



wwPDB EM Validation Summary Report ⓘ

Jul 28, 2026 – 06:23 PM EDT

PDB ID : 11YE / pdb_000011ye
EMDB ID : EMD-76184
Title : Curved structure of mPiezo1 in plasma membrane vesicles
Authors : Vaisey, G.V.; MacKinnon, R.M.
Deposited on : 2026-03-18
Resolution : 3.70 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:

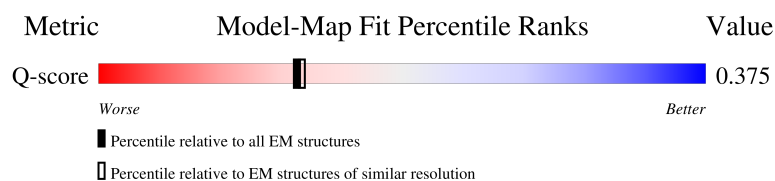
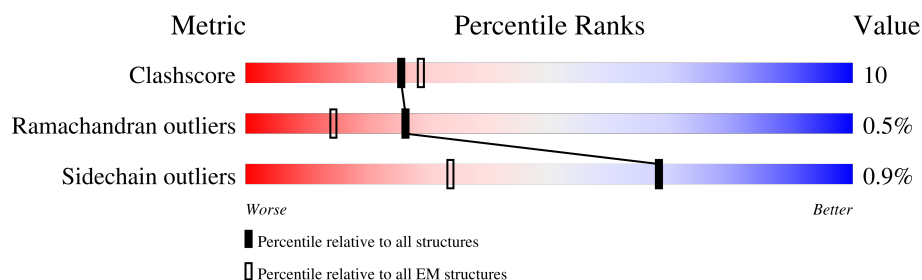
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 3.70 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	11569 (3.20 - 4.20)

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 ≥ 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	C	2561	
1	D	2561	
1	E	2561	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 29295 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 Piezo-type mechanosensitive ion channel component 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	1335	Total	C	N	O	S	0	0
			9765	6243	1715	1756	51		
1	D	1335	Total	C	N	O	S	0	0
			9765	6243	1715	1756	51		
1	E	1335	Total	C	N	O	S	0	0
			9765	6243	1715	1756	51		

There are 42 discrepancies between the modelled and reference sequences:

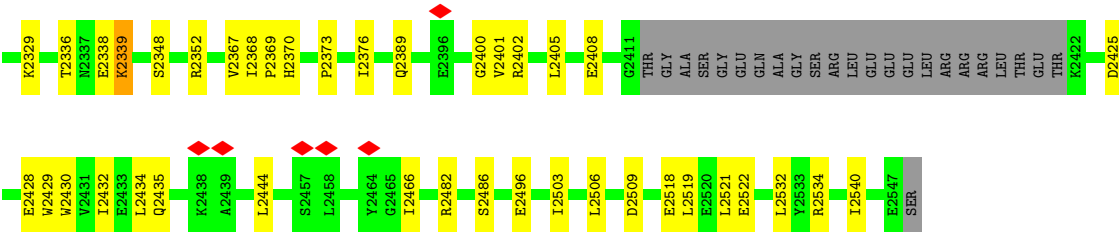
Chain	Residue	Modelled	Actual	Comment	Reference
C	2420A	SER	-	insertion	UNP E2JF22
C	2420B	ARG	-	insertion	UNP E2JF22
C	2420C	LEU	-	insertion	UNP E2JF22
C	2420D	GLU	-	insertion	UNP E2JF22
C	2420E	GLU	-	insertion	UNP E2JF22
C	2420F	GLU	-	insertion	UNP E2JF22
C	2420G	LEU	-	insertion	UNP E2JF22
C	2420H	ARG	-	insertion	UNP E2JF22
C	2420I	ARG	-	insertion	UNP E2JF22
C	2430J	ARG	-	insertion	UNP E2JF22
C	2420K	LEU	-	insertion	UNP E2JF22
C	2420L	THR	-	insertion	UNP E2JF22
C	2420M	GLU	-	insertion	UNP E2JF22
C	2548	SER	-	expression tag	UNP E2JF22
D	2420A	SER	-	insertion	UNP E2JF22
D	2420B	ARG	-	insertion	UNP E2JF22
D	2420C	LEU	-	insertion	UNP E2JF22
D	2420D	GLU	-	insertion	UNP E2JF22
D	2420E	GLU	-	insertion	UNP E2JF22
D	2420F	GLU	-	insertion	UNP E2JF22
D	2420G	LEU	-	insertion	UNP E2JF22
D	2420H	ARG	-	insertion	UNP E2JF22
D	2420I	ARG	-	insertion	UNP E2JF22
D	2420J	ARG	-	insertion	UNP E2JF22

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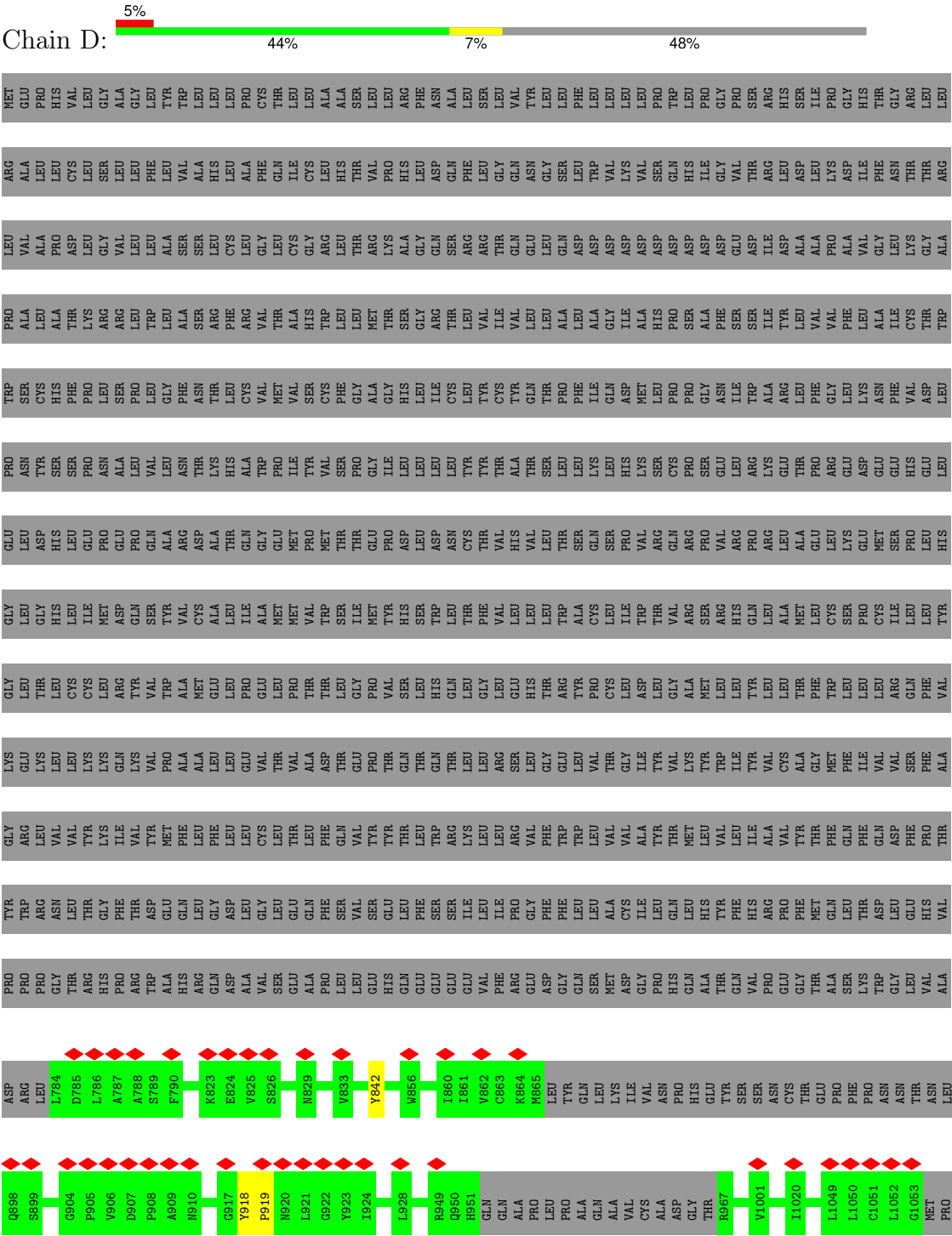
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Chain	Residue	Modelled	Actual	Comment	Reference
D	2420K	LEU	-	insertion	UNP E2JF22
D	2420L	THR	-	insertion	UNP E2JF22
D	2420M	GLU	-	insertion	UNP E2JF22
D	2548	SER	-	expression tag	UNP E2JF22
E	2420A	SER	-	insertion	UNP E2JF22
E	2420B	ARG	-	insertion	UNP E2JF22
E	2420C	LEU	-	insertion	UNP E2JF22
E	2420D	GLU	-	insertion	UNP E2JF22
E	2420E	GLU	-	insertion	UNP E2JF22
E	2420F	GLU	-	insertion	UNP E2JF22
E	2420G	LEU	-	insertion	UNP E2JF22
E	2420H	ARG	-	insertion	UNP E2JF22
E	2420I	ARG	-	insertion	UNP E2JF22
E	2420J	ARG	-	insertion	UNP E2JF22
E	2420K	LEU	-	insertion	UNP E2JF22
E	2420L	THR	-	insertion	UNP E2JF22
E	2420M	GLU	-	insertion	UNP E2JF22
E	2548	SER	-	expression tag	UNP E2JF22





● Molecule 1: Piezo-type mechanosensitive ion channel component 1





E2547
SER

- Molecule 1: Piezo-type mechanosensitive ion channel component 1

Chain E: 44% 8% 48%

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

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

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LY	RG	LAL	LAL	YR	YS	LE	LAL	YR	HE	EU	HE	EU	YS	YS	HR	HR	EU	HE	LN	LN	YR	HR	RP	RG	YS	YS	EU	EU	RG	RG	LAL	LAL	RP	RP	RP	RP	LA	LA	YR	HR	ET	ET	EU	EU	LE	LA	LAL	LAL	YR	HR	HE	HE	LN	LN	HE	HE	RSP	RSP	RO	RO
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Age Group	Percentage
18-24	18%
25-34	22%
35-44	15%
45-54	12%
55-64	10%
65-74	8%
75-84	5%
85+	3%

SER	LYS	ALA	ILE	PRO	M1072	Y1081	F1086	Q1120	ARG	MET	ALA	GLY	ILE	ASN	THR	ASP	HIS	LEU	GLU	PRO	LEU	R1134	G1135	F1143	I1144	H1145	C1146	R1147	S1148	Y1149	L1150	D1151	M1152	F1158	F1170	R1176	I1177	Y1184	C1188	L1191	G1195	L1198	L1207
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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	69370	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 ($e^-/\text{\AA}^2$)	60.00	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	34.226	Depositor
Minimum map value	-19.697	Depositor
Average map value	-0.010	Depositor
Map value standard deviation	0.997	Depositor
Recommended contour level	4.5	Depositor
Map size (Å)	376.0, 376.0, 376.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.94, 0.94, 0.94	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	C	0.16	0/9982	0.34	0/13408
1	D	0.16	0/9982	0.34	0/13408
1	E	0.16	0/9982	0.34	0/13408
All	All	0.16	0/29946	0.34	0/40224

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	C	9765	0	9060	202	0
1	D	9765	0	9060	198	0
1	E	9765	0	9060	198	0
All	All	29295	0	27180	583	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 10.

The worst 5 of 583 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:1744:LYS:CG	1:C:1776:LEU:HD22	1.59	1.31

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1744:LYS:CG	1:E:1776:LEU:HD22	1.59	1.30
1:D:1744:LYS:CG	1:D:1776:LEU:HD22	1.59	1.30
1:C:1523:PHE:HZ	1:C:1686:HIS:NE2	1.37	1.21
1:D:1744:LYS:HG2	1:D:1776:LEU:CD2	1.71	1.21

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	C	1313/2561 (51%)	1197 (91%)	110 (8%)	6 (0%)	24	56
1	D	1313/2561 (51%)	1197 (91%)	110 (8%)	6 (0%)	24	56
1	E	1313/2561 (51%)	1197 (91%)	110 (8%)	6 (0%)	24	56
All	All	3939/7683 (51%)	3591 (91%)	330 (8%)	18 (0%)	26	56

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	919	PRO
1	D	919	PRO
1	E	919	PRO
1	C	1177	ILE
1	D	1177	ILE

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	C	940/2260 (42%)	932 (99%)	8 (1%)	70	75
1	D	940/2260 (42%)	932 (99%)	8 (1%)	70	75
1	E	940/2260 (42%)	932 (99%)	8 (1%)	70	75
All	All	2820/6780 (42%)	2796 (99%)	24 (1%)	68	75

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	2020	PHE
1	E	1258	TYR
1	E	1184	TYR
1	E	1300	HIS
1	C	2020	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	2116	HIS
1	E	2347	ASN
1	D	2347	ASN
1	E	2080	GLN
1	D	2310	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.

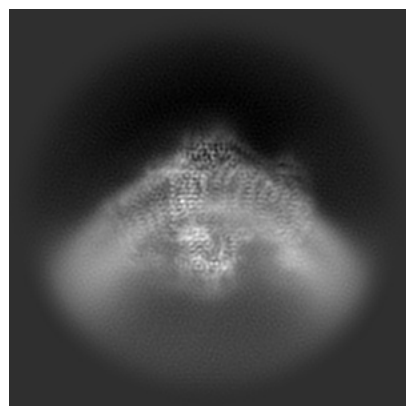
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-76184. These allow visual inspection of the internal detail of the map and identification of artifacts.

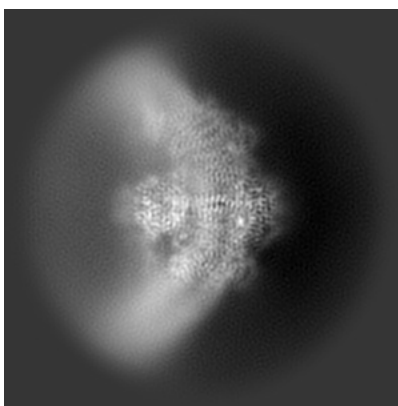
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

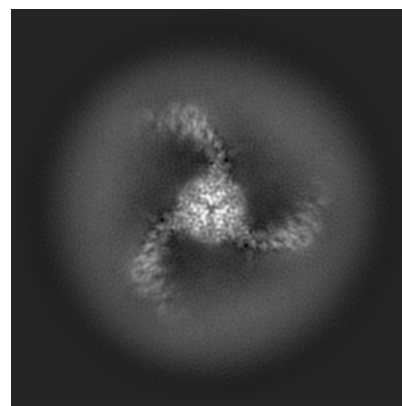
6.1.1 Primary map



X

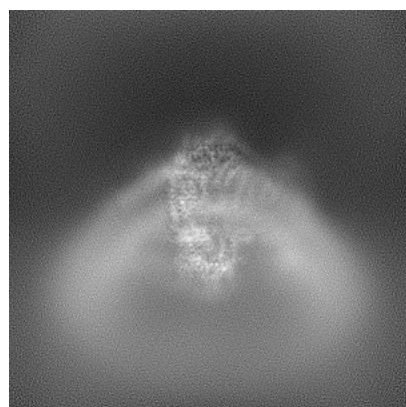


Y

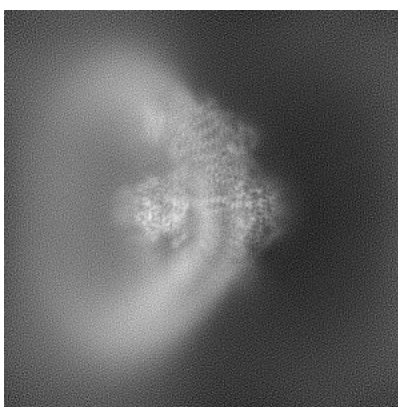


Z

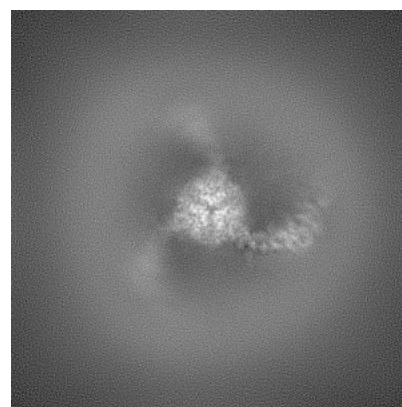
6.1.2 Raw map



X



Y

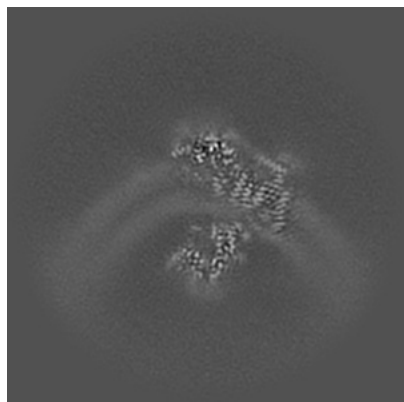


Z

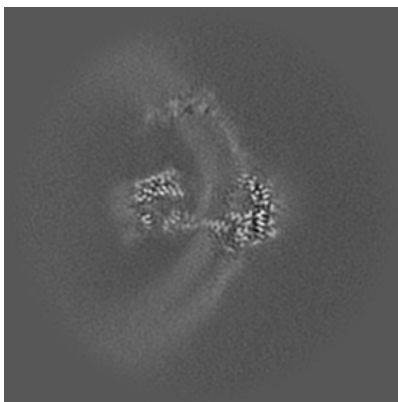
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

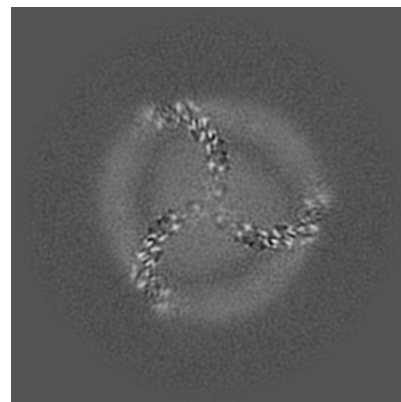
6.2.1 Primary map



X Index: 200

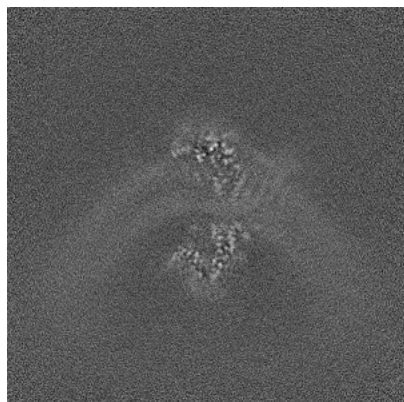


Y Index: 200

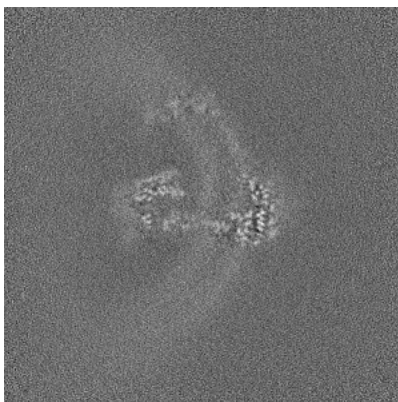


Z Index: 200

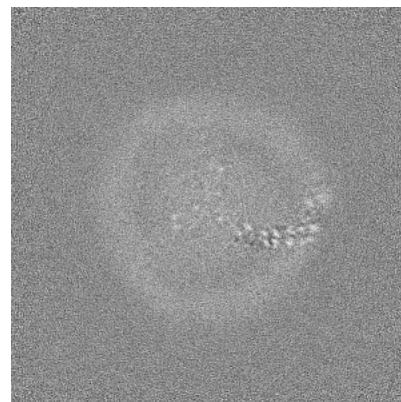
6.2.2 Raw map



X Index: 200



Y Index: 200

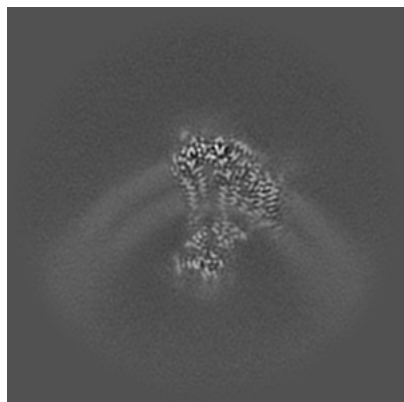


Z Index: 200

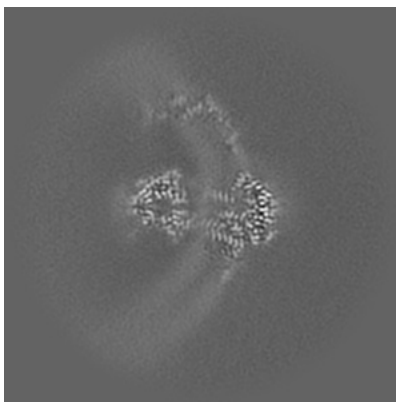
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

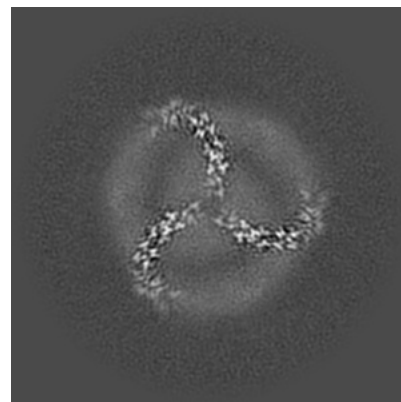
6.3.1 Primary map



X Index: 208

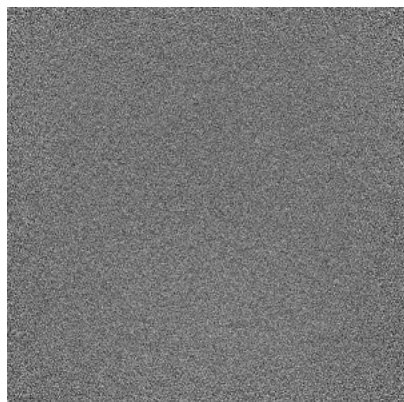


Y Index: 197

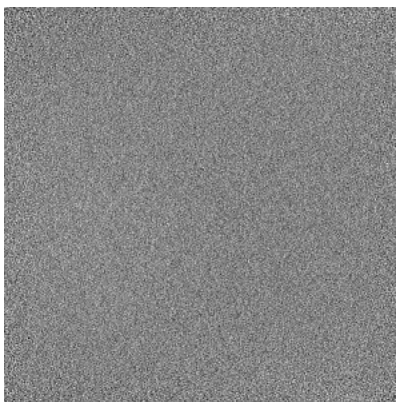


Z Index: 207

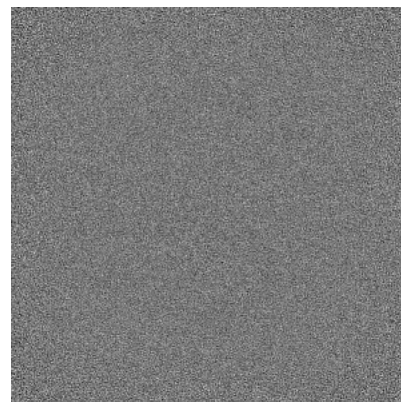
6.3.2 Raw map



X Index: 0



Y Index: 0

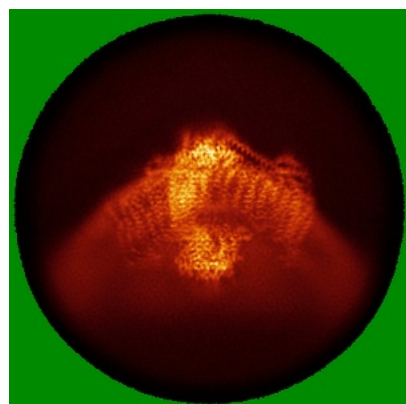


Z Index: 399

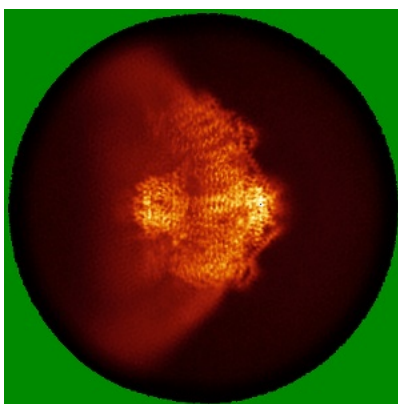
The images above show the largest variance slices of the map in three orthogonal directions.

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

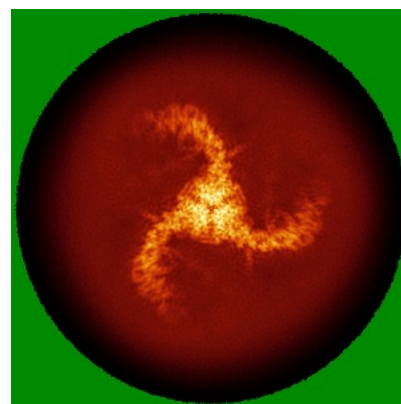
6.4.1 Primary map



X

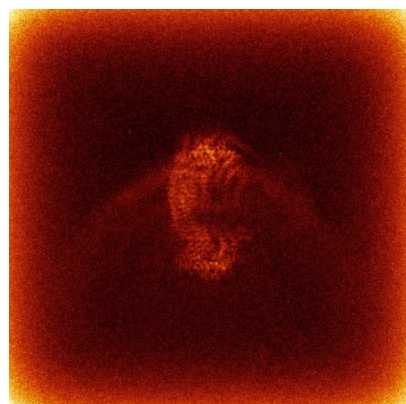


Y

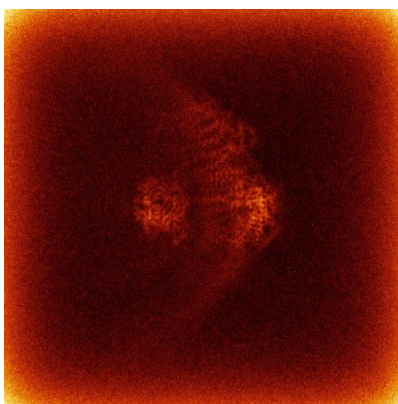


Z

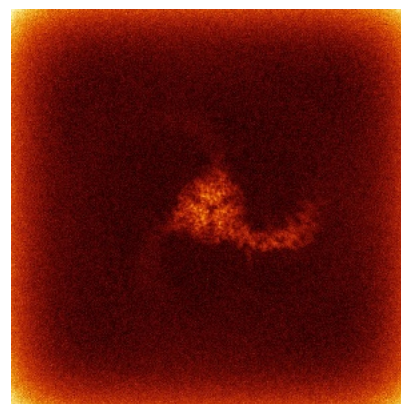
6.4.2 Raw map



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.

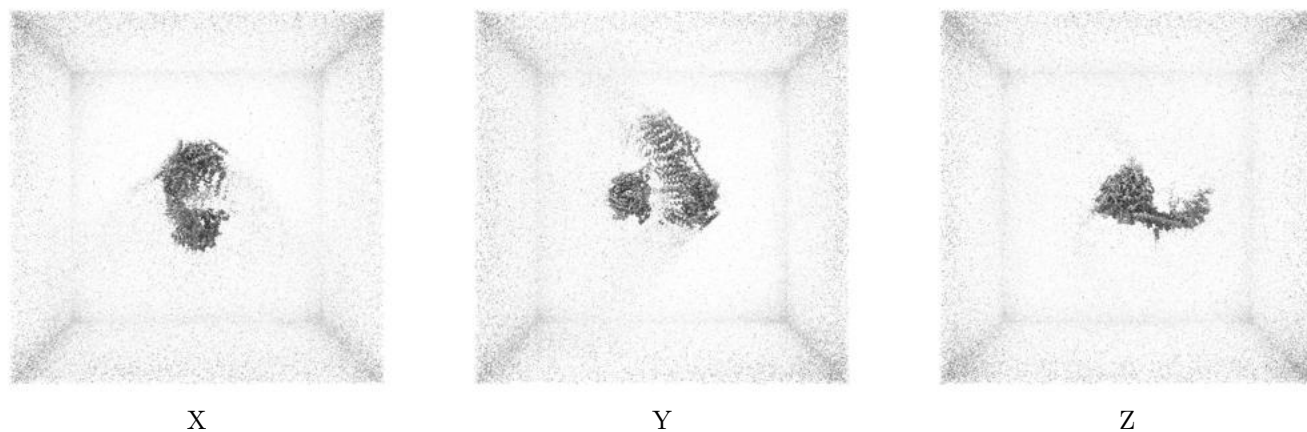
6.5 Orthogonal surface views [i](#)

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.

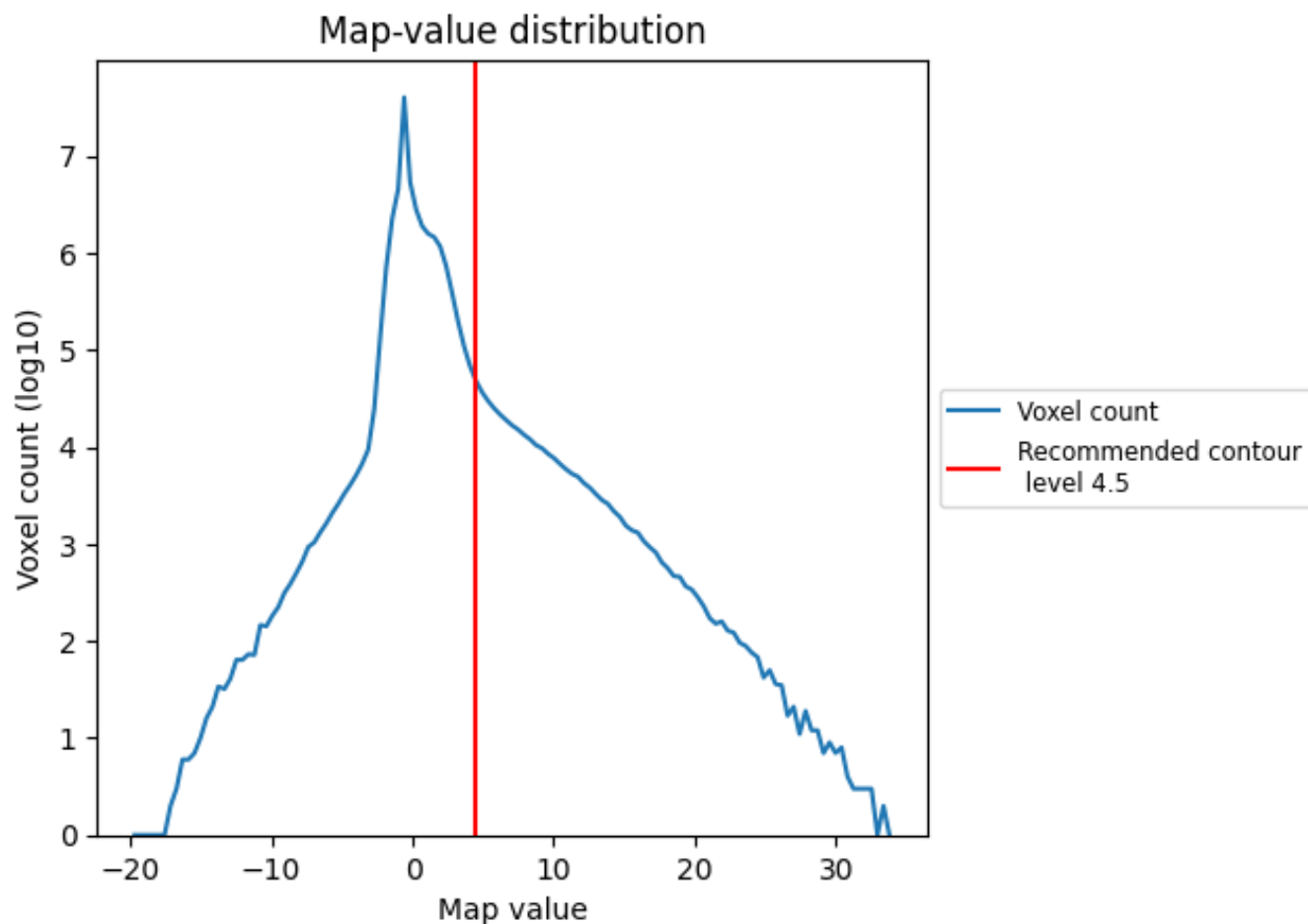
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

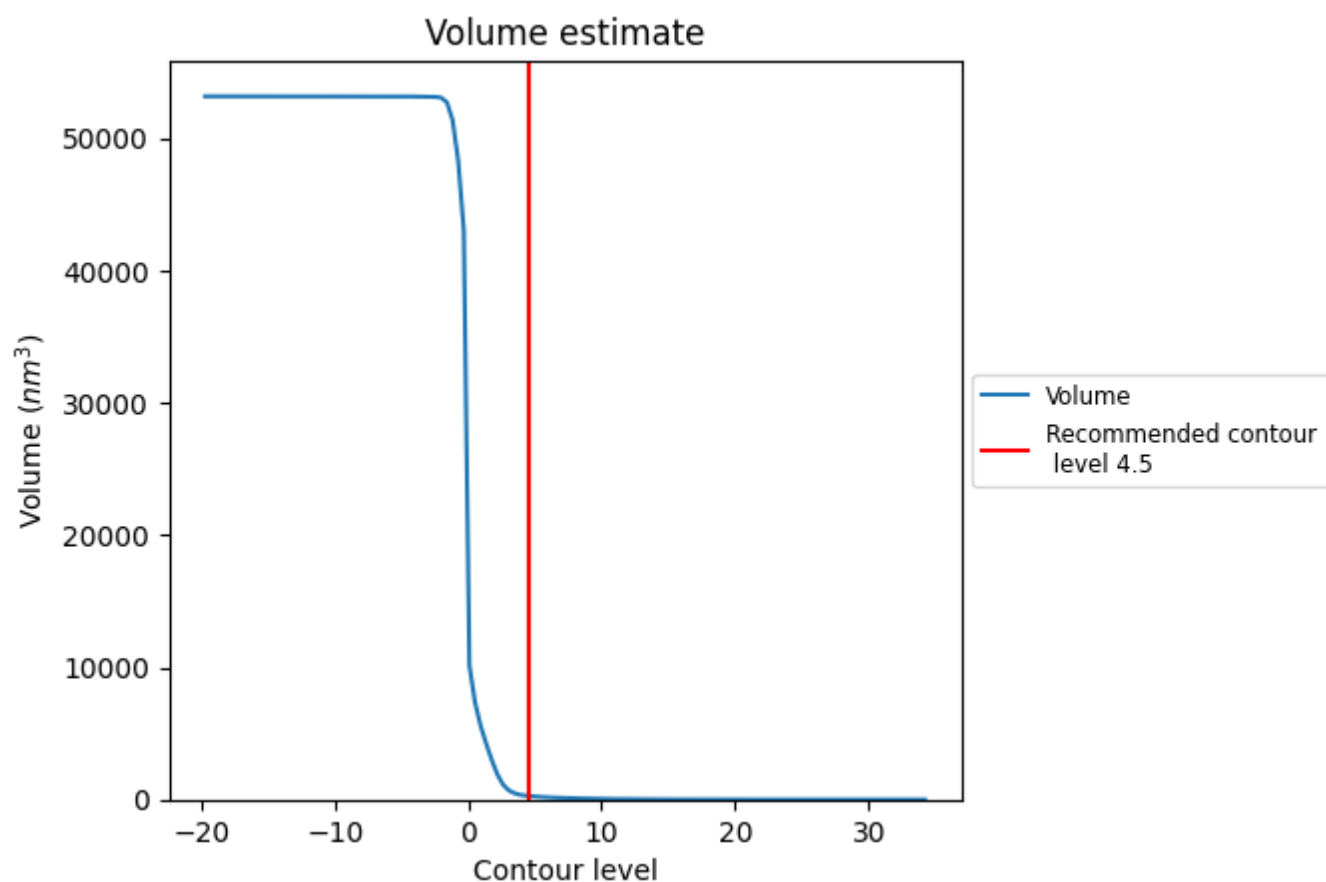
This section contains the results of statistical analysis of the map.

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.

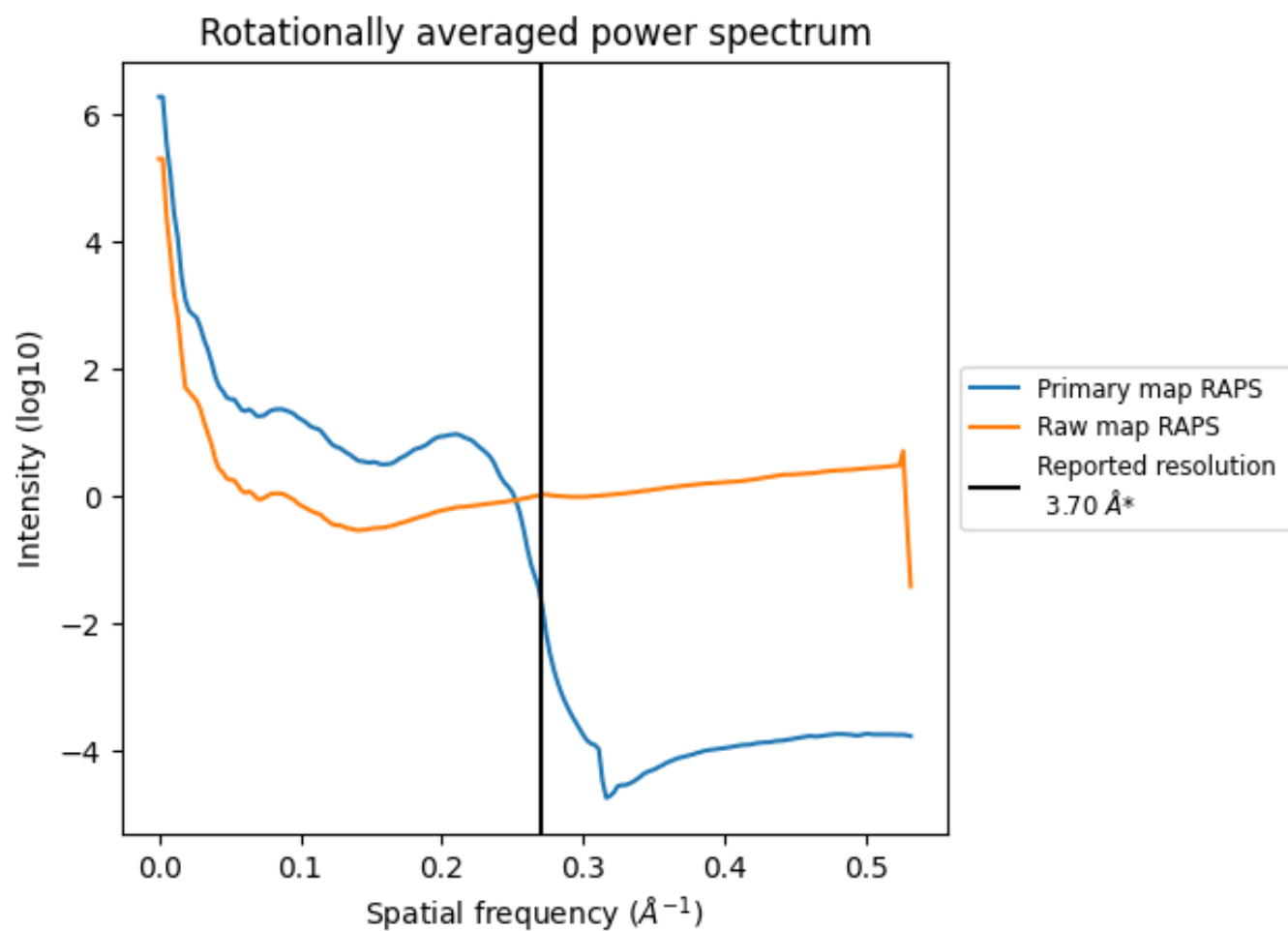
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 276 nm³; this corresponds to an approximate mass of 249 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 ⓘ

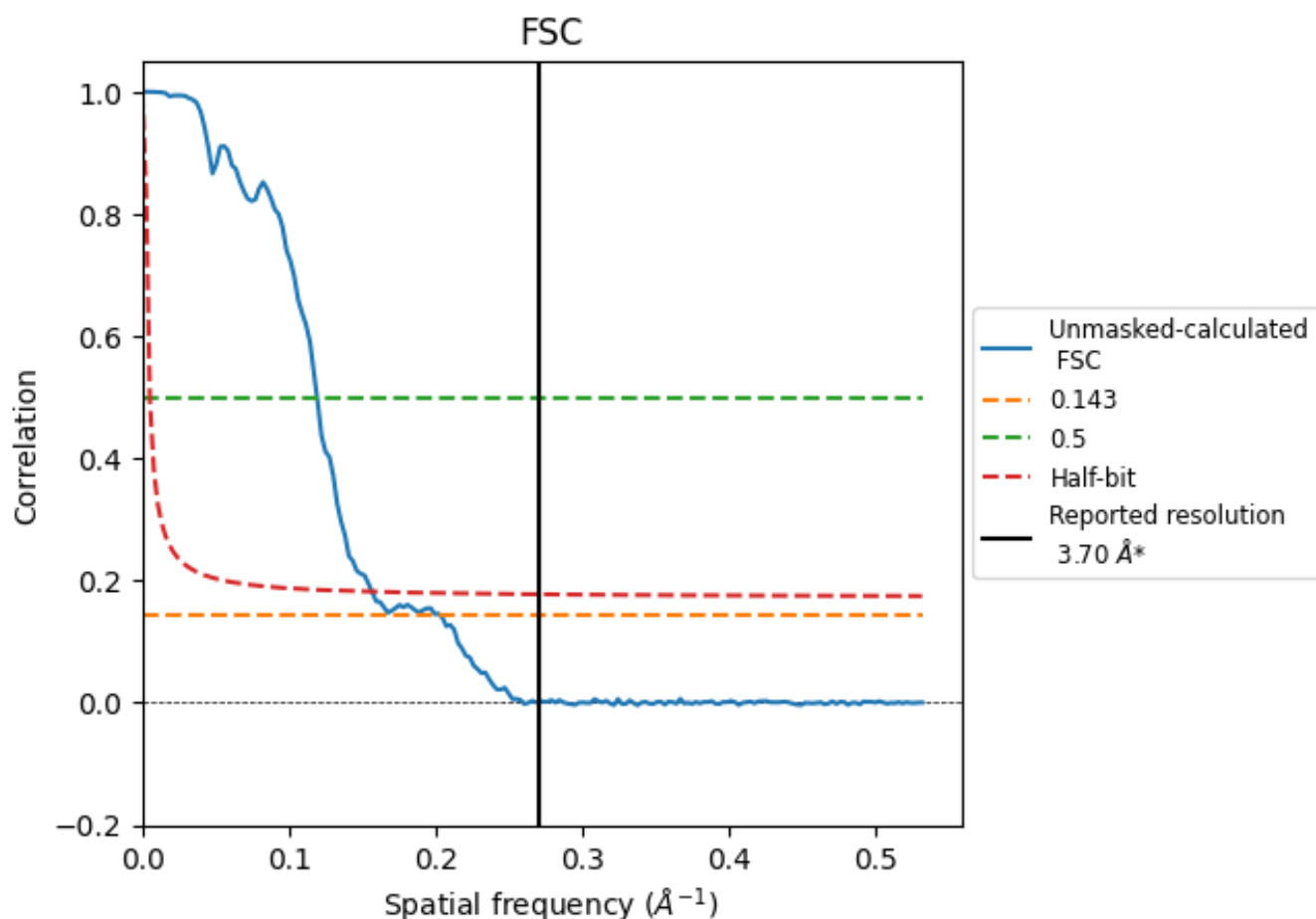


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

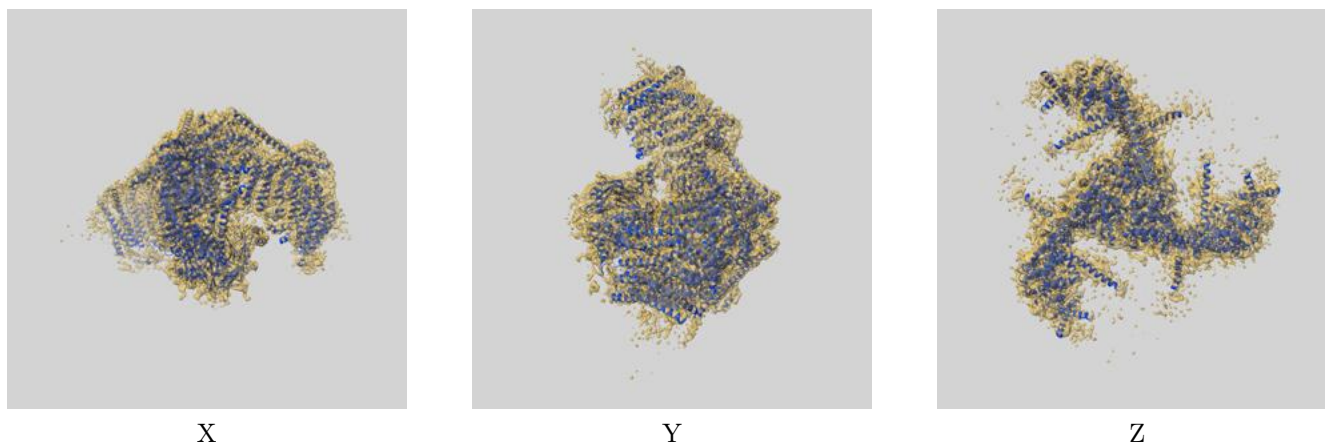
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.92	8.39	6.38

*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 4.92 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

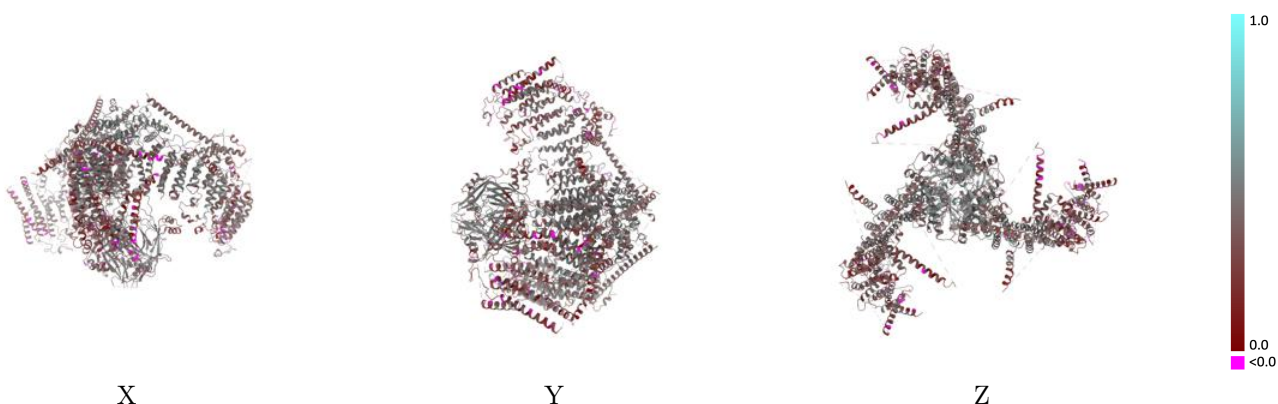
This section contains information regarding the fit between EMDB map EMD-76184 and PDB model 11YE. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



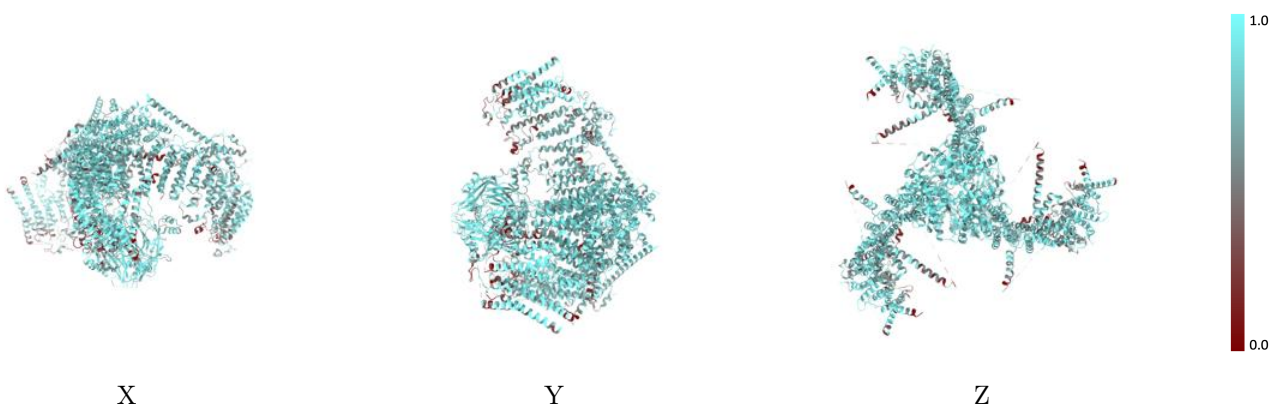
The images above show the 3D surface view of the map at the recommended contour level 4.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



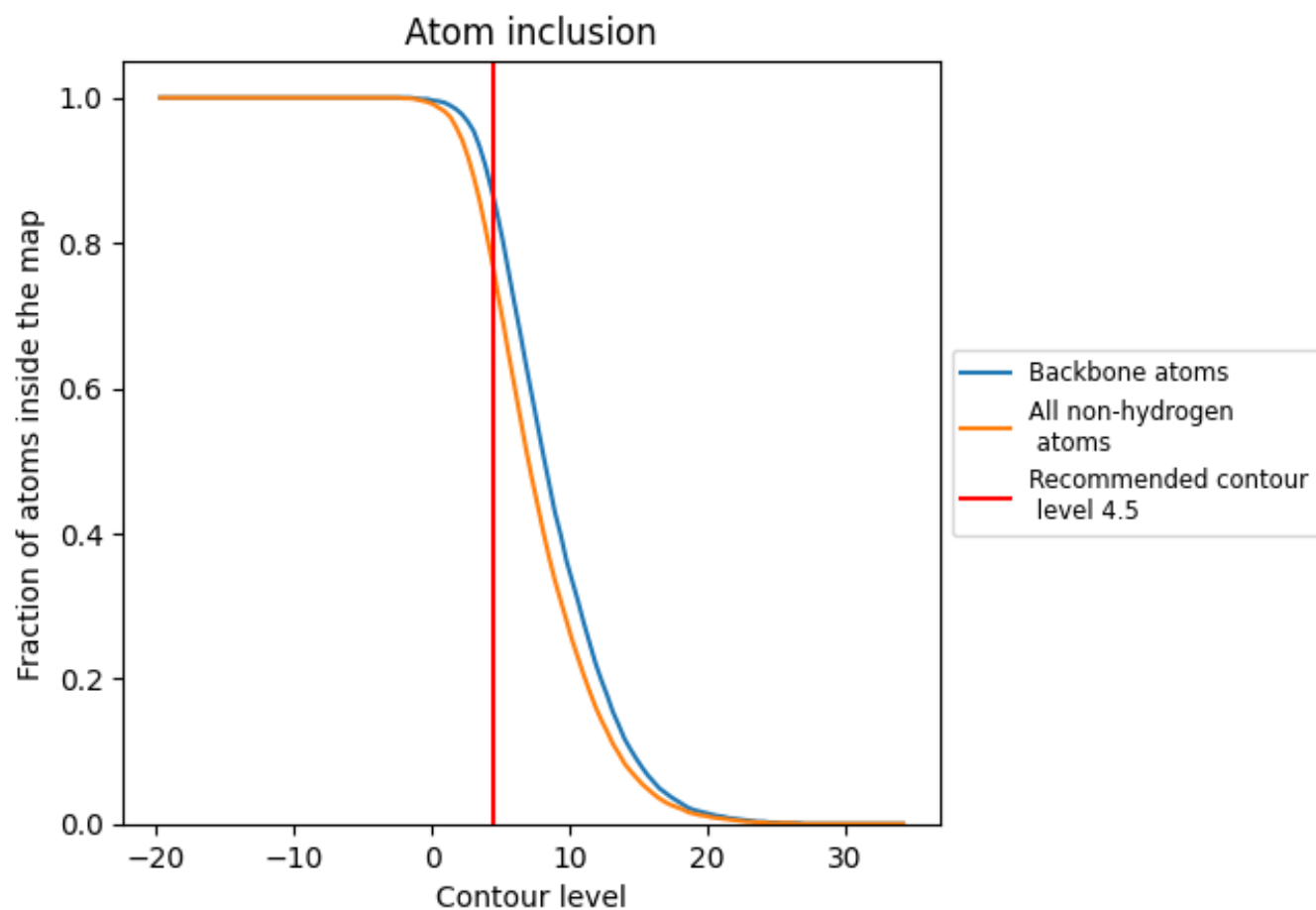
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 76% 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	0.7630	0.3750
C	0.7690	0.3790
D	0.7510	0.3680
E	0.7690	0.3780

