



# wwPDB EM Validation Summary Report ⓘ

Apr 28, 2026 – 07:15 pm BST

PDB ID : 9HMV / pdb\_00009hmv  
EMDB ID : EMD-52298  
Title : Cryo-EM structure of SA2-SCC1 complex at 2.9 angstrom  
Authors : Yu, J.; Schmidt, S.; Botto, M.; Boland, A.  
Deposited on : 2024-12-09  
Resolution : 2.90 Å(reported)  
Based on initial model : 4PJU

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.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

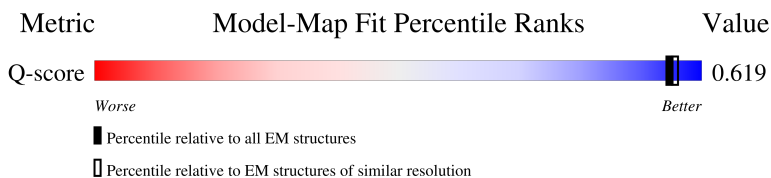
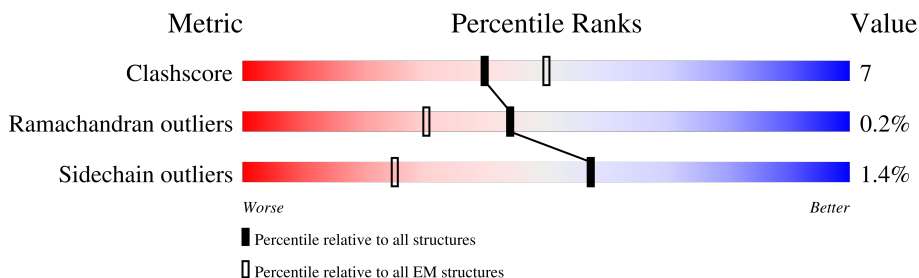
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*



The reported resolution of this entry is 2.90 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	13054 ( 2.40 - 3.40 )

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	1271	 61% 13% 26%
2	B	241	 24% 6% 70%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8234 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 Cohesin subunit SA-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	940	Total	C	N	O	S	0	0
			7647	4868	1288	1436	55		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1232	SER	-	expression tag	UNP Q8N3U4
A	1233	SER	-	expression tag	UNP Q8N3U4
A	1234	LEU	-	expression tag	UNP Q8N3U4
A	1235	ALA	-	expression tag	UNP Q8N3U4
A	1236	GLU	-	expression tag	UNP Q8N3U4
A	1237	GLU	-	expression tag	UNP Q8N3U4
A	1238	ASN	-	expression tag	UNP Q8N3U4
A	1239	LEU	-	expression tag	UNP Q8N3U4
A	1240	TYR	-	expression tag	UNP Q8N3U4
A	1241	PHE	-	expression tag	UNP Q8N3U4
A	1242	GLN	-	expression tag	UNP Q8N3U4
A	1243	SER	-	expression tag	UNP Q8N3U4
A	1244	TRP	-	expression tag	UNP Q8N3U4
A	1245	SER	-	expression tag	UNP Q8N3U4
A	1246	HIS	-	expression tag	UNP Q8N3U4
A	1247	PRO	-	expression tag	UNP Q8N3U4
A	1248	GLN	-	expression tag	UNP Q8N3U4
A	1249	PHE	-	expression tag	UNP Q8N3U4
A	1250	GLU	-	expression tag	UNP Q8N3U4
A	1251	LYS	-	expression tag	UNP Q8N3U4
A	1252	GLY	-	expression tag	UNP Q8N3U4
A	1253	GLY	-	expression tag	UNP Q8N3U4
A	1254	GLY	-	expression tag	UNP Q8N3U4
A	1255	SER	-	expression tag	UNP Q8N3U4
A	1256	GLY	-	expression tag	UNP Q8N3U4
A	1257	GLY	-	expression tag	UNP Q8N3U4
A	1258	GLY	-	expression tag	UNP Q8N3U4
A	1259	SER	-	expression tag	UNP Q8N3U4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1260	GLY	-	expression tag	UNP Q8N3U4
A	1261	GLY	-	expression tag	UNP Q8N3U4
A	1262	GLY	-	expression tag	UNP Q8N3U4
A	1263	SER	-	expression tag	UNP Q8N3U4
A	1264	TRP	-	expression tag	UNP Q8N3U4
A	1265	SER	-	expression tag	UNP Q8N3U4
A	1266	HIS	-	expression tag	UNP Q8N3U4
A	1267	PRO	-	expression tag	UNP Q8N3U4
A	1268	GLN	-	expression tag	UNP Q8N3U4
A	1269	PHE	-	expression tag	UNP Q8N3U4
A	1270	GLU	-	expression tag	UNP Q8N3U4
A	1271	LYS	-	expression tag	UNP Q8N3U4

- Molecule 2 is a protein called Double-strand-break repair protein rad21 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	73	Total	C	N	O	S	0	0
			587	379	99	106	3		



PRO	ASP	PHE	PHE	ASP	PRO	ALA	SER	ILE	MET	ASP	GLU	SER	VAL	LEU	GLY	VAL	SER	MET	PHE	SER	SER	LEU	ALA	GLU	GLU	ASN	LEU	TYR	PHE	GLN	SER	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS	GLY	GLY	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS
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● Molecule 2: Double-strand-break repair protein rad21 homolog



ASP	ILE	THR	VAL	PHE	LYS	GLU	THR	LYS	ALA	LYS	ARG	LYS	R322	V326	V329	D333	S334	K335	T336	I337	R338	D343	A354	P355	L360	W363	V369	K387	T394	PRO	LEU	VAL	PRO	GLU	ASP	LEU	ARG	LYS	LYS	ARG	GLY	GLY	GLY	GLY	ALA	PRO	ASP	ASN	LEU	ASP	GLY
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PHE	LEU	LYS	GLU	PHE	ALA	GLN	ASN	PRO	GLU	VAL	PRO	ARG	GLU	VAL	GLU	ASP	GLN	GLN	HIS	GLN	GLN	MET	ARG	ASP	VAL	ILE	ASP	PRO	ILE	GLU	GLU	PRO	SER	PRO	ARG	ASN	LEU	GLN	GLU	SER	VAL	MET	ILE	PRO	GLU	ALA	SER	ARG	THR	LEU	LEU	PRO	ILE	GLU	LYS	GLY	SER	GLU	PRO	PRO	PRO	PRO	GLN	ASP
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VAL	LYS	ARG	GLU	GLU	ASP	GLN	ILE	ASP	PRO	GLU	PRO	MET	GLN	GLN	VAL	GLU	MET	ILE	PRO	PRO	VAL	LEU	LEU	PRO	GLU	GLU	PRO	ILE	ILE	CYS	GLN	LEU	ILE	PRO	GLU	LEU	LEU	GLU	LEU	PRO	GLU	LYS	GLY	LYS	GLU	LYS	GLU	LYS	GLU	GLU	LYS	GLY	GLN	ASP
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ASP	GLU	GLU	GLU	ASP	GLU	ASP	ALA	SER	GLY	GLY	ASP	GLN	ASP
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	768540	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	24.758	Depositor
Minimum map value	-0.826	Depositor
Average map value	-0.024	Depositor
Map value standard deviation	0.311	Depositor
Recommended contour level	4.5	Depositor
Map size (Å)	360.96002, 360.96002, 360.96002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9024001, 0.9024001, 0.9024001	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	0.95	0/7782	1.18	2/10489 (0.0%)
2	B	0.96	0/597	1.20	1/807 (0.1%)
All	All	0.95	0/8379	1.19	3/11296 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	193	ASP	CA-CB-CG	6.65	119.25	112.60
1	A	1035	GLU	N-CA-C	-5.94	105.79	113.16
2	B	343	ASP	CA-CB-CG	5.06	117.66	112.60

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	7647	0	7661	113	0
2	B	587	0	626	8	0
All	All	8234	0	8287	118	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 7.

The worst 5 of 118 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:224:MET:HB3	1:A:311:GLU:HG3	1.56	0.87
1:A:159:TYR:CZ	1:A:162:THR:HG23	2.20	0.75
1:A:128:LYS:HD2	1:A:153:ASP:HB2	1.69	0.74
1:A:159:TYR:CE1	1:A:162:THR:HG23	2.27	0.69
1:A:316:MET:HG3	1:A:354:LEU:HD21	1.77	0.67

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	932/1271 (73%)	902 (97%)	28 (3%)	2 (0%)	43	72
2	B	71/241 (30%)	67 (94%)	4 (6%)	0	100	100
All	All	1003/1512 (66%)	969 (97%)	32 (3%)	2 (0%)	44	72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1037	VAL
1	A	752	SER

### 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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	848/1136 (75%)	837 (99%)	11 (1%)	61 86
2	B	68/224 (30%)	66 (97%)	2 (3%)	37 71
All	All	916/1360 (67%)	903 (99%)	13 (1%)	57 85

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	779	VAL
1	A	794	ILE
2	B	387	LYS
1	A	1014	ASP
2	B	326	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	786	GLN
1	A	928	ASN
1	A	909	GLN
1	A	932	GLN
1	A	286	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.

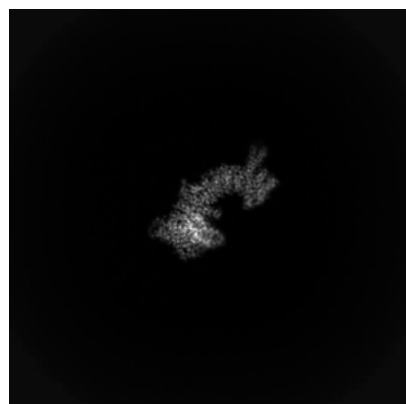
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52298. These allow visual inspection of the internal detail of the map and identification of artifacts.

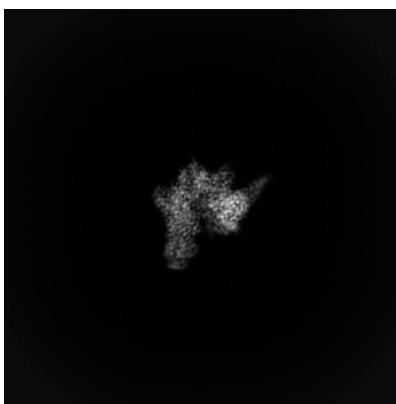
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

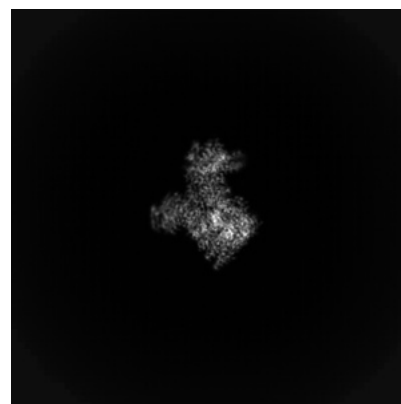
#### 6.1.1 Primary map



X

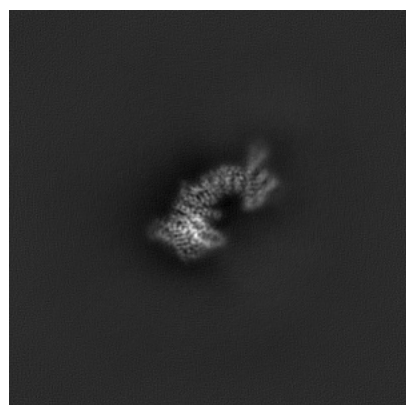


Y

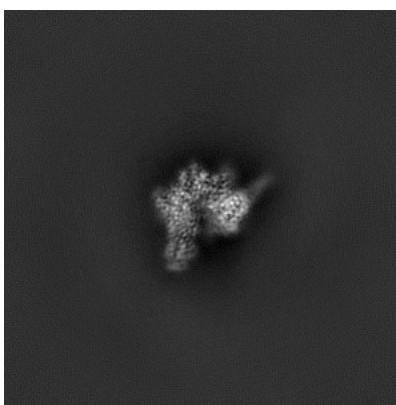


Z

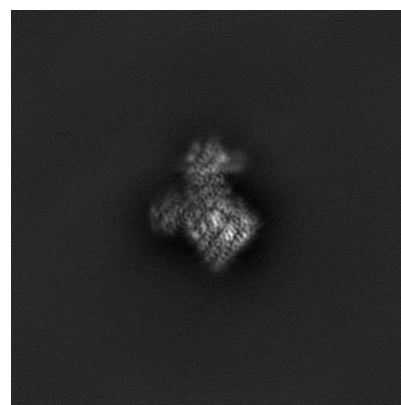
#### 6.1.2 Raw map



X



Y

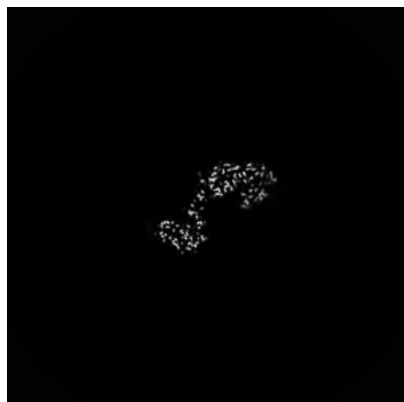


Z

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

## 6.2 Central slices [i](#)

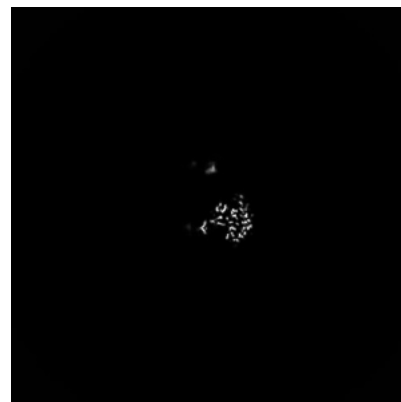
### 6.2.1 Primary map



X Index: 200

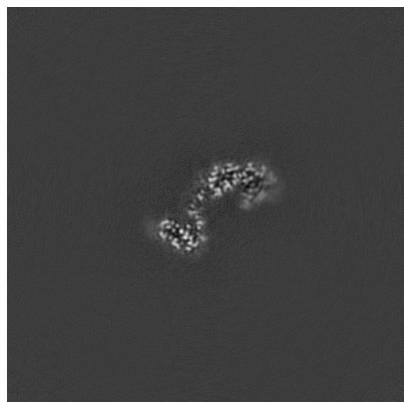


Y Index: 200



Z Index: 200

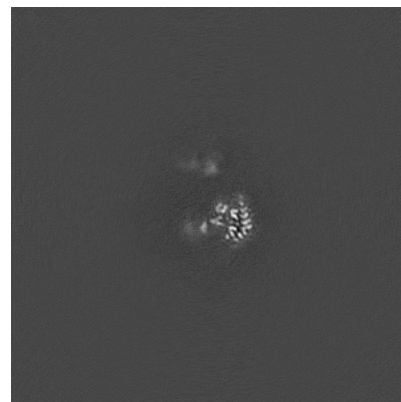
### 6.2.2 Raw map



X Index: 200



Y Index: 200

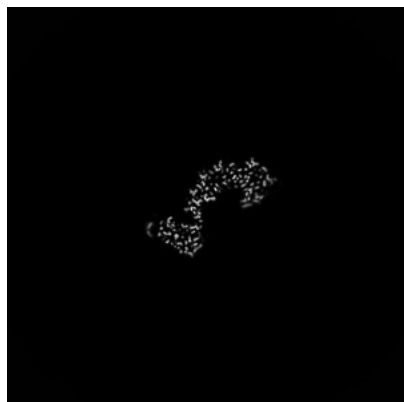


Z Index: 200

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

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

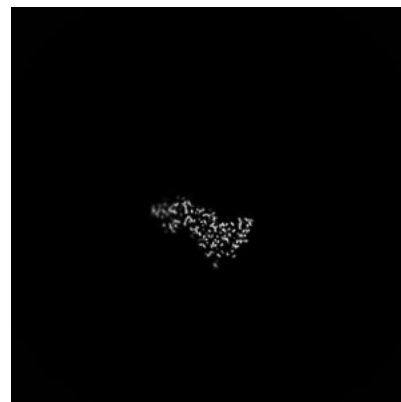
### 6.3.1 Primary map



X Index: 203

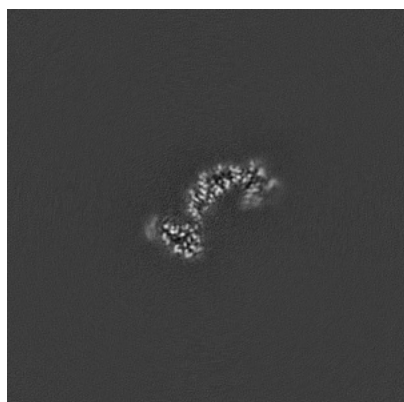


Y Index: 187

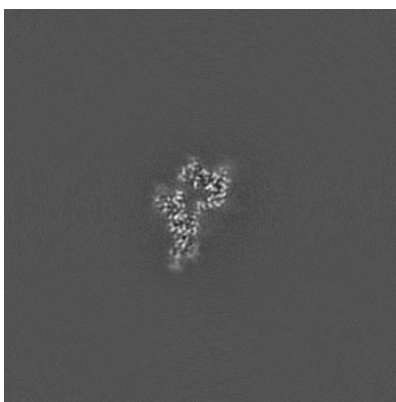


Z Index: 180

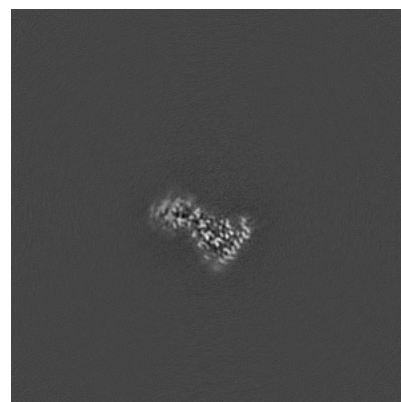
### 6.3.2 Raw map



X Index: 205



Y Index: 186



Z Index: 177

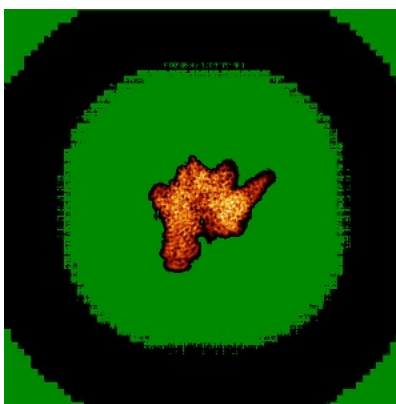
The images above show the largest variance slices of the map in three orthogonal directions.

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

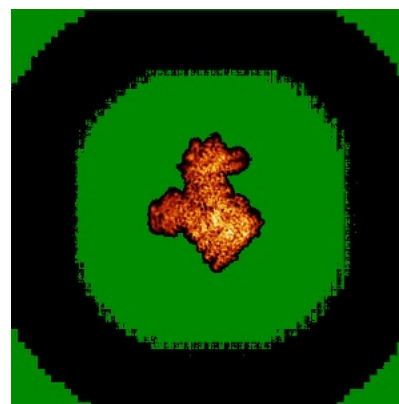
### 6.4.1 Primary map



X

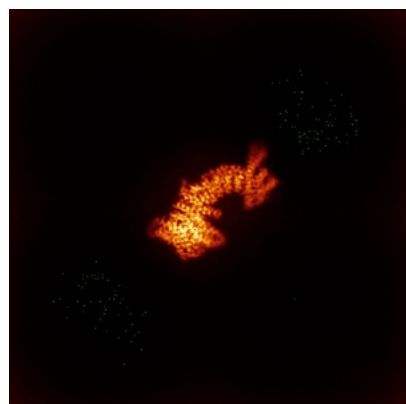


Y

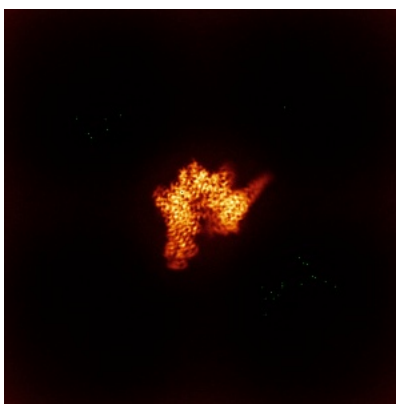


Z

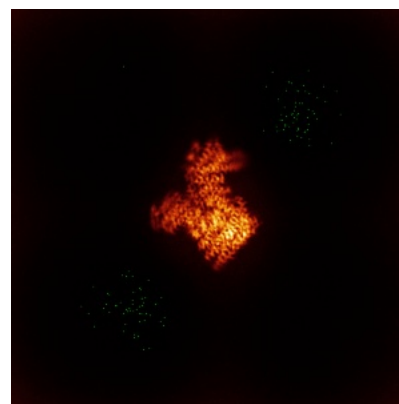
### 6.4.2 Raw map



X



Y

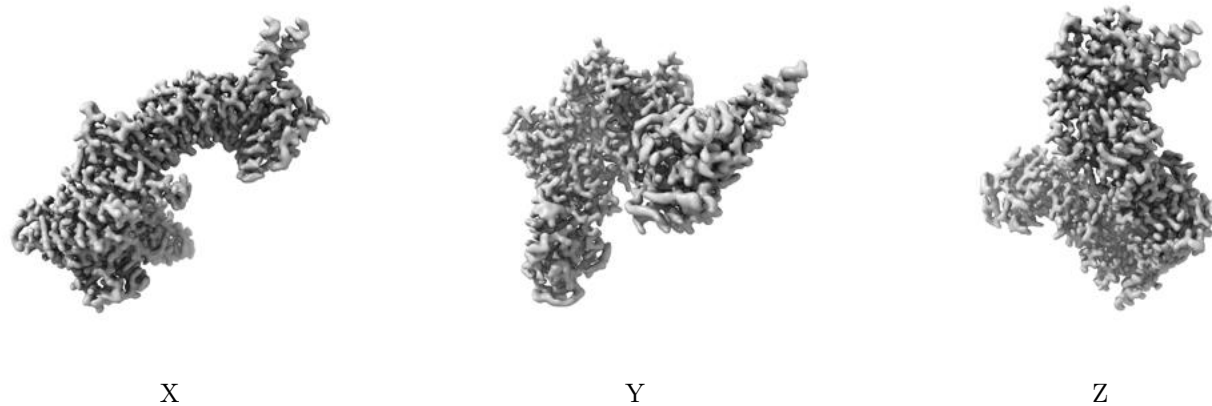


Z

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.

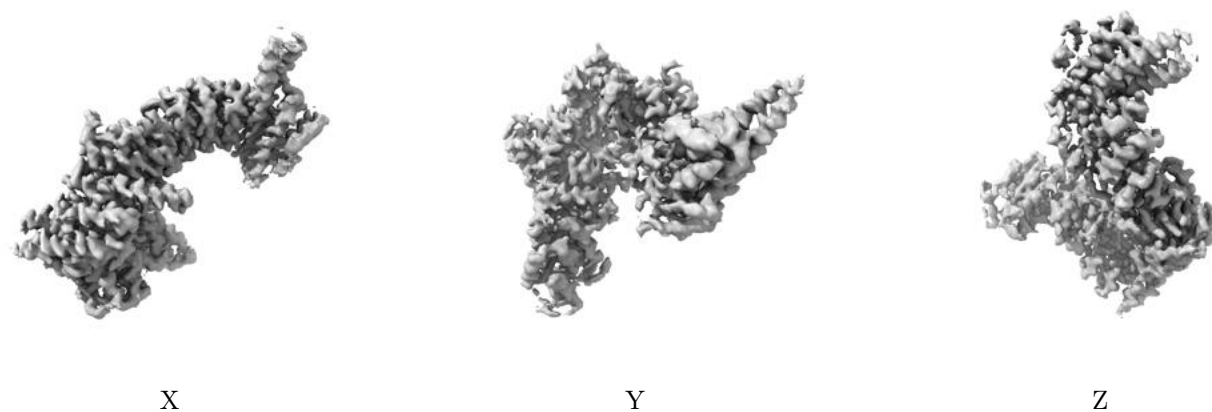
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.5. 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](#)

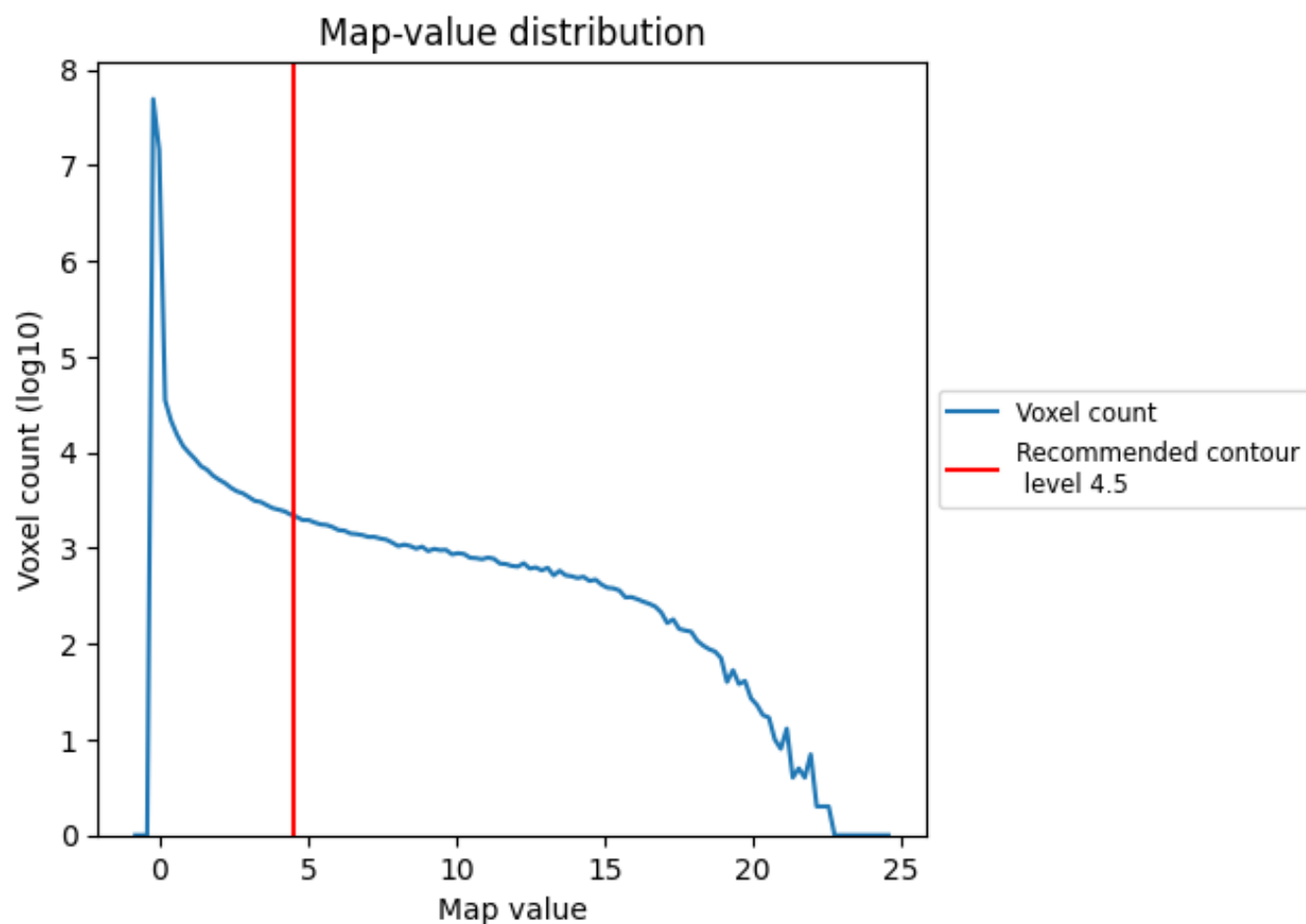
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

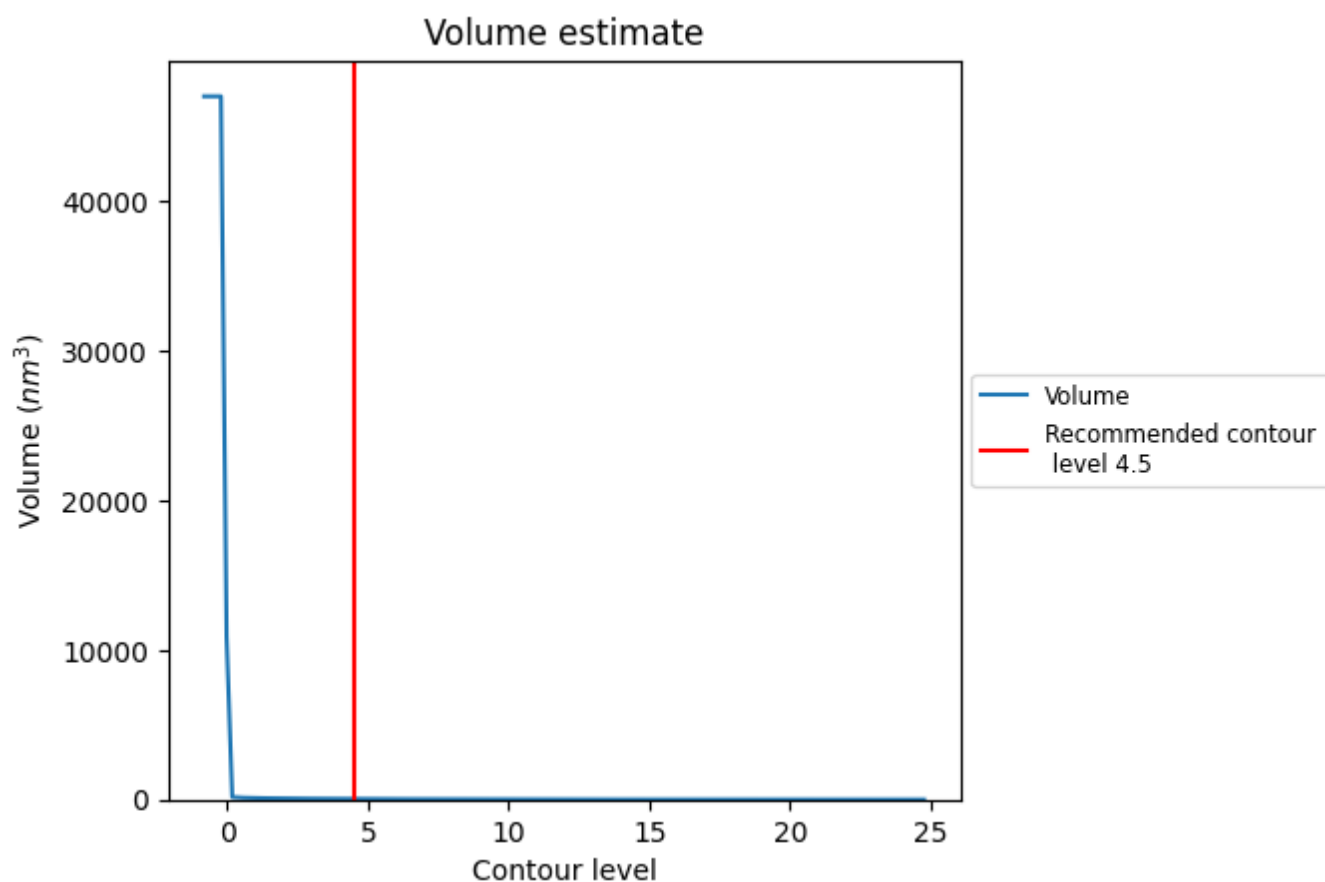
This section contains the results of statistical analysis of the map.

### 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.

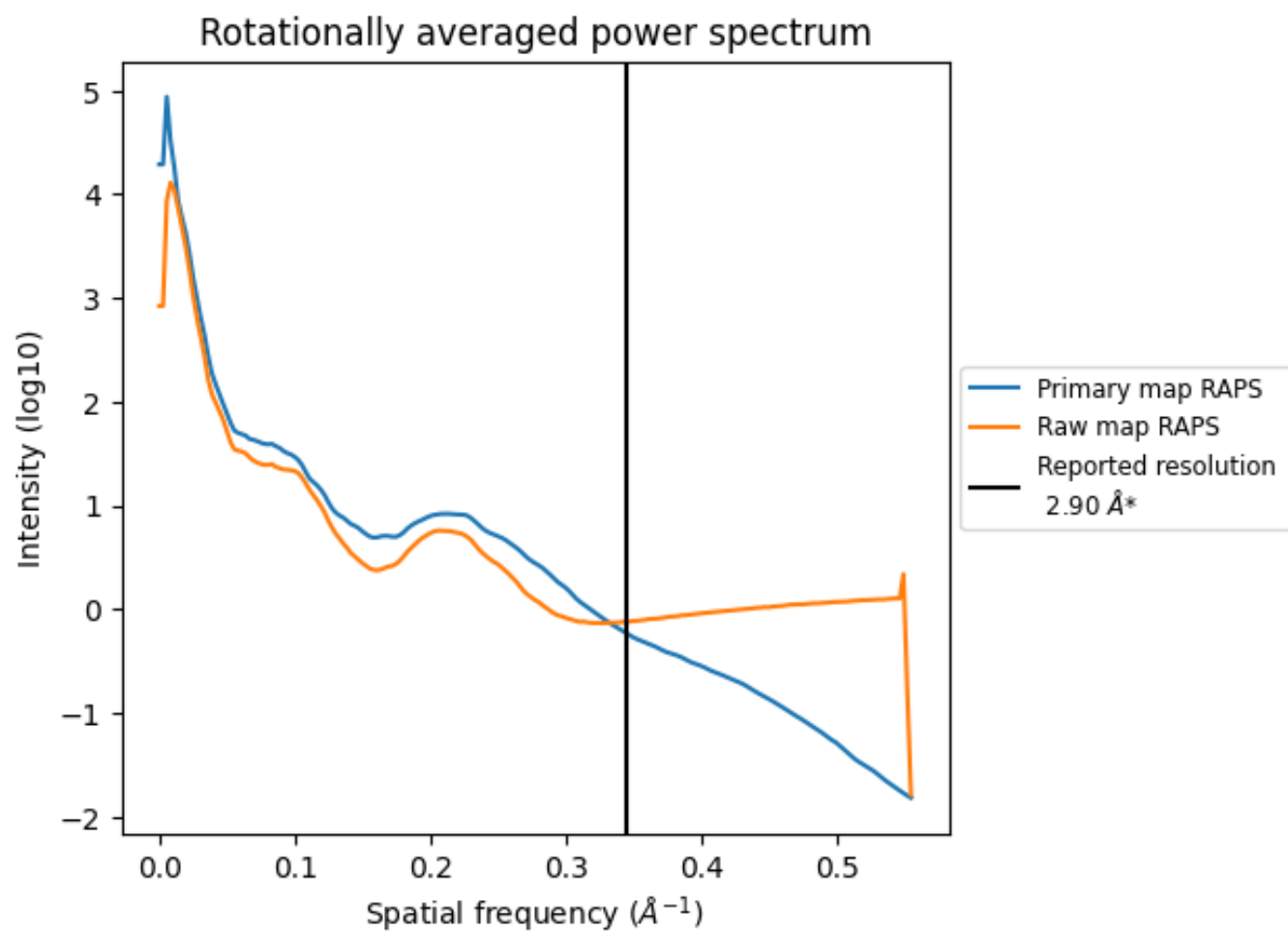
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 43  $\text{nm}^3$ ; 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 ⓘ

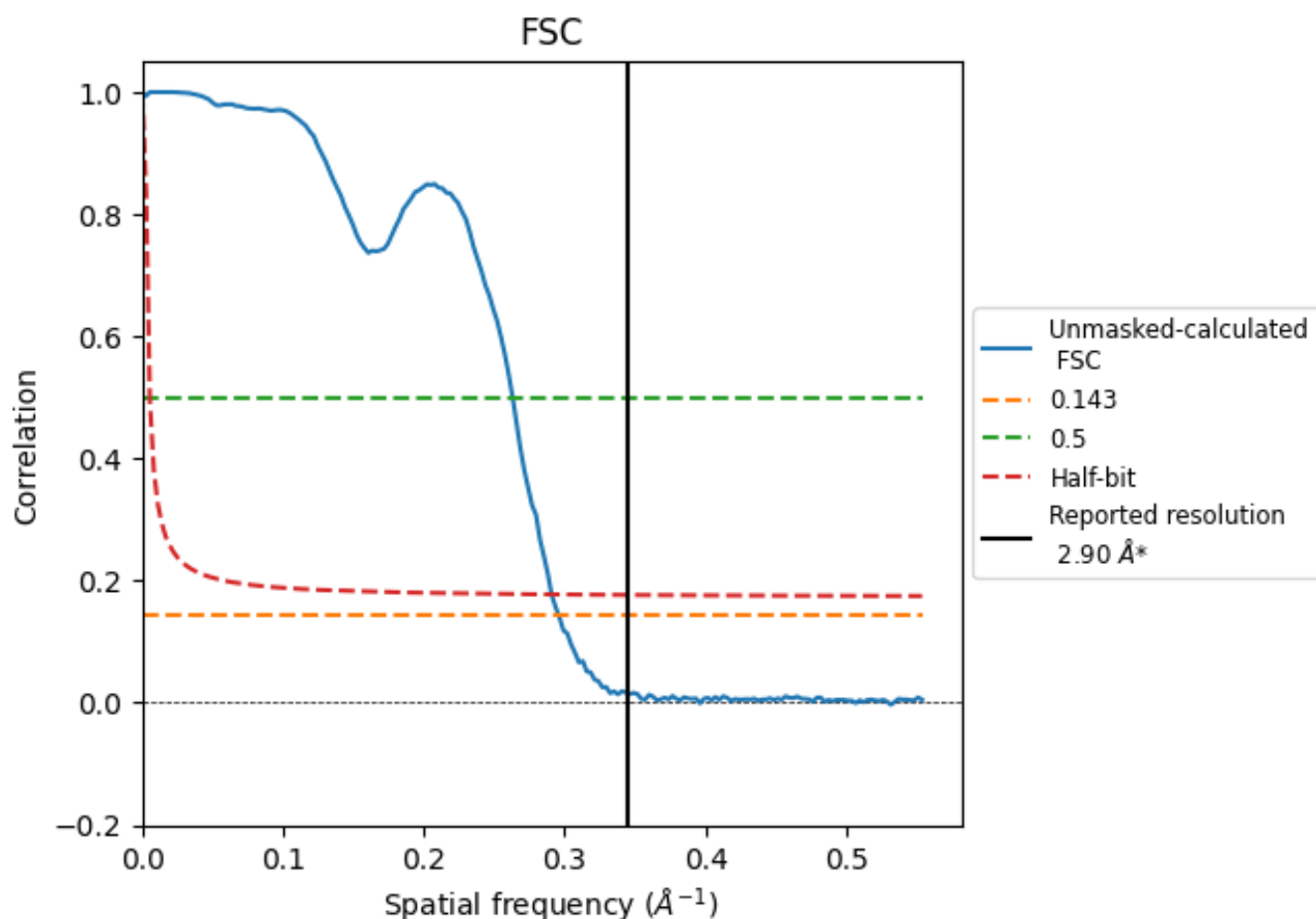


\*Reported resolution corresponds to spatial frequency of 0.345 Å<sup>-1</sup>

## 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  $0.345 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

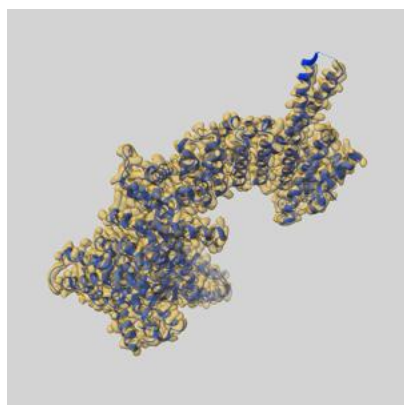
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.38	3.80	3.44

\*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 3.38 differs from the reported value 2.9 by more than 10 %

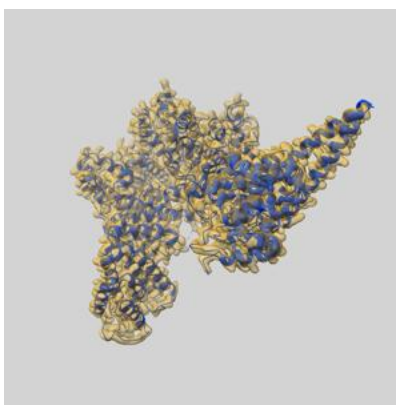
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-52298 and PDB model 9HMY. Per-residue inclusion information can be found in section [3](#) on page [5](#).

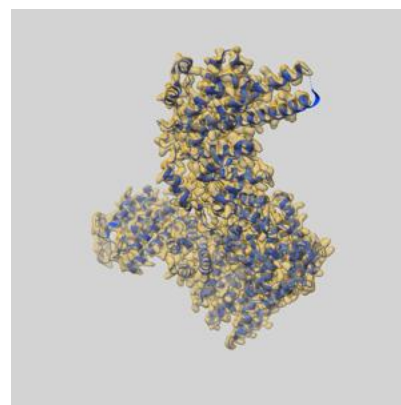
### 9.1 Map-model overlay [i](#)



X



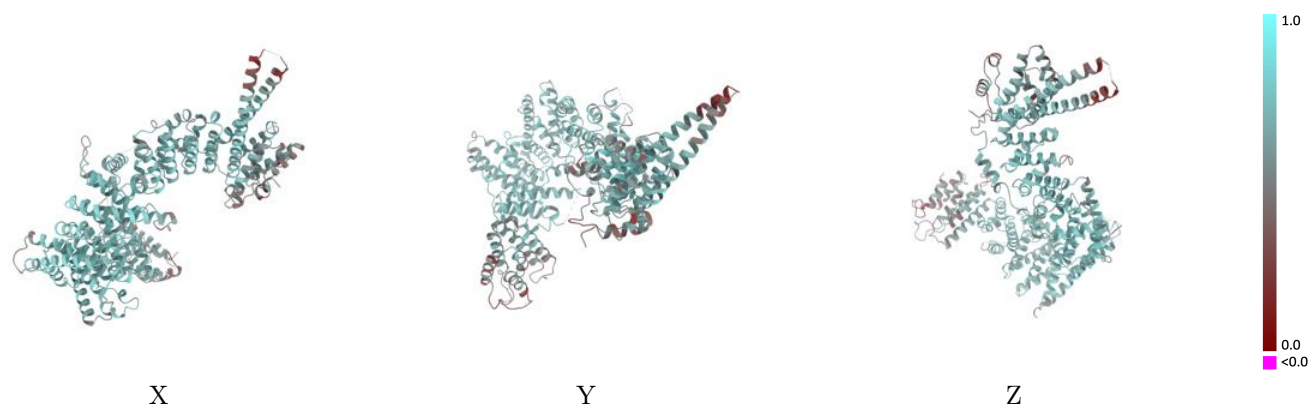
Y



Z

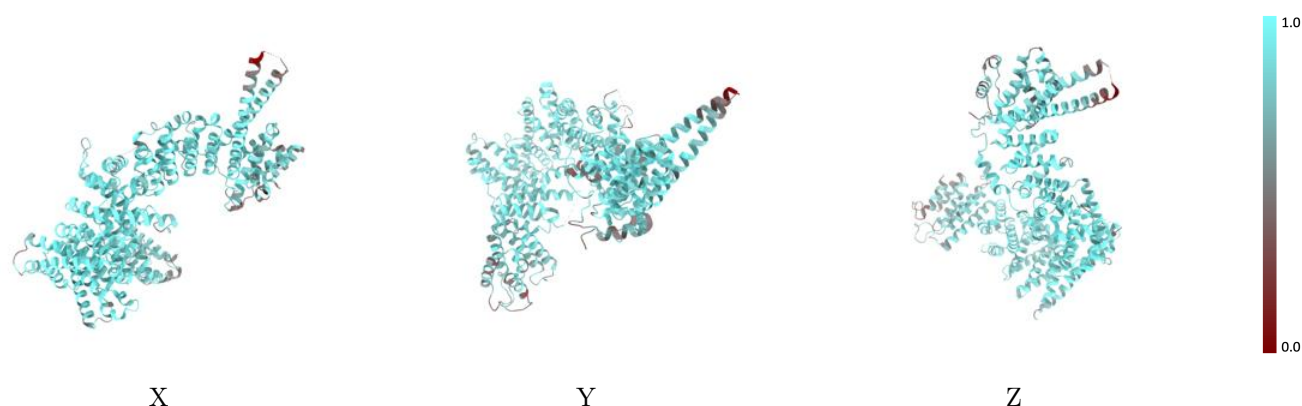
The images above show the 3D surface view of the map at the recommended contour level 4.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



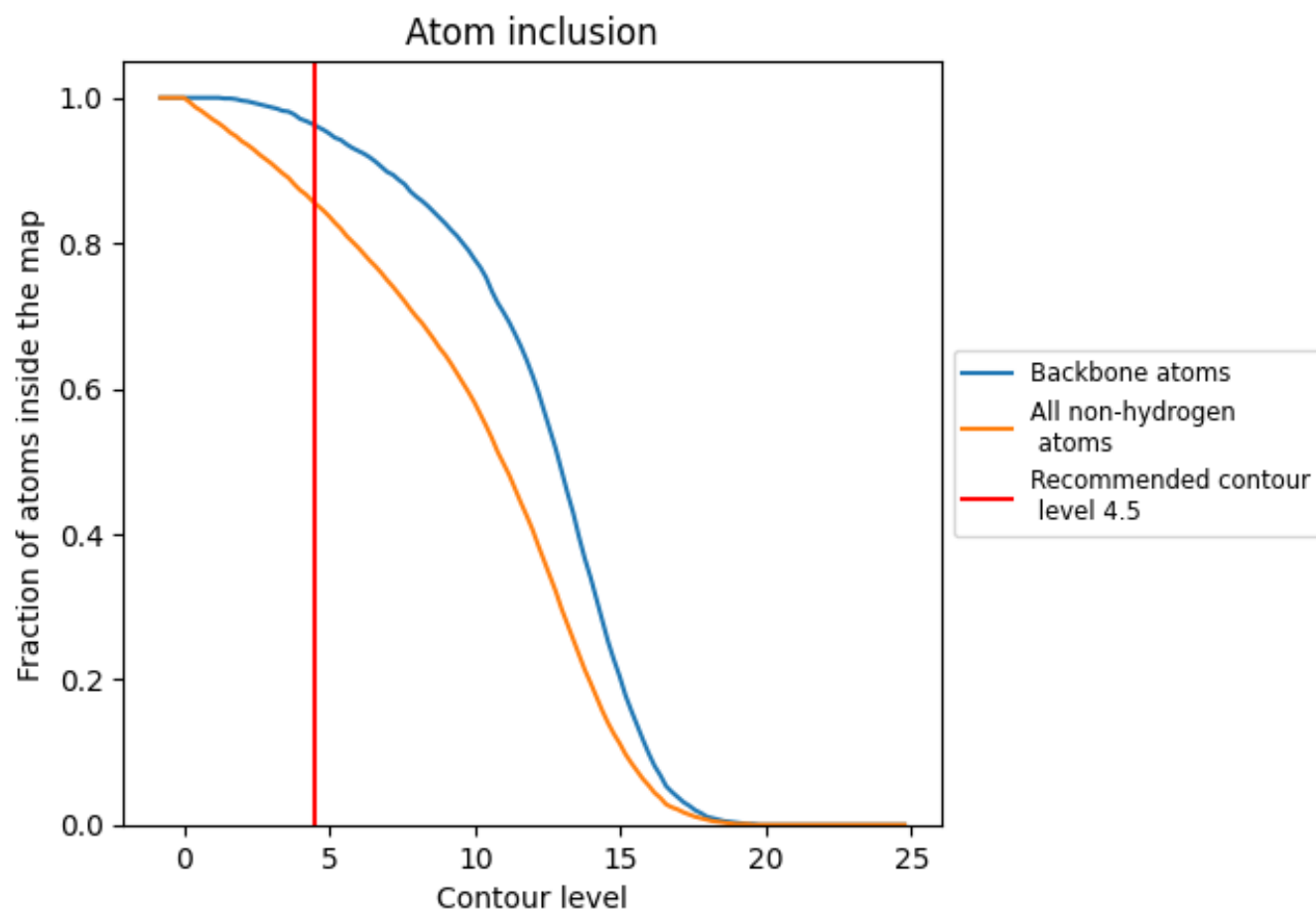
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.5).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 85% 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 (4.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8540</div>	<div><div></div>0.6190</div>
A	<div><div></div>0.8520</div>	<div><div></div>0.6180</div>
B	<div><div></div>0.8770</div>	<div><div></div>0.6420</div>

