



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2022 – 04:51 am GMT

PDB ID : 7QKW
EMDB ID : EMD-14055
Title : In vitro assembled 266-391 S356D tau filaments with KCl (44a)
Authors : Lovestam, S.; Scheres, S.H.W.
Deposited on : 2021-12-19
Resolution : 2.32 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.0.dev97
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.27

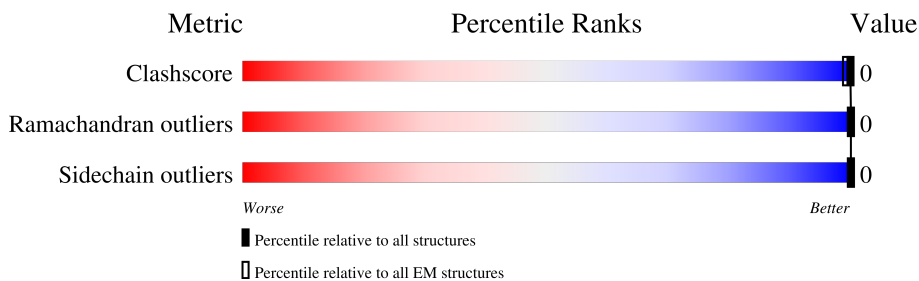
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.32 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	 5% 12% 12% 88%
1	B	441	 6% 12% 12% 88%
1	C	441	 6% 12% 12% 88%
1	D	441	 11% 11% 11% 89%
1	E	441	 11% 11% 11% 89%
1	F	441	 11% 11% 11% 89%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4707 atoms, of which 2439 are hydrogens and 0 are deuteriums.

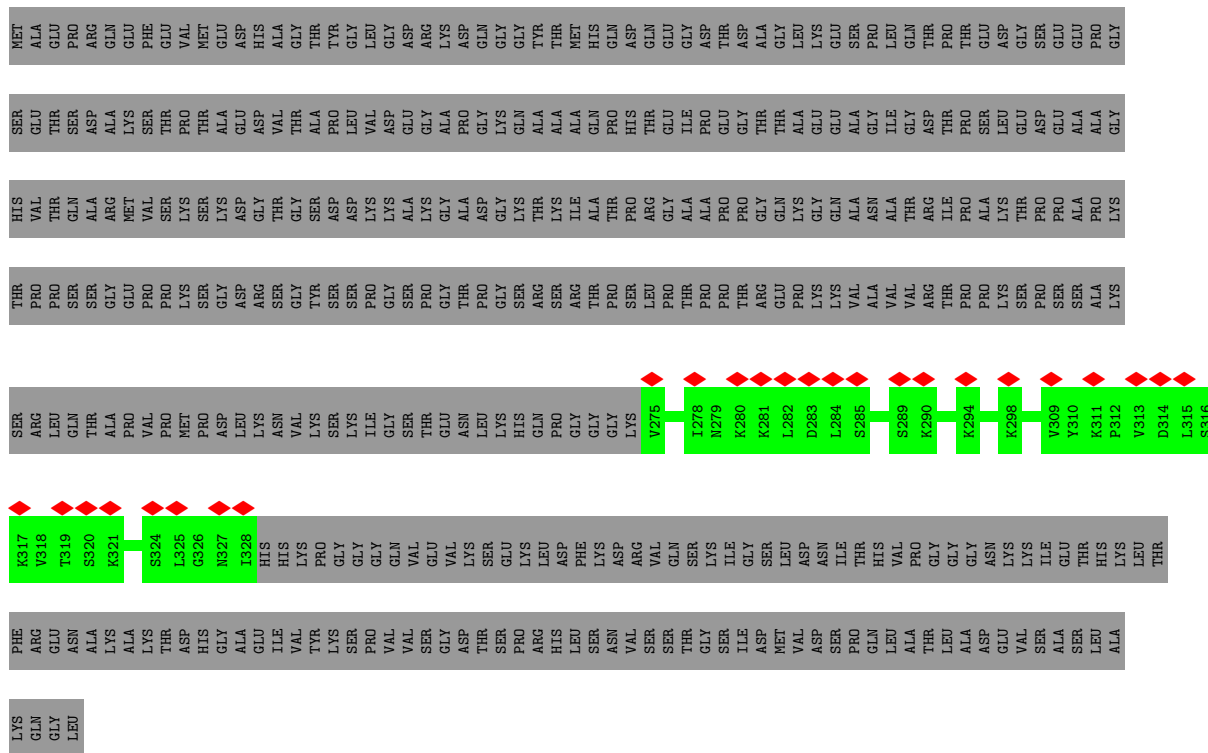
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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

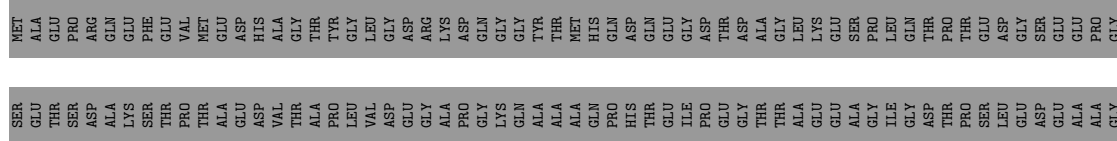
Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	B	54	Total 823	C 248	H 426	N 71	O 76	S 2	0	0
1	A	54	Total 823	C 248	H 426	N 71	O 76	S 2	0	0
1	C	54	Total 823	C 248	H 426	N 71	O 76	S 2	0	0
1	D	48	Total 746	C 225	H 387	N 64	O 68	S 2	0	0
1	E	48	Total 746	C 225	H 387	N 64	O 68	S 2	0	0
1	F	48	Total 746	C 225	H 387	N 64	O 68	S 2	0	0



• Molecule 1: Microtubule-associated protein tau



• Molecule 1: Microtubule-associated protein tau



SER	ARG	LEU	GLN	THR	ALA	PRO	VAL	PRO	MET	PRO	ASP	LEU	LYS	ASN	VAL	LYS	SER	SER	LYS	ILE	GLY	GLY	GLY	LYS	V275	I278	N279	K280	K281	L282	D283	L284	S285	K290	I308	K311	L315	S316	K317	S320	K321	C322	GLY	SER																				
LEU	GLY	ASN	ILE	HIS	HIS	LYS	PRO	GLY	GLY	GLN	VAL	GLU	VAL	VAL	LYS	GLY	GLU	LYS	THR	LEU	ASP	PHE	LYS	ASP	ARG	VAL	GLN	SER	LYS	ILE	GLY	SER	LEU	ASP	ASN	ILE	THR	HIS	VAL	PRO	GLN	GLY	ALA	GLY	ASN	LYS	LYS	ILE	GLU	THR	ALA	HIS	LYS	LEU	THR	PHE	LYS	ARG	GLY	ASN	ALA	LYS	ALA	ALA
LYS	THR	ASP	HIS	GLY	ALA	GLU	ILE	VAL	TYR	SER	PRO	VAL	VAL	VAL	SER	ASP	THR	SER	PRO	ARG	HIS	LEU	SER	ASN	VAL	VAL	SER	THR	GLY	SER	ILE	ASP	MET	VAL	ASP	SER	PRO	GLN	LEU	ALA	THR	LEU	ALA	ASP	VAL	SER	ALA	SER	LEU	ALA	LYS	LYS	GLN	GLY	LEU									

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-1.01°, rise=4.78 Å, axial sym=C1	Depositor
Number of segments used	9794	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	0.047	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0114	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	0.47	0/400	0.89	0/536
1	B	0.48	0/400	0.91	0/536
1	C	0.48	0/400	0.88	0/536
1	D	0.49	0/362	0.92	0/485
1	E	0.49	0/362	0.95	0/485
1	F	0.49	0/362	0.90	0/485
All	All	0.48	0/2286	0.91	0/3063

There are no bond length outliers.

There are no bond angle outliers.

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	397	426	425	0	0
1	B	397	426	425	0	0
1	C	397	426	425	0	0
1	D	359	387	386	0	0
1	E	359	387	386	0	0
1	F	359	387	386	0	0
All	All	2268	2439	2433	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	52/441 (12%)	49 (94%)	3 (6%)	0	100	100
1	B	52/441 (12%)	49 (94%)	3 (6%)	0	100	100
1	C	52/441 (12%)	51 (98%)	1 (2%)	0	100	100
1	D	46/441 (10%)	42 (91%)	4 (9%)	0	100	100
1	E	46/441 (10%)	44 (96%)	2 (4%)	0	100	100
1	F	46/441 (10%)	43 (94%)	3 (6%)	0	100	100
All	All	294/2646 (11%)	278 (95%)	16 (5%)	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	48/358 (13%)	48 (100%)	0	100	100
1	B	48/358 (13%)	48 (100%)	0	100	100
1	C	48/358 (13%)	48 (100%)	0	100	100
1	D	44/358 (12%)	44 (100%)	0	100	100
1	E	44/358 (12%)	44 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	44/358 (12%)	44 (100%)	0	100	100
All	All	276/2148 (13%)	276 (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 monosaccharides 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.

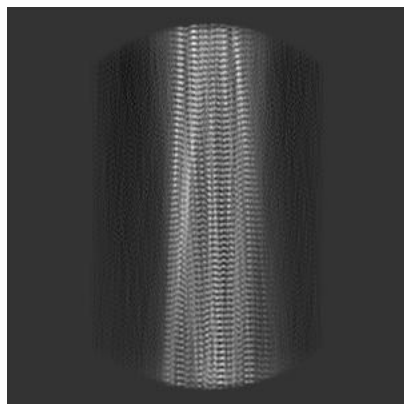
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14055. These allow visual inspection of the internal detail of the map and identification of artifacts.

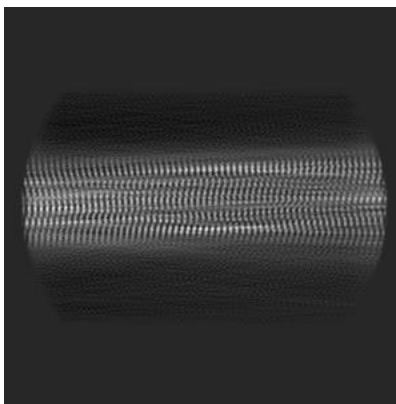
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

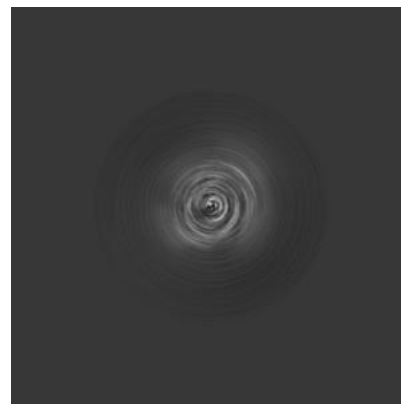
6.1.1 Primary map



X

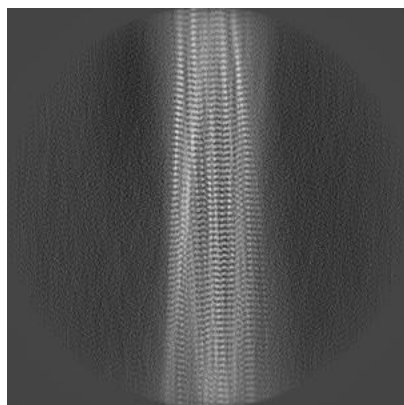


Y

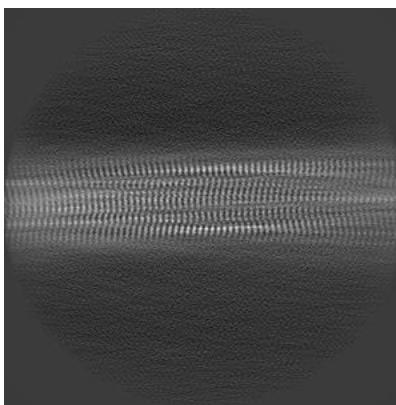


Z

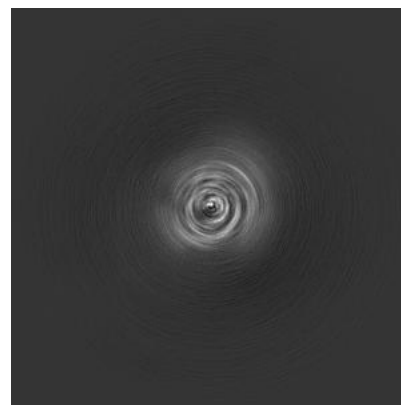
6.1.2 Raw map



X



Y

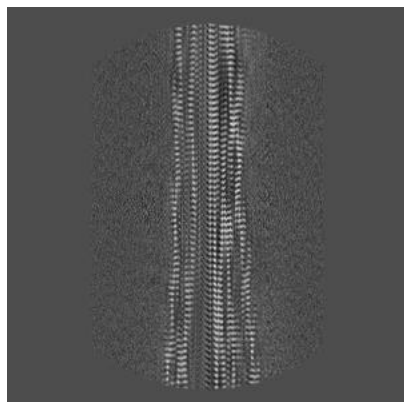


Z

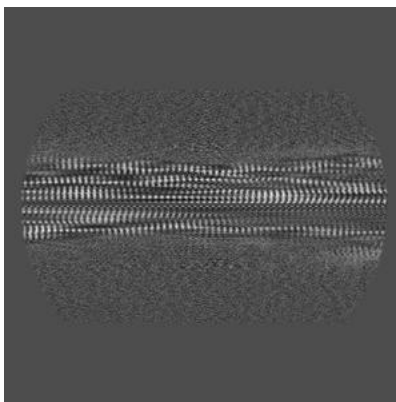
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

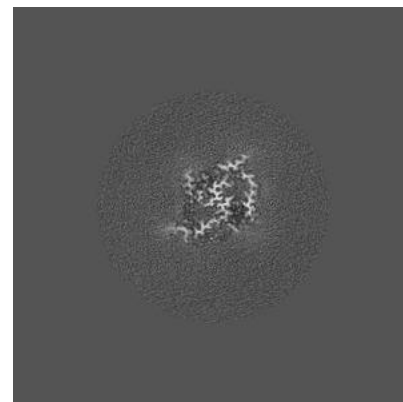
6.2.1 Primary map



X Index: 192

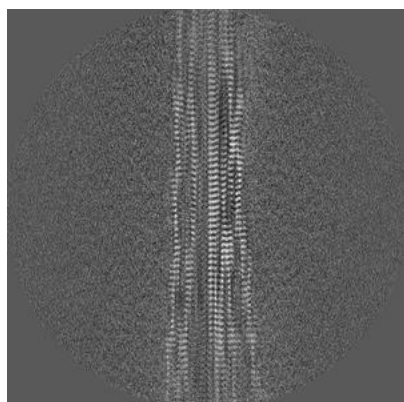


Y Index: 192

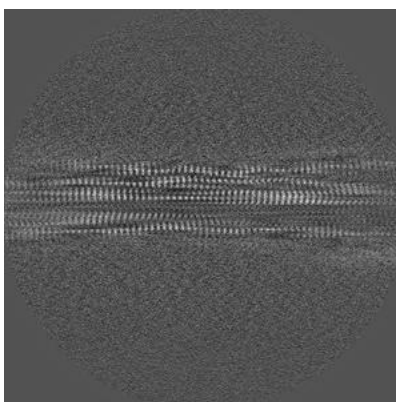


Z Index: 192

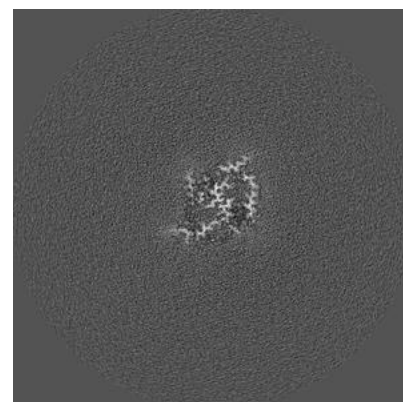
6.2.2 Raw map



X Index: 192



Y Index: 192

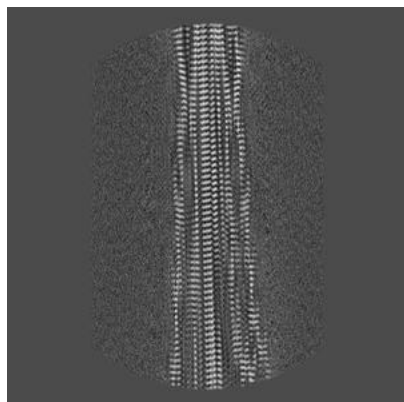


Z Index: 192

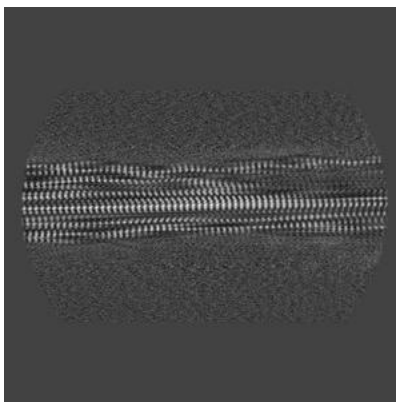
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

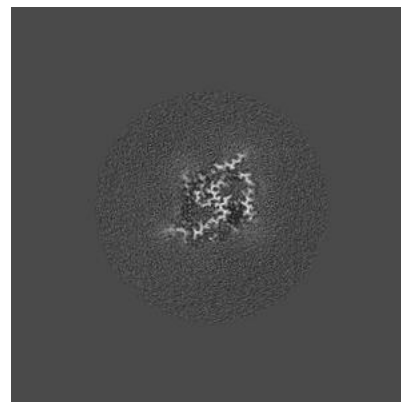
6.3.1 Primary map



X Index: 200

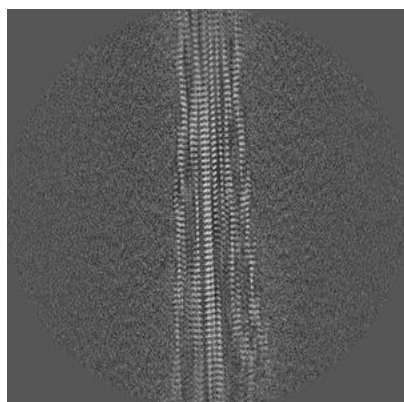


Y Index: 199

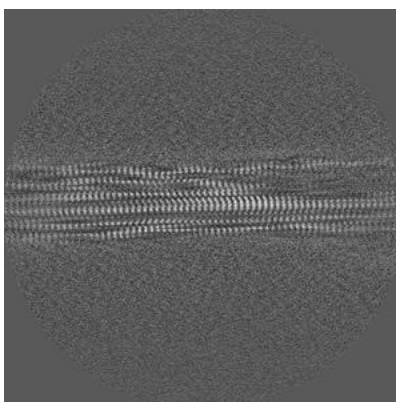


Z Index: 180

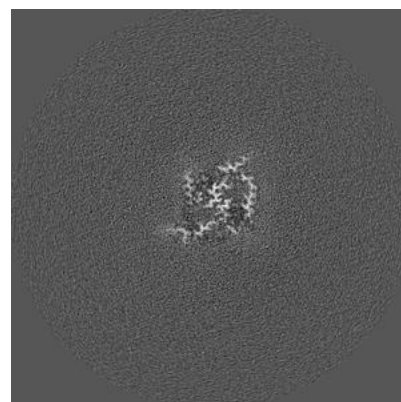
6.3.2 Raw map



X Index: 202



Y Index: 199

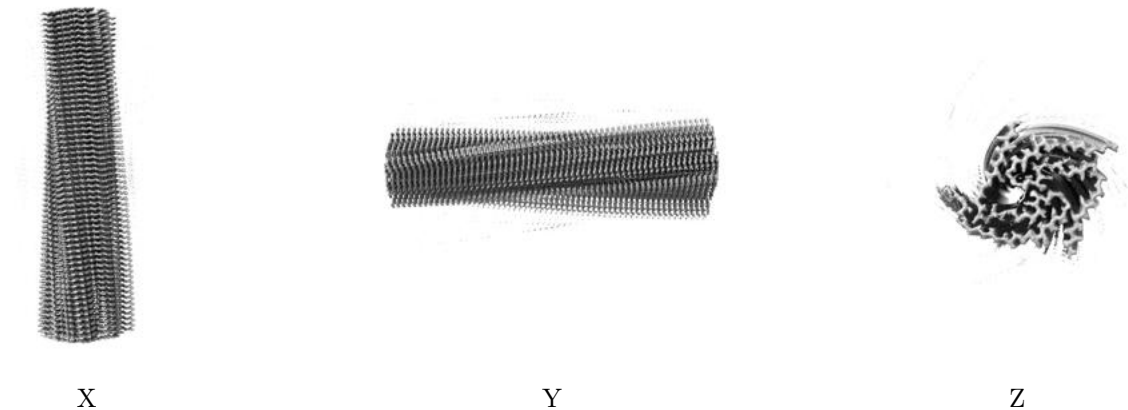


Z Index: 198

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

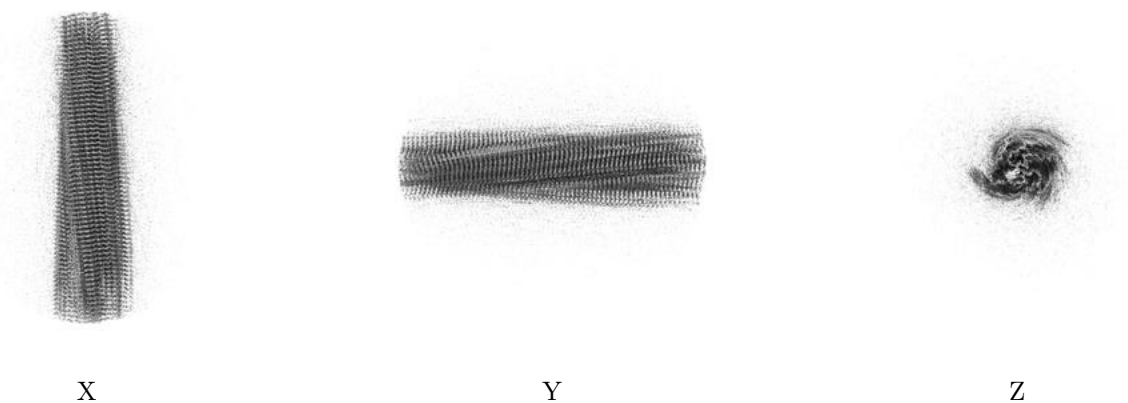
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0114. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

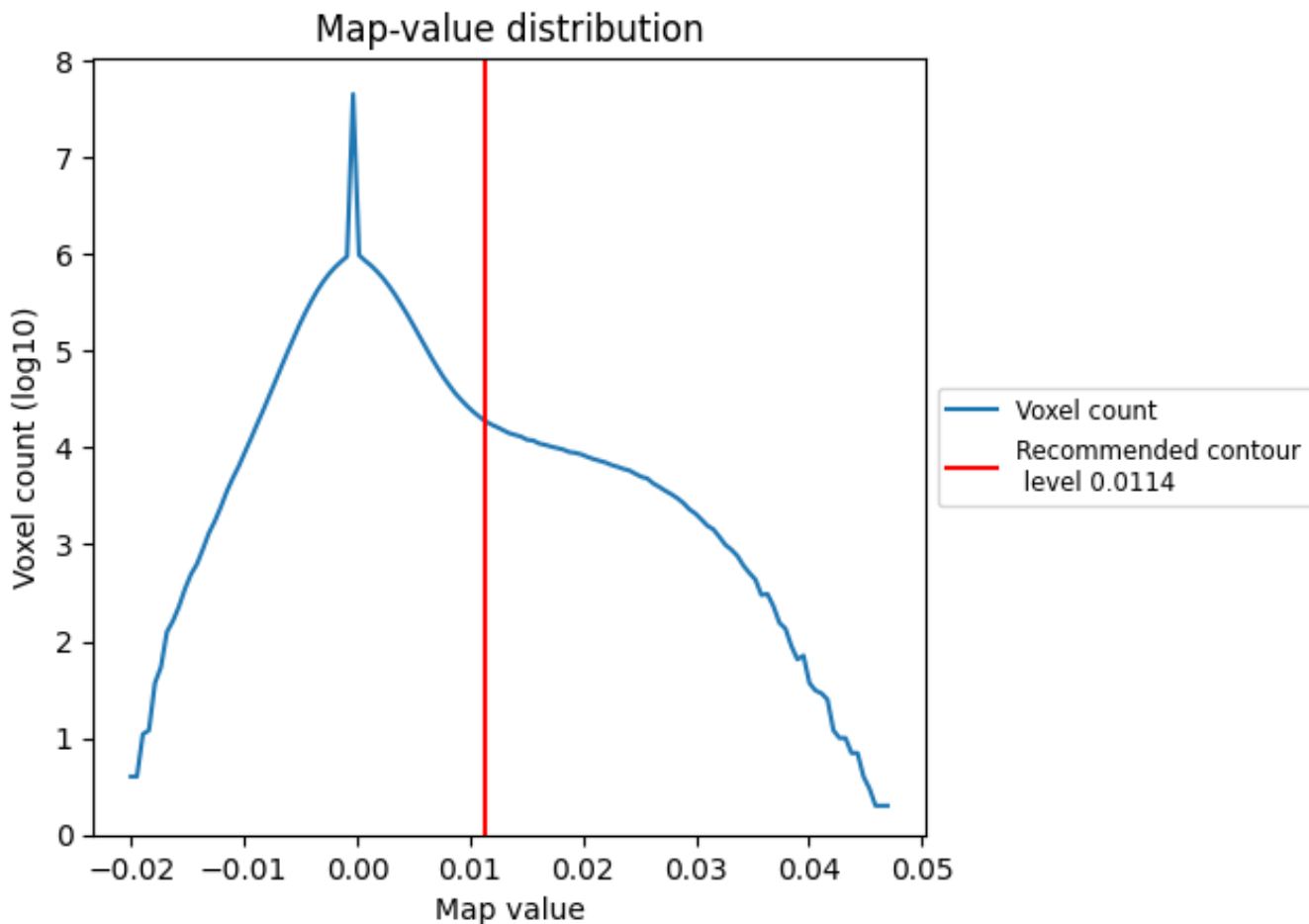
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

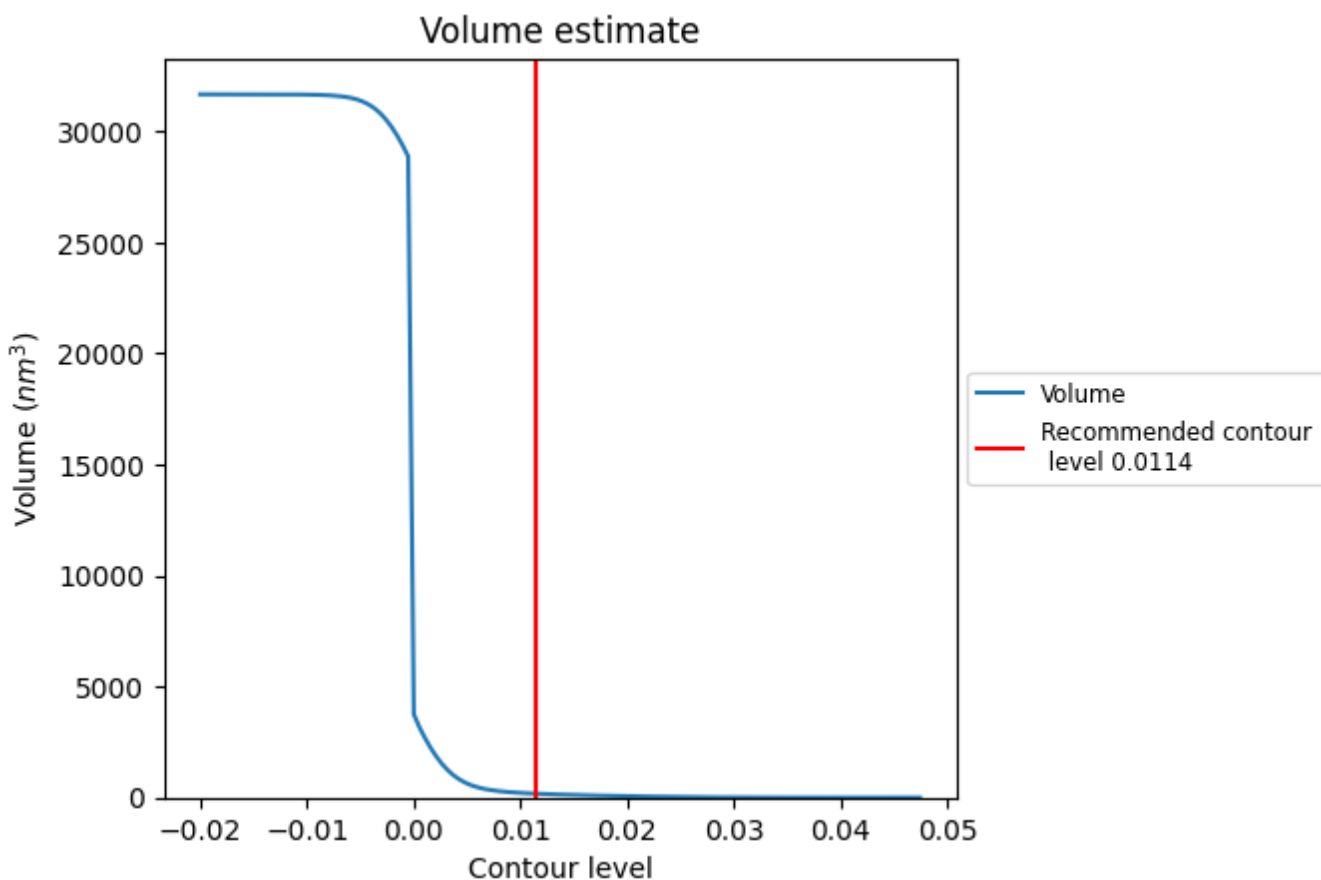
This section contains the results of statistical analysis of the map.

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.

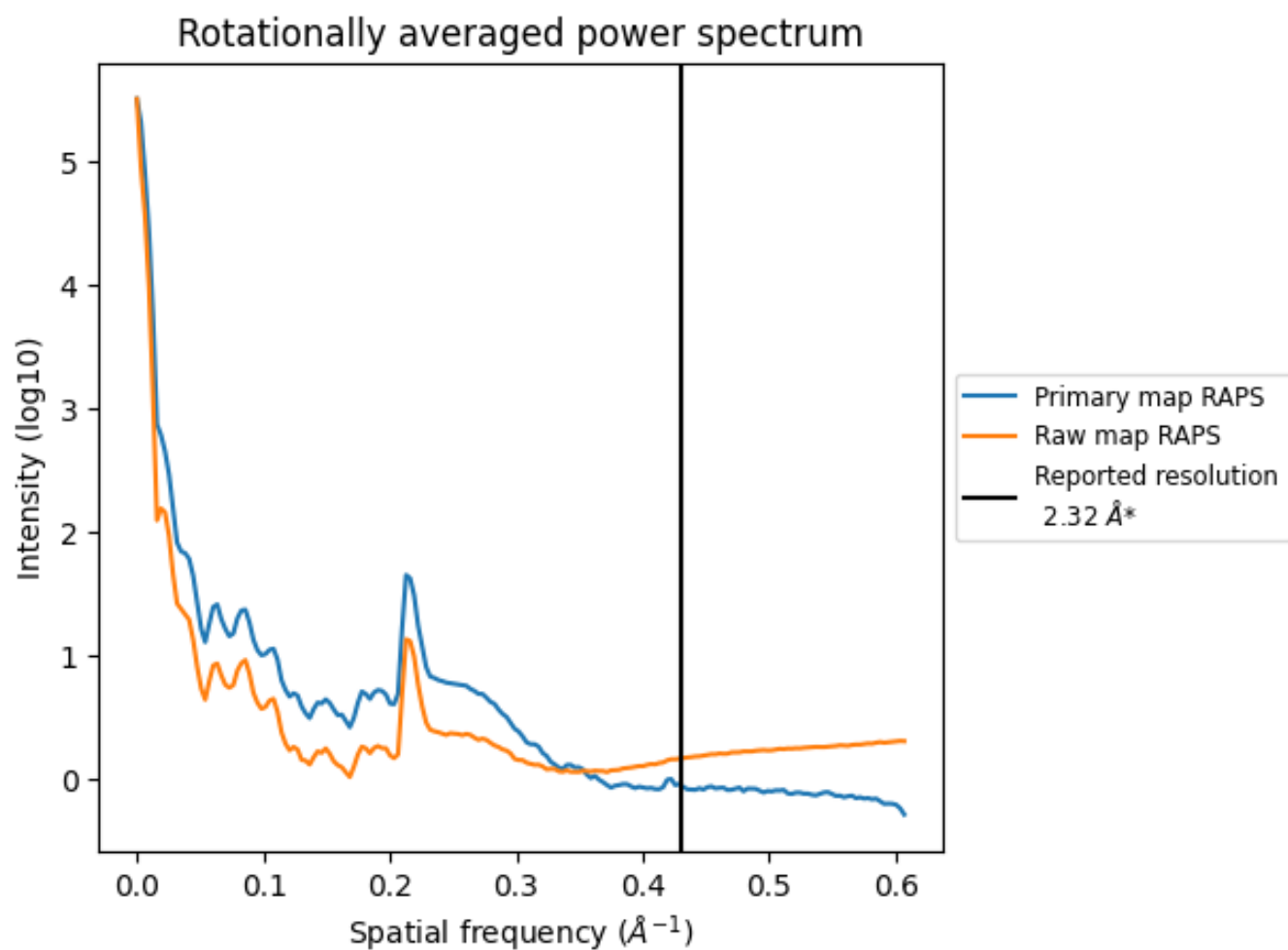
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 177 nm³; this corresponds to an approximate mass of 159 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

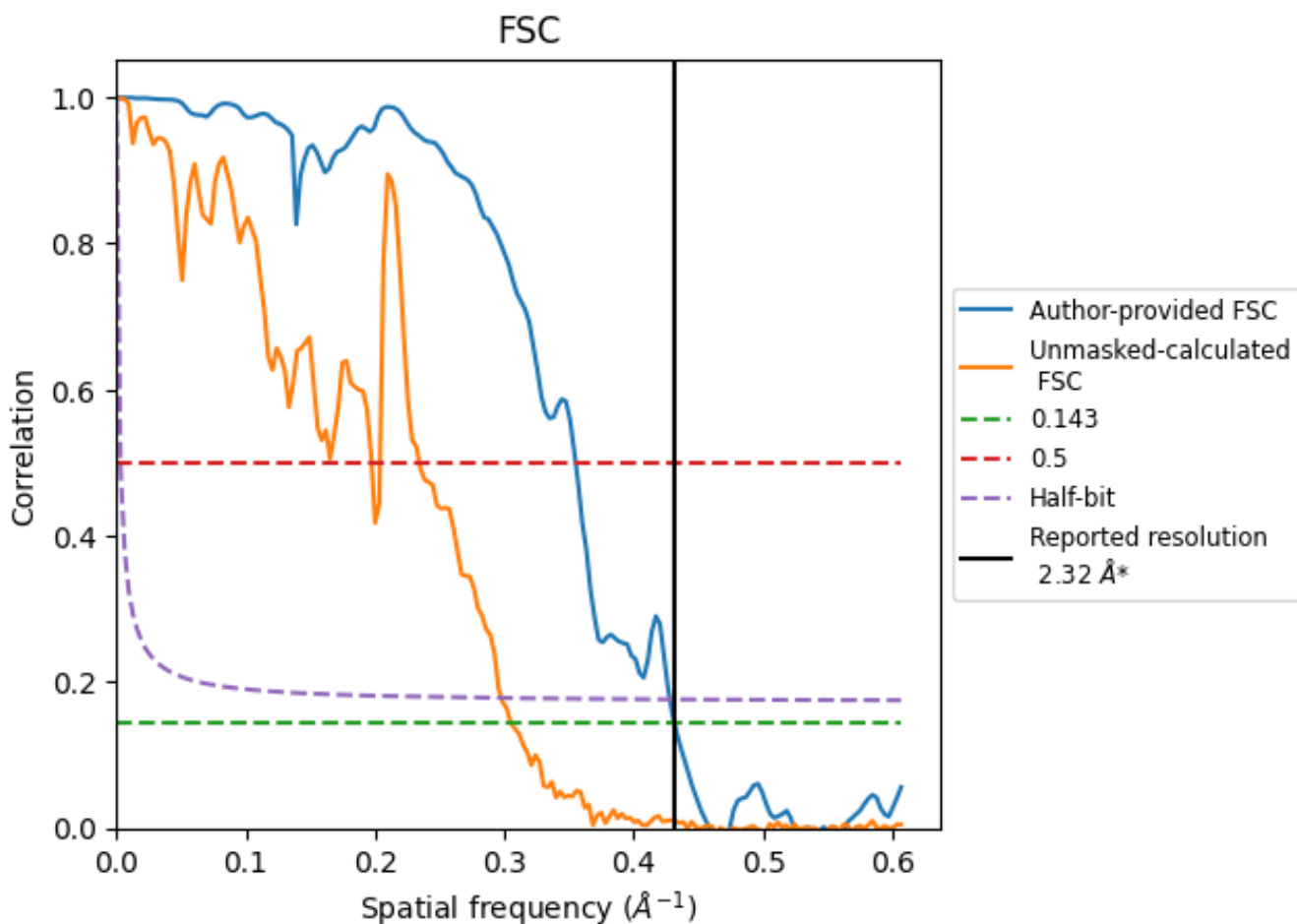


*Reported resolution corresponds to spatial frequency of 0.431 \AA^{-1}

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 0.431 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.32	-	-
Author-provided FSC curve	2.32	2.82	2.34
Unmasked-calculated*	3.28	5.07	3.36

*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 3.28 differs from the reported value 2.32 by more than 10 %

9 Map-model fit [i](#)

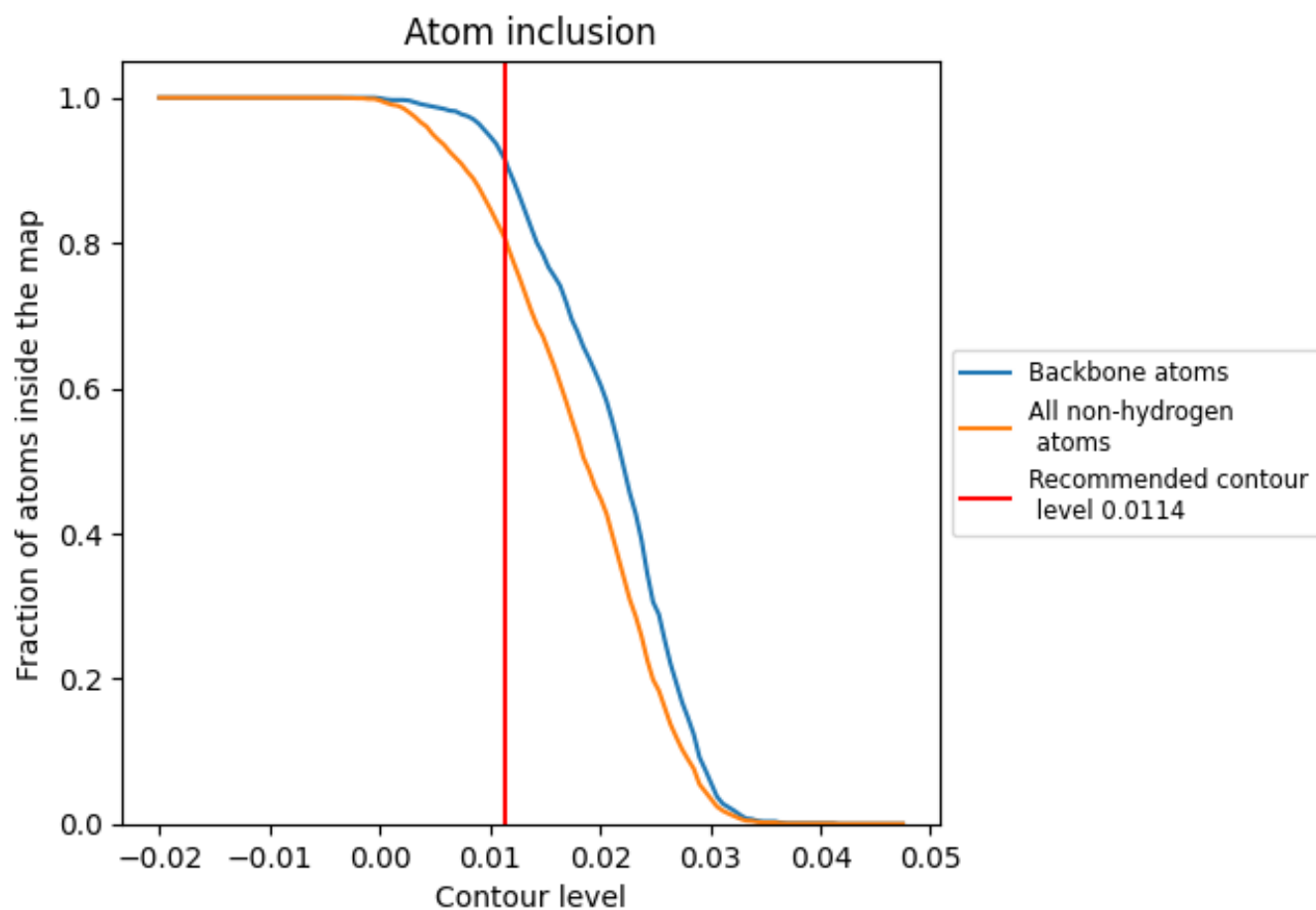
This section contains information regarding the fit between EMDB map EMD-14055 and PDB model 7QKW. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0114 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 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.