



## wwPDB EM Validation Summary Report ⓘ

Sep 8, 2025 – 02:10 pm BST

PDB ID : 9GNI / pdb\_00009gni  
EMDB ID : EMD-51471  
Title : NONO/SFPQ filament: composite structure  
Authors : Rasmussen, T.; Bottcher, B.  
Deposited on : 2024-09-03  
Resolution : 3.90 Å (reported)  
Based on initial models : 9GLC, 9GLD, 6WMZ

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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 3.90 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 2 unique types of molecules in this entry. The entry contains 74499 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 Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	AC	304	Total	C	N	O	S	0	0
			2527	1561	469	482	15		
1	AE	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	AG	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	BA	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	BC	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	BE	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	BG	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	CA	275	Total	C	N	O	S	0	0
			2251	1405	406	429	11		
1	CC	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	CE	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	CG	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	DA	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	DC	276	Total	C	N	O	S	0	0
			2262	1411	410	430	11		
1	DG	239	Total	C	N	O	S	0	0
			1932	1215	339	371	7		
1	DE	236	Total	C	N	O	S	0	0
			1901	1195	334	365	7		

- Molecule 2 is a protein called Non-POU domain-containing octamer-binding protein isoform X2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	AD	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	AF	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	AH	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	BB	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	BD	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	BF	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	BH	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	CB	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	CD	243	Total	C	N	O	S	0	0
			1979	1246	355	368	10		
2	CF	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	CH	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	DB	244	Total	C	N	O	S	0	0
			1987	1252	356	369	10		
2	DD	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	DH	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	DF	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		

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	2974535	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 ( $e^-/\text{\AA}^2$ )	70	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	130000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	85.165	Depositor
Minimum map value	-51.683	Depositor
Average map value	-0.012	Depositor
Map value standard deviation	1.132	Depositor
Recommended contour level	5	Depositor
Map size (Å)	484.352, 484.352, 484.352	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.946, 0.946, 0.946	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.

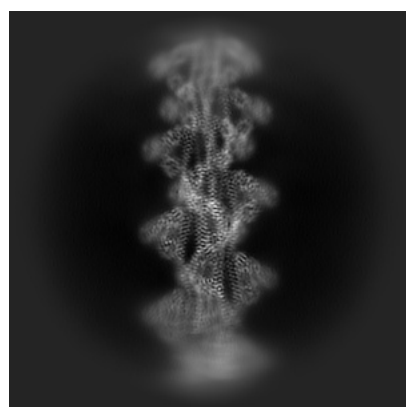
## 5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51471. These allow visual inspection of the internal detail of the map and identification of artifacts.

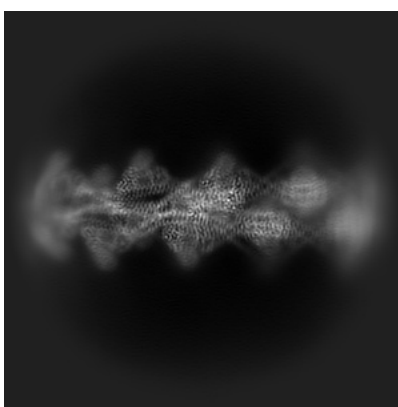
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 5.1 Orthogonal projections [i](#)

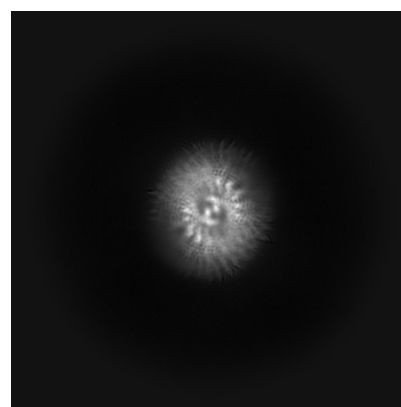
#### 5.1.1 Primary map



X



Y

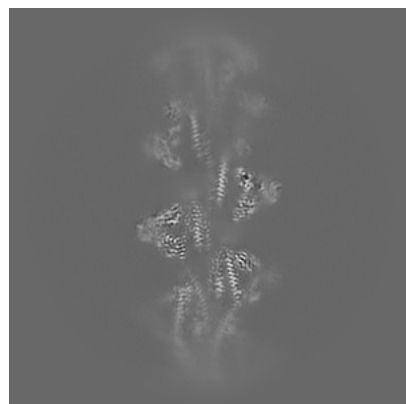


Z

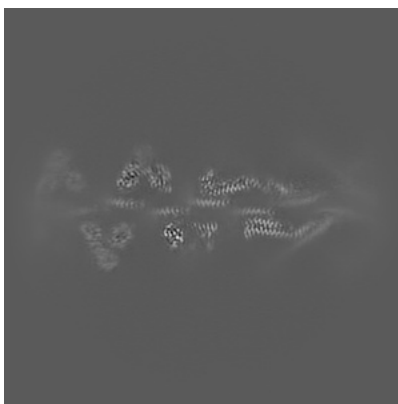
The images above show the map projected in three orthogonal directions.

### 5.2 Central slices [i](#)

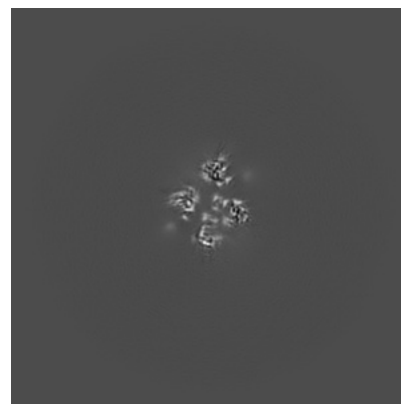
#### 5.2.1 Primary map



X Index: 256



Y Index: 256



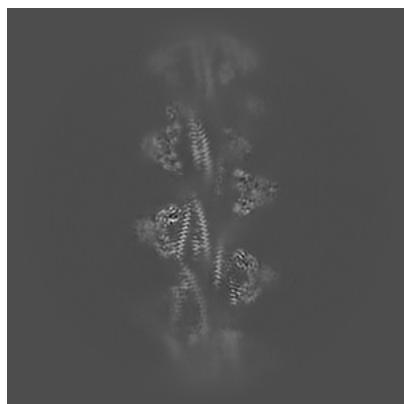
Z Index: 256



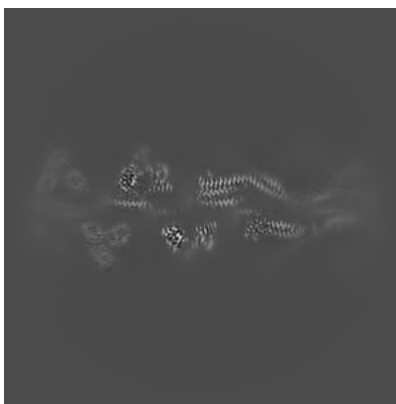
The images above show central slices of the map in three orthogonal directions.

## 5.3 Largest variance slices [i](#)

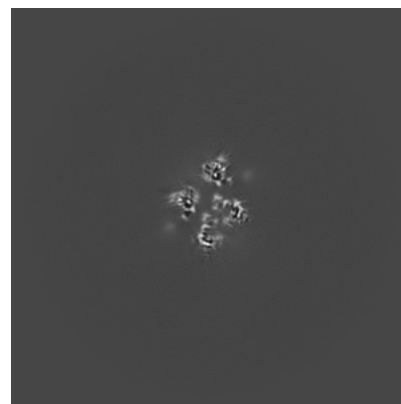
### 5.3.1 Primary map



X Index: 251



Y Index: 260

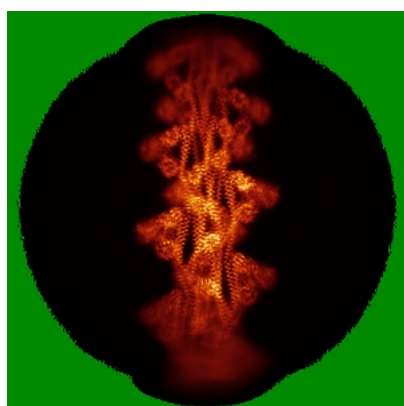


Z Index: 255

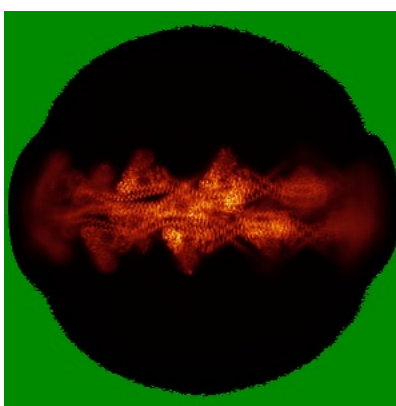
The images above show the largest variance slices of the map in three orthogonal directions.

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

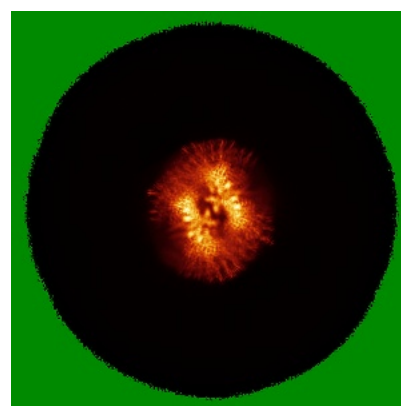
### 5.4.1 Primary map



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



X



Y



Z

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.

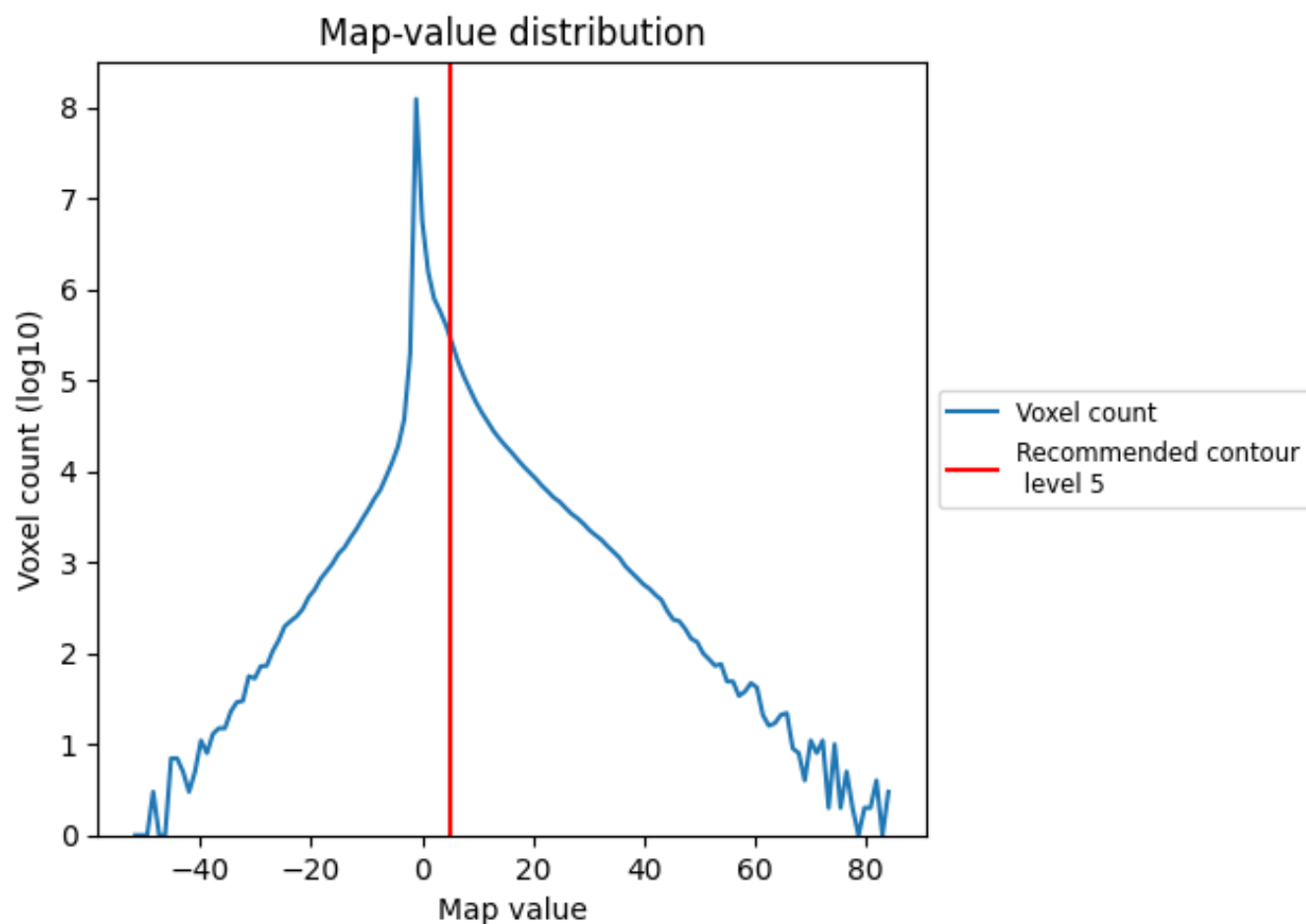
## 5.6 Mask visualisation [i](#)

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

## 6 Map analysis [i](#)

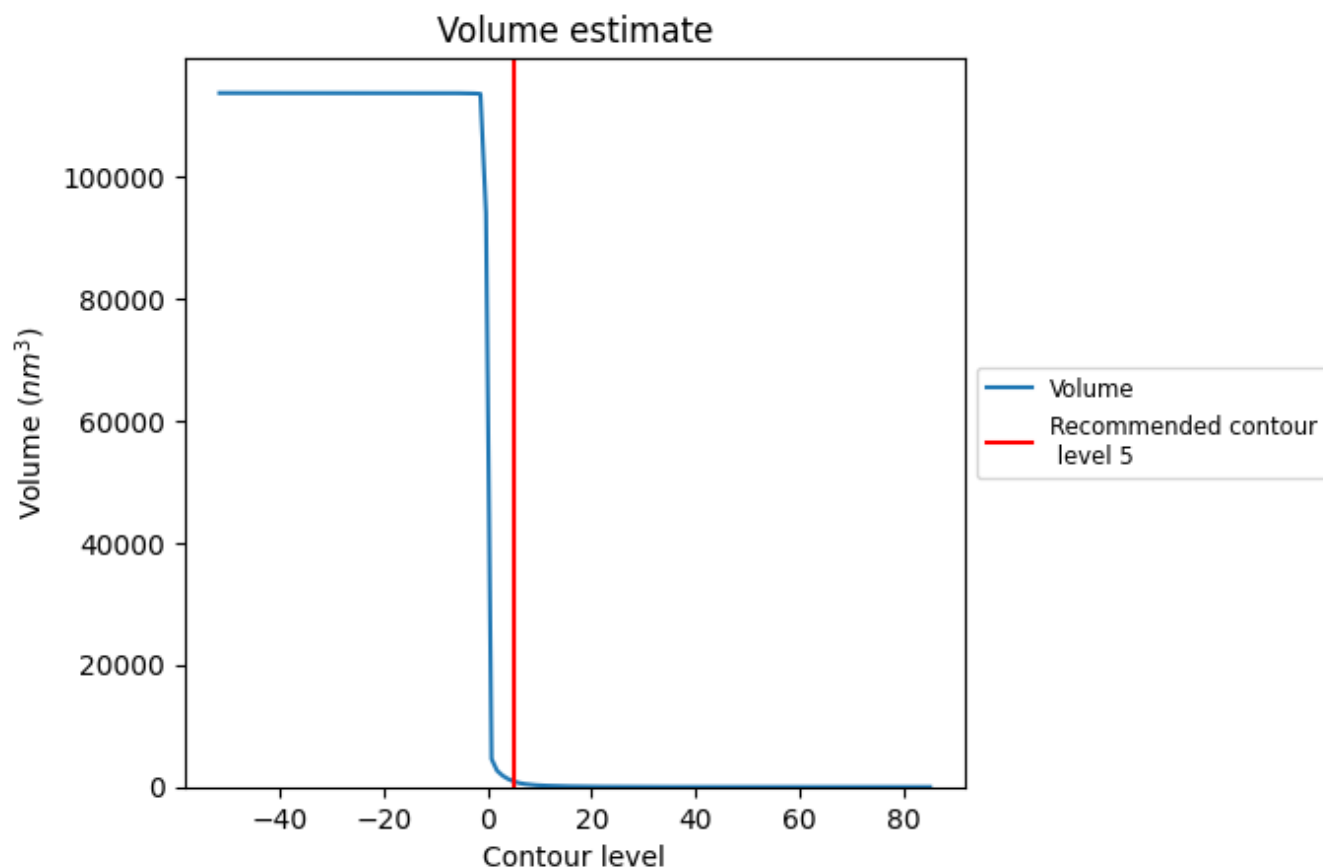
This section contains the results of statistical analysis of the map.

### 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.

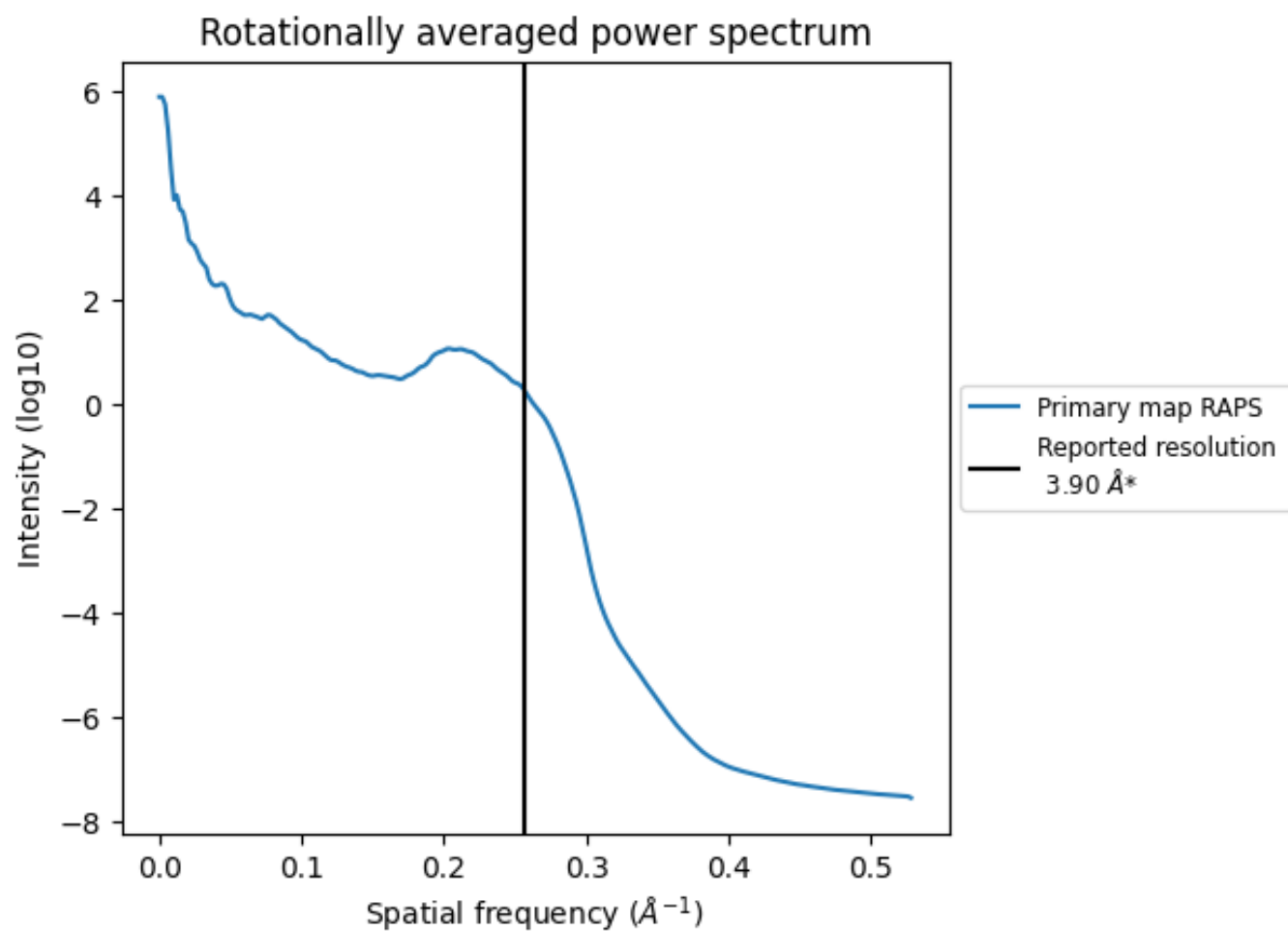
## 6.2 Volume estimate [i](#)



The volume at the recommended contour level is 899 nm<sup>3</sup>; this corresponds to an approximate mass of 812 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 0.256 Å<sup>-1</sup>

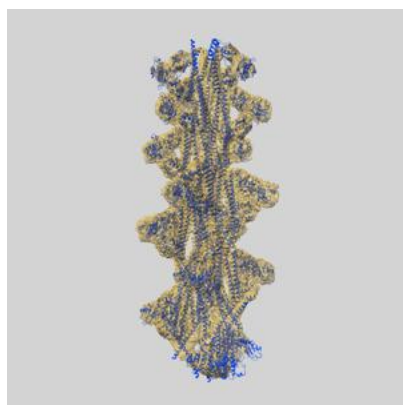
## 7 Fourier-Shell correlation ⓘ

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

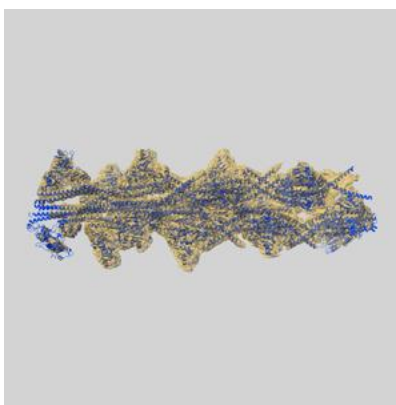
## 8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51471 and PDB model 9GNI. Per-residue inclusion information can be found in section ?? on page ??.

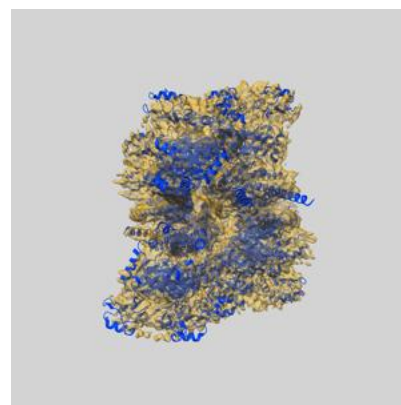
### 8.1 Map-model overlay [i](#)



X



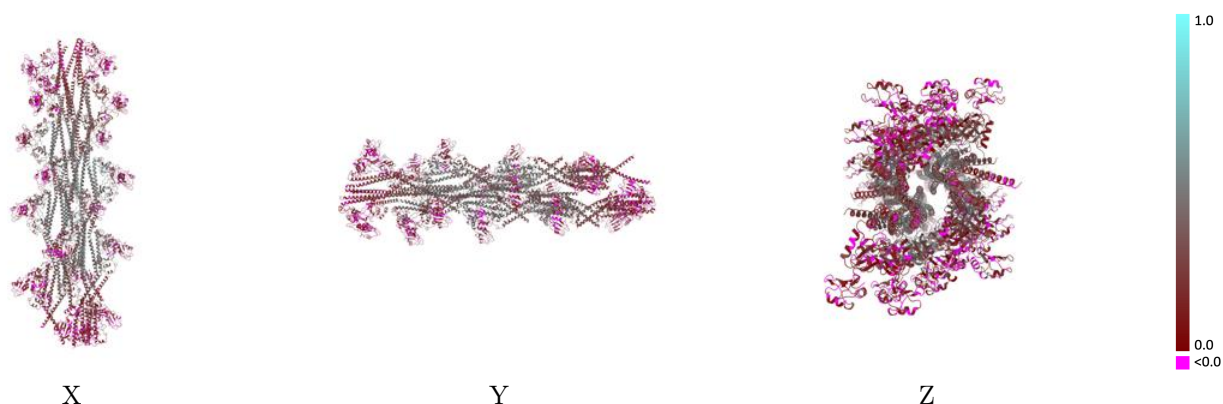
Y



Z

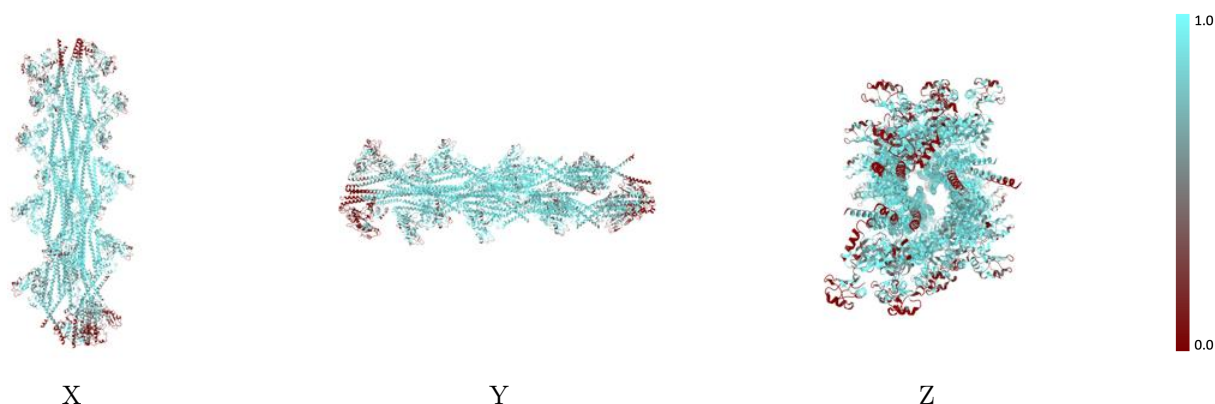
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

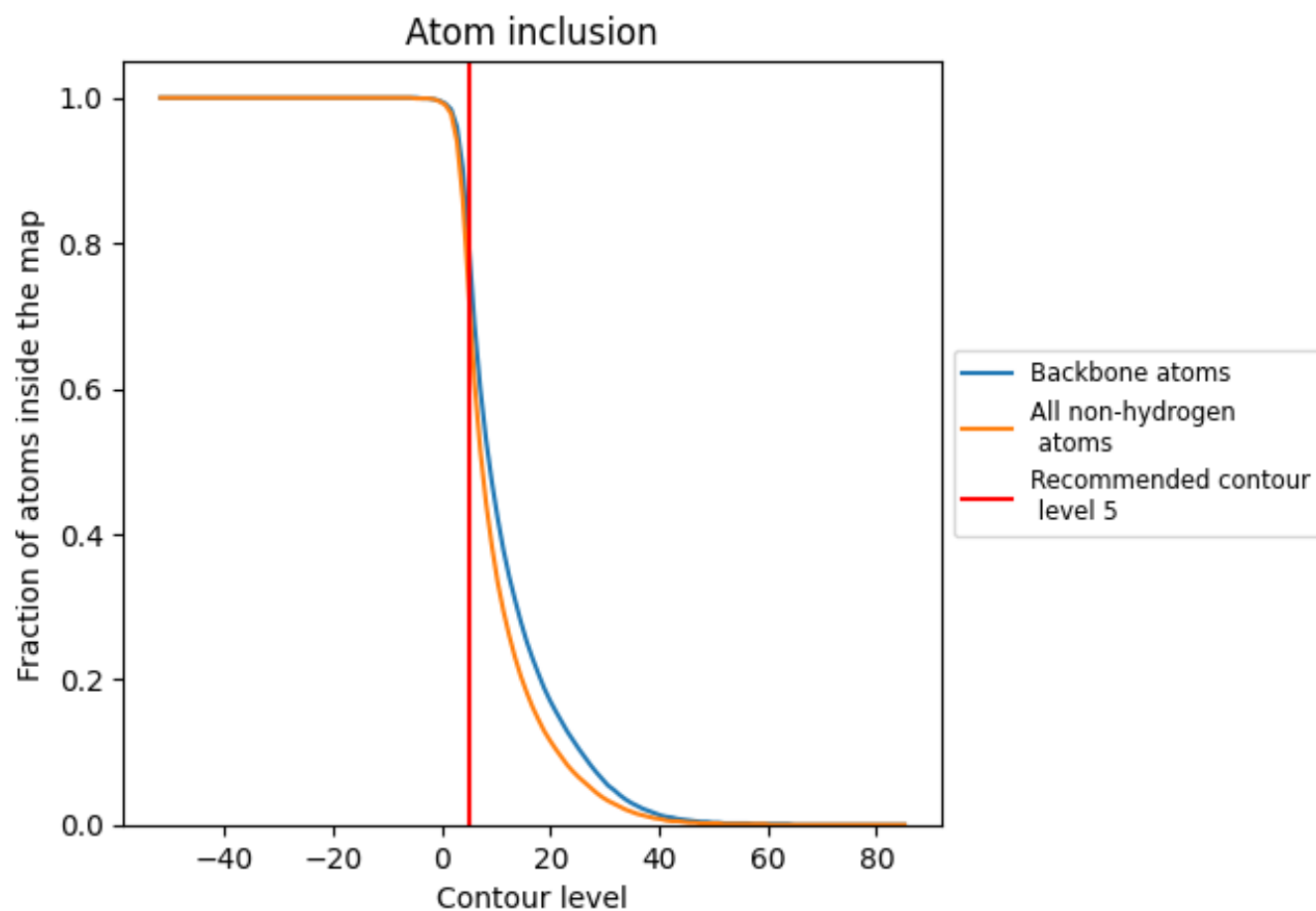
## 8.3 Atom inclusion mapped to coordinate model [i](#)



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, 80% of all backbone atoms, 73% 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	 0.7330	 0.2560
AA	 0.8540	 0.3370
AB	 0.8020	 0.3120
AC	 0.8610	 0.3170
AD	 0.8920	 0.3490
AE	 0.7600	 0.2560
AF	 0.6970	 0.2230
AG	 0.7340	 0.2710
AH	 0.8550	 0.3320
BA	 0.8620	 0.3240
BB	 0.8870	 0.3340
BC	 0.8490	 0.3390
BD	 0.8270	 0.3380
BE	 0.8890	 0.3660
BF	 0.8860	 0.3630
BG	 0.8840	 0.3350
BH	 0.9210	 0.3860
CA	 0.6580	 0.1700
CB	 0.7230	 0.2190
CC	 0.6340	 0.1850
CD	 0.5030	 0.1360
CE	 0.7270	 0.2620
CF	 0.8450	 0.3280
CG	 0.8080	 0.2670
CH	 0.7570	 0.2360
DA	 0.5990	 0.1850
DB	 0.4670	 0.1260
DC	 0.6580	 0.1500
DD	 0.7500	 0.2100
DE	 0.2690	 0.1010
DF	 0.3480	 0.0940
DG	 0.4390	 0.0860
DH	 0.5500	 0.1230

