



wwPDB EM Validation Summary Report ⓘ

Apr 5, 2026 – 11:10 PM UTC

PDB ID : 9PW3 / pdb_00009pw3
EMDB ID : EMD-71898
Title : Cryo-EM structure of renal amyloid fibril from a variant apolipoprotein A-I R173P amyloidosis patient
Authors : Nguyen, B.A.; Saelices, L.
Deposited on : 2025-08-04
Resolution : 2.73 Å(reported)
Based on initial model : 9PVY

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

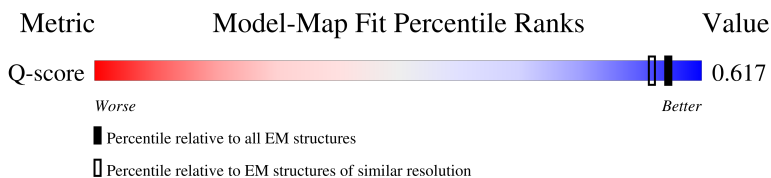
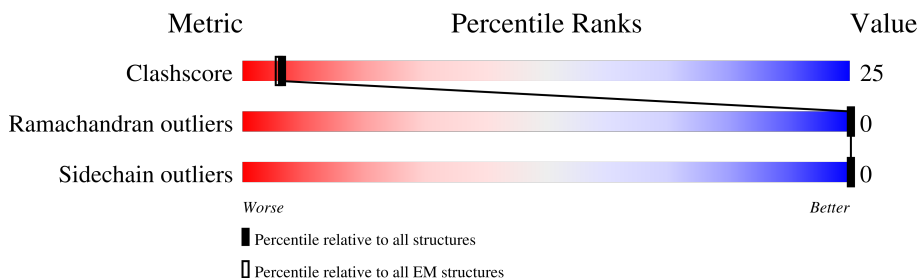
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY





The reported resolution of this entry is 2.73 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	10432 (2.23 - 3.23)

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	243	
1	B	243	
1	C	243	
1	D	243	

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Mol	Chain	Length	Quality of chain
1	E	243	 16% 7% 76%
1	F	243	 16% 7% 76%
1	G	243	 16% 7% 76%
1	H	243	 16% 7% 76%
1	I	243	 19% 5% 76%
1	J	243	 17% 7% 76%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4650 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.

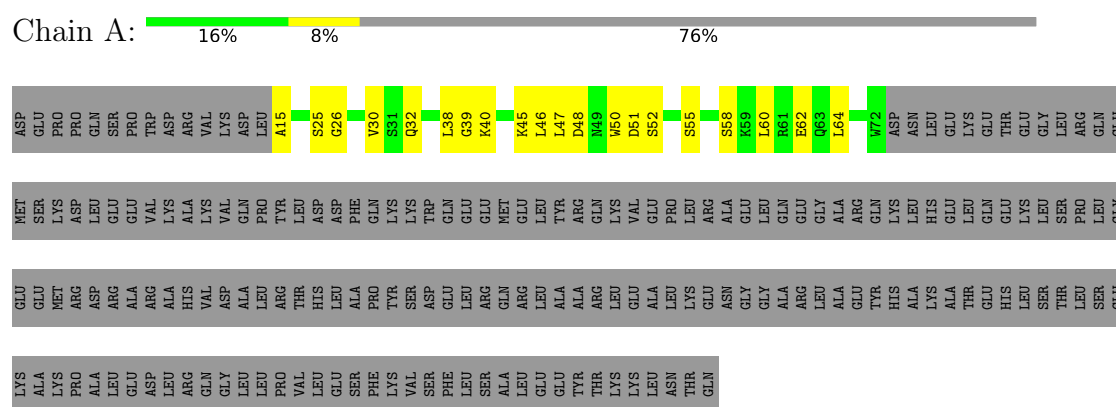
- Molecule 1 is a protein called Apolipoprotein A-I.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	58	Total	C	N	O	0	0
			465	297	76	92		
1	B	58	Total	C	N	O	0	0
			465	297	76	92		
1	C	58	Total	C	N	O	0	0
			465	297	76	92		
1	D	58	Total	C	N	O	0	0
			465	297	76	92		
1	E	58	Total	C	N	O	0	0
			465	297	76	92		
1	F	58	Total	C	N	O	0	0
			465	297	76	92		
1	G	58	Total	C	N	O	0	0
			465	297	76	92		
1	H	58	Total	C	N	O	0	0
			465	297	76	92		
1	I	58	Total	C	N	O	0	0
			465	297	76	92		
1	J	58	Total	C	N	O	0	0
			465	297	76	92		

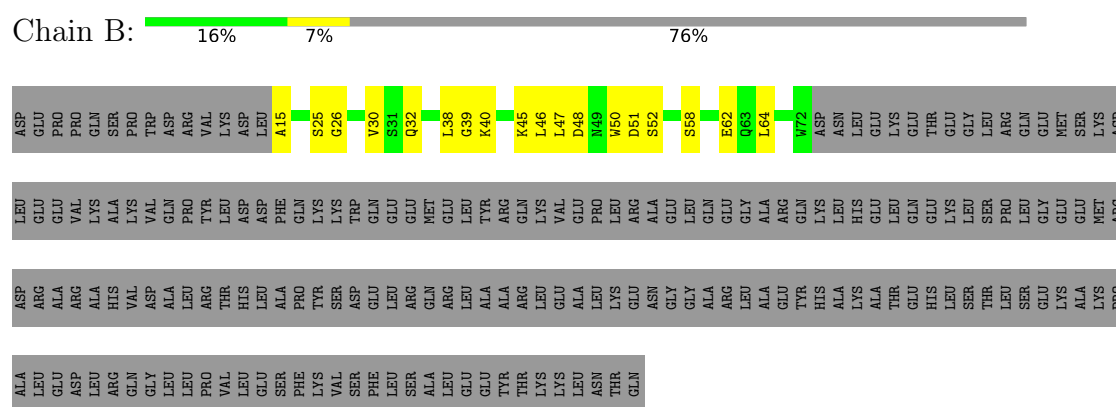
3 Residue-property plots [i](#)

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.

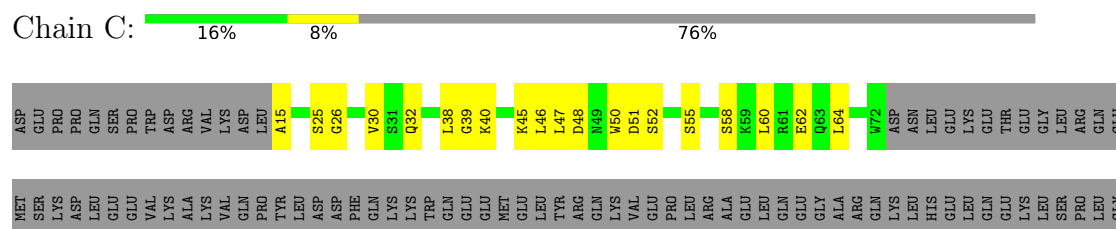
• Molecule 1: Apolipoprotein A-I



• Molecule 1: Apolipoprotein A-I



• Molecule 1: Apolipoprotein A-I



- Molecule 1: Apolipoprotein A-I

Chain D:  18% 6% 76%

[illegible]

- Molecule 1: Apolipoprotein A-I

Chain E: 16% 7% 76%

[illegible]

- Molecule 1: Apolipoprotein A-I

Chain F:  16% 7% 76%

[illegible]

- Molecule 1: Apolipoprotein A-I

ASP	GLU	PRO	GLU	ASP	GLN	SER	PRO	TRP	ASP	VAL	LYS	ASP	LEU	A15	K23	D24	S25	L38	G39	K40	K45	L46	L47	D48	N49	W50	D51	S52	E62	Q63	L64	G65	P66	W72	ASN	ASN	GLU	LYS	GLU	THR	GLU	GLY	ARG	GLN	GLU	GLU	ASP	GLU	GLU			
ARG	ALA	HIS	VAL	ASP	ALA	LEU	THR	THR	HIS	LEU	ALA	PRO	TYR	LYS	GLN	GLU	MET	GLU	LEU	TYR	ARG	GLN	VAL	GLU	PRO	LEU	ARG	GLY	GLU	ALA	GLN	GLY	ALA	ARG	GLN	LYS	LEU	HIS	GLU	LEU	GLN	GLU	GLY	PRO	LEU	GLY	GLU	ARG	ALA	LEU	GLU	GLU
ASP	LEU	ARG	GLN	GLY	LEU	LEU	PRO	PRO	VAL	GLU	SER	GLU	GLU	GLU	PHE	SER	THR	LEU	GLU	TYR	THR	LYS	LYS	ASN	THR	THR	GLN	GLY	GLY	ALA	ALA	TYR	HIS	GLY	ALA	ALA	LYS	THR	THR	THR	GLY	GLY	LYS	ALA	LYS	ASN	PRO	ARG	ASP	LEU	GLU	GLU

[illegible]

GLN	GLN	VAL	LYS	ASP
LEU	ASP	VAL	GLN	GLU
LEU	ALA	GLN	GLN	PRO
PRO	LEU	PRO	TYR	GLN
VAL	THR	ARG	LEU	SER
LEU	HIS	HIS	ASP	PRO
GLU	LEU	ALA	ASP	TRP
SER	SER	ALA	PHE	ASP
LYS	LYS	PRO	GLN	ARG
VAL	TYR	TYR	LYS	VAL
SER	SER	ASP	TRP	LYS
PHE	PHE	GLU	GLN	ASP
LEU	LEU	LEU	GLU	LEU
SER	ARG	GLU	GLU	A15
ALA	GLN	GLN	MET	K23
LEU	ARG	ARG	GLU	D24
GLU	LEU	LEU	LEU	
GLU	ALA	TYR	TYR	G39
THR	ALA	ALA	ARG	
LYS	LEU	ARG	GLN	K45
LYS	GLU	LEU	LYS	L46
LEU	ALA	GLU	VAL	L47
ASN	LEU	PRO	GLU	D48
THR	THR	LYS	LEU	M49
GLN	GLN	ASN	ARG	M50
	ASN	ALA	ALA	D51
	GLY	GLY	GLU	S52
	GLY	GLY	LEU	E62
	ALA	GLN	GLN	Q63
	ARG	GLU	GLY	L64
	ALA	ALA	ARG	G65
	GLU	ARG	ALA	P66
	TYR	GLN	GLN	G72
	HIS	LYS	LYS	ASP
	ALA	ALA	LEU	ASN
	LYS	HIS	HIS	LEU
	ALA	ALA	GLU	GLU
	THR	THR	LEU	LYS
	GLU	GLU	GLN	GLU
	HIS	HIS	GLU	THR
	LEU	LEU	LYS	GLY
	SER	SER	LEU	GLY
	THR	THR	SER	LEU
	LEU	LEU	PRO	ARG
	SER	SER	LEU	GLN
	LYS	LYS	GLY	LEU
	GLY	GLY	GLU	MET
	ALA	ALA	ALA	SER
	PRO	PRO	MET	LYS
	ALA	ARG	ARG	ASP
	LEU	ASP	ASP	LEU
	GLU	ARG	GLU	GLU
	ASP	GLU	ARG	VAL
	ARG	ALA	ALA	LYS
	LEU	THR	HIS	ALA

ASP	GLU	PRO	PRO	GLN	SER	PRO	TRP	ASP	ARG	VAL	LYS	ASP	LEU	A15		K23	D24	S25		L38	G39	K40		K45	L46	L47	D48	A49	H50	D51	S52		E62	G63	L64	P66		H72	ASP	ASN	LEU	GLU	LYS	GLU	THR	GLU	GLY	LEU	ARG	GLN	GLY	MET	SER	LYS	ASP	LEU	GLU	ARG	VAL
VAL	LYS	ALA	LYS	VAL	GLN	PRO	TYR	LEU	ASP	ASP	PHE	GLN	LYS	LYS	TRP	GLN	GLU	GLU	MET	LEU	GLU	TYR	ARG	GLN	LYS	VAL	GLU	PRO	LEU	ARG	ALA	GLU	LEU	GLN	GLY	ALA	ARG	GLN	LYS	LEU	HIS	LEU	LEU	LYS	GLU	GLY	PRO	ASP	ARG	VAL	ARG	ALA							

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

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-0.67°, rise=4.85 Å, axial sym=C1	Depositor
Number of segments used	133438	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; RELION 4 built in CTFFIND	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.189	Depositor
Minimum map value	-0.112	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	279.9, 279.9, 279.9	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93299997, 0.93299997, 0.93299997	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	0.16	0/474	0.35	0/642
1	B	0.17	0/474	0.35	0/642
1	C	0.17	0/474	0.35	0/642
1	D	0.17	0/474	0.35	0/642
1	E	0.17	0/474	0.35	0/642
1	F	0.14	0/474	0.37	0/642
1	G	0.14	0/474	0.37	0/642
1	H	0.14	0/474	0.37	0/642
1	I	0.14	0/474	0.37	0/642
1	J	0.14	0/474	0.37	0/642
All	All	0.15	0/4740	0.36	0/6420

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	465	0	453	52	0
1	B	465	0	453	45	0
1	C	465	0	453	53	0
1	D	465	0	453	35	0
1	E	465	0	453	31	0
1	F	465	0	453	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	465	0	453	44	0
1	H	465	0	453	44	0
1	I	465	0	453	24	0
1	J	465	0	453	34	0
All	All	4650	0	4530	231	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 25.

The worst 5 of 231 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:B:38:LEU:CD2	1:G:64:LEU:HD23	1.71	1.19
1:A:38:LEU:CD2	1:F:64:LEU:HD23	1.72	1.18
1:C:38:LEU:CD2	1:H:64:LEU:HD23	1.74	1.16
1:E:38:LEU:CD2	1:J:64:LEU:HD23	1.75	1.15
1:D:38:LEU:CD2	1:I:64:LEU:HD23	1.76	1.15

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	56/243 (23%)	54 (96%)	2 (4%)	0	100	100
1	B	56/243 (23%)	54 (96%)	2 (4%)	0	100	100
1	C	56/243 (23%)	54 (96%)	2 (4%)	0	100	100
1	D	56/243 (23%)	54 (96%)	2 (4%)	0	100	100
1	E	56/243 (23%)	54 (96%)	2 (4%)	0	100	100
1	F	56/243 (23%)	55 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	56/243 (23%)	55 (98%)	1 (2%)	0	100	100
1	H	56/243 (23%)	55 (98%)	1 (2%)	0	100	100
1	I	56/243 (23%)	55 (98%)	1 (2%)	0	100	100
1	J	56/243 (23%)	55 (98%)	1 (2%)	0	100	100
All	All	560/2430 (23%)	545 (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	52/214 (24%)	52 (100%)	0	100	100
1	B	52/214 (24%)	52 (100%)	0	100	100
1	C	52/214 (24%)	52 (100%)	0	100	100
1	D	52/214 (24%)	52 (100%)	0	100	100
1	E	52/214 (24%)	52 (100%)	0	100	100
1	F	52/214 (24%)	52 (100%)	0	100	100
1	G	52/214 (24%)	52 (100%)	0	100	100
1	H	52/214 (24%)	52 (100%)	0	100	100
1	I	52/214 (24%)	52 (100%)	0	100	100
1	J	52/214 (24%)	52 (100%)	0	100	100
All	All	520/2140 (24%)	520 (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 (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	GLN

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Mol	Chain	Res	Type
1	B	41	GLN
1	C	41	GLN
1	D	41	GLN
1	E	41	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.

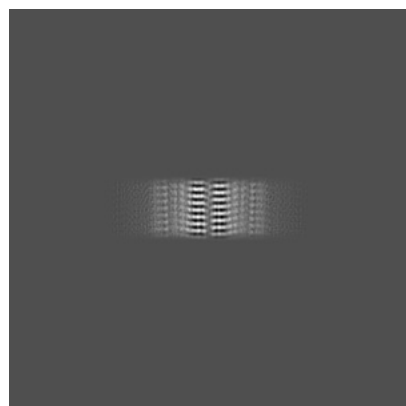
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71898. These allow visual inspection of the internal detail of the map and identification of artifacts.

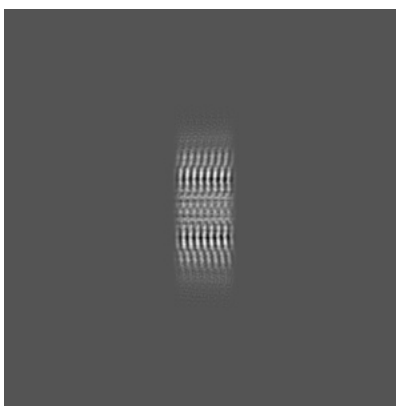
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

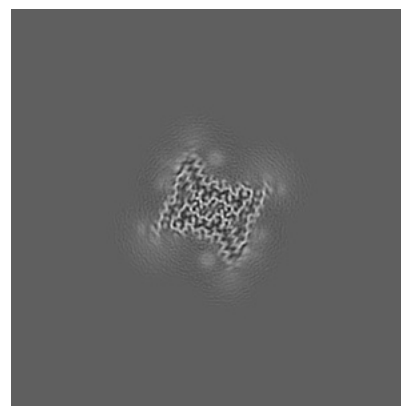
6.1.1 Primary map



X

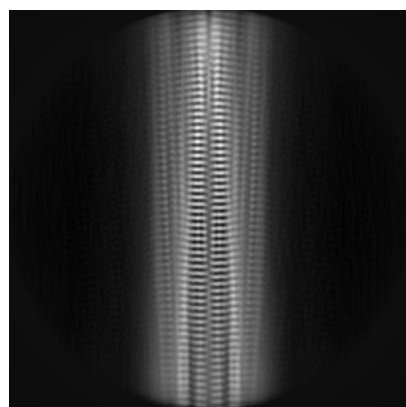


Y

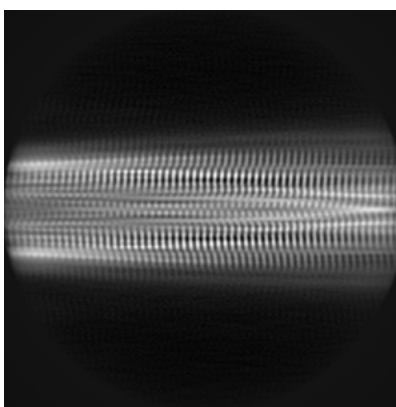


Z

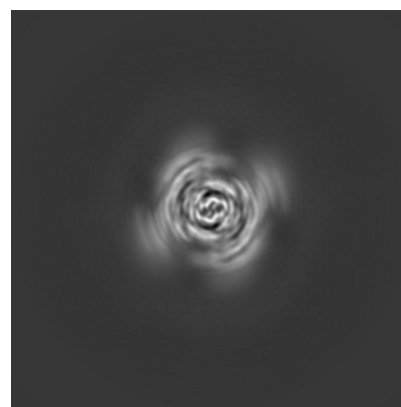
6.1.2 Raw map



X



Y

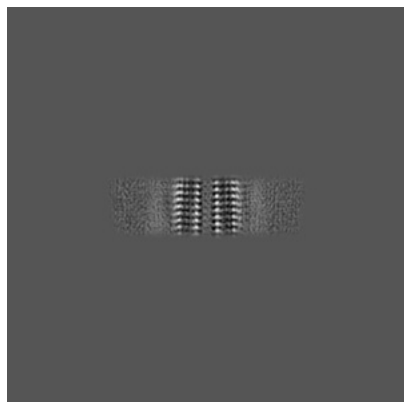


Z

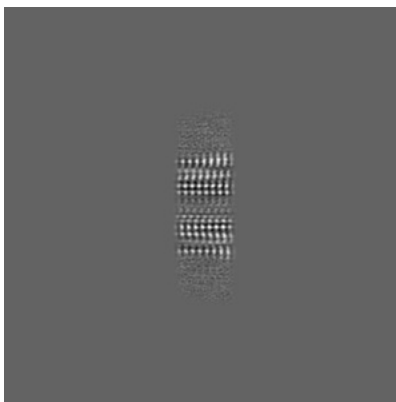
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

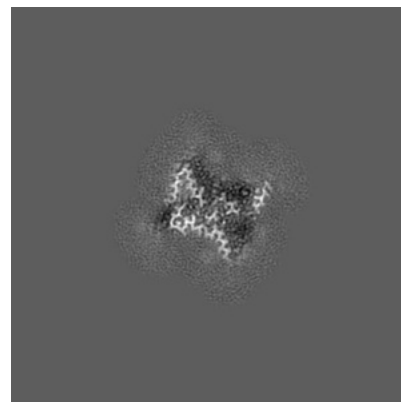
6.2.1 Primary map



X Index: 150

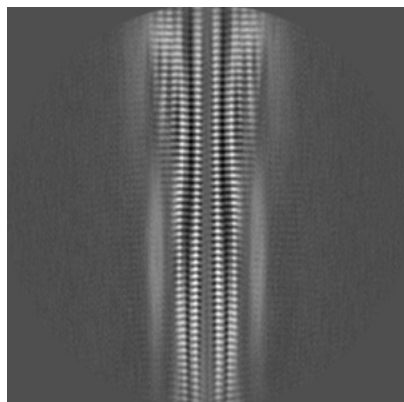


Y Index: 150

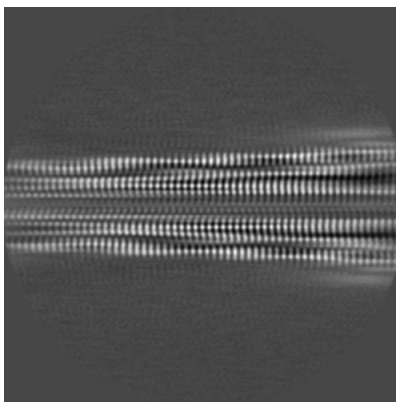


Z Index: 150

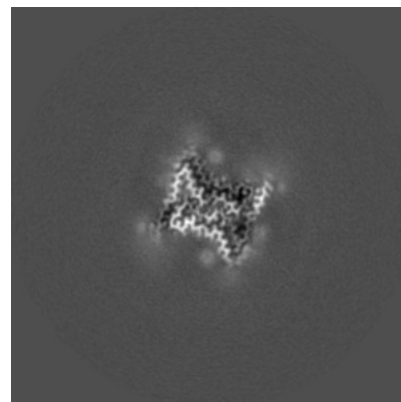
6.2.2 Raw map



X Index: 150



Y Index: 150

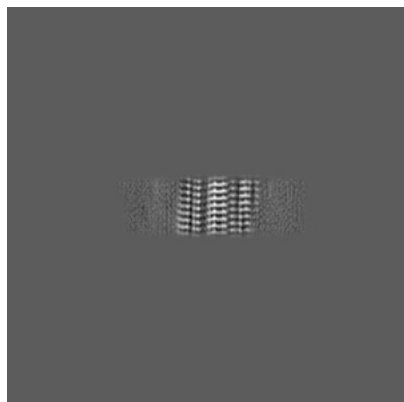


Z Index: 150

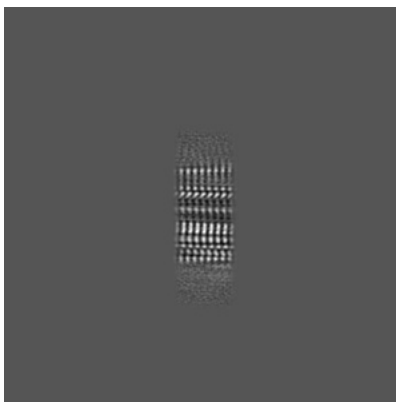
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

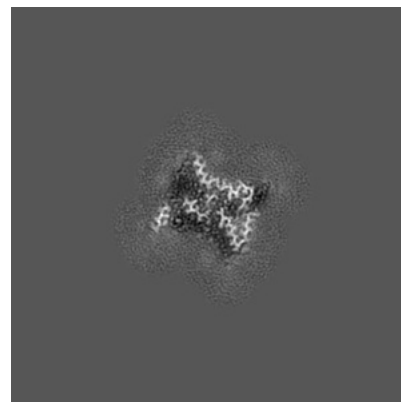
6.3.1 Primary map



X Index: 142

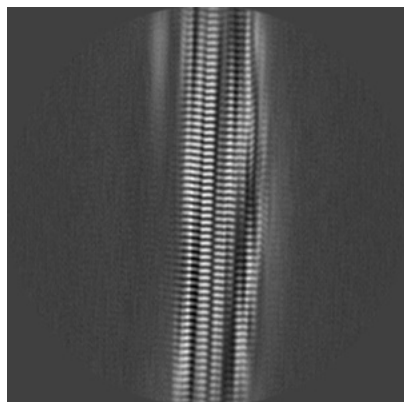


Y Index: 138

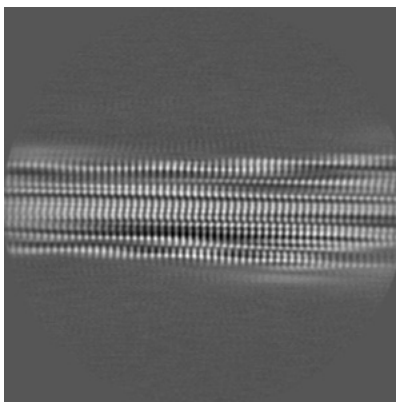


Z Index: 158

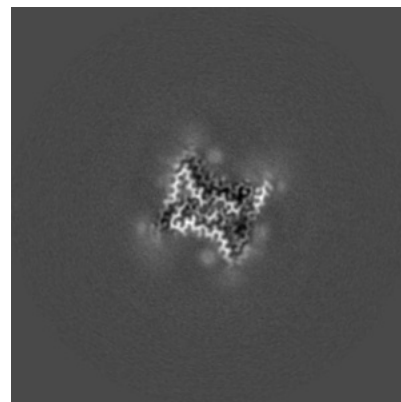
6.3.2 Raw map



X Index: 135



Y Index: 142

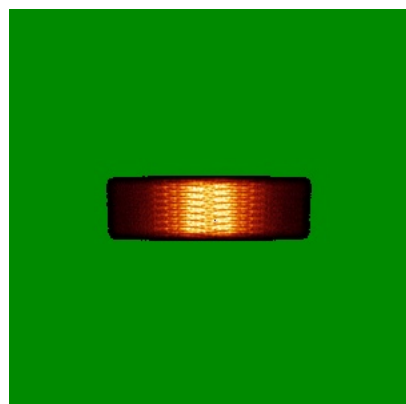


Z Index: 145

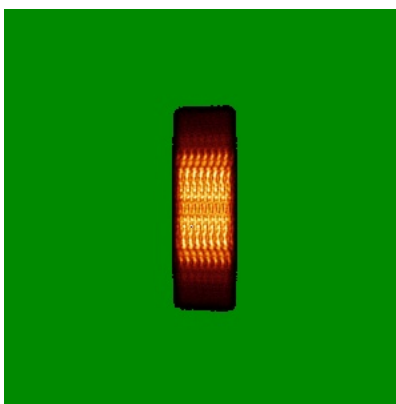
The images above show the largest variance slices of the map in three orthogonal directions.

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

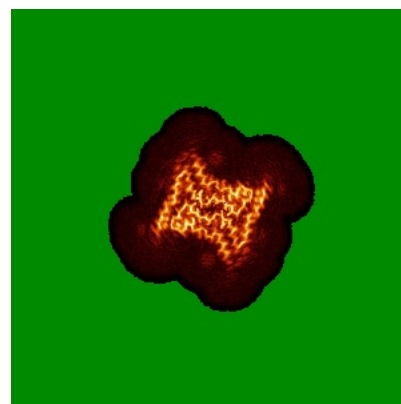
6.4.1 Primary map



X

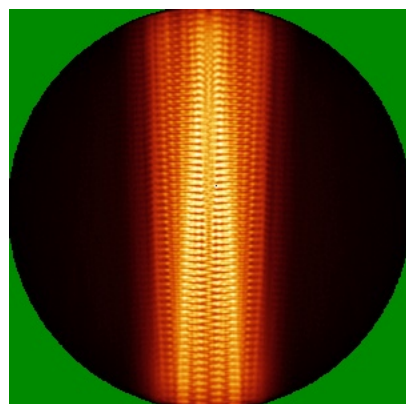


Y

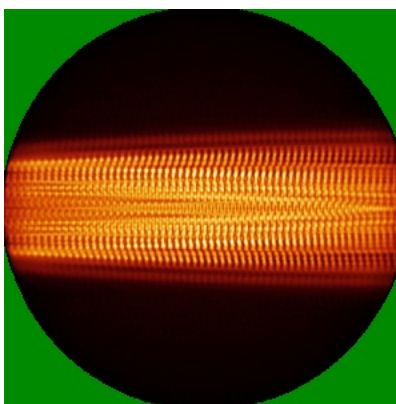


Z

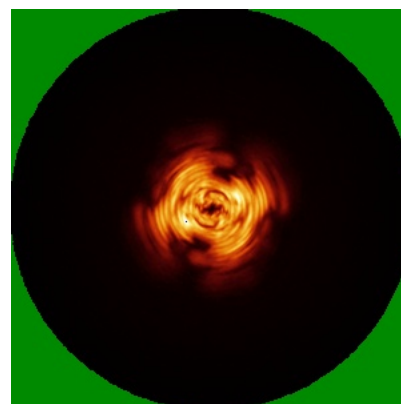
6.4.2 Raw map



X



Y

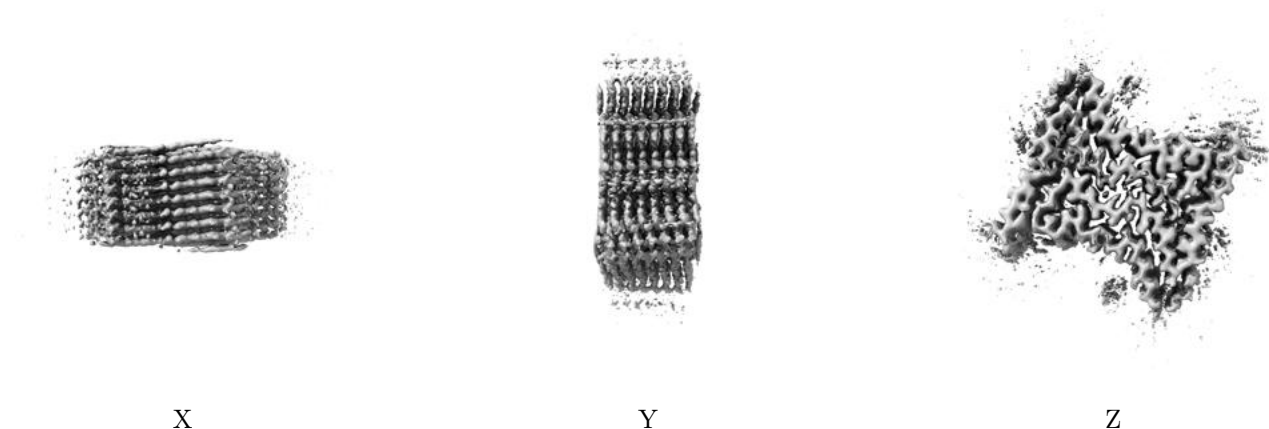


Z

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.

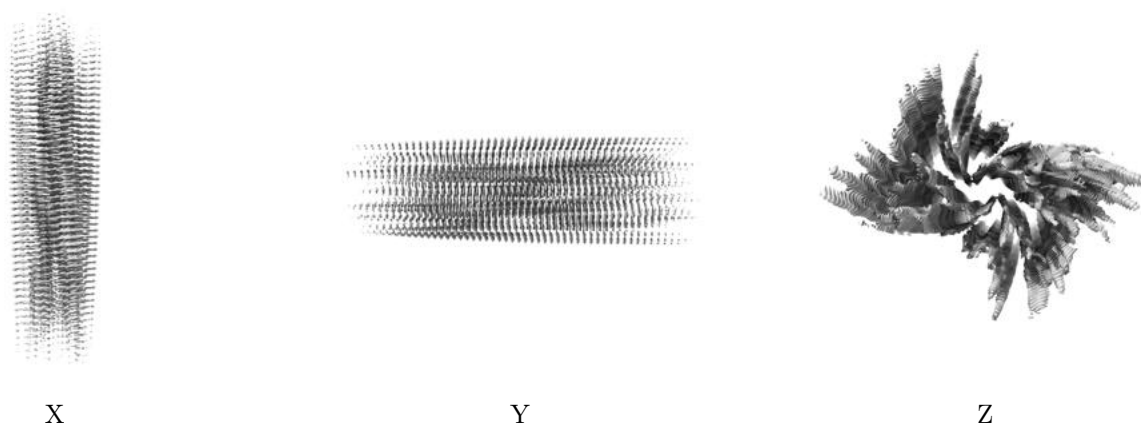
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. 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.

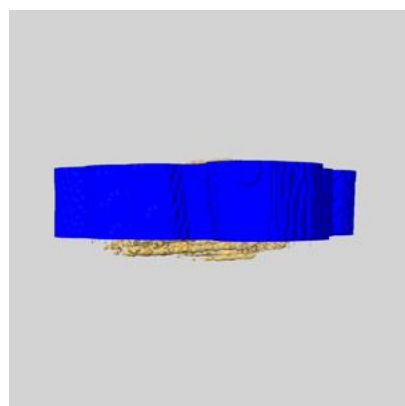
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

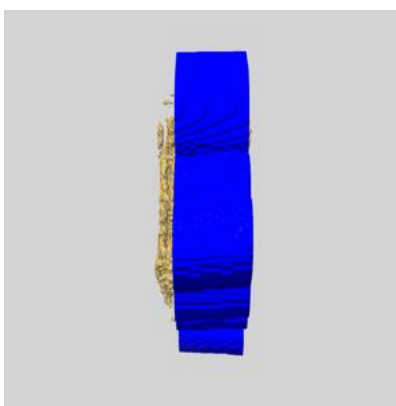
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

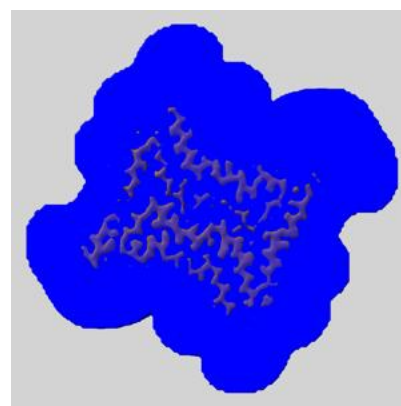
6.6.1 emd_71898_msk_1.map [i](#)



X



Y

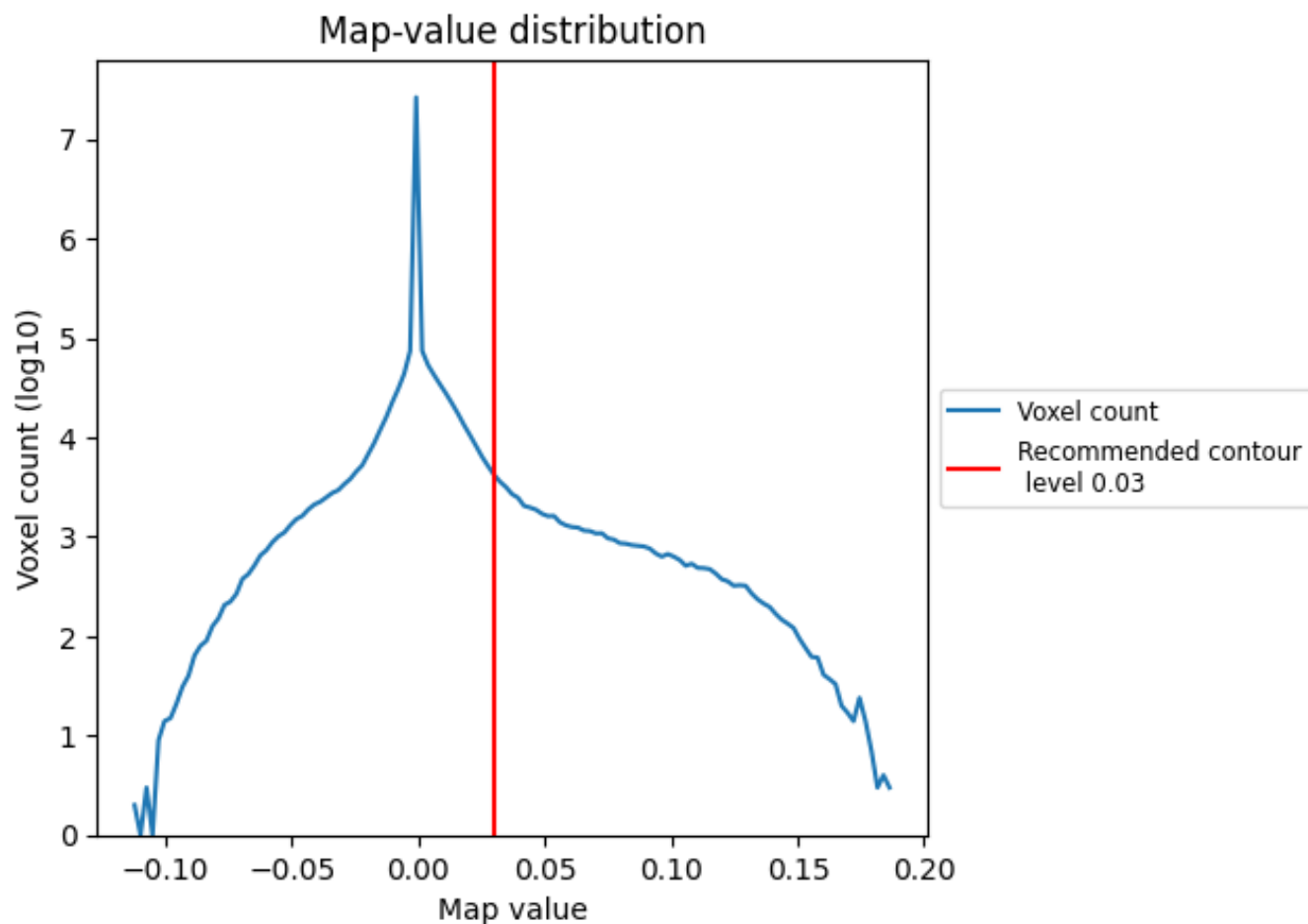


Z

7 Map analysis [i](#)

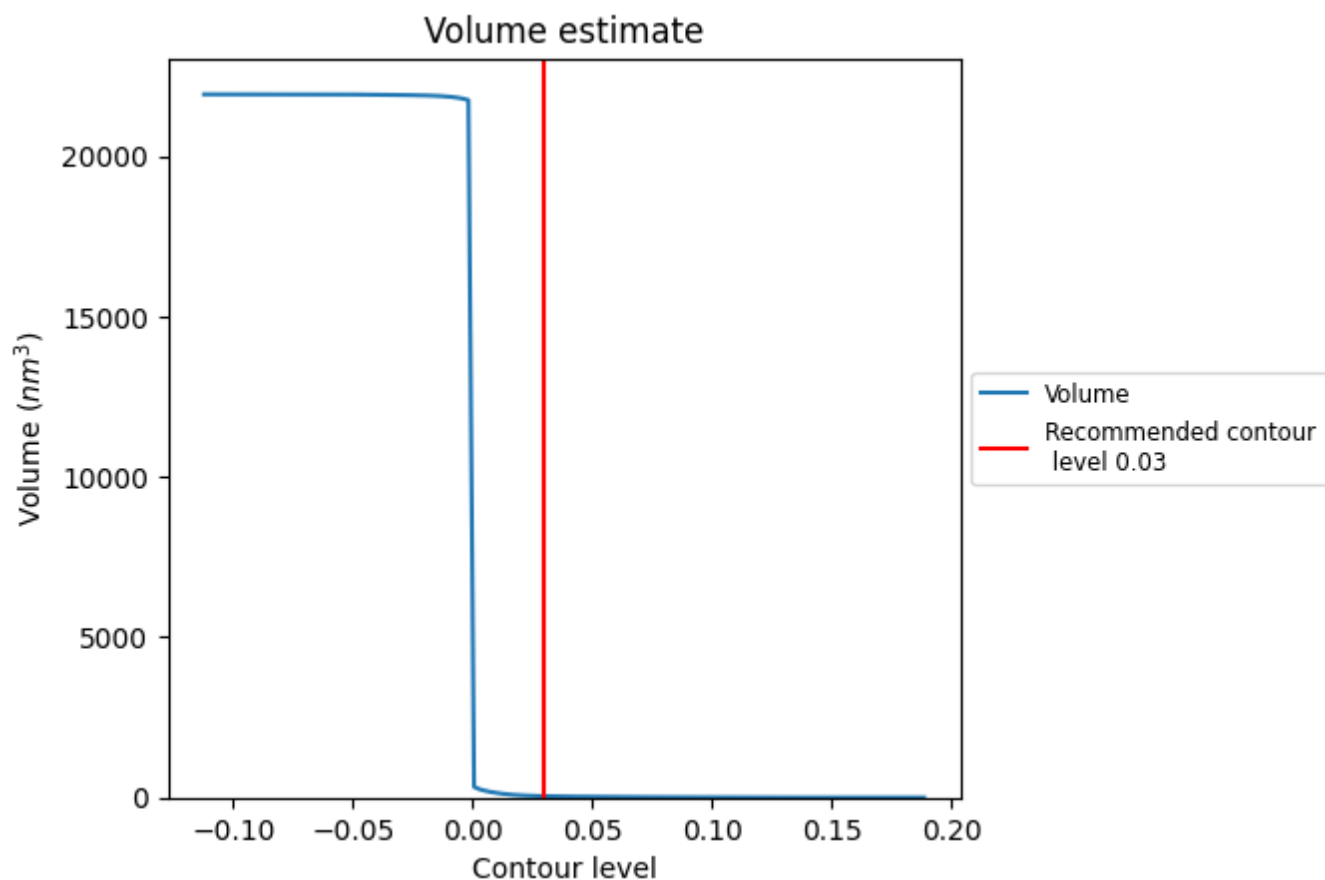
This section contains the results of statistical analysis of the map.

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.

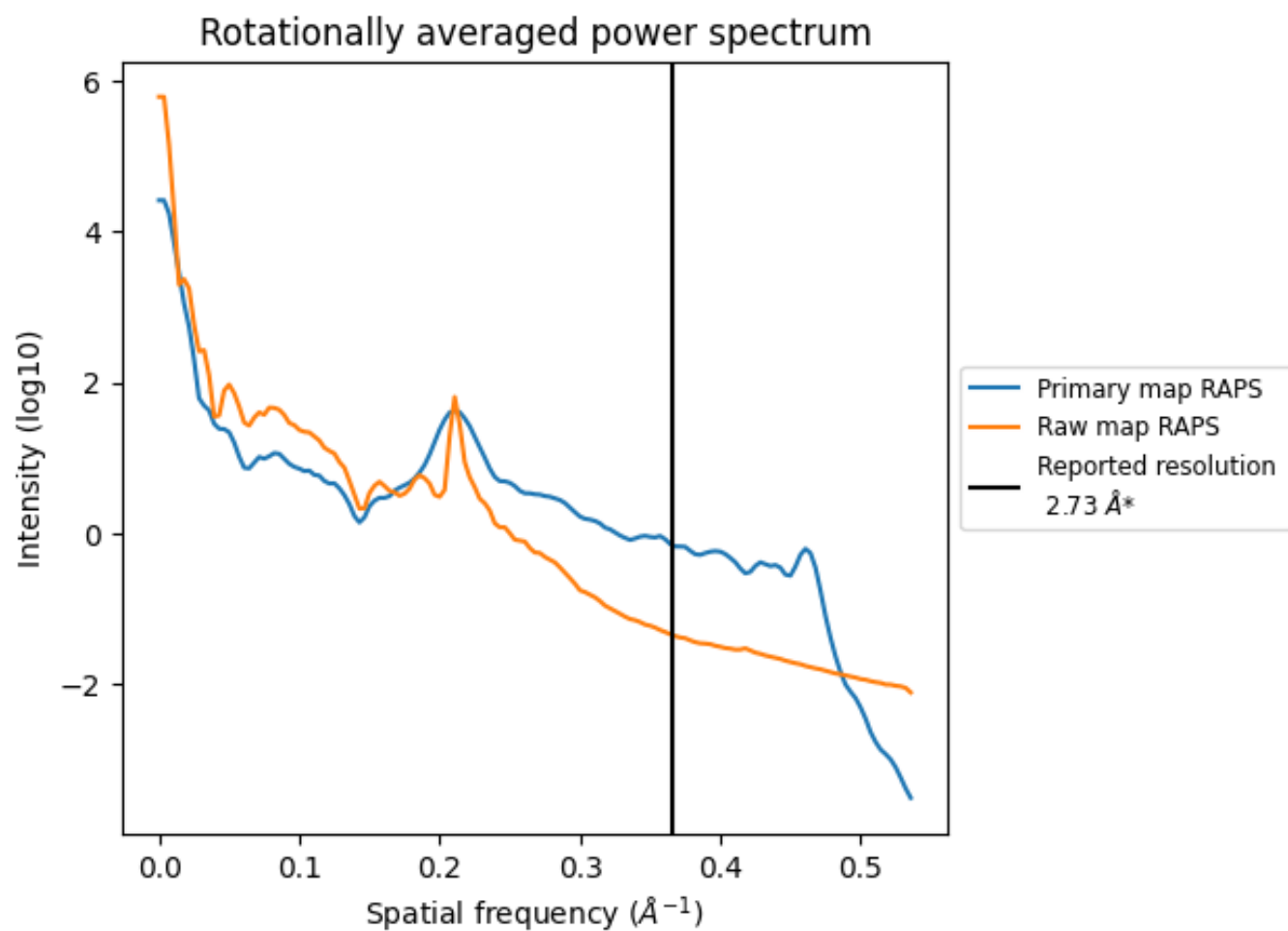
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 43 nm³; this corresponds to an approximate mass of 39 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 ⓘ

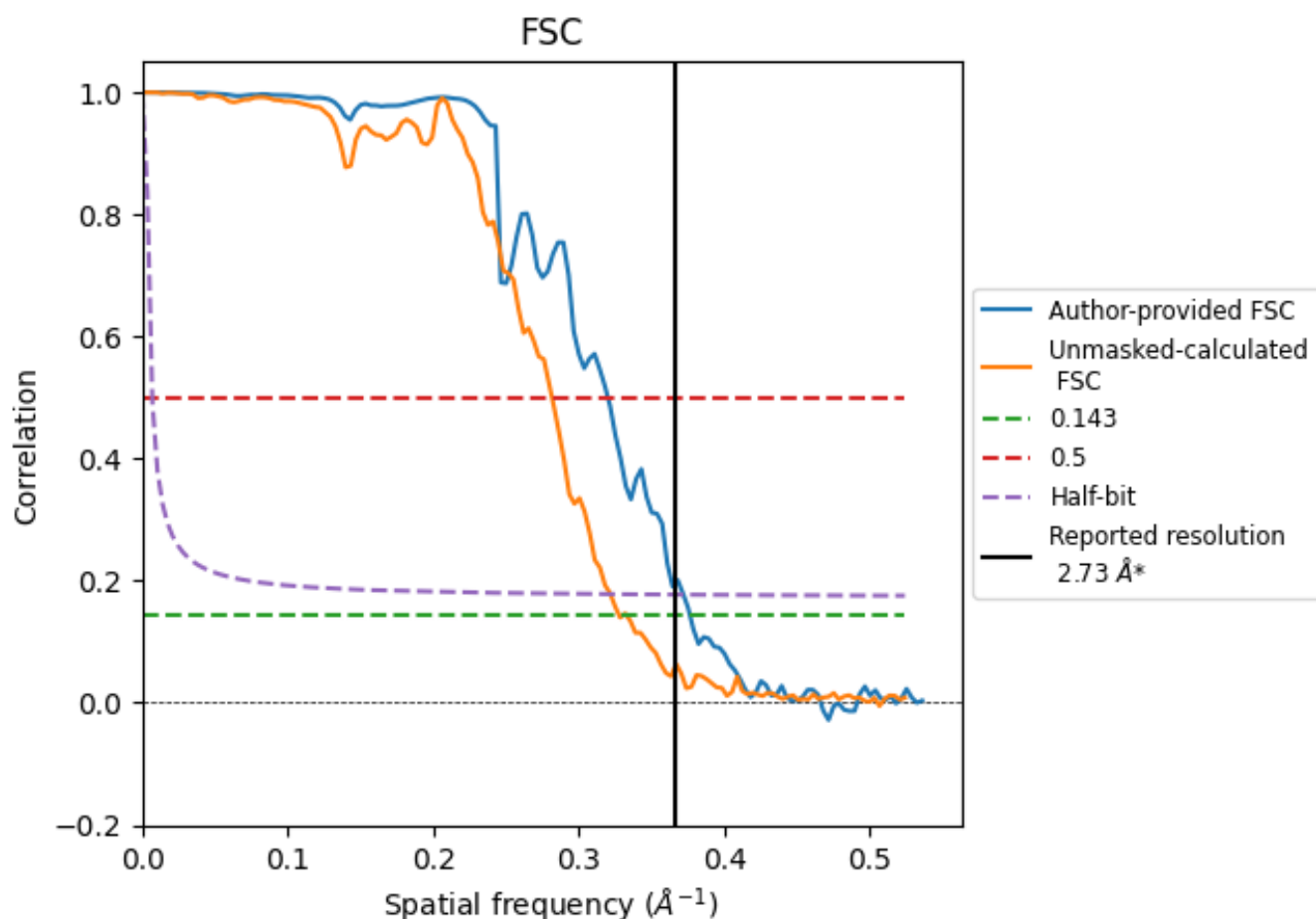


*Reported resolution corresponds to spatial frequency of 0.366 Å⁻¹

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 0.366 \AA^{-1}

8.2 Resolution estimates [i](#)

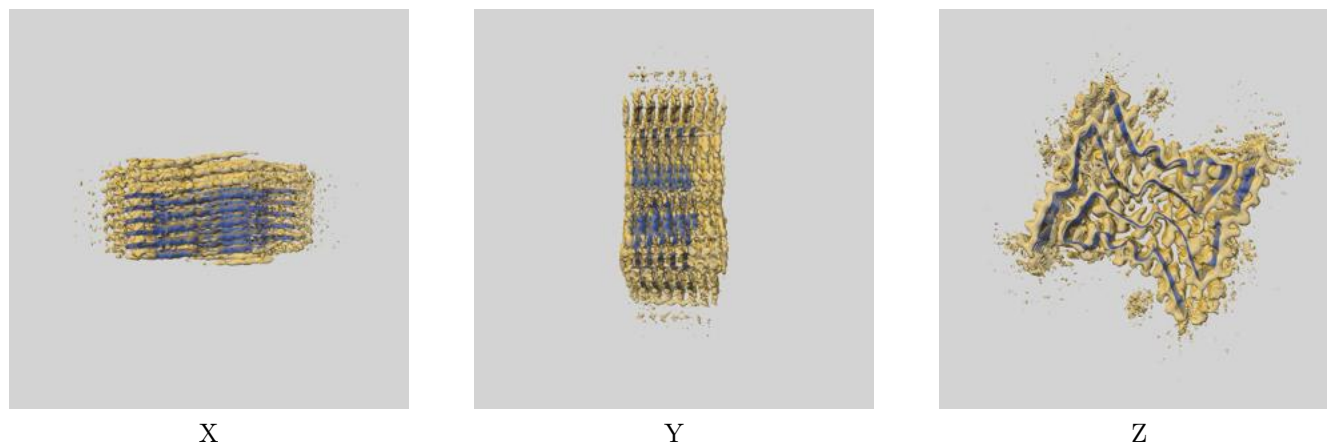
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.73	-	-
Author-provided FSC curve	2.66	3.12	2.69
Unmasked-calculated*	3.05	3.55	3.11

*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 3.05 differs from the reported value 2.73 by more than 10 %

9 Map-model fit [i](#)

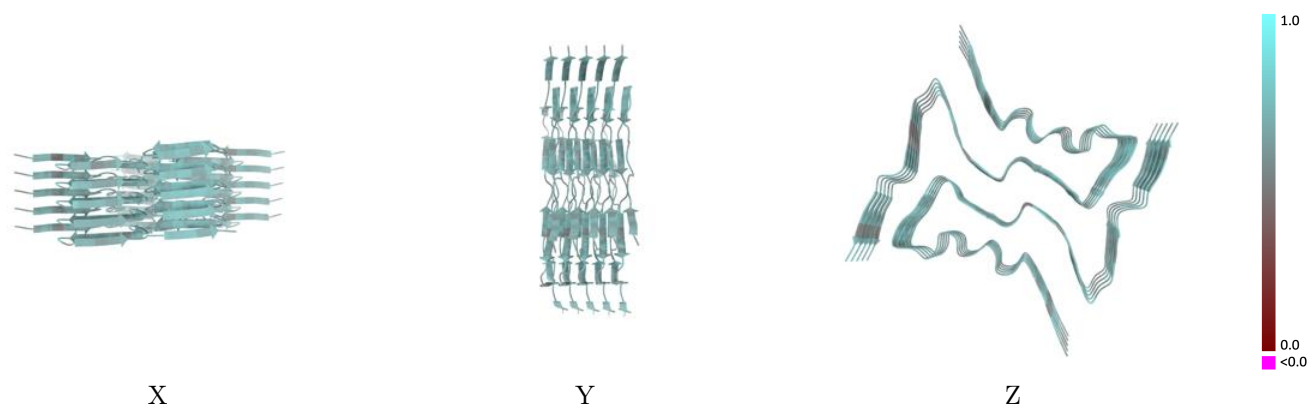
This section contains information regarding the fit between EMDB map EMD-71898 and PDB model 9PW3. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



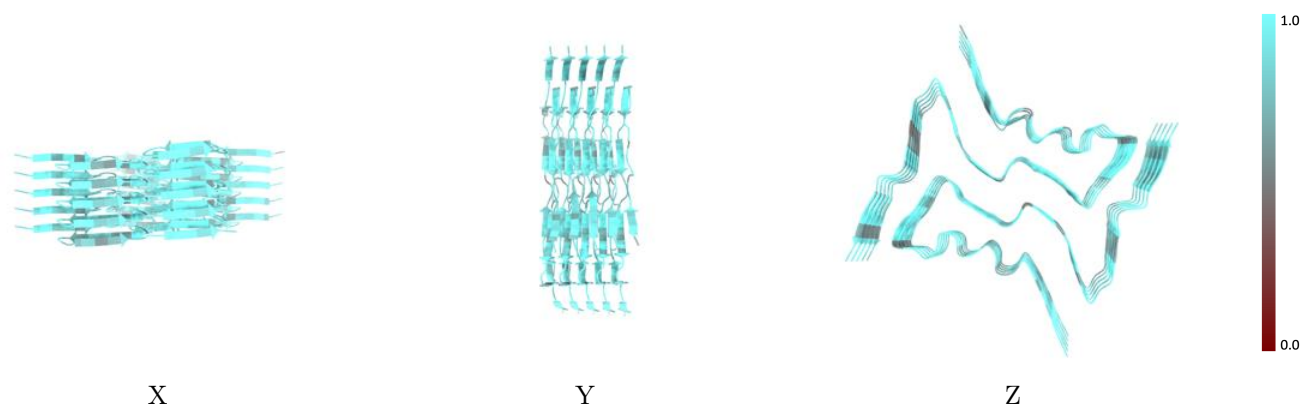
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



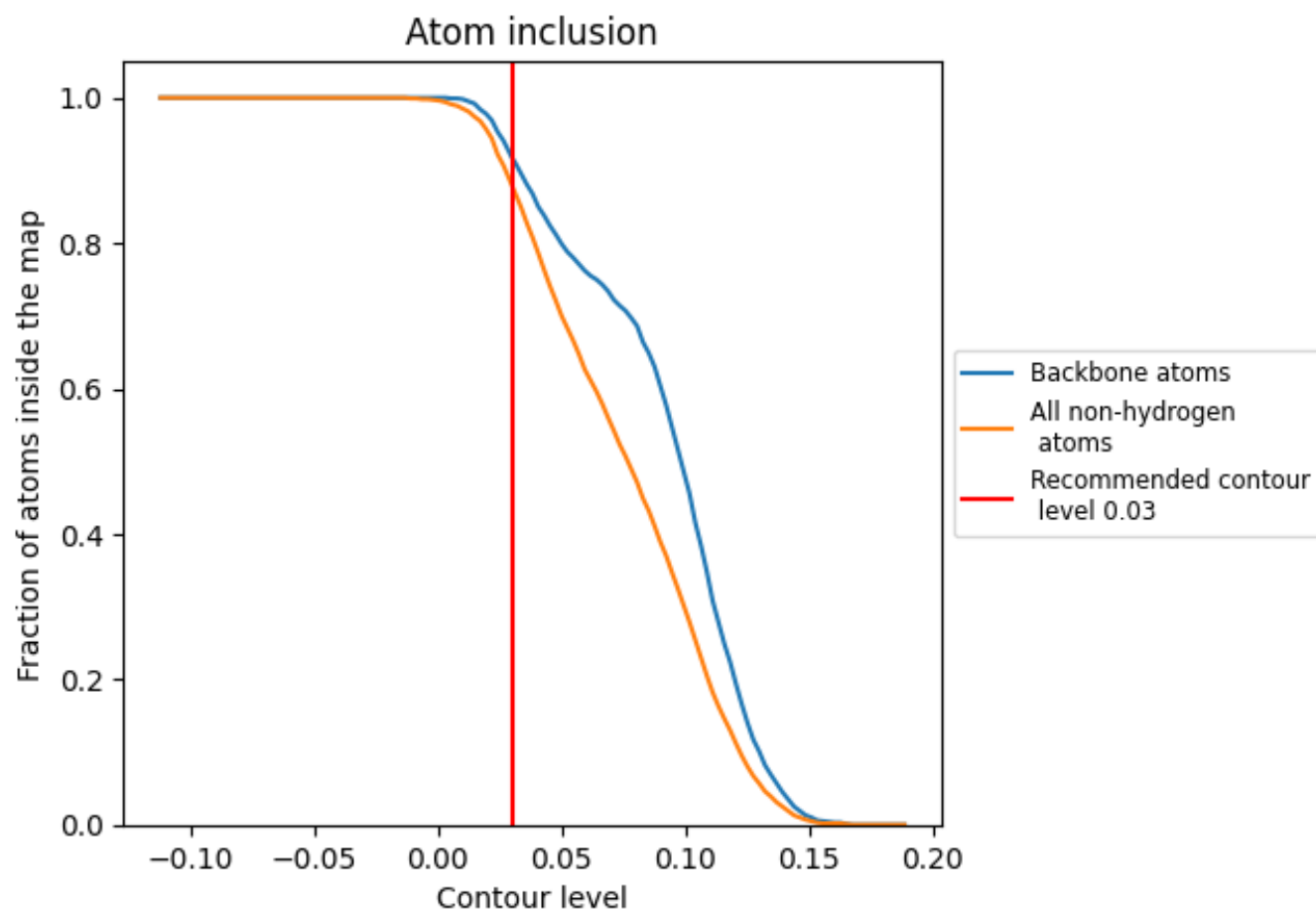
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).























9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 88% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8790	 0.6170
A	 0.8990	 0.6330
B	 0.8930	 0.6240
C	 0.8880	 0.6260
D	 0.8770	 0.6130
E	 0.8360	 0.6150
F	 0.9010	 0.6220
G	 0.8880	 0.6180
H	 0.8800	 0.6150
I	 0.8670	 0.6000
J	 0.8640	 0.6020

