



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 05:22 PM UTC

PDB ID : 8OZN / pdb_00008ozn
EMDB ID : EMD-17315
Title : In situ cryoEM structure of the Prototype Foamy Virus capsid, hexamer 2 localised reconstruction
Authors : Calcraft, T.; Nans, A.; Rosenthal, P.B.
Deposited on : 2023-05-09
Resolution : 3.50 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.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

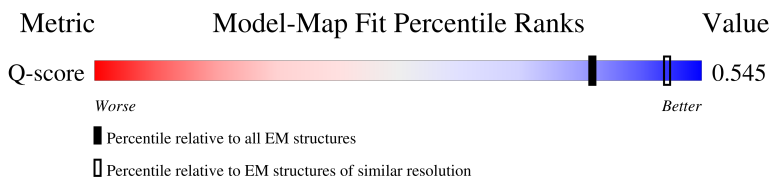
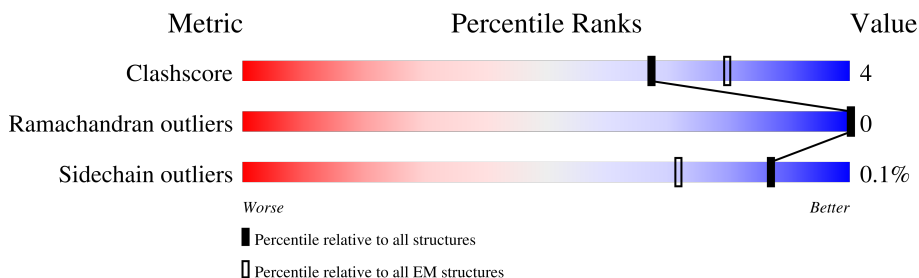
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	H	648	
1	I	648	
1	J	648	
1	K	648	

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Mol	Chain	Length	Quality of chain
1	L	648	23% 73%
1	M	648	25% 73%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8030 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	H	175	Total	C	N	O	S	0	0
			1342	848	242	247	5		
1	I	175	Total	C	N	O	S	0	0
			1342	848	242	247	5		
1	J	174	Total	C	N	O	S	0	0
			1331	842	238	246	5		
1	K	175	Total	C	N	O	S	0	0
			1342	848	242	247	5		
1	L	174	Total	C	N	O	S	0	0
			1331	842	238	246	5		
1	M	175	Total	C	N	O	S	0	0
			1342	848	242	247	5		

[illegible]

- Molecule 1: Gag polyprotein



ALA	GLY	ARG	GLY	ARG	GLY	ASN	THR	ARG	ALA	ARG	ALA	THR	THR	ASP	MET
GLY	ARG	GLY	THR	THR	GLN	THR	GLN	GLN	SER	GLY	GLN	GLY	GLY	PRO	ALA
GLY	ARG	GLY	THR	THR	GLN	THR	THR	THR	THR	T303	THR	GLN	SER	ASN	SER
GLY	ASN	HIS	GLN	GLN	THR	THR	THR	THR	THR	V304	THR	GLY	SER	GLY	GLY
GLY	ASN	ARG	GLN	GLN	THR	THR	THR	THR	THR	T305	THR	ILE	SER	LEU	ASN
ASN	ASN	GLY	GLN	GLN	THR	THR	THR	THR	THR	P306	THR	SER	ARG	GLN	VAL
ASN	ASN	GLY	GLN	GLN	THR	THR	THR	THR	THR	R311	THR	PRO	THR	GLN	GLY
ASN	ASN	GLY	GLN	GLN	THR	THR	THR	THR	THR	S312	THR	GLY	PRO	PRO	GLY
ASN	ASN	GLY	GLN	GLN	THR	THR	THR	THR	THR	V313	THR	ALA	VAL	ARG	TYR
ASN	ASN	GLY	GLN	GLN	THR	THR	THR	THR	THR	E316	THR	VAL	THR	GLY	LEU
GLN	GLN	THR	THR	THR	THR	THR	THR	THR	THR	P317	THR	SER	ARG	ALA	ASP
ARG	ARG	THR	THR	THR	THR	THR	THR	THR	THR	P318	THR	HIS	ARG	GLY	VAL
SER	SER	THR	THR	THR	THR	THR	THR	THR	THR	R319	THR	PRO	PRO	ALA	ALA
SER	SER	THR	THR	THR	THR	THR	THR	THR	THR	GLY	THR	ASN	VAL	GLN	LEU
GLY	GLY	ARG	ARG	ARG	GLY	GLN	GLY	GLY	ASN	T324	THR	PRO	SER	VAL	VAL
ALA	ALA	GLY	ASN	ASN	GLN	GLN	GLN	GLN	PRO	P325	THR	SER	THR	ASN	VAL
GLY	GLY	THR	THR	THR	THR	THR	THR	THR	THR	I326	THR	PHE	ARG	PRO	VAL
ASP	ASP	ARG	ARG	ARG	THR	THR	THR	THR	THR	V327	THR	VAL	ARG	THR	VAL
ARG	ARG	THR	THR	THR	THR	THR	THR	THR	THR	L328	THR	GLY	ASP	HIS	ILE
ARG	ARG	THR	THR	THR	THR	THR	THR	THR	THR	GLY	THR	GLY	THR	ARG	ARG
ALA	ALA	THR	THR	THR	THR	THR	THR	THR	THR	V338	THR	GLY	LEU	MET	ASP
VAL	VAL	ASN	THR	THR	THR	THR	THR	THR	THR	GLY	THR	PRO	GLY	PHE	ARG
ASN	ASN	THR	THR	THR	THR	THR	THR	THR	THR	T359	THR	SER	ASP	MET	ASN
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ARG	THR	LEU	VAL	ILE	THR
VAL	VAL	THR	THR	THR	THR	THR	THR	THR	THR	D367	THR	PRO	LEU	SER	PRO
GLN	GLN	THR	THR	THR	THR	THR	THR	THR	THR	GLN	THR	SER	ASN	GLY	ASN
SER	SER	THR	THR	THR	THR	THR	THR	THR	THR	S373	THR	PRO	GLN	GLY	THR
ALA	ALA	ARG	ARG	ARG	GLY	GLY	GLY	GLY	SER	A374	THR	PRO	GLY	SER	ALA
THR	THR	PRO	PRO	PRO	ARG	ARG	ARG	ARG	ARG	V375	THR	GLY	GLY	LEU	LEU
SER	SER	THR	THR	THR	GLY	GLY	GLY	GLY	GLY	A376	THR	ILE	GLY	HIS	THR
SER	SER	THR	THR	THR	THR	THR	THR	THR	THR	T377	THR	HIS	ILE	GLY	GLY
THR	THR	ASP	GLY	GLY	GLN	GLY	GLY	GLY	ARG	P387	THR	ARG	GLN	ALA	ILE
ASP	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ARG	GLY	THR	ALA	MET	GLY	GLY
GLY	GLY	SER	SER	SER	PRO	PRO	PRO	PRO	PRO	Q390	THR	SER	ILE	GLN	LEU
SER	SER	THR	THR	THR	ALA	ALA	ALA	ALA	ALA	L391	THR	PRO	ASN	ARG	ARG
SER	SER	PRO	PRO	PRO	GLY	GLY	GLY	GLY	GLY	GLY	THR	LEU	LEU	LEU	THR
SER	SER	ALA	ALA	ALA	GLN	GLN	GLN	GLN	GLN	V394	THR	ARG	LEU	ASP	THR
VAL	VAL	THR	THR	THR	ASN	ASN	ASN	ASN	ASN	PRO	THR	ALA	GLY	LEU	GLY
THR	THR	ASN	ASN	ASN	SER	SER	SER	SER	SER	T398	THR	THR	LEU	PRO	GLY
ALA	ALA	GLN	GLN	GLN	ARG	ARG	ARG	ARG	ARG	A407	THR	SER	GLY	TRP	TRP
ALA	ALA	SER	SER	SER	GLY	GLY	GLY	GLY	GLY	ALA	THR	PRO	VAL	PRO	GLY
GLY	GLY	GLY	GLY	GLY	SER	SER	SER	SER	SER	M413	THR	PRO	GLY	LEU	GLY
ASP	ASP	VAL	VAL	VAL	THR	THR	THR	THR	THR	L421	THR	MET	ARG	PHE	ILE
GLN	GLN	ARG	ARG	ARG	ASN	ASN	ASN	ASN	ASN	ILE	THR	ILE	ALA	GLY	ARG
ARG	ARG	GLY	GLY	GLY	GLN	GLN	GLN	GLN	GLN	R427	THR	GLN	LEU	PRO	PHE
ASP	ASP	GLN	GLN	GLN	ASN	ASN	ASN	ASN	ASN	V435	THR	TYR	ARG	GLY	GLN
						</									

- Molecule 1: Gag polyprotein



NET	ALA	SER	GLY	SER	ASN	VAL	GLU	LEU	GLU	ASP	VAL	GLU	ALA	ALA	LEU	VAL	VAL	ILE	PRO	ARG	ASN	ASN	PRO	LEU	HIS	GLY	GLU	VAL	ILE	GLY	LEU	ARG	LEU	THR	GLU	GLY	TRP	TRP	GLY	GLN	ILE	GLN	GLU	ARG	PHE	GLN	NET	VAL	VAL	ARG	ARG	LEU	ILE	LEU	LEU	ASN	GLN
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ALA	THR	SER	SER	THR	ASP	ARG	GLY	ILE	SER	THR	ASP	ASP	MET
THR	SER	SER	ASP	THR	GLN	PRO	ARG	GLY	SER	GLY	PRO	ASP	ALA
SER	SER	SER	ASP	THR	GLN	GLN	ARG	T303	PHE	GLN	TYR	ASP	SER
THR	THR	GLN	GLN	GLN	GLN	GLN	ARG	V304	PRO	GLY	SER	GLY	SER
ASP	ASP	GLY	ARG	ARG	PRO	PRO	ARG	P306	PRO	ILE	SER	LEU	ASN
GLU	SER	SER	SER	THR	THR	THR	ALA	I307	SER	SER	TYR	GLN	VAL
SER	SER	SER	THR	THR	PRO	PRO	GLY	R319	ARG	ALA	ARG	GLU	VAL
SER	SER	GLN	GLN	GLN	GLN	GLN	GLN	T324	VAL	PRO	THR	GLU	TYR
ALA	VAL	ARG	PRO	ARG	ASN	ASN	SER	P325	SER	ARG	GLU	LEU	ASP
THR	THR	ASN	ASN	ASN	ASN	ASN	PHE	G325	SER	SER	ALA	VAL	ASP
ALA	ALA	GLN	ARG	ARG	GLY	GLY	ARG	A332	HIS	ARG	ILE	VAL	VAL
ALA	ALA	GLY	GLY	GLY	GLY	GLY	GLY	P333	PRO	PRO	THR	GLN	GLN
SER	SER	GLY	GLY	SER	SER	SER	SER	G356	ASN	VAL	ALA	ALA	ALA
GLY	GLY	GLY	THR	THR	THR	THR	THR	G357	PRO	SER	MET	VAL	VAL
ASP	ASP	VAL	VAL	VAL	GLN	GLN	GLN	N358	PHE	SER	THR	ASN	VAL
GLN	GLN	ARG	ARG	ARG	ASN	ASN	ASN	L361	GLY	SER	ARG	PRO	ILE
ARG	ARG	GLY	GLY	GLN	GLN	GLN	GLN	S362	GLU	GLY	GLU	THR	ARG
ASP	ASP	GLN	SER	SER	ASP	ASP	ASN	L363	GLY	PRO	GLU	PHE	ASP
		GLN	ASN	ASN	ASN	ASN	ASN	L369	HIS	SER	ASP	MET	ASN
		THR	THR	LEU	LEU	LEU	LEU	L378	ARG	LEU	VAL	ILE	ILE
		PRO	PRO	ASN	ASN	ASN	GLN	L378	PRO	PRO	LEU	SER	PRO
		ARG	ARG	GLN	GLY	GLY	GLY	T437	ARG	ILE	THR	ASN	ASN
		PRO	PRO	GLY	GLY	GLY	GLY		SER	ILE	PRO	PRO	ASN
		ALA	ALA	ALA	ALA	ALA	ALA		GLN	PRO	GLN	LEU	GLN
		ALA	ALA	ALA	ALA	ALA	ALA		SER	GLY	SER	ALA	LEU
		GLY	GLY	GLY	GLY	GLY	GLY	R477	ARG	ILE	GLU	GLU	HIS
		GLY	GLY	GLY	GLY	GLY	GLY	ALA	GLU	HIS	ILE	GLY	GLY
		ARG	ARG	ARG	ARG	ARG	ARG	SER	ARG	PRO	GLN	GLN	GLU
		GLY	GLY	GLY	GLY	GLY	GLY	VAL	ARG	ARG	ILE	LEU	VAL
		GLY	GLY	GLY	GLY	GLY	GLY	THR	ARG	ALA	GLN	ALA	ILE
		ASN	ASN	ASN	ASN	ASN	ASN	PRO	ILE	SER	MET	PHE	GLY
		HIS	HIS	HIS	HIS	HIS	THR	GLN	LEU	ASN	GLN	ARG	LEU
		ASN	ASN	ASN	ASN	ASN	TYR	PRO	PRO	ILE	ILE	GLN	THR
		ARG	ARG	ARG	ARG	ARG	THR	ARG	ALA	PRO	GLY	LEU	GLY
		ASN	ASN	ASN	ASN	ASN	ASN	GLN	VAL	ALA	TYR	GLU	GLY
		GLN	GLN	GLN	GLN	GLN	TYR	ARG	PRO	THR	GLU	PRO	TRP
		ARG	ARG	ARG	ARG	ARG	GLY	GLY	SER	SER	GLY	TRP	TRP
		SER	SER	SER	SER	SER	GLY	GLY	ARG	PRO	GLY	TRP	TRP
		GLY	GLY	GLY	GLY	GLY	ARG	ARG	PRO	GLY	GLY	GLY	GLY
		ALA	ALA	ALA	ALA	ALA	ALA	GLY	PRO	ASN	THR	ARG	ILE
		GLY	GLY	GLY	GLY	GLY	ARG	GLN	MET	ILE	PHE	GLY	ARG
		ASP	ASP	ASP	ASP	ASP	ASP	ASN	ILE	PRO	ALA	GLY	ARG
		SER	SER	SER	SER	SER	TRP	THR	GLN	TRP	LEU	PRO	PHE
		ARG	ARG	ARG	ARG	ARG	ASN	TYR	SER	SER	ARG	ALA	GLY
		ALA	ALA	ALA	ALA	ALA	ASP	ILE	ILE	LEU	ARG	ALA	MET
		VAL	VAL	VAL									

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	340192	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	0.089	Depositor
Minimum map value	-0.058	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0153	Depositor
Map size (Å)	345.6, 345.6, 345.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	H	1.06	0/1368	1.52	2/1866 (0.1%)
1	I	1.06	0/1368	1.54	6/1866 (0.3%)
1	J	1.06	0/1357	1.54	3/1852 (0.2%)
1	K	1.08	0/1368	1.54	5/1866 (0.3%)
1	L	1.09	0/1357	1.54	6/1852 (0.3%)
1	M	1.08	0/1368	1.49	2/1866 (0.1%)
All	All	1.07	0/8186	1.53	24/11168 (0.2%)

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	477	ARG	CA-C-O	8.64	135.49	120.80
1	L	384	GLY	CA-C-O	-6.70	117.63	122.45
1	J	387	PRO	N-CA-CB	-6.64	98.36	102.81
1	J	317	PRO	N-CA-CB	6.20	106.66	103.19
1	I	432	GLY	CA-C-O	-5.88	117.88	122.52

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	H	1342	0	1360	11	0
1	I	1342	0	1360	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	1331	0	1347	11	0
1	K	1342	0	1360	7	0
1	L	1331	0	1347	11	0
1	M	1342	0	1360	8	0
All	All	8030	0	8134	62	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 62 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:M:363:LEU:HD21	1:M:378:LEU:CD1	2.17	0.74
1:L:391:LEU:HD23	1:L:421:LEU:HD21	1.73	0.69
1:M:358:ASN:OD1	1:M:361:LEU:HD12	1.96	0.65
1:M:363:LEU:HD21	1:M:378:LEU:HD11	1.79	0.62
1:I:313:VAL:HG21	1:I:338:VAL:HG21	1.81	0.61

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	H	173/648 (27%)	160 (92%)	13 (8%)	0	100	100
1	I	173/648 (27%)	157 (91%)	16 (9%)	0	100	100
1	J	172/648 (26%)	153 (89%)	19 (11%)	0	100	100
1	K	173/648 (27%)	161 (93%)	12 (7%)	0	100	100
1	L	172/648 (26%)	157 (91%)	15 (9%)	0	100	100
1	M	173/648 (27%)	160 (92%)	13 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1036/3888 (27%)	948 (92%)	88 (8%)	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	H	145/543 (27%)	145 (100%)	0	100	100
1	I	145/543 (27%)	145 (100%)	0	100	100
1	J	144/543 (26%)	143 (99%)	1 (1%)	76	78
1	K	145/543 (27%)	145 (100%)	0	100	100
1	L	144/543 (26%)	144 (100%)	0	100	100
1	M	145/543 (27%)	145 (100%)	0	100	100
All	All	868/3258 (27%)	867 (100%)	1 (0%)	87	87

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	427	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	309	HIS
1	M	308	GLN
1	M	440	GLN
1	L	331	ASN
1	I	441	GLN

5.3.3 RNA [i](#)

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 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.

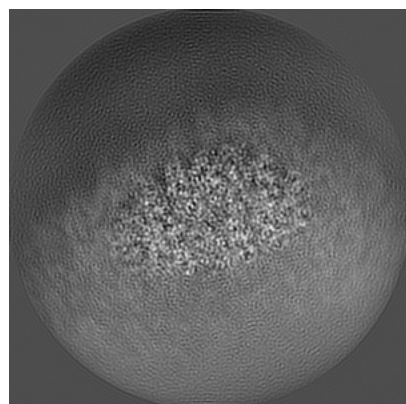
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17315. These allow visual inspection of the internal detail of the map and identification of artifacts.

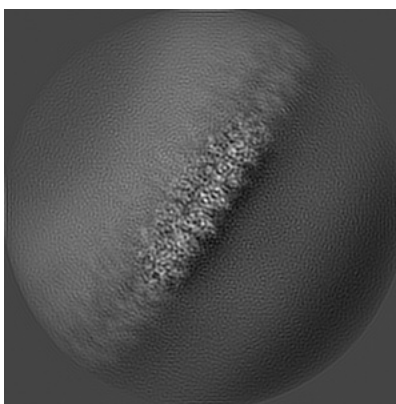
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

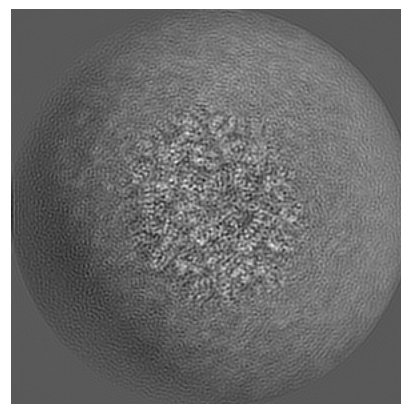
6.1.1 Primary map



X

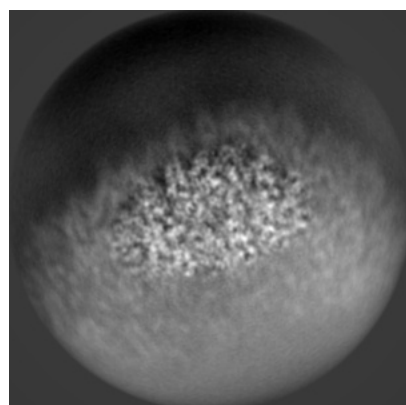


Y

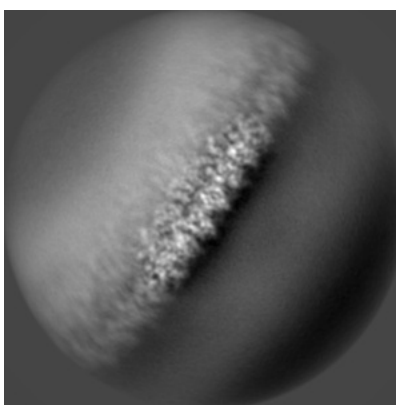


Z

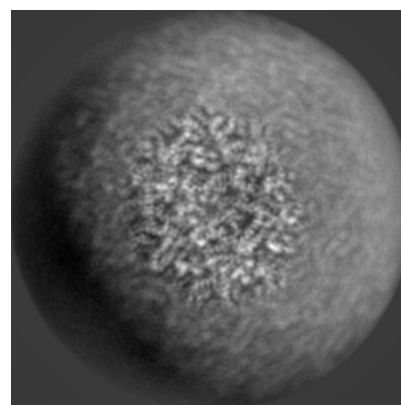
6.1.2 Raw map



X



Y

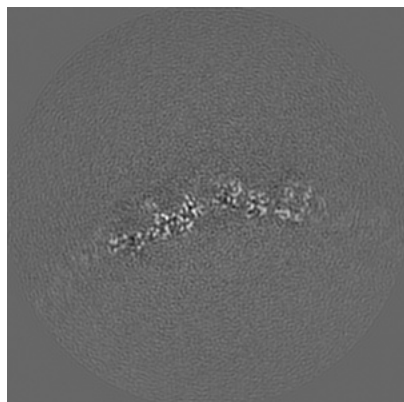


Z

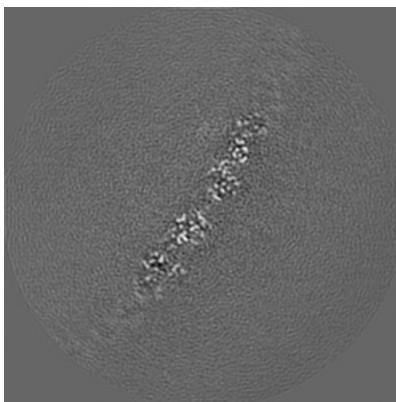
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

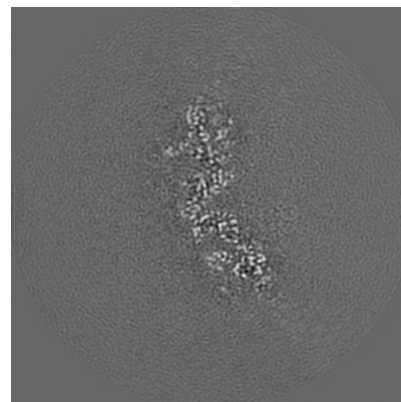
6.2.1 Primary map



X Index: 160

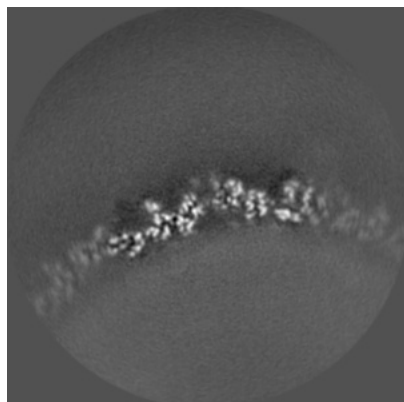


Y Index: 160

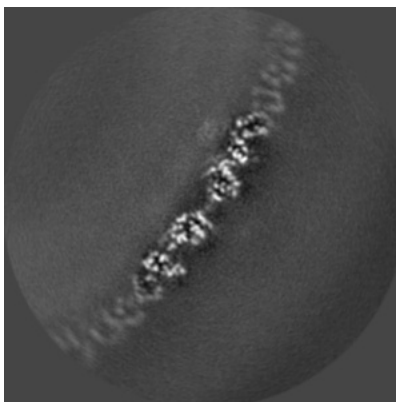


Z Index: 160

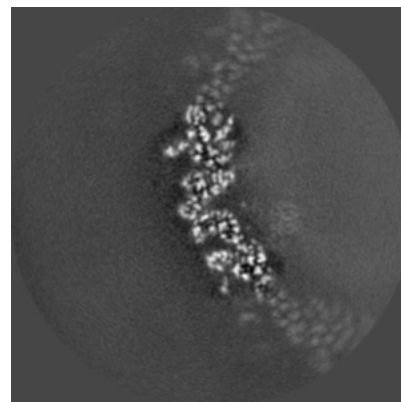
6.2.2 Raw map



X Index: 160



Y Index: 160

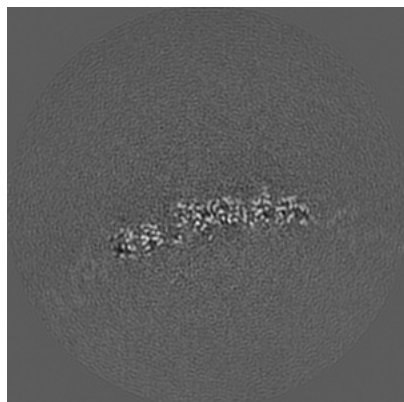


Z Index: 160

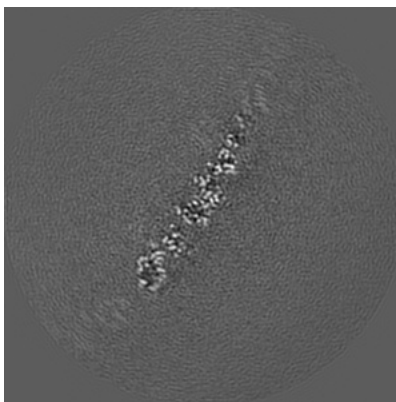
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

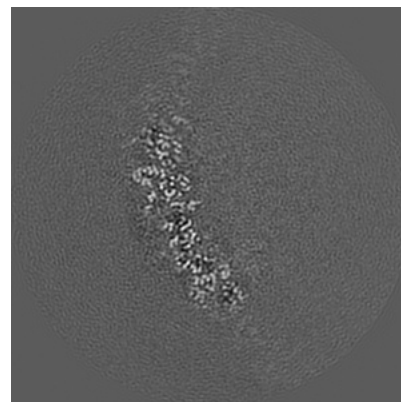
6.3.1 Primary map



X Index: 147

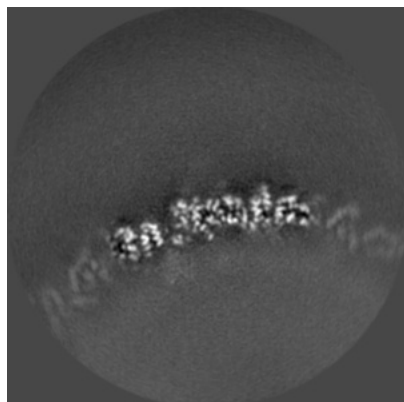


Y Index: 142

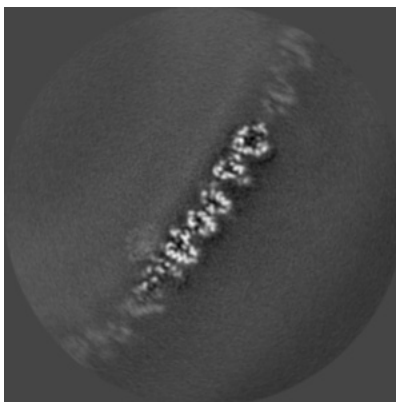


Z Index: 136

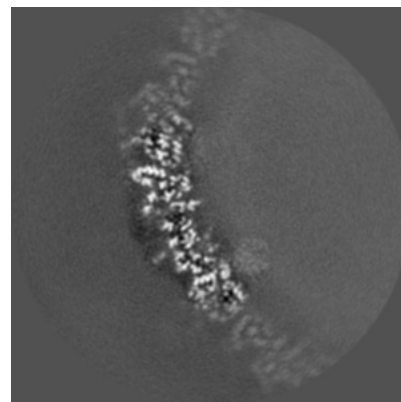
6.3.2 Raw map



X Index: 147



Y Index: 177

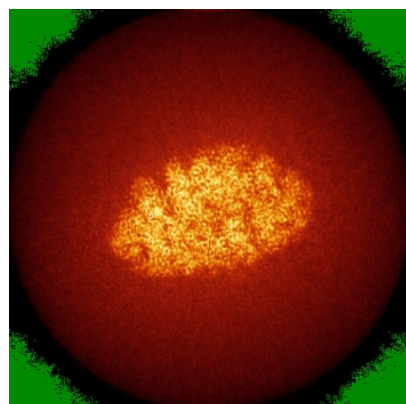


Z Index: 136

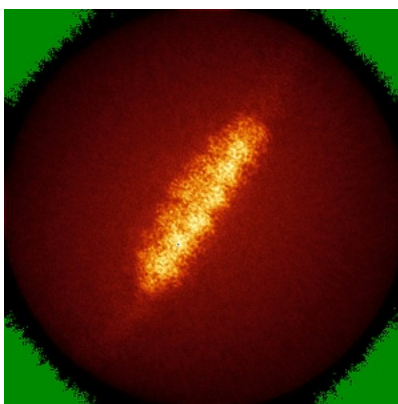
The images above show the largest variance slices of the map in three orthogonal directions.

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

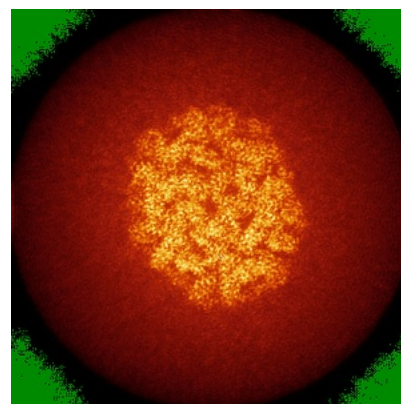
6.4.1 Primary map



X

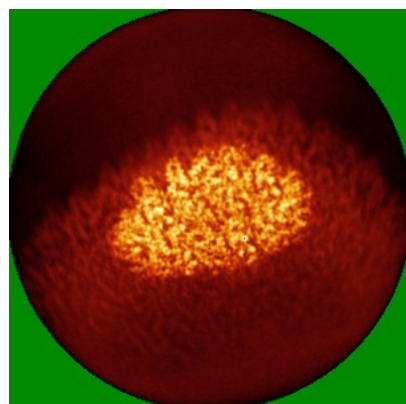


Y

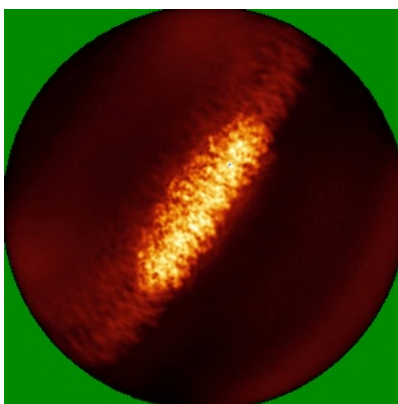


Z

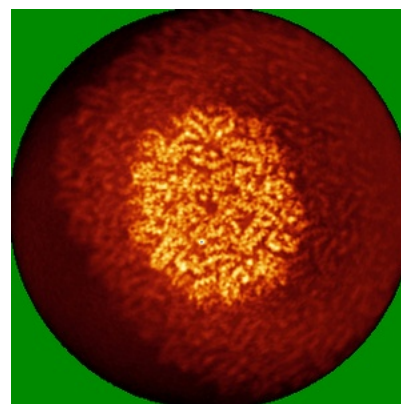
6.4.2 Raw map



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.

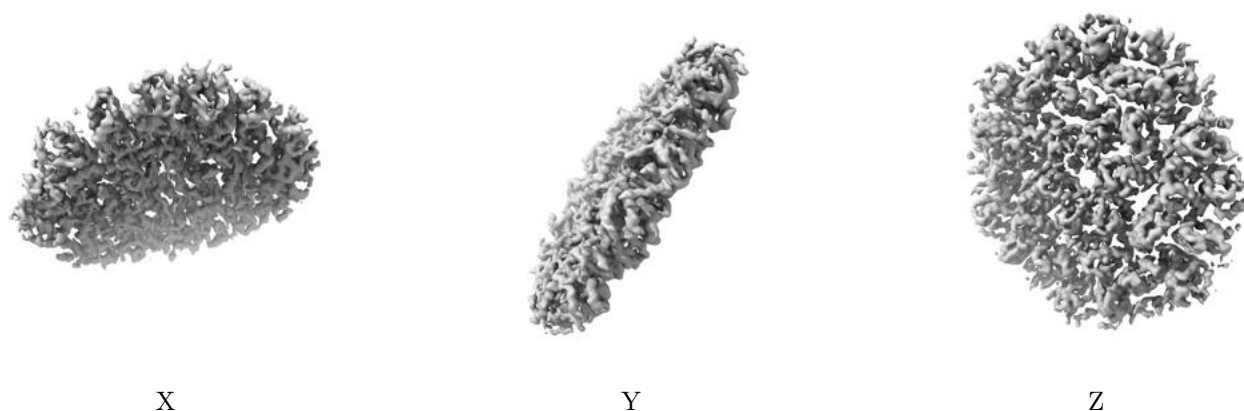
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0153. 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.

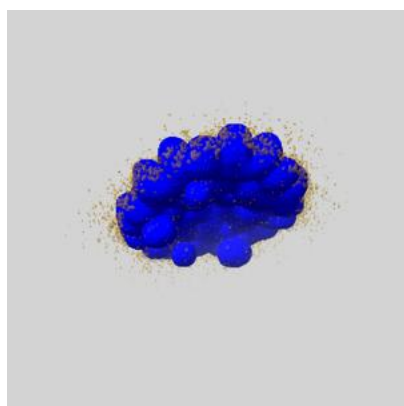
6.6 Mask visualisation [i](#)

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

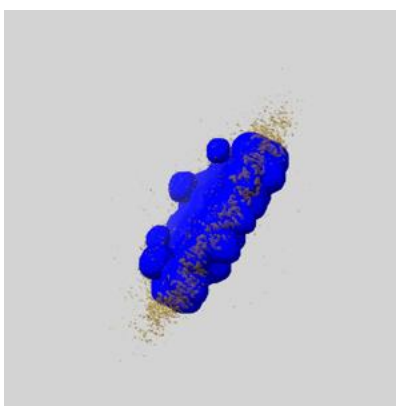
A mask typically either:

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

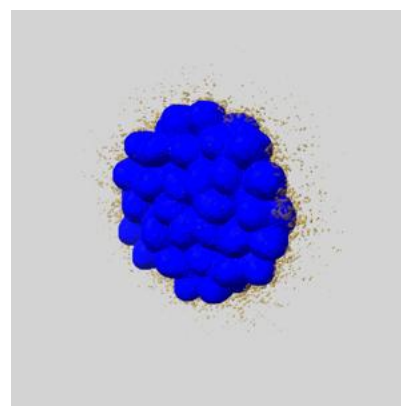
6.6.1 emd_17315_msk_1.map [i](#)



X



Y

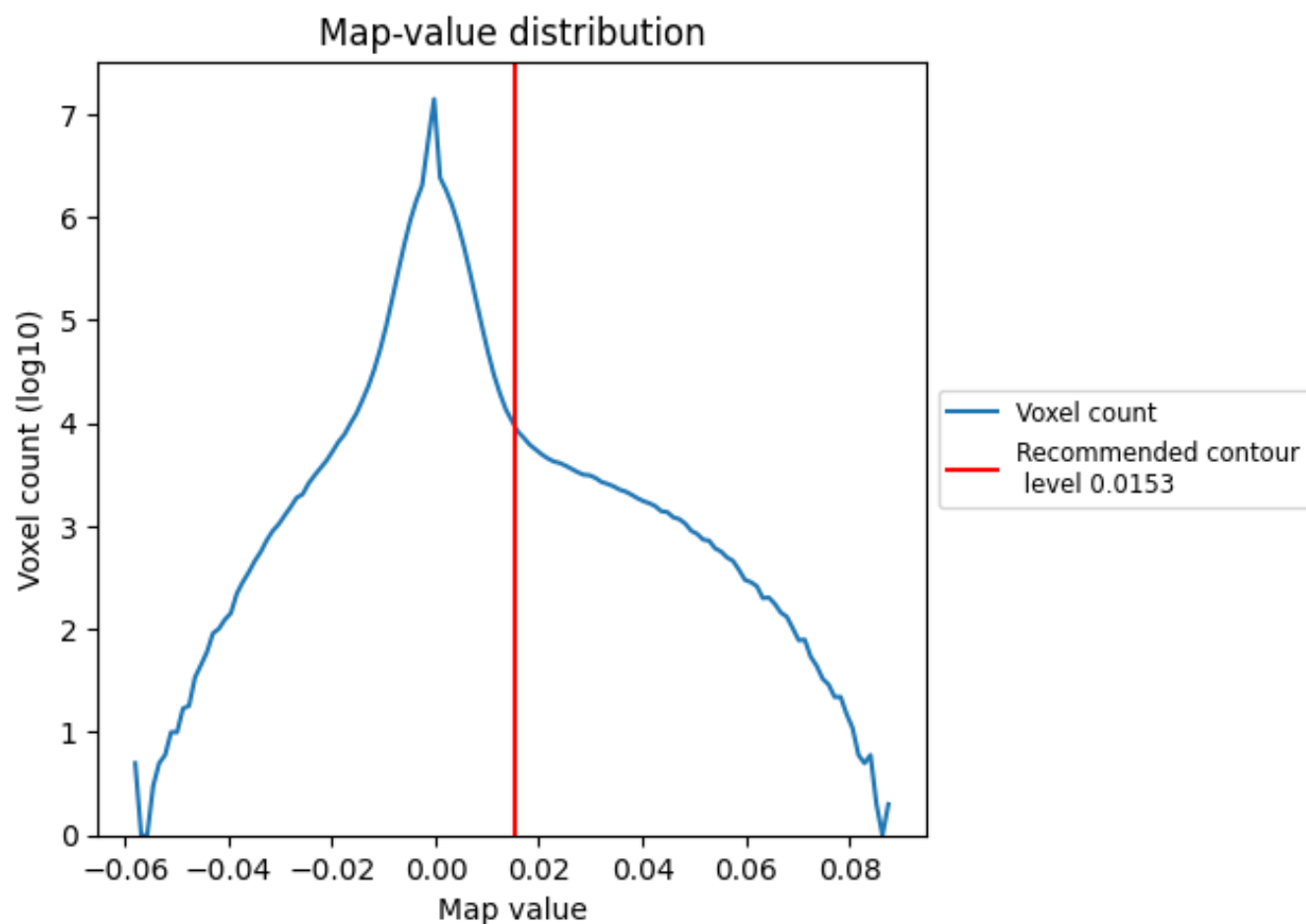


Z

7 Map analysis [i](#)

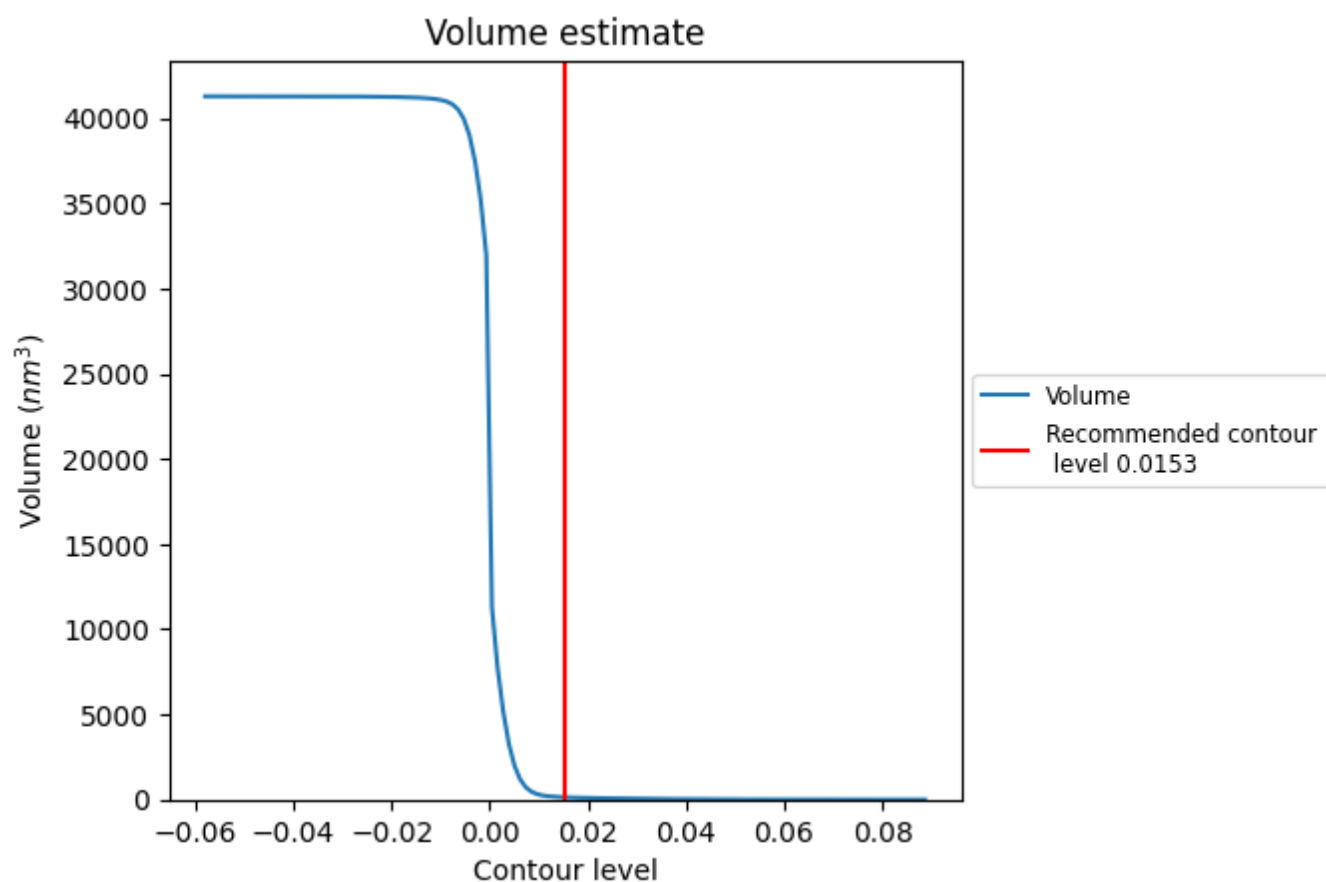
This section contains the results of statistical analysis of the map.

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.

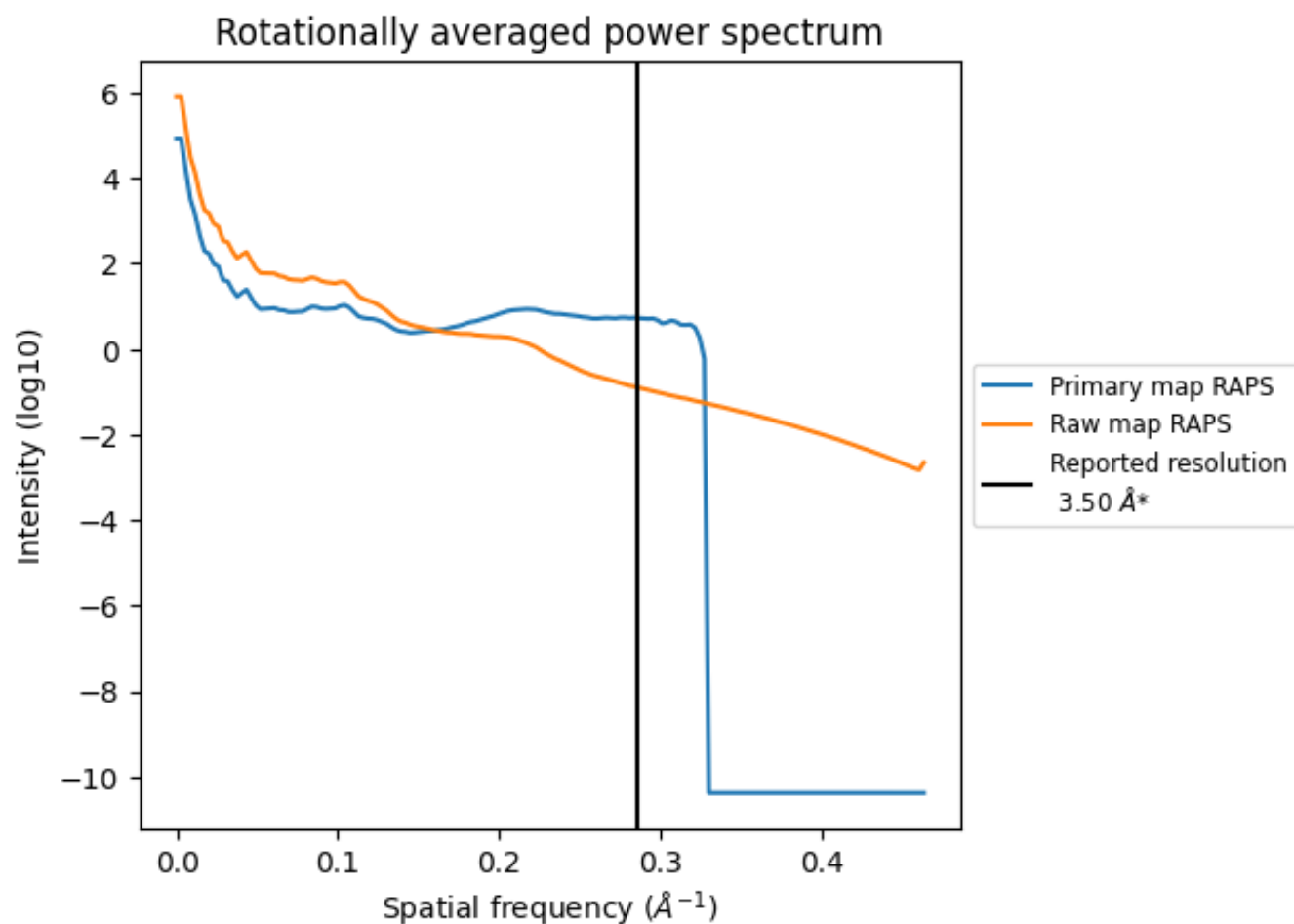
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 133 nm³; this corresponds to an approximate mass of 120 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 ⓘ

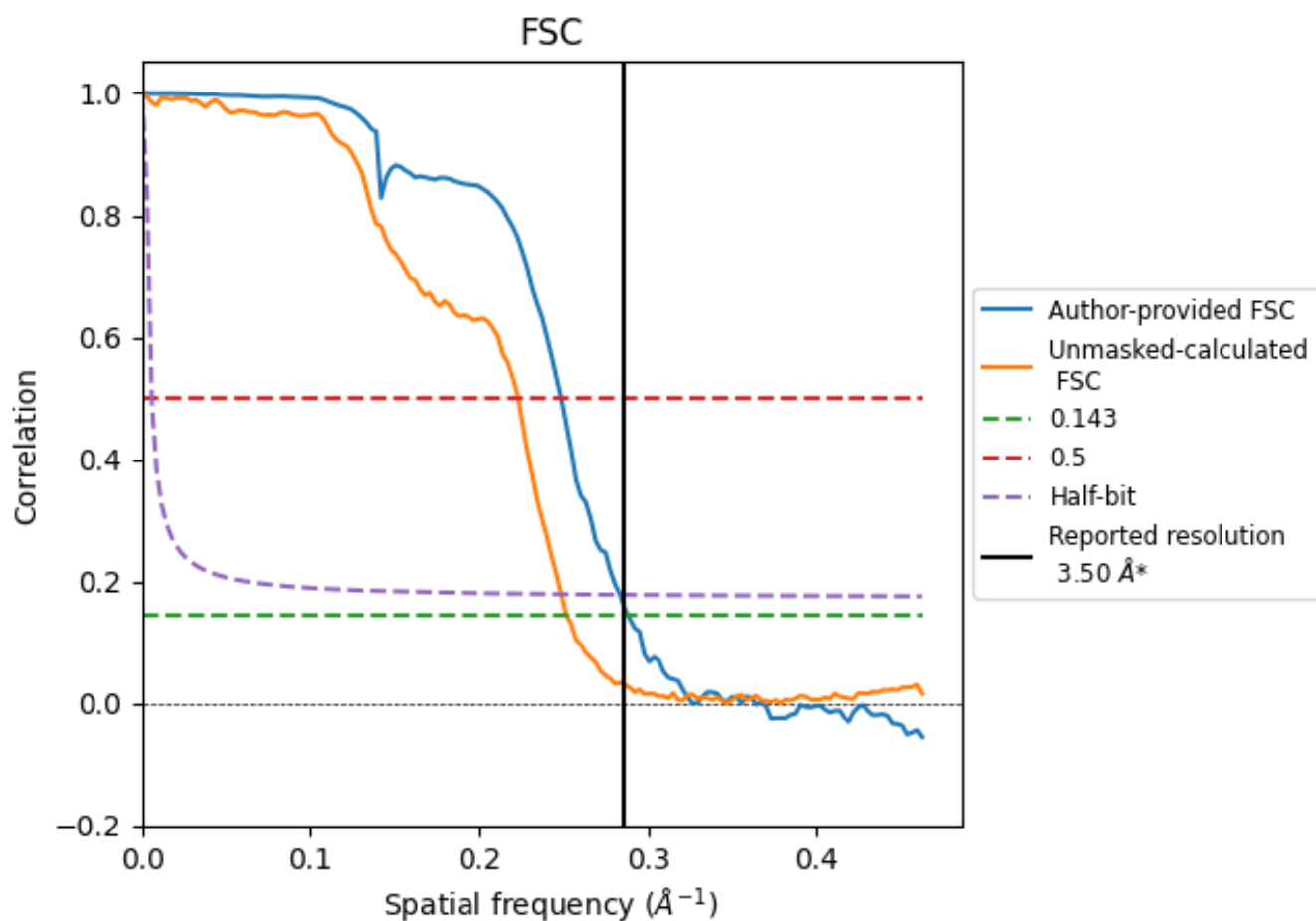


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 $0.286 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

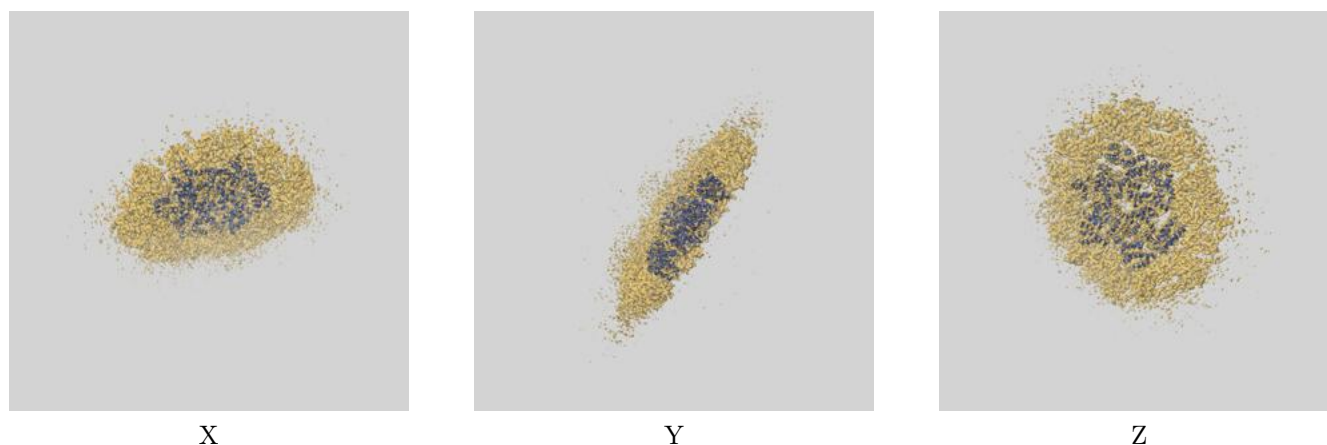
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.47	4.02	3.53
Unmasked-calculated*	3.97	4.48	4.02

*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 3.97 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

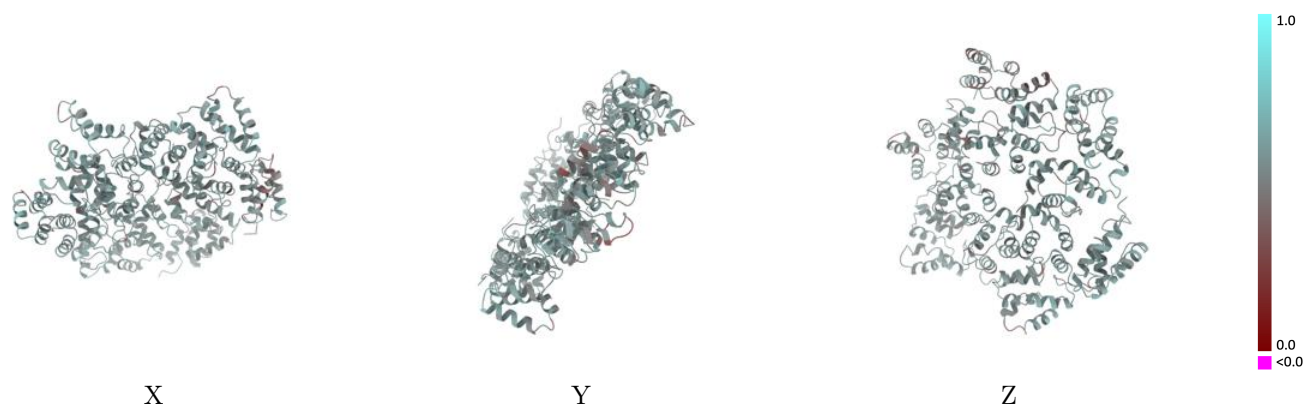
This section contains information regarding the fit between EMDB map EMD-17315 and PDB model 8OZN. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



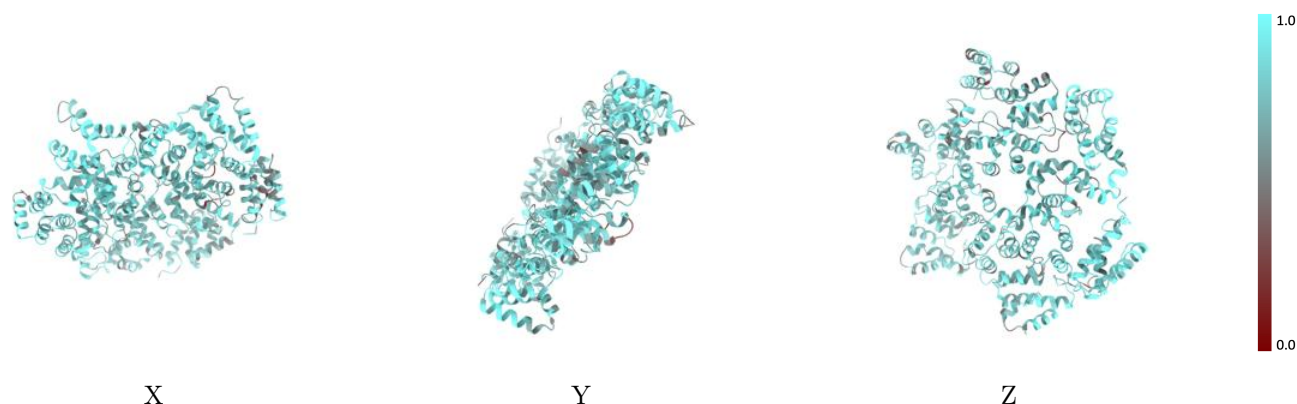
The images above show the 3D surface view of the map at the recommended contour level 0.0153 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



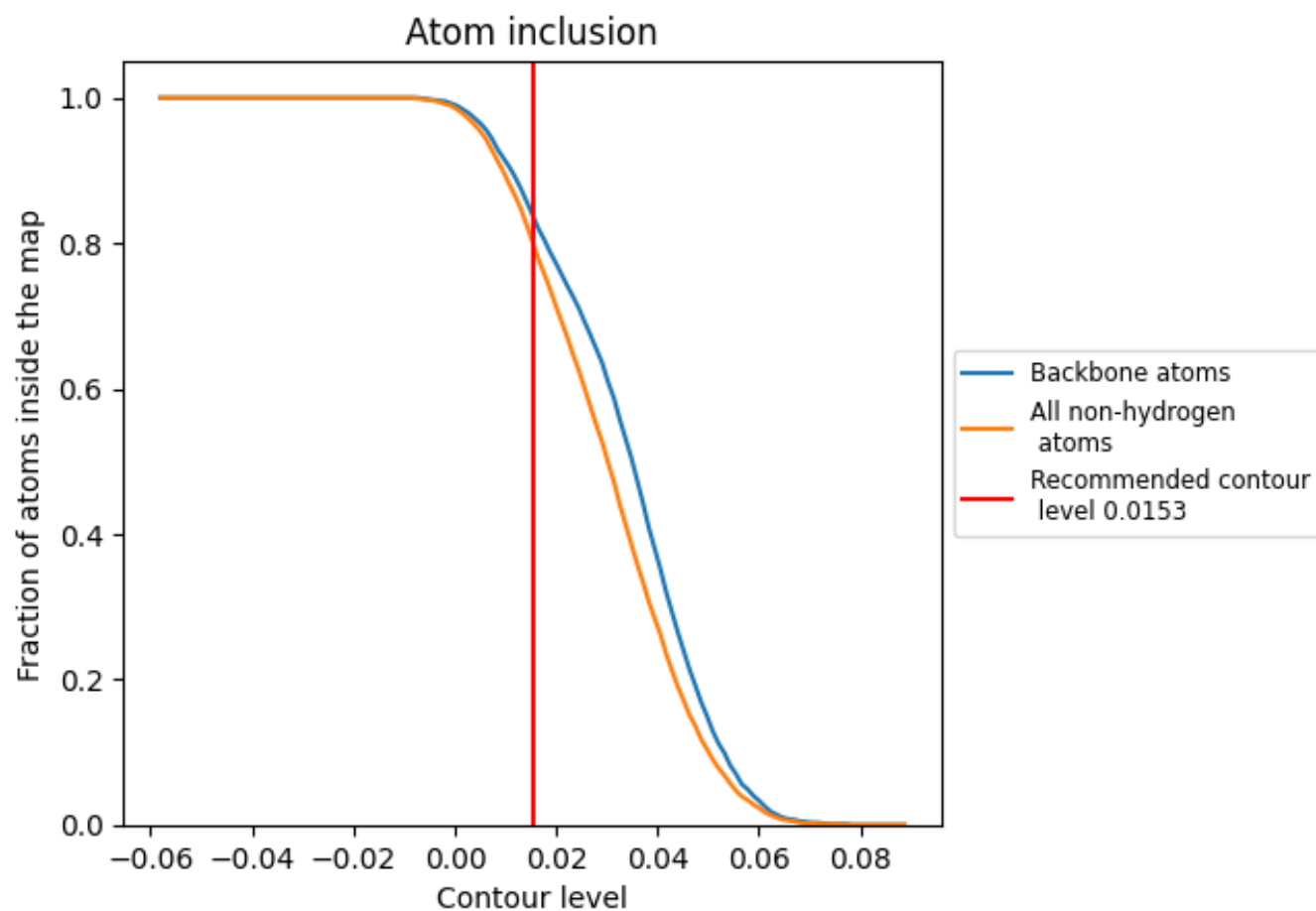
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0153).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 80% 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 (0.0153) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8030	0.5450
H	0.8110	0.5490
I	0.8290	0.5550
J	0.7430	0.5160
K	0.8140	0.5520
L	0.8210	0.5540
M	0.7960	0.5450

