



## Full wwPDB EM Validation Report ⓘ

Jun 8, 2025 – 12:05 PM EDT

PDB ID : 9MU3 / pdb\_00009mu3  
EMDB ID : EMD-48618  
Title : SaPI1 neck structure  
Authors : Kizziah, J.L.; Dokland, T.  
Deposited on : 2025-01-13  
Resolution : 3.14 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](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.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
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) : 2.43.1

# 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 3.14 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	110	
1	B	110	
2	C	100	
3	D	127	
4	E	193	
4	F	193	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4822 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 Head-tail connector protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	96	Total	C	N	O	S	0	0
			780	489	128	159	4		
1	B	96	Total	C	N	O	S	0	0
			780	489	128	159	4		

- Molecule 2 is a protein called adaptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	100	Total	C	N	O	S	0	0
			832	527	145	158	2		

- Molecule 3 is a protein called DUF3168 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	127	Total	C	N	O	S	0	0
			1037	656	163	214	4		


- Molecule 4 is a protein called Major tail protein.

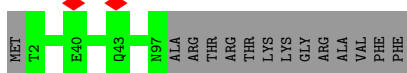
Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	162	Total	C	N	O	S	0	0
			1288	809	214	260	5		
4	F	12	Total	C	N	O		0	0
			105	66	18	21			

### 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.

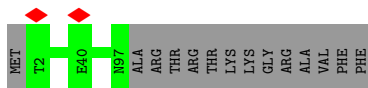
- Molecule 1: Head-tail connector protein

Chain A:  87% 13%



- Molecule 1: Head-tail connector protein

Chain B:  87% 13%



- Molecule 2: adaptor

Chain C:  100%


There are no outlier residues recorded for this chain.

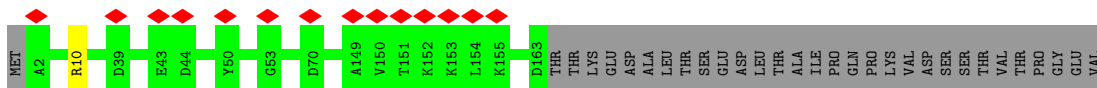
- Molecule 3: DUF3168 domain-containing protein

Chain D:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: Major tail protein

Chain E:  7% 83% 16%



- Molecule 4: Major tail protein

Chain F:  6% 94%

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

PRO	GLY
GLY	GLU
GLU	VAL
VAL	

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23206	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 ( $e^-/\text{\AA}^2$ )	35.26	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	6.342	Depositor
Minimum map value	-3.431	Depositor
Average map value	-0.018	Depositor
Map value standard deviation	0.257	Depositor
Recommended contour level	1	Depositor
Map size ( $\text{\AA}$ )	319.2, 319.2, 319.2	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.33, 1.33, 1.33	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	0.28	0/789	0.63	0/1058
1	B	0.28	0/789	0.66	0/1058
2	C	0.31	0/847	0.56	0/1145
3	D	0.30	0/1061	0.59	0/1442
4	E	0.30	0/1314	0.64	0/1764
4	F	0.30	0/107	0.47	0/143
All	All	0.30	0/4907	0.62	0/6610

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	E	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	E	10	ARG	Sidechain

### 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	780	0	770	0	0
1	B	780	0	770	0	0
2	C	832	0	841	0	0
3	D	1037	0	984	0	0
4	E	1288	0	1210	0	0
4	F	105	0	94	0	0
All	All	4822	0	4669	0	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 0.

There are no clashes within the asymmetric unit.

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	94/110 (86%)	91 (97%)	3 (3%)	0	100	100
1	B	94/110 (86%)	91 (97%)	3 (3%)	0	100	100
2	C	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
3	D	125/127 (98%)	124 (99%)	1 (1%)	0	100	100
4	E	160/193 (83%)	155 (97%)	5 (3%)	0	100	100
4	F	10/193 (5%)	10 (100%)	0	0	100	100
All	All	581/833 (70%)	563 (97%)	18 (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	86/97 (89%)	86 (100%)	0	100	100
1	B	86/97 (89%)	86 (100%)	0	100	100
2	C	95/95 (100%)	95 (100%)	0	100	100
3	D	121/121 (100%)	121 (100%)	0	100	100
4	E	132/160 (82%)	132 (100%)	0	100	100
4	F	11/160 (7%)	11 (100%)	0	100	100
All	All	531/730 (73%)	531 (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 (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	21	GLN
1	B	94	ASN
2	C	72	HIS
3	D	74	HIS
3	D	102	ASN
3	D	105	GLN
4	E	136	ASN

### 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 ⓘ

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.

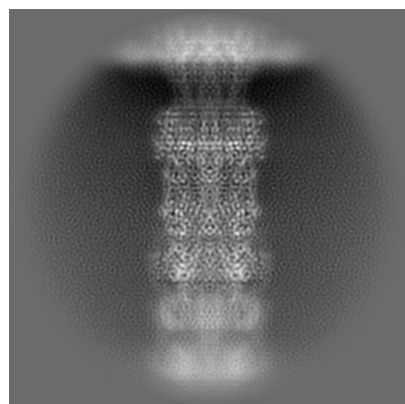
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48618. These allow visual inspection of the internal detail of the map and identification of artifacts.

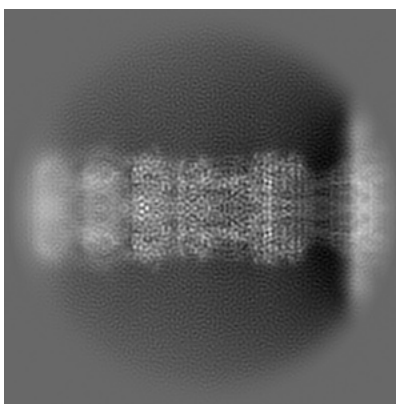
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

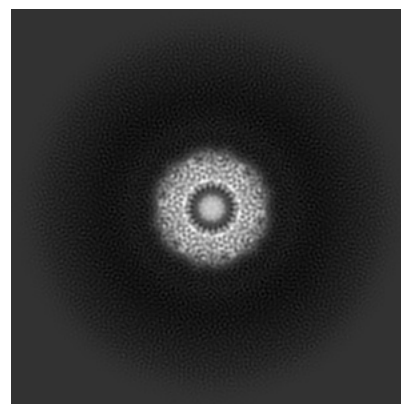
#### 6.1.1 Primary map



X

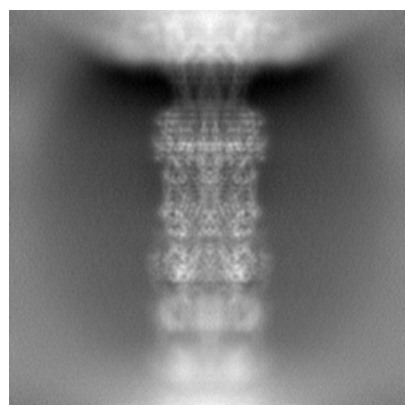


Y

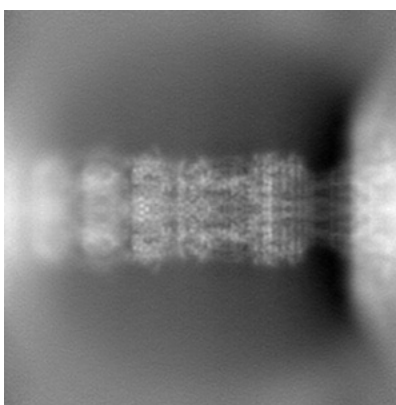


Z

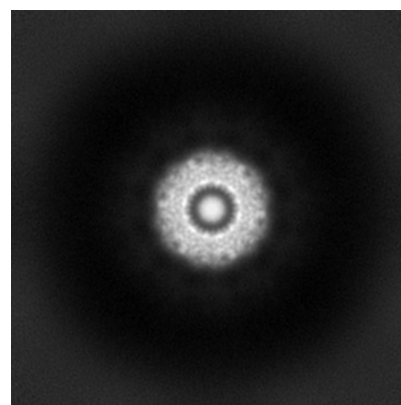
#### 6.1.2 Raw map



X



Y

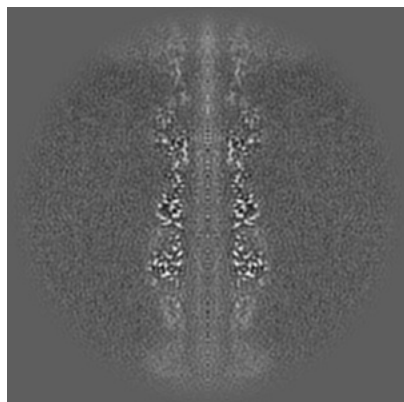


Z

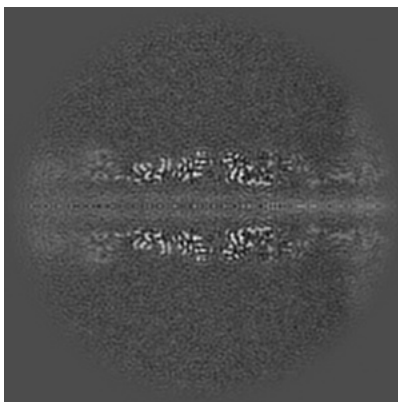
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

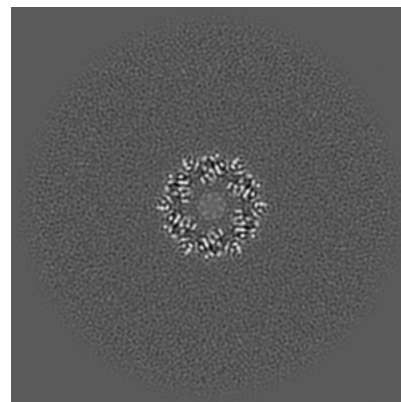
### 6.2.1 Primary map



X Index: 120

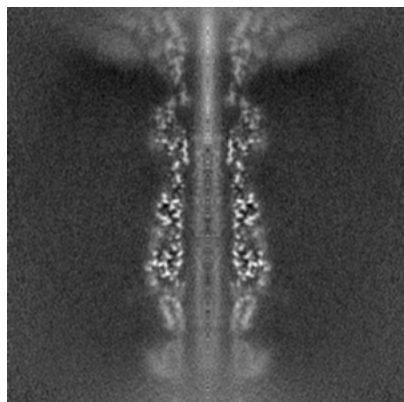


Y Index: 120

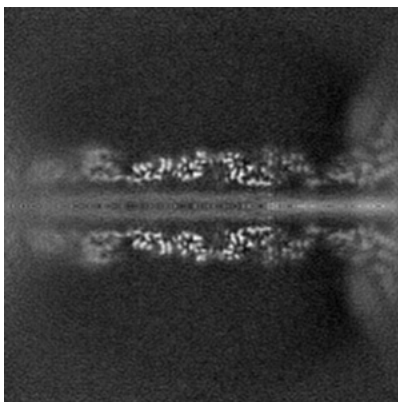


Z Index: 120

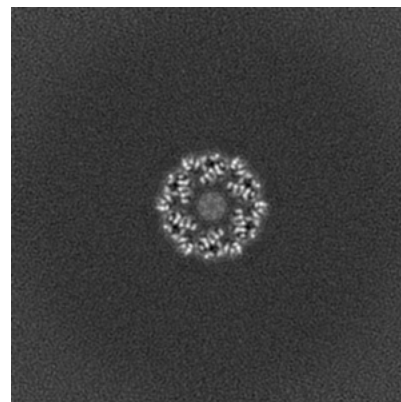
### 6.2.2 Raw map



X Index: 120



Y Index: 120

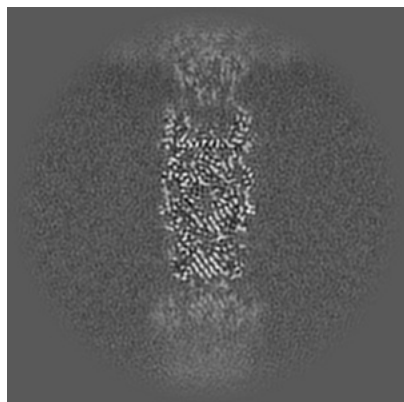


Z Index: 120

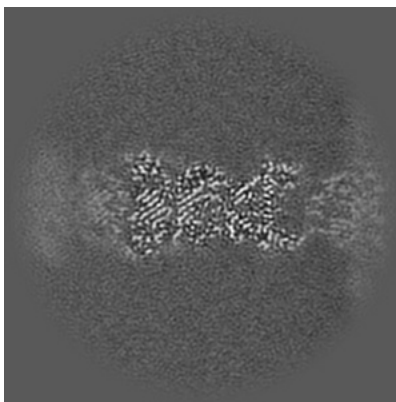
The images above show central slices of the map in three orthogonal directions.

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

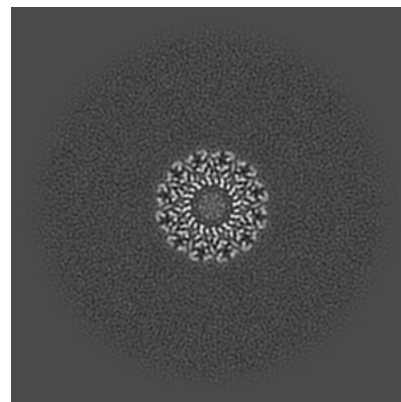
### 6.3.1 Primary map



X Index: 104

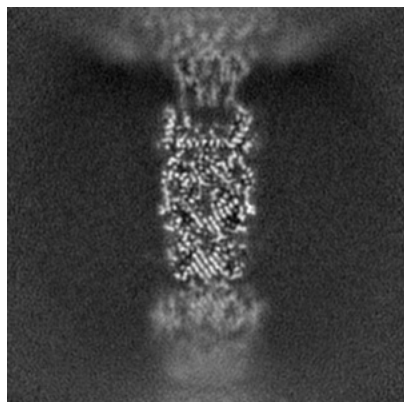


Y Index: 104

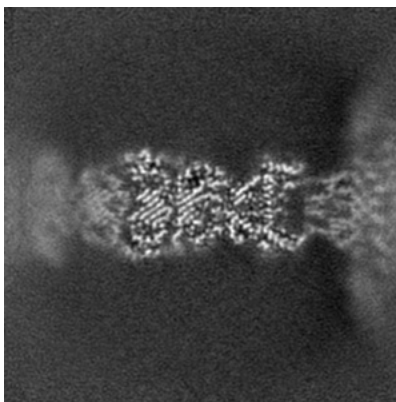


Z Index: 159

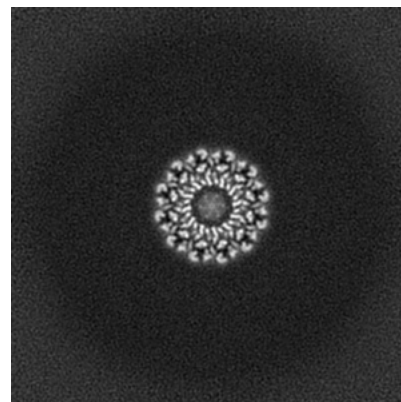
### 6.3.2 Raw map



X Index: 104



Y Index: 104



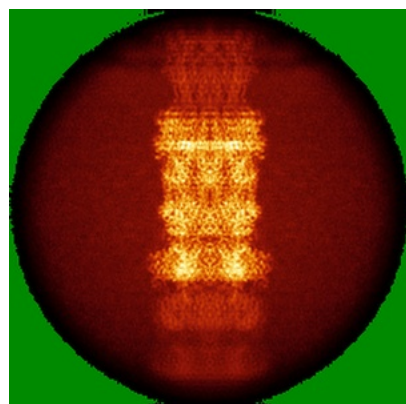
Z Index: 159

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

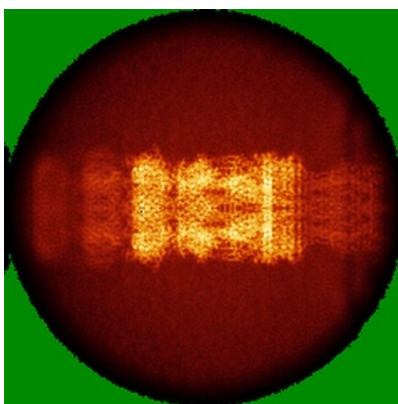


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

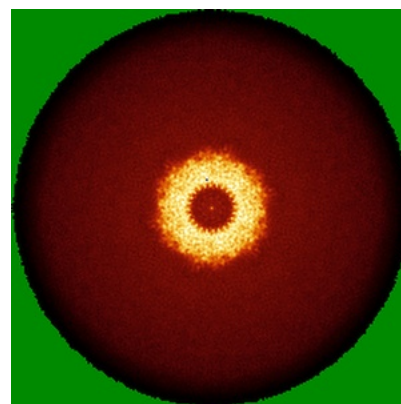
### 6.4.1 Primary map



X

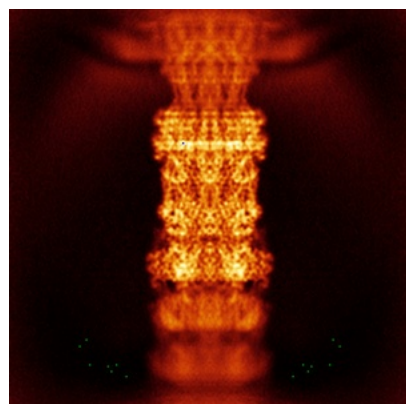


Y

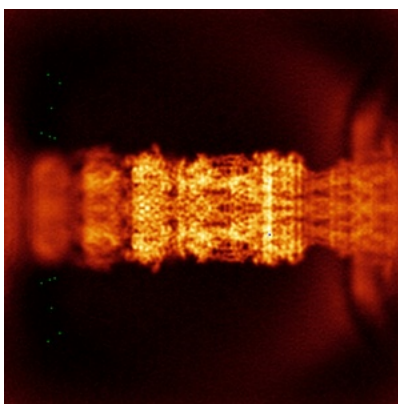


Z

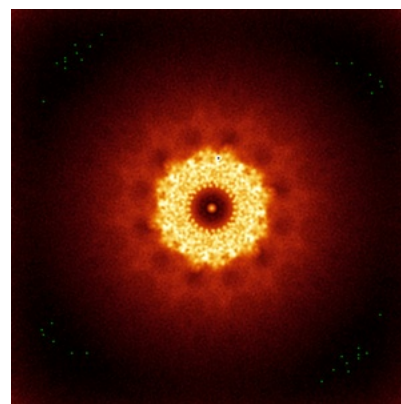
### 6.4.2 Raw map



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.

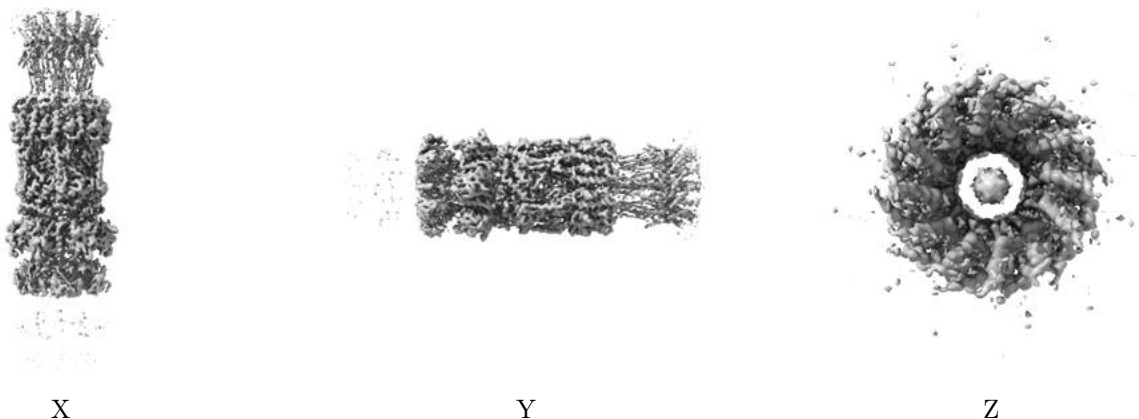
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. 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.

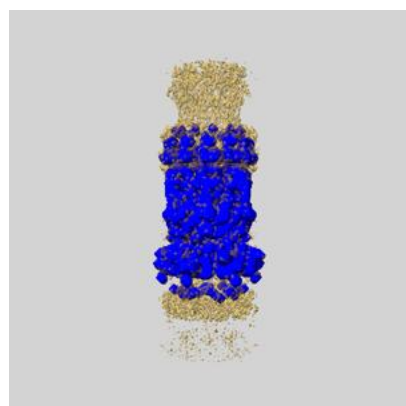
## 6.6 Mask visualisation [i](#)

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

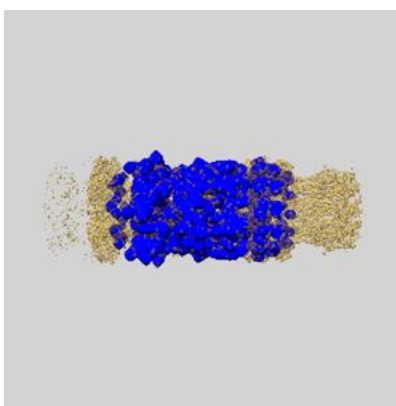
A mask typically either:

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

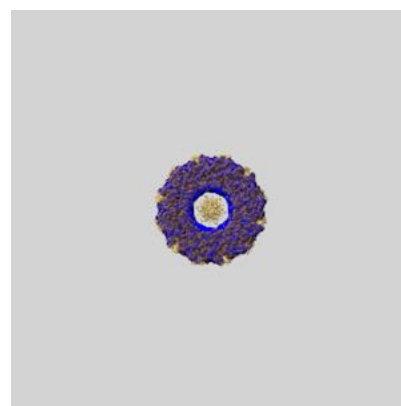
### 6.6.1 emd\_48618\_msk\_1.map [i](#)



X



Y



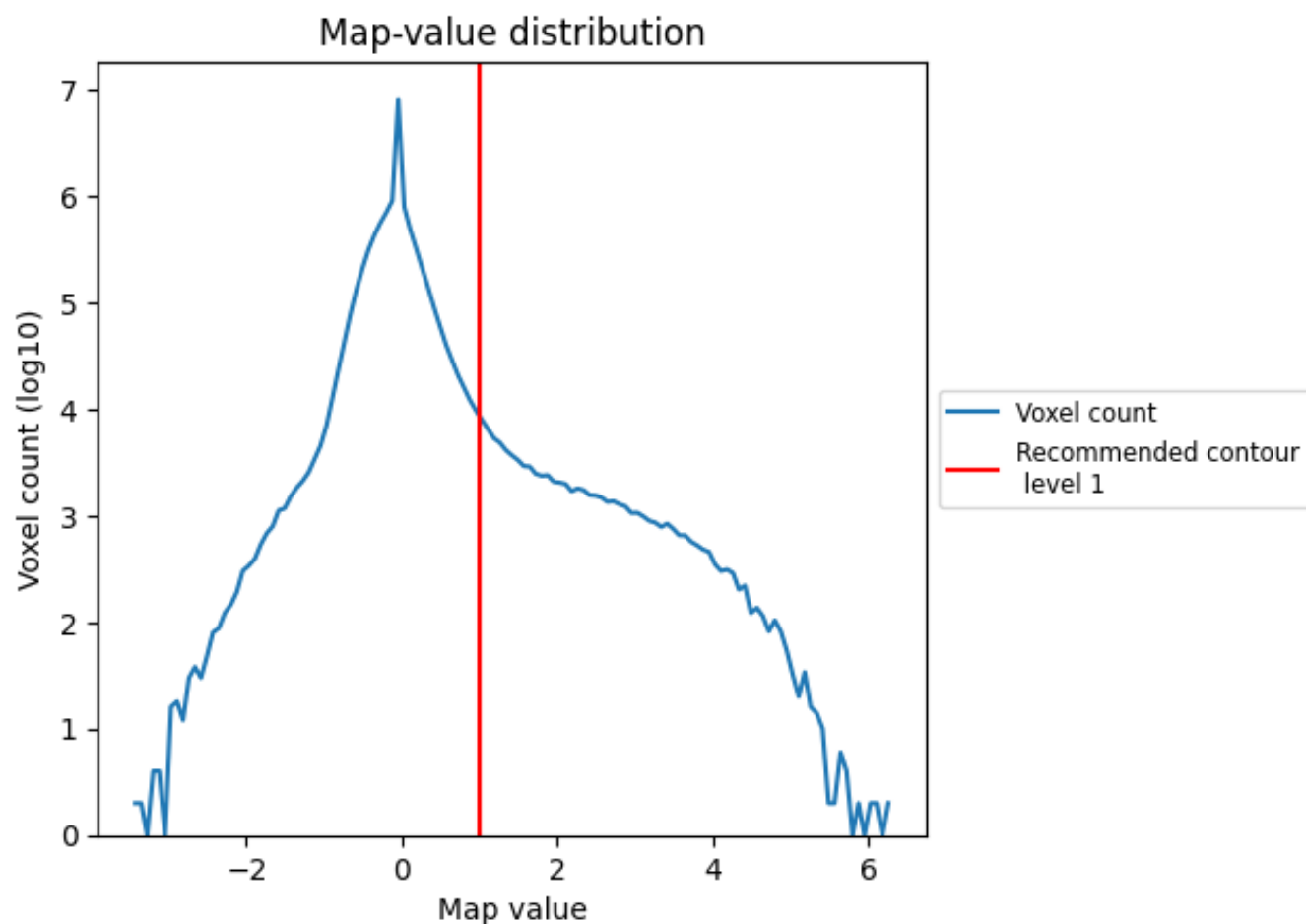
Z



## 7 Map analysis [i](#)

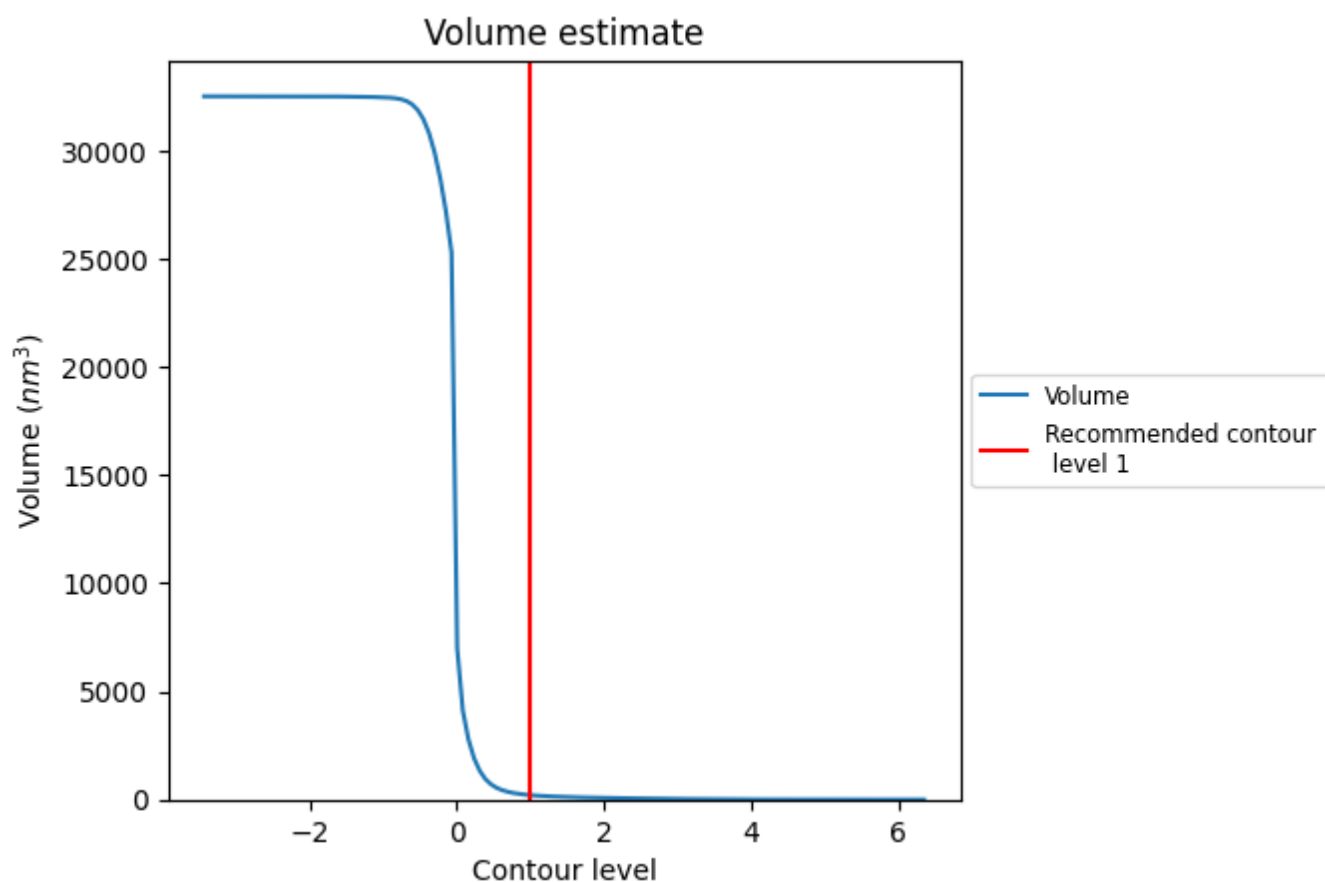
This section contains the results of statistical analysis of the map.

### 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.

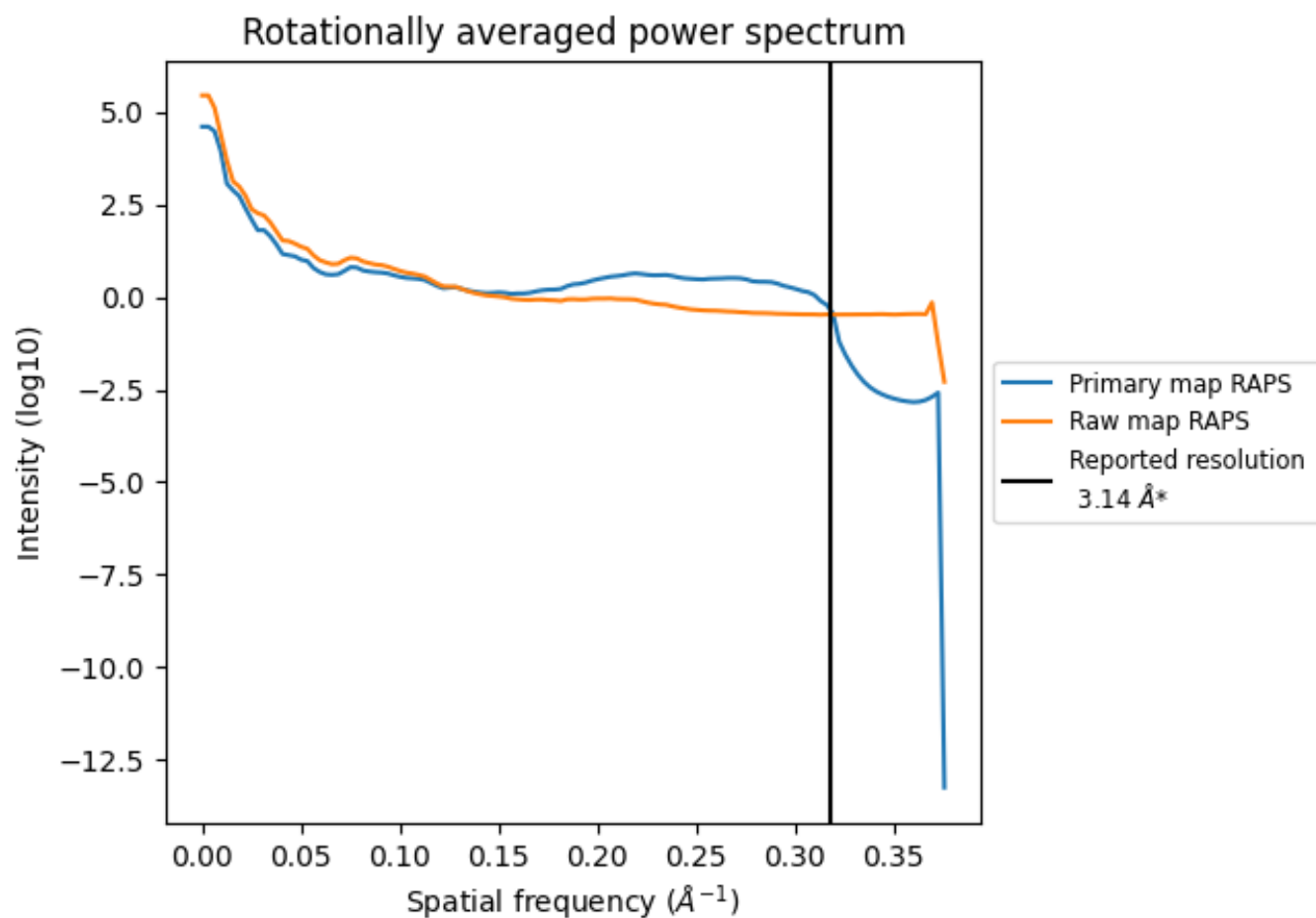
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 204 nm<sup>3</sup>; this corresponds to an approximate mass of 184 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 ⓘ

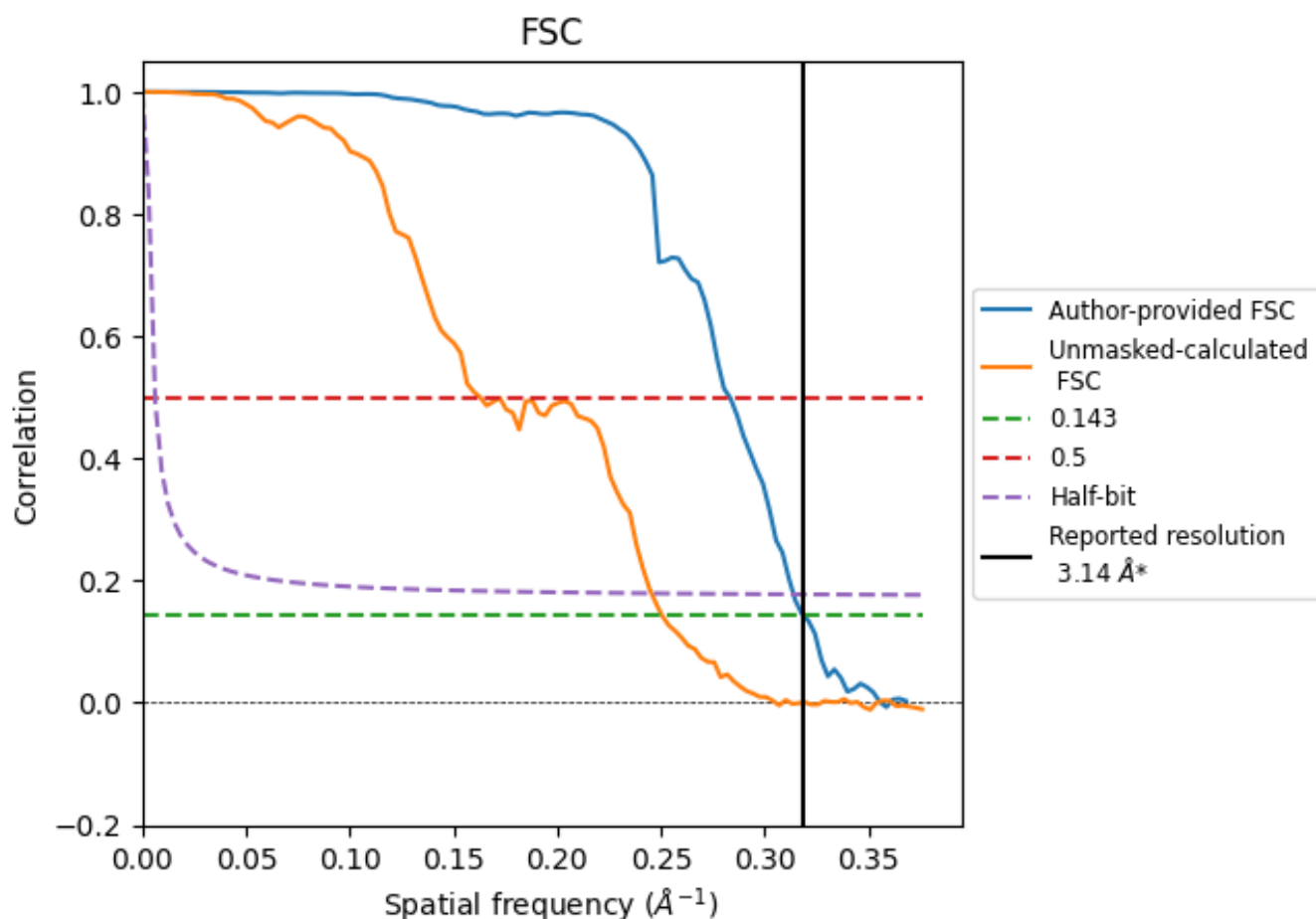


\*Reported resolution corresponds to spatial frequency of 0.318 Å<sup>-1</sup>

## 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 0.318  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.14	-	-
Author-provided FSC curve	3.14	3.53	3.18
Unmasked-calculated*	3.99	6.14	4.07

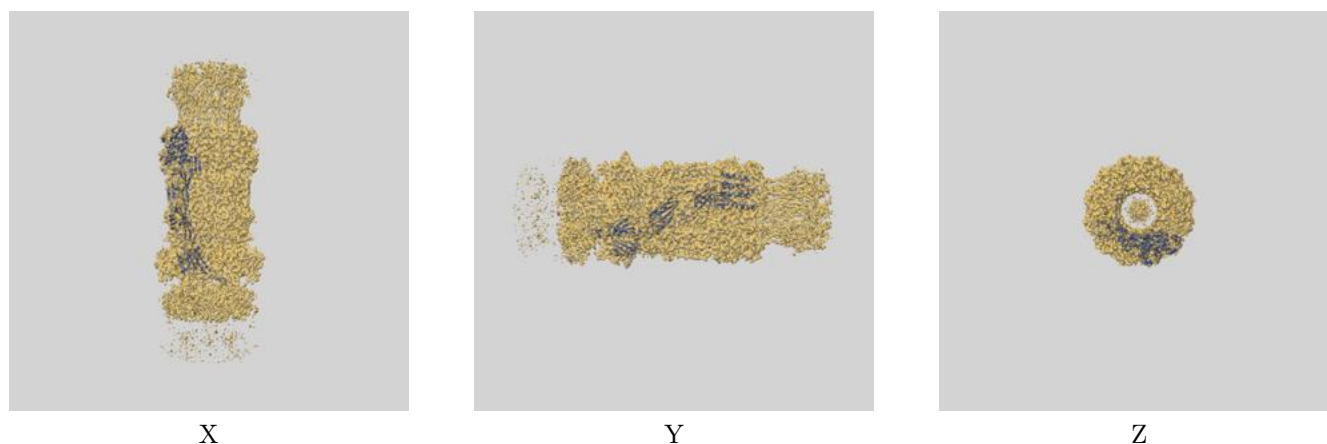
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.99 differs from the reported value 3.14 by more than 10 %

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

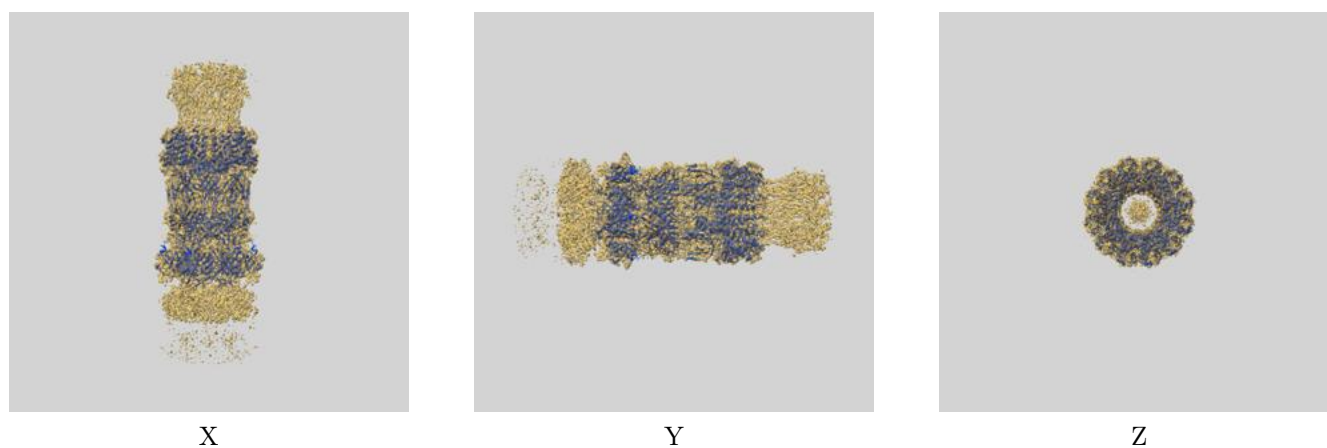
This section contains information regarding the fit between EMDB map EMD-48618 and PDB model 9MU3. Per-residue inclusion information can be found in section 3 on page 4.

### 9.1 Map-model overlays

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



#### 9.1.2 Map-model assembly overlay [i](#)



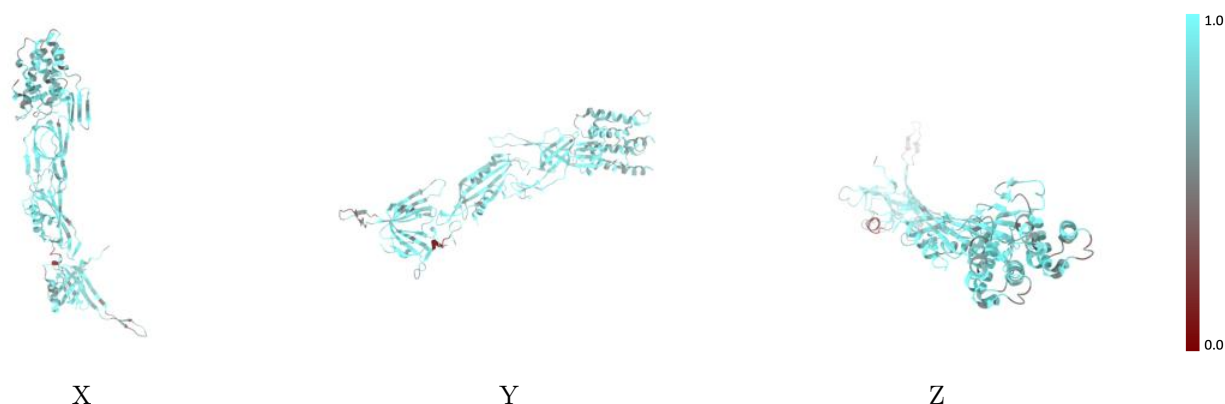
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



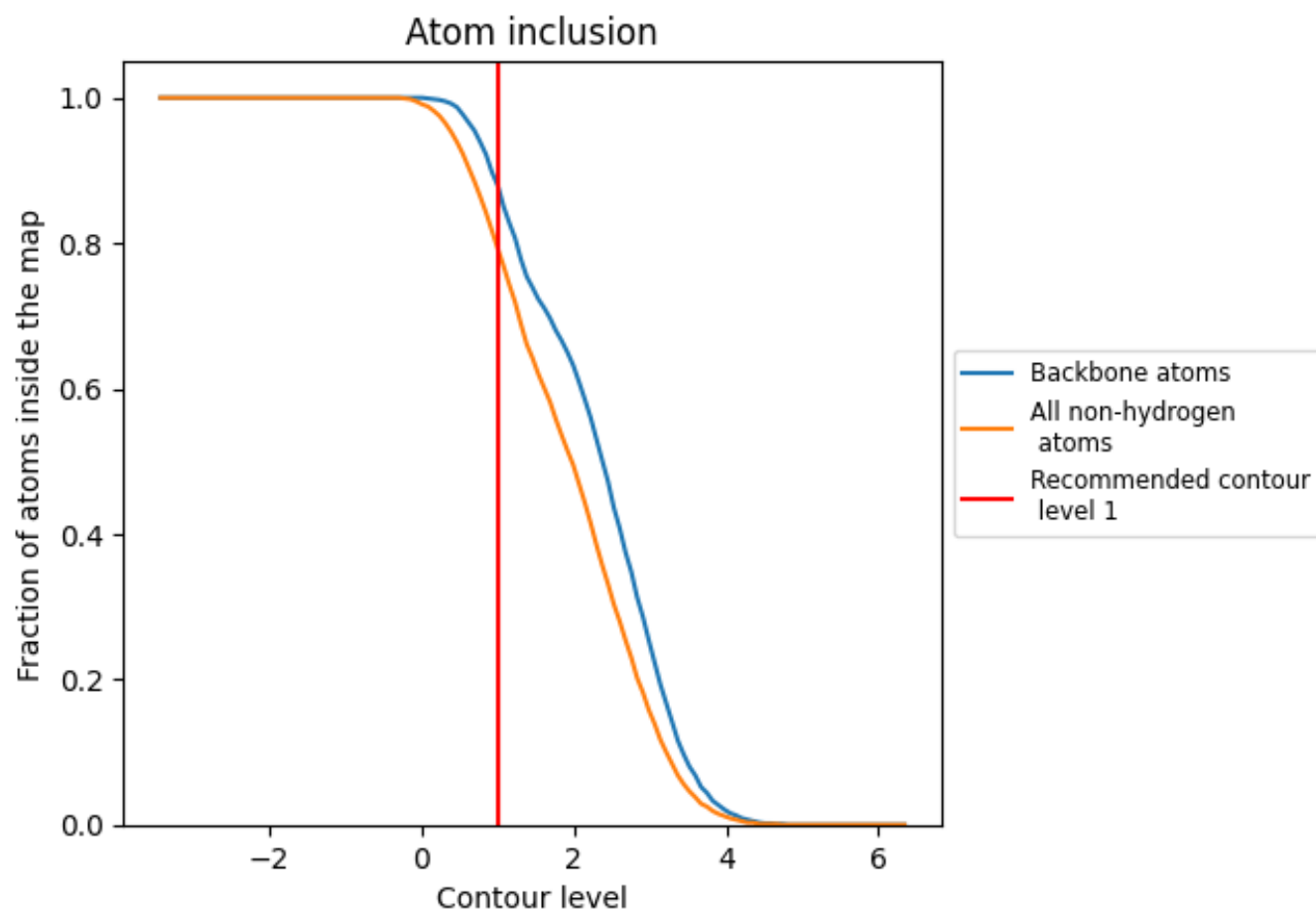
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 79% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.7920	<div><div></div></div> 0.5480
A	<div><div></div></div> 0.7480	<div><div></div></div> 0.5400
B	<div><div></div></div> 0.7780	<div><div></div></div> 0.5460
C	<div><div></div></div> 0.8490	<div><div></div></div> 0.5660
D	<div><div></div></div> 0.8400	<div><div></div></div> 0.5630
E	<div><div></div></div> 0.7490	<div><div></div></div> 0.5320
F	<div><div></div></div> 0.8140	<div><div></div></div> 0.5310

1.0

0.0

<0.0