



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 06:11 AM UTC

PDB ID : 9QJ5 / pdb_00009qj5
EMDB ID : EMD-53199
Title : Structure of the Complement classical and lectin pathway proconvertase, C4b2
Authors : De la O Becerra, K.I.; Brondijk, T.H.C.; Gros, P.
Deposited on : 2025-03-18
Resolution : 3.50 Å(reported)
Based on initial models : 5JTW, 3ERB, 2I6Q

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
Mogul : 2022.3.0, CSD as543be (2022)
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

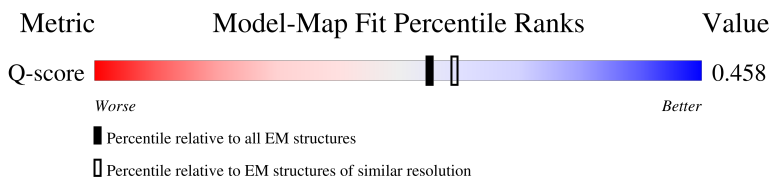
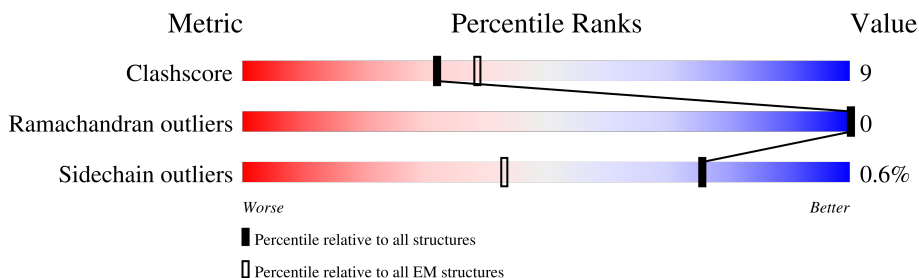
1 Overall quality at a glance

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	A	1744	 31% 6% 63%
1	B	1744	 14% 82%
1	C	1744	 12% 84%
2	D	752	 44% 10% 46%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 12950 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.

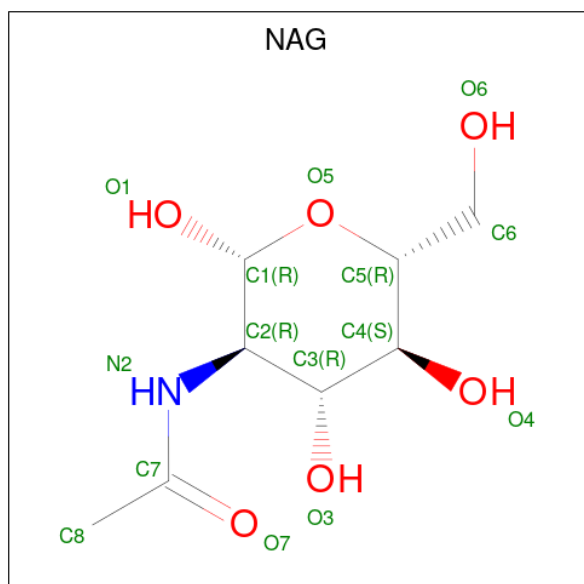
- Molecule 1 is a protein called Complement C4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	651	Total	C	N	O	S	0	0
			5012	3185	872	939	16		
1	C	281	Total	C	N	O	S	0	0
			2241	1407	400	417	17		
1	B	321	Total	C	N	O	S	0	0
			2531	1604	438	482	7		

- Molecule 2 is a protein called Complement C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	404	Total	C	N	O	S	1	0
			3123	1951	547	600	25		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
4	D	1	Total	Mg	0
			1	1	

[illegible]

- Molecule 1: Complement C4-A

[illegible]



Chain B: 14% 82%





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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	112621	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.220	Depositor
Minimum map value	-0.833	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.12	Depositor
Map size ($\text{\AA}$)	401.28, 401.28, 401.28	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.836, 0.836, 0.836	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, MG

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	0.12	0/5128	0.31	0/6961
1	B	0.14	0/2579	0.39	0/3500
1	C	0.15	0/2288	0.43	0/3090
2	D	0.12	0/3192	0.33	0/4323
All	All	0.13	0/13187	0.35	0/17874

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	5012	0	5025	76	0
1	B	2531	0	2518	60	0
1	C	2241	0	2184	57	0
2	D	3123	0	3005	50	0
3	A	14	0	13	0	0
3	B	28	0	26	0	0
4	D	1	0	0	0	0
All	All	12950	0	12771	221	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 9.

The worst 5 of 221 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:LEU:HD21	1:A:134:PHE:HD2	1.53	0.73
1:A:200:ASP:OD1	1:A:201:ASP:N	2.22	0.73
2:D:261:CYS:SG	2:D:331:HIS:ND1	2.64	0.69
1:C:1656:ASP:HB2	1:C:1699:PRO:HG2	1.73	0.69
1:C:1583:CYS:HA	1:C:1588:CYS:CB	2.24	0.68

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	649/1744 (37%)	630 (97%)	19 (3%)	0	100	100
1	B	315/1744 (18%)	296 (94%)	19 (6%)	0	100	100
1	C	279/1744 (16%)	263 (94%)	16 (6%)	0	100	100
2	D	399/752 (53%)	392 (98%)	7 (2%)	0	100	100
All	All	1642/5984 (27%)	1581 (96%)	61 (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	557/1480 (38%)	552 (99%)	5 (1%)	70	76
1	B	282/1480 (19%)	280 (99%)	2 (1%)	76	78
1	C	240/1480 (16%)	239 (100%)	1 (0%)	84	81
2	D	346/647 (54%)	346 (100%)	0	100	100
All	All	1425/5087 (28%)	1417 (99%)	8 (1%)	76	79

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	940	HIS
1	B	764	GLU
1	A	548	TYR
1	A	460	LEU
1	C	1509	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	39	HIS
2	D	447	GLN
1	A	659	GLN
1	C	1598	GLN
1	C	1698	HIS

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

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	B	1801	1	14,14,15	0.72	0	17,19,21	1.23	1 (5%)
3	NAG	B	1802	1	14,14,15	0.78	0	17,19,21	1.45	2 (11%)
3	NAG	A	1801	1	14,14,15	0.72	0	17,19,21	1.09	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	B	1801	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1802	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1801	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1802	NAG	C2-N2-C7	3.48	127.57	122.90
3	B	1801	NAG	C2-N2-C7	3.10	127.05	122.90
3	A	1801	NAG	C1-O5-C5	2.96	116.15	112.19
3	B	1802	NAG	C1-O5-C5	2.88	116.05	112.19

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1801	NAG	C8-C7-N2-C2
3	A	1801	NAG	O7-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
3	B	1802	NAG	O5-C5-C6-O6
3	B	1801	NAG	C1-C2-N2-C7
3	B	1802	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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.

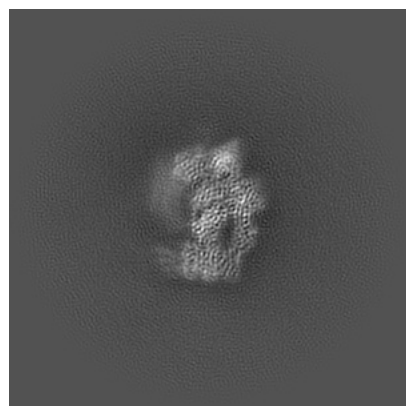
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53199. These allow visual inspection of the internal detail of the map and identification of artifacts.

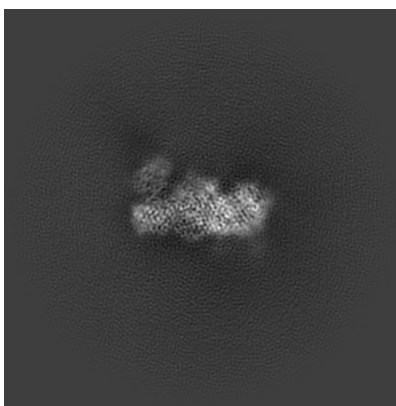
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

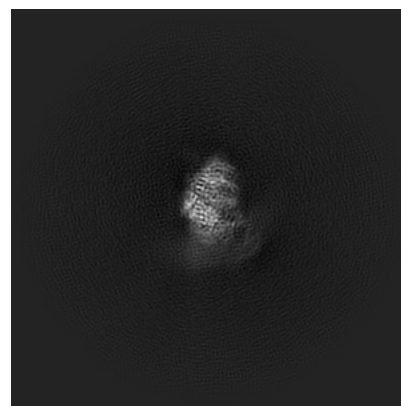
6.1.1 Primary map



X

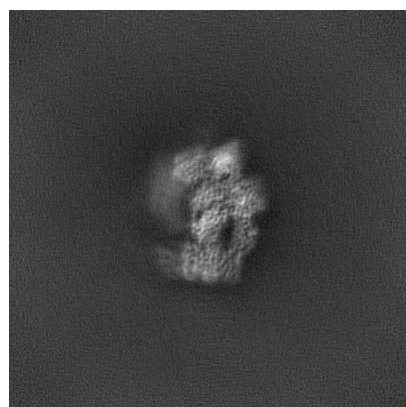


Y

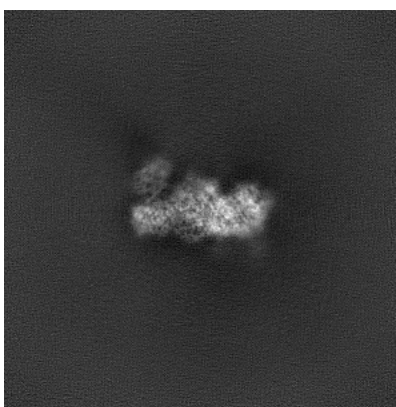


Z

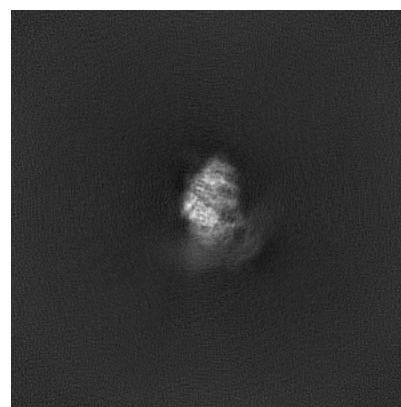
6.1.2 Raw map



X



Y

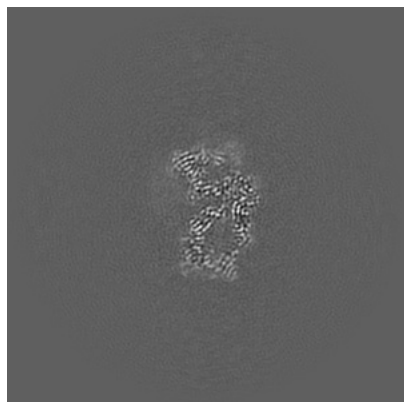


Z

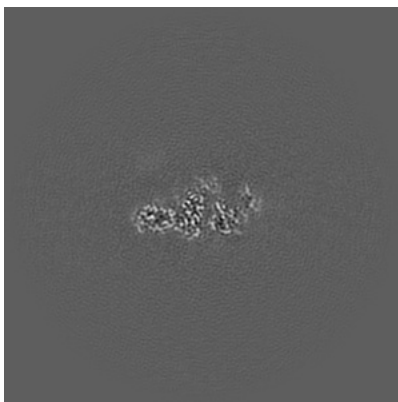
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

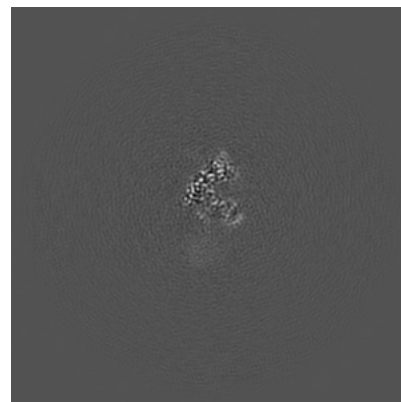
6.2.1 Primary map



X Index: 240

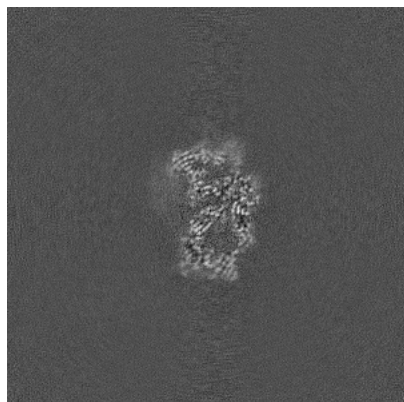


Y Index: 240

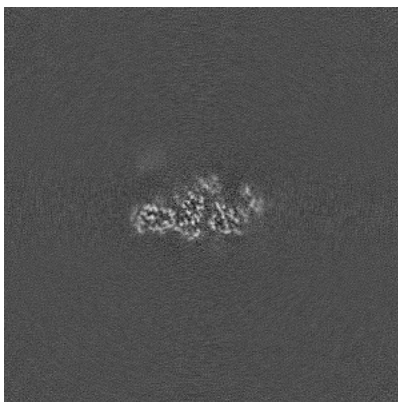


Z Index: 240

6.2.2 Raw map



X Index: 240



Y Index: 240

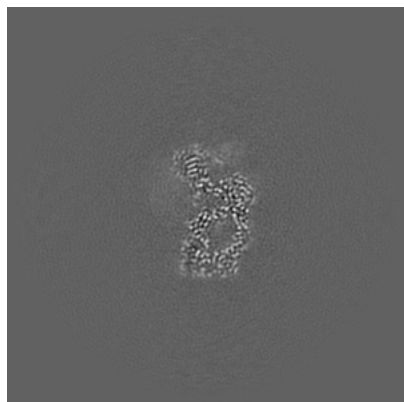


Z Index: 240

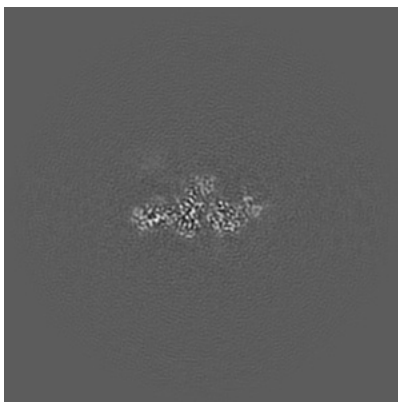
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

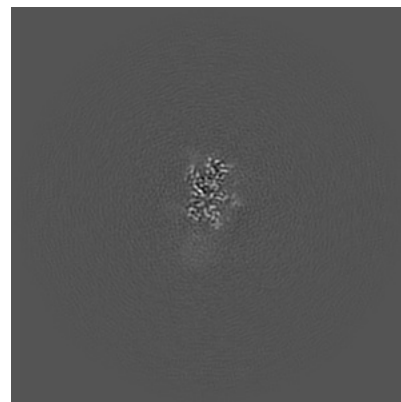
6.3.1 Primary map



X Index: 235

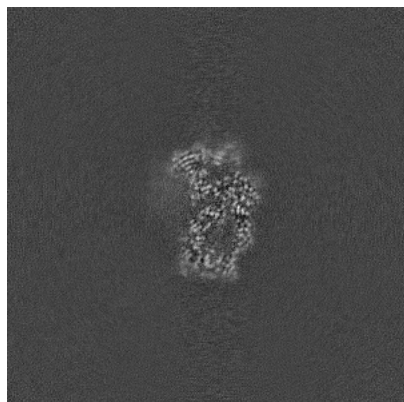


Y Index: 236



Z Index: 256

6.3.2 Raw map



X Index: 239



Y Index: 249

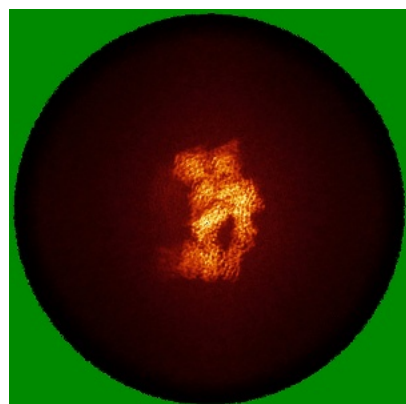


Z Index: 249

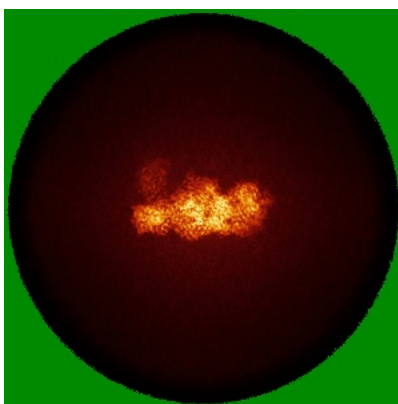
The images above show the largest variance slices of the map in three orthogonal directions.

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

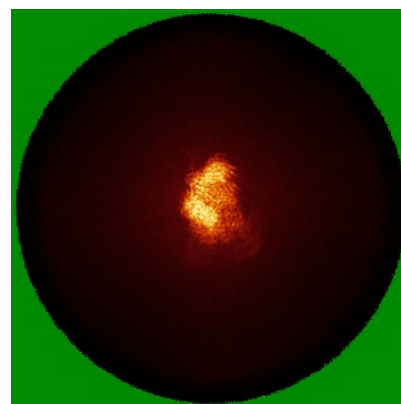
6.4.1 Primary map



X

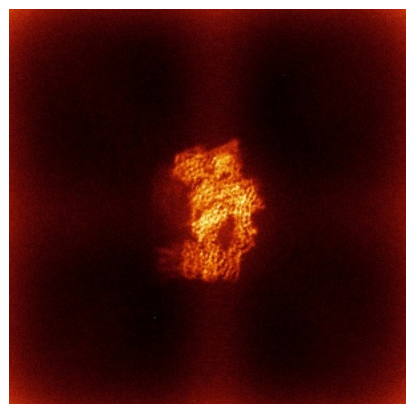


Y

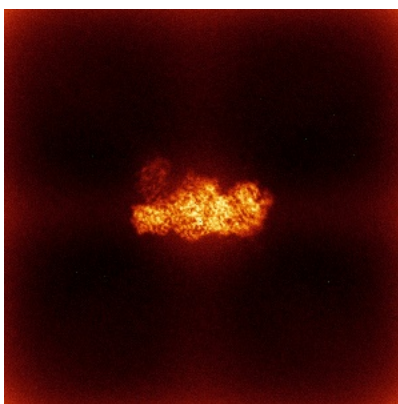


Z

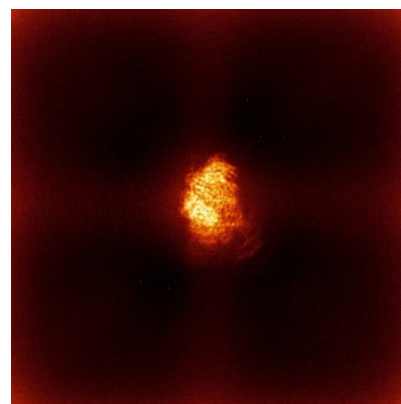
6.4.2 Raw map



X



Y

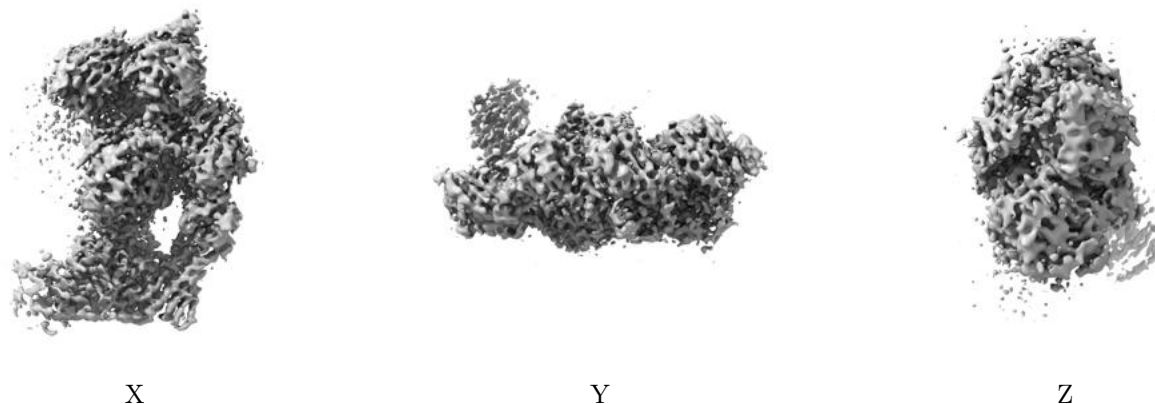


Z

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.

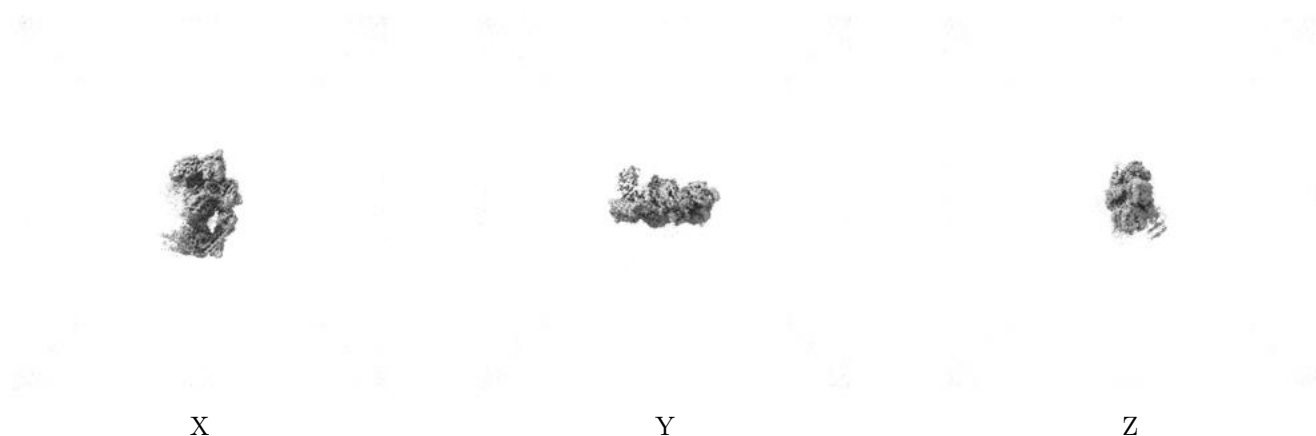
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. 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.

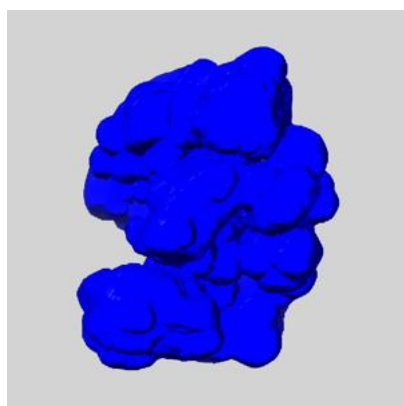
6.6 Mask visualisation [i](#)

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

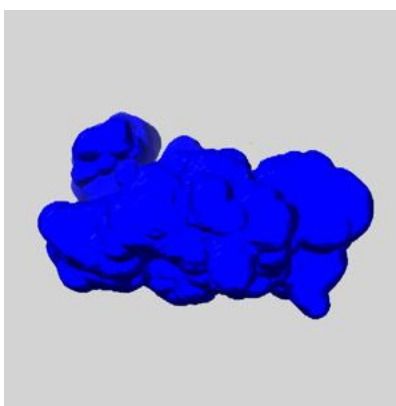
A mask typically either:

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

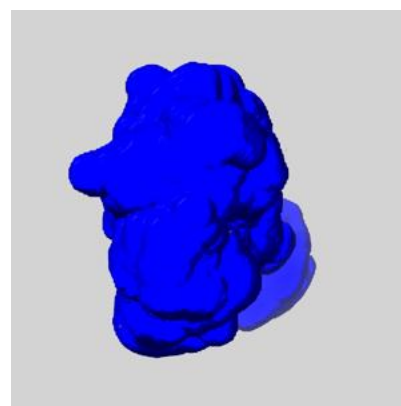
6.6.1 emd_53199_msk_2.map [i](#)



X

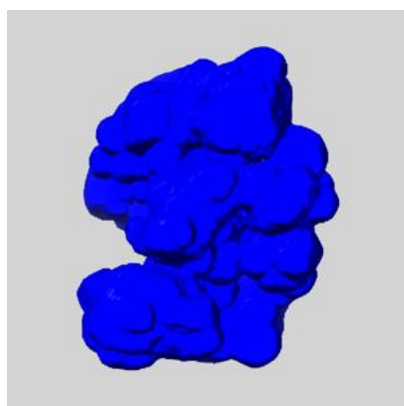


Y

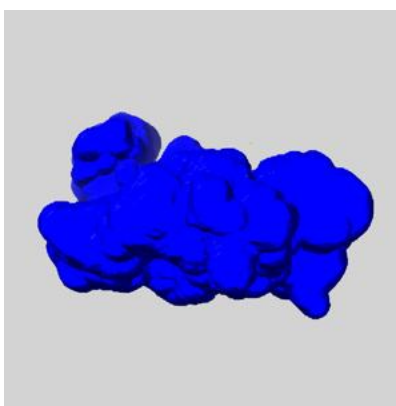


Z

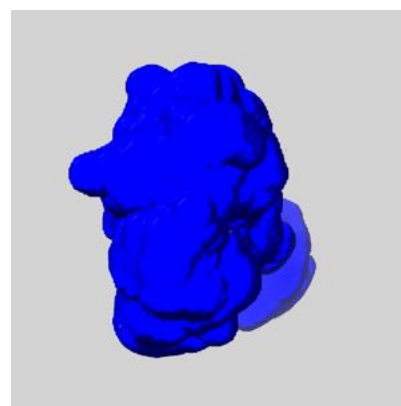
6.6.2 emd_53199_msk_1.map [i](#)



X



Y

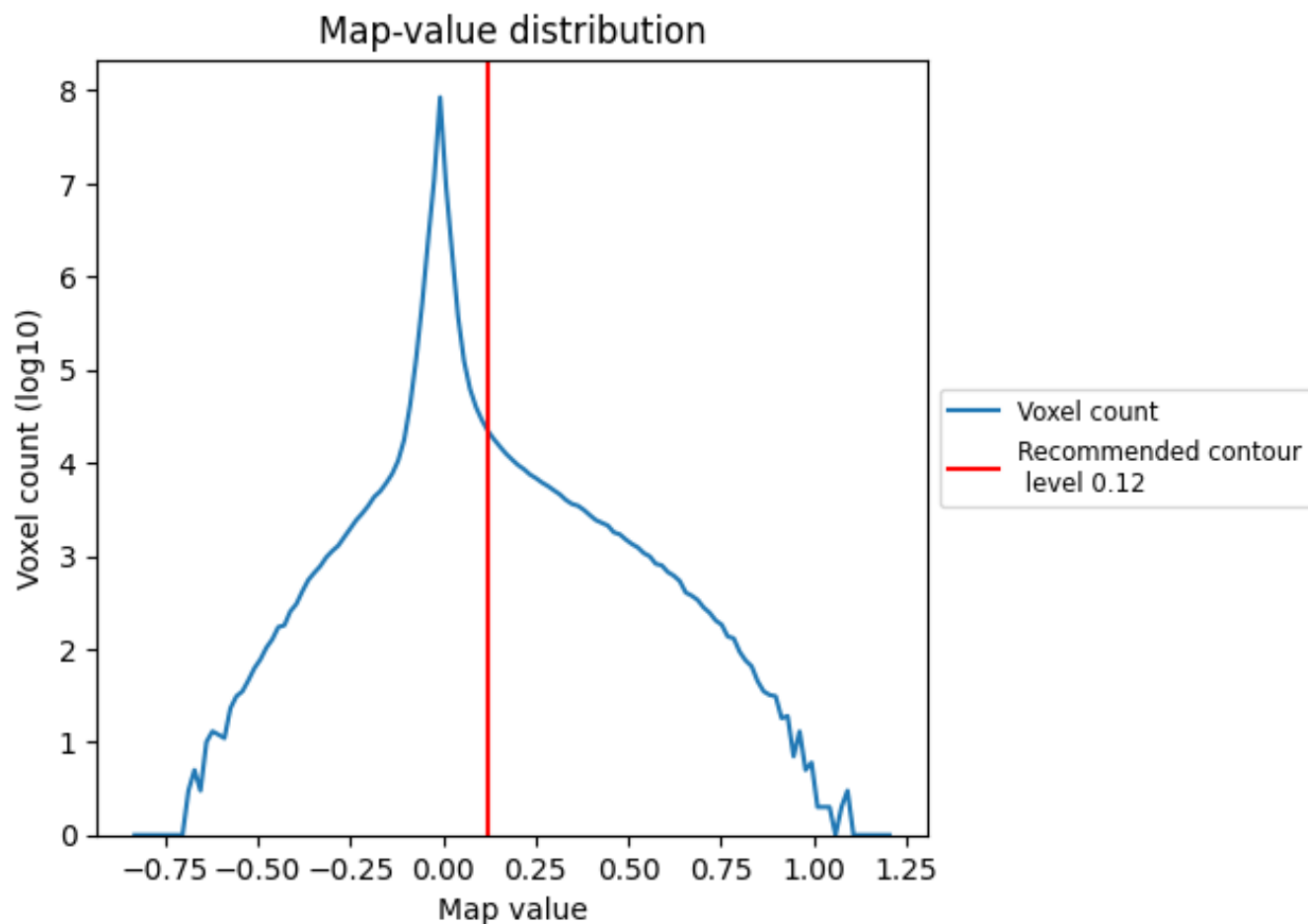


Z

7 Map analysis [i](#)

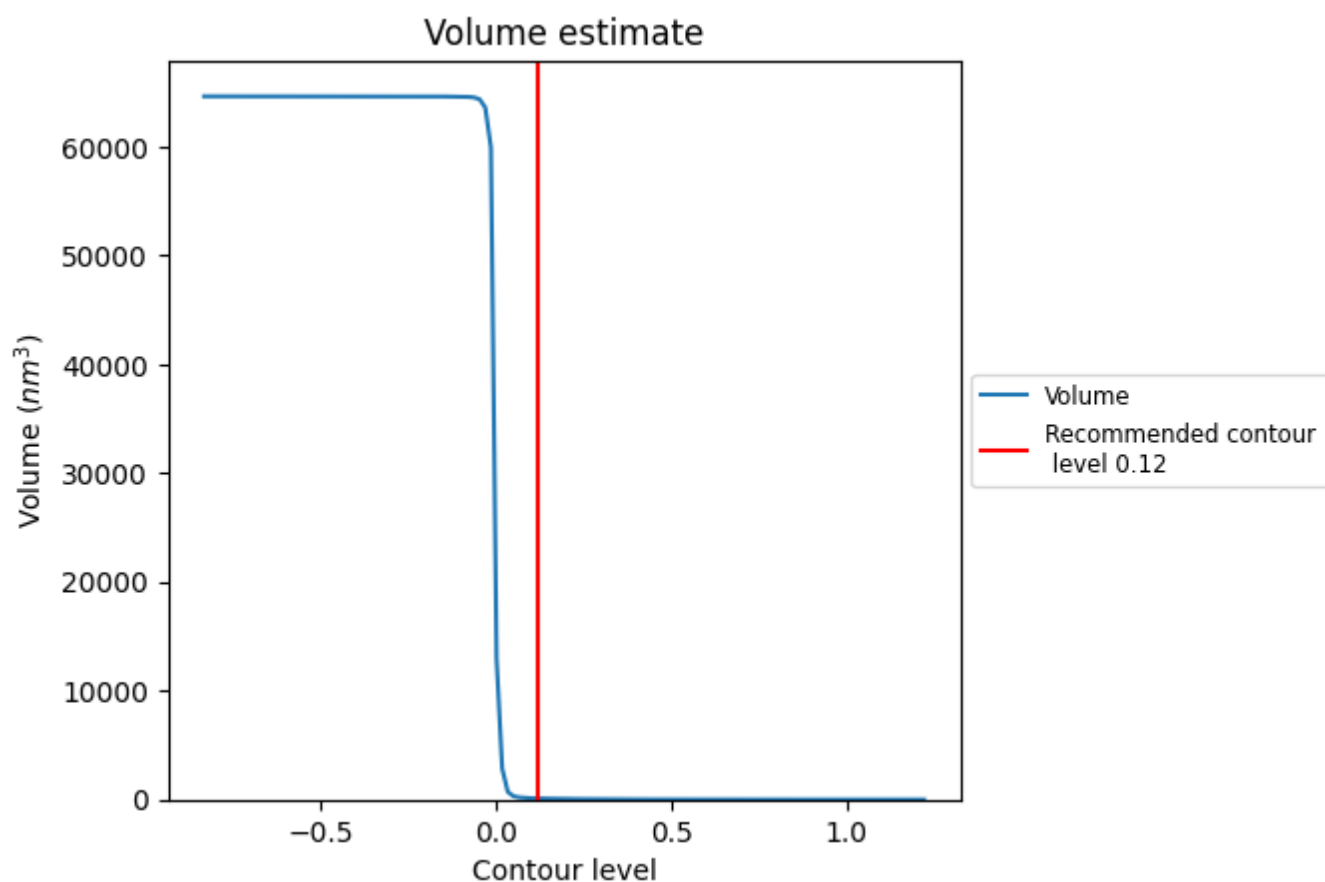
This section contains the results of statistical analysis of the map.

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.

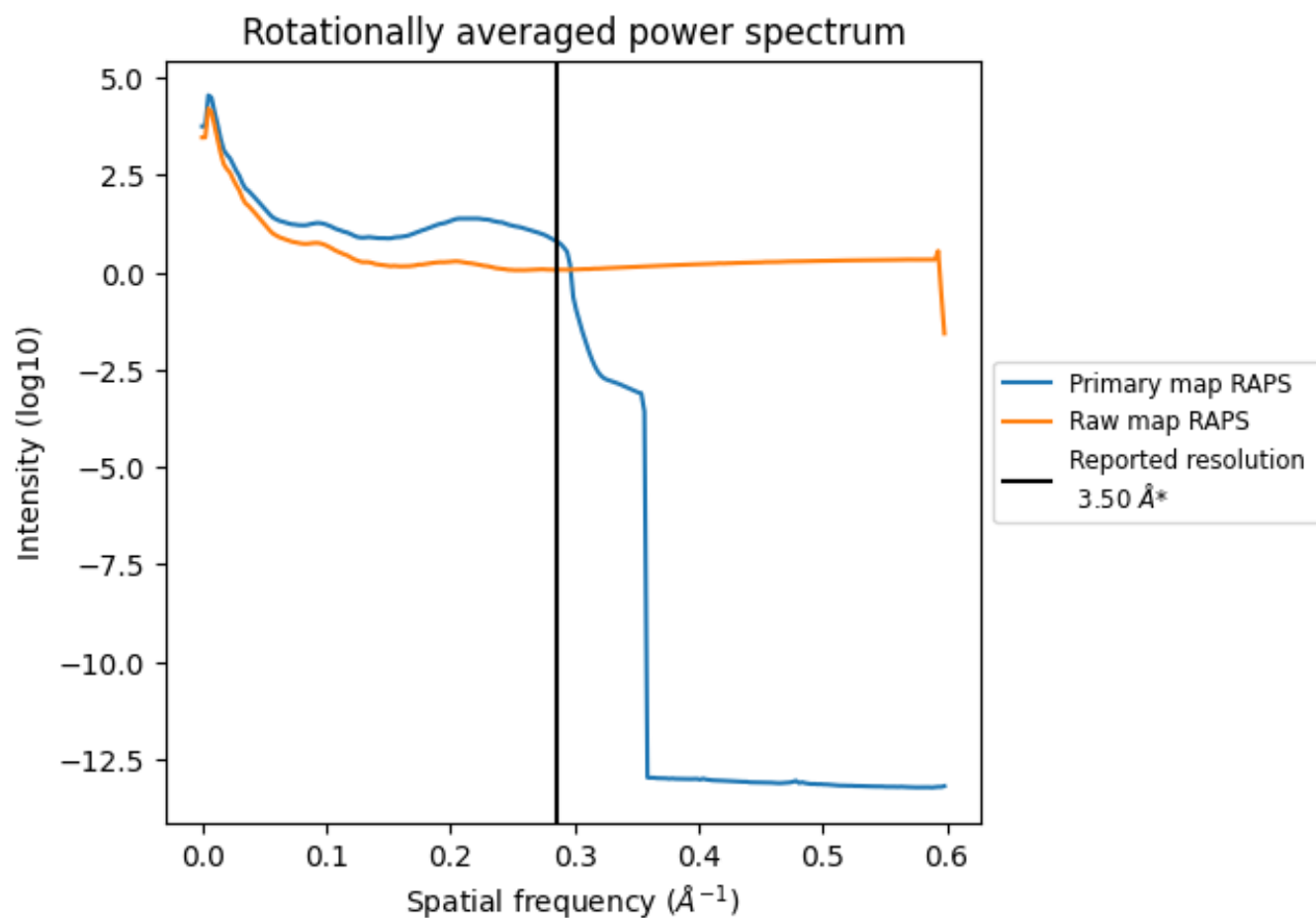
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 101 nm³; this corresponds to an approximate mass of 92 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 ⓘ

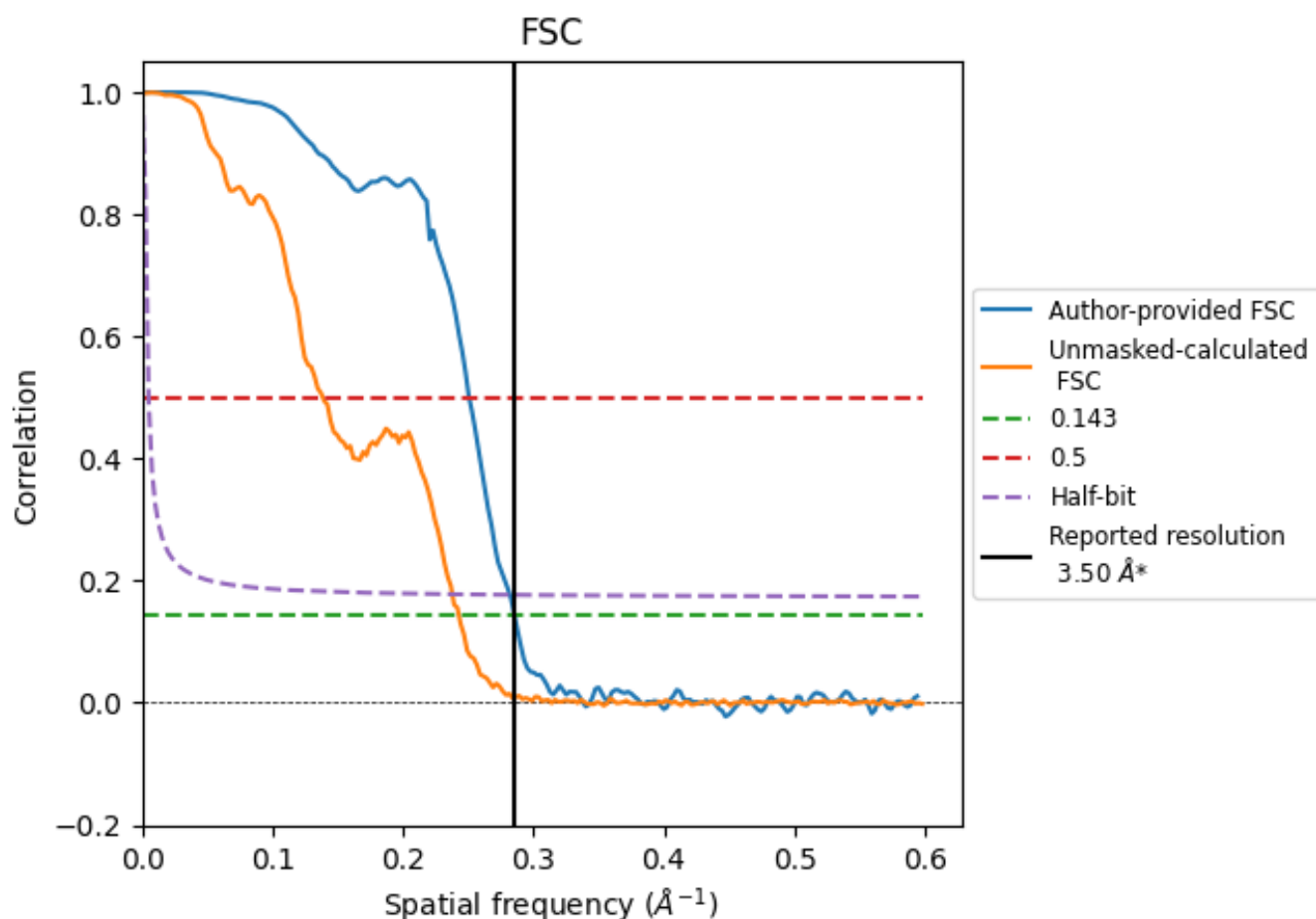


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 Å⁻¹

8.2 Resolution estimates [i](#)

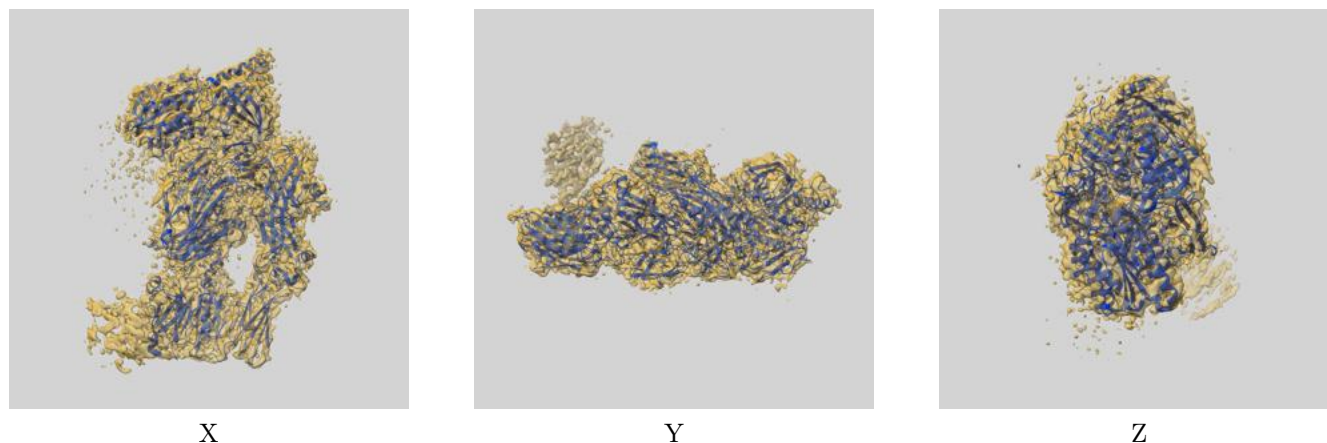
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.50	3.99	3.55
Unmasked-calculated*	4.12	7.22	4.20

*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 4.12 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-53199 and PDB model 9QJ5. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



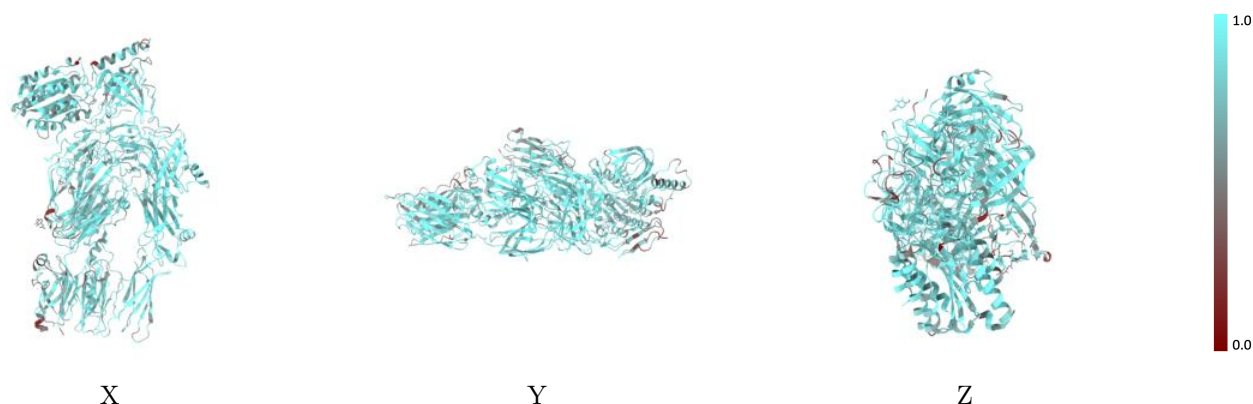
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



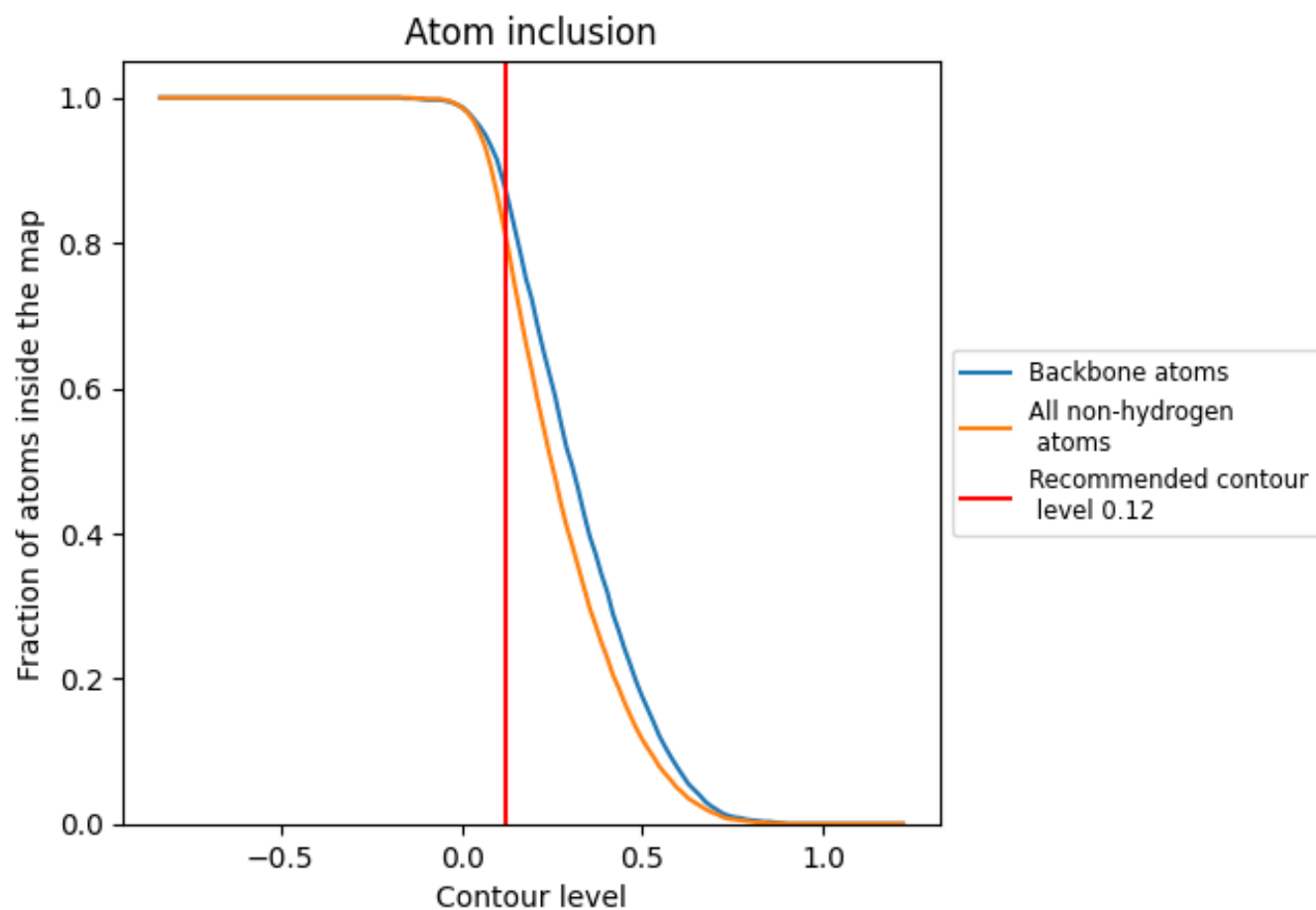
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8130	0.4580
A	0.8210	0.4750
B	0.8050	0.4670
C	0.8280	0.4510
D	0.7970	0.4300

