



wwPDB EM Validation Summary Report ⓘ

Sep 8, 2025 – 02:07 pm BST

PDB ID : 9QZC / pdb_00009qzc
EMDB ID : EMD-53467
Title : Proximal A-C linker of Tetrahymena centriole, one repeating unit
Authors : Cai, B.; Xu, J.W.; Luo, L.; Aarts, E.; Leitner, A.; Ishikawa, T.; Beltro, P.;
Pilhofer, M.; Wieczorek, M.
Deposited on : 2025-04-22
Resolution : 3.80 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.dev126
MolProbity : **FAILED**
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

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 3.80 Å.

There are no overall percentile quality scores available for this entry.

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 22355 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 WD repeat WRAP73-like protein, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	i	429	Total	C	N	O	0	0
			2129	1271	429	429		

- Molecule 2 is a protein called Centrosomal protein, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	q	284	Total	C	N	O	0	0
			1415	847	284	284		
2	y	258	Total	C	N	O	0	0
			1288	772	258	258		

- Molecule 3 is a protein called Rab-GAP TBC domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	7	813	Total	C	N	O	0	0
			4040	2414	813	813		

- Molecule 4 is a protein called TBC1 domain family member 31.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	AE	518	Total	C	N	O	0	0
			2584	1548	518	518		
4	AU	354	Total	C	N	O	0	0
			1752	1044	354	354		

- Molecule 5 is a protein called POC1 centriolar protein homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	AM	365	Total	C	N	O	0	0
			1806	1076	365	365		

- Molecule 6 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	Ac	32	Total	C	N	O	0	0
			160	96	32	32		

- Molecule 7 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	As	153	Total	C	N	O	0	0
			765	459	153	153		

- Molecule 8 is a protein called SWIM-type domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	Az	151	Total	C	N	O	0	0
			748	446	151	151		
8	A7	158	Total	C	N	O	0	0
			783	467	158	158		

- Molecule 9 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	Bw	151	Total	C	N	O	0	0
			755	453	151	151		

- Molecule 10 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	B4	164	Total	C	N	O	0	0
			820	492	164	164		

- Molecule 11 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	CA	167	Total	C	N	O	0	0
			835	501	167	167		

- Molecule 12 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	CH	161	Total	C	N	O	0	0
			805	483	161	161		

- Molecule 13 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	CO	105	Total	C	N	O	0	0
			525	315	105	105		

- Molecule 14 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	CV	127	Total	C	N	O	0	0
			635	381	127	127		

- Molecule 15 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	Cc	102	Total	C	N	O	0	0
			510	306	102	102		

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	155485	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 ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	13.599	Depositor
Minimum map value	0.000	Depositor
Average map value	0.223	Depositor
Map value standard deviation	1.035	Depositor
Recommended contour level	5	Depositor
Map size (Å)	631.2, 631.2, 631.2	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.315, 1.315, 1.315	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

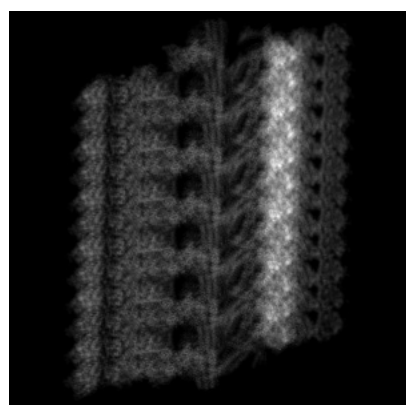
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53467. These allow visual inspection of the internal detail of the map and identification of artifacts.

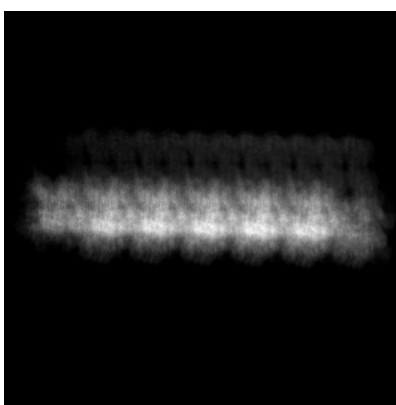
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

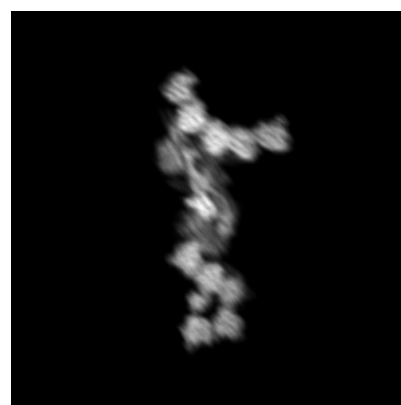
5.1.1 Primary map



X



Y

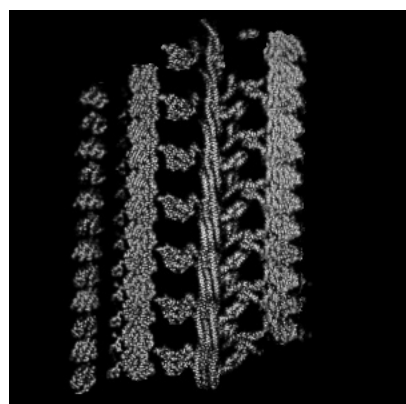


Z

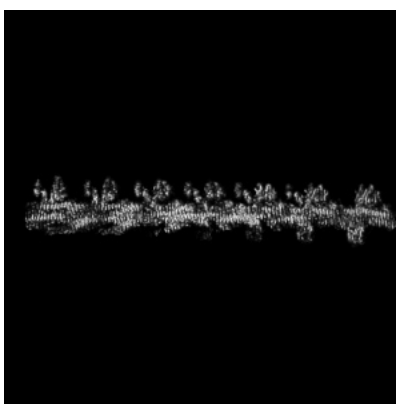
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

5.2.1 Primary map



X Index: 240



Y Index: 240

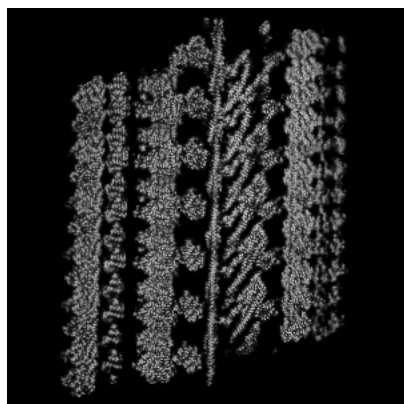


Z Index: 240

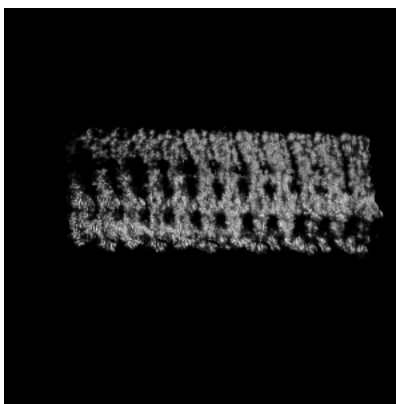
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

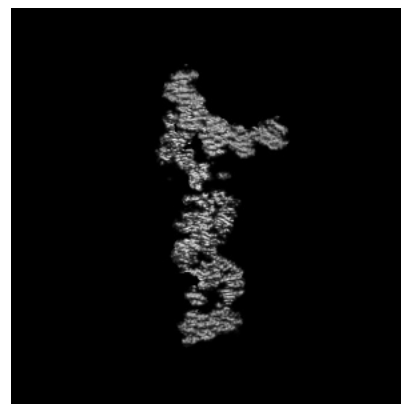
5.3.1 Primary map



X Index: 218



Y Index: 335

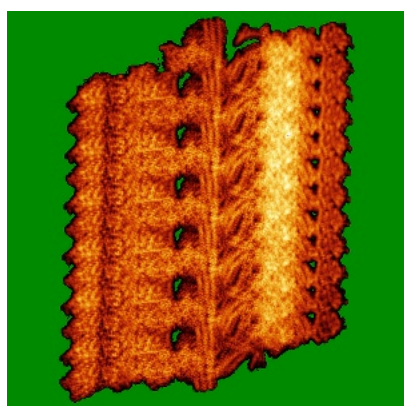


Z Index: 311

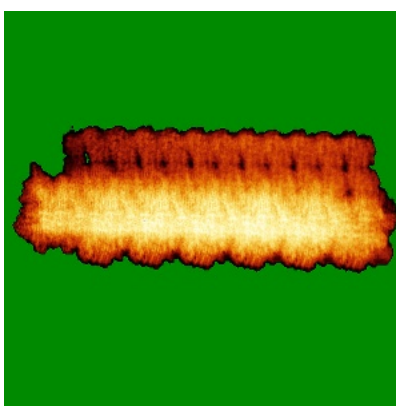
The images above show the largest variance slices of the map in three orthogonal directions.

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

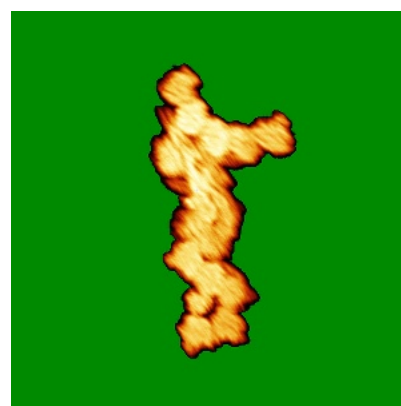
5.4.1 Primary map



X



Y

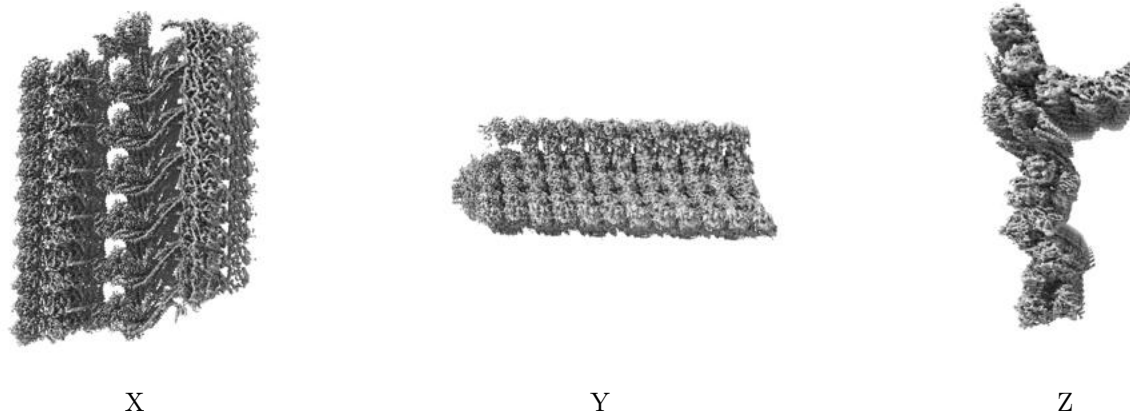


Z

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.

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

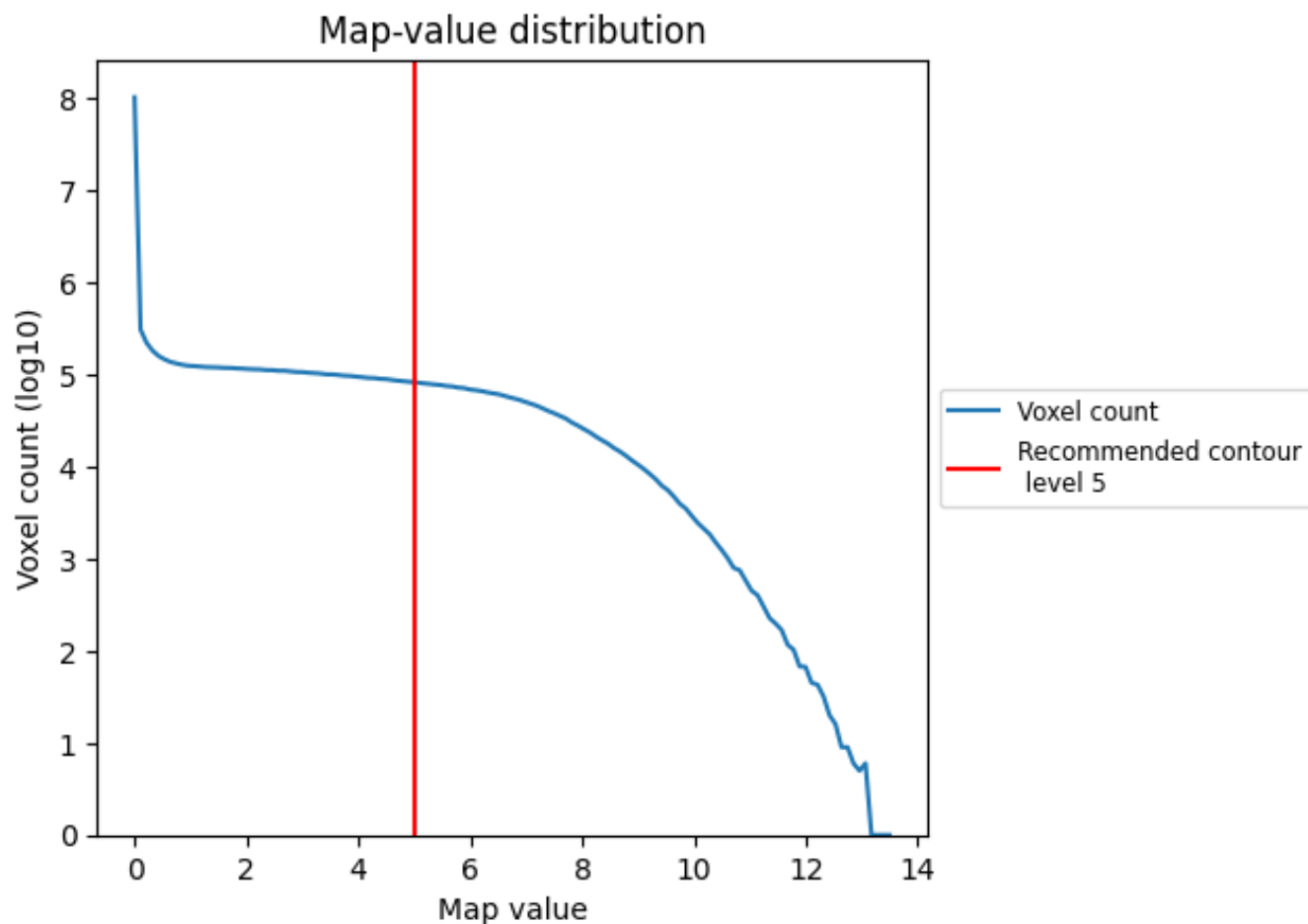
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

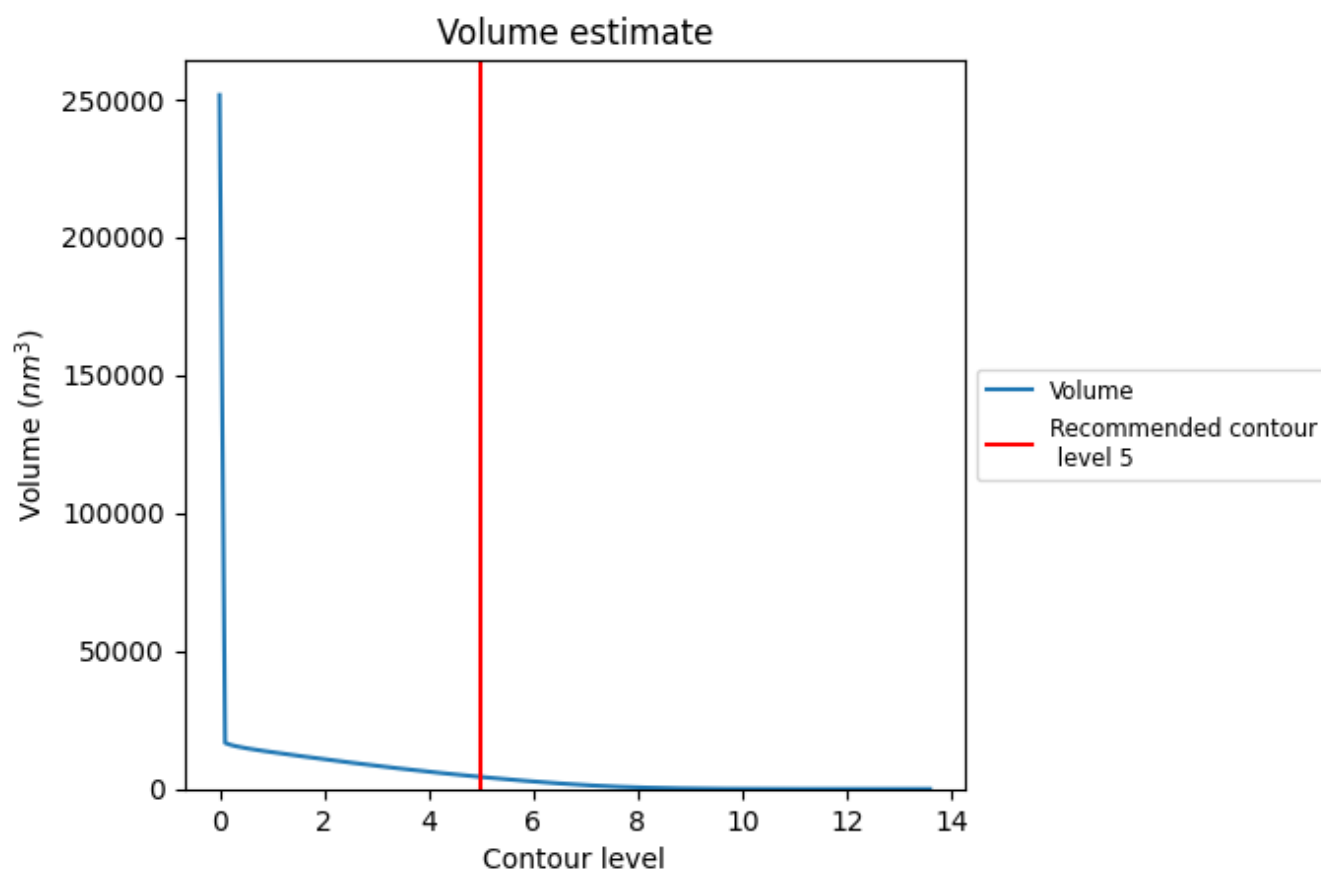
This section contains the results of statistical analysis of the map.

6.1 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.

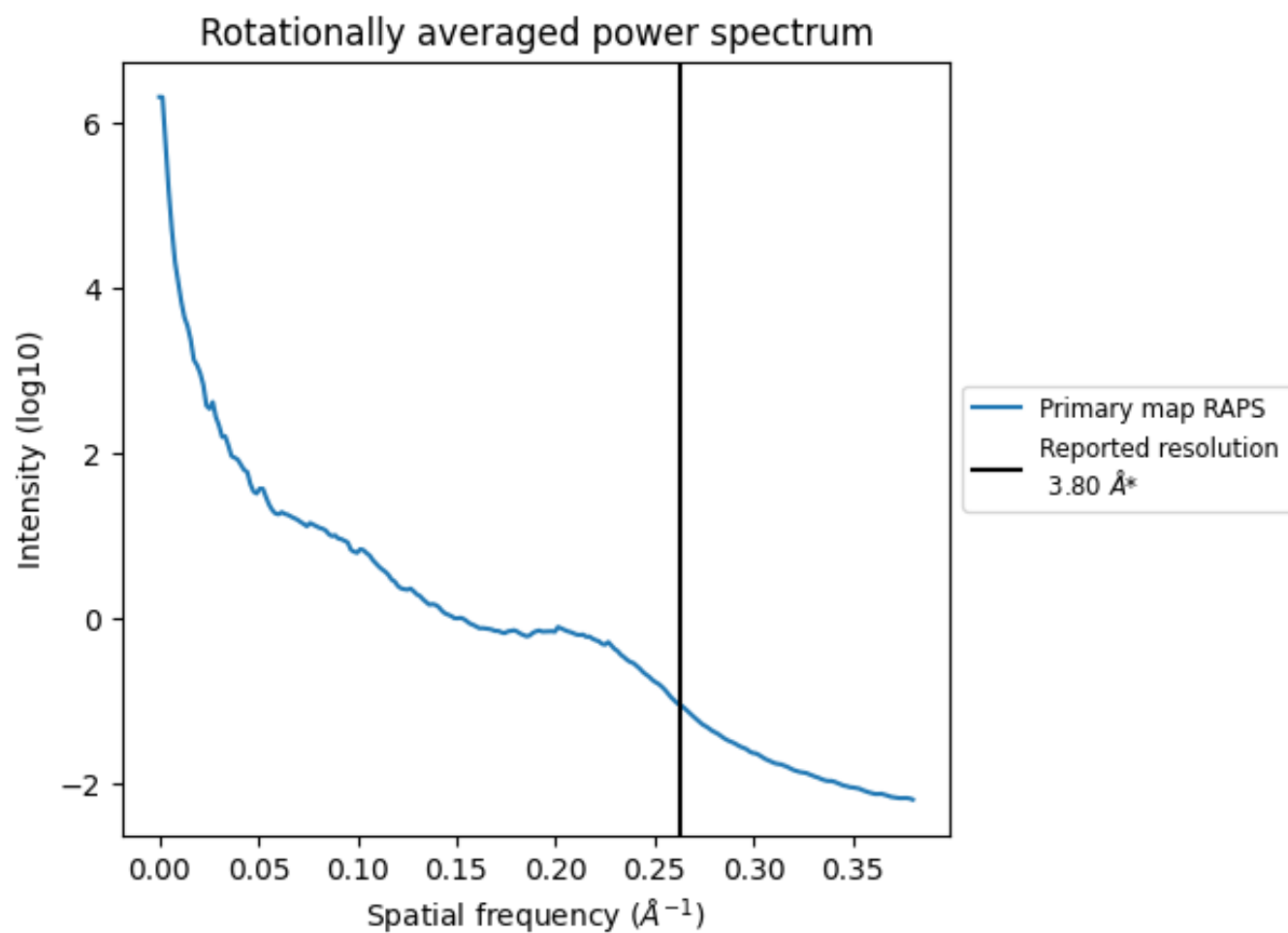
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 4355 nm^3 ; this corresponds to an approximate mass of 3934 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.

6.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

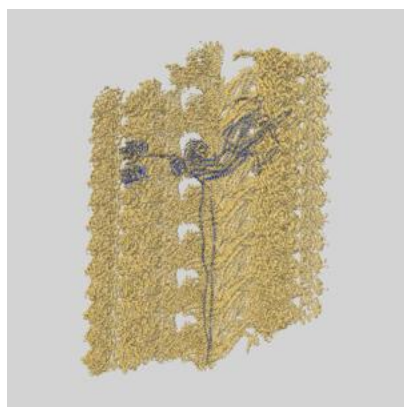
7 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

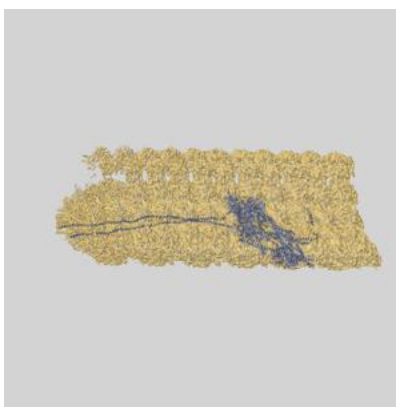
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53467 and PDB model 9QZC. Per-residue inclusion information can be found in section ?? on page ??.

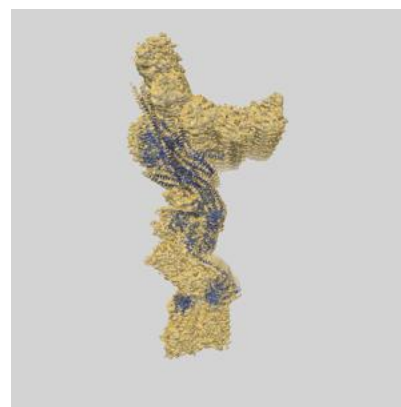
8.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 5.0 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.

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



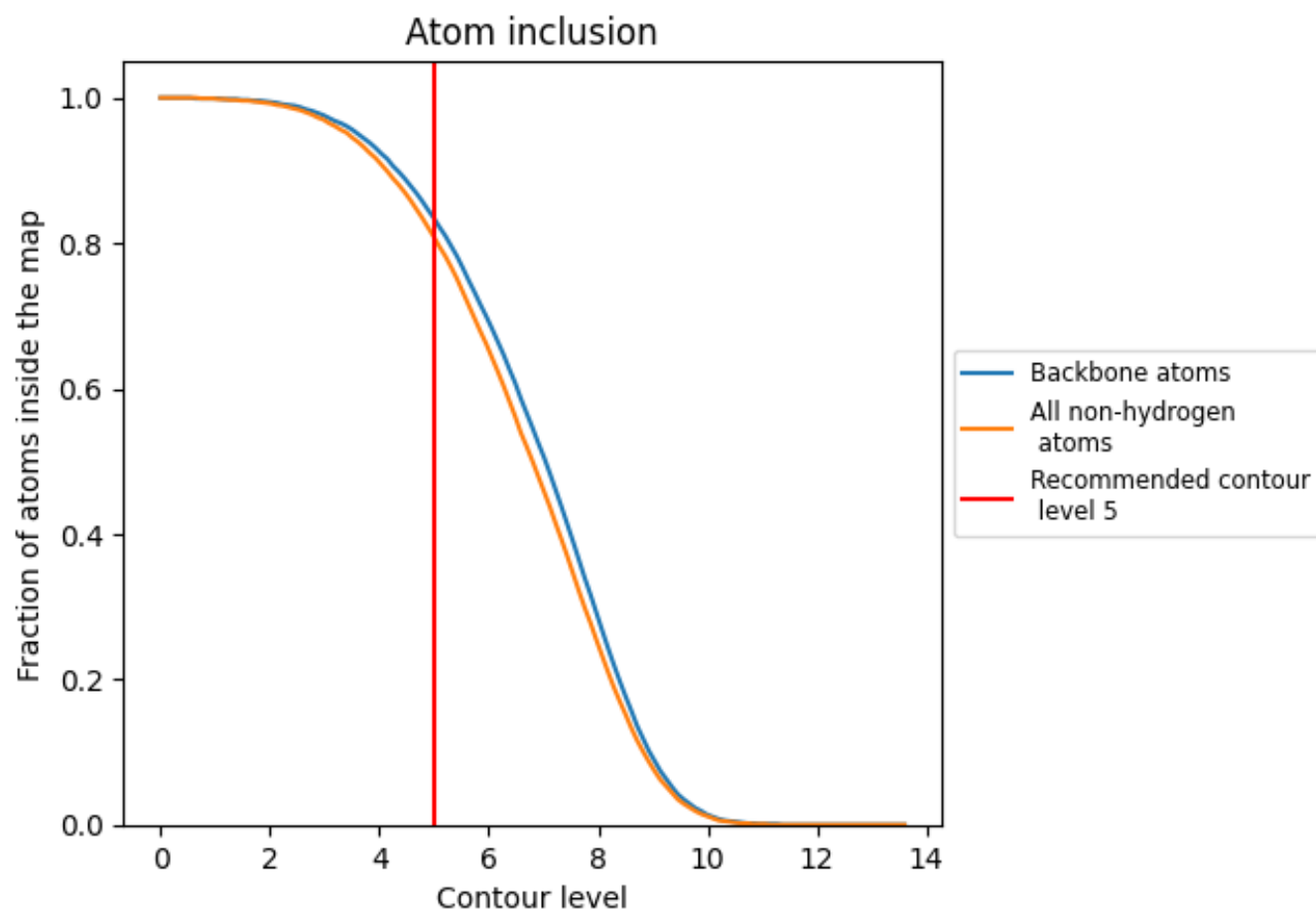
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

8.3 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 (5).







































8.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8080	 0.3410
7	 0.7440	 0.3410
A7	 0.7940	 0.3400
AE	 0.8500	 0.3580
AM	 0.7320	 0.2870
AU	 0.5010	 0.2140
Ac	 0.8440	 0.4140
As	 0.8990	 0.3380
Az	 0.7940	 0.3240
B4	 0.8520	 0.3670
Bw	 0.9430	 0.3710
CA	 0.8520	 0.3760
CH	 0.9430	 0.3910
CO	 0.9330	 0.3750
CV	 0.9200	 0.3590
Cc	 0.9250	 0.3730
i	 0.8760	 0.3990
q	 0.8820	 0.3490
y	 0.8370	 0.3210

