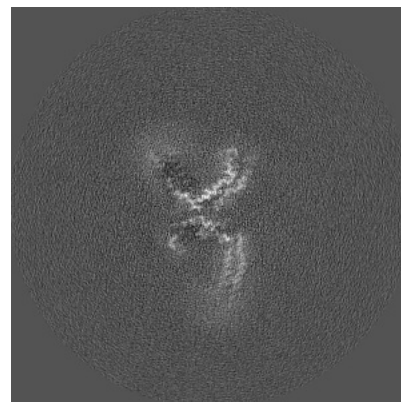
6.2.2 Raw map



X Index: 192



Y Index: 192

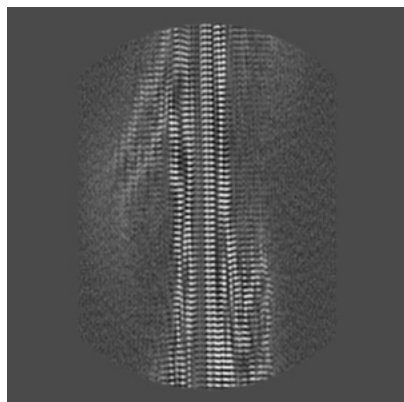


Z Index: 192

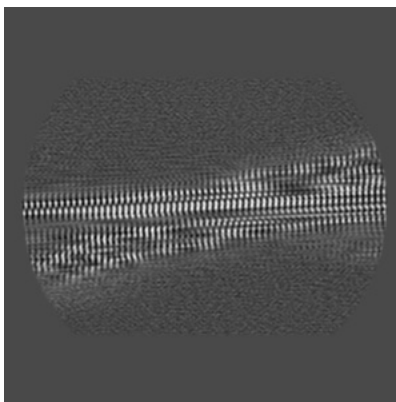
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

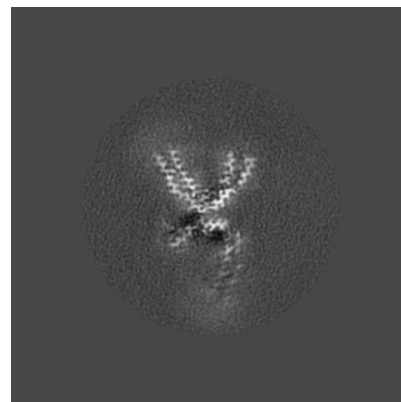
6.3.1 Primary map



X Index: 196

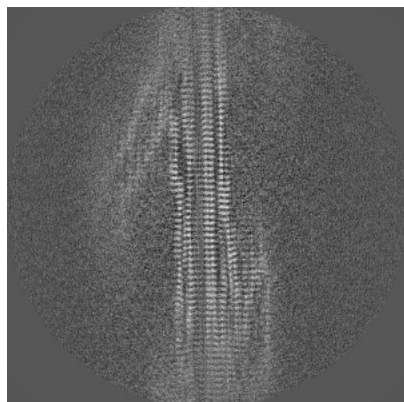


Y Index: 205

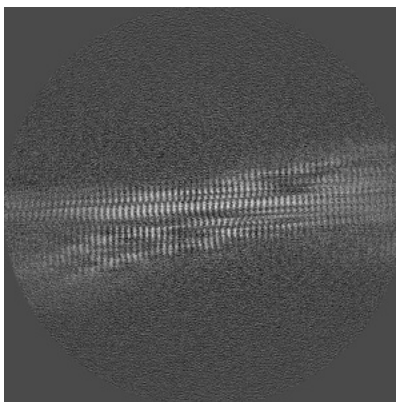


Z Index: 205

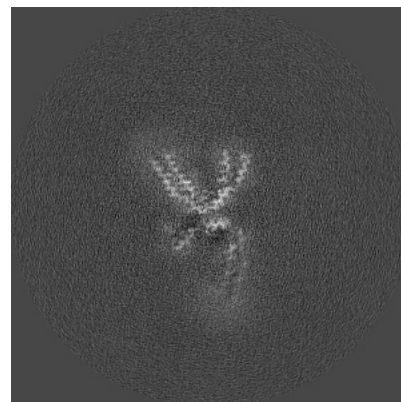
6.3.2 Raw map



X Index: 196



Y Index: 205

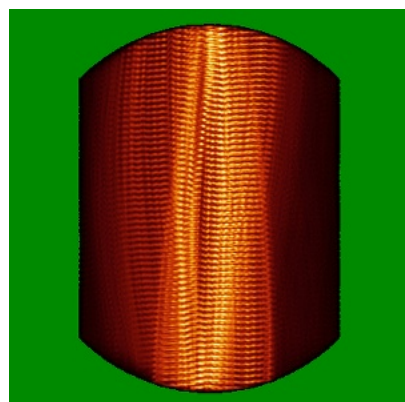


Z Index: 182

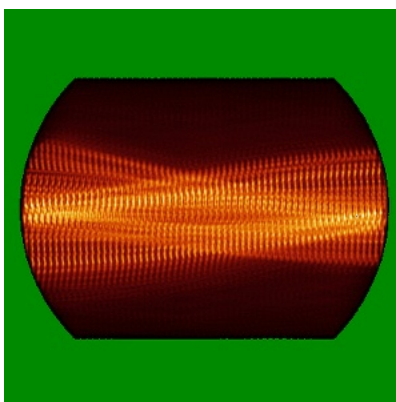
The images above show the largest variance slices of the map in three orthogonal directions.

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

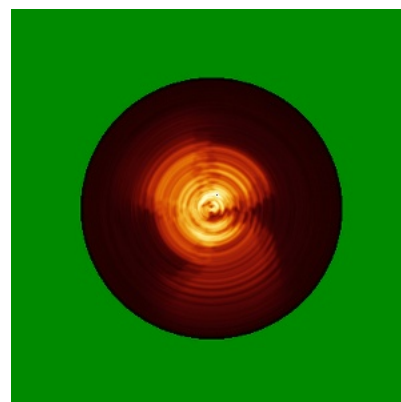
6.4.1 Primary map



X

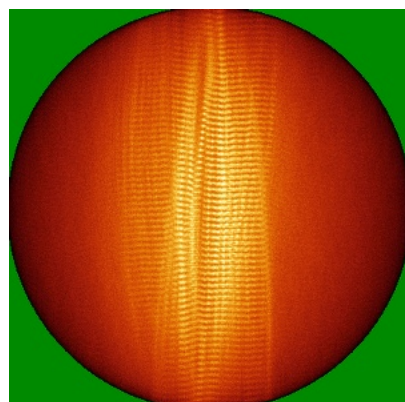


Y

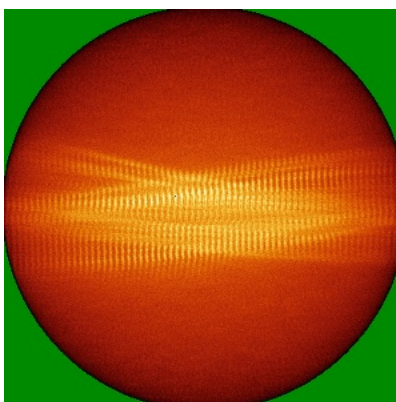


Z

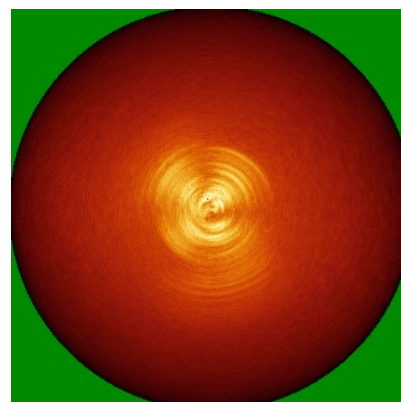
6.4.2 Raw map



X



Y

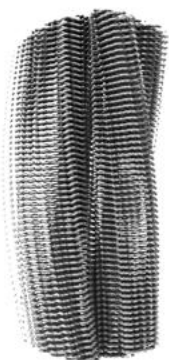


Z

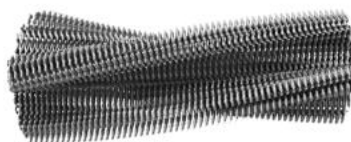
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.00802. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

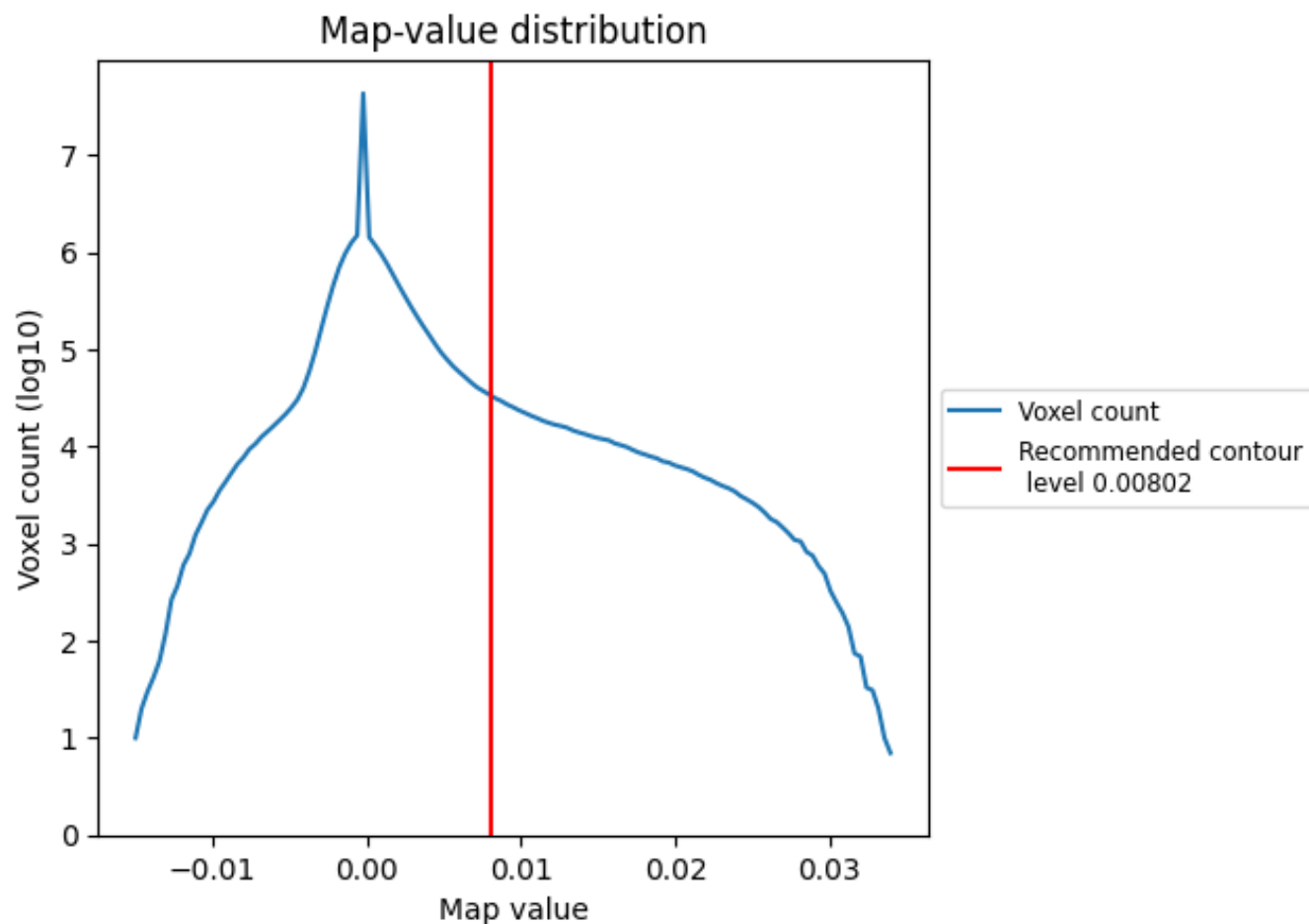
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

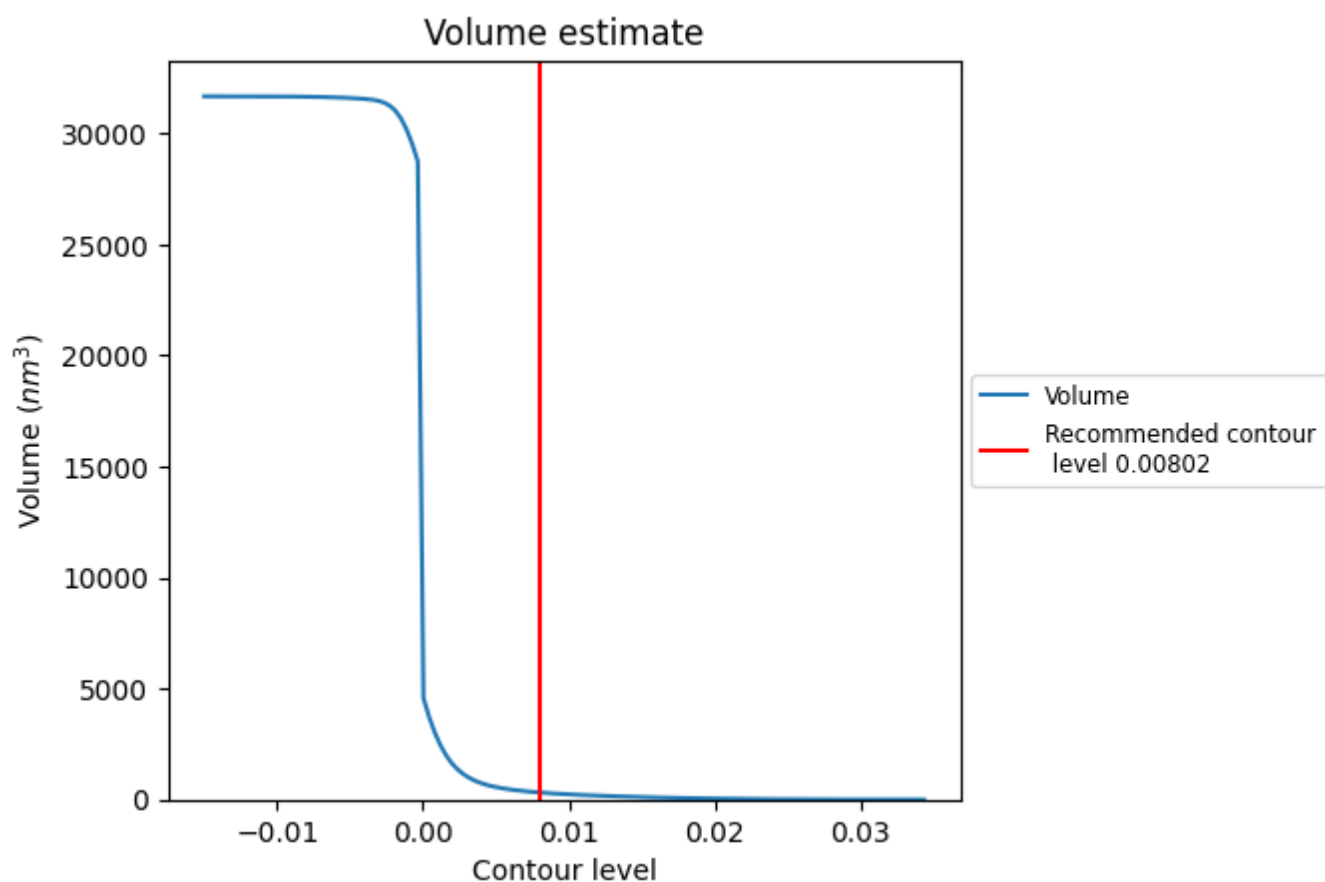
This section contains the results of statistical analysis of the map.

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.

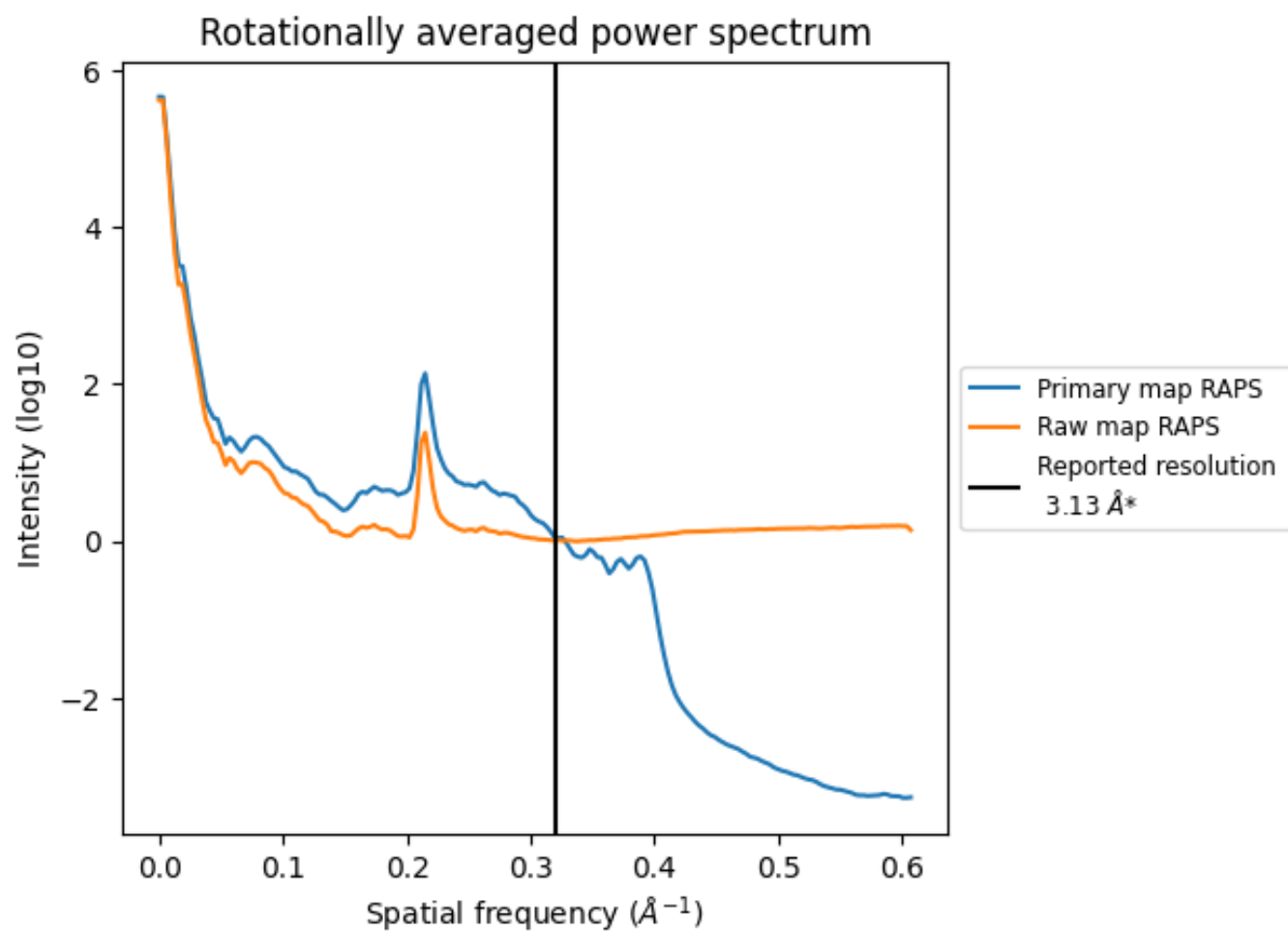
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 317 nm³; this corresponds to an approximate mass of 286 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 ⓘ

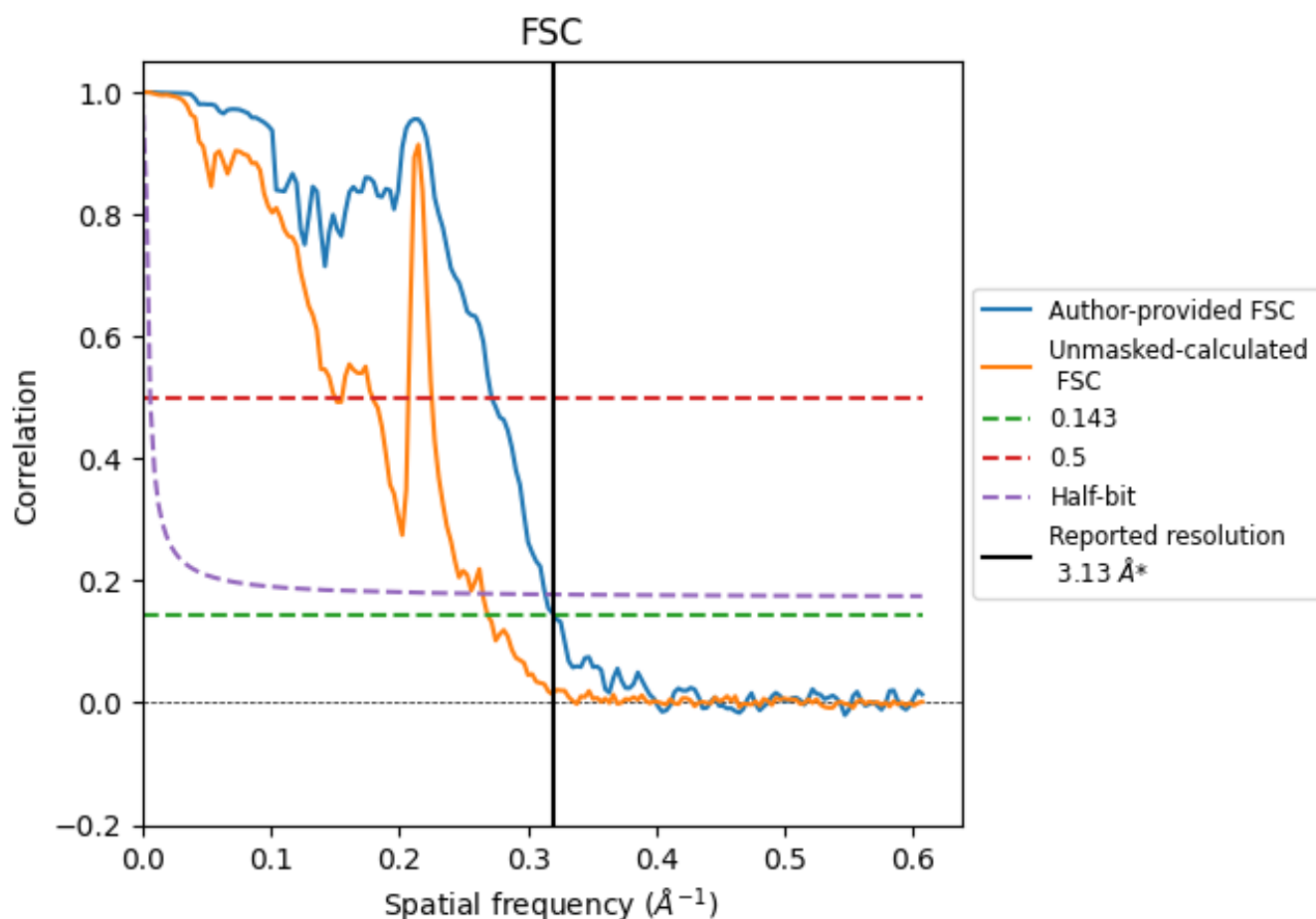


*Reported resolution corresponds to spatial frequency of 0.319 Å⁻¹

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 $0.319 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

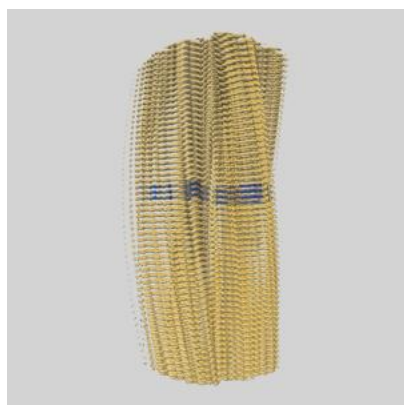
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.13	-	-
Author-provided FSC curve	3.12	3.68	3.19
Unmasked-calculated*	3.72	6.67	3.77

*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 3.72 differs from the reported value 3.13 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14059 and PDB model 7QL0. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



X



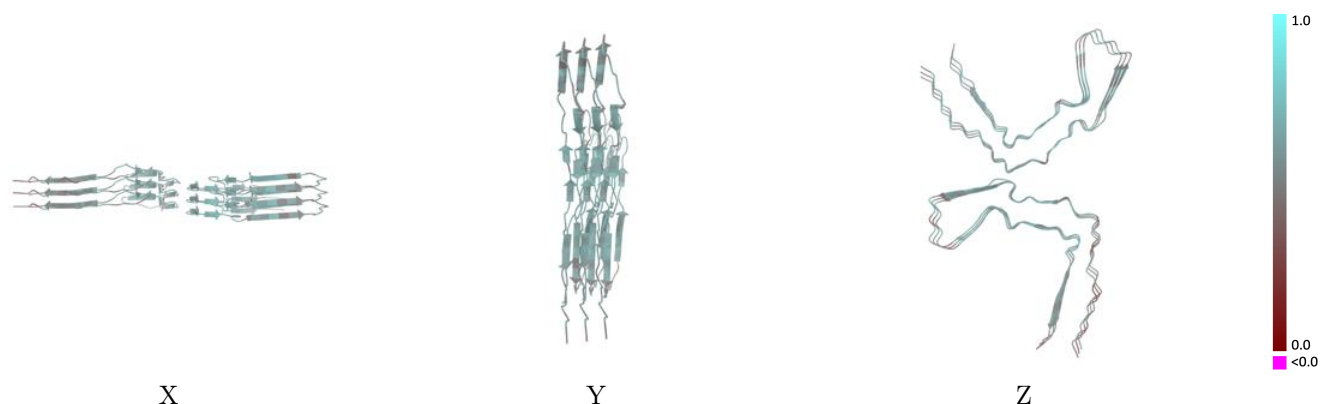
Y



Z

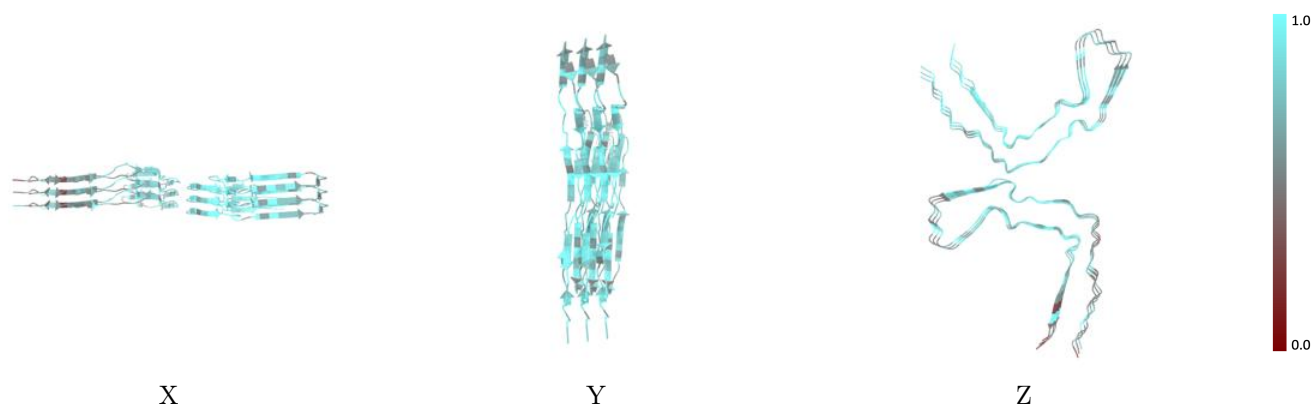
The images above show the 3D surface view of the map at the recommended contour level 0.00802 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



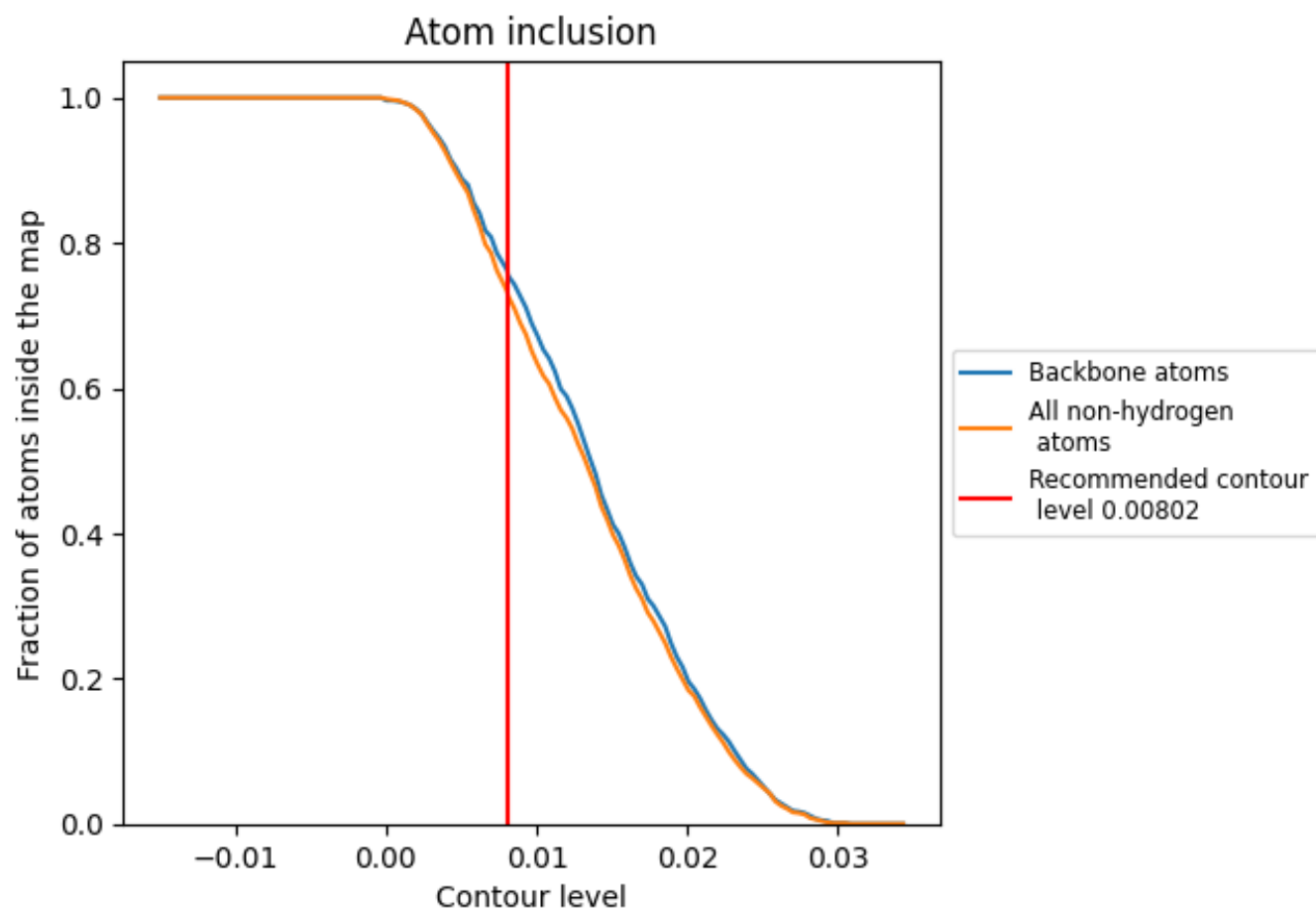
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00802).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 73% 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 (0.00802) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7340	0.5510
A	0.6880	0.5400
B	0.6860	0.5420
C	0.7820	0.5670
D	0.7820	0.5610
E	0.7780	0.5610
c	0.6690	0.5350

1.0

0.0

<0.0