



## wwPDB EM Validation Summary Report ⓘ

May 18, 2025 – 01:03 PM EDT

PDB ID : 9O12 / pdb\_00009o12  
EMDB ID : EMD-49995  
Title : Kv2.1 in an intermediate conformation with 2 voltage sensors down and an open pore  
Authors : Mandala, V.S.; MacKinnon, R.  
Deposited on : 2025-04-03  
Resolution : 4.30 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](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

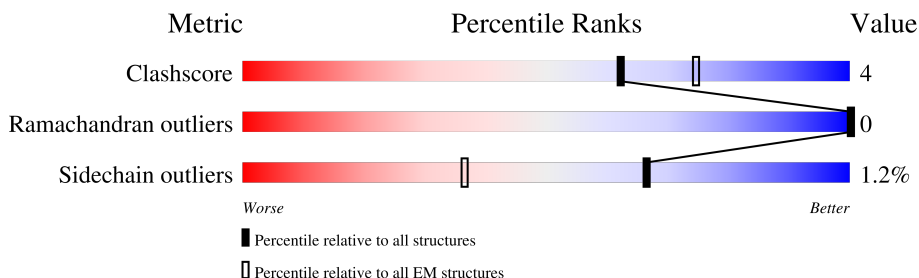
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.30 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	858	<div> <div>9%</div> <div>27%</div> <div>70%</div> </div>
1	B	858	<div> <div>8%</div> <div>27%</div> <div>70%</div> </div>
1	C	858	<div> <div>7%</div> <div>27%</div> <div>70%</div> </div>
1	D	858	<div> <div>9%</div> <div>27%</div> <div>70%</div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 17136 atoms, of which 8772 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 Potassium voltage-gated channel subfamily B member 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	261	Total	C	H	N	O	S	0	0
			4284	1380	2193	339	361	11		
1	B	261	Total	C	H	N	O	S	0	0
			4284	1380	2193	339	361	11		
1	C	261	Total	C	H	N	O	S	0	0
			4284	1380	2193	339	361	11		
1	D	261	Total	C	H	N	O	S	0	0
			4284	1380	2193	339	361	11		







S285	V286	L287	Q288	F289	Q290	N291	V292	R293	R294	V295	Q297	I298	F299	R300	I301	M302	R303	I304	L305	L310	A311	R312	F322	R325	E330	L336	F350	F351	A352	E353	K354	D355	E356	D357	K360	F361	I364	P365	M375	T376	Y380	G381	D382	I383	T387	K391					
G394	G401	F419	K424	R425	Q426	E427	LYS	ALA	ALA	ILE	LYS	ARG	ARG	GLU	ALA	LEU	GLU	THR	ALA	LYS	ARG	ASN	GLY	ILE	VAL	SER	MET	ASN	MET	LYS	ASP	ALA	PHE	ALA	ARG	SER	ILE	SER	PRO	MET	GLN	HIS	ARG	GLY	ILE	VAL	ASN	GLY	LYS	LYS	ASP
LYS	VAL	THR	GLN	ASP	ASN	HIS	LEU	SER	PRO	ASN	LYS	TRP	LYS	TRP	LYS	TRP	THR	THR	LEU	SER	GLU	THR	THR	LYS	GLU	GLN	GLY	THR	LYS	GLU	VAL	ALA	ARG	SER	SER	PRO	MET	GLN	ILE	SER	ASP	PHE	GLY	THR	ASN	GLY	LYS	MET			
ALA	LYS	THR	GLN	SER	ALA	GLN	PRO	ILE	LEU	THR	ALA	ALA	LYS	GLN	SER	LYS	PRO	GLY	LEU	GLU	THR	THR	PRO	LYS	GLY	GLU	THR	LEU	GLU	MET	GLU	VAL	THR	ARG	THR	GLY	VAL	ILE	ASP	GLN	THR	ARG	GLY	THR	ASN	GLY	THR				
ASP	PHE	PRO	GLU	SER	ALA	THR	ARG	PHE	ASN	SER	ILE	THR	HIS	PRO	LEU	LYS	PRO	GLY	THR	ALA	PRO	GLY	THR	ARG	GLY	ALA	LEU	TYR	GLY	VAL	ALA	GLY	PHE	ASN	VAL	GLY	ALA	ASN	PRO	SER	GLN	HIS	SER	PHE	THR	GLY	SER				
PRO	LYS	SER	MET	LYS	THR	THR	THR	ASN	THR	ARG	LEU	ALA	ASN	VAL	PRO	PHE	THR	GLY	GLY	GLY	THR	ALA	PRO	SER	PRO	GLY	LEU	VAL	LEU	GLY	ALA	GLY	LEU	VAL	ASP	ALA	GLY	SER	GLN	THR	GLY	GLU	CYS	ALA	THR	LEU	ASP	LYS			
ALA	VAL	LEU	SER	PRO	GLY	THR	SER	SER	THR	ALA	ALA	LYS	THR	PRO	PRO	ARG	SER	GLY	GLY	GLY	THR	HIS	THR	PRO	ALA	THR	ILE	THR	ALA	VAL	GLY	THR	ASP	THR	ASP	GLY	LEU	THR	TYR	GLN	THR	VAL	VAL	SER	PRO	GLY	THR				
SER	LEU	PRO	GLY	THR	SER	THR	SER	PRO	THR	THR	ARG	THR	THR	GLY	GLY	ALA	THR	THR	THR	THR	ARG	THR	THR	PRO	LEU	PRO	ALA	THR	ILE	THR	ALA	VAL	GLY	THR	ASP	GLY	LEU	THR	GLN	THR	GLY	GLU	CYS	LYS	LEU	GLY	ASN	HIS			
ILE	SER	PRO	ASP	VAL	ARG	VAL	LEU	PRO	GLY	GLY	ALA	HIS	GLY	THR	THR	ASP	GLN	SER	ILE																																

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	13810	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 ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.177	Depositor
Minimum map value	-0.081	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.055	Depositor
Map size (Å)	213.984, 213.984, 213.984	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.743, 0.743, 0.743	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	0.14	0/2137	0.27	0/2893
1	B	0.14	0/2137	0.30	0/2893
1	C	0.14	0/2137	0.28	0/2893
1	D	0.14	0/2137	0.27	0/2893
All	All	0.14	0/8548	0.28	0/11572

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	2091	2193	2192	19	0
1	B	2091	2193	2192	16	0
1	C	2091	2193	2192	19	0
1	D	2091	2193	2192	20	0
All	All	8364	8772	8768	70	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 4.

The worst 5 of 70 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:C:330:GLU:OE1	1:C:330:GLU:N	2.16	0.78
1:D:219:GLU:OE1	1:D:219:GLU:N	2.21	0.73
1:C:215:GLN:NE2	1:C:225:ASP:OD1	2.24	0.71
1:D:176:TRP:NE1	1:D:180:GLU:OE1	2.24	0.69
1:B:376:THR:O	1:B:377:THR:OG1	2.11	0.69

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	259/858 (30%)	250 (96%)	9 (4%)	0	100	100
1	B	259/858 (30%)	245 (95%)	14 (5%)	0	100	100
1	C	259/858 (30%)	247 (95%)	12 (5%)	0	100	100
1	D	259/858 (30%)	249 (96%)	10 (4%)	0	100	100
All	All	1036/3432 (30%)	991 (96%)	45 (4%)	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	232/753 (31%)	230 (99%)	2 (1%)	75	83
1	B	232/753 (31%)	228 (98%)	4 (2%)	56	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	232/753 (31%)	229 (99%)	3 (1%)	65	77
1	D	232/753 (31%)	230 (99%)	2 (1%)	75	83
All	All	928/3012 (31%)	917 (99%)	11 (1%)	66	79

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	353	GLU
1	C	380	TYR
1	D	380	TYR
1	D	172	ARG
1	B	380	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	313	HIS
1	B	329	ASN
1	C	415	ASN
1	D	283	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 ⓘ

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.

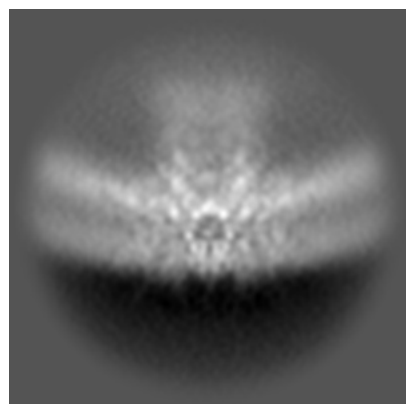
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49995. These allow visual inspection of the internal detail of the map and identification of artifacts.

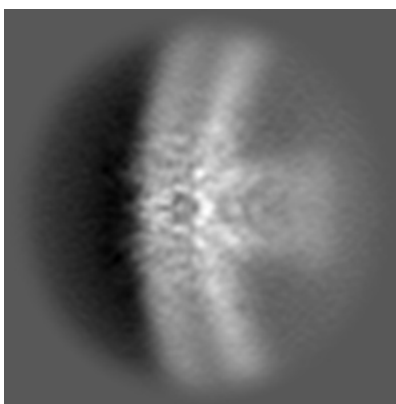
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

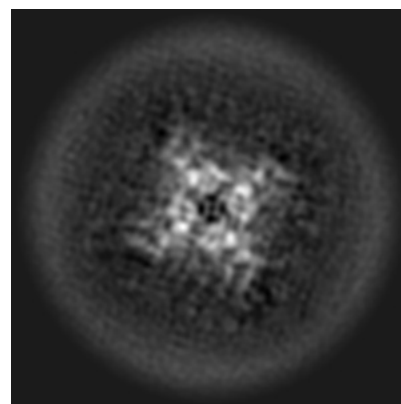
#### 6.1.1 Primary map



X

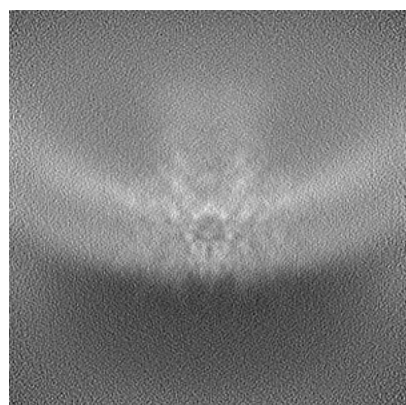


Y

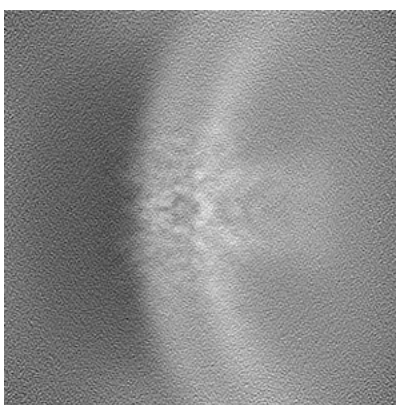


Z

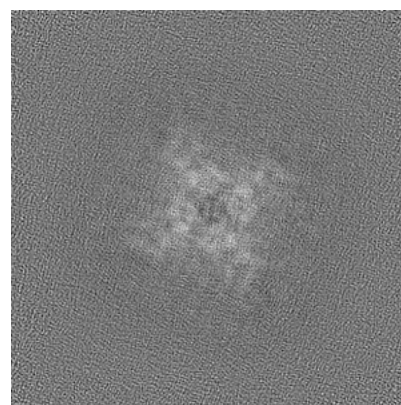
#### 6.1.2 Raw map



X



Y

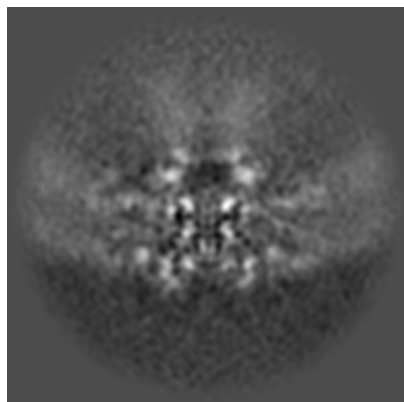


Z

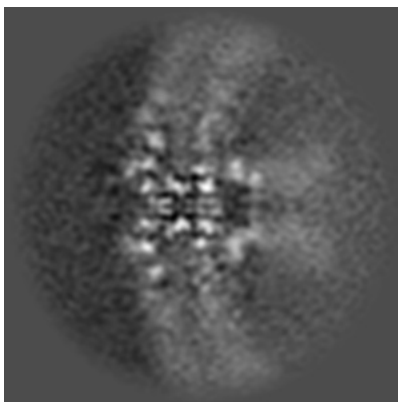
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

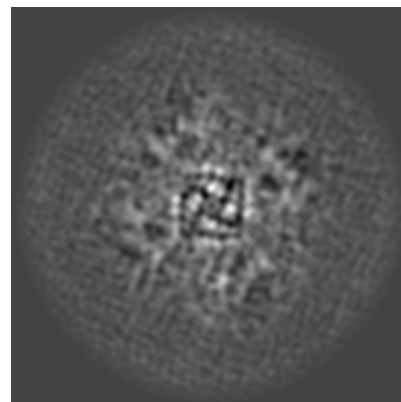
### 6.2.1 Primary map



X Index: 144

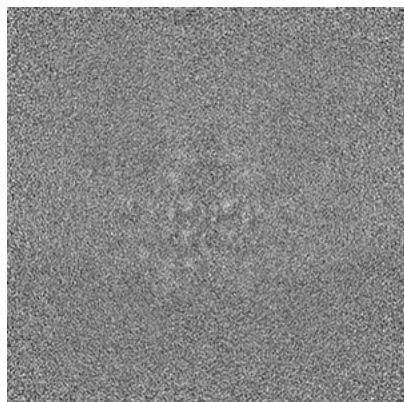


Y Index: 144

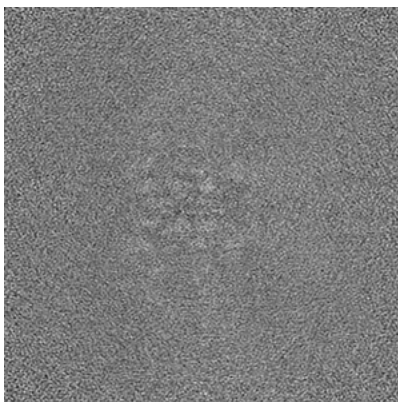


Z Index: 144

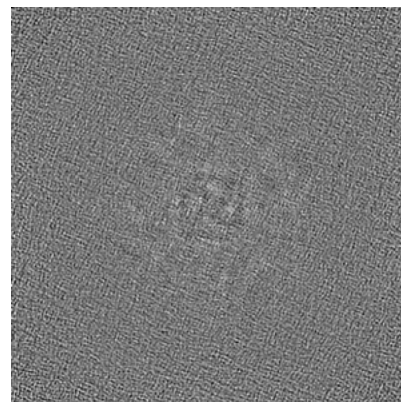
### 6.2.2 Raw map



X Index: 144



Y Index: 144



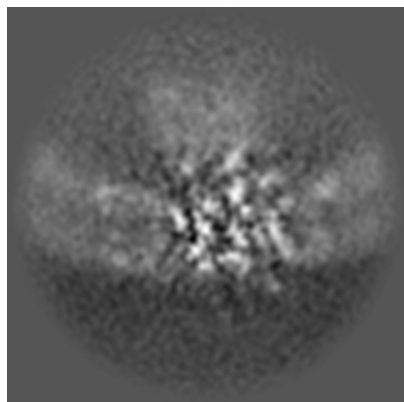
Z Index: 144

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

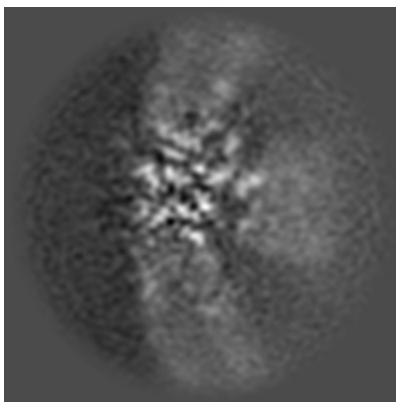


## 6.3 Largest variance slices [i](#)

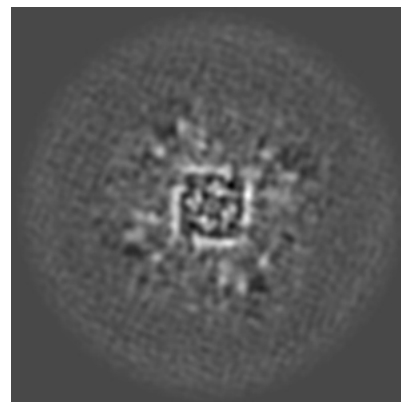
### 6.3.1 Primary map



X Index: 131

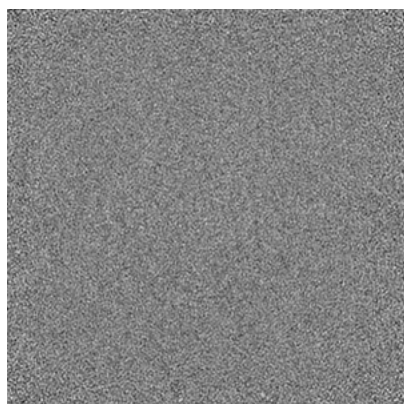


Y Index: 157

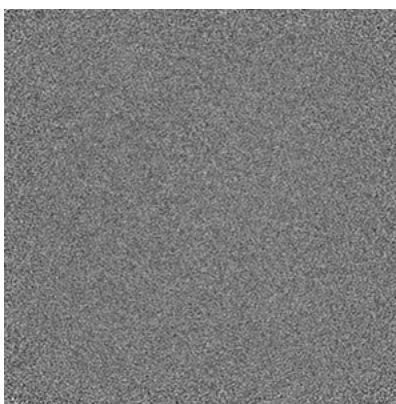


Z Index: 141

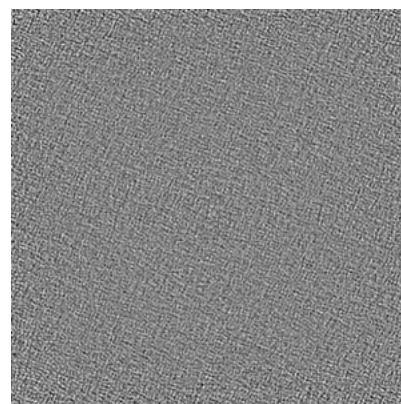
### 6.3.2 Raw map



X Index: 0



Y Index: 0

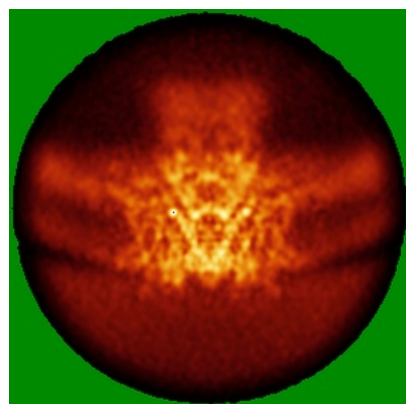


Z Index: 0

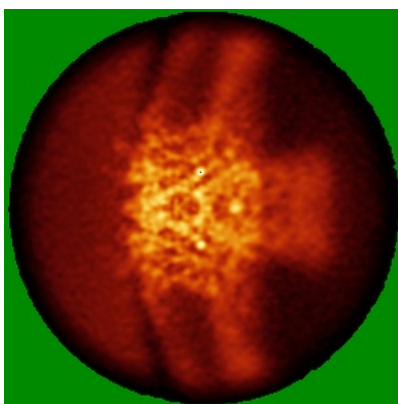
The images above show the largest variance slices of the map in three orthogonal directions.

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

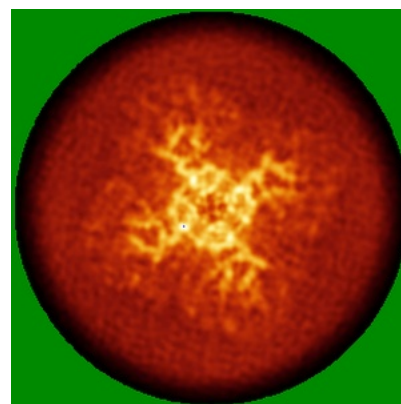
### 6.4.1 Primary map



X

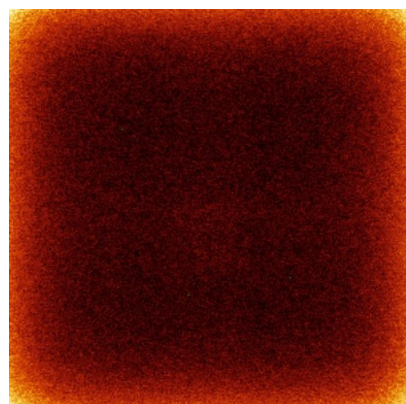


Y

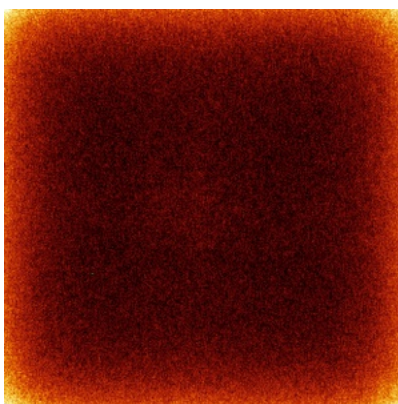


Z

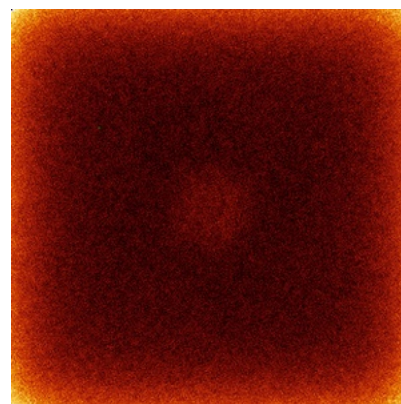
### 6.4.2 Raw map



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.



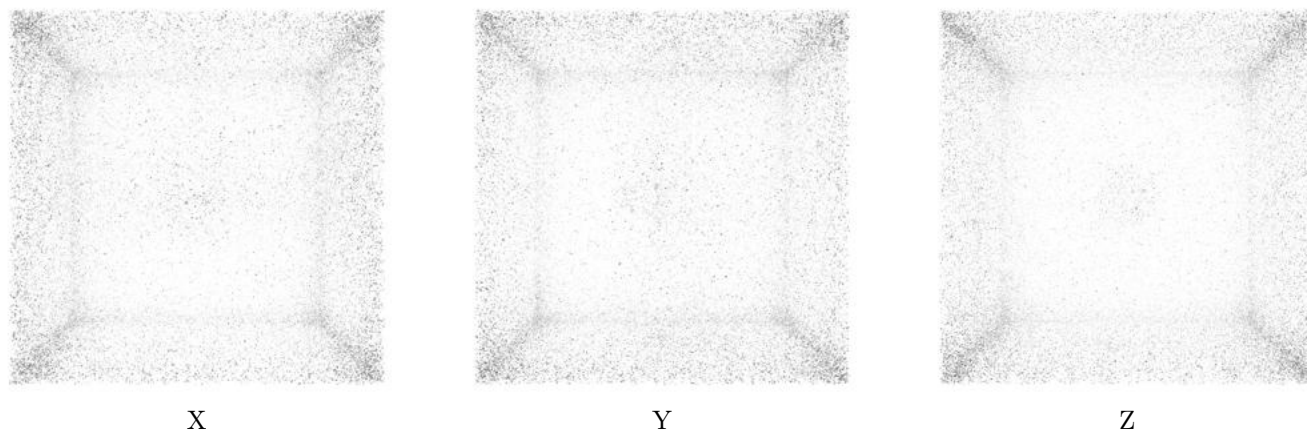
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.055. 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.

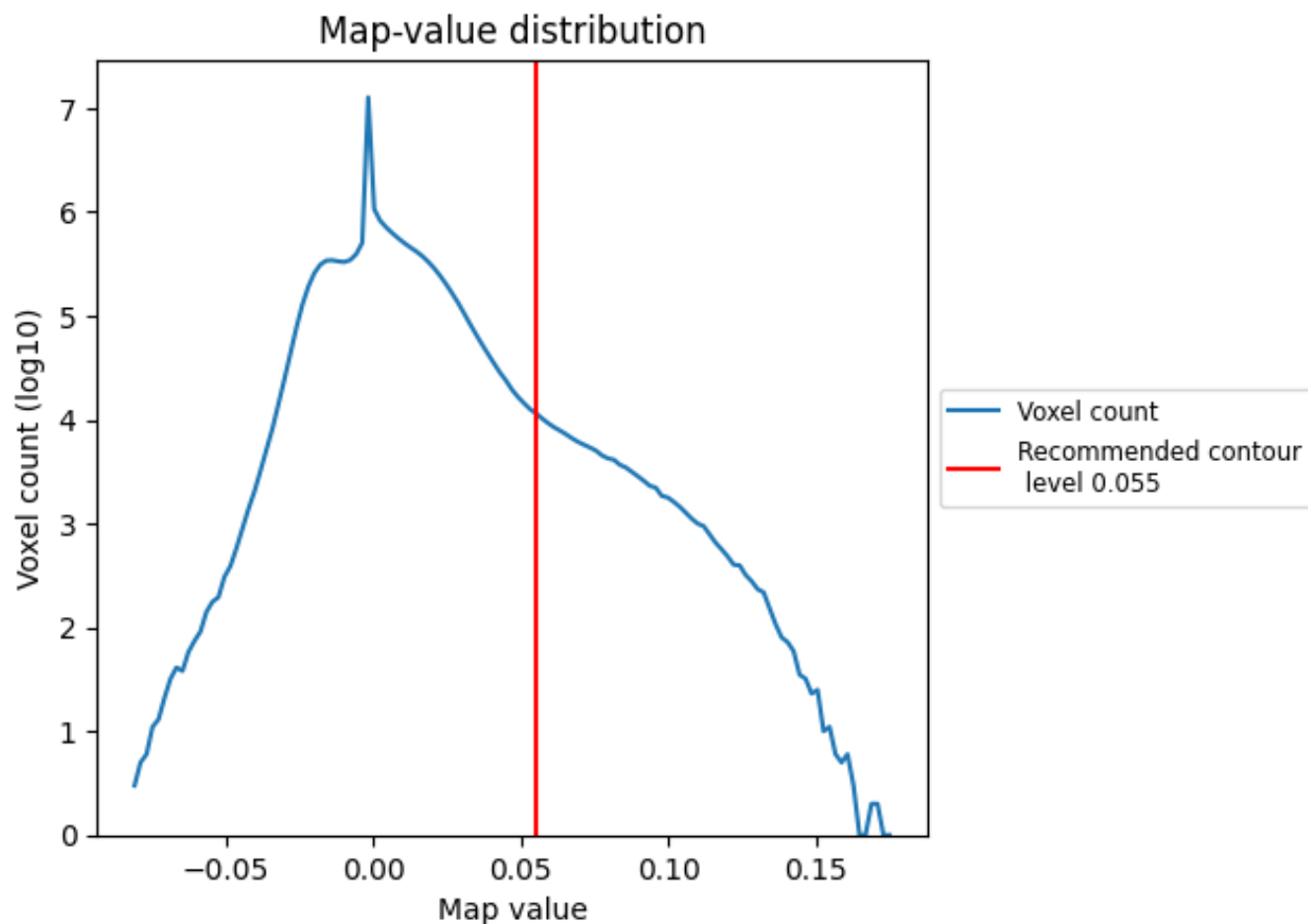
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

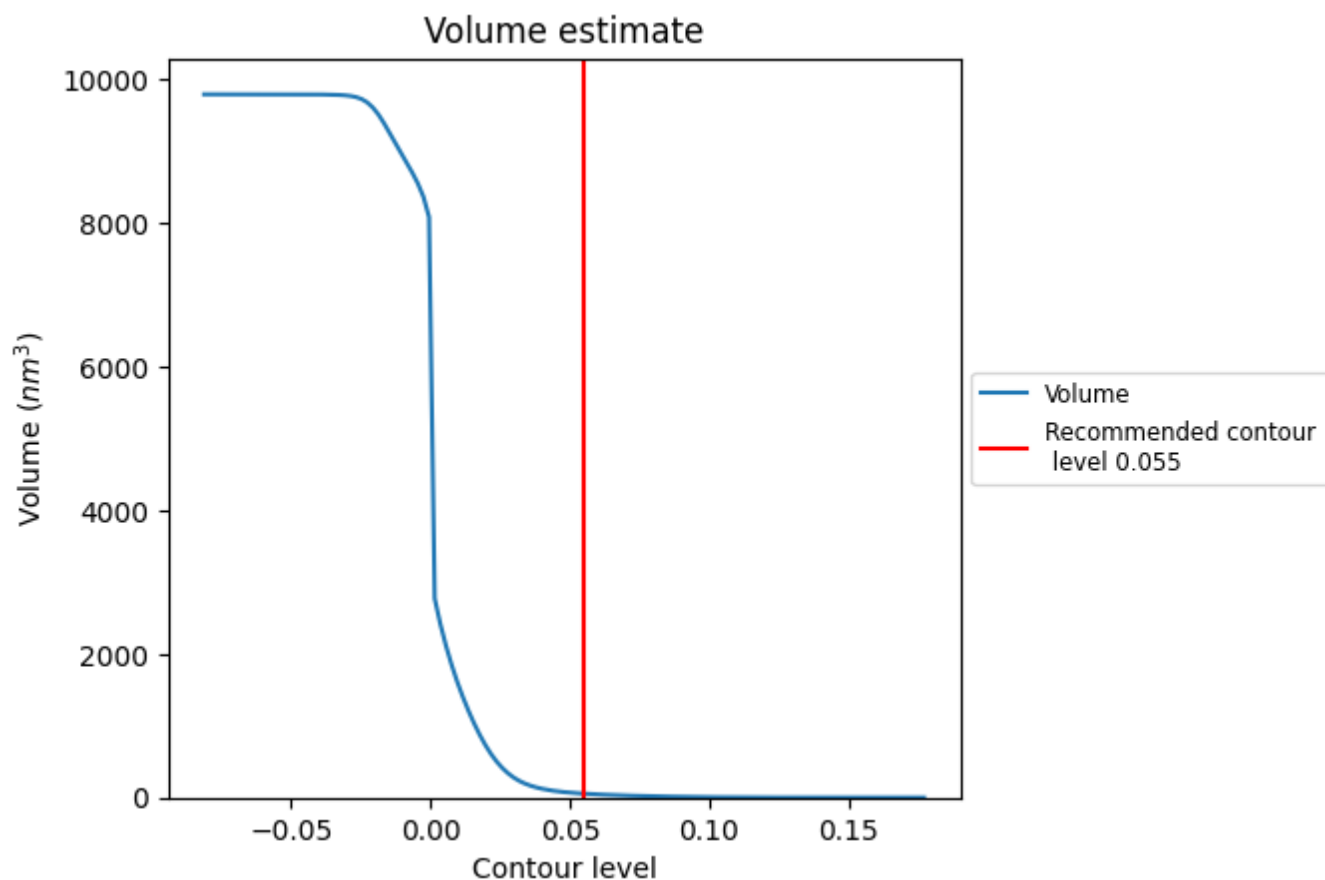
This section contains the results of statistical analysis of the map.

### 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.

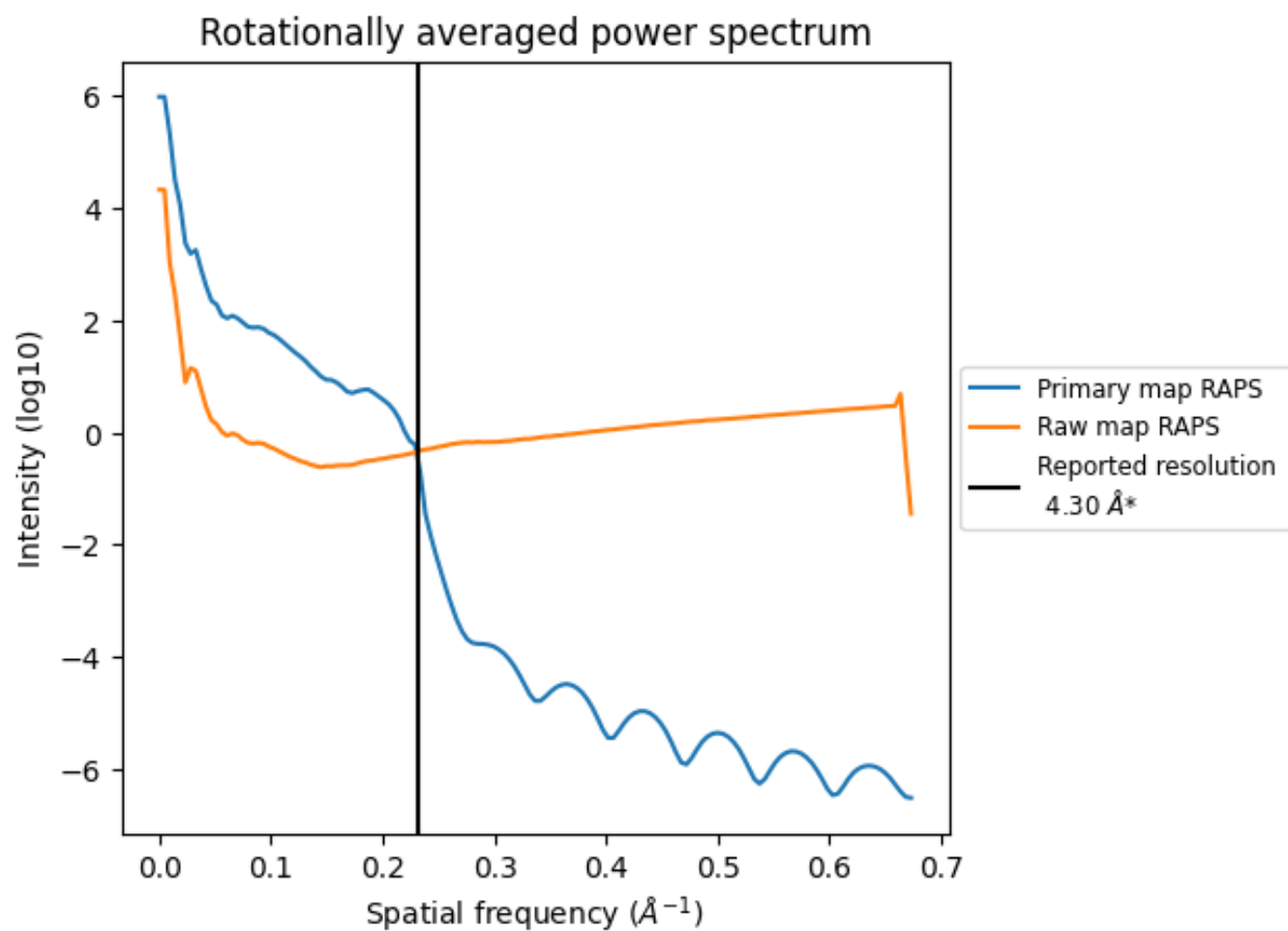
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 55 nm<sup>3</sup>; this corresponds to an approximate mass of 49 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 ⓘ

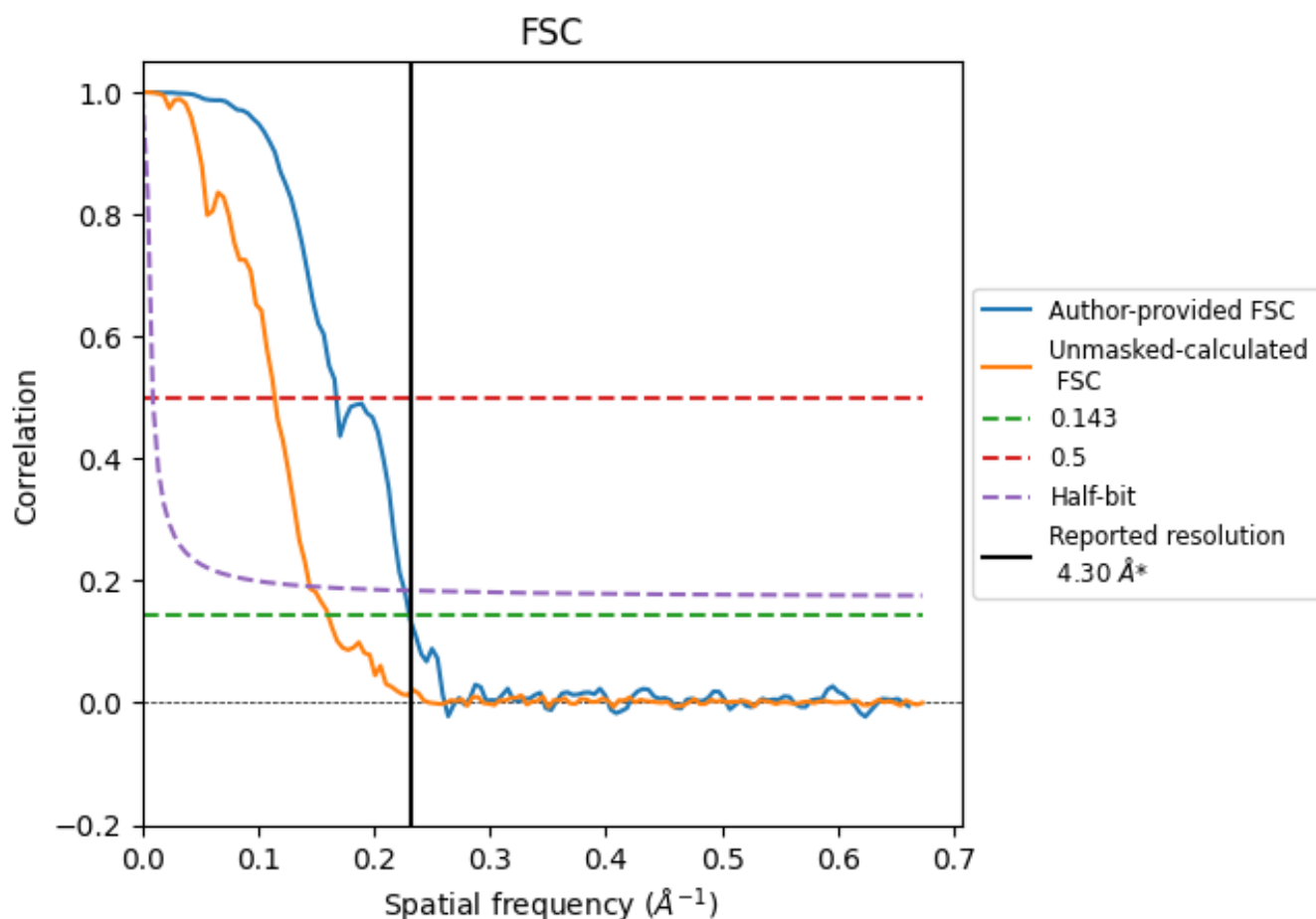


\*Reported resolution corresponds to spatial frequency of 0.233  $\text{\AA}^{-1}$

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

## 8.2 Resolution estimates [i](#)

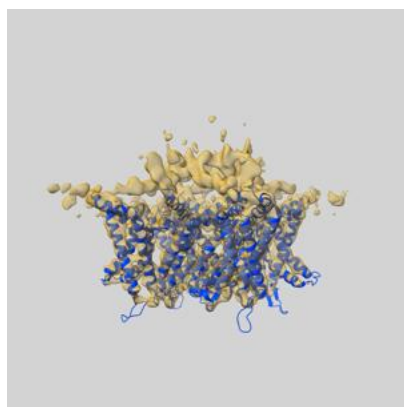
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.34	5.97	4.42
Unmasked-calculated*	6.23	8.75	6.92

\*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 6.23 differs from the reported value 4.3 by more than 10 %

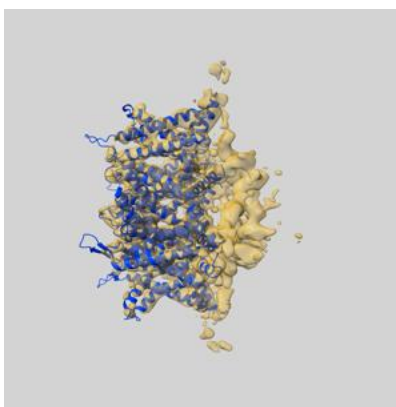
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-49995 and PDB model 9O12. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

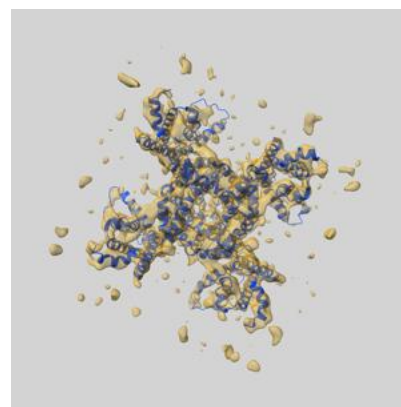
### 9.1 Map-model overlay [i](#)



X



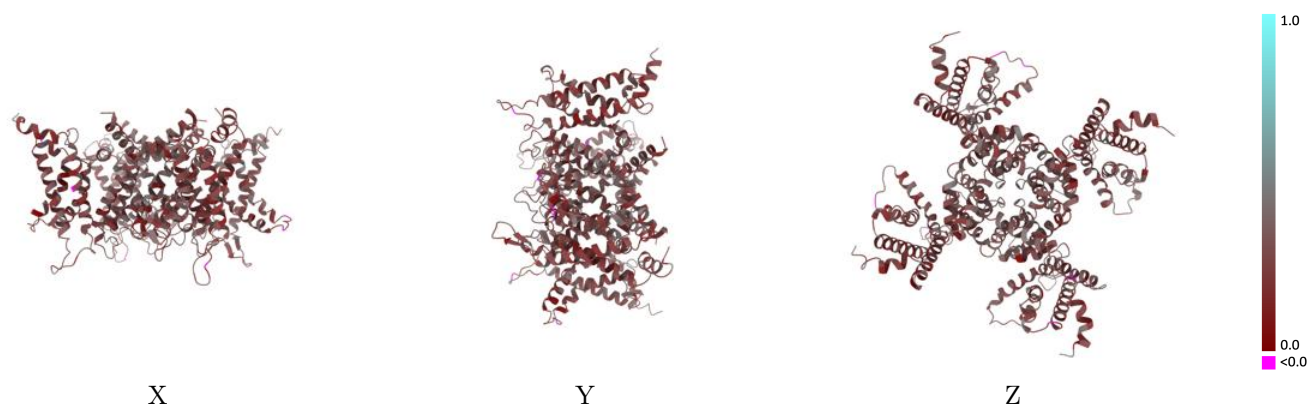
Y



Z

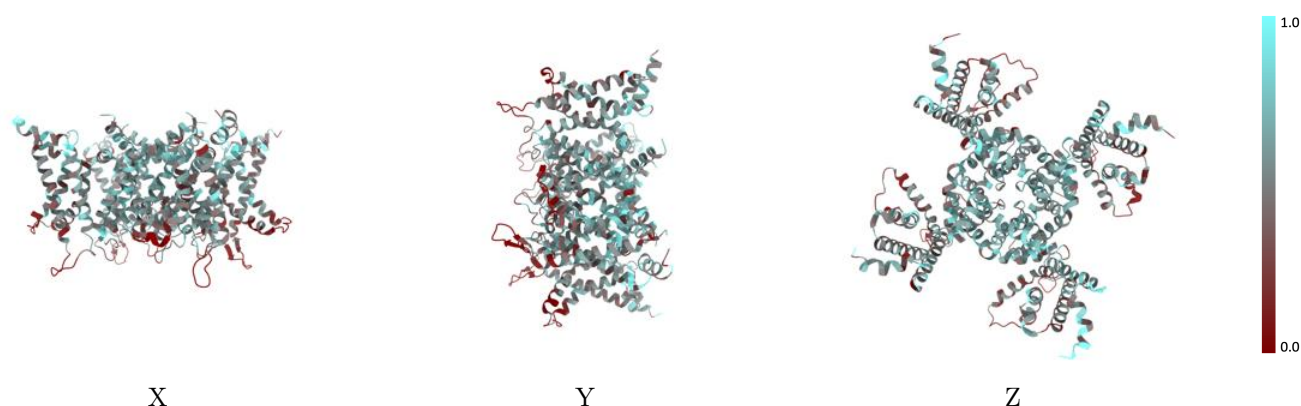
The images above show the 3D surface view of the map at the recommended contour level 0.055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

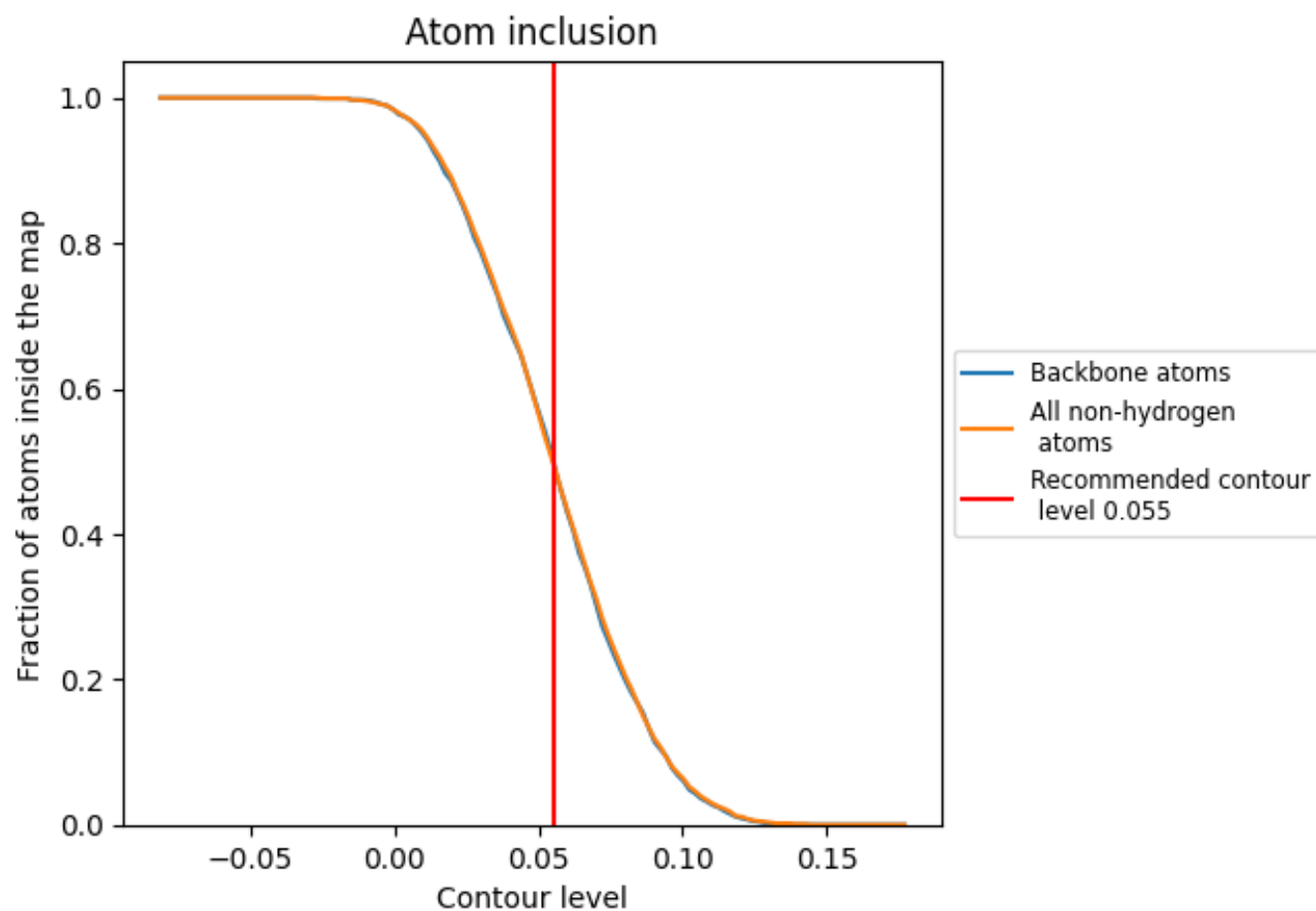
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.055).



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 50% 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 (0.055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4990	<div></div> 0.2940
A	<div></div> 0.4960	<div></div> 0.2880
B	<div></div> 0.5230	<div></div> 0.3000
C	<div></div> 0.5220	<div></div> 0.2940
D	<div></div> 0.5040	<div></div> 0.2950

