



wwPDB EM Validation Summary Report ⓘ

Jul 4, 2026 – 01:18 PM JST

PDB ID : 9VY0 / pdb_00009vy0
EMDB ID : EMD-65447
Title : Cryo-EM Structure of Peste Des Petits Ruminants Virus Polymerase in complex with ERDRP-0519
Authors : Xue, L.; Gui, J.; Chang, T.; Pan, H.; Xiong, X.
Deposited on : 2025-07-20
Resolution : 2.71 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

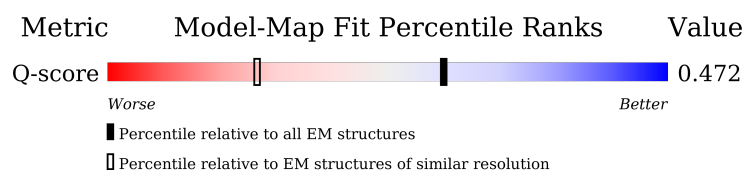
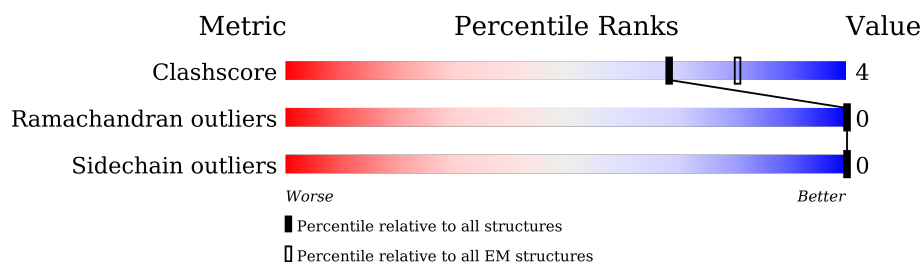
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.71 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	10297 (2.21 - 3.21)

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	2183	
2	B	509	
2	C	509	
2	D	509	

Continued on next page...

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Mol	Chain	Length	Quality of chain
2	E	509	10% . 87%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12256 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	1180	Total	C	N	O	S	0	0
			9442	6048	1596	1744	54		

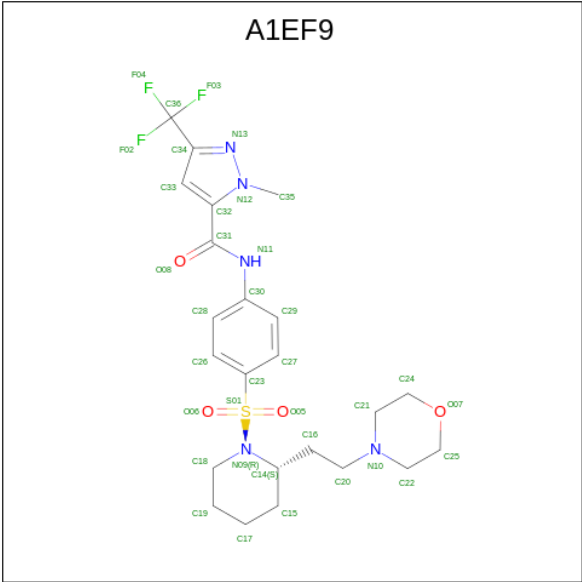
- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	157	Total	C	N	O	S	1	0
			1221	771	216	232	2		
2	C	79	Total	C	N	O	S	0	0
			608	383	103	121	1		
2	D	59	Total	C	N	O	S	0	0
			452	286	77	88	1		
2	E	65	Total	C	N	O	S	0	0
			496	315	84	96	1		

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

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	

- Molecule 4 is 2-methyl- {N}-[4-[(2 {S})-2-(2-morpholin-4-ylethyl)piperidin-1-yl]sulfonylphenyl]-5-(trifluoromethyl)pyrazole-3-carboxamide (CCD ID: A1EF9) (formula: C₂₃H₃₀F₃N₅O₄S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
			Total	C	F	N	O	S	
4	A	1	36	23	3	5	4	1	0

[illegible]

- Molecule 2: Phosphoprotein

[illegible]

- Molecule 2: Phosphoprotein



SER	ARG	ASP	ASN	THR	ASP	THR	GLY	GLN	ASN	MET
ARG	ASP	ASP	ASN	VAL	VAL	VAL	GLY	GLN	ASN	ALA
ASN	SER	SER	SER	THR	GLU	THR	LEU	SER	GLU	GLU
VAL	GLY	GLU	GLU	THR	LYS	THR	GLU	CYS	GLU	GLU
ILE	ARG	ARG	TYR	LEU	LEU	LEU	ASP	PRO	GLN	ALA
ARG	ALA	ALA	TYR	SER	GLY	SER	ASP	ALA	ALA	TYR
SER	LEU	LEU	GLU	ILE	ALA	ILE	SER	ILE	HIS	HIS
ILE	ALA	GLU	GLU	SER	ASP	SER	LEU	VAL	GLY	VAL
ILE	GLU	ASP	ASP	SER	ASP	GLY	VAL	GLY	VAL	ASP
LYS	VAL	VAL	LEU	GLY	ILE	ALA	VAL	ASN	ASN	LYS
SER	LYS	LYS	PHE	THR	GLU	THR	GLN	LYS	GLY	GLY
LYS	LYS	LYS	GLU	GLN	VAL	ALA	ALA	VAL	LEU	LEU
LEU	PRO	ALA	GLU	ALA	LEU	ALA	ASP	TYR	GLU	GLU
ASN	ALA	ILE	GLN	VAL	ASN	VAL	PRO	LEU	CYS	ILE
THR	VAL	VAL	ASN	PRO	GLU	GLU	SER	PRO	LYS	LYS
ASP	ASP	ARG	I317	SER	GLY	GLY	VAL	GLY	ASP	SER
HIS	ASP	ARG	I318	ARG	LYS	TPP	ALA	ASN	LEU	ALA
LYS	SER	SER	R319	THR	LYS	GLY	VAL	ASN	ASP	LEU
ASP	GLN	LYS		GLY	GLY	GLY	PHE	LEU	ALA	ALA
TYR	LYS	LYS		SER	GLY	SER	GLY	GLY	GLY	LYS
LEU	ILE	ILE		SER	GLY	SER	ARG	PHE	ASN	GLY
LEU	GLY	GLY		THR	GLY	GLU	GLY	GLY	ARG	PRO
ASP	THR	LYS		LYS	GLN	GLN	ASP	GLU	ASP	PRO
LEU	LYS	ALA		ALA	ASN	ASN	ASP	ILE	LEU	LEU
LEU	ALA	ASN		ALA	ALA	ALA	GLY	THR	SER	THR
ASN	ASN	SER		SER	SER	SER	LYS	GLY	ASN	ILE
VAL	SER	SER		VAL	VAL	VAL	ASP	ASN	ASP	ILE
LYS	SER	SER		GLY	GLY	SER	LEU	ASP	CYS	ARG
GLY	LYS	LYS		LYS	ARG	SER	SER	GLY	GLY	THR
SER	GLY	GLN		VAL	VAL	VAL	ASP	ASP	GLU	THR
LYS	LYS	LEU		PRO	PRO	LEU	ASP	ALA	ALA	ILE
ASP	LEU	LEU		ILE	LYS	LYS	ASP	GLY	GLY	ILE
LEU	LEU	LYS		ALA	ALA	ALA	PRO	GLY	TRP	SER
GLU	ASP	ASP		ASP	ASP	ARG	PRO	GLY	GLY	ARG
PHE	LEU	LEU		SER	VAL	SER	VAL	VAL	VAL	GLU
HIS	GLN	GLN		ALA	LYS	SER	ASP	GLN	GLN	GLY
LYS	LEU	LEU		THR	THR	GLU	PRO	LYS	LYS	LEU
MET	LYS	LYS		LYS	THR	THR	ASP	ARG	ARG	SER
LEU	PRO	PRO		PRO	ILE	ILE	ASP	PRO	PRO	PRO
THR	VAL	VAL		LYS	GLN	GLY	ASP	SER	SER	GLY
ALA	ASP	ASP		LYS	GLY	GLY	THR	ASN	GLY	ASN
ILE	LYS	LYS		PRO	ASP	LEU	ARG	SER	ARG	ARG
LEU	GLN	GLN		THR	THR	THR	TYR	SER	GLN	ALA
ALA	ALA	ALA		GLN	SER	GLN	VAL	VAL	VAL	THR
LYS	SER	SER		GLU	SER	GLY	ARG	GLN	GLN	ASN
HIS	SER	SER		VAL	LYS	LYS	GLY	ARG	ARG	TYR
PRO	ALA	ALA		ILE	GLY	THR	VAL	SER	PRO	ASP
	THR	THR		THR	THR	THR	GLY	GLY	ASP	GLY
	ILE	ILE		ILE	THR	ILE	VAL	THR	ASP	THR
	GLY	PHE		GLY	THR	THR	ALA	VAL	VAL	THR
	VAL	VAL		ALA	ALA	ALA	GLY	GLY	SER	SER
	PRO	PRO		VAL	ASP	LEU	ASN	ASN	HIS	GLY
	SER	ARG		LEU	LEU	THR	ASP	GLY	GLY	ASP
	ASP	ASP		ARG	ARG	GLN	VAL	VAL	ALA	HIS
	HIS	HIS		ILE	ILE	PRO	VAL	ARG	GLY	GLY
	GLU	GLU		ILE	ILE	LYS	SER	GLU	GLU	GLN
	SER	SER		SER	SER	LYS	GLY	SER	SER	GLU
										ILE

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	3880076	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	1.918	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	262.8, 262.8, 262.8	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.876, 0.876, 0.876	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, A1EF9

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	0.14	0/9653	0.32	0/13076
2	B	0.15	0/1235	0.34	0/1655
2	C	0.19	0/613	0.35	0/824
2	D	0.18	0/454	0.39	0/609
2	E	0.20	0/499	0.45	0/668
All	All	0.15	0/12454	0.33	0/16832

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	9442	0	9409	64	0
2	B	1221	0	1308	12	0
2	C	608	0	645	8	0
2	D	452	0	493	5	0
2	E	496	0	536	11	0
3	A	1	0	0	0	0
4	A	36	0	0	0	0
All	All	12256	0	12391	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 4.

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)
2:B:469:LYS:HA	2:B:478:LYS:HD3	1.74	0.70
1:A:1180:CYS:SG	1:A:1364:HIS:CE1	2.86	0.69
1:A:530:LEU:HB3	1:A:705:LEU:HD22	1.79	0.64
1:A:1171:ILE:HB	1:A:1360:VAL:HB	1.80	0.64
2:E:348:THR:HA	2:E:351:LYS:HD2	1.80	0.63

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	1170/2183 (54%)	1136 (97%)	34 (3%)	0	100	100
2	B	152/509 (30%)	145 (95%)	7 (5%)	0	100	100
2	C	77/509 (15%)	75 (97%)	2 (3%)	0	100	100
2	D	57/509 (11%)	55 (96%)	2 (4%)	0	100	100
2	E	63/509 (12%)	62 (98%)	1 (2%)	0	100	100
All	All	1519/4219 (36%)	1473 (97%)	46 (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	1042/1937 (54%)	1042 (100%)	0	100	100
2	B	143/436 (33%)	143 (100%)	0	100	100
2	C	72/436 (16%)	72 (100%)	0	100	100
2	D	54/436 (12%)	54 (100%)	0	100	100
2	E	58/436 (13%)	58 (100%)	0	100	100
All	All	1369/3681 (37%)	1369 (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	A	941	ASN
1	A	979	HIS
2	D	357	ASN
2	C	356	GLN
1	A	711	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 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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
4	A1EF9	A	2202	-	39,39,39	0.45	1 (2%)	54,57,57	0.92	3 (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
4	A1EF9	A	2202	-	-	2/31/50/50	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	2202	A1EF9	C18-N09	2.01	1.51	1.48

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2202	A1EF9	C23-S01-N09	-3.40	101.31	107.36
4	A	2202	A1EF9	C34-N13-N12	2.83	106.92	104.36
4	A	2202	A1EF9	C32-C33-C34	2.74	106.38	103.64

There are no chirality outliers.

All (2) torsion outliers are listed below:

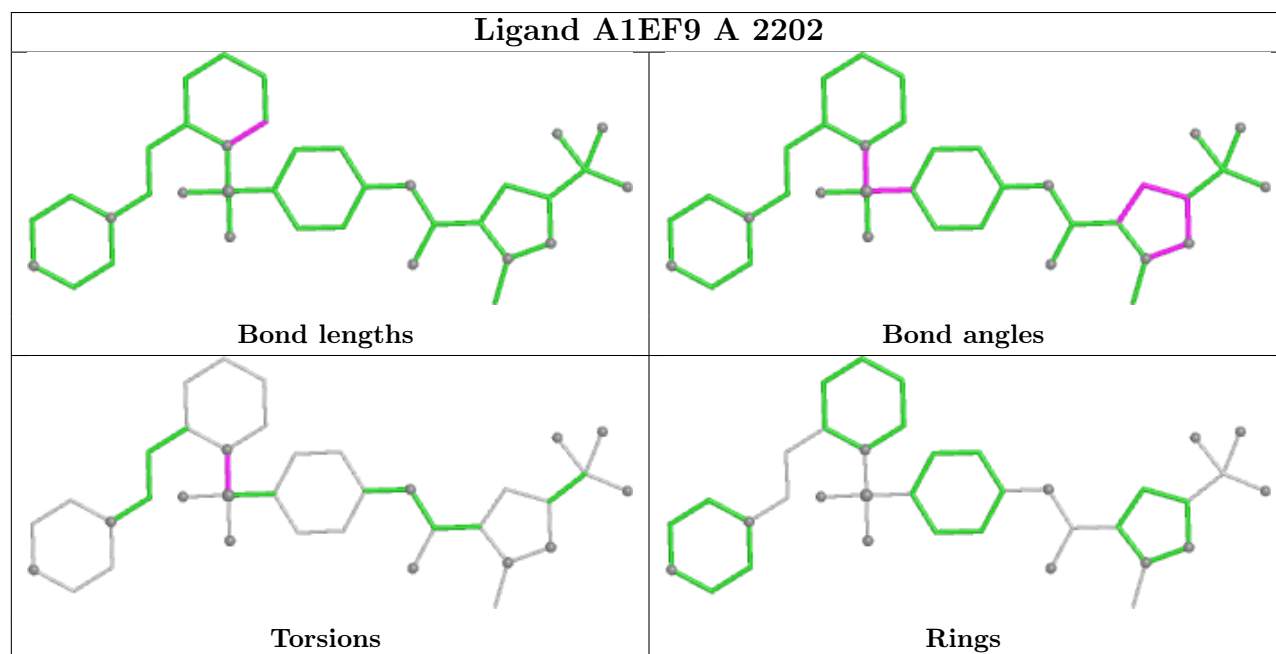
Mol	Chain	Res	Type	Atoms
4	A	2202	A1EF9	C14-N09-S01-O05
4	A	2202	A1EF9	C14-N09-S01-O06

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

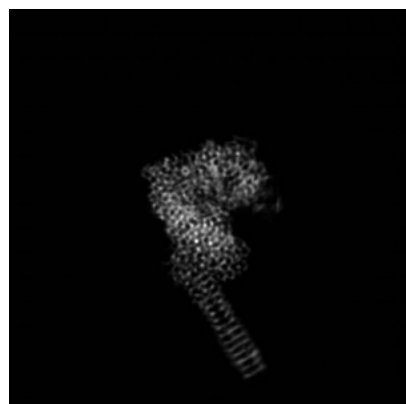
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65447. These allow visual inspection of the internal detail of the map and identification of artifacts.

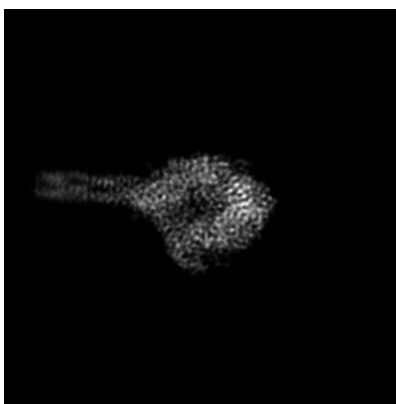
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

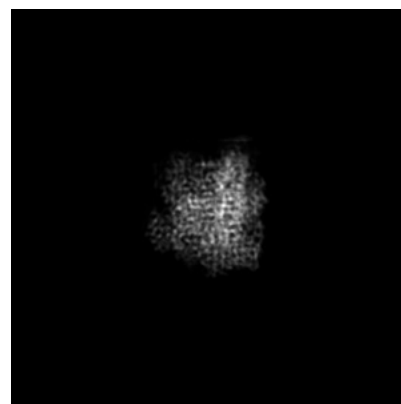
6.1.1 Primary map



X

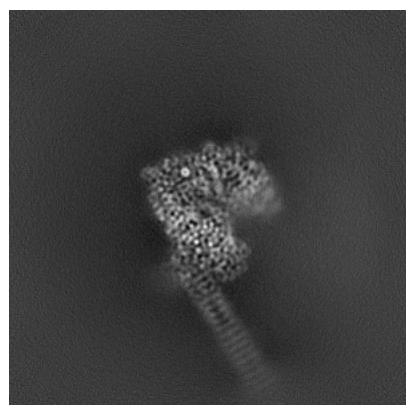


Y

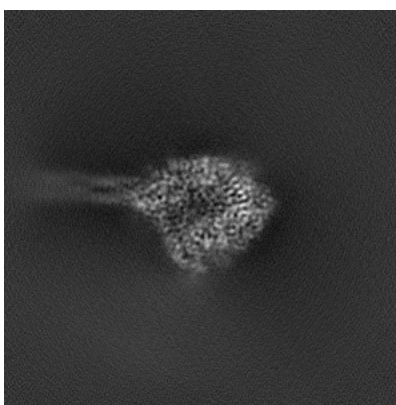


Z

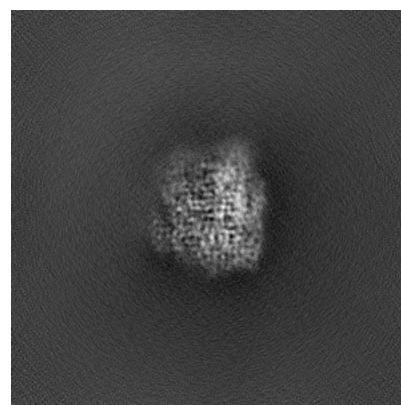
6.1.2 Raw map



X



Y

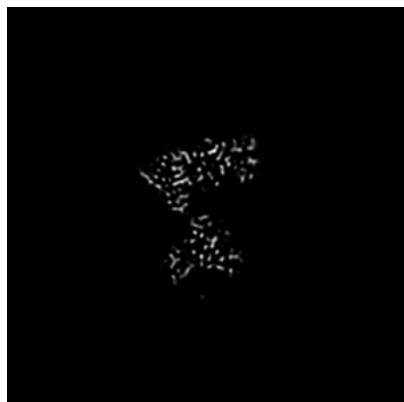


Z

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

6.2 Central slices [i](#)

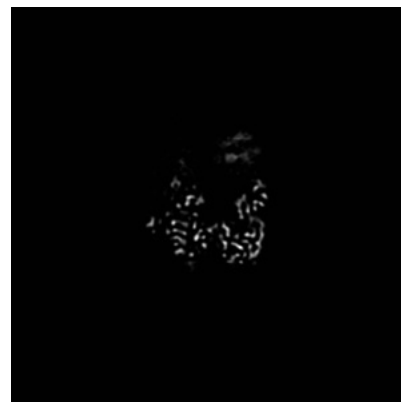
6.2.1 Primary map



X Index: 150

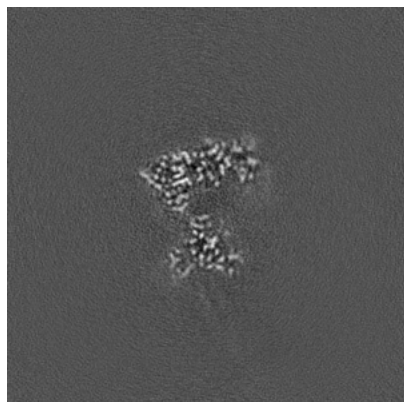


Y Index: 150

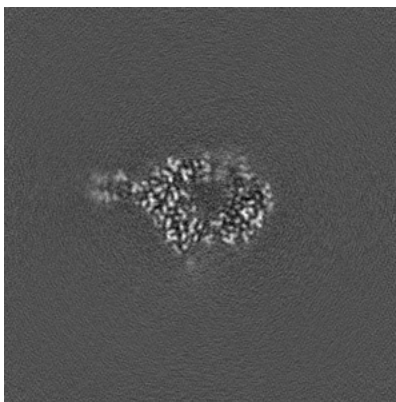


Z Index: 150

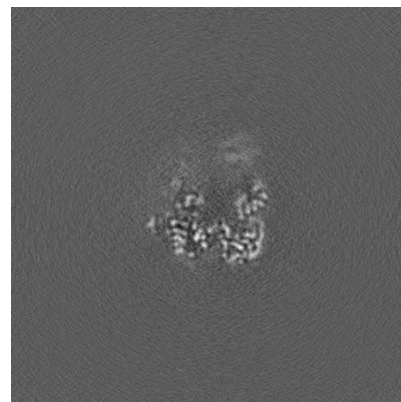
6.2.2 Raw map



X Index: 150



Y Index: 150



Z Index: 150

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: 158

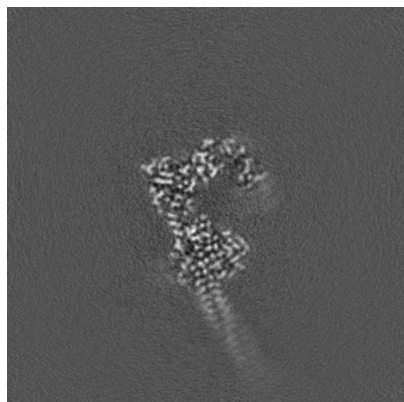


Y Index: 151

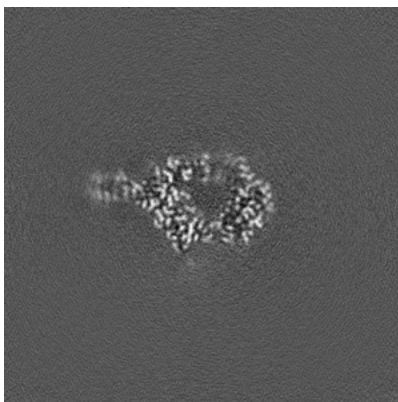


Z Index: 170

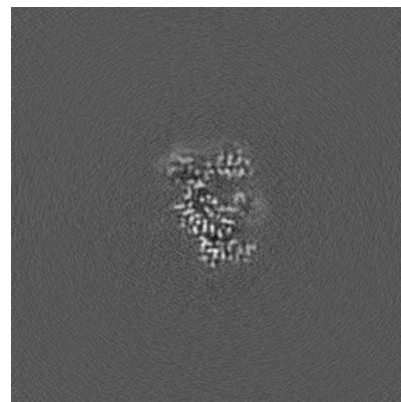
6.3.2 Raw map



X Index: 158



Y Index: 151



Z Index: 170

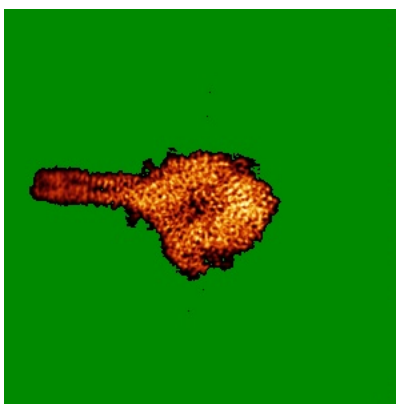
The images above show the largest variance slices of the map in three orthogonal directions.

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

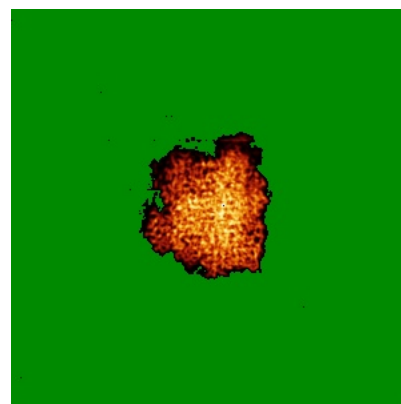
6.4.1 Primary map



X

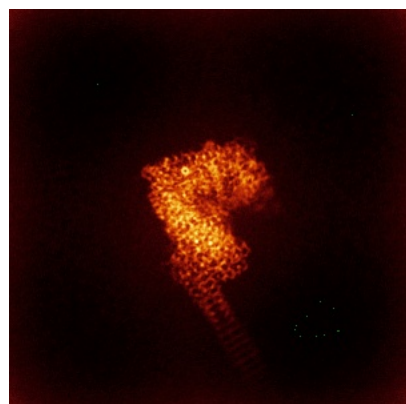


Y

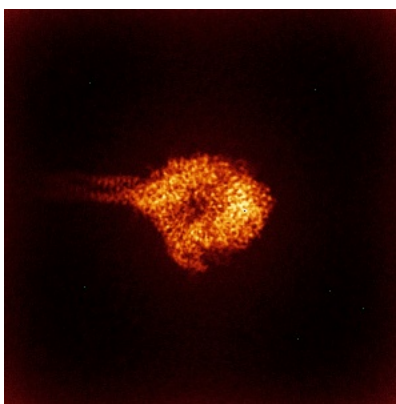


Z

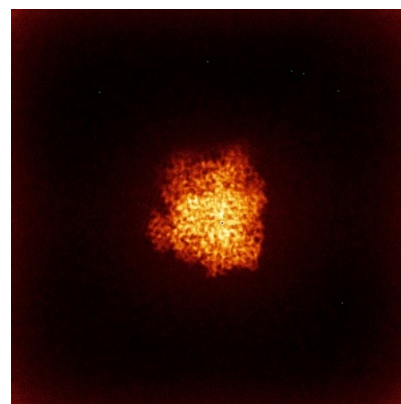
6.4.2 Raw map



X



Y

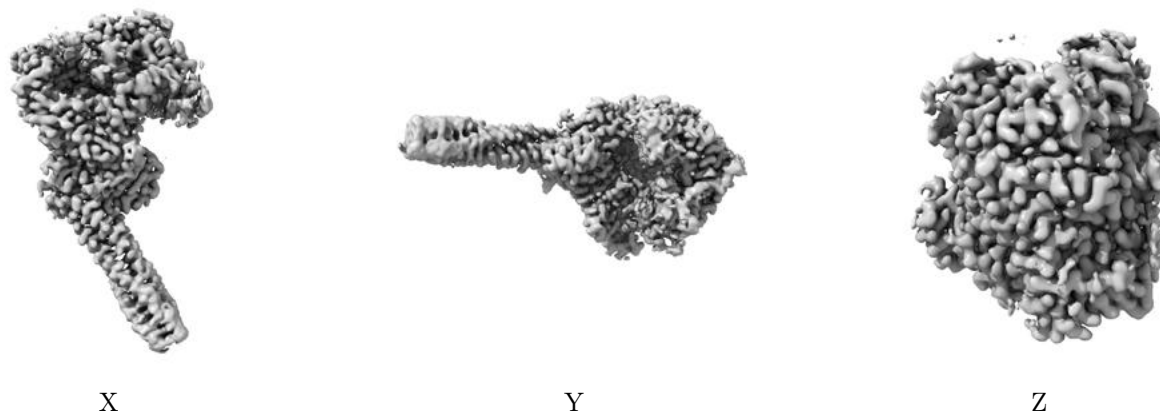


Z

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.

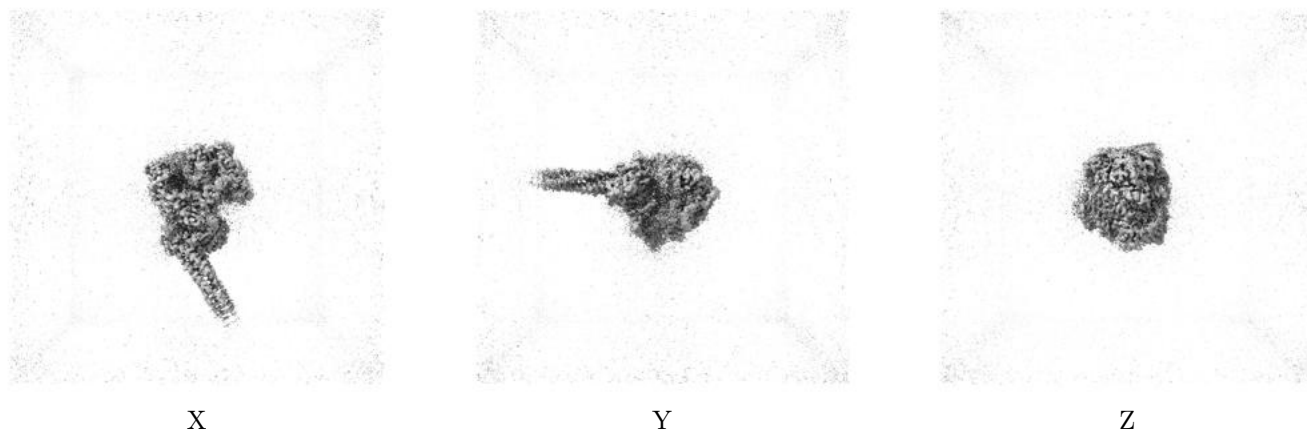
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. 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.

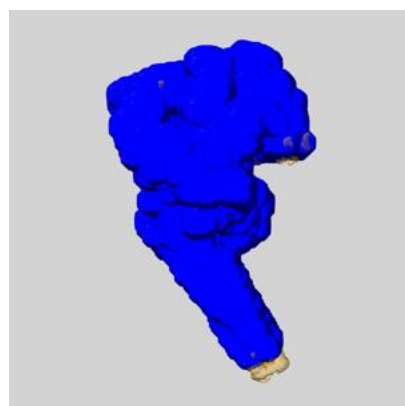
6.6 Mask visualisation [i](#)

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

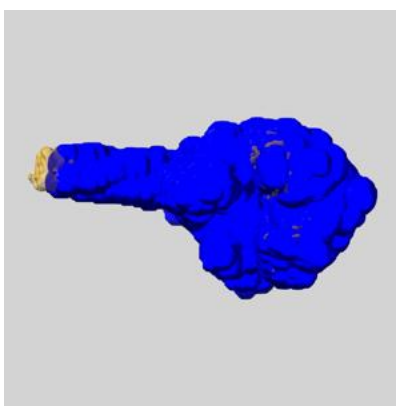
A mask typically either:

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

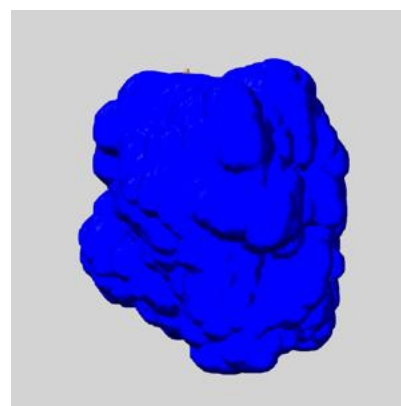
6.6.1 emd_65447_msk_1.map [i](#)



X



Y

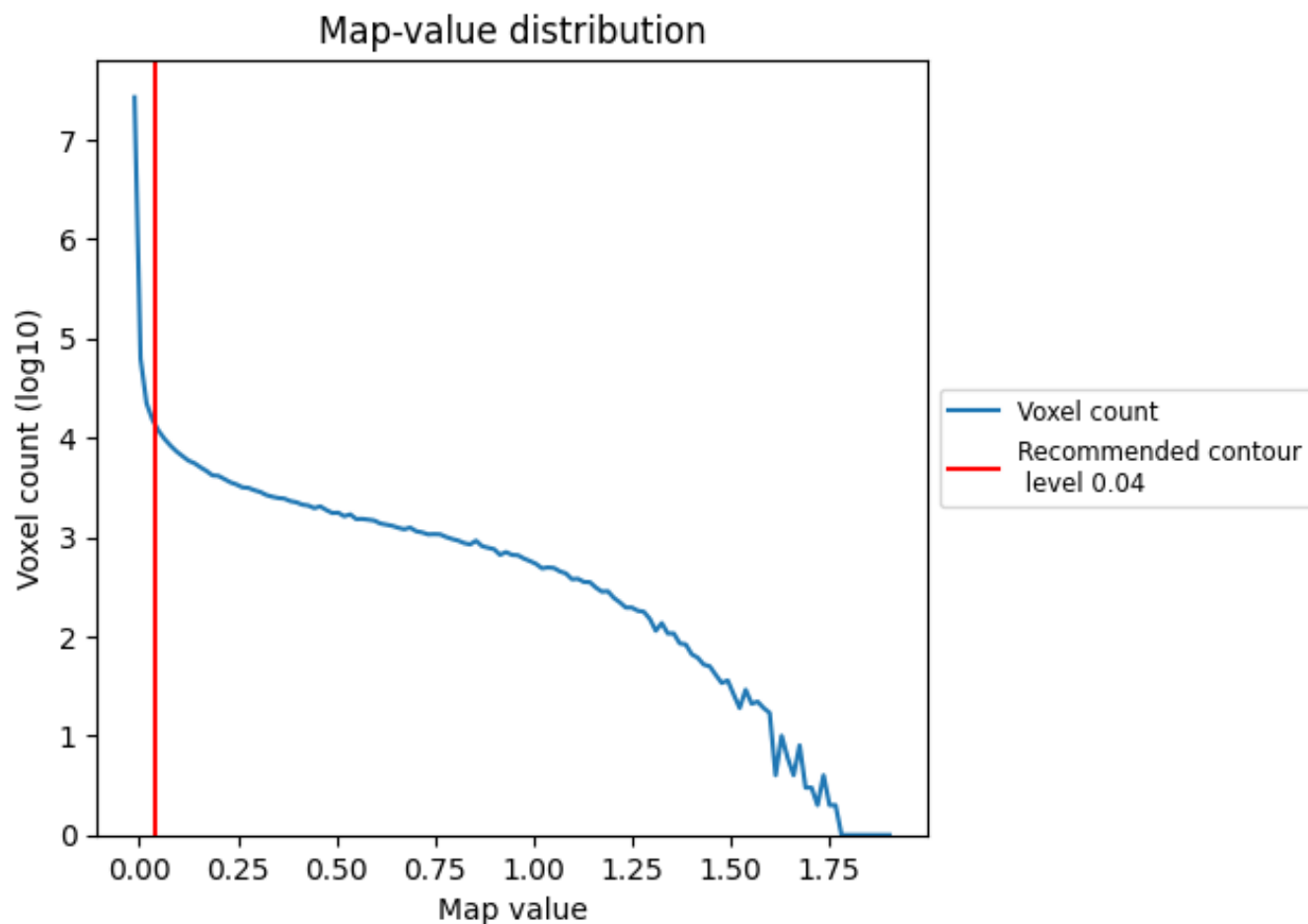


Z

7 Map analysis [i](#)

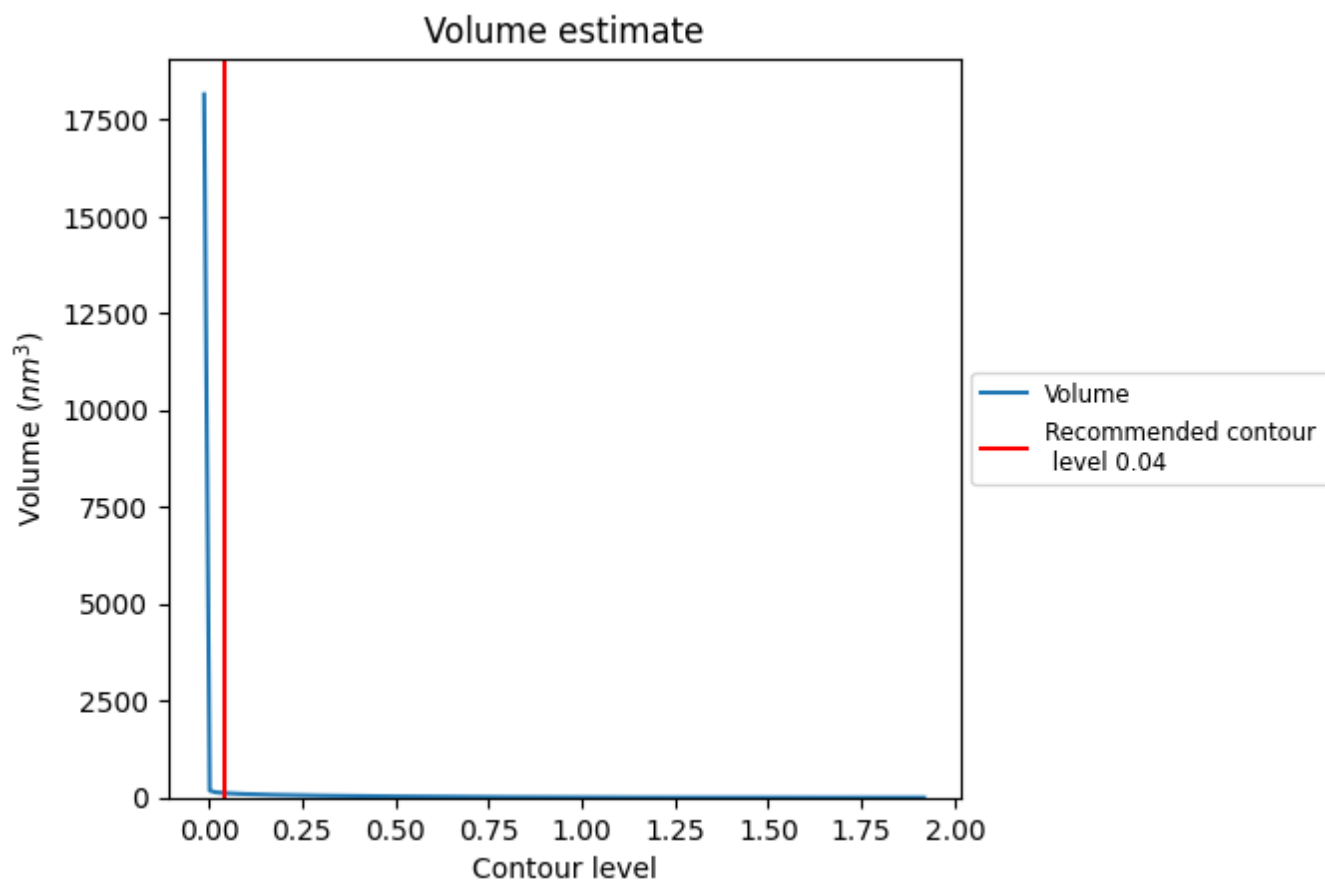
This section contains the results of statistical analysis of the map.

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.

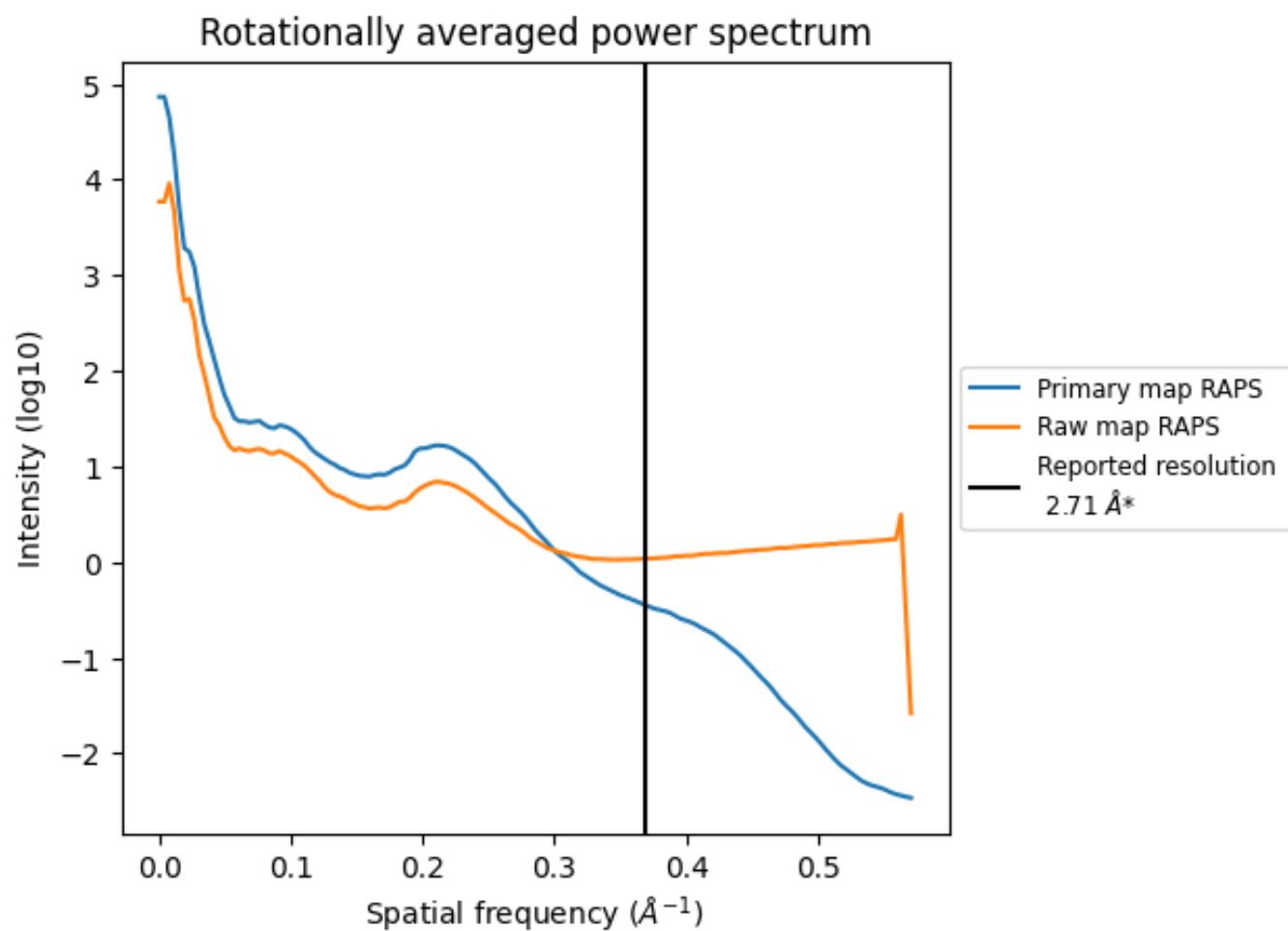
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 117 nm^3 ; this corresponds to an approximate mass of 106 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 ⓘ

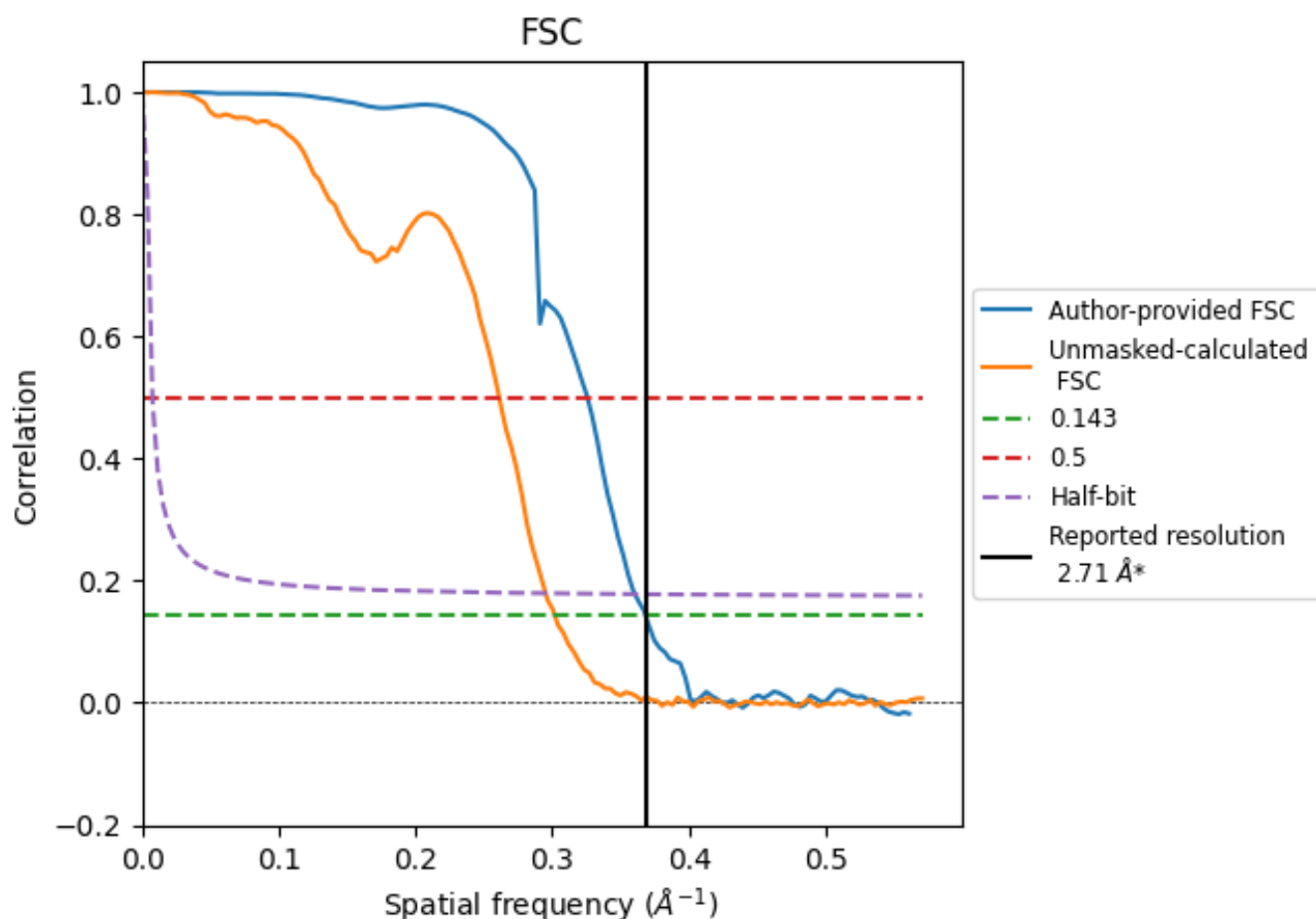


*Reported resolution corresponds to spatial frequency of 0.369 Å⁻¹

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 $0.369 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

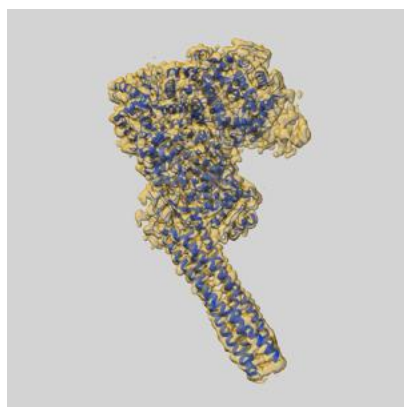
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.71	-	-
Author-provided FSC curve	2.71	3.07	2.77
Unmasked-calculated*	3.31	3.83	3.39

*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 3.31 differs from the reported value 2.71 by more than 10 %

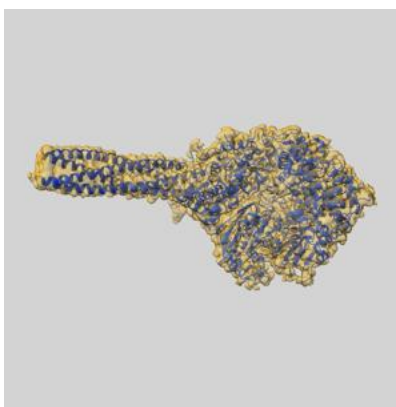
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65447 and PDB model 9VY0. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

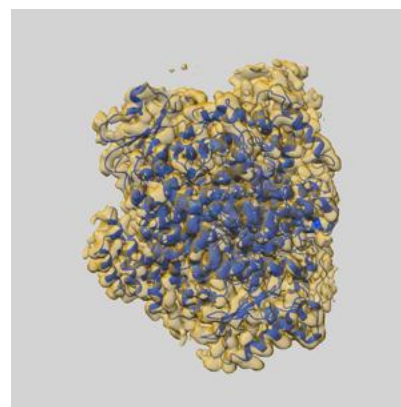
9.1 Map-model overlay [i](#)



X



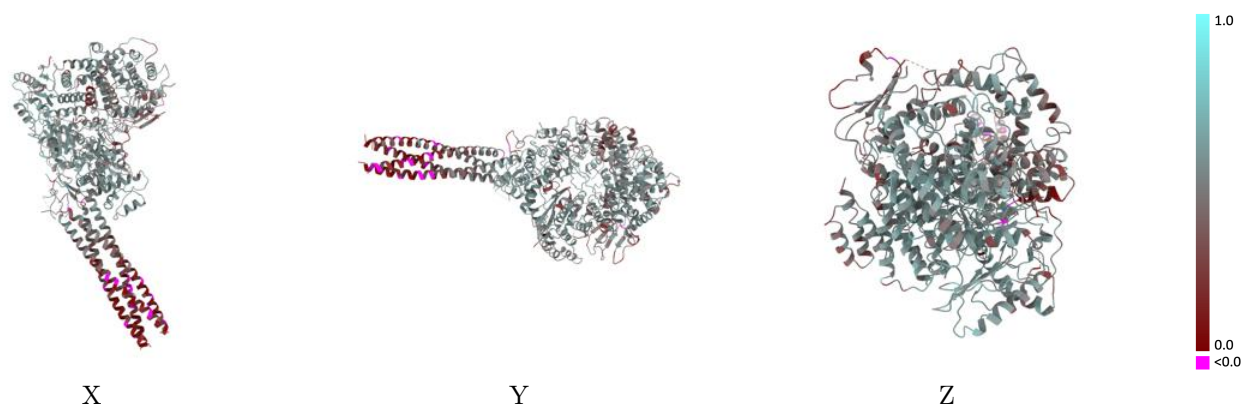
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04 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](#)



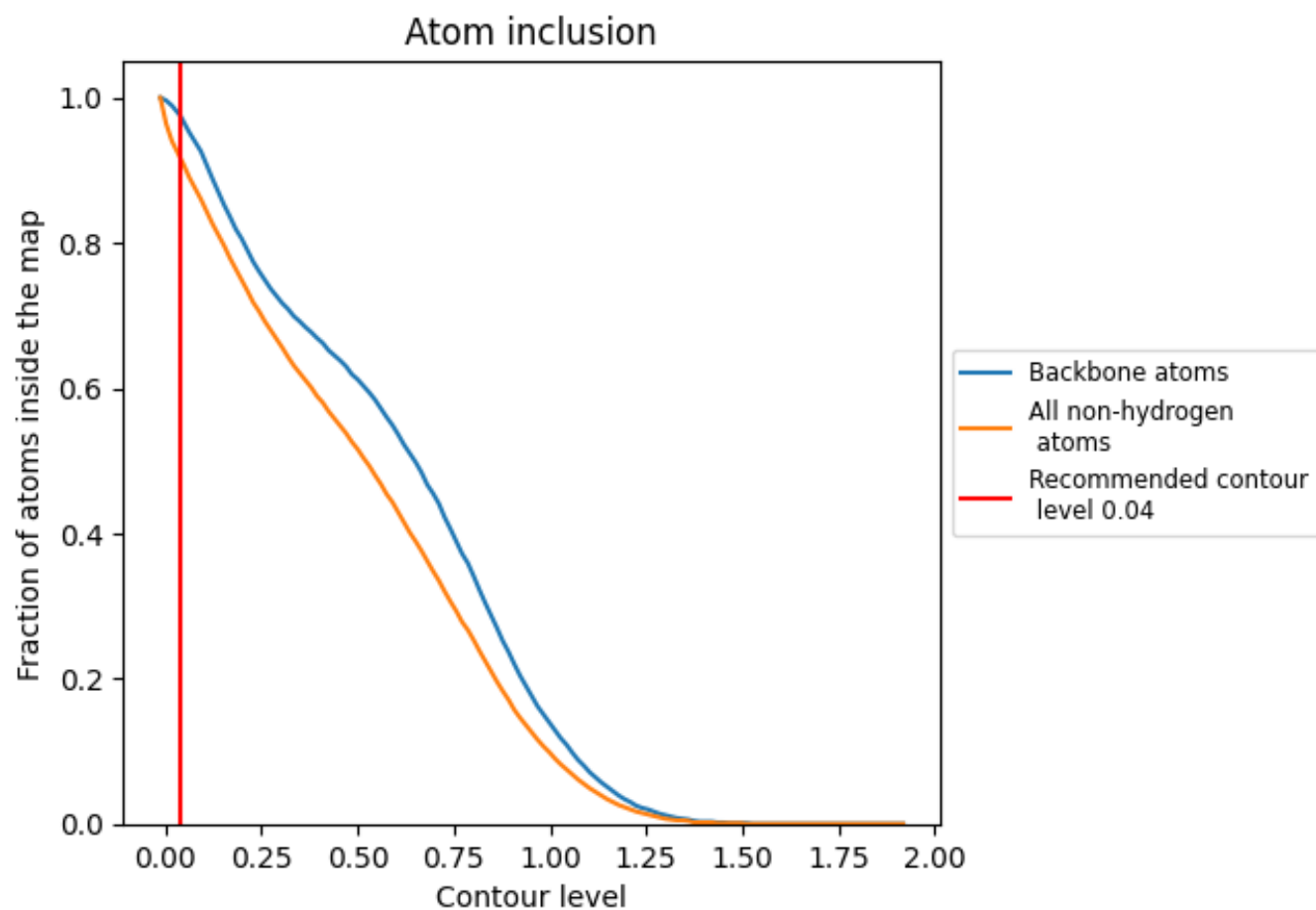
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion ⓘ



At the recommended contour level, 98% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9170	0.4720
A	0.9330	0.5090
B	0.8820	0.4100
C	0.8460	0.3130
D	0.8160	0.2520
E	0.8640	0.3080

