



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 08:51 AM UTC

PDB ID : 7P6C / pdb_00007p6c
EMDB ID : EMD-13225
Title : Limbic-predominant neuronal inclusion body 4R tauopathy type 2 tau filament
Authors : Shi, Y.; Zhang, W.; Yang, Y.; Murzin, A.G.; Falcon, B.; Kotecha, A.; van Beers, M.; Tarutani, A.; Kametani, F.; Garringer, H.J.; Vidal, R.; Hallinan, G.I.; Lashley, T.; Saito, Y.; Murayama, S.; Yoshida, M.; Tanaka, H.; Kakita, A.; Ikeuchi, T.; Robinson, A.C.; Mann, D.M.A.; Kovacs, G.G.; Revesz, T.; Ghetti, B.; Hasegawa, M.; Goedert, M.; Scheres, S.H.W.
Deposited on : 2021-07-15
Resolution : 2.50 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

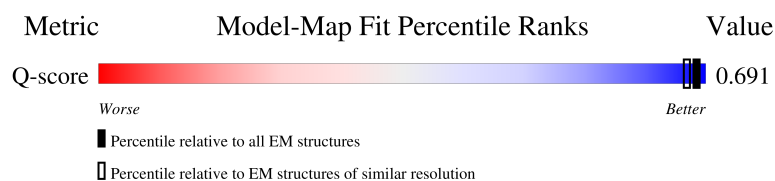
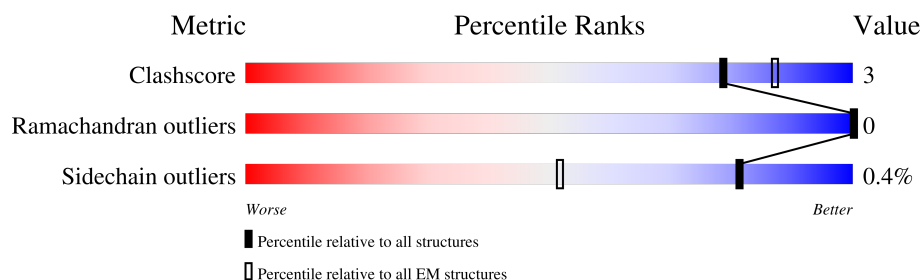
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.50 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	7115 (2.00 - 3.00)

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	
1	B	441	
1	C	441	
1	D	441	

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Mol	Chain	Length	Quality of chain
1	E	441	 23% • 76%
1	F	441	 23% • 76%
1	G	441	 23% • 76%
1	H	441	 23% • 76%
1	I	441	 23% • 76%
1	J	441	 23% • 76%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8120 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.

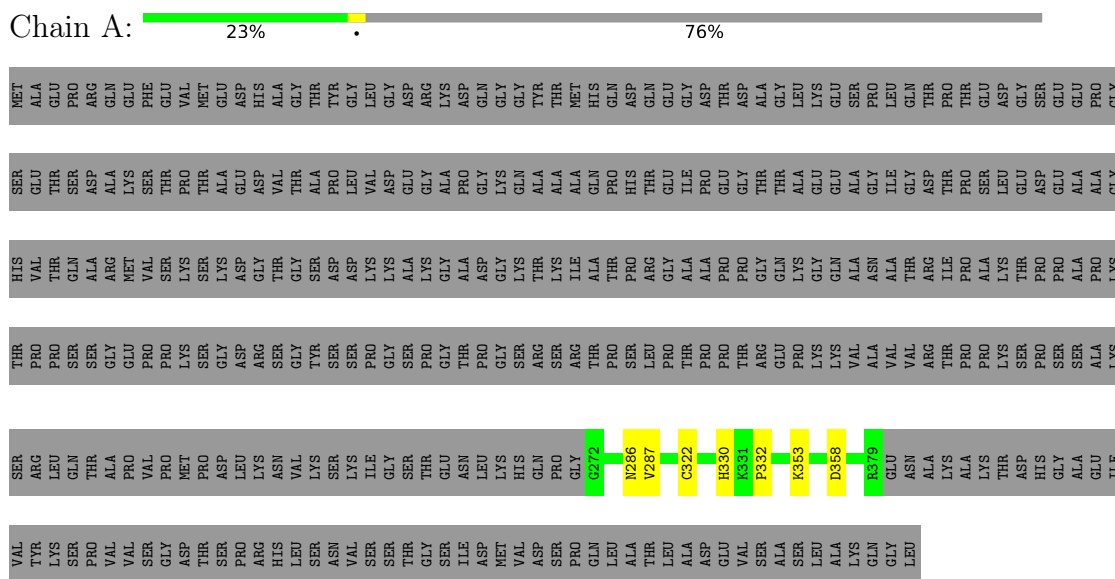
- Molecule 1 is a protein called Microtubule-associated protein tau.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	108	Total	C	N	O	S	0	0
			812	506	152	152	2		
1	B	108	Total	C	N	O	S	0	0
			812	506	152	152	2		
1	C	108	Total	C	N	O	S	0	0
			812	506	152	152	2		
1	D	108	Total	C	N	O	S	0	0
			812	506	152	152	2		
1	E	108	Total	C	N	O	S	0	0
			812	506	152	152	2		
1	F	108	Total	C	N	O	S	0	0
			812	506	152	152	2		
1	G	108	Total	C	N	O	S	0	0
			812	506	152	152	2		
1	H	108	Total	C	N	O	S	0	0
			812	506	152	152	2		
1	I	108	Total	C	N	O	S	0	0
			812	506	152	152	2		
1	J	108	Total	C	N	O	S	0	0
			812	506	152	152	2		

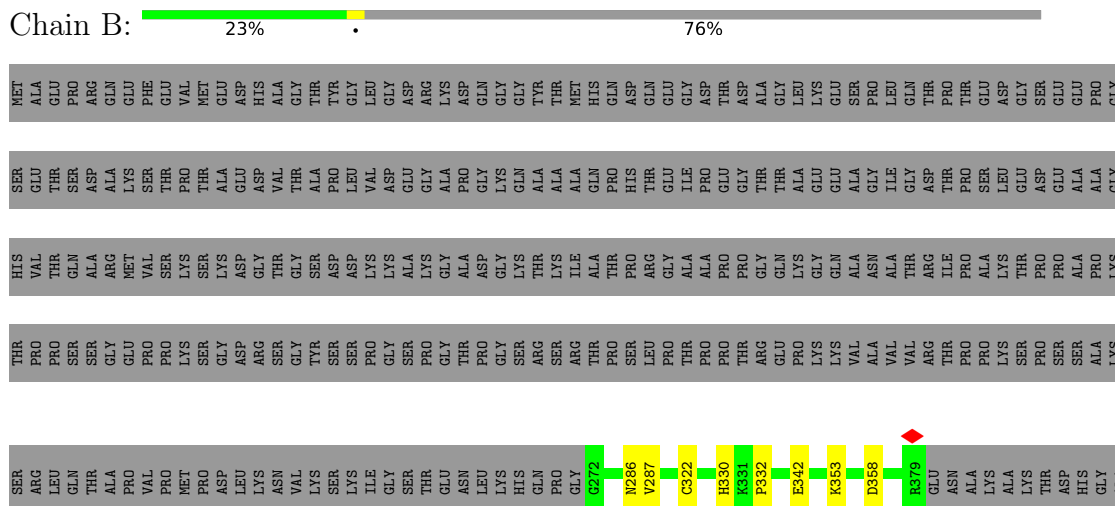
3 Residue-property plots

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.

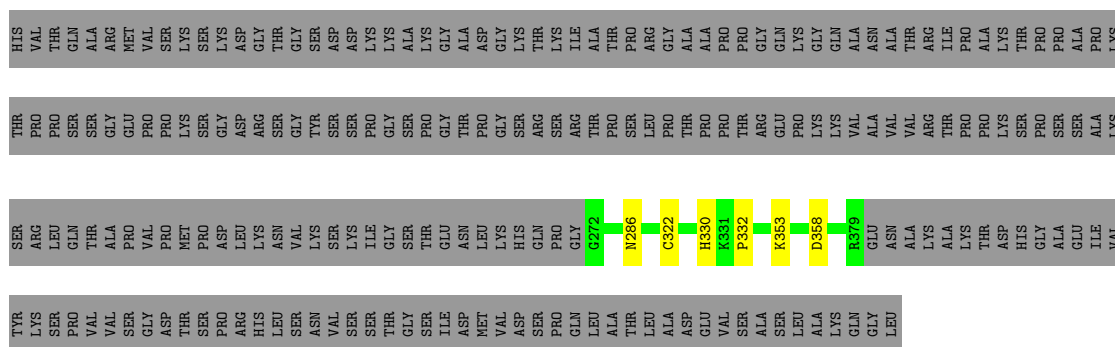
• Molecule 1: Microtubule-associated protein tau



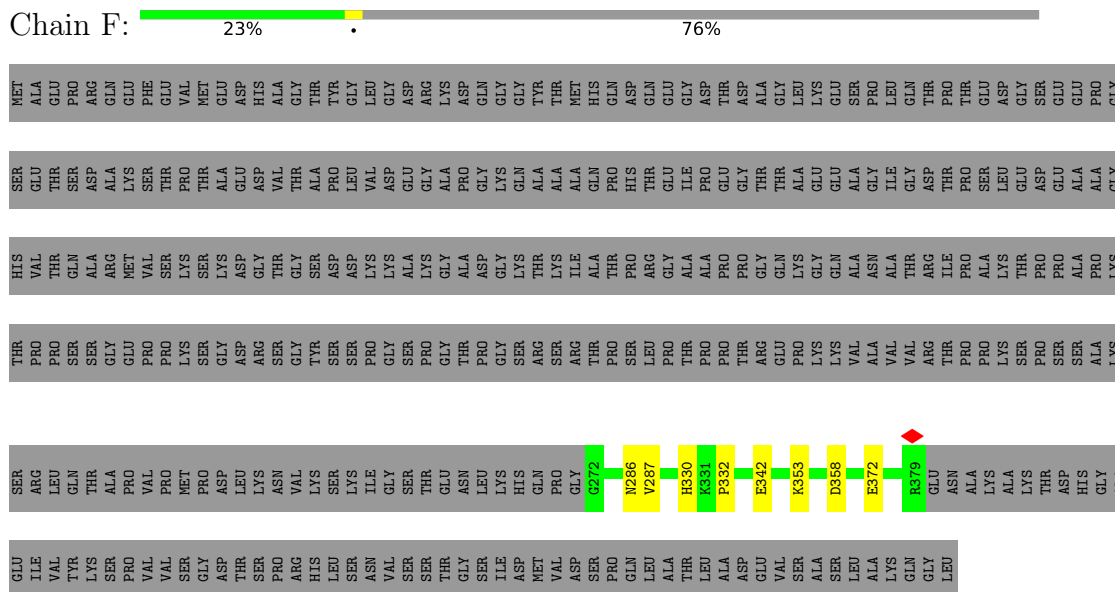
• Molecule 1: Microtubule-associated protein tau



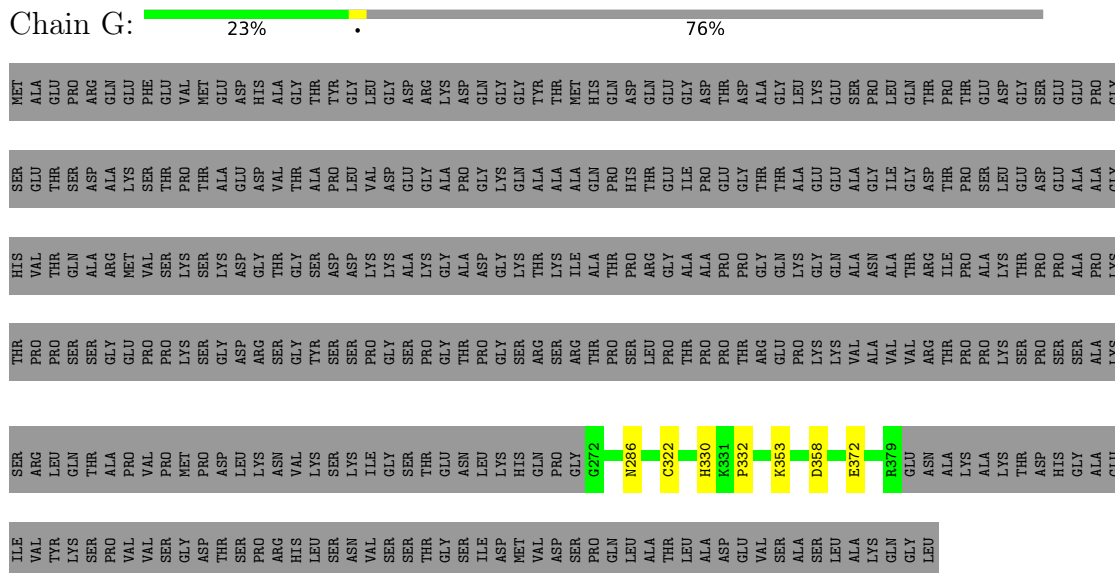
SER	GLU	THR	THR	SER	ASP	ALA	LYS	SER	THR	THR	THR	ALA	GLU	ASP	VAL	THR	ALA	ALA	PRO	LEU	VAL	ASP	GLU	GLY	ALA	ALA	PRO	GLY	LYS	GLN	ALA	ALA	ALA	GLN	GLU	GLY	THR	THR	ALA	GLU	GLU	ILE	PRO	GLU	GLY	THR	THR	THR	PRO	LEU	GLY	ASP	GLU	GLA	ALA	ALA	TYR
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- Molecule 1: Microtubule-associated protein tau



- Molecule 1: Microtubule-associated protein tau



- Molecule 1: Microtubule-associated protein tau

VAL	VAL	SER	THR	HIS	SER	MET
TYR	ARG	ARG	PRO	VAL	THR	ALA
LYS	LEU	LEU	PRO	THR	THR	GLU
SER	GLN	GLN	SER	GLN	SER	PRO
PRO	THR	THR	SER	ALA	ASP	ARG
VAL	ALA	ALA	GLY	ARG	ALA	GLN
VAL	PRO	PRO	GLU	MET	LYS	GLU
SER	VAL	VAL	PRO	VAL	SER	PHE
GLY	PRO	PRO	PRO	GLU	THR	GLU
ASP	MET	MET	LYS	SER	PRO	VAL
THR	PRO	PRO	SER	SER	THR	MET
SER	THR	ASP	GLY	LYS	ALA	GLU
PRO	LEU	LEU	ASP	ASP	GLU	ASP
ARG	LYS	LYS	ARG	GLY	ASP	HIS
HIS	ASN	ASN	SER	THR	VAL	ALA
LEU	VAL	VAL	GLY	GLY	THR	GLY
SER	VAL	THR	TYR	SER	ALA	THR
ASN	SER	SER	SER	ASP	PRO	TYR
VAL	LYS	LYS	SER	ASP	LEU	GLY
SER	ILE	ILE	PRO	LYS	VAL	LEU
SER	GLY	GLY	GLY	LYS	ASP	GLY
THR	SER	SER	SER	ALA	GLU	ASP
GLY	THR	THR	PRO	LYS	GLY	ARG
SER	GLU	GLU	GLY	GLY	ALA	LYS
ILE	ASN	ASN	THR	ALA	PRO	ASP
ASP	LEU	LEU	PRO	ASP	GLY	GLN
MET	LEU	LEU	GLY	GLY	LYS	GLY
VAL	HIS	HIS	SER	LYS	GLN	GLY
ASP	GLN	GLN	ARG	THR	ALA	TYR
SER	PRO	PRO	SER	LYS	ALA	THR
PRO	GLY	GLY	ARG	ILE	ALA	MET
GLN	G772	G772	THR	ALA	GLN	HIS
LEU	LEU	LEU	PRO	THR	PRO	GLN
ALA	N286	N286	SER	PRO	HIS	ASP
THR	V287	V287	LEU	ARG	THR	GLN
LEU	LEU	LEU	PRO	GLY	GLU	GLU
ALA	H330	H330	THR	ALA	ILE	GLY
ASP	K331	K331	PRO	ALA	PRO	ASP
GLU	P332	P332	PRO	PRO	GLU	THR
VAL	THR	THR	THR	PRO	GLY	ASP
SER	K353	K353	ARG	GLY	THR	GLY
ALA	LEU	LEU	GLU	GLN	THR	ALA
SER	LEU	LEU	PRO	LYS	ALA	LEU
LEU	D358	D358	LYS	GLY	GLU	LYS
ALA	E372	E372	LYS	GLN	GLU	GLU
LYS	GLY	GLY	VAL	ALA	SER	GLY
GLN	P379	P379	ALA	ASN	GLY	PRO
GLY	GLU	GLU	VAL	ALA	ILE	LEU
LEU	ASN	ASN	VAL	THR	GLN	GLN
	ALA	ALA	ARG	ARG	ASP	THR
	LYS	LYS	THR	ILE	THR	PRO
	ALA	ALA	PRO	PRO	PRO	GLU
	LYS	LYS	PRO	LYS	LEU	ASP
	THR	THR	SER	THR	GLY	GLY
	ASP	ASP	SER	PRO	ASP	SER
	HIS	HIS	PRO	PRO	GLU	GLU
	GLY	GLY	SER	ALA	ALA	GLU
	ALA	ALA	SER	ALA	GLY	PRO
	GLU	GLU	ALA	LYS	GLY	PRO
	TYR	TYR	LYS	PRO	GLY	GLY

[illegible][illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=179.82°, rise=2.39 Å, axial sym=C1	Depositor
Number of segments used	16813	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 ($e^-/\text{Å}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.064	Depositor
Minimum map value	-0.030	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.013	Depositor
Map size (Å)	290.8, 290.8, 290.8	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	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	0.32	0/823	0.50	0/1099
1	B	0.32	0/823	0.50	0/1099
1	C	0.32	0/823	0.50	0/1099
1	D	0.32	0/823	0.50	0/1099
1	E	0.32	0/823	0.50	0/1099
1	F	0.32	0/823	0.50	0/1099
1	G	0.32	0/823	0.51	0/1099
1	H	0.32	0/823	0.50	0/1099
1	I	0.32	0/823	0.51	0/1099
1	J	0.32	0/823	0.50	0/1099
All	All	0.32	0/8230	0.50	0/10990

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	812	0	851	9	0
1	B	812	0	851	8	0
1	C	812	0	851	4	0
1	D	812	0	851	9	0
1	E	812	0	851	5	0
1	F	812	0	851	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	812	0	851	12	0
1	H	812	0	851	7	0
1	I	812	0	851	12	0
1	J	812	0	851	6	0
All	All	8120	0	8510	47	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 3.

The worst 5 of 47 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:A:358:ASP:HA	1:B:358:ASP:O	2.11	0.51
1:A:358:ASP:O	1:D:358:ASP:HA	2.12	0.50
1:I:358:ASP:O	1:J:358:ASP:HA	2.12	0.49
1:F:358:ASP:HA	1:G:358:ASP:O	2.12	0.49
1:D:358:ASP:O	1:E:358:ASP:HA	2.13	0.49

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	106/441 (24%)	103 (97%)	3 (3%)	0	100	100
1	B	106/441 (24%)	103 (97%)	3 (3%)	0	100	100
1	C	106/441 (24%)	103 (97%)	3 (3%)	0	100	100
1	D	106/441 (24%)	103 (97%)	3 (3%)	0	100	100
1	E	106/441 (24%)	103 (97%)	3 (3%)	0	100	100
1	F	106/441 (24%)	103 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	106/441 (24%)	103 (97%)	3 (3%)	0	100	100
1	H	106/441 (24%)	103 (97%)	3 (3%)	0	100	100
1	I	106/441 (24%)	103 (97%)	3 (3%)	0	100	100
1	J	106/441 (24%)	103 (97%)	3 (3%)	0	100	100
All	All	1060/4410 (24%)	1030 (97%)	30 (3%)	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	93/358 (26%)	93 (100%)	0	100	100
1	B	93/358 (26%)	92 (99%)	1 (1%)	65	84
1	C	93/358 (26%)	93 (100%)	0	100	100
1	D	93/358 (26%)	93 (100%)	0	100	100
1	E	93/358 (26%)	93 (100%)	0	100	100
1	F	93/358 (26%)	92 (99%)	1 (1%)	65	84
1	G	93/358 (26%)	93 (100%)	0	100	100
1	H	93/358 (26%)	93 (100%)	0	100	100
1	I	93/358 (26%)	92 (99%)	1 (1%)	65	84
1	J	93/358 (26%)	92 (99%)	1 (1%)	65	84
All	All	930/3580 (26%)	926 (100%)	4 (0%)	81	93

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	342	GLU
1	F	342	GLU
1	I	342	GLU
1	J	342	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	351	GLN
1	E	330	HIS
1	J	374	HIS
1	H	279	ASN
1	J	330	HIS

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.

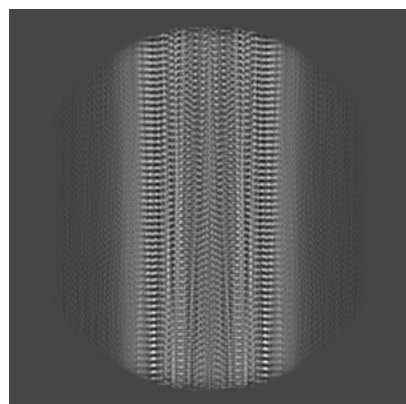
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13225. These allow visual inspection of the internal detail of the map and identification of artifacts.

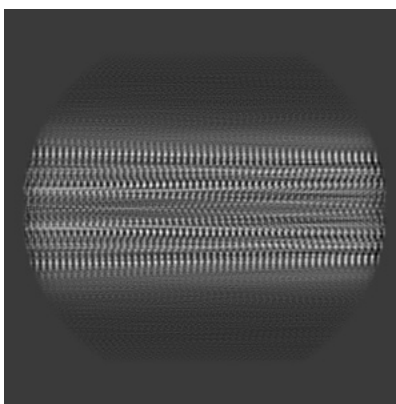
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

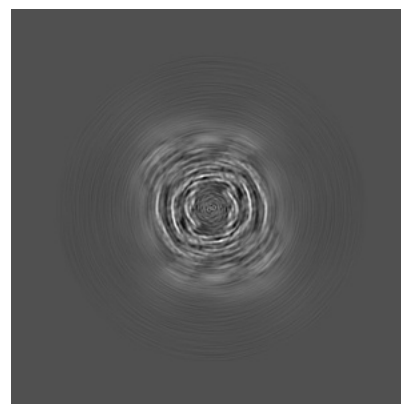
6.1.1 Primary map



X

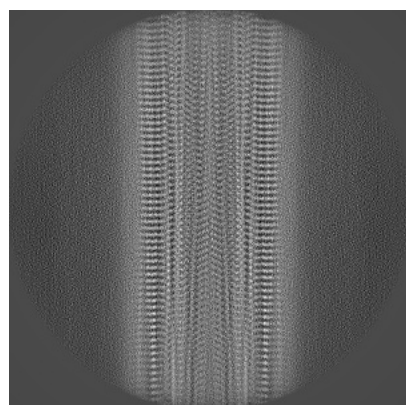


Y

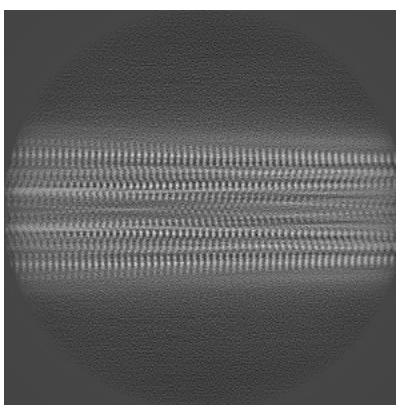


Z

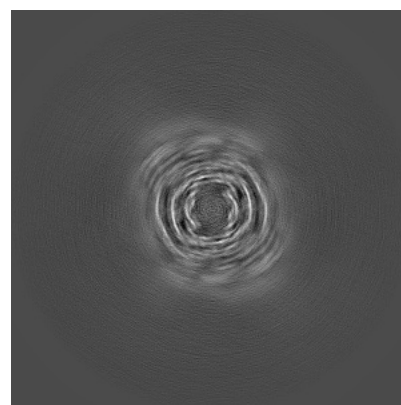
6.1.2 Raw map



X



Y

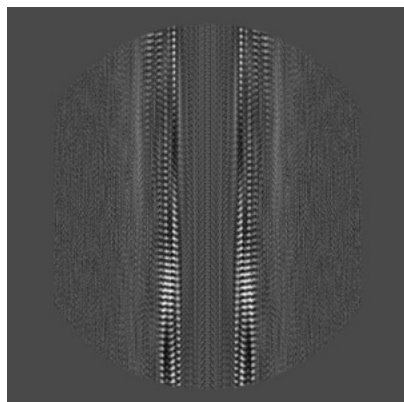


Z

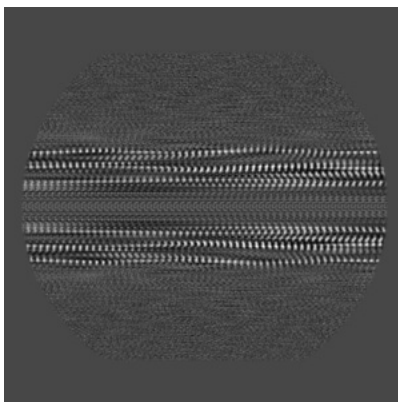
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

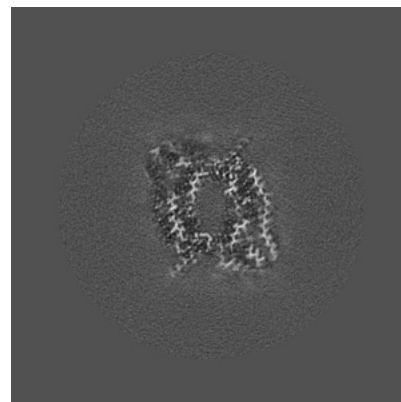
6.2.1 Primary map



X Index: 200

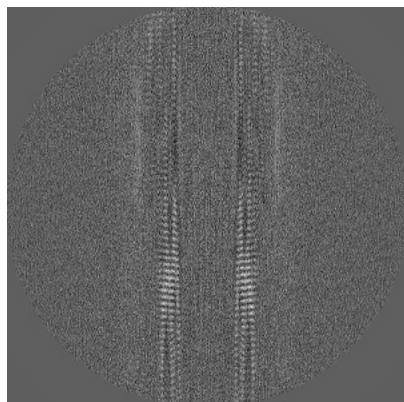


Y Index: 200

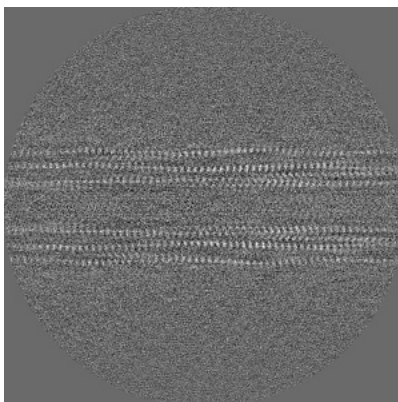


Z Index: 200

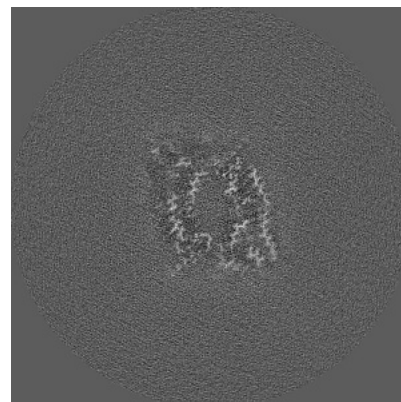
6.2.2 Raw map



X Index: 200



Y Index: 200

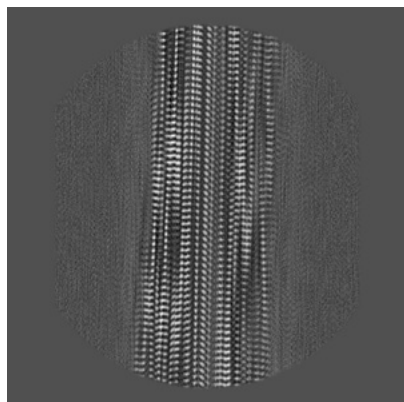


Z Index: 200

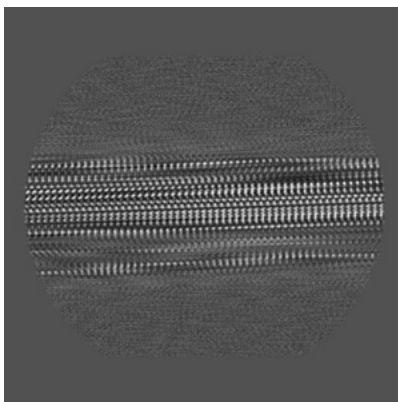
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

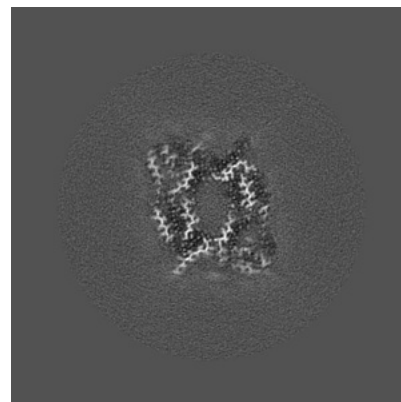
6.3.1 Primary map



X Index: 179

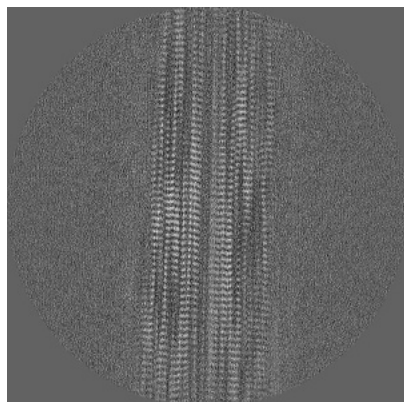


Y Index: 233

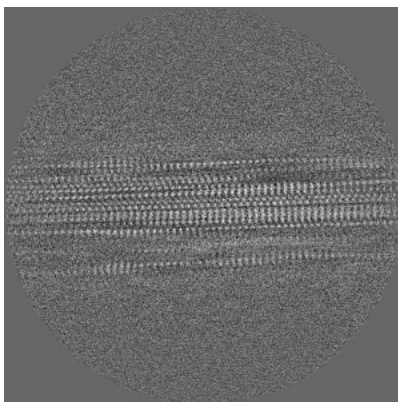


Z Index: 222

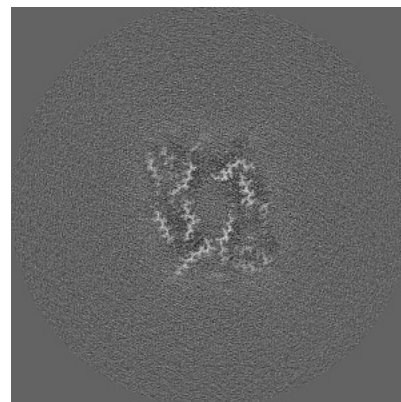
6.3.2 Raw map



X Index: 181



Y Index: 233

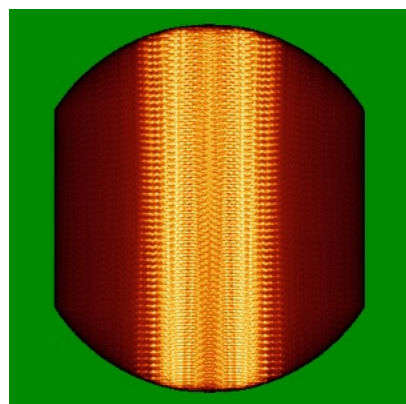


Z Index: 189

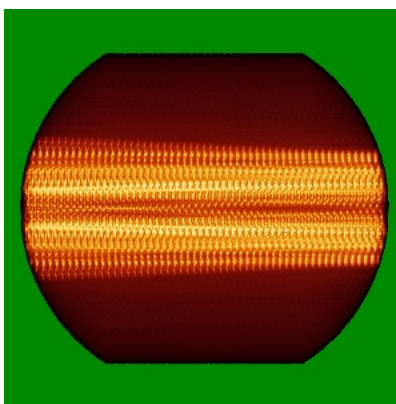
The images above show the largest variance slices of the map in three orthogonal directions.

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

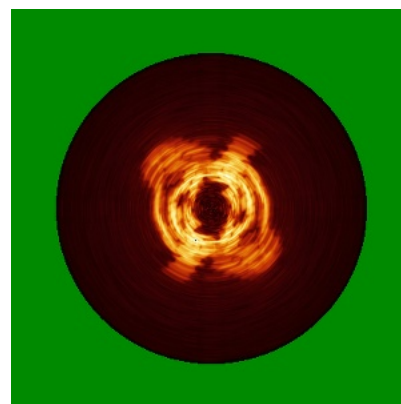
6.4.1 Primary map



X

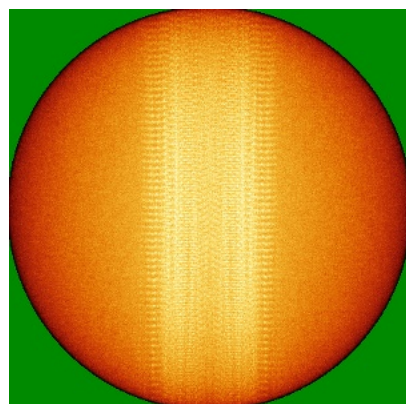


Y

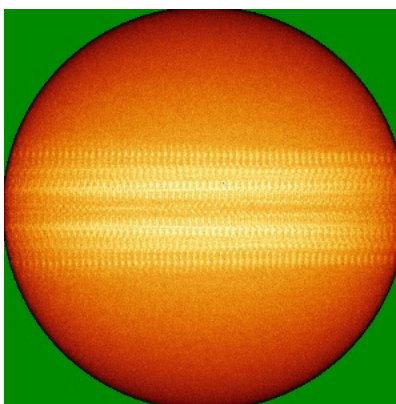


Z

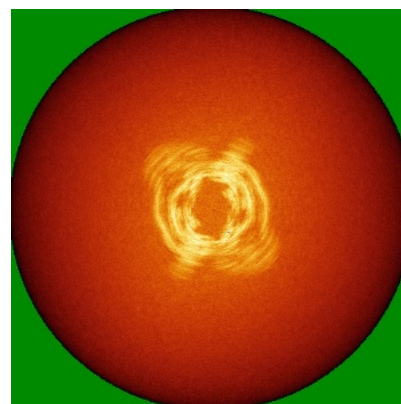
6.4.2 Raw map



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](#)

This section was not generated.

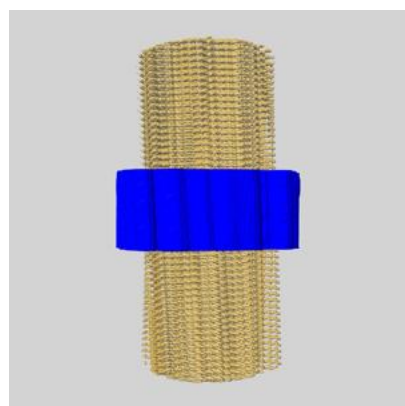
6.6 Mask visualisation [i](#)

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

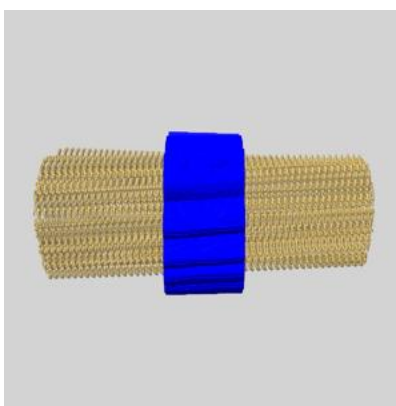
A mask typically either:

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

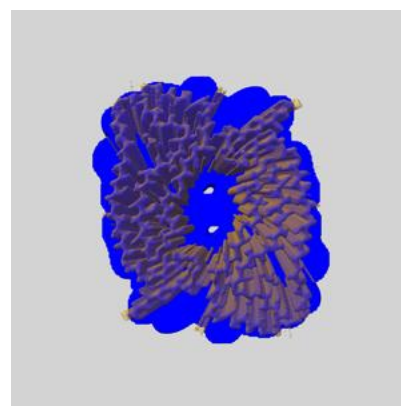
6.6.1 emd_13225_msk_1.map [i](#)



X



Y

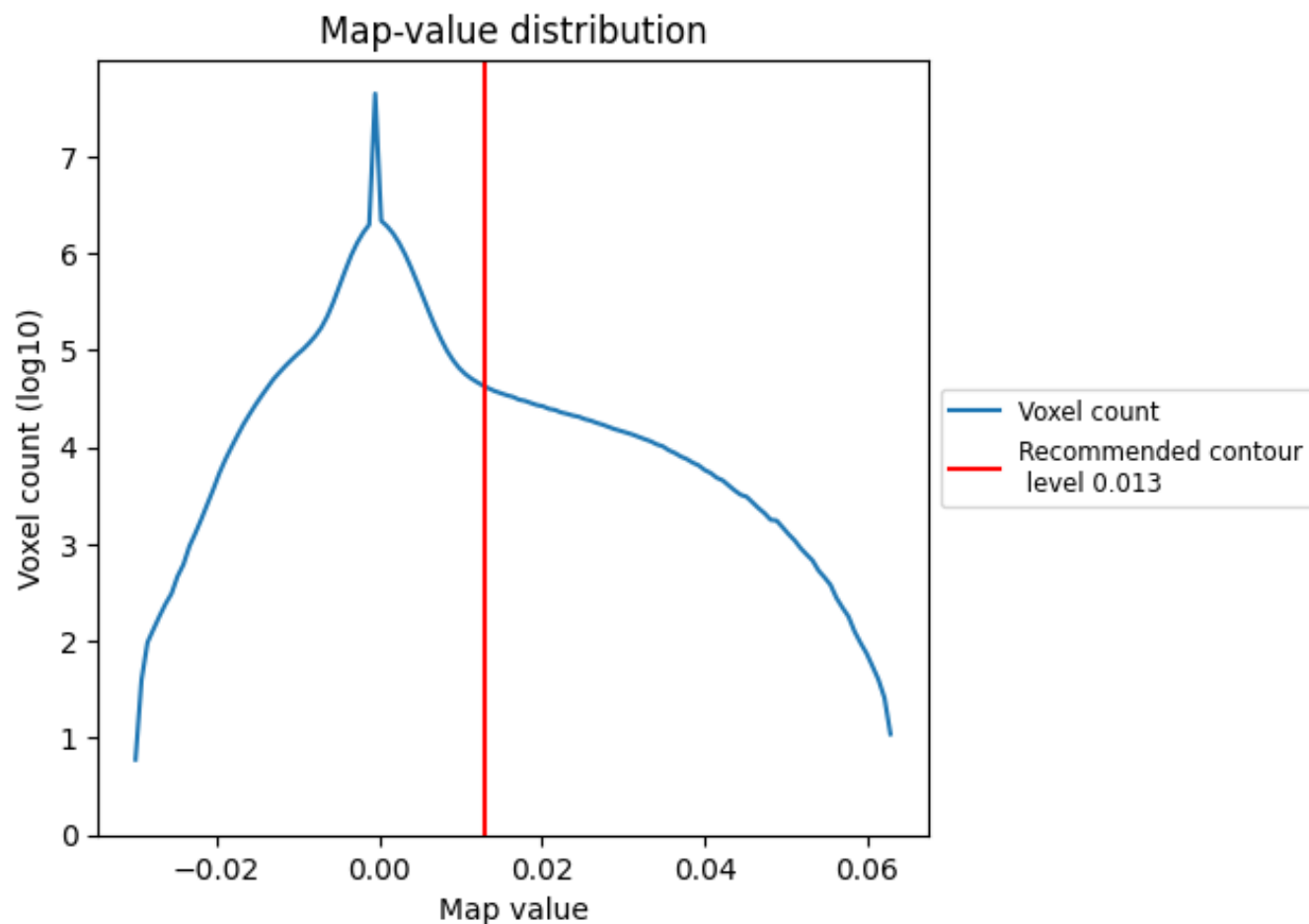


Z

7 Map analysis [i](#)

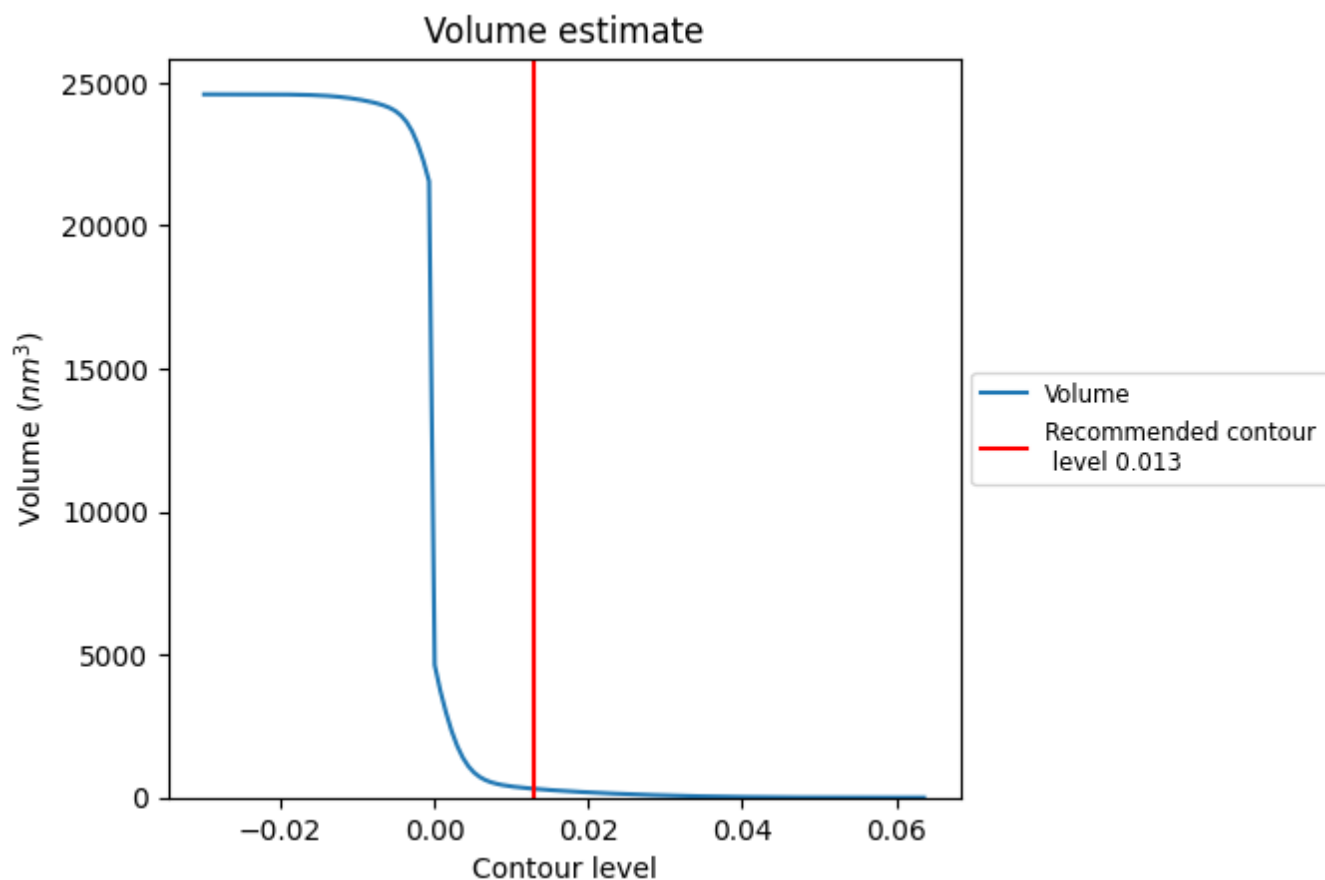
This section contains the results of statistical analysis of the map.

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.

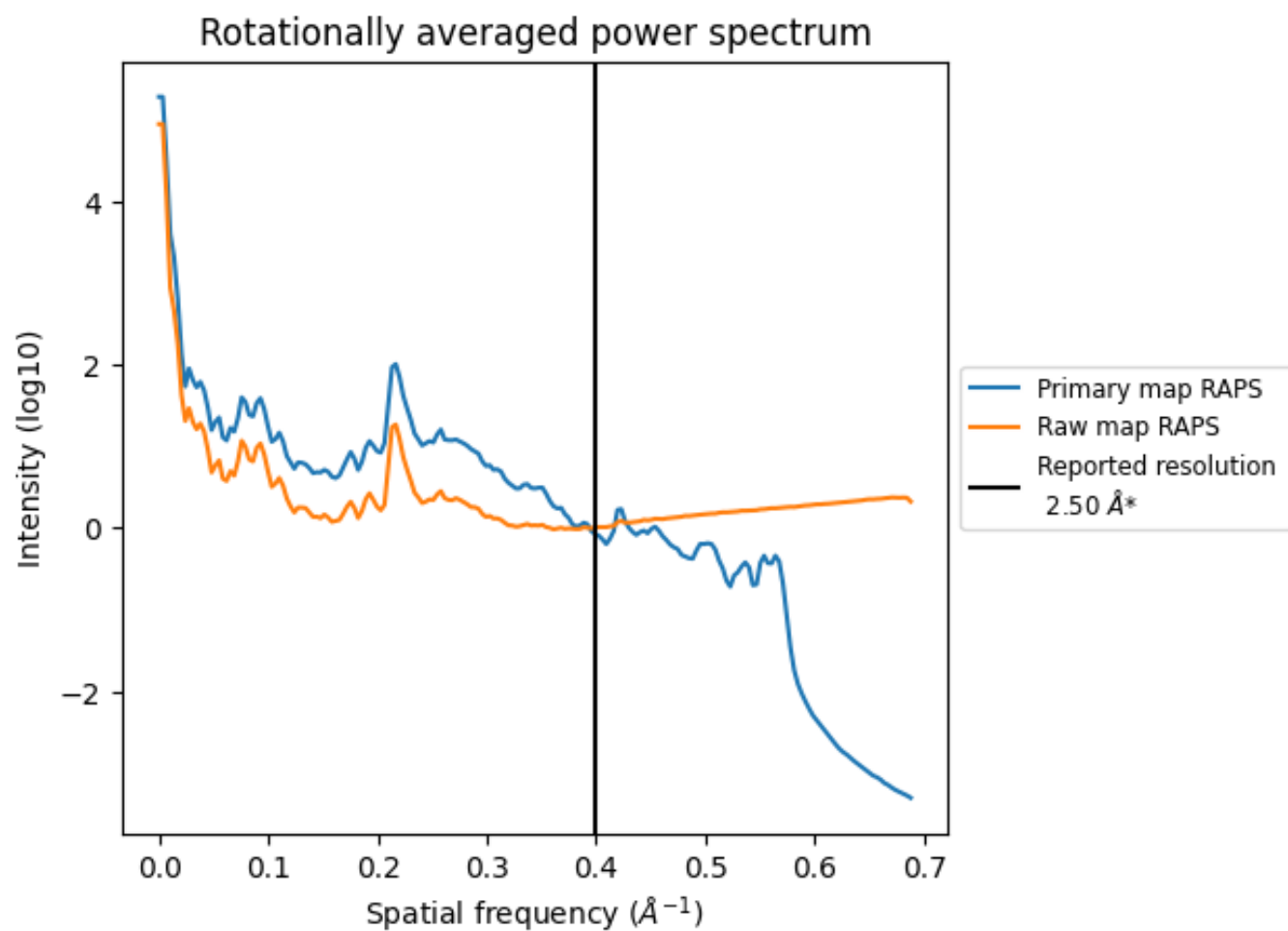
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 306 nm³; this corresponds to an approximate mass of 276 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 ⓘ

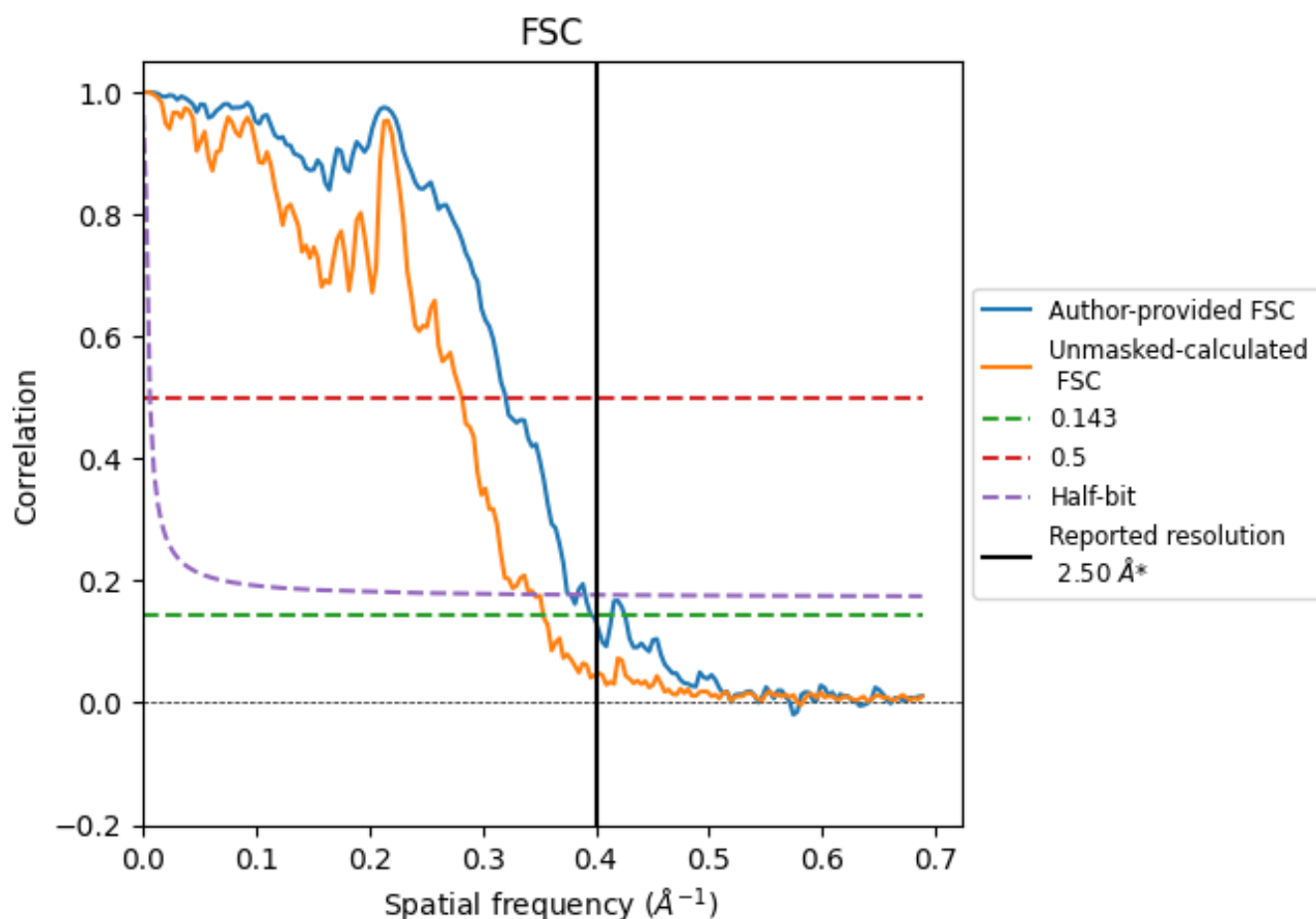


*Reported resolution corresponds to spatial frequency of 0.400 Å⁻¹

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 0.400 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

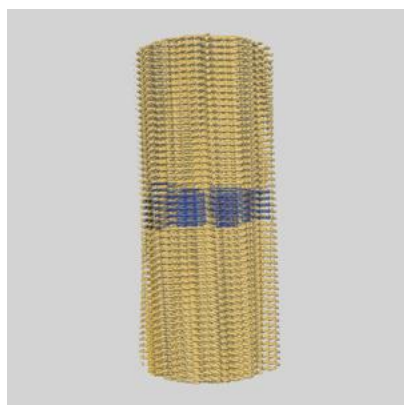
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	2.52	3.12	2.65
Unmasked-calculated*	2.83	3.55	2.89

*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 2.83 differs from the reported value 2.5 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13225 and PDB model 7P6C. Per-residue inclusion information can be found in section [3](#) on page [5](#).

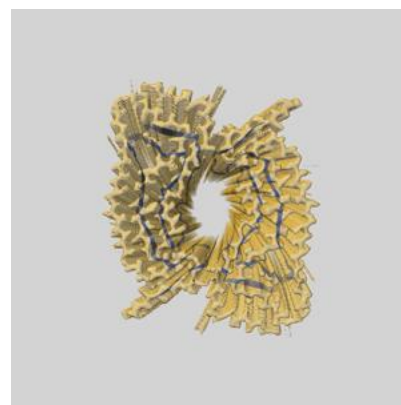
9.1 Map-model overlay [i](#)



X



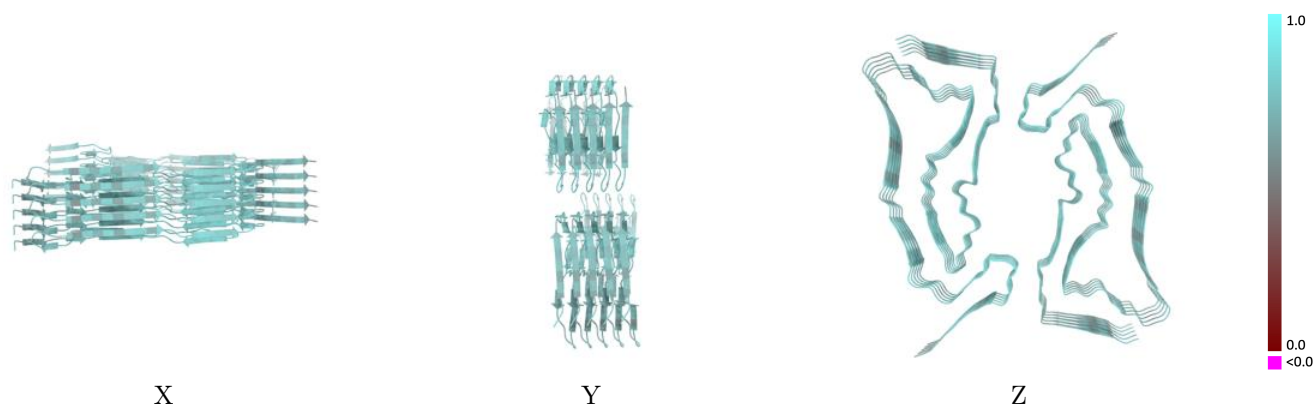
Y



Z

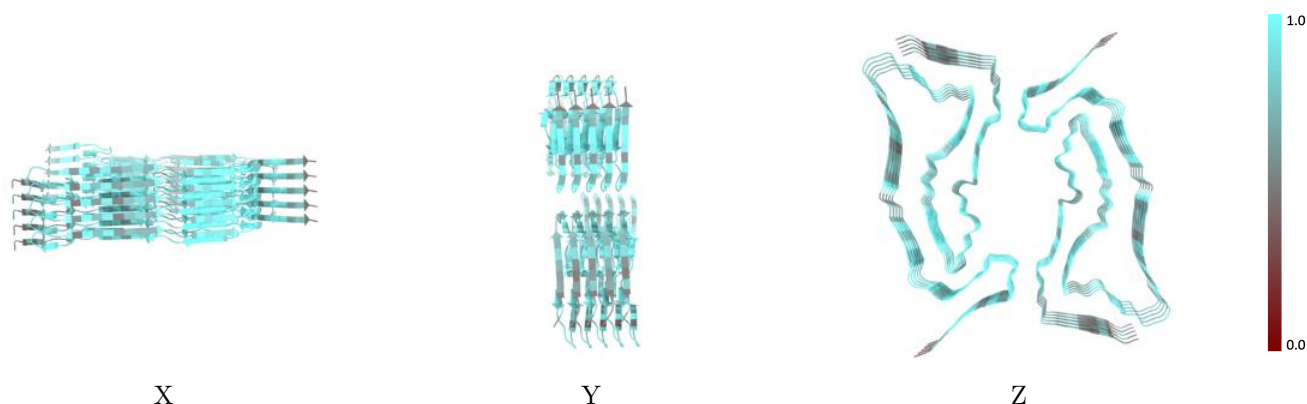
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



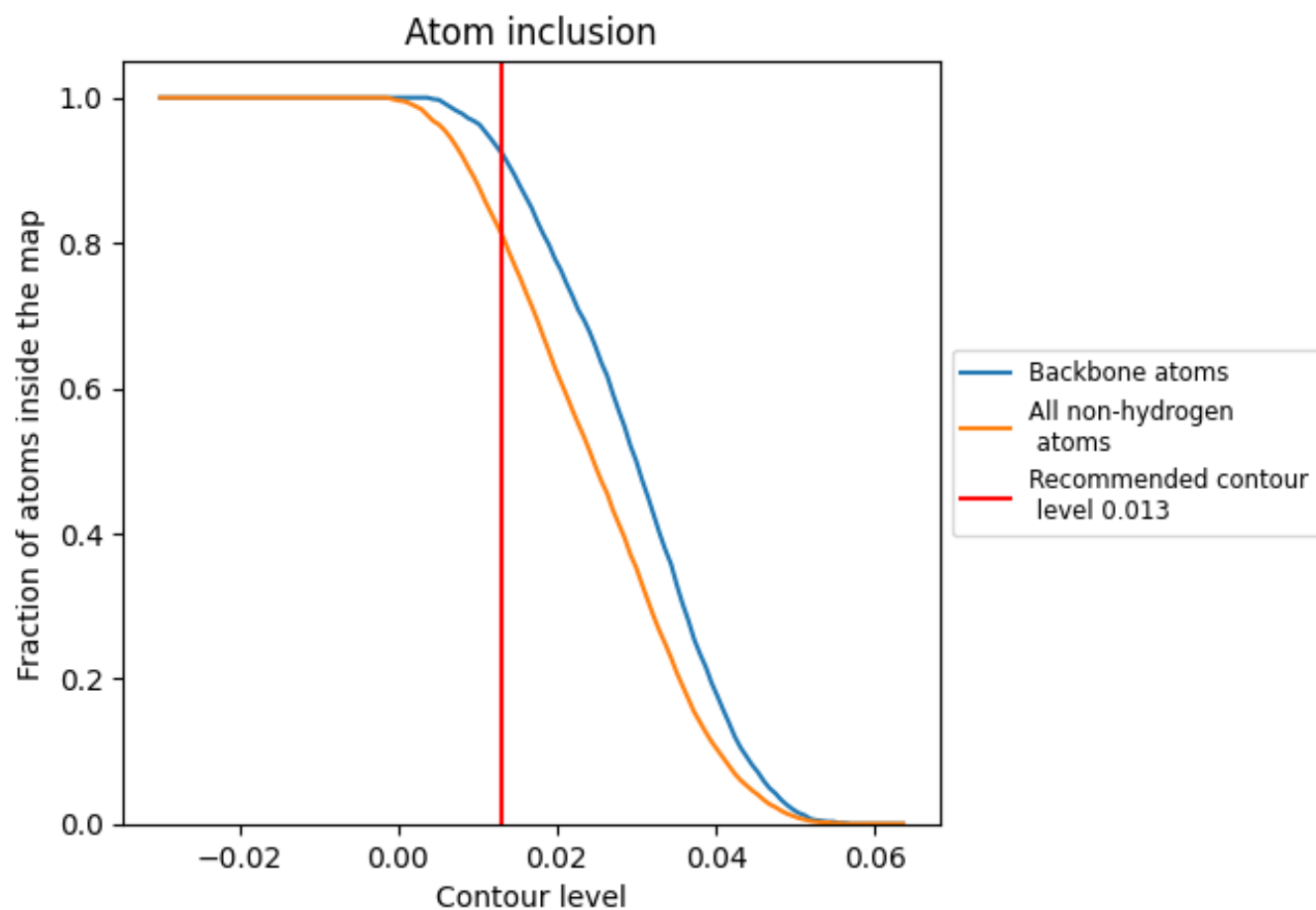
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.013).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 81% 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 (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8130	0.6910
A	0.8200	0.6910
B	0.8130	0.6900
C	0.8140	0.6920
D	0.8070	0.6900
E	0.8130	0.6910
F	0.8090	0.6930
G	0.8190	0.6910
H	0.8130	0.6920
I	0.8090	0.6920
J	0.8100	0.6920

1.0

0.0

<0.0