



Full wwPDB EM Validation Report ⓘ

Sep 28, 2026 – 10:18 PM JST

PDB ID : 26SG / pdb_000026sg
EMDB ID : EMD-80851
Title : Sunflower protein amyloid fibrils
Authors : Li, S.; Cao, Q.; Cao, Y.
Deposited on : 2026-05-13
Resolution : 3.05 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.dev133
MolProbity : 4-5-2 with Phenix2.2
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) : 2.51

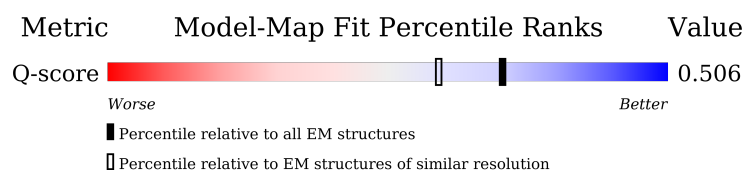
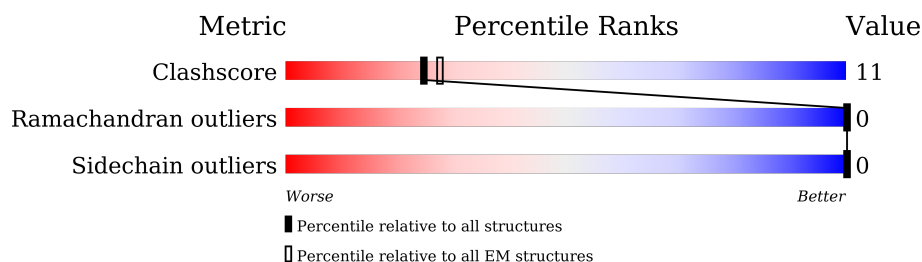
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.05 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	13971 (2.55 - 3.55)

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	251	10% • 86%
1	B	251	10% • 86%
1	C	251	10% • 86%
1	D	251	12% • 86%

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Mol	Chain	Length	Quality of chain
1	E	251	 11% . 86%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1275 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.

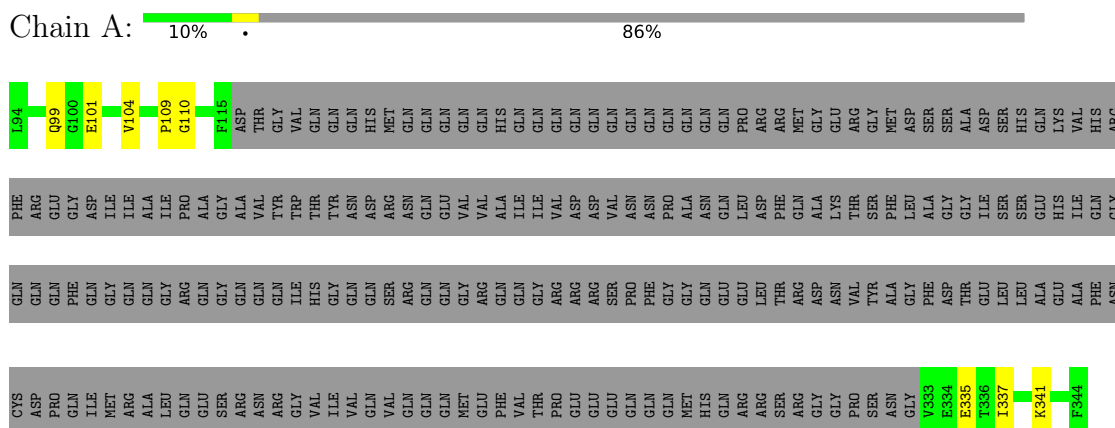
- Molecule 1 is a protein called 11-S seed storage protein, plant.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	34	Total	C	N	O	S	0	0
			255	167	37	49	2		
1	B	34	Total	C	N	O	S	0	0
			255	167	37	49	2		
1	C	34	Total	C	N	O	S	0	0
			255	167	37	49	2		
1	D	34	Total	C	N	O	S	0	0
			255	167	37	49	2		
1	E	34	Total	C	N	O	S	0	0
			255	167	37	49	2		

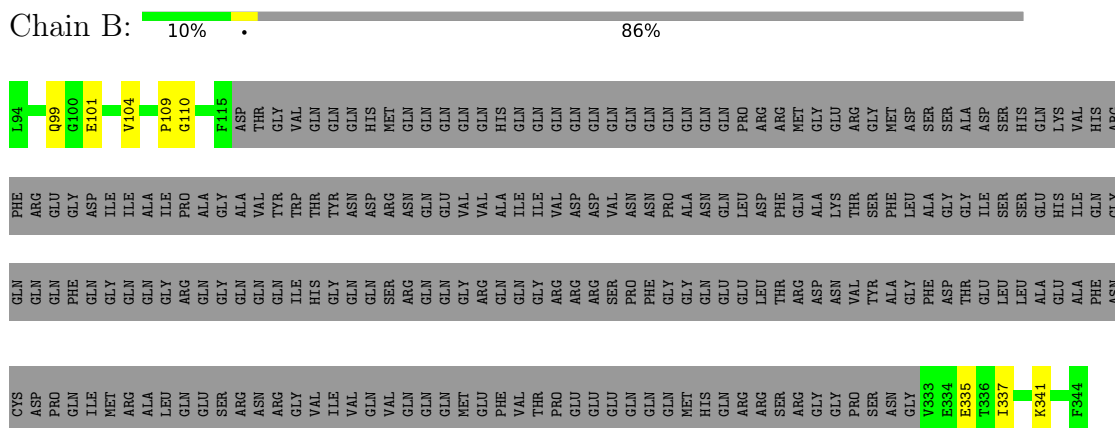
3 Residue-property plots [i](#)

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.

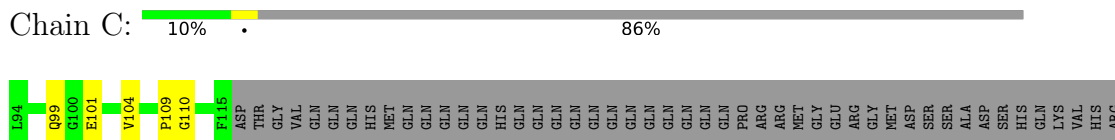
- Molecule 1: 11-S seed storage protein, plant



- Molecule 1: 11-S seed storage protein, plant



- Molecule 1: 11-S seed storage protein, plant



CYS	ASP	PRO	GLN	GLN	MET	ARG	ALA	LEU	GLU	GLU	SER	ARG	ASN	ARG	GLY	VAL	ILE	VAL	GLN	VAL	GLN	GLN	GLN	MET	GLU	GLU	PHE	THR	PRO	GLU	GLU	GLN	GLN	GLN	MET	HIS	GLN	ARG	ARG	SER	ARG	GLY	GLY	PRO	SER	ASN	GLY	V333	E334	E335	E336	I337	K341	F344
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- Molecule 1: 11-S seed storage protein, plant

Chain D: 12% 86%

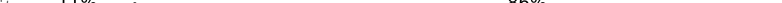
L94
Q99
G100
E101
V104
P109
G110
F115
ASP
THR
GLY
VAL
GLN
GLN
GLN
MET
MET
GLM
GLM
GLN
GLN
GLM
HIS
HIS
GLM
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GLM
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GLM
PRO
ARG
ARG
MET
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GLU
GLU
ARG
GLY
MET
ASP
SER
SER
ALA
ASP
SER
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GLM
LVS
VAL
HIS
ARG

PHE	ARG	GLU	GLY	ASP	ILE	ILE	ALA	ILE	PRO	ALA	GLY	ALA	VAL	TYR	TRP	THR	THR	ASN	ASP	ARG	ASN	GLN	GLU	VAL	VAL	ALA	ILE	ILE	VAL	ASP	ASP	VAL	ASN	ASN	PRO	ALA	ASN	GLN	LEU	ASP	PHE	GLN	ALA	ALA	LYS	THR	SER	PHE	SER	LEU	ALA	GLY	ILE	ILE	GLN	TYR
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[illegible]

CYS ASP PRO ARG MET ILE ALA LEU GLN CYS SER ARG ASN ARG GLY VAL ILE VAL GLN GLN GLN GLN GLN MET MET HIS GLN ARG ARG SER ARG GLY GLY PRO SER SER ASN GLY V333 F344

- Molecule 1: 11-S seed storage protein, plant

Chain E:  11% 86%

L94 Q99 G100 E101 V104 P109 G110 F115 ASP THR GLY VAL GLN GLN GLN HIS HTS MET MET GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN PRO ARG ARG MET MET ARG ASP SER SER LYS VAL VAL HTS

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

CYS	ASP	PRO	ARG	GLN	ILE	GLN	MET	ARG	ALA	ARG	LEU	GLN	GLU	GLU	SER	ARG	ASN	ARG	ARG	GLY	VAL	GLY	ILE	VAL	GLN	VAL	GLN	GLN	GLN	MET	MET	GLU	GLU	PHE	VAL	THR	PRO	GLU	GLU	GLN	GLN	GLN	MET	MET	GLN	GLN	GLY	GLY	GLY	PRO	GLY	ASN	GLY	V333	K341	F344
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4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-2.2017, -2.2017°, rise=4.757, 4.757 Å, axial sym=C1, C1	Depositor
Number of segments used	296338	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.039	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	335.52, 335.52, 335.52	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.932, 0.932, 0.932	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	0.18	0/257	0.38	0/345
1	B	0.18	0/257	0.38	0/345
1	C	0.18	0/257	0.38	0/345
1	D	0.18	0/257	0.38	0/345
1	E	0.18	0/257	0.38	0/345
All	All	0.18	0/1285	0.38	0/1725

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	255	0	255	7	0
1	B	255	0	255	12	0
1	C	255	0	255	12	0
1	D	255	0	255	10	0
1	E	255	0	255	6	0
All	All	1275	0	1275	27	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.

All (27) 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:C:99:GLN:O	1:D:99:GLN:HA	2.10	0.52
1:D:99:GLN:O	1:E:99:GLN:HA	2.10	0.52
1:D:110:GLY:O	1:E:110:GLY:HA2	2.10	0.52
1:B:99:GLN:O	1:C:99:GLN:HA	2.10	0.52
1:A:99:GLN:O	1:B:99:GLN:HA	2.10	0.52
1:C:110:GLY:O	1:D:110:GLY:HA2	2.10	0.52
1:B:110:GLY:O	1:C:110:GLY:HA2	2.10	0.51
1:A:110:GLY:O	1:B:110:GLY:HA2	2.10	0.51
1:D:109:PRO:HA	1:E:109:PRO:HD2	1.94	0.50
1:C:109:PRO:HA	1:D:109:PRO:HD2	1.93	0.50
1:B:109:PRO:HA	1:C:109:PRO:HD2	1.94	0.49
1:A:109:PRO:HA	1:B:109:PRO:HD2	1.94	0.49
1:A:104:VAL:O	1:B:104:VAL:HA	2.14	0.47
1:B:104:VAL:O	1:C:104:VAL:HA	2.14	0.47
1:C:104:VAL:O	1:D:104:VAL:HA	2.14	0.47
1:D:104:VAL:O	1:E:104:VAL:HA	2.14	0.47
1:C:341:LYS:HE3	1:C:341:LYS:HB3	1.84	0.45
1:A:341:LYS:HE3	1:A:341:LYS:HB3	1.84	0.42
1:D:101:GLU:HA	1:E:101:GLU:O	2.20	0.42
1:B:341:LYS:HE3	1:B:341:LYS:HB3	1.84	0.42
1:C:101:GLU:HA	1:D:101:GLU:O	2.20	0.42
1:A:101:GLU:HA	1:B:101:GLU:O	2.20	0.41
1:B:101:GLU:HA	1:C:101:GLU:O	2.20	0.41
1:B:335:GLU:OE1	1:B:337:ILE:HD11	2.21	0.40
1:E:341:LYS:HB3	1:E:341:LYS:HE3	1.84	0.40
1:A:335:GLU:OE1	1:A:337:ILE:HD11	2.21	0.40
1:C:335:GLU:OE1	1:C:337:ILE:HD11	2.21	0.40

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	30/251 (12%)	29 (97%)	1 (3%)	0	100	100
1	B	30/251 (12%)	29 (97%)	1 (3%)	0	100	100
1	C	30/251 (12%)	29 (97%)	1 (3%)	0	100	100
1	D	30/251 (12%)	29 (97%)	1 (3%)	0	100	100
1	E	30/251 (12%)	29 (97%)	1 (3%)	0	100	100
All	All	150/1255 (12%)	145 (97%)	5 (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	28/212 (13%)	28 (100%)	0	100	100
1	B	28/212 (13%)	28 (100%)	0	100	100
1	C	28/212 (13%)	28 (100%)	0	100	100
1	D	28/212 (13%)	28 (100%)	0	100	100
1	E	28/212 (13%)	28 (100%)	0	100	100
All	All	140/1060 (13%)	140 (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 ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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.

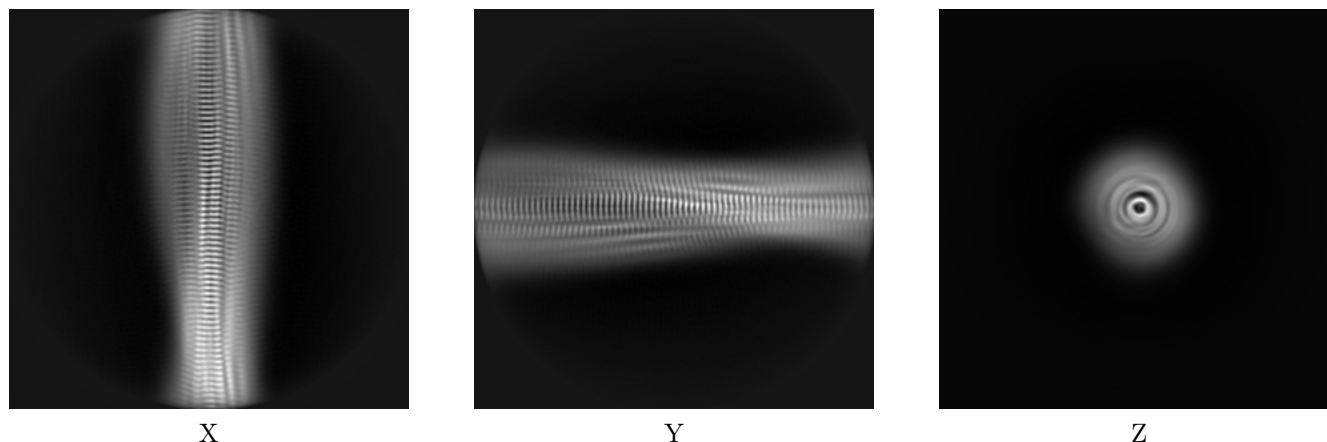
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-80851. These allow visual inspection of the internal detail of the map and identification of artifacts.

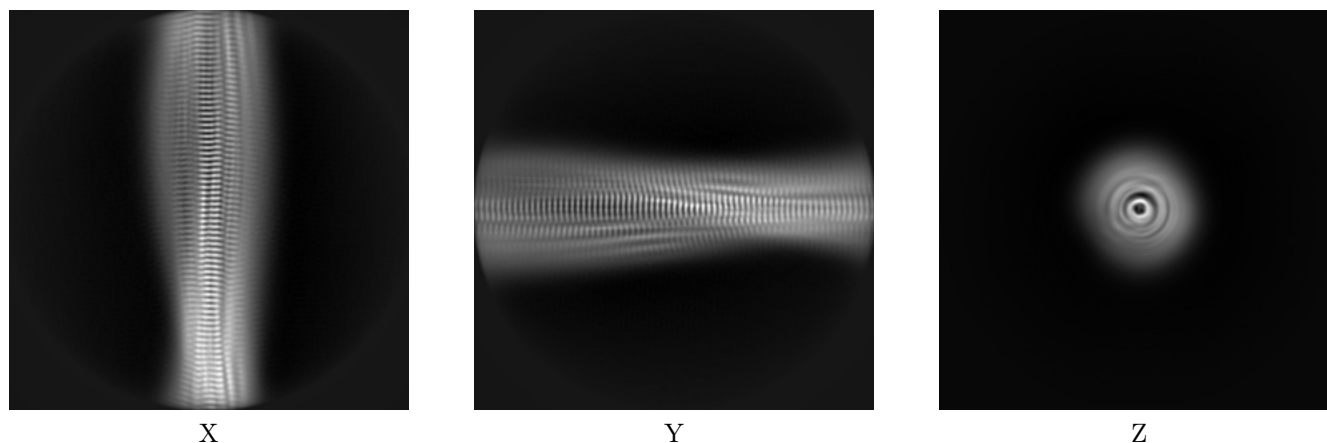
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



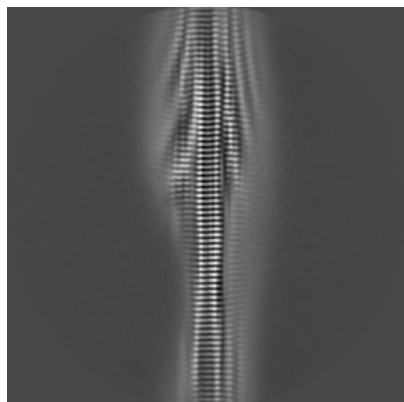
6.1.2 Raw map



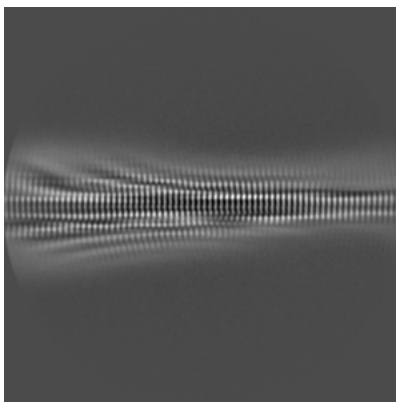
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

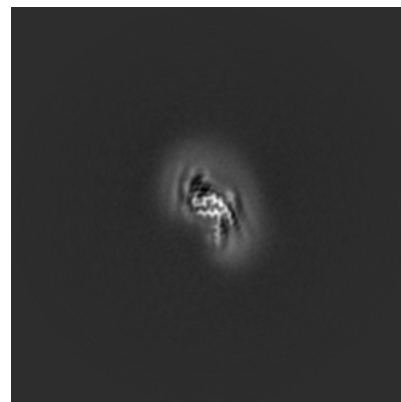
6.2.1 Primary map



X Index: 180

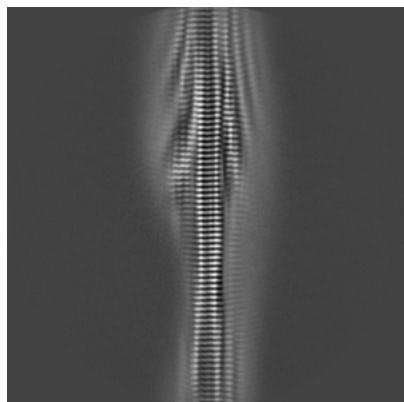


Y Index: 180

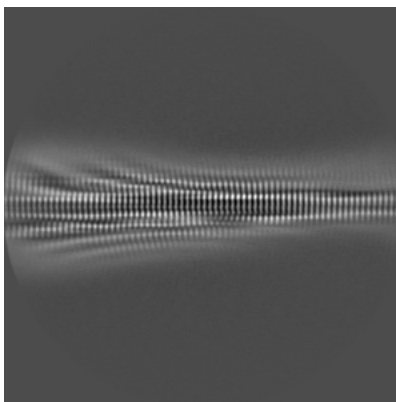


Z Index: 180

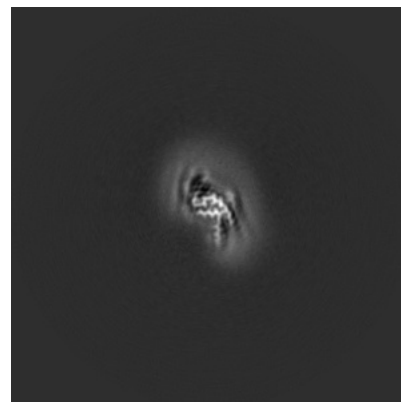
6.2.2 Raw map



X Index: 180



Y Index: 180

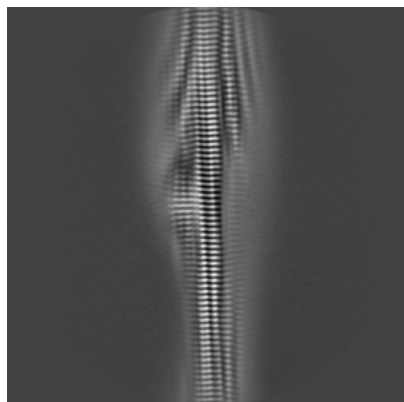


Z Index: 180

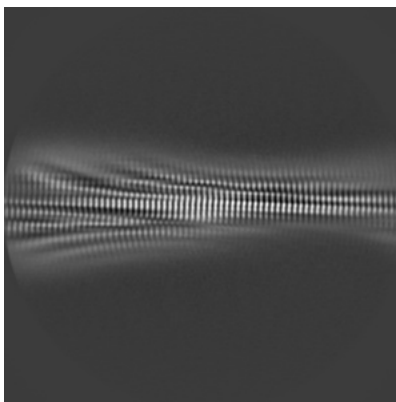
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

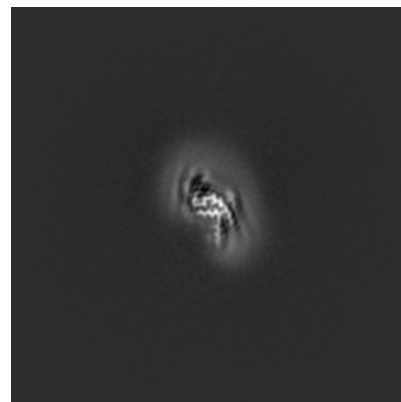
6.3.1 Primary map



X Index: 186

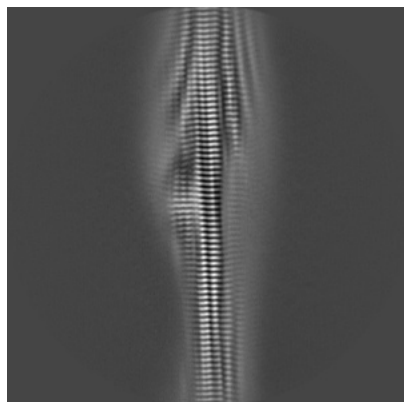


Y Index: 174

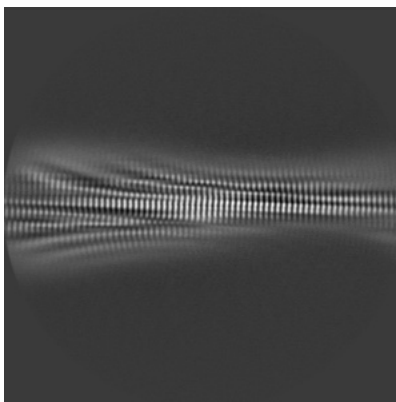


Z Index: 180

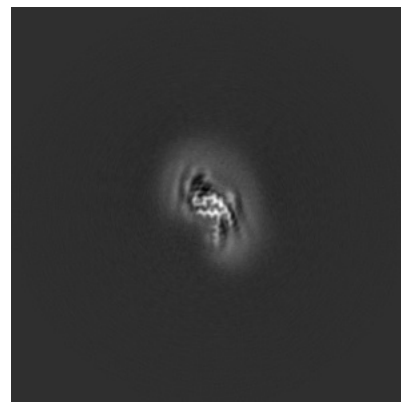
6.3.2 Raw map



X Index: 186



Y Index: 174

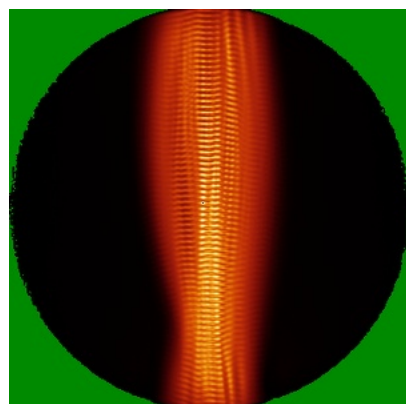


Z Index: 185

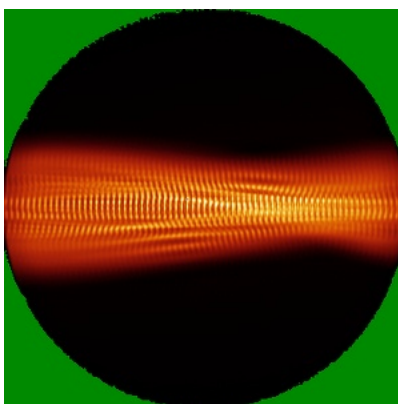
The images above show the largest variance slices of the map in three orthogonal directions.

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

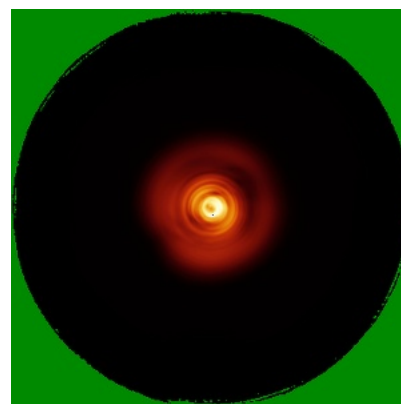
6.4.1 Primary map



X

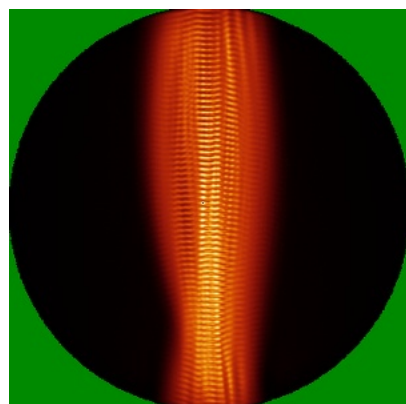


Y

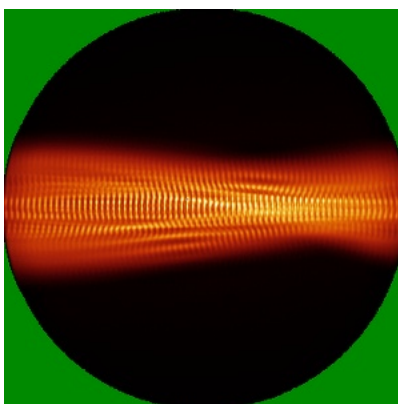


Z

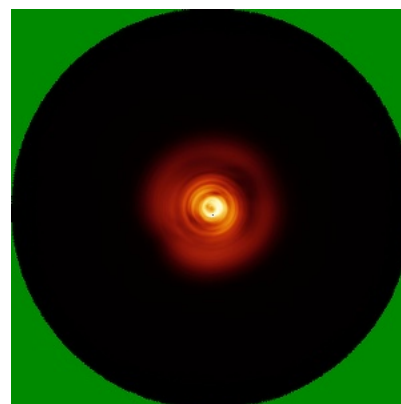
6.4.2 Raw map



X



Y

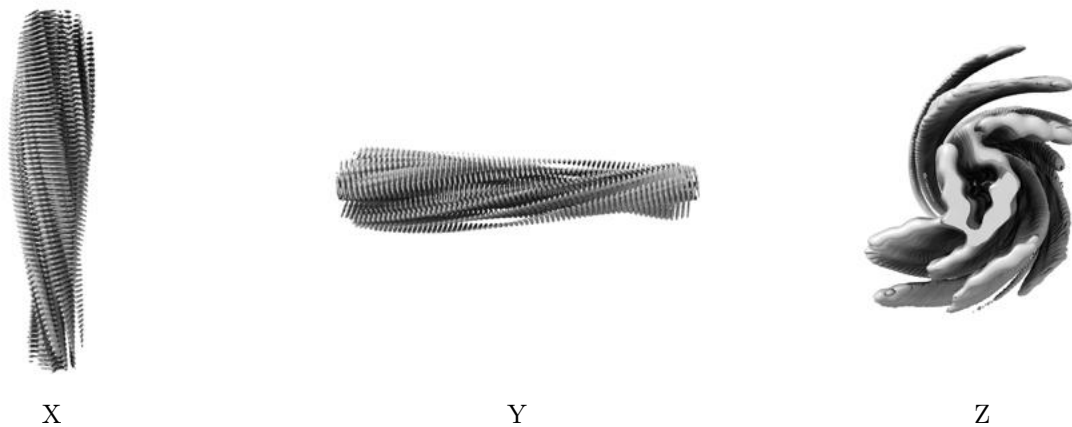


Z

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.

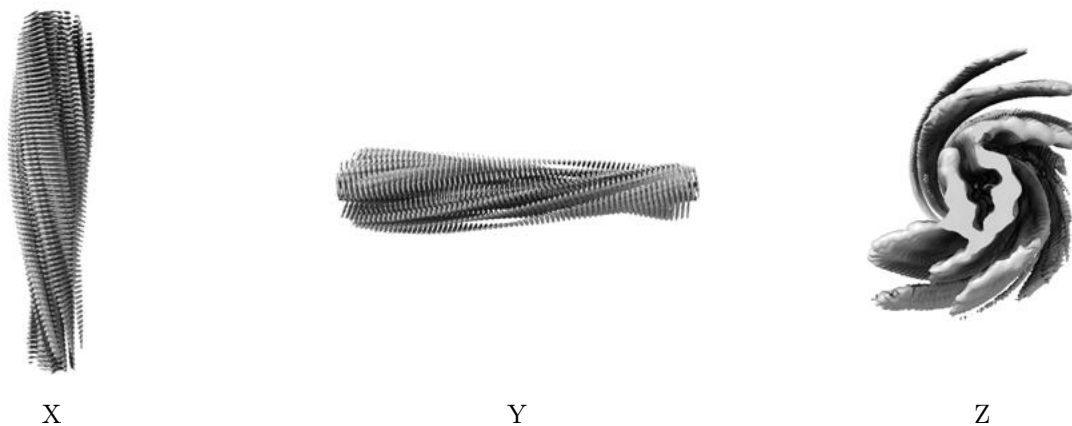
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

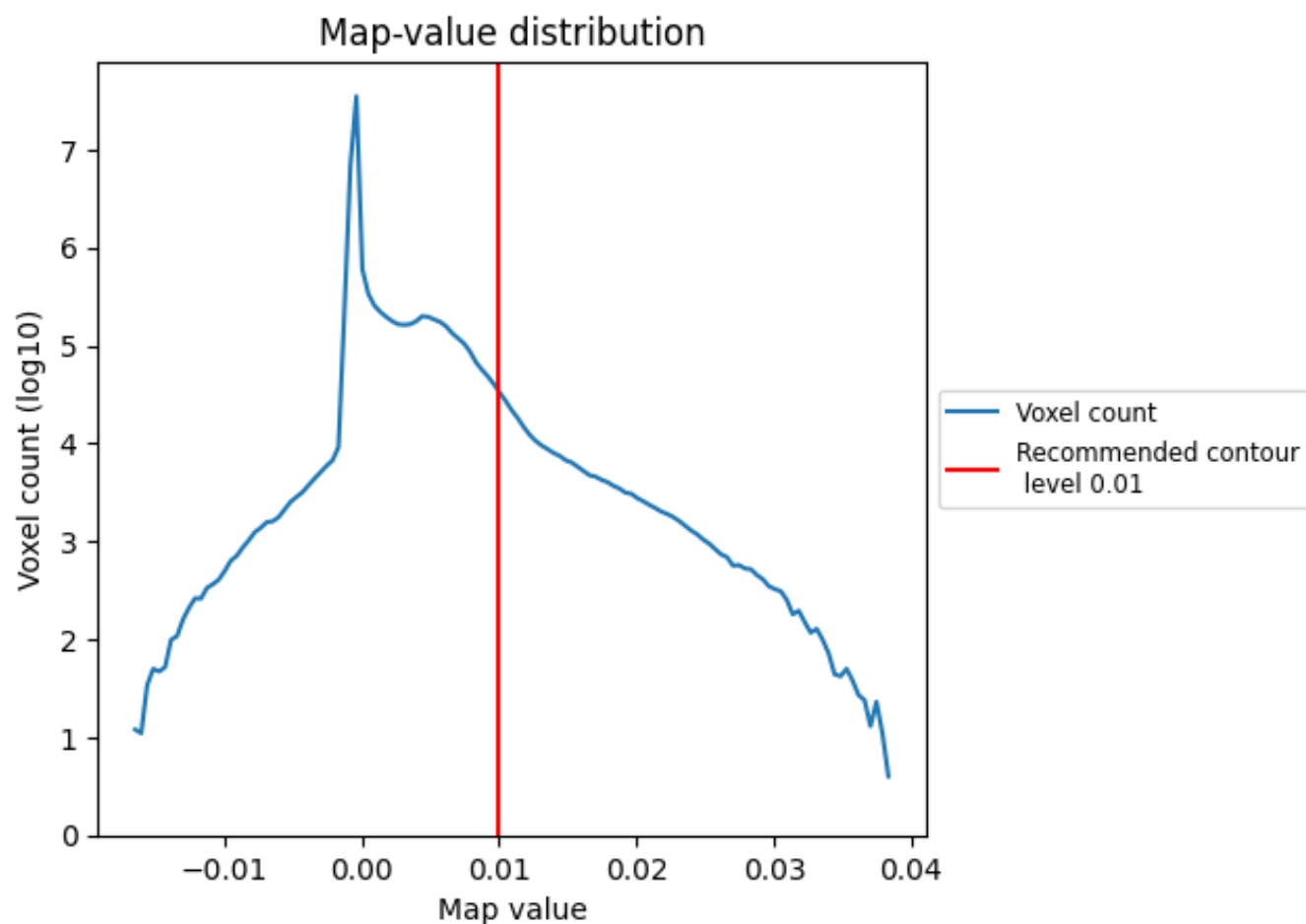
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

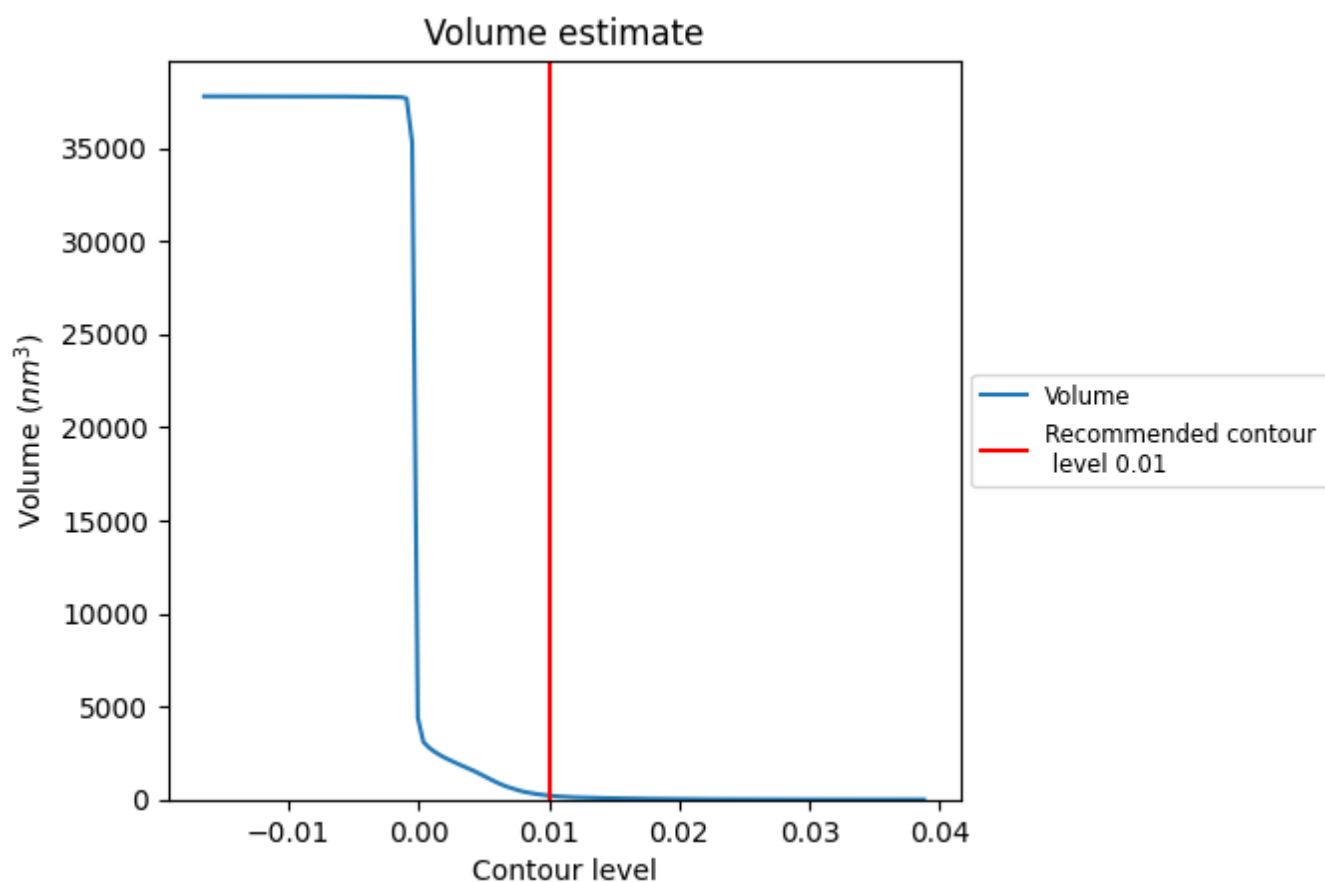
This section contains the results of statistical analysis of the map.

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.

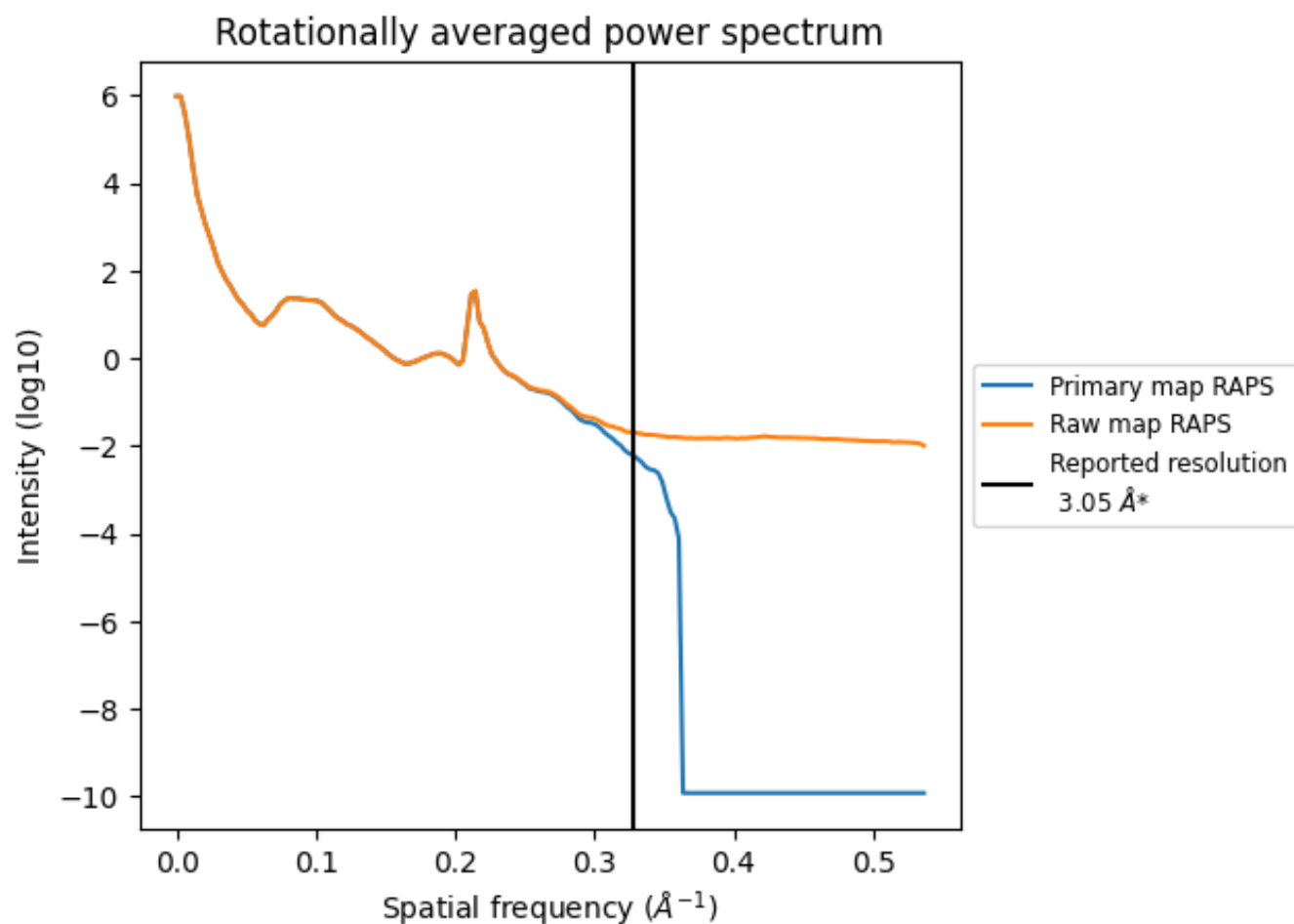
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 213 nm³; this corresponds to an approximate mass of 193 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 ⓘ

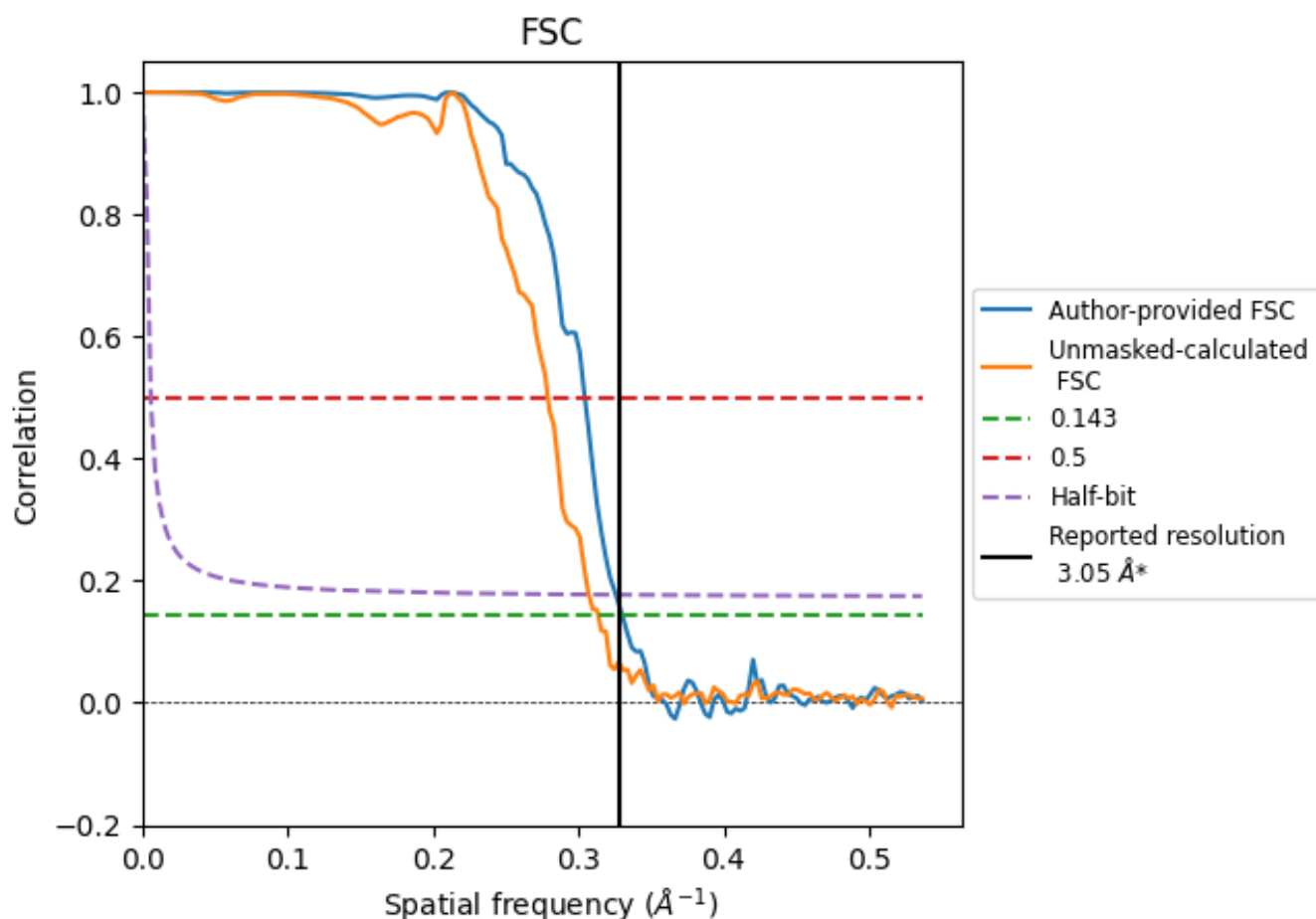


*Reported resolution corresponds to spatial frequency of 0.328 Å⁻¹

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 0.328 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.05	-	-
Author-provided FSC curve	3.03	3.28	3.07
Unmasked-calculated*	3.19	3.58	3.26

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-80851 and PDB model 26SG. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



X



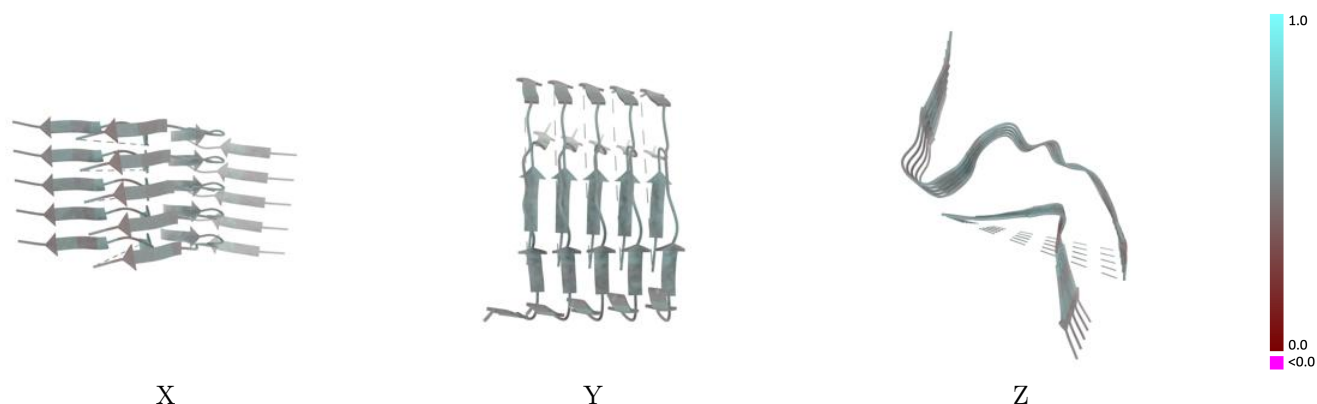
Y



Z

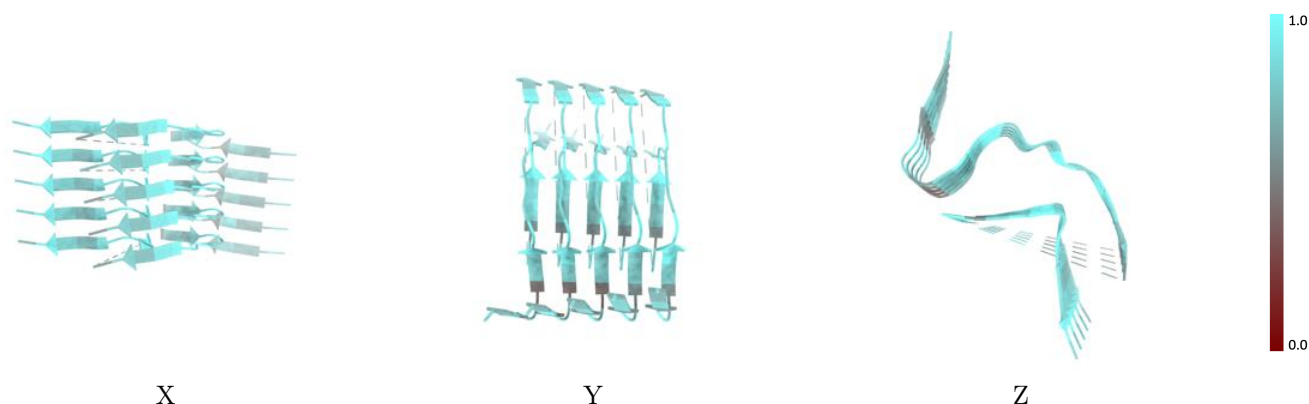
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



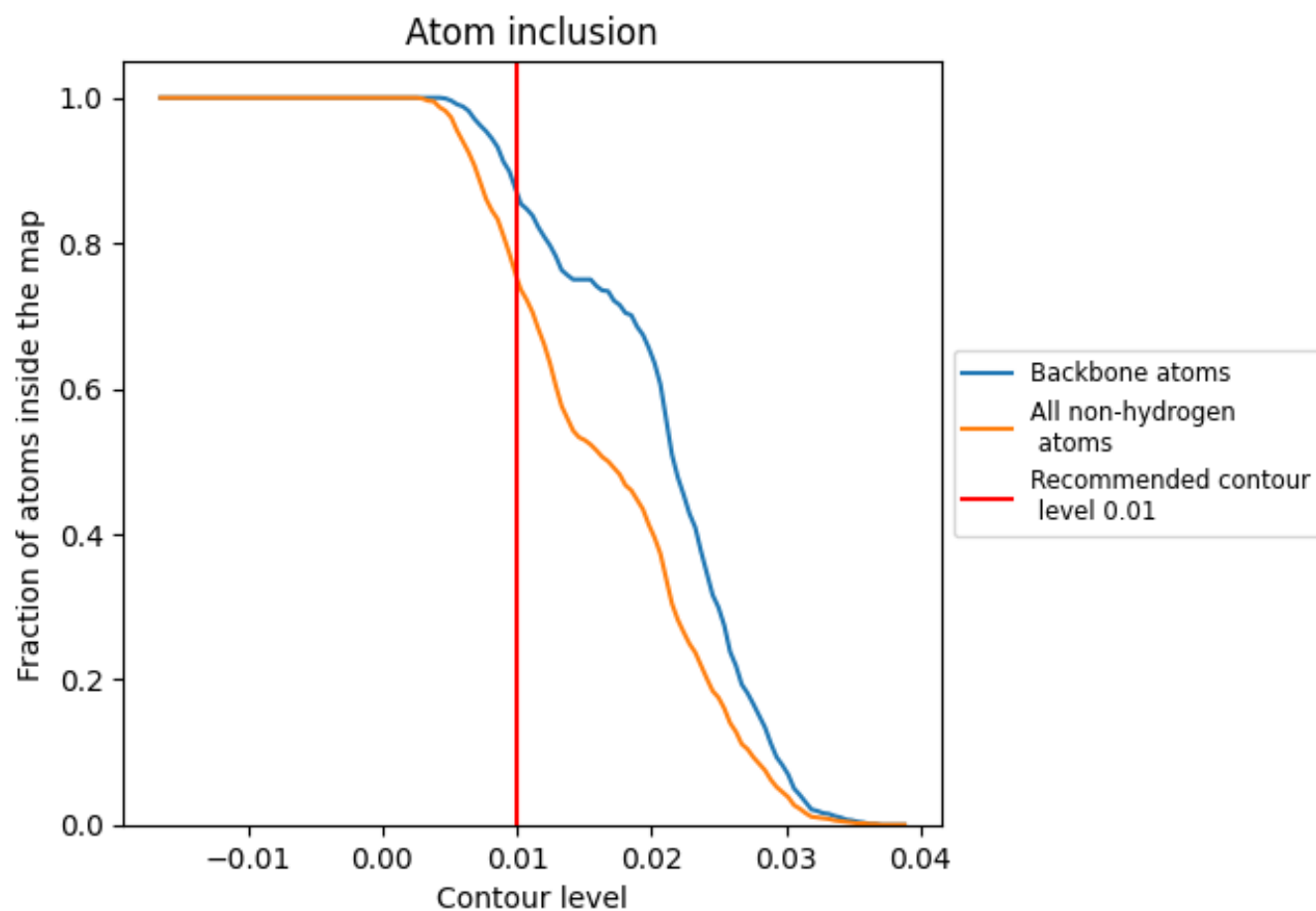
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 75% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7510	0.5060
A	0.7450	0.5030
B	0.7490	0.5030
C	0.7490	0.5070
D	0.7570	0.5090
E	0.7570	0.5080

