



wwPDB EM Validation Summary Report ⓘ

Jul 1, 2024 – 10:20 am BST

PDB ID : 8OZM
EMDB ID : EMD-17314
Title : In situ cryoEM structure of the Prototype Foamy Virus capsid, hexamer 1 localised reconstruction
Authors : Calcraft, T.; Nans, A.; Rosenthal, P.B.
Deposited on : 2023-05-09
Resolution : 3.40 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.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

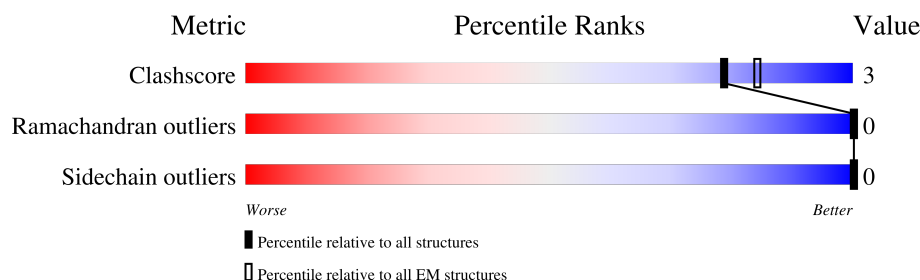
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY





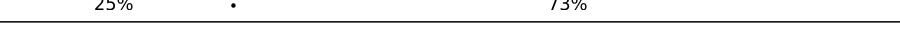
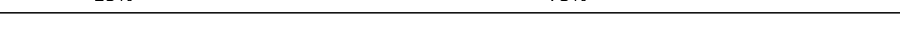
The reported resolution of this entry is 3.40 Å.

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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	B	648	 24% 73%
1	C	648	 26% 73%
1	D	648	 26% 73%
1	E	648	 25% 73%
1	F	648	 25% 73%
1	G	648	 25% 73%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8052 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.

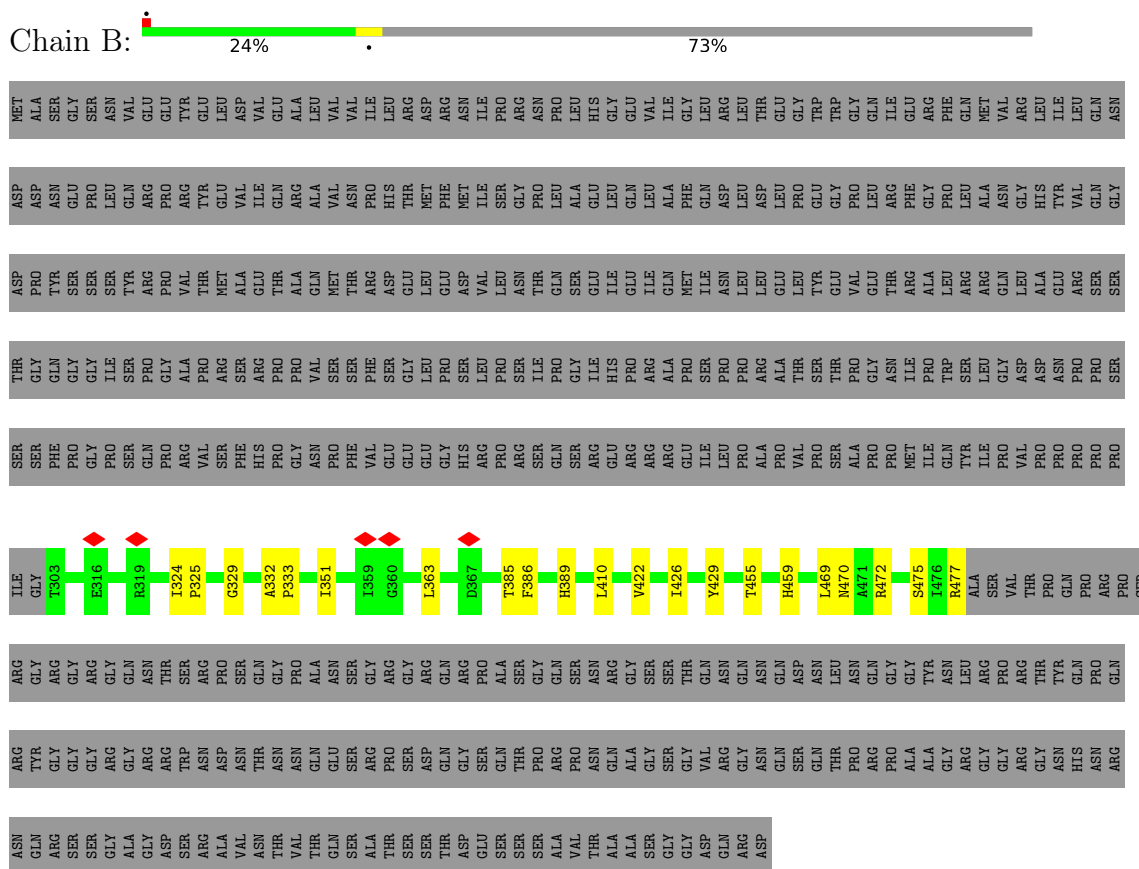
- Molecule 1 is a protein called Gag polyprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	175	Total	C	N	O	S	0	0
			1342	848	242	247	5		
1	C	175	Total	C	N	O	S	0	0
			1342	848	242	247	5		
1	D	175	Total	C	N	O	S	0	0
			1342	848	242	247	5		
1	E	175	Total	C	N	O	S	0	0
			1342	848	242	247	5		
1	F	175	Total	C	N	O	S	0	0
			1342	848	242	247	5		
1	G	175	Total	C	N	O	S	0	0
			1342	848	242	247	5		

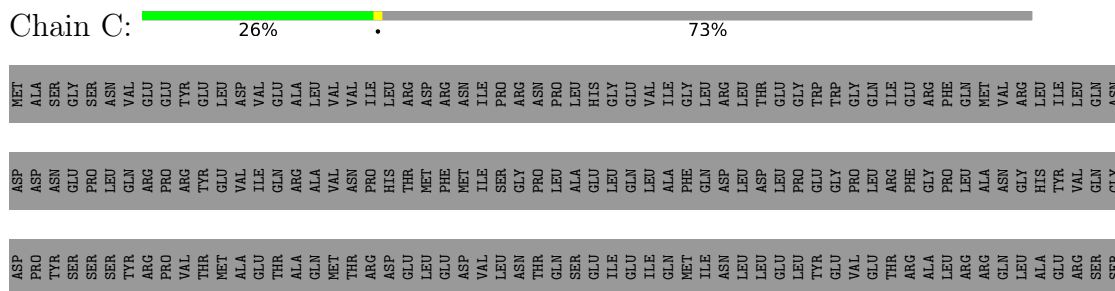
3 Residue-property plots

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: Gag polyprotein



• Molecule 1: Gag polyprotein







THR	PRO	ARG	ILE	SER	THR	ASP	ASP	MET
THR	PRO	ARG	ILE	SER	THR	ASP	ASP	MET
SER	SER	GLY	GLY	SER	GLN	TYR	ASP	ALA
THR	GLN	GLN	THR	PRO	GLY	SER	GLY	SER
ASP	GLY	ARG	V313	PRO	ILE	SER	PRO	ASN
GLU	SER	PRO	V313	PRO	ILE	SER	LEU	ASN
SER	THR	ALA	A332	SER	SER	TYR	GLN	VAL
SER	THR	SER	P233	GLN	PRO	ARG	ARG	GLU
ALA	PRO	GLY	P233	PRO	GLY	PRO	PRO	GLU
SER	ARG	GLN	V338	ARG	ALA	VAL	ARG	TVR
VAL	PRO	SER	V338	VAL	PRO	THR	TYR	GLU
THR	ASN	ASN	R347	SER	ARG	MET	GLU	LEU
ALA	GLN	ARG	R347	PHE	SER	ALA	VAL	ASP
ALA	ALA	GLY	I398	HIS	ARG	GLU	ILE	GLU
SER	GLY	SER	I398	PRO	PRO	THR	GLN	VAL
GLY	SER	THR	V404	GLY	PRO	ALA	ARG	ALA
GLY	THR	SER	V404	ASN	VAL	GLN	ALA	VAL
ASP	VAL	GLN	L410	PRO	SER	MET	VAL	VAL
GLN	ARG	ASN	L410	PHE	SER	THR	ASN	THR
ARG	GLY	GLN	L430	VAL	PHE	ARG	PRO	ILE
ASN	ASN	ASN	L430	GLU	GLU	ASP	HIS	LEU
GLN	GLN	GLN	V435	GLU	GLY	GLY	THR	GLY
SER	SER	ASN	V435	GLY	LEU	LEU	MET	ASP
GLN	GLN	ASN	D449	GLY	PRO	GLU	PHE	ARG
THR	THR	LEU	D449	HIS	SER	ASP	MET	ASN
PRO	PRO	ASN	R452	ARG	LEU	VAL	ILE	ASN
ARG	GLN	GLN	R452	PRO	PRO	SER	SER	PRO
PRO	GLY	GLY	L467	ARG	ARG	ASN	GLY	ASN
ALA	ALA	GLY	L467	SER	ILE	THR	PRO	ASN
ALA	ALA	TYR	R477	GLN	PRO	GLN	LEU	PRO
GLY	GLY	ASN	R477	SER	GLY	SER	ALA	LEU
ARG	ARG	LEU	ALA	ARG	ILE	GLU	ALA	ALA
GLY	GLY	ARG	VAL	GLU	THR	ILE	LEU	GLY
GLY	ARG	PRO	THR	ARG	ARG	ILE	GLN	VAL
GLY	THR	ARG	GLN	ARG	ALA	GLN	ALA	ILE
ASN	ASN	TYR	GLN	GLU	PRO	MET	PHE	GLY
HIS	GLN	GLN	ARG	ILE	SER	ILE	GLN	LEU
ASN	ASN	PRO	PRO	LEU	PRO	ASN	ASP	ARG
ARG	ARG	GLN	SER	PRO	PRO	LEU	LEU	THR
ASN	ASN	ARG	ARG	ALA	ARG	ASP	ASP	GLU
GLN	GLN	TYR	GLY	PRO	ALA	GLU	LEU	THR
ARG	ARG	GLY	GLY	VAL	THR	PRO	PRO	GLY
SER	SER	GLY	GLY	PRO	SER	TYR	GLU	TRP
ALA	GLY	ARG	GLY	ALA	THR	GLU	GLY	TRP
GLY	GLY	GLY	GLY	PRO	GLY	VAL	PRO	GLN
ASP	ASP	ARG	ASN	PRO	THR	ARG	LEU	ILE
THR	THR	ARG	THR	MET	ILE	ARG	ARG	GLY
ARG	ARG	ASN	SER	ILE	TRP	ALA	PHE	THR
ALA	ALA	ASP	PRO	TYR	SER	ARG	GLN	MET
ASN	ASN	ASN	SER	PRO	GLY	ALA	ASN	VAL
THR	THR	ASN	GLN	VAL	ASP	GLY	GLY	ARG
VAL	VAL	ASN	GLY	VAL	THR	LEU	HIS	THR
GLN	GLN	GLN	GLY	PRO	ASP	GLU	TYR	ILE
ASP	GLN	GLU	ALA	PRO	VAL	THR	GLN	GLN
	ALA	ARG	SER	PRO	SER	SER	GLY	ASN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	346237	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.093	Depositor
Minimum map value	-0.056	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0167	Depositor
Map size (\AA)	345.6, 345.6, 345.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	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	B	0.75	0/1368	0.93	1/1866 (0.1%)
1	C	0.74	0/1368	0.90	0/1866
1	D	0.74	0/1368	0.88	0/1866
1	E	0.73	0/1368	0.90	2/1866 (0.1%)
1	F	0.72	0/1368	0.89	1/1866 (0.1%)
1	G	0.73	0/1368	0.86	1/1866 (0.1%)
All	All	0.74	0/8208	0.89	5/11196 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	381	ARG	CG-CD-NE	-6.03	99.14	111.80
1	B	477	ARG	NE-CZ-NH1	5.65	123.13	120.30
1	E	347	ARG	NE-CZ-NH2	-5.45	117.58	120.30
1	F	338	VAL	CA-CB-CG1	5.17	118.66	110.90
1	G	347	ARG	NE-CZ-NH1	5.12	122.86	120.30

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	B	1342	0	1360	16	0
1	C	1342	0	1360	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1342	0	1360	3	0
1	E	1342	0	1360	5	0
1	F	1342	0	1360	10	0
1	G	1342	0	1360	7	0
All	All	8052	0	8160	45	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 3.

The worst 5 of 45 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:F:313:VAL:HG21	1:F:338:VAL:HG21	1.59	0.85
1:G:398:ILE:HD13	1:G:410:LEU:HD23	1.64	0.79
1:G:313:VAL:HG21	1:G:338:VAL:HG21	1.82	0.60
1:B:455:THR:HG22	1:B:459:HIS:CD2	2.36	0.60
1:B:422:VAL:O	1:B:426:ILE:HG12	2.02	0.59

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	B	173/648 (27%)	158 (91%)	15 (9%)	0	100	100
1	C	173/648 (27%)	169 (98%)	4 (2%)	0	100	100
1	D	173/648 (27%)	161 (93%)	12 (7%)	0	100	100
1	E	173/648 (27%)	163 (94%)	10 (6%)	0	100	100
1	F	173/648 (27%)	168 (97%)	5 (3%)	0	100	100
1	G	173/648 (27%)	164 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1038/3888 (27%)	983 (95%)	55 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	B	145/543 (27%)	145 (100%)	0	100	100
1	C	145/543 (27%)	145 (100%)	0	100	100
1	D	145/543 (27%)	145 (100%)	0	100	100
1	E	145/543 (27%)	145 (100%)	0	100	100
1	F	145/543 (27%)	145 (100%)	0	100	100
1	G	145/543 (27%)	145 (100%)	0	100	100
All	All	870/3258 (27%)	870 (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. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	390	GLN
1	F	440	GLN
1	G	420	GLN
1	F	445	GLN
1	D	461	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides 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.

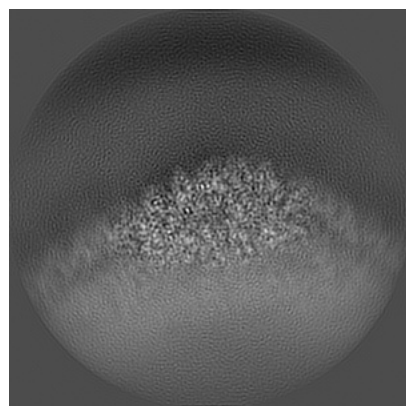
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17314. These allow visual inspection of the internal detail of the map and identification of artifacts.

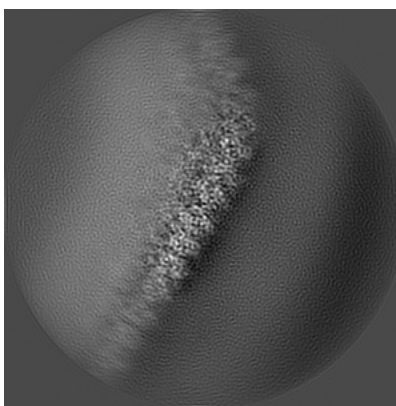
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

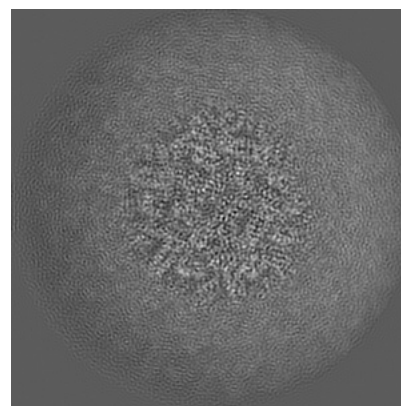
6.1.1 Primary map



X

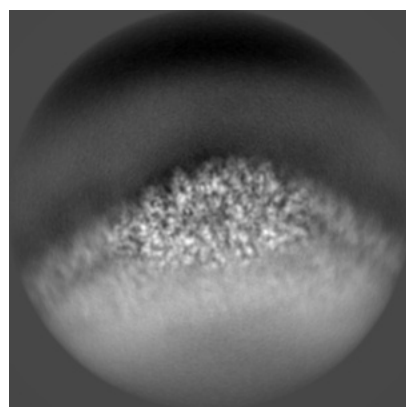


Y

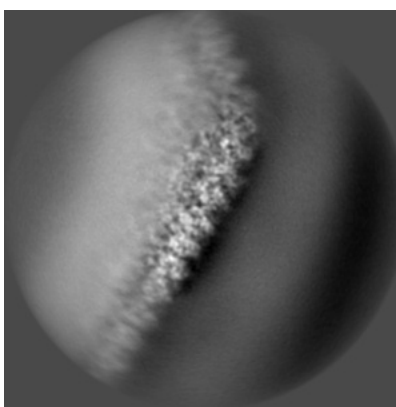


Z

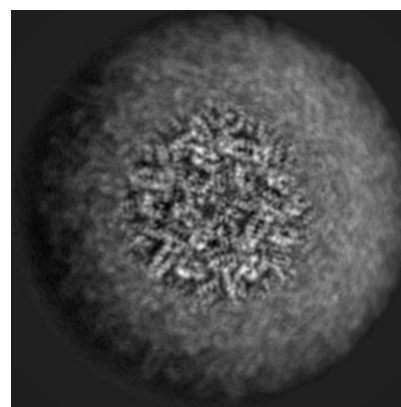
6.1.2 Raw map



X



Y

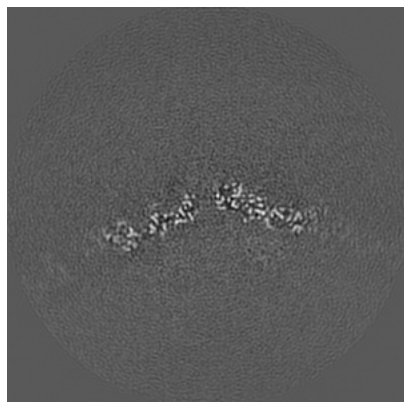


Z

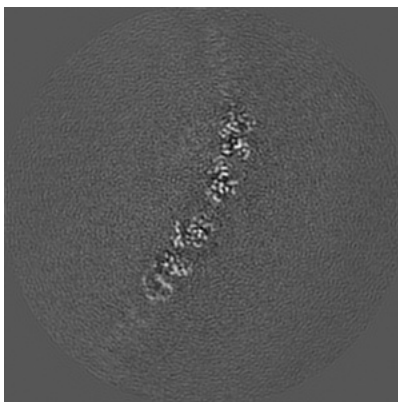
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

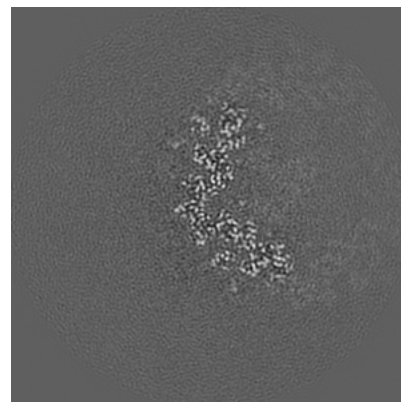
6.2.1 Primary map



X Index: 160

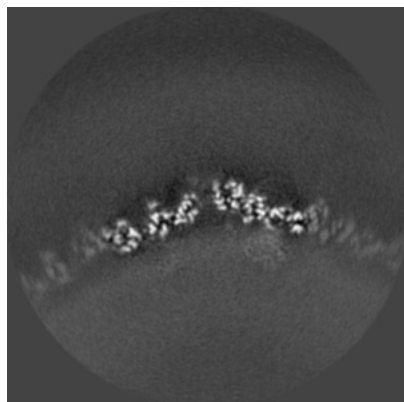


Y Index: 160

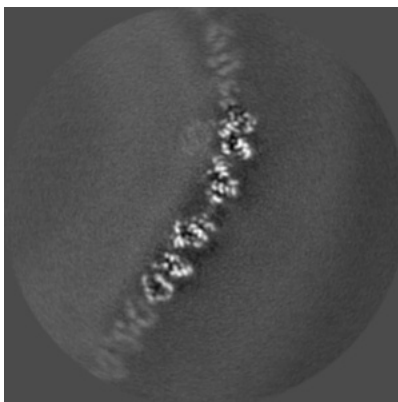


Z Index: 160

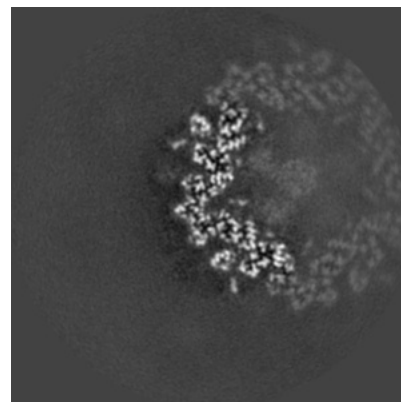
6.2.2 Raw map



X Index: 160



Y Index: 160

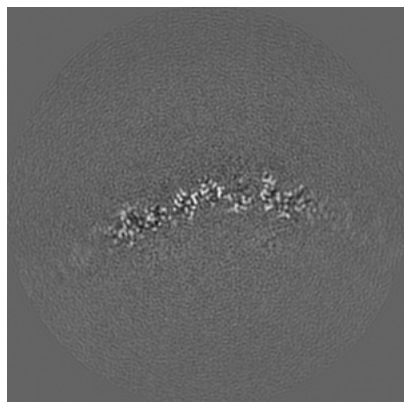


Z Index: 160

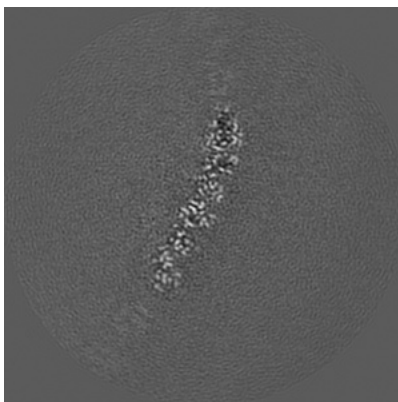
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

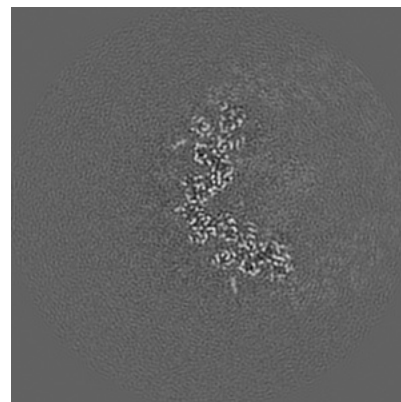
6.3.1 Primary map



X Index: 176

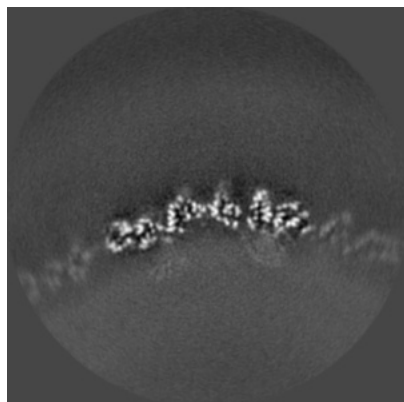


Y Index: 138

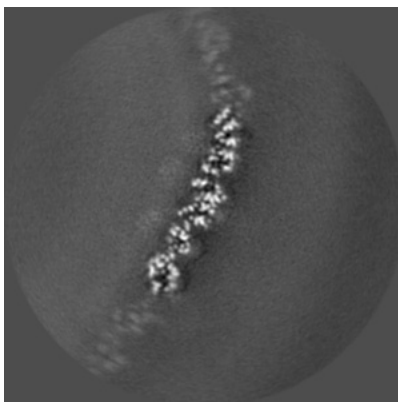


Z Index: 159

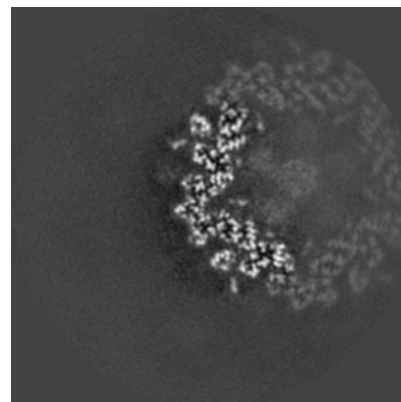
6.3.2 Raw map



X Index: 152



Y Index: 142

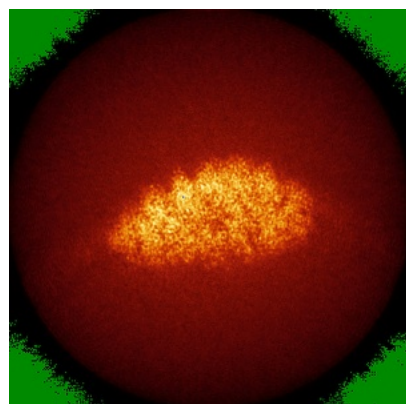


Z Index: 160

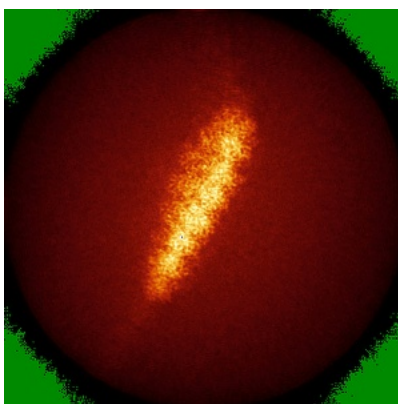
The images above show the largest variance slices of the map in three orthogonal directions.

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

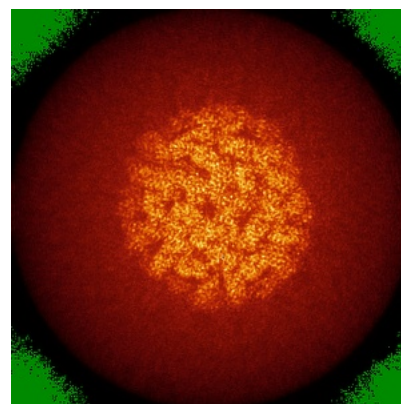
6.4.1 Primary map



X

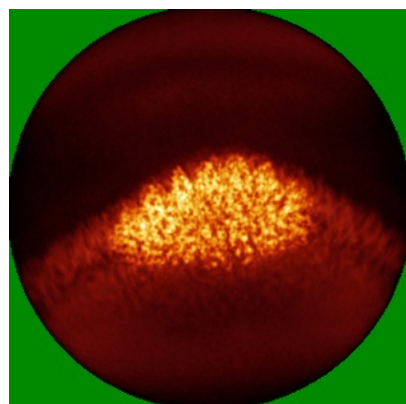


Y

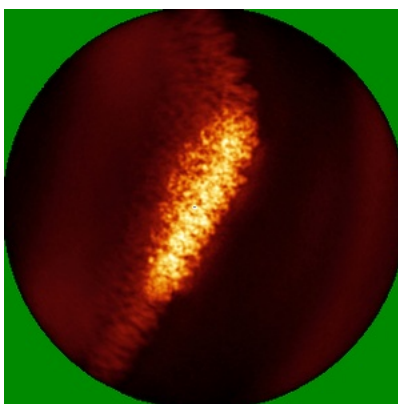


Z

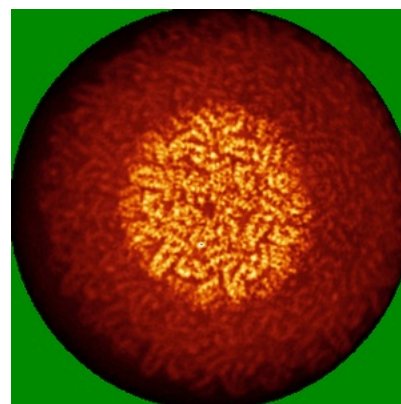
6.4.2 Raw map



X



Y

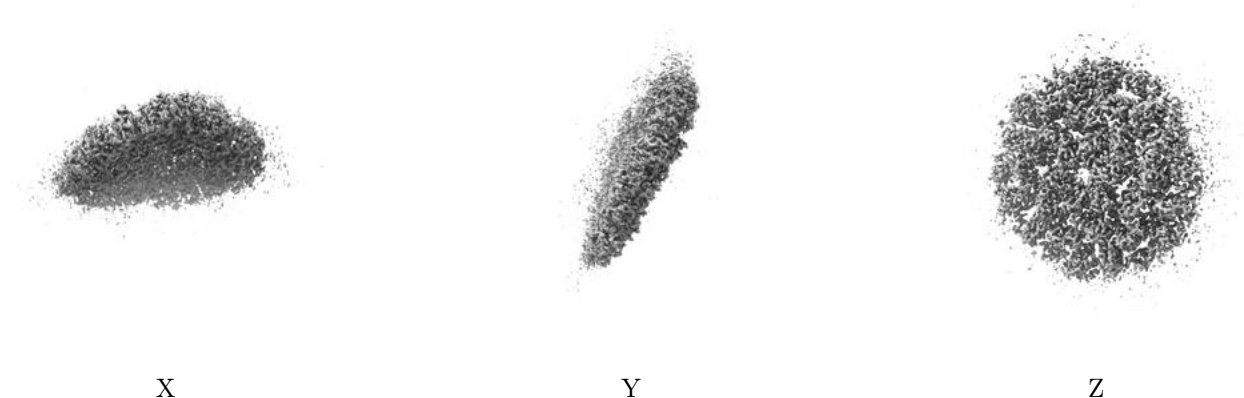


Z

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 0.0167. 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.

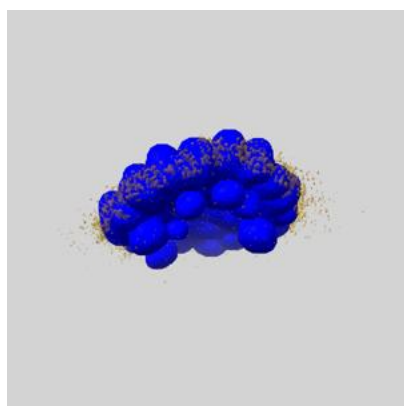
6.6 Mask visualisation [i](#)

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

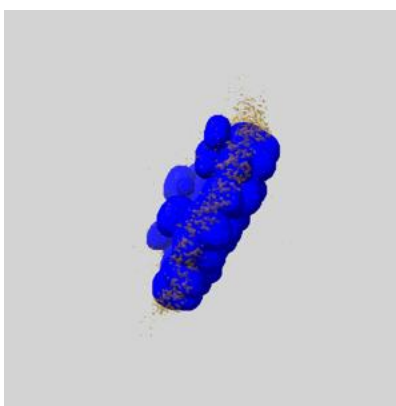
A mask typically either:

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

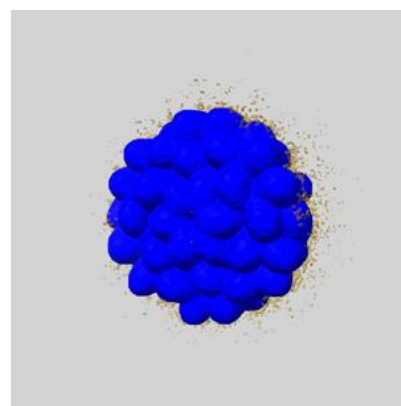
6.6.1 emd_17314_msk_1.map [i](#)



X



Y

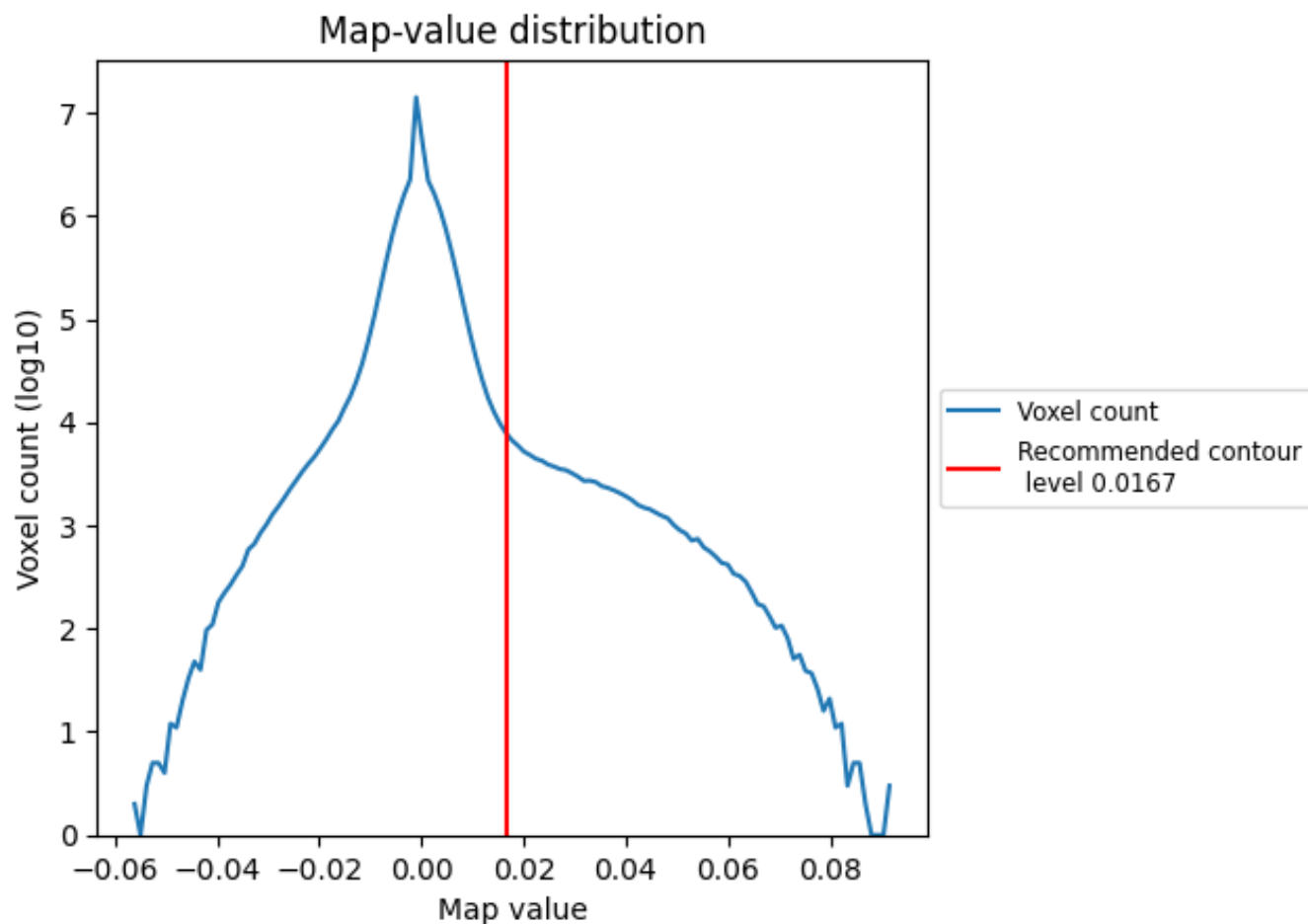


Z

7 Map analysis [i](#)

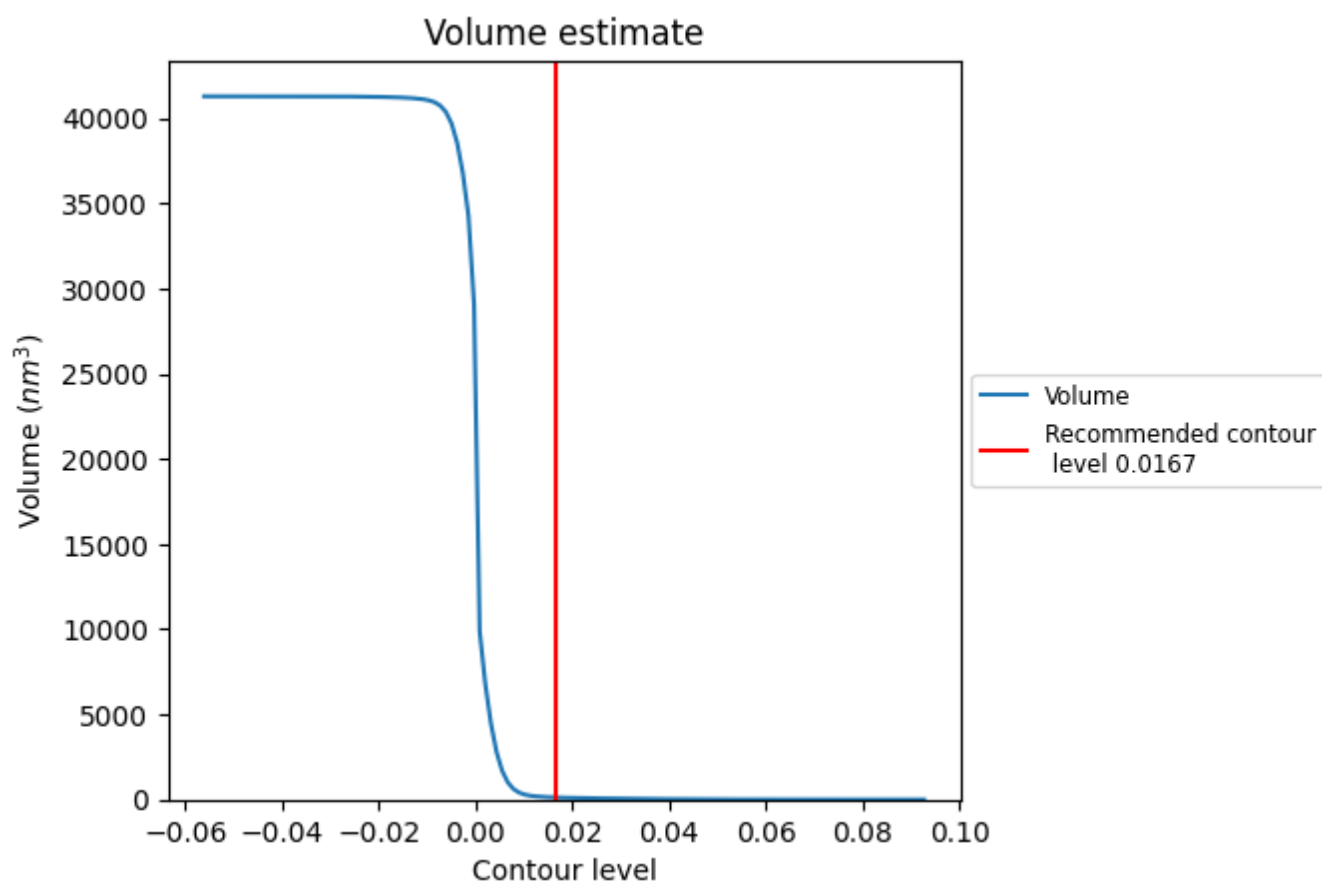
This section contains the results of statistical analysis of the map.

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.

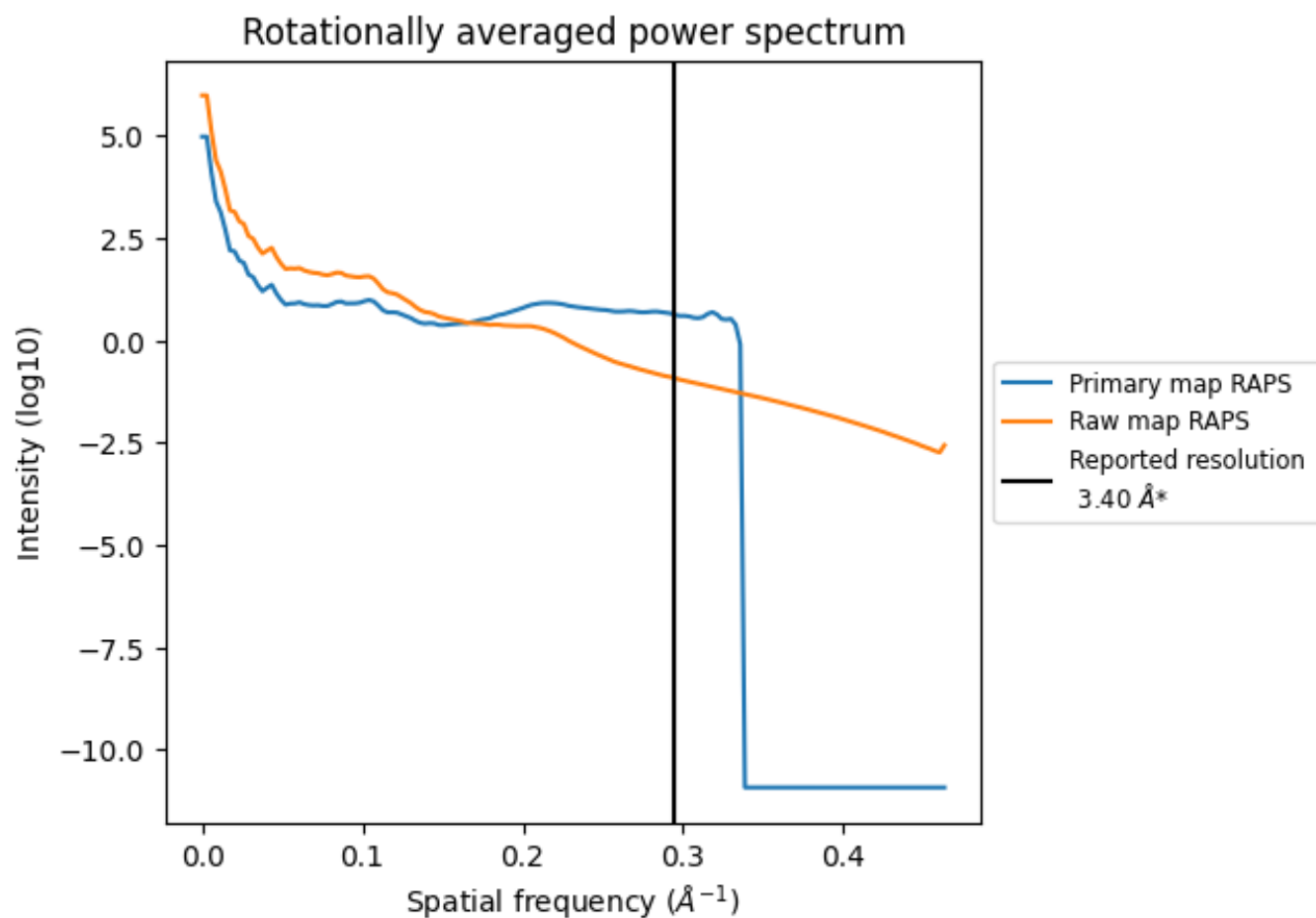
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 122 nm³; this corresponds to an approximate mass of 111 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 ⓘ

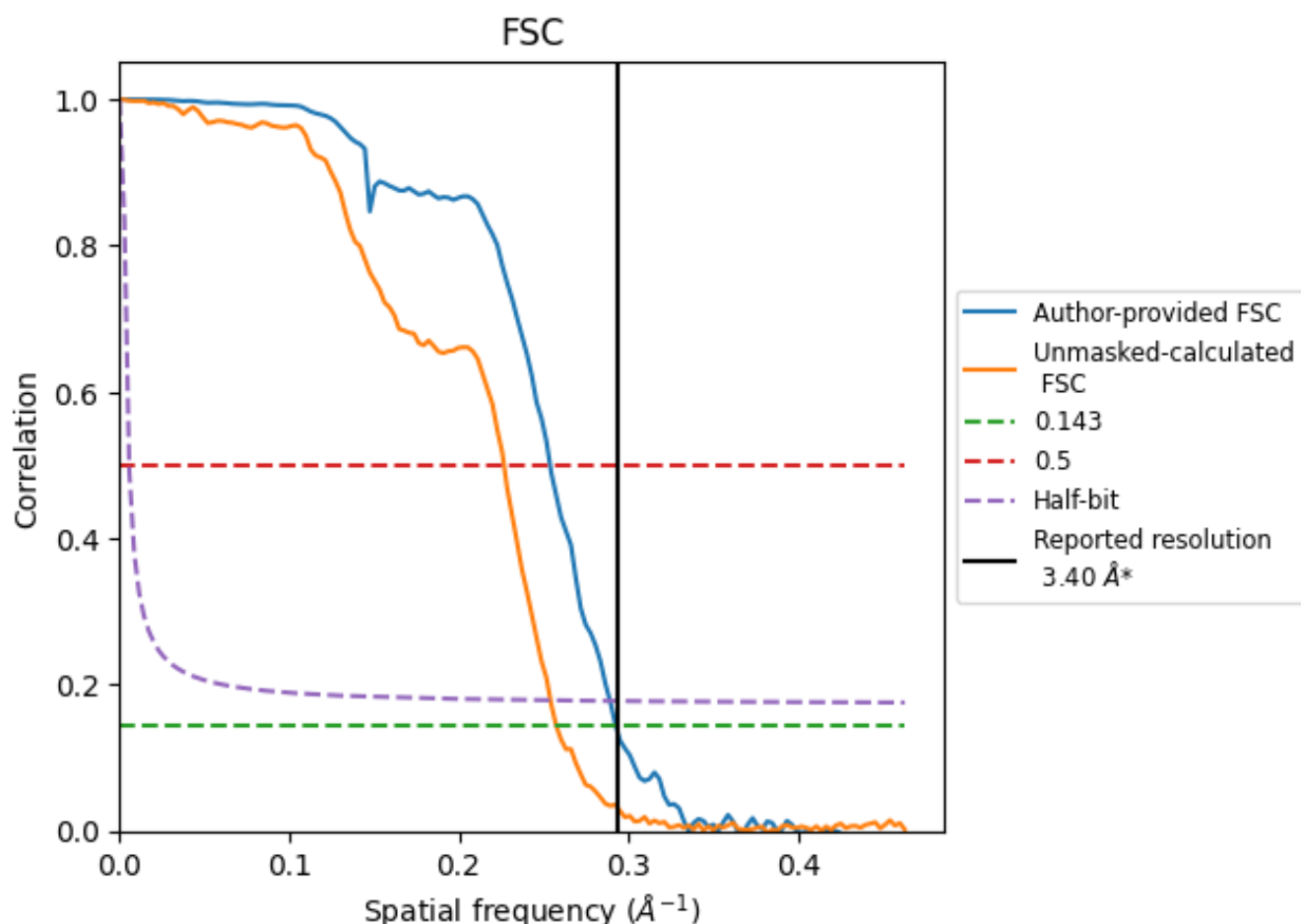


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

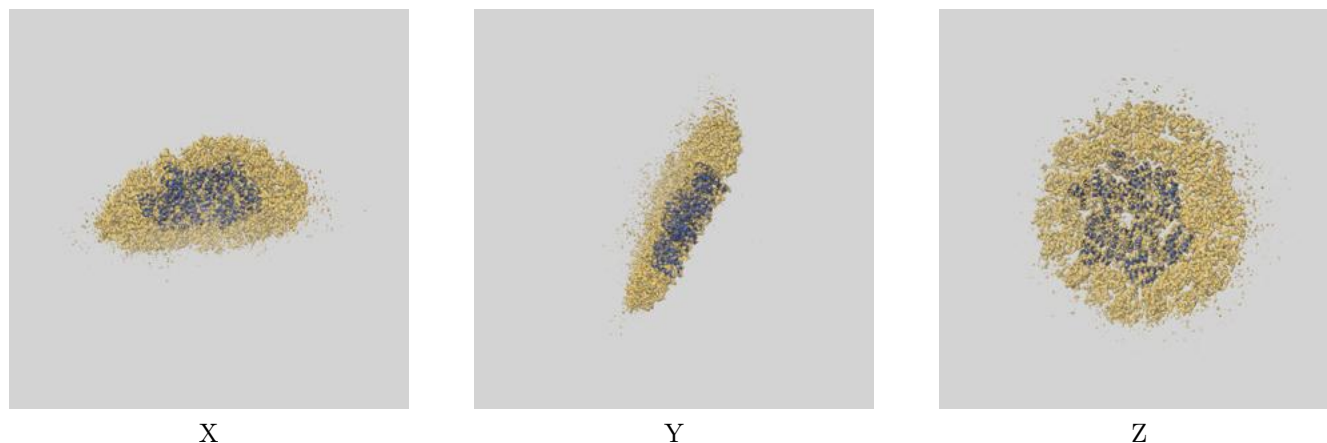
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.42	3.94	3.46
Unmasked-calculated*	3.88	4.41	3.94

*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 3.88 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

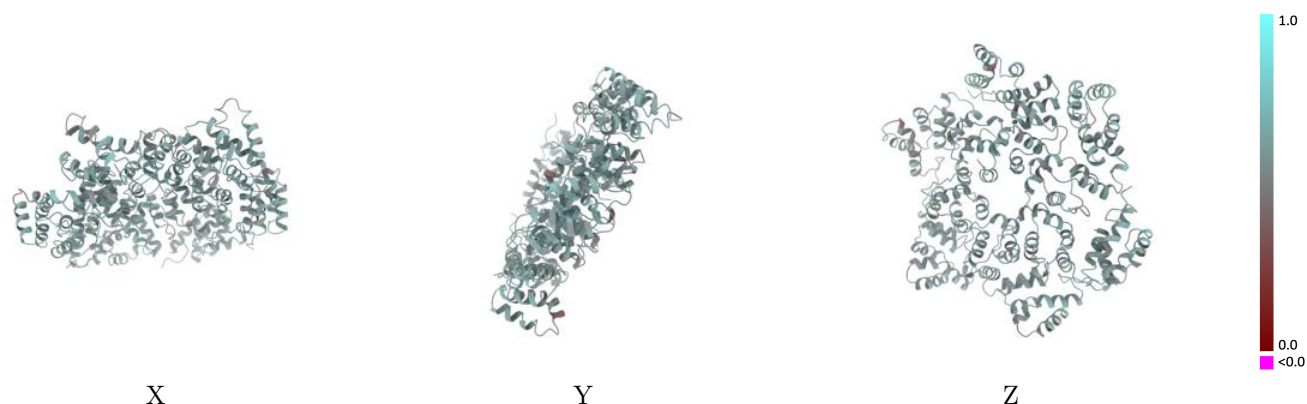
This section contains information regarding the fit between EMDB map EMD-17314 and PDB model 8OZM. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



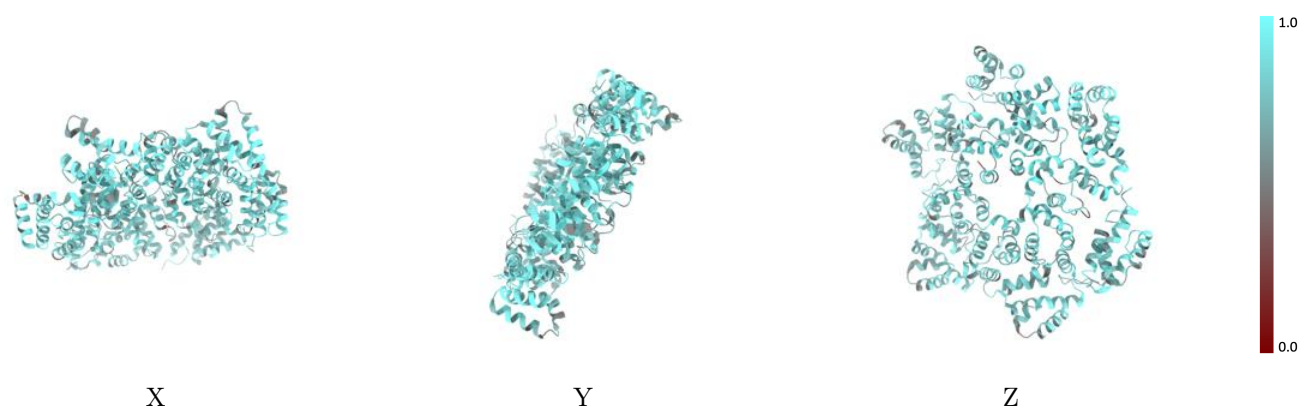
The images above show the 3D surface view of the map at the recommended contour level 0.0167 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



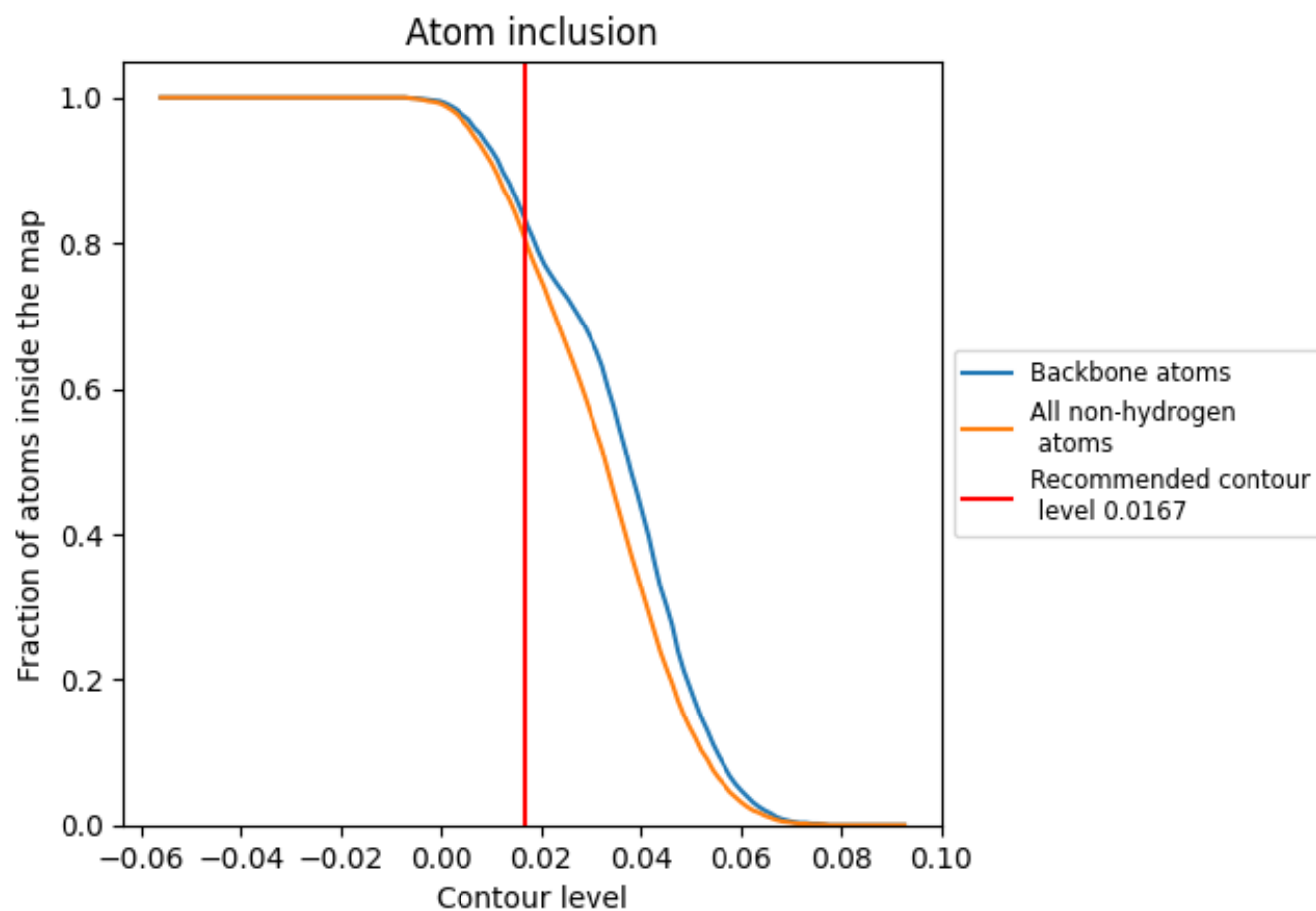
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0167).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 81% 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 (0.0167) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8080	<div><div></div></div> 0.5650
B	<div><div></div></div> 0.8090	<div><div></div></div> 0.5630
C	<div><div></div></div> 0.7960	<div><div></div></div> 0.5670
D	<div><div></div></div> 0.8160	<div><div></div></div> 0.5710
E	<div><div></div></div> 0.8100	<div><div></div></div> 0.5640
F	<div><div></div></div> 0.8130	<div><div></div></div> 0.5650
G	<div><div></div></div> 0.8040	<div><div></div></div> 0.5610

