



wwPDB EM Validation Summary Report ⓘ

May 14, 2025 – 06:13 AM JST

PDB ID : 9IVA / pdb_00009iva
EMDB ID : EMD-60923
Title : Cryo-EM structure of the full-length Nipah Virus L Protein bound by Phosphoprotein Tetramer
Authors : Xue, L.; Chang, T.; Gui, J.; Li, Z.; Zhao, H.; Zou, B.; Li, M.; He, J.; Chen, X.; Xiong, X.
Deposited on : 2024-07-23
Resolution : 2.52 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

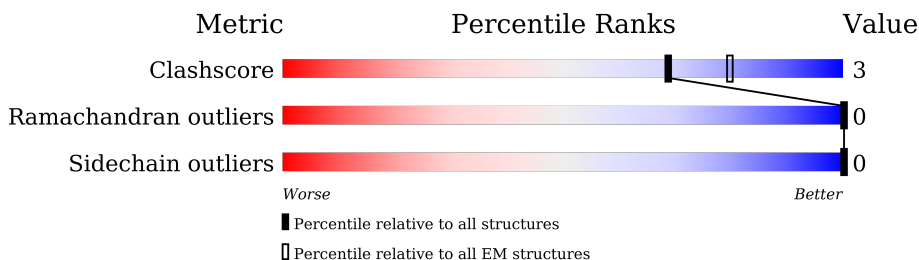
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.52 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	2244	
2	B	709	
2	C	709	
2	D	709	
2	E	709	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12944 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1275	Total	C	N	O	S	1	0
			10269	6543	1758	1902	66		

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	151	Total	C	N	O	S	1	0
			1215	761	207	242	5		
2	C	55	Total	C	N	O	S	0	0
			437	278	75	80	4		
2	D	71	Total	C	N	O	S	0	0
			558	351	101	102	4		
2	E	59	Total	C	N	O	S	0	0
			463	294	81	84	4		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Zn	0
			2	2	

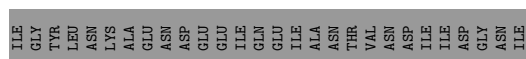
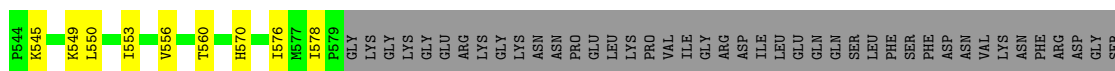
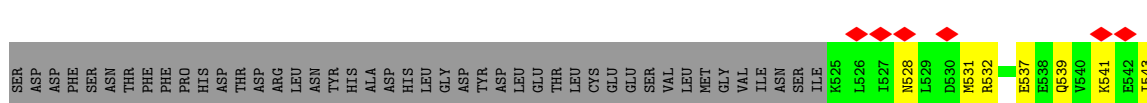
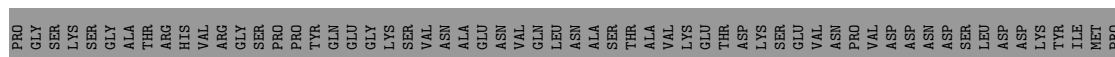
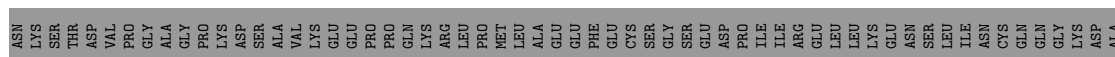
[illegible]

- Molecule 2: Phosphoprotein

[illegible]



- Molecule 2: Phosphoprotein



- Molecule 2: Phosphoprotein



- Molecule 2: Phosphoprotein

[illegible]

ASN	GLY	SER	ILE	K525	L526	I527	N528	R532	N548	P579	K583	GLY	GLU	ARG	LYS
ALA	LYS	ASP	ILE												
SER	ASN	ASP	ASN												
GLN	ASN	PHE	PRO												
PHE	GLU	SER	GLU												
VAL	LEU	ASN	THR												
PRO	LEU	THR	THR												
MET	LYS	PHE	LYS												
ALA	PRO	PHE	VAL												
ASP	VAL	ASP	ILE												
SER	ASP	ASP	GLY												
SER	ARG	THR	ARG												
ARG	ASP	ASP	ASP												
VAL	ILE	LEU	ILE												
LYS	GLN	ASN	GLU												
THR	GLN	THR	THR												
LEU	SER	ALA	SER												
ILE	LEU	ASP	LEU												
ARG	PHE	HIS	PHE												
THR	SER	THR	SER												
HIS	PHE	PHE	PHE												
ILE	ASP	ASP	ASN												
LYS	ASN	TYR	ASN												
ASP	VAL	ASP	VAL												
ARG	LYS	ASP	LYS												
GLU	ASN	GLU	ASN												
LEU	PHE	THR	PHE												
ARG	ARG	LEU	ARG												
SER	ASP	ASP	ASP												
GLU	GLY	GLU	GLY												
LEU	SER	GLU	SER												
ILE	LEU	ILE	LEU												
GLY	THR	THR	ASN												
LEU	GLU	MET	LEU												
ASN	PRO	GLY	GLU												
LYS	TYR	VAL	VAL												
ALA	GLY	ILE	ILE												
GLU	ALA	ASN	ALA												
ASN	VAL	SER	VAL												
ASP	GLN	ILE	GLN												
GLU	LEU	LEU	LEU												
ILE	ARG	ARG	ARG												
GLN	ILE	GLU	GLU												
GLU	ASN	ASN	ASN												
ILE	GLN	ILE	ILE												
ASN	LEU	LEU	LEU												
LYS	PRO	GLY	GLY												
ALA	TYR	VAL	VAL												
GLU	ASN	GLU	GLU												
ASN	LEU	LEU	LEU												
THR	PRO	GLU	GLU												
VAL	VAL	THR	THR												
ASN	LEU	LEU	LEU												
ASP	ASN	ASN	ASN												
ILE	PHE	PHE	PHE												
ILE	GLU	GLU	GLU												
ASP	GLU	GLU	GLU												
GLY	THR	THR	THR												

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	224424	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	2.072	Depositor
Minimum map value	-1.052	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.13	Depositor
Map size (Å)	262.80002, 262.80002, 262.80002	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9125001, 0.9125001, 0.9125001	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: ZN

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	0.16	0/10482	0.36	0/14167
2	B	0.19	0/1227	0.45	0/1652
2	C	0.26	0/440	0.58	0/591
2	D	0.19	0/562	0.44	0/749
2	E	0.19	0/466	0.40	0/623
All	All	0.17	0/13177	0.38	0/17782

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	10269	0	10316	57	0
2	B	1215	0	1248	20	0
2	C	437	0	476	16	0
2	D	558	0	608	10	0
2	E	463	0	508	4	0
3	A	2	0	0	0	0
All	All	12944	0	13156	91	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 91 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:1239:CYS:SG	1:A:1423:HIS:CE1	2.72	0.81
1:A:291:GLU:HG2	1:A:292:PRO:HD3	1.72	0.69
1:A:26:LEU:HD22	1:A:234:MET:HE1	1.76	0.67
1:A:1239:CYS:SG	1:A:1423:HIS:HE1	2.15	0.65
2:B:549:LYS:HB3	2:C:550:LEU:HD23	1.79	0.64

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	1266/2244 (56%)	1219 (96%)	47 (4%)	0	100	100
2	B	146/709 (21%)	142 (97%)	4 (3%)	0	100	100
2	C	53/709 (8%)	52 (98%)	1 (2%)	0	100	100
2	D	69/709 (10%)	69 (100%)	0	0	100	100
2	E	57/709 (8%)	56 (98%)	1 (2%)	0	100	100
All	All	1591/5080 (31%)	1538 (97%)	53 (3%)	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	1145/2046 (56%)	1145 (100%)	0	100	100
2	B	142/625 (23%)	142 (100%)	0	100	100
2	C	52/625 (8%)	52 (100%)	0	100	100
2	D	64/625 (10%)	64 (100%)	0	100	100
2	E	54/625 (9%)	54 (100%)	0	100	100
All	All	1457/4546 (32%)	1457 (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 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1029	HIS
1	A	1371	ASN
2	B	686	ASN
2	B	648	ASN
1	A	929	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 ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

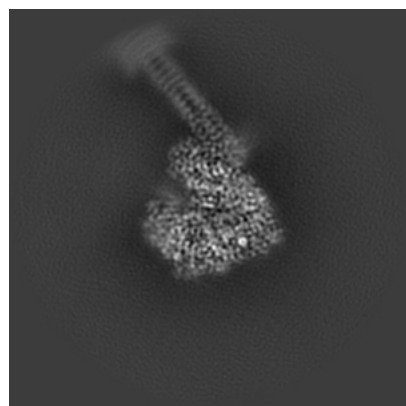
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60923. These allow visual inspection of the internal detail of the map and identification of artifacts.

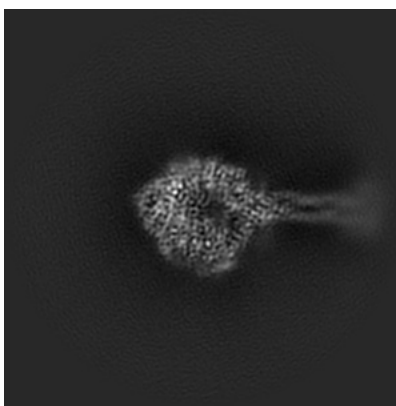
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

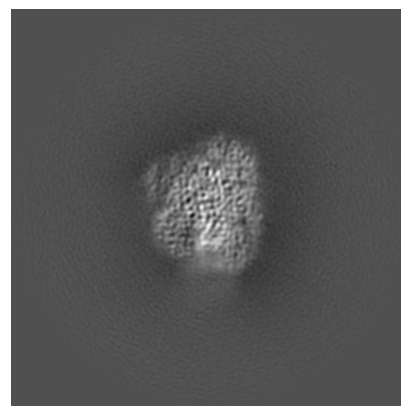
6.1.1 Primary map



X

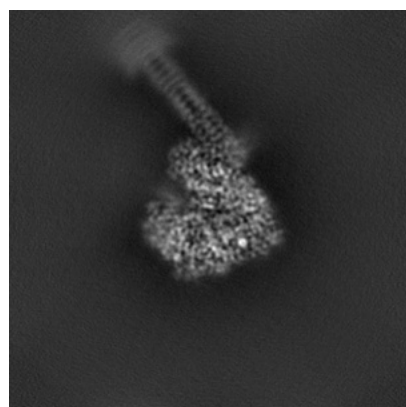


Y

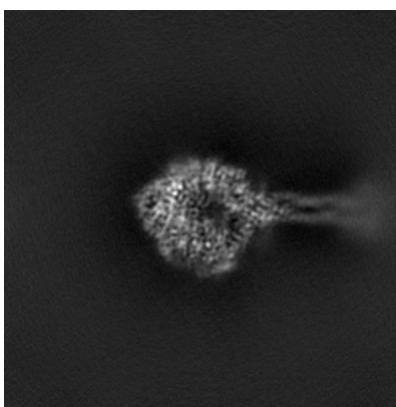


Z

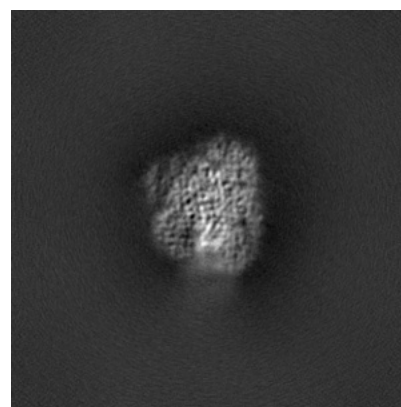
6.1.2 Raw map



X



Y

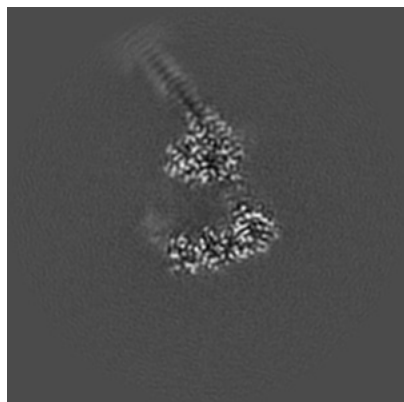


Z

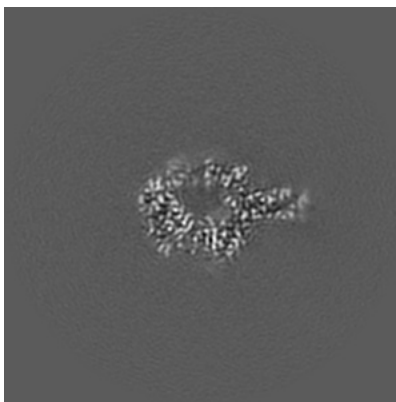
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

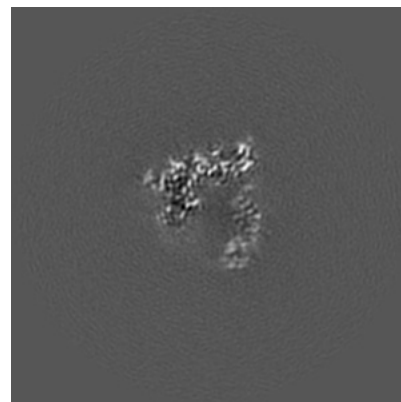
6.2.1 Primary map



X Index: 144

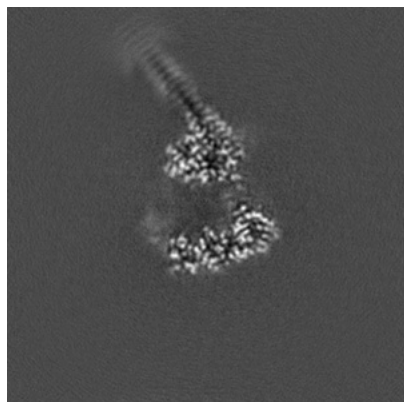


Y Index: 144

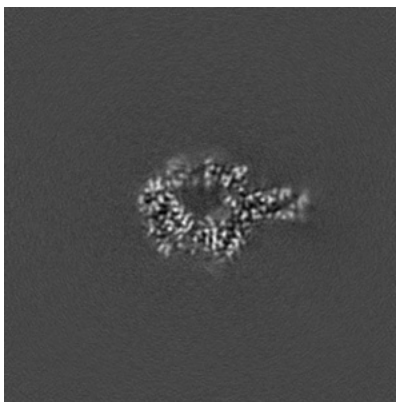


Z Index: 144

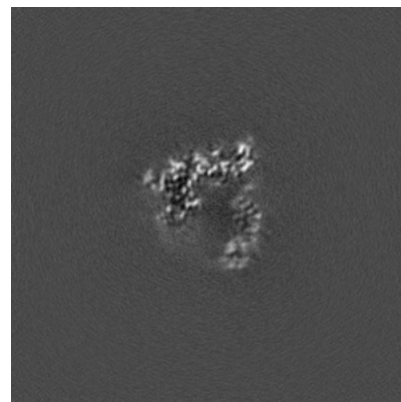
6.2.2 Raw map



X Index: 144



Y Index: 144

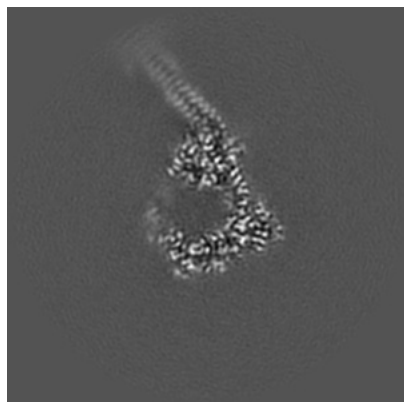


Z Index: 144

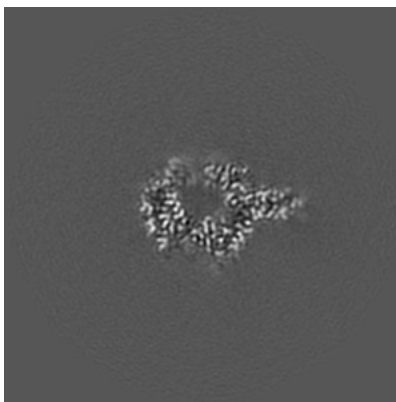
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

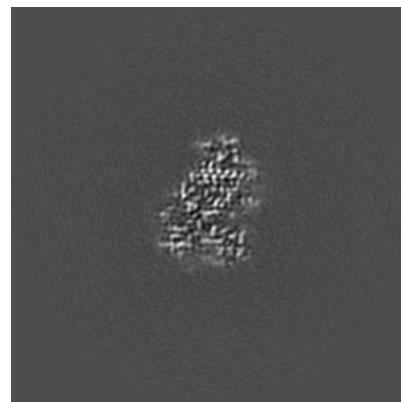
6.3.1 Primary map



X Index: 149

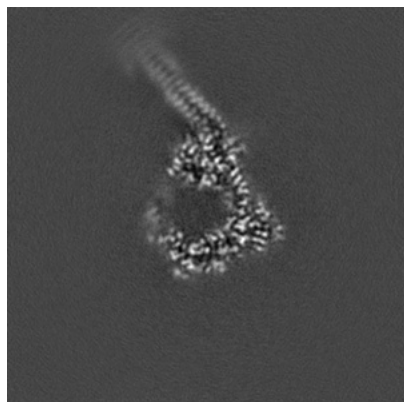


Y Index: 146

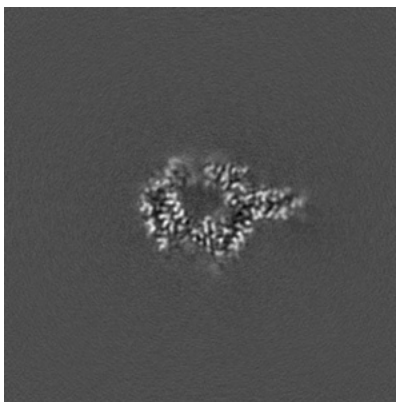


Z Index: 120

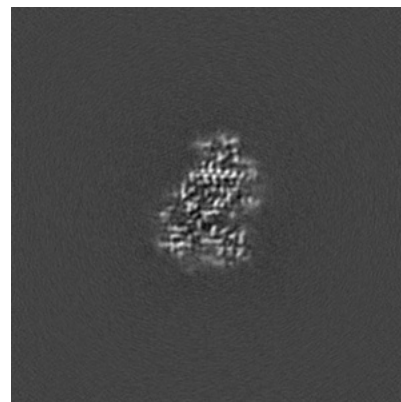
6.3.2 Raw map



X Index: 149



Y Index: 146

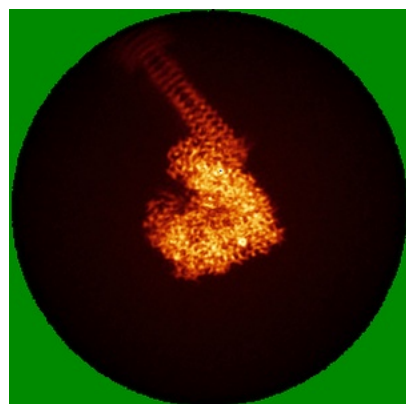


Z Index: 120

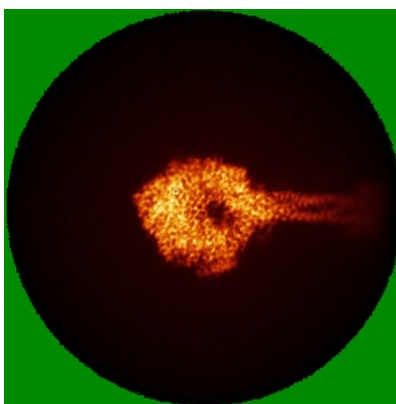
The images above show the largest variance slices of the map in three orthogonal directions.

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

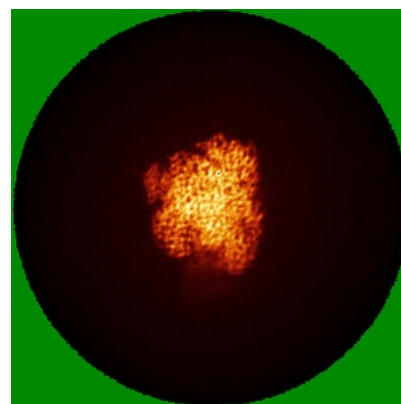
6.4.1 Primary map



X

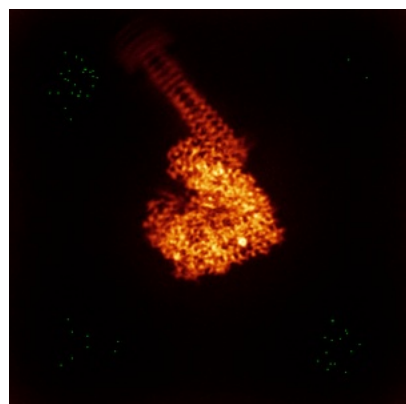


Y

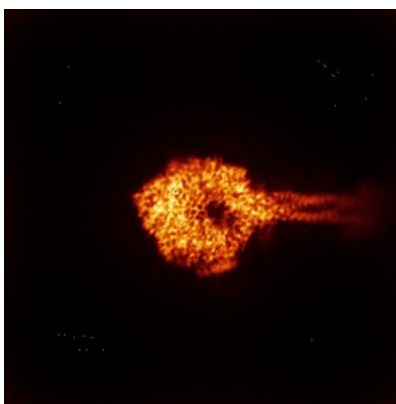


Z

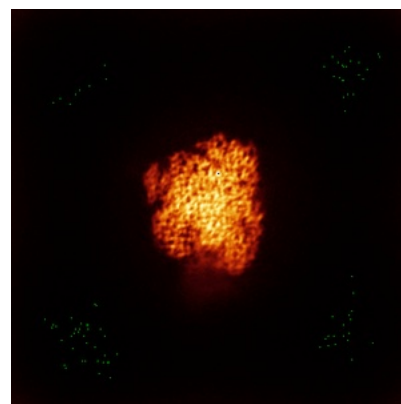
6.4.2 Raw map



X



Y

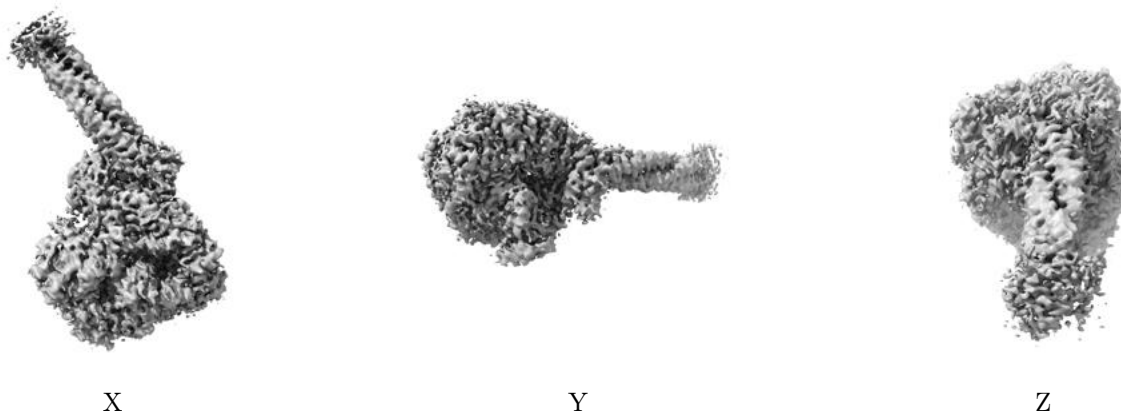


Z

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.

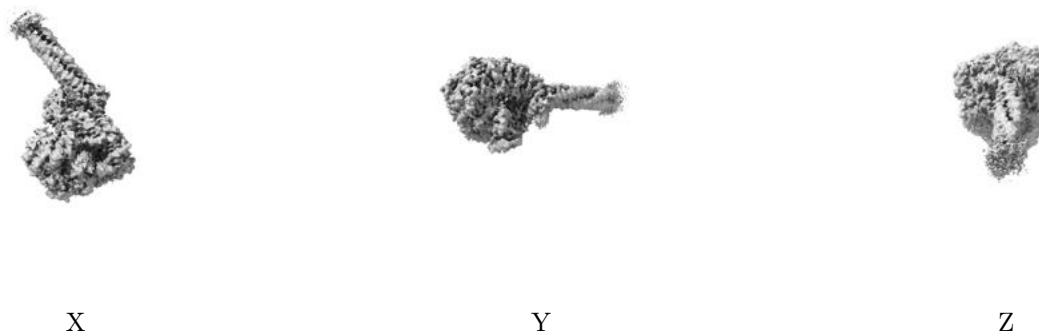
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.13. 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.

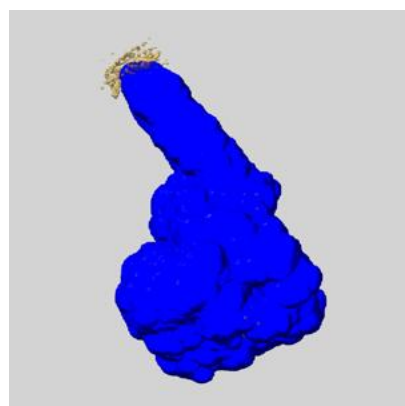
6.6 Mask visualisation [i](#)

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

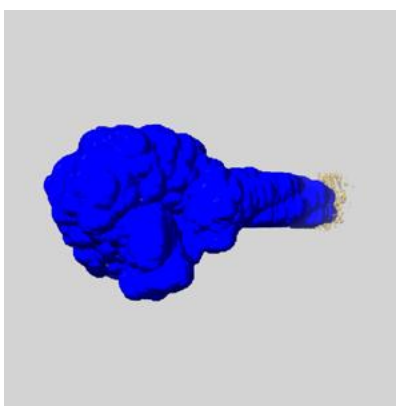
A mask typically either:

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

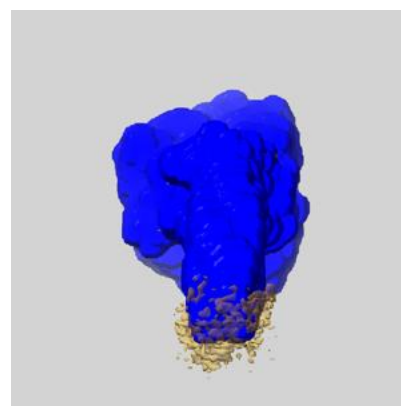
6.6.1 emd_60923_msk_1.map [i](#)



X



Y

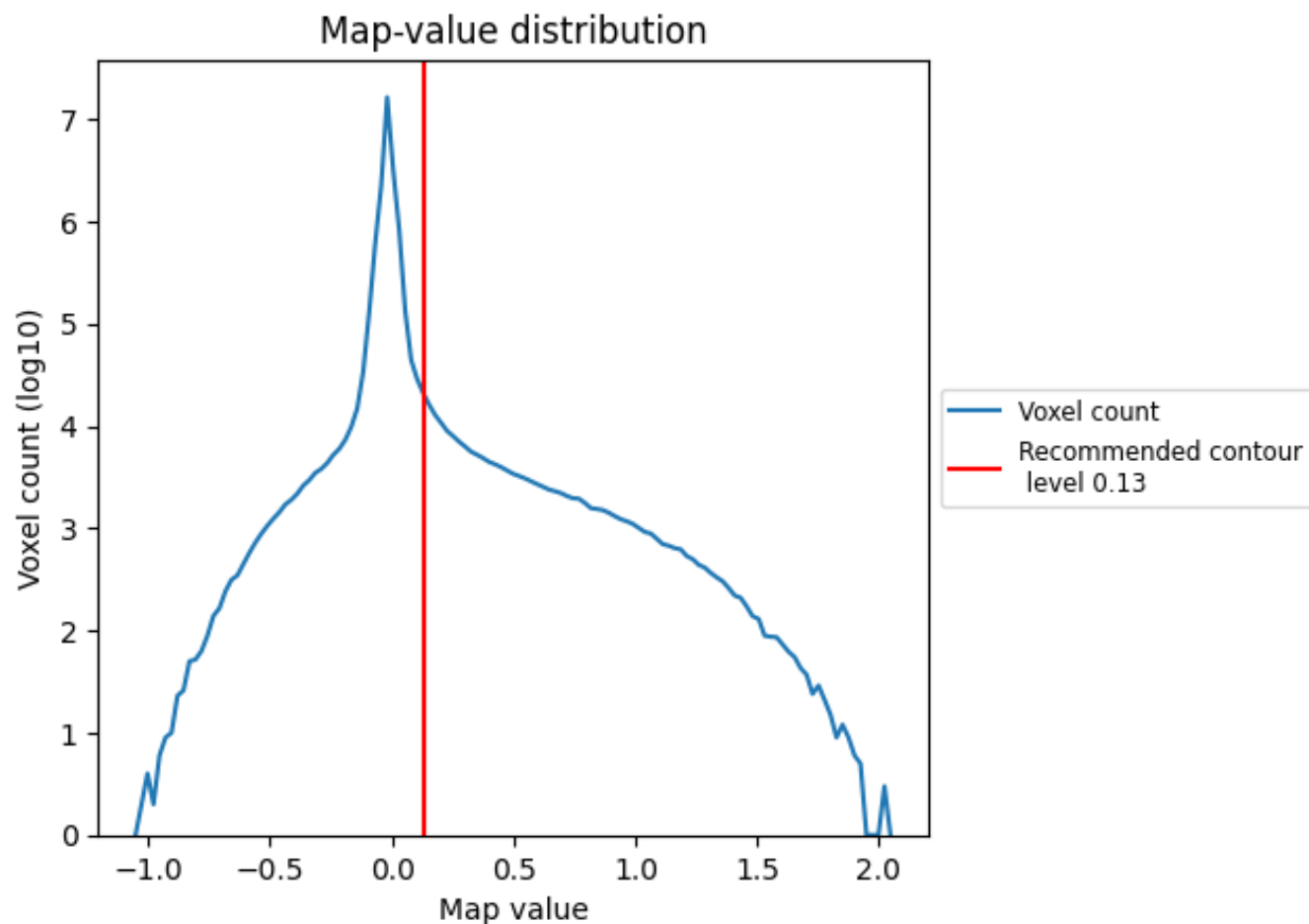


Z

7 Map analysis [i](#)

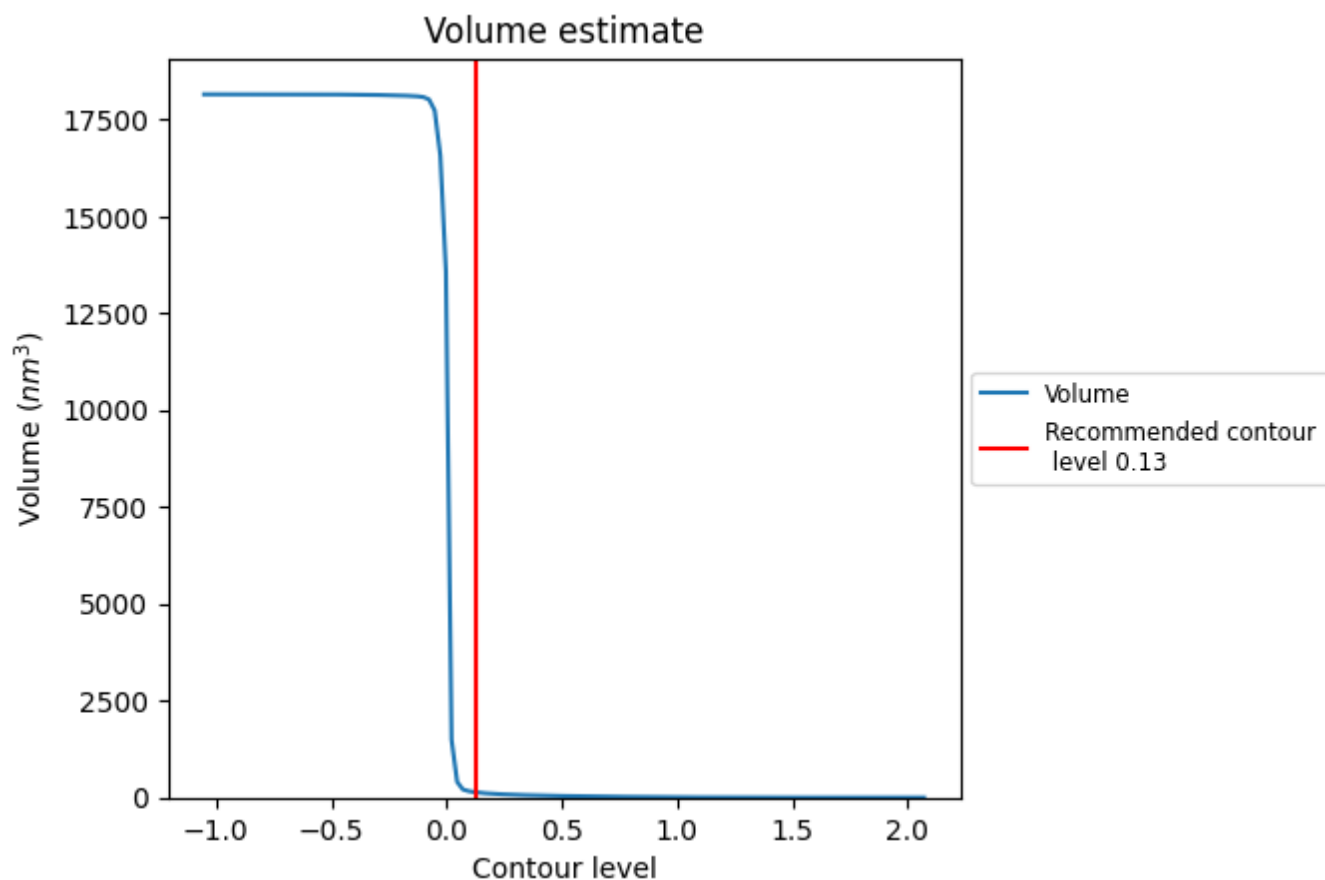
This section contains the results of statistical analysis of the map.

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.

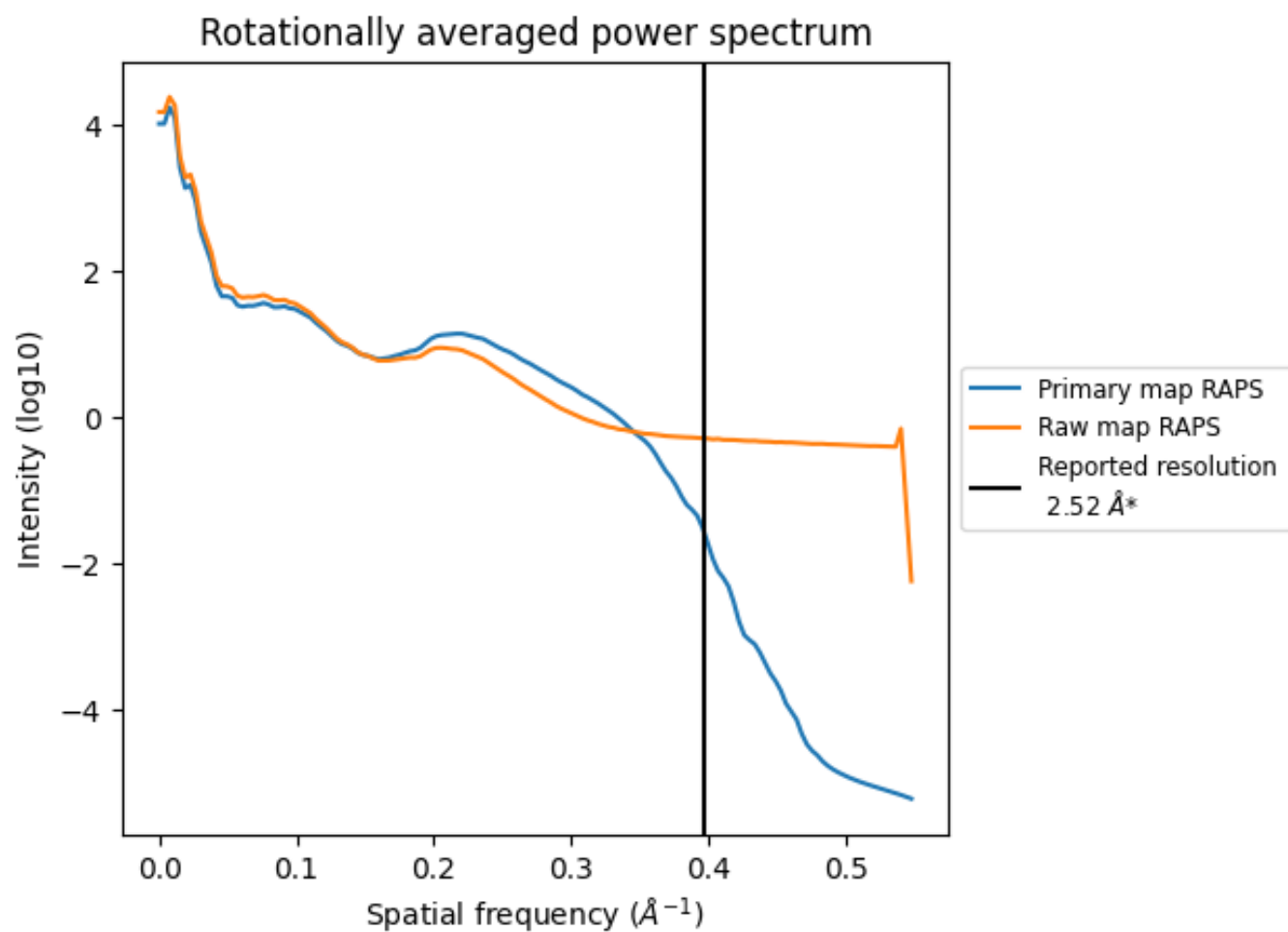
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 134 nm^3 ; this corresponds to an approximate mass of 121 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 ⓘ

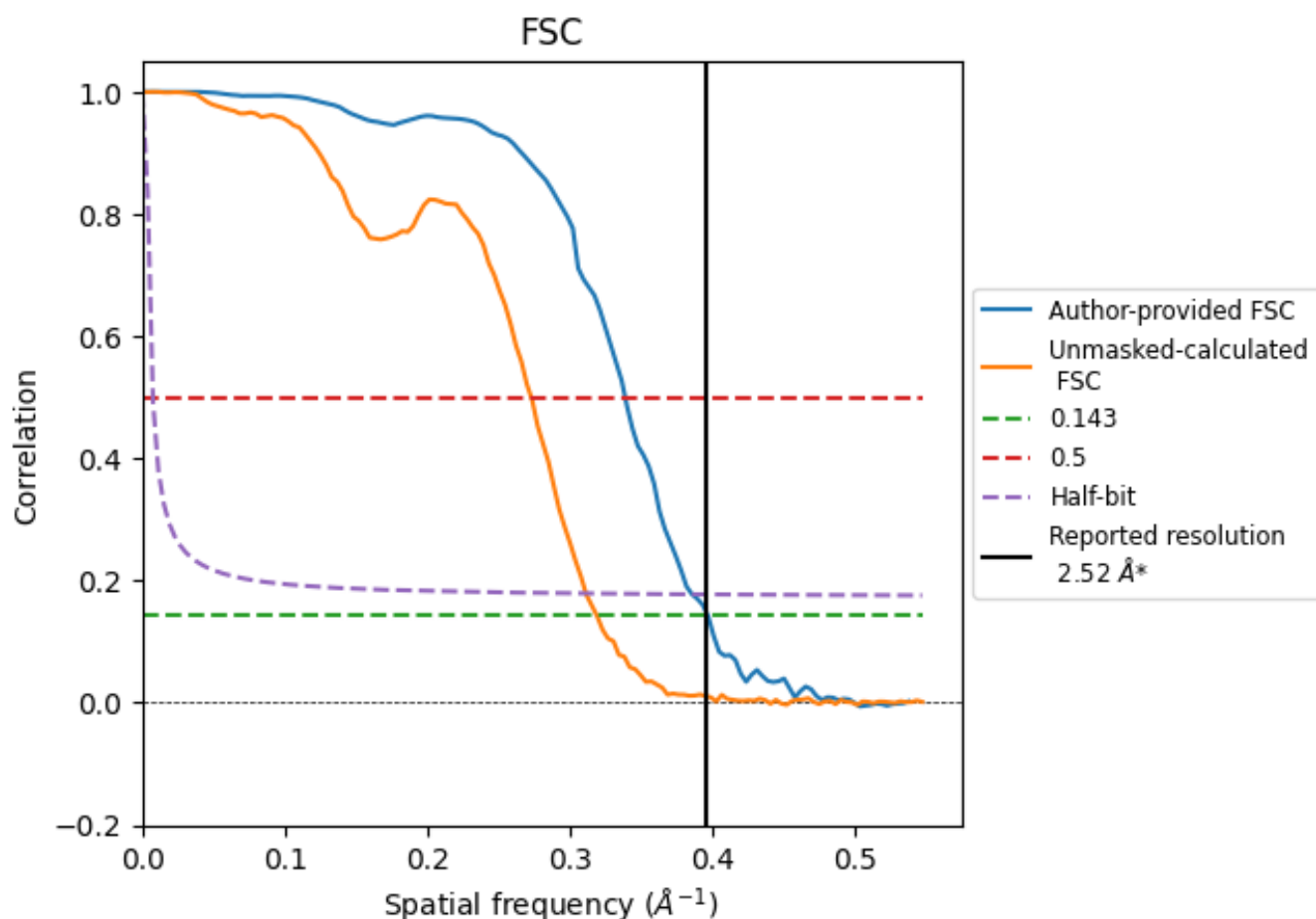


*Reported resolution corresponds to spatial frequency of 0.397 Å⁻¹

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 0.397 \AA^{-1}

8.2 Resolution estimates [i](#)

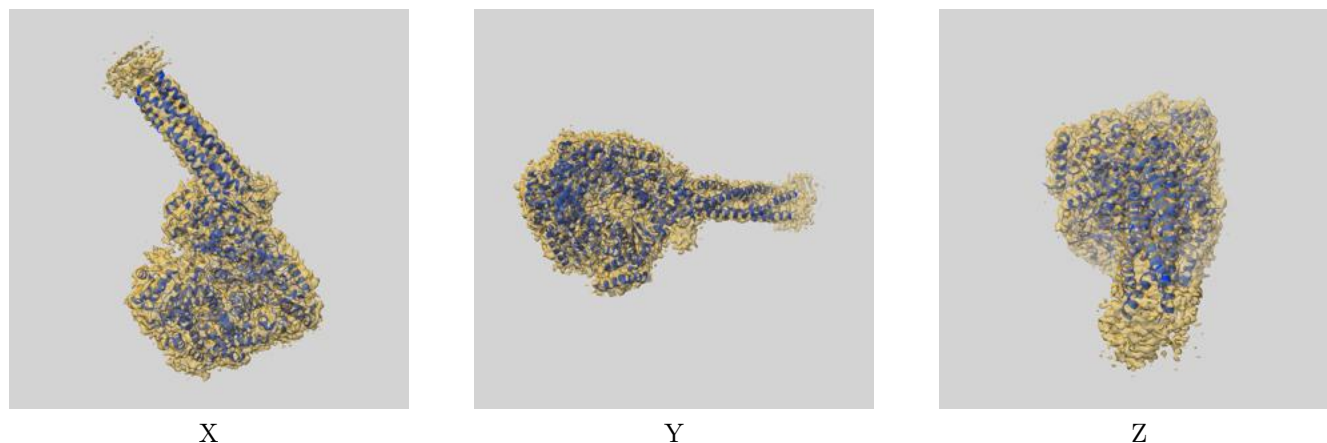
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.52	-	-
Author-provided FSC curve	2.52	2.95	2.59
Unmasked-calculated*	3.13	3.66	3.21

*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 3.13 differs from the reported value 2.52 by more than 10 %

9 Map-model fit [i](#)

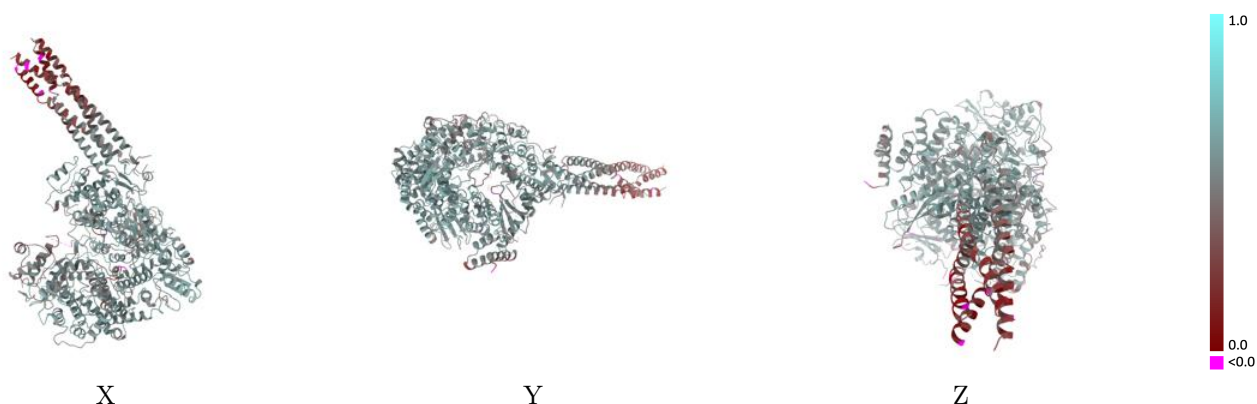
This section contains information regarding the fit between EMDB map EMD-60923 and PDB model 9IVA. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



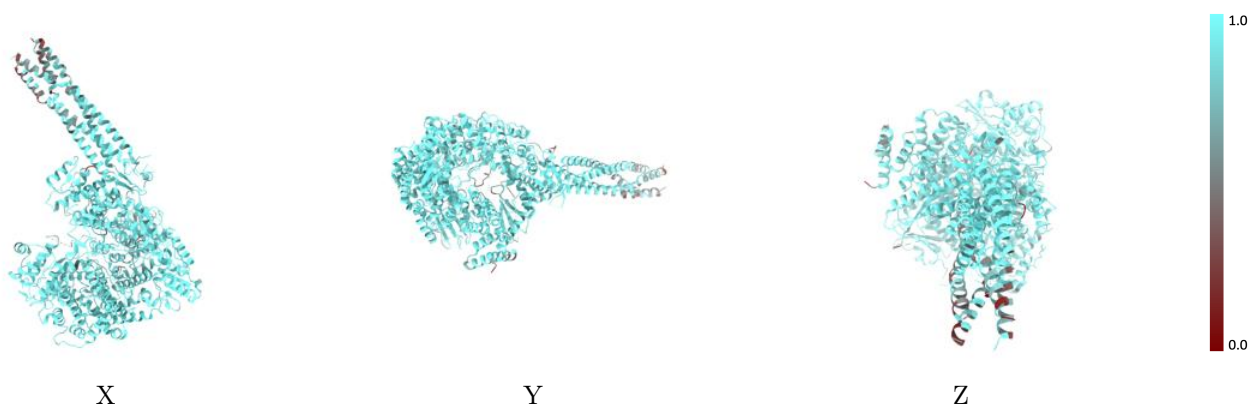
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



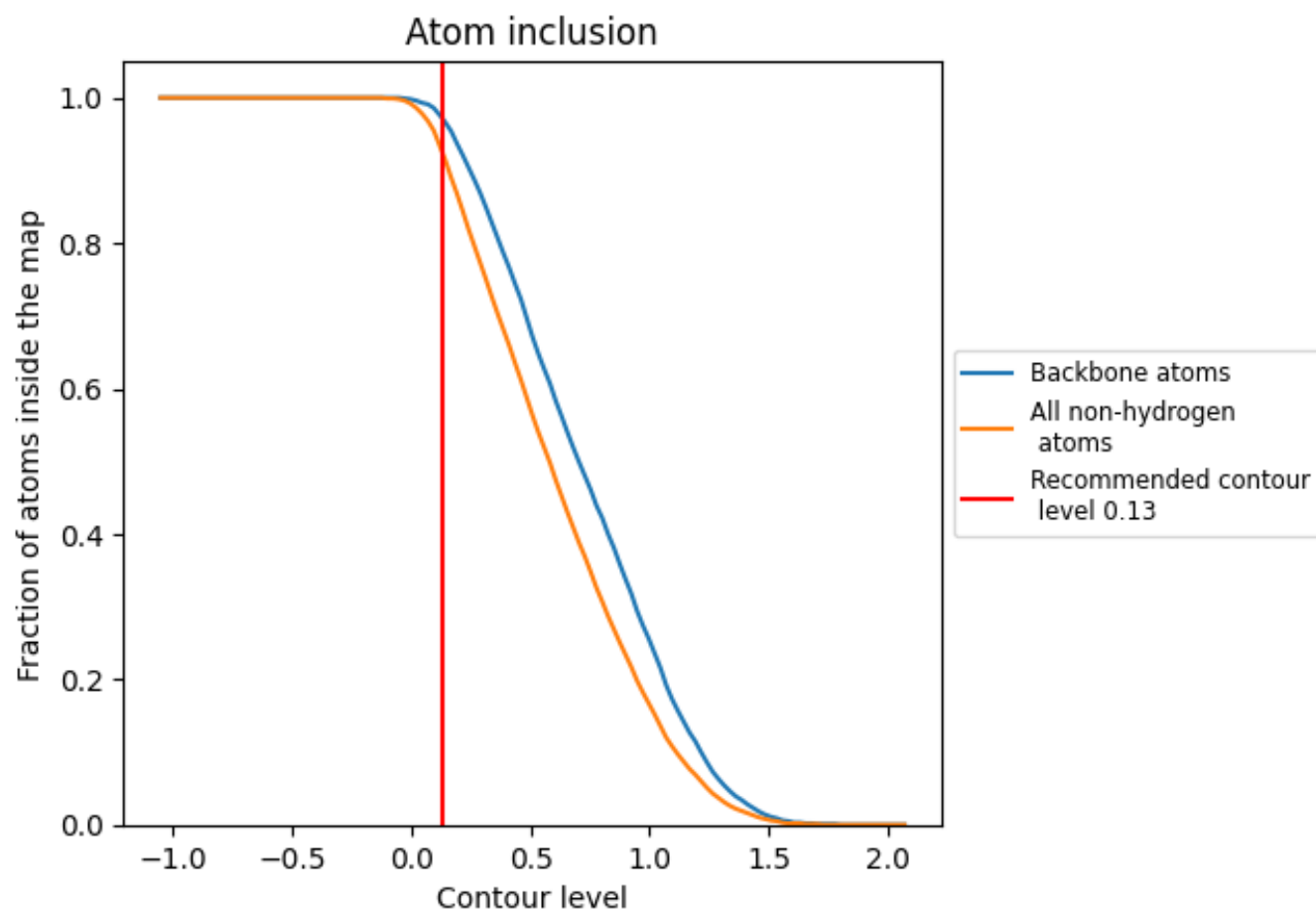
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 92% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9250	<div></div> 0.5190
A	<div></div> 0.9530	<div></div> 0.5500
B	<div></div> 0.8630	<div></div> 0.4420
C	<div></div> 0.7530	<div></div> 0.3200
D	<div></div> 0.7840	<div></div> 0.3880
E	<div></div> 0.8130	<div></div> 0.3810

